(12) STANDARD PATENT APPLICATION (11) Application No. **AU 2026202266 A1**
(19) AUSTRALIAN PATENT OFFICE

(54) Title
Alpha-amylase variants and polynucleotides encoding same

(51) International Patent Classification(s)
C12N 9/28 (2006.01) ***C11D 3/386*** (2006.01)

(21) Application No: **2026202266** (22) Date of Filing: **2026.03.24**

(43) Publication Date: **2026.04.16**
(43) Publication Journal Date: **2026.04.16**

(62) Divisional of:
2020242303

(71) Applicant(s)
Novozymes A/S

(72) Inventor(s)
ANDERSEN, Carsten;ARNEHED, Sofia;CHRISTENSEN, Lars Lehmann Hylling;FALLAH-ARAGHI, Ali;KLINGER, Markus;SANDSTRÖM, Anders Gunnar

(74) Agent / Attorney
Spruson & Ferguson, GPO Box 3898, Sydney, NSW, 2001, AU

24 Mar 2026
2026202266

ABSTRACT

The present invention relates to alpha-amylase variants of a parent alpha-amylase wherein said alpha-amylase variants have an improved wash performance as compared to said parent alpha-amylase. The invention also relates to compositions comprising the variants of the invention, uses of said variants and methods of producing said variants.

24 Mar 2026
2026202266

ALPHA-AMYLASE VARIANTS AND POLYNUCLEOTIDES ENCODING SAME

Related Applications

This application is a divisional of Australian Application No. 2020242303, filed 20 March 2020, is related to PCT/EP2020/057818, and claims priority from European Provisional Application No. 19164228.9, filed 21 March 2019, each of which are herein incorporated by reference in their entirety.

Reference to a Sequence Listing

Preceding applications contained a sequence listing which was originally submitted electronically in ASCII format and is hereby incorporated by reference in its entirety. The instant application contains a sequence listing which has been submitted electronically as an XML document in the ST26 format and is hereby incorporated by reference in its entirety. Said XML copy, created on 10 March 2026, is named 113956AUP00D1 ST.26 Sequence Listing (10Mar2026).xml and is 29 kilobytes in size.

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates to alpha-amylase variants, polynucleotides encoding the variants, methods of producing the variants, and methods of using the variants.

Description of the Related Art

Alpha-amylases (α-1,4-glucan-4-glucanohydrolases, E.C. 3.2.1.) are a group of enzymes that hydrolyzes starch, glycogen, and other related polysaccharides by cleaving the internal α-1,4-glucosidic bonds. It has been used for many years been in, *e.g.*, laundry where is it well-known that alpha-amylases have a beneficial effect in removal of starch containing, or starch-based, stains. However, in other commercial applications the enzyme has become important, such as in the initial stages (liquefaction) of starch processing, in textile desizing, in alcohol production and as cleaning agents in detergent compositions.

In recent years there has been a desire to improve the properties of various amylases. In particular, the object of reducing the temperature of the laundry in order to reduce the energy consumption has been of primary focus when referring to the household care sector. Thus, many efforts have been put into finding improved alpha-amylase variants.

Regardless, there remains a need for alpha-amylase variants that possess altered properties and offer improved performance in various industrial applications. Thus, the present

24 Mar 2026
2026202266

invention provides such further improved alpha-amylase variants with improved properties compared to its parent.

It is an object of the present invention to provide polypeptides having alpha-amylase activity (alpha-amylases) which have improved wash performance, especially for use in automatic washing machines and/or dishwashers.

SUMMARY OF THE INVENTION

The present invention relates to an alpha-amylase variant of a parent alpha-amylase comprising a modification at one or more positions corresponding to positions: H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98,

24 Mar 2026
2026202266

V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering, and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17, and wherein the said variant has improved wash performance compared to said parent alpha-amylase and wherein said parent alpha-amylase has amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.

The present invention also relates to polynucleotides encoding the variants; nucleic acid constructs, vectors, and host cells comprising the polynucleotides; and methods of producing the variants.

The present invention also relates to methods of improving wash performance of a parent alpha-amylase.

DETAILED DESCRIPTION OF THE INVENTION

Definitions

In accordance with this detailed description, the following definitions apply. Note that the singular forms "a," "an," and "the" include plural references unless the context clearly dictates otherwise.

Reference to “about” a value or parameter herein includes aspects that are directed to that value or parameter per se. For example, description referring to “about X” includes the aspect “X”.

Unless defined otherwise or clearly indicated by context, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs.

The term “alpha-amylase” is synonymous with the term “polypeptides having alpha-amylase activity”. “Alpha-amylase activity” means the activity of alpha-1,4-glucan-4-glucanohydrolases, E.C. 3.2.1.1, which constitute a group of enzymes, catalyzing hydrolysis of starch and other linear and branched 1,4-glucosidic oligo- and polysaccharides.

24 Mar 2026
2026202266

Thus, the term “alpha-amylase” as used herein, refers to an enzyme that has alpha-amylase activity (Enzyme Class; EC 3.2.1.1) that hydrolyses alpha bonds of large, alpha-linked polysaccharides, such as starch and glycogen, yielding glucose and maltose. The terms “alpha-amylase” and “amylase” may be used interchangeably and constitute the same meaning and purpose herein. For purposes of the present invention, alpha-amylase activity is determined according to the procedure described under the sub-heading Methods, below. In one aspect, the alpha-amylases 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 alpha-amylase activity of one or more of the polypeptides of SEQ ID NOs:1-17.

The term ‘amino acid’ as used herein, refers to the standard twenty genetically-encoded amino acids and their corresponding stereoisomers in the ‘d’ form (as compared to the natural ‘l’ form), omega-amino acids other naturally-occurring amino acids, unconventional amino acids (*e.g.* α, α -disubstituted amino acids, N-alkyl amino acids, *etc.*) and chemically derivatised amino acids. Chemical derivatives of one or more amino acids may be achieved by reaction with a functional side group. Such derivatised molecules include, for example, those molecules in which free amino groups have been derivatised to form amine hydrochlorides, *p*-toluene sulphonyl groups, carboxybenzoxy groups, *t*-butyloxycarbonyl groups, chloroacetyl groups or formyl groups. Free carboxyl groups may be derivatised to form salts, methyl and ethyl esters or other types of esters and hydrazides. Free hydroxyl groups may be derivatised to form O-acyl or O-alkyl derivatives. Also included as chemical derivatives are those peptides which contain naturally occurring amino acid derivatives of the twenty standard amino acids. For example: 4-hydroxyproline may be substituted for proline; 5-hydroxylysine may be substituted for lysine; 3-methylhistidine may be substituted for histidine; homoserine may be substituted for serine and ornithine for lysine. Derivatives also include peptides containing one or more additions or deletions as long as the requisite activity is maintained. Other included modifications are amidation, amino terminal acylation (*e.g.* acetylation or thioglycolic acid amidation), terminal carboxylamidation (*e.g.* with ammonia or methylamine), and the like terminal modifications.

When an amino acid is being specifically enumerated, such as ‘alanine’ or ‘Ala’ or ‘A’, the term refers to both l-alanine and d-alanine unless explicitly stated otherwise. Other unconventional amino acids may also be suitable components for polypeptides of the present invention, as long as the desired functional property is retained by the polypeptide. For the peptides shown, each encoded amino acid residue, where appropriate, is represented by a single letter designation, corresponding to the trivial name of the conventional amino acid. In one embodiment, the polypeptides of the invention comprise or consist of l-amino acids.

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

24 Mar 2026
2026202266

The term "cDNA" means a DNA molecule that can be prepared by reverse transcription from a mature, spliced, mRNA molecule obtained from a 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 “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 “corresponding to” as used herein, refers to a way of determining the specific amino acid of a sequence wherein reference is made to a specific amino acid sequence. *E.g.* for the purposes of the present invention, when references are made to specific amino acid positions, the skilled person would be able to align another amino acid sequence to said amino acid sequence that reference has been made to, in order to determine which specific amino acid may be of interest in said another amino acid sequence. Alignment of another amino acid sequence with *e.g.* the sequence as set forth in SEQ ID NO: 1, or any other sequence listed herein, has been described elsewhere herein. Alignment of another amino acid sequence with e.g. the sequence as set forth in SEQ ID NOs: 1, 2, 3,4 5, 6, 7, 8, 9, 10,11, 12, 13, 14, 15, 16 or 17, or any other sequence listed herein, has been described elsewhere herein. Alternative alignment methods may be used and are well-known for the skilled person.

The term “dish washing composition" as used herein, refers to all forms of compositions for cleaning hard surfaces. The present invention is not restricted to any particular type of dish wash composition or any particular detergent. Thus, in one embodiment, the dish washing composition is a liquid dish washing composition, a powder dish washing composition, wherein the composition may optionally be in the form of a unit dose.

The term “enzyme detergency benefit” used herein, refers to the advantageous effect an

24 Mar 2026
2026202266

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

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

The term “expression vector” as used herein, refers to a linear or circular DNA molecule that comprises a polynucleotide encoding a variant and is operably linked to control sequences that provide for its expression.

The term “fragment” means a polypeptide having one or more (several) amino acids deleted from the amino and/or carboxyl terminus of a mature polypeptide; wherein the fragment has alpha-amylase activity.

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 “hard surface cleaning” as used herein, refers to cleaning of hard surfaces wherein hard surfaces may include floors, tables, walls, roofs etc. as well as surfaces of hard objects such as cars (car wash) and dishes (dish wash). Dish washing includes but are not limited to cleaning of plates, cups, glasses, bowls, cutlery such as spoons, knives, forks, serving utensils, ceramics, plastics, metals, china, glass and acrylics.

The term “improved property” is defined herein as a characteristic associated with a

24 Mar 2026
2026202266

variant that is improved compared to the parent alpha-amylase. Such improved properties include, but are not limited to, increased amylolytic activity, increased catalytic efficiency, increased catalytic rate, increased chemical stability, increased oxidation stability, increased pH activity, increased pH stability, increased relative specific activity, increased specific activity, increased substrate binding, increased substrate cleavage, increased substrate specificity, increased substrate stability, increased surface properties, increased thermal activity, increased thermostability, increased wash performance such as soil removal performance e.g. performance to starch-containing soils, stain removal, anti-greying, stability e.g. thermostability, pH stability, or stability in the presence of builders, including chelant, stability in powder, liquid or gel detergent formulation or dishwashing composition, altered temperature-dependent performance and activity profile, pH activity, substrate specificity, product specificity, and chemical stability. The improved property may be any of those herein defined and described, such as wash performance.

The term “improved wash performance” is defined herein as displaying a modification of the wash performance of an amylase of the present invention relative to the wash performance of the parent alpha-amylase of SEQ ID NO: 1 or SEQ ID NO: 2. The modification may *e.g.* be seen as increased stain removal. The wash performance is improved if the Improvement Factor (IF) is at least 1.1, at least 1.2, at least 1.3.

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

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 “mature polypeptide” as used herein, refers to 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*. It is known in the art that a host cell

24 Mar 2026
2026202266

may produce a mixture of two of more different mature polypeptides (*i.e.*, with a different C-terminal and/or N-terminal amino acid) expressed by the same polynucleotide.

The term “mature polypeptide coding sequence” as used herein, refers to a polynucleotide that encodes a mature polypeptide having alpha-amylase activity.

The term “modification”, in the context of the polypeptides of the invention, means that one or more amino acids within the reference amino acid sequence (*i.e.* SEQ ID NOs: 1 or 2) are altered by substitution with a different amino acid, by insertion of an amino acid or by deletion, preferably by at least two deletion. The terms “modification”, “alteration”, and “mutation” may be used interchangeably and constitute the same meaning and purpose.

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 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 “mutant” means a polynucleotide encoding a variant.

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 “parent” or “parent alpha-amylase” means an alpha-amylase to which a modification is made to produce the enzyme variants of the present invention. The parent may be a naturally occurring (wild-type) polypeptide or a variant thereof.

The term “sequence identity” as used herein refers to relatedness between two amino acid sequences or between two nucleotide sequences is described by the parameter “sequence identity”.

For purposes of the present invention, the sequence identity between two amino acid

24 Mar 2026
2026202266

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

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

Alternatively, the parameters used may be gap open penalty of 10, gap extension penalty of 0.5, and the EDNAFULL (EMBOSS version of NCBI NUC4.4) substitution matrix. The output of Needle labeled "longest identity" (obtained using the –nobrief option) is used as the percent identity and is calculated as follows:

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

The term "subsequence" as used herein, refers to a polynucleotide having one or more (*e.g.*, several) nucleotides absent from the 5' and/or 3' end of a mature polypeptide coding sequence; wherein the subsequence encodes a fragment having alpha-amylase activity.

The term "textile" refers to woven fabrics, as well as staple fibres 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) fibres. The term, "textile materials" is a general term for fibres, yarn intermediates, yarn, fabrics, and products made from fabrics (*e.g.,* garments and other articles).

The term "textile care benefits", as used herein, is defined as not being directly related to catalytic stain removal or prevention of re-deposition of soils, are also important for enzyme detergency benefits. Examples of such textile care benefits are prevention or reduction of dye transfer from one textile to another textile or another part of the same textile (an effect that is also termed dye transfer inhibition or anti-backstaining), removal of protruding or broken fibers from a textile surface to decrease pilling tendencies or remove already existing pills or fuzz (an effect that also is termed anti-pilling), improvement of the textile-softness, colour clarification of the textile and removal of particulate soils which are trapped in the fibers of the textile. Enzymatic bleaching is a further enzyme detergency benefit where the catalytic activity generally is used to catalyze the formation of bleaching component such as hydrogen peroxide or other peroxides or other bleaching species."

The terms "variant" or "polypeptide variant" or "polypeptide" or "alpha-amylase variant" when used in relation to a variant of the present invention, as used herein, refer to a polypeptide

24 Mar 2026
2026202266

having alpha-amylase activity comprising a modification, *i.e.*, a substitution, insertion, and/or deletion, at one or more (*e.g.*, several) positions relative to the 'parent' alpha-amylase of SEQ ID NOs:1 or 2. A substitution means replacement of the amino acid occupying a position with a different amino acid; a deletion means removal of the amino acid occupying a position; and an insertion means adding an amino acid adjacent to and immediately following the amino acid occupying a position The 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 alpha-amylase activity of the polypeptide of SEQ ID NOs: 1-17.

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 "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 "wash performance" is defined herein as displaying an alteration of the wash performance of an amylase of the present invention relative to the wash performance of the parent amylase of SEQ ID NO: 1 or the amylase of SEQ ID NO: 2. Improved wash performance may be measured by comparing of the so-called Intensity value.

The term "wild-type alpha-amylase" as used herein refers to an alpha-amylase expressed by a naturally occurring microorganism, such as a bacterium, yeast, or filamentous fungus found in nature.

The term "wash cycle" is defined herein with respect to dishwashing as a washing operation wherein dishware are exposed to the wash liquor for a period of time by circulating the wash liquor and spraying the wash liquor onto the dishware in order to clean the dishware and finally the superfluous wash liquor is removed. A wash cycle may be repeated one, two, three, four, five or even six times at the same or at different temperatures. Hereafter the dishware is generally rinsed and dried. One of the wash cycles can be a soaking step, where the dishware is left soaking in the wash liquor for a period.

The term "wash liquor" is defined herein as the solution or mixture of water and detergent components.

The term "wash time" with respect to automatic dishwashing is defined herein as the time it takes for the entire washing process; i.e. the time for the wash cycle(s) and rinse cycle(s)

24 Mar 2026
2026202266

together.

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").

The term “automatic dishwashing detergent composition” refers to compositions comprising detergent components, which composition is intended for cleaning dishware such as plates, cups, glasses, bowls, cutlery such as spoons, knives, forks, serving utensils, ceramics, plastics, metals, china, glass and acrylics in a dishwashing machine. 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 enzymes herein described, the detergents compositions may comprise, *e.g.* one or more additional components selected from stabilizing agents, surfactants, hydrotopes, builders, co-builders, chelating agents, bleaching systems, bleach activators, bleach catalysts, polymers, metal care agents, glass care agents, crystal growth inhibitors and fabric-hueing agents.

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)

24 Mar 2026
2026202266

composition is required, and the like. The term "effective amount" of an enzyme refers to the quantity of enzyme described hereinbefore that achieves a desired level of enzymatic activity, *e.g.,* in a defined detergent composition. In one embodiment, the effective amount of a protease is the same as the effective amount of an alpha-amylase. In another embodiment, the effective amount of a protease is different to the effective amount of an alpha-amylase, *e.g.,* the effective amount of a protease may be more or may be less than the effective amount of an alpha-amylase.

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 enzymes 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

24 Mar 2026
2026202266

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.

The term “liquid laundry detergent composition” as used herein refers to a detergent composition which is in a stabilized liquid form and used in a method for laundering a fabric. Thus, the detergent composition has been formulated to be in fluid form.

The term “powder laundry detergent composition” as used herein refers to a detergent composition which is in a solid form, such as a granulate, non-dusting granulate or powder, which is used in a method for laundering a fabric.

The term “liquid dishwash detergent composition” as used herein refers to a detergent composition which is in a stabilized liquid form and used in dishwash. Dishwash may be any kind of dishwash, such as manual dishwash and such as automated dishwash (ADW).

The term “powder dishwash detergent composition” as used herein refers to a detergent composition which is in a solid form, such as a granulate, powder or compact unit and used in dishwash. A powder dishwash detergent composition is typically used in automated dishwash, but the used is not limited to such ADW, and may also be intended for used in any other kind of dishwash, such as manual dishwash.

The terms “Delta intensity” or “Delta intensity value” are defined herein as the result of an intensity measurement of a test material, *e.g.* a Melamine tiles stained with starch DM-277 (Center For Testmaterials BV, P.O. Box 120, 3133 KT Vlaardingen, the Netherlands) or a hard surface. The delta intensity is the intensity value of the test material washed with amylase subtracting the intensity value of the test material washed without amylase.

The term “numbering is according to” as used herein, refers to the way each of the amino acid residues in a polypeptide of the present invention is numbered. *I.e.* the skilled person would know that when, *e.g.* position 202 is numbered according to SEQ ID NO: 1, he would know that by alignment of any other polypeptide with SEQ ID NO: 1, he will be able to determine the corresponding amino acid residue in the other polypeptide. Alignment of two or more amino acid sequences has been described elsewhere herein.

Conventions for Designation of Variants

For purposes of the present invention, the polypeptide disclosed in SEQ ID NO: 1 is used to determine the corresponding amino acid residue in another alpha-amylase. The amino acid

24 Mar 2026
2026202266

sequence of another alpha-amylase is aligned with the polypeptide disclosed in SEQ ID NO: 1, and based on the alignment, the amino acid position number corresponding to any amino acid residue in the polypeptide disclosed in SEQ ID NO: 1 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.

Identification of the corresponding amino acid residue in another alpha-amylase can be confirmed by an alignment of multiple polypeptide sequences using "ClustalW" (Larkin *et al.*, 2007, *Bioinformatics* 23: 2947-2948).

When the other enzyme has diverged from the polypeptide of SEQ ID NO: 1 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 superfamilies 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).

24 Mar 2026
2026202266

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 letter amino acid abbreviation is employed.

Substitutions: For an amino acid substitution, the following nomenclature is used: Original amino acid, position, substituted amino acid. Accordingly, the substitution of threonine at position 226 with alanine is designated as "Thr226Ala" or "T226A". Multiple mutations are separated by addition marks ("+"), *e.g.*, "Gly205Arg + Ser411Phe" or "G205R + S411F", representing substitutions at positions 205 and 411 of glycine (G) with arginine (R) and serine (S) with phenylalanine (F), respectively.

Deletions: For an amino acid deletion, the following nomenclature is used: Original amino acid, position, *. Accordingly, the deletion of glycine at position 195 is designated as "Gly195*" or "G195*". Multiple deletions are separated by addition marks ("+"), *e.g.*, "Gly195* + Ser411*" or "G195* + S411*".

Insertions. For an amino acid insertion, the following nomenclature is used: Original amino acid, position, original amino acid, inserted amino acid. Accordingly, the insertion of lysine after glycine at position 195 is designated "Gly195GlyLys" or "G195GK". An insertion of multiple amino acids is designated [Original amino acid, position, original amino acid, inserted amino acid #1, inserted amino acid #2; etc.]. For example, the insertion of lysine and alanine after glycine at position 195 is indicated as "Gly195GlyLysAla" or "G195GKA".

In such cases the inserted amino acid residue(s) are 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 the above example, the sequence would thus be:

Parent:	Variant:
195	195 195a 195b
G	G - K - A

Multiple modifications: Variants comprising multiple modifications are separated by addition marks ("+"), *e.g.*, "Arg170Tyr+Gly195Glu" or "R170Y+G195E" representing a substitution of arginine and glycine at positions 170 and 195 with tyrosine and glutamic acid, respectively.

Different modifications: Where different modifications may be introduced at a position, the different alterations are separated by a comma, *e.g.*, "Arg170Tyr,Glu" represents a substitution of arginine at position 170 with tyrosine or glutamic acid. Thus, "Tyr167Gly,Ala + Arg170Gly,Ala" designates the following variants:
"Tyr167Gly+Arg170Gly", "Tyr167Gly+Arg170Ala", "Tyr167Ala+Arg170Gly", and "Tyr167Ala+Arg170Ala".

24 Mar 2026
2026202266

DETAILED DESCRIPTION OF THE INVENTION

The present invention relates an alpha-amylase variant of a parent alpha-amylase comprising a modification in one or more (e.g., several) positions corresponding to position: 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17, and wherein said variant has alpha-amylase activity and wherein the said variant has improved wash performance compared to said parent polypeptide.

In one aspect, the present invention relates to alpha-amylase variant of a parent alpha-amylase polypeptide having alpha-amylase activity. Thus, in particular aspect, the present invention relates to variant of a parent alpha-amylase polypeptide having alpha-amylase activity, wherein said variant has an improved wash performance, and wherein said variant has alpha-amylase activity.

In one aspect, the present invention relates to an alpha-amylase variant of a parent alpha-amylase comprising a modification in one or more (e.g., several) positions corresponding to position: 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering, and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17, and wherein said variant has alpha-amylase activity and wherein the said variant has improved wash

24 Mar 2026
2026202266

performance compared to said parent polypeptide and wherein said parent alpha-amylase has amino acid sequence of SEQ ID NO: 1 or SEQ ID NO: 2.

In one aspect, the number of alterations is 1-50, e.g., 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 alterations.

In one aspect, the number of substitutions is 1-50, e.g., 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 substitutions.

In one aspect, the substituted amino acid residue is different from the naturally-occurring amino acid residue in that position. In one embodiment, the substitution is selected from the group consisting of A, C, D, E, F, G, H, I, K, L, M, N, P, Q, R, S, T, V, W and Y, with the proviso that the substituted amino acid residue is different from the naturally-occurring amino acid residue in that position.

In certain embodiments, the variant may comprise a pairwise deletion within a particular loop of the alpha-amylase which has been found to further stabilize the alpha-amylase. Thus, in one embodiment, the variant further comprises a pairwise deletion of the amino acid residues corresponding to R181, G182, D183 and G184, using SEQ ID NO: 1 for numbering, with the proviso that when the amino acids in positions corresponding to R181 and/or G184 has been substituted, the pairwise deletion is in the positions corresponding to G182 and D183, using SEQ ID NO: 1 for numbering.

The term “pairwise deletion” as used herein, refers to one deletion in two separate positions. Such positions may be adjacent to one another but are not limited to such adjacent pairs. A pairwise deletion may thus, also be deletion of one amino acid and another amino acid which may be up to three amino acids further downstream or upstream from the first deletion. Accordingly, in one embodiment, the variant comprises a pairwise deletion of the amino acid residues selected from the group consisting of; R181+G182, R181+D183, R181+G184, G182+D183, G182+G182, and D183+G184, using SEQ ID NO:1 for numbering.

In one aspect, SEQ ID NO: 2 is the amino acid sequence comprising a double deletion of the amino acid residues selected from the group consisting of; R181+G182, R181+D183, R181+G184, G182+D183, G182+G182, and D183+G184, preferably D183+G184, using SEQ ID NO: 1 for numbering.

In one aspect, the number of deletion is 1-50, e.g., 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5, such as 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48,

24 Mar 2026
2026202266

49 or 50 deletion.

In another aspect, a variant comprises a modification at one or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at two or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at three or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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%

24 Mar 2026
2026202266

sequence identity sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at four or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at five or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at six or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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%

24 Mar 2026
2026202266

sequence identity sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at seven or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at eight or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at nine or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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%

24 Mar 2026
2026202266

sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at ten or more positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, a variant comprises a modification at each positions corresponding to any of positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In one aspect, a variant useful herein comprises one or more of the following modification at position corresponding to positions 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein said variant has alpha-amylase activity and wherein said variant has at least 60%, at least 65%, at least 70%, 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%

24 Mar 2026
2026202266

sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In one aspect, the variant comprises one or more of the following modification at position corresponding to positions: H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17.

In another aspect, the variant comprises or consists of a deletion at a position corresponding to position 1. In another aspect, the amino acid at a position corresponding to position 1 is deleted of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion H1* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion at a position corresponding to position 2. In another aspect, the amino acid at a position corresponding to position 2 is deleted of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion H2* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 7. In another aspect, the amino acid at a position corresponding to position 7 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution G7A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 9. In another aspect, the amino acid at a position corresponding to position 9 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution I9M of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 11. In another aspect, the amino acid at a position corresponding to position 11 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro,

24 Mar 2026
2026202266

Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution Q11H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 16. In another aspect, the amino acid at a position corresponding to position 16 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution N16E or N16H or N16Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 19. In another aspect, the amino acid at a position corresponding to position 19 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution N19D of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 25. In another aspect, the amino acid at a position corresponding to position 25 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution N25K or N25M or N25T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 37. In another aspect, the amino acid at a position corresponding to position 37 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution A37V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 43. In another aspect, the amino acid at a position corresponding to position 43 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution W43Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 48. In another aspect, the amino acid at a position corresponding to position 48 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution W48Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 54. In another aspect, the amino acid at a position corresponding to position 54 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution

24 Mar 2026
2026202266

N54Q or N54S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 56. In another aspect, the amino acid at a position corresponding to position 56 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Tyr. In another aspect, the variant comprises or consists of the substitution V56I or V56T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 58. In another aspect, the amino acid at a position corresponding to position 58 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y58F of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 59. In another aspect, the amino acid at a position corresponding to position 59 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution G59A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 60. In another aspect, the amino acid at a position corresponding to position 60 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution A60S or A60T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 63. In another aspect, the amino acid at a position corresponding to position 63 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution L63F of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 81. In another aspect, the amino acid at a position corresponding to position 81 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution T81A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 84. In another aspect, the amino acid at a position corresponding to position 84 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution E84Q of the polypeptide of SEQ ID NO: 2.

24 Mar 2026
2026202266

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 86. In another aspect, the amino acid at a position corresponding to position 86 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution E86L of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 90. In another aspect, the amino acid at a position corresponding to position 90 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution R90H or R90N or R90Q of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 98. In another aspect, the amino acid at a position corresponding to position 98 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution Q98N of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 104. In another aspect, the amino acid at a position corresponding to position 104 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp or Tyr. In another aspect, the variant comprises or consists of the substitution V104A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 109. In another aspect, the amino acid at a position corresponding to position 109 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution G109A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 111. In another aspect, the amino acid at a position corresponding to position 111 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution A111T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 113. In another aspect, the amino acid at a position corresponding to position 113 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution F113A or F113G or F113N or F113Q or F113T or F113Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position

24 Mar 2026
2026202266

corresponding to position 116. In another aspect, the amino acid at a position corresponding to position 116 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution R116C or R116D or R116F or R116H or R116K or R116N or R116S or R116Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 118. In another aspect, the amino acid at a position corresponding to position 118 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution Q118N or Q118T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 125. In another aspect, the amino acid at a position corresponding to position 125 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution Q125G or Q125S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 127. In another aspect, the amino acid at a position corresponding to position 127 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution R127A or R127F or R127H or R127L or R127N or R127T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 130. In another aspect, the amino acid at a position corresponding to position 130 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution E130D or E130F or E130I or E130K or E130L or E130N or E130S or E130T or E130V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 132. In another aspect, the amino acid at a position corresponding to position 132 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution S132A or S132D or S132F or S132L or S132M or S132P or S132T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 133. In another aspect, the amino acid at a position corresponding to position 133 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe,

24 Mar 2026
2026202266

Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution G133D of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 134. In another aspect, the amino acid at a position corresponding to position 134 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution T134C or T134E or T134N or T134P or T134R or T134S or T134W or T134Y or T134A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 135. In another aspect, the amino acid at a position corresponding to position 135 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y135H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 136. In another aspect, the amino acid at a position corresponding to position 136 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution Q136D or Q136E or Q136G or 136N or Q136R or Q136S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 139. In another aspect, the amino acid at a position corresponding to position 139 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution A139T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 142. In another aspect, the amino acid at a position corresponding to position 142 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution G142H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 144. In another aspect, the amino acid at a position corresponding to position 144 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution N144H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 149. In another aspect, the amino acid at a position corresponding to

24 Mar 2026
2026202266

position 149 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution G149A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 158. In another aspect, the amino acid at a position corresponding to position 158 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution R158C or R158H or R158K or R158Q or R158S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 160. In another aspect, the amino acid at a position corresponding to position 160 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y160D or Y160F or Y160H or Y160N of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 163. In another aspect, the amino acid at a position corresponding to position 163 is substituted with Ala, Arg, Asn, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution D163H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion at a position corresponding to position 167. In another aspect, the variant comprises or consists of the deletion W167* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 169. In another aspect, the amino acid at a position corresponding to position 169 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the deletion Q169* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 170. In another aspect, the amino acid at a position corresponding to position 170 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution S170A of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion S170* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 171. In another aspect, the amino acid at a position corresponding to position 171 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists

24 Mar 2026
2026202266

of the substitution R171H or R171K or R171L or R171Y of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion R171* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 172. In another aspect, the amino acid at a position corresponding to position 172 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution Q172K or Q172N or Q172S of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion Q172* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 173. In another aspect, the amino acid at a position corresponding to position 173 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution L173K of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion L173* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 174. In another aspect, the amino acid at a position corresponding to position 174 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution A174N or A174S of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion A174* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 175. In another aspect, the amino acid at a position corresponding to position 175 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution N175S of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion N175* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 176. In another aspect, the amino acid at a position corresponding to position 176 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution R176A of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion R176* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 178. In another aspect, the amino acid at a position corresponding to

24 Mar 2026
2026202266

position 178 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y178F of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 181. In another aspect, the amino acid at a position corresponding to position 181 is substituted with Ala, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution R181A or R181C or R181E or R181G or R181H or R181K or R181N or R181Q of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion R181* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a deletion or substitution at a position corresponding to position 182. In another aspect, the amino acid at a position corresponding to position 182 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr, or Val. In another aspect, the variant comprises or consists of the substitution G182T N175S of the polypeptide of SEQ ID NO: 2. In another aspect, the variant comprises or consists of deletion G182* of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 186. In another aspect, the amino acid at a position corresponding to position 186 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution A186D or A186E or A186H or A186K or A186N or A186T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 187. In another aspect, the amino acid at a position corresponding to position 187 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr or Val. In another aspect, the variant comprises or consists of the substitution W187M of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 195. In another aspect, the amino acid at a position corresponding to position 195 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution N195D or N195F or N195H or N195Q or N195Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 202. In another aspect, the amino acid at a position corresponding to position 202 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution

24 Mar 2026
2026202266

M202L of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 203. In another aspect, the amino acid at a position corresponding to position 203 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y203L of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 204. In another aspect, the amino acid at a position corresponding to position 204 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution A204V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 206. In another aspect, the amino acid at a position corresponding to position 206 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Tyr. In another aspect, the variant comprises or consists of the substitution V206L of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 209. In another aspect, the amino acid at a position corresponding to position 209 is substituted with Ala, Arg, Asn, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution D209N of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 210. In another aspect, the amino acid at a position corresponding to position 210 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution H210K or H210N of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 212. In another aspect, the amino acid at a position corresponding to position 212 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution E212D of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 227. In another aspect, the amino acid at a position corresponding to position 227 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution T227K or T227N of the polypeptide of SEQ ID NO: 2.

24 Mar 2026
2026202266

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 235. In another aspect, the amino acid at a position corresponding to position 235 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution L235I of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 238. In another aspect, the amino acid at a position corresponding to position 238 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Tyr. In another aspect, the variant comprises or consists of the substitution V238A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 246. In another aspect, the amino acid at a position corresponding to position 246 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution M246I or M246L or M246T or M246V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 256. In another aspect, the amino acid at a position corresponding to position 256 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q256H or Q256N of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 259. In another aspect, the amino acid at a position corresponding to position 259 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution K259G or K259H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 264. In another aspect, the amino acid at a position corresponding to position 264 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Tyr. In another aspect, the variant comprises or consists of the substitution V264A or V246I or V264T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 265. In another aspect, the amino acid at a position corresponding to position 265 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution A265G of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position

24 Mar 2026
2026202266

corresponding to position 266. In another aspect, the amino acid at a position corresponding to position 266 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution E266V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 267. In another aspect, the amino acid at a position corresponding to position 267 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y267F or Y267H or Y267L of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 269. In another aspect, the amino acid at a position corresponding to position 269 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution K269M or K269Q or K269R of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 270. In another aspect, the amino acid at a position corresponding to position 270 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution N270G or N270P of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 272. In another aspect, the amino acid at a position corresponding to position 272 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution L272I of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 273. In another aspect, the amino acid at a position corresponding to position 273 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution G273V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 274. In another aspect, the amino acid at a position corresponding to position 274 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution A274K or A274S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 275. In another aspect, the amino acid at a position corresponding to

24 Mar 2026
2026202266

position 275 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution L275A or L275I or L275V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 276. In another aspect, the amino acid at a position corresponding to position 276 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution E276N of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 291. In another aspect, the amino acid at a position corresponding to position 291 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution V291A or V291I or V291T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 284. In another aspect, the amino acid at a position corresponding to position 284 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr or Val. In another aspect, the variant comprises or consists of the substitution W284R or W284Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 286. In another aspect, the amino acid at a position corresponding to position 286 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution M286L of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 291. In another aspect, the amino acid at a position corresponding to position 291 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Tyr. In another aspect, the variant comprises or consists of the substitution V291A or V291I or V291T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 293. In another aspect, the amino acid at a position corresponding to position 293 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution L293I or L293V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 295. In another aspect, the amino acid at a position corresponding to position 295 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe,

24 Mar 2026
2026202266

Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y295F of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 298. In another aspect, the amino acid at a position corresponding to position 298 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y298E or Y298N of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 299. In another aspect, the amino acid at a position corresponding to position 299 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q299N or Q299Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 302. In another aspect, the amino acid at a position corresponding to position 302 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution N302A or N302H or N302K or N302Q of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 303. In another aspect, the amino acid at a position corresponding to position 303 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution S303G of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 304. In another aspect, the amino acid at a position corresponding to position 304 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution S304G or S304Q of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 306. In another aspect, the amino acid at a position corresponding to position 306 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution N306H or N306K or N306Q or N306R or N306Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 310. In another aspect, the amino acid at a position corresponding to position 310 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the

24 Mar 2026
2026202266

substitution R310N or R310S or R310Q of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 311. In another aspect, the amino acid at a position corresponding to position 311 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution N311K or N311R of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 314. In another aspect, the amino acid at a position corresponding to position 314 is substituted with Ala, Arg, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution N314Q of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 315. In another aspect, the amino acid at a position corresponding to position 315 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution G315N of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 317. In another aspect, the amino acid at a position corresponding to position 317 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution L317V of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 319. In another aspect, the amino acid at a position corresponding to position 319 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q319H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 320. In another aspect, the amino acid at a position corresponding to position 320 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution R320K or R320Q or R320S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 323. In another aspect, the amino acid at a position corresponding to position 323 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution S323T or S323K of the polypeptide of SEQ ID NO: 2.

24 Mar 2026
2026202266

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 328. In another aspect, the amino acid at a position corresponding to position 328 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution F328L of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 337. In another aspect, the amino acid at a position corresponding to position 337 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution G337D or G337E of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 339. In another aspect, the amino acid at a position corresponding to position 339 is substituted with Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution A339S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 345. In another aspect, the amino acid at a position corresponding to position 345 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q345N or Q345R of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 357. In another aspect, the amino acid at a position corresponding to position 357 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution L357F of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 365. In another aspect, the amino acid at a position corresponding to position 365 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q365A or Q365C or Q365E or Q365H or Q365K or Q365M or Q365S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 377. In another aspect, the amino acid at a position corresponding to position 377 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution P377K or P377T of the polypeptide of SEQ ID NO: 2.

24 Mar 2026
2026202266

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 375. In another aspect, the amino acid at a position corresponding to position 375 is substituted with Ala, Arg, Asn, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution D375H or D375N or D375Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 386. In another aspect, the amino acid at a position corresponding to position 386 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q386L of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 391. In another aspect, the amino acid at a position corresponding to position 391 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution K391A of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 395. In another aspect, the amino acid at a position corresponding to position 395 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q395K of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 400. In another aspect, the amino acid at a position corresponding to position 400 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution R400S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 406. In another aspect, the amino acid at a position corresponding to position 406 is substituted with Ala, Arg, Asn, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution D406H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 408. In another aspect, the amino acid at a position corresponding to position 408 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr or Val. In another aspect, the variant comprises or consists of the substitution W408H of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position

24 Mar 2026
2026202266

corresponding to position 410. In another aspect, the amino acid at a position corresponding to position 410 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Tyr. In another aspect, the variant comprises or consists of the substitution V410I of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 431. In another aspect, the amino acid at a position corresponding to position 431 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution S431F of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 435. In another aspect, the amino acid at a position corresponding to position 435 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution G435C of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 439. In another aspect, the amino acid at a position corresponding to position 439 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr or Val. In another aspect, the variant comprises or consists of the substitution W439R or W439T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 444. In another aspect, the amino acid at a position corresponding to position 444 is substituted with Ala, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution R444T of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 445. In another aspect, the amino acid at a position corresponding to position 445 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q445S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 178. In another aspect, the amino acid at a position corresponding to position 178 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, or Val. In another aspect, the variant comprises or consists of the substitution Y178F of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 458. In another aspect, the amino acid at a position corresponding to

24 Mar 2026
2026202266

position 458 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution R458K of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 465. In another aspect, the amino acid at a position corresponding to position 465 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution N465G of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 466. In another aspect, the amino acid at a position corresponding to position 466 is substituted with Ala, Arg, Asn, Asp, Cys, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Q466S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 469. In another aspect, the amino acid at a position corresponding to position 469 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Tyr or Val. In another aspect, the variant comprises or consists of the substitution W469N or W469Y of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 178. In another aspect, the amino acid at a position corresponding to position 178 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution Y178F of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 473. In another aspect, the amino acid at a position corresponding to position 473 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution F473I or F473P or F473S of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 476. In another aspect, the amino acid at a position corresponding to position 476 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, His, Ile, Leu, Lys, Met, Phe, Pro, Ser, Thr, Trp, Tyr or Val. In another aspect, the variant comprises or consists of the substitution G476K of the polypeptide of SEQ ID NO: 2.

In another aspect, the variant comprises or consists of a substitution at a position corresponding to position 481. In another aspect, the amino acid at a position corresponding to position 481 is substituted with Ala, Arg, Asn, Asp, Cys, Gln, Glu, Gly, His, Ile, Leu, Lys, Met, Phe,

24 Mar 2026
2026202266

Pro, Ser, Thr, Trp, or Tyr. In another aspect, the variant comprises or consists of the substitution V481A of the polypeptide of SEQ ID NO: 2.

In one aspect, the variant comprises one or more of the following modification at position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17.

The variants 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 alpha-amylase activity of the polypeptide of SEQ ID NOs: 1-17.

In an embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, but

24 Mar 2026
2026202266

less than 100%, to the amino acid sequence of the parent polypeptide having alpha-amylase activity.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 1.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 2.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 3.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 4.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 5.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 6.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 7.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 8.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%,

24 Mar 2026
2026202266

at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 9.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 10.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 11.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 12.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 13.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 14.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 15.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 16.

In another embodiment, the variant has sequence identity of at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, such as at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to SEQ ID NO: 17.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M;

24 Mar 2026
2026202266

N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 1.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F;

24 Mar 2026
2026202266

S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 2.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N;

24 Mar 2026
2026202266

Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 3.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at

24 Mar 2026
2026202266

least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100% sequence identity to the polypeptide of SEQ ID NO: 4.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 5.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K;

24 Mar 2026
2026202266

E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 6.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L;

24 Mar 2026
2026202266

D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 7.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T;

24 Mar 2026
2026202266

D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 8.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 9.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M;

24 Mar 2026
2026202266

N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 10.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F;

24 Mar 2026
2026202266

S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 11.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N;

24 Mar 2026
2026202266

Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 12.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at

24 Mar 2026
2026202266

least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100% sequence identity to the polypeptide of SEQ ID NO: 13.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 14.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K;

24 Mar 2026
2026202266

E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 15.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L;

24 Mar 2026
2026202266

D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 16.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T;

24 Mar 2026
2026202266

D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 17.

In one aspect, the modification in one or more positions correspond to the following: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: A174*+A339S, A174*+G109A, A174*+G149A, A174*+G182T, A174*+H1*, A174*+I9M, A174*+K391A, A174*+M202L, A174*+N16Y, A174*+N195F, A174*+N54S, A174*+Q169E, A174*+Q169E, A174*+Q172K, A174*+Q299Y, A174*+Q345R, A174*+Q365S, A174*+R320K, A174*+R458K, A174*+S323T, A174*+V206L, A174*+Y295F,

24 Mar 2026
2026202266

A339S+G109A, A339S+G149A, A339S+G182T, A339S+H1*, A339S+I9M, A339S+K391A, A339S+M202L, A339S+N16Y, A339S+N195F, A339S+N54S, A339S+Q169E, A339S+Q169E, A339S+Q172K, A339S+Q299Y, A339S+Q345R, A339S+Q365S, A339S+R320K, A339S+R458K, A339S+S323T, A339S+V206L, A339S+Y295F, G109A+G149A, G109A+G182T, G109A+H1*, G109A+I9M, G109A+K391A, G109A+M202L, G109A+N16Y, G109A+N195F, G109A+N54S, G109A+Q169E, G109A+Q169E, G109A+Q172K, G109A+Q299Y, G109A+Q345R, G109A+Q365S, G109A+R320K, G109A+R458K, G109A+S323T, G109A+V206L, G109A+Y295F, G149A+G182T, G149A+H1*, G149A+I9M, G149A+K391A, G149A+M202L, G149A+N16Y, G149A+N195F, G149A+N54S, G149A+Q169E, G149A+Q169E, G149A+Q172K, G149A+Q299Y, G149A+Q345R, G149A+Q365S, G149A+R320K, G149A+R458K, G149A+S323T, G149A+V206L, G149A+Y295F, G182T+H1*, G182T+I9M, G182T+K391A, G182T+M202L, G182T+N16Y, G182T+N195F, G182T+N54S, G182T+Q169E, G182T+Q169E, G182T+Q172K, G182T+Q299Y, G182T+Q345R, G182T+Q365S, G182T+R320K, G182T+R458K, G182T+S323T, G182T+V206L, G182T+Y295F, H1*+I9M, H1*+K391A, H1*+M202L, H1*+N16Y, H1*+N195F, H1*+N54S, H1*+Q169E, H1*+Q169E, H1*+Q172K, H1*+Q299Y, H1*+Q345R, H1*+Q365S, H1*+R320K, H1*+R458K, H1*+S323T, H1*+V206L, H1*+Y295F, I9M+K391A, I9M+M202L, I9M+N16Y, I9M+N195F, I9M+N54S, I9M+Q169E, I9M+Q169E, I9M+Q172K, I9M+Q299Y, I9M+Q345R, I9M+Q365S, I9M+R320K, I9M+R458K, I9M+S323T, I9M+V206L, I9M+Y295F, K391A+M202L, K391A+N16Y, K391A+N195F, K391A+N54S, K391A+Q169E, K391A+Q169E, K391A+Q172K, K391A+Q299Y, K391A+Q345R, K391A+Q365S, K391A+R320K, K391A+R458K, K391A+S323T, K391A+V206L, K391A+Y295F, M202L+N16Y, M202L+N195F, M202L+N54S, M202L+Q169E, M202L+Q169E, M202L+Q172K, M202L+Q299Y, M202L+Q345R, M202L+Q365S, M202L+R320K, M202L+R458K, M202L+S323T, M202L+V206L, M202L+Y295F, N16Y+N195F, N16Y+N54S, N16Y+Q169E, N16Y+Q169E, N16Y+Q172K, N16Y+Q299Y, N16Y+Q345R, N16Y+Q365S, N16Y+R320K, N16Y+R458K, N16Y+S323T, N16Y+V206L, N16Y+Y295F, N195F+N54S, N195F+Q169E, N195F+Q169E, N195F+Q172K, N195F+Q299Y, N195F+Q345R, N195F+Q365S, N195F+R320K, N195F+R458K, N195F+S323T, N195F+V206L, N195F+Y295F, N54S+Q169E, N54S+Q169E, N54S+Q172K, N54S+Q299Y, N54S+Q345R, N54S+Q365S, N54S+R320K, N54S+R458K, N54S+S323T, N54S+V206L, N54S+Y295F, Q169E+Q169E, Q169E+Q172K, Q169E+Q299Y, Q169E+Q345R, Q169E+Q365S, Q169E+R320K, Q169E+R458K, Q169E+S323T, Q169E+V206L, Q169E+Y295F, Q172K+Q299Y, Q172K+Q345R, Q172K+Q365S, Q172K+R320K, Q172K+R458K, Q172K+S323T, Q172K+V206L, Q172K+Y295F, Q299Y+Q345R, Q299Y+Q365S, Q299Y+R320K, Q299Y+R458K,

24 Mar 2026

2026202266

Q299Y+S323T, Q299Y+V206L, Q299Y+Y295F, Q345R+Q365S, Q345R+R320K, Q345R+R458K, Q345R+S323T, Q345R+V206L, Q345R+Y295F, Q365S+R320K, Q365S+R458K, Q365S+S323T, Q365S+V206L, Q365S+Y295F, R320K+R458K, R320K+S323T, R320K+V206L, R320K+Y295F, R458K+S323T, R458K+V206L, R458K+Y295F, S323T+V206L, S323T+Y295F, V206L+Y295F, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID Nos; 1-17.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: A174*+A339S+G109A, A174*+A339S+G149A, A174*+A339S+G182T, A174*+A339S+H1*, A174*+A339S+I9M, A174*+A339S+K391A, A174*+A339S+M202L, A174*+A339S+N16Y, A174*+A339S+N195F, A174*+A339S+N54S, A174*+A339S+Q169E, A174*+A339S+Q169E, A174*+A339S+Q172K, A174*+A339S+Q299Y, A174*+A339S+Q345R, A174*+A339S+Q365S, A174*+A339S+R320K, A174*+A339S+R458K, A174*+A339S+S323T, A174*+A339S+V206L, A174*+A339S+Y295F, A174*+G109A+G149A, A174*+G109A+G182T, A174*+G109A+H1*, A174*+G109A+I9M, A174*+G109A+K391A, A174*+G109A+M202L, A174*+G109A+N16Y, A174*+G109A+N195F, A174*+G109A+N54S, A174*+G109A+Q169E, A174*+G109A+Q169E, A174*+G109A+Q172K, A174*+G109A+Q299Y, A174*+G109A+Q345R, A174*+G109A+Q365S, A174*+G109A+R320K, A174*+G109A+R458K, A174*+G109A+S323T, A174*+G109A+V206L, A174*+G109A+Y295F, A174*+G149A+G182T, A174*+G149A+H1*, A174*+G149A+I9M, A174*+G149A+K391A, A174*+G149A+M202L, A174*+G149A+N16Y, A174*+G149A+N195F, A174*+G149A+N54S, A174*+G149A+Q169E, A174*+G149A+Q169E, A174*+G149A+Q172K, A174*+G149A+Q299Y, A174*+G149A+Q345R, A174*+G149A+Q365S, A174*+G149A+R320K, A174*+G149A+R458K, A174*+G149A+S323T, A174*+G149A+V206L, A174*+G149A+Y295F, A174*+G182T+H1*, A174*+G182T+I9M, A174*+G182T+K391A, A174*+G182T+M202L, A174*+G182T+N16Y, A174*+G182T+N195F, A174*+G182T+N54S, A174*+G182T+Q169E, A174*+G182T+Q169E, A174*+G182T+Q172K, A174*+G182T+Q299Y, A174*+G182T+Q345R, A174*+G182T+Q365S, A174*+G182T+R320K, A174*+G182T+R458K, A174*+G182T+S323T, A174*+G182T+V206L, A174*+G182T+Y295F, A174*+H1*+I9M, A174*+H1*+K391A, A174*+H1*+M202L, A174*+H1*+N16Y, A174*+H1*+N195F, A174*+H1*+N54S, A174*+H1*+Q169E, A174*+H1*+Q169E, A174*+H1*+Q172K, A174*+H1*+Q299Y, A174*+H1*+Q345R, A174*+H1*+Q365S, A174*+H1*+R320K, A174*+H1*+R458K, A174*+H1*+S323T, A174*+H1*+V206L, A174*+H1*+Y295F, A174*+I9M+K391A, A174*+I9M+M202L, A174*+I9M+N16Y, A174*+I9M+N195F, A174*+I9M+N54S, A174*+I9M+Q169E, A174*+I9M+Q169E, A174*+I9M+Q172K, A174*+I9M+Q299Y, A174*+I9M+Q345R, A174*+I9M+Q365S,

24 Mar 2026
2026202266

A174*+I9M+R320K, A174*+I9M+R458K, A174*+I9M+S323T, A174*+I9M+V206L, A174*+I9M+Y295F, A174*+K391A+M202L, A174*+K391A+N16Y, A174*+K391A+N195F, A174*+K391A+N54S, A174*+K391A+Q169E, A174*+K391A+Q169E, A174*+K391A+Q172K, A174*+K391A+Q299Y, A174*+K391A+Q345R, A174*+K391A+Q365S, A174*+K391A+R320K, A174*+K391A+R458K, A174*+K391A+S323T, A174*+K391A+V206L, A174*+K391A+Y295F, A174*+M202L+N16Y, A174*+M202L+N195F, A174*+M202L+N54S, A174*+M202L+Q169E, A174*+M202L+Q169E, A174*+M202L+Q172K, A174*+M202L+Q299Y, A174*+M202L+Q345R, A174*+M202L+Q365S, A174*+M202L+R320K, A174*+M202L+R458K, A174*+M202L+S323T, A174*+M202L+V206L, A174*+M202L+Y295F, A174*+N16Y+N195F, A174*+N16Y+N54S, A174*+N16Y+Q169E, A174*+N16Y+Q169E, A174*+N16Y+Q172K, A174*+N16Y+Q299Y, A174*+N16Y+Q345R, A174*+N16Y+Q365S, A174*+N16Y+R320K, A174*+N16Y+R458K, A174*+N16Y+S323T, A174*+N16Y+V206L, A174*+N16Y+Y295F, A174*+N195F+N54S, A174*+N195F+Q169E, A174*+N195F+Q169E, A174*+N195F+Q172K, A174*+N195F+Q299Y, A174*+N195F+Q345R, A174*+N195F+Q365S, A174*+N195F+R320K, A174*+N195F+R458K, A174*+N195F+S323T, A174*+N195F+V206L, A174*+N195F+Y295F, A174*+N54S+Q169E, A174*+N54S+Q169E, A174*+N54S+Q172K, A174*+N54S+Q299Y, A174*+N54S+Q345R, A174*+N54S+Q365S, A174*+N54S+R320K, A174*+N54S+R458K, A174*+N54S+S323T, A174*+N54S+V206L, A174*+N54S+Y295F, A174*+Q169E+Q169E, A174*+Q169E+Q172K, A174*+Q169E+Q299Y, A174*+Q169E+Q345R, A174*+Q169E+Q365S, A174*+Q169E+R320K, A174*+Q169E+R458K, A174*+Q169E+S323T, A174*+Q169E+V206L, A174*+Q169E+Y295F, A174*+Q169E+Q172K, A174*+Q169E+Q299Y, A174*+Q169E+Q345R, A174*+Q169E+Q365S, A174*+Q169E+R320K, A174*+Q169E+R458K, A174*+Q169E+S323T, A174*+Q169E+V206L, A174*+Q169E+Y295F, A174*+Q172K+Q299Y, A174*+Q172K+Q345R, A174*+Q172K+Q365S, A174*+Q172K+R320K, A174*+Q172K+R458K, A174*+Q172K+S323T, A174*+Q172K+V206L, A174*+Q172K+Y295F, A174*+Q299Y+Q345R, A174*+Q299Y+Q365S, A174*+Q299Y+R320K, A174*+Q299Y+R458K, A174*+Q299Y+S323T, A174*+Q299Y+V206L, A174*+Q299Y+Y295F, A174*+Q345R+Q365S, A174*+Q345R+R320K, A174*+Q345R+R458K, A174*+Q345R+S323T, A174*+Q345R+V206L, A174*+Q345R+Y295F, A174*+Q365S+R320K, A174*+Q365S+R458K, A174*+Q365S+S323T, A174*+Q365S+V206L, A174*+Q365S+Y295F, A174*+R320K+R458K, A174*+R320K+S323T, A174*+R320K+V206L, A174*+R320K+Y295F, A174*+R458K+S323T, A174*+R458K+V206L, A174*+R458K+Y295F, A174*+S323T+V206L, A174*+S323T+Y295F, A174*+V206L+Y295F, A339S+G109A+G149A, A339S+G109A+G182T, A339S+G109A+H1*, A339S+G109A+I9M, A339S+G109A+K391A, A339S+G109A+M202L, A339S+G109A+N16Y, A339S+G109A+N195F,A339S+G109A+N54S, A339S+G109A+Q169E, A339S+G109A+Q169E, A339S+G109A+Q172K,A339S+G109A+Q299Y,A339S+G109A+Q345R,A339S+G109A+Q365S ,A339S+G109A+R320K,A339S+G109A+R458K,A339S+G109A+S323T,A339S+G109A+V206L,

2026202266 24 Mar 2026

A339S+G109A+Y295F, A339S+G149A+G182T, A339S+G149A+H1*, A339S+G149A+I9M, A339S+G149A+K391A, A339S+G149A+M202L, A339S+G149A+N16Y, A339S+G149A+N195F, A339S+G149A+N54S,A339S+G149A+Q169E,A339S+G149A+Q169E,A339S+G149A+Q172K, A339S+G149A+Q299Y,A339S+G149A+Q345R,A339S+G149A+Q365S,A339S+G149A+R320K ,A339S+G149A+R458K,A339S+G149A+S323T,A339S+G149A+V206L,A339S+G149A+Y295F, A339S+G182T+H1*,A339S+G182T+I9M,A339S+G182T+K391A,A339S+G182T+M202L, A339S+G182T+N16Y, A339S+G182T+N195F, A339S+G182T+N54S, A339S+G182T+Q169E, A339S+G182T+Q169E,A339S+G182T+Q172K,A339S+G182T+Q299Y,A339S+G182T+Q345R ,A339S+G182T+Q365S,A339S+G182T+R320K,A339S+G182T+R458K,A339S+G182T+S323T, A339S+G182T+V206L,A339S+G182T+Y295F,A339S+H1*+I9M,A339S+H1*+K391A,A339S+H 1*+M202L, A339S+H1*+N16Y, A339S+H1*+N195F, A339S+H1*+N54S, A339S+H1*+Q169E, A339S+H1*+Q169E,A339S+H1*+Q172K,A339S+H1*+Q299Y,A339S+H1*+Q345R,A339S+H1* +Q365S,A339S+H1*+R320K,A339S+H1*+R458K,A339S+H1*+S323T,A339S+H1*+V206L, A339S+H1*+Y295F,A339S+I9M+K391A,A339S+I9M+M202L,A339S+I9M+N16Y,A339S+I9M+ N195F, A339S+I9M+N54S, A339S+I9M+Q169E, A339S+I9M+Q169E, A339S+I9M+Q172K, A339S+I9M+Q299Y,A339S+I9M+Q345R,A339S+I9M+Q365S,A339S+I9M+R320K,A339S+I9M +R458K,A339S+I9M+S323T,A339S+I9M+V206L,A339S+I9M+Y295F, A339S+K391A+M202L, A339S+K391A+N16Y, A339S+K391A+N195F, A339S+K391A+N54S, A339S+K391A+Q169E, A339S+K391A+Q169E,A339S+K391A+Q172K,A339S+K391A+Q299Y,A339S+K391A+Q345R, A339S+K391A+Q365S,A339S+K391A+R320K, A339S+K391A+R458K, A339S+K391A+S323T, A339S+K391A+V206L, A339S+K391A+Y295F, A339S+M202L+N16Y, A339S+M202L+N195F, A339S+M202L+N54S, A339S+M202L+Q169E, A339S+M202L+Q169E, A339S+M202L+Q172K, A339S+M202L+Q299Y,A339S+M202L+Q345R,A339S+M202L+Q365S,A339S+M202L+R320K, A339S+M202L+R458K, A339S+M202L+S323T, A339S+M202L+V206L, A339S+M202L+Y295F, A339S+N16Y+N195F, A339S+N16Y+N54S, A339S+N16Y+Q169E, A339S+N16Y+Q169E, A339S+N16Y+Q172K, A339S+N16Y+Q299Y, A339S+N16Y+Q345R, A339S+N16Y+Q365S, A339S+N16Y+R320K, A339S+N16Y+R458K, A339S+N16Y+S323T, A339S+N16Y+V206L, A339S+N16Y+Y295F, A339S+N195F+N54S, A339S+N195F+Q169E, A339S+N195F+Q169E, A339S+N195F+Q172K,A339S+N195F+Q299Y,A339S+N195F+Q345R, A339S+N195F+Q365S, A339S+N195F+R320K, A339S+N195F+R458K, A339S+N195F+S323T, A339S+N195F+V206L, A339S+N195F+Y295F, A339S+N54S+Q169E, A339S+N54S+Q169E, A339S+N54S+Q172K, A339S+N54S+Q299Y, A339S+N54S+Q345R, A339S+N54S+Q365S, A339S+N54S+R320K, A339S+N54S+R458K, A339S+N54S+S323T, A339S+N54S+V206L, A339S+N54S+Y295F, A339S+Q169E+Q169E,A339S+Q169E+Q172K,A339S+Q169E+Q299Y,A339S+Q169E+Q345R ,A339S+Q169E+Q365S,A339S+Q169E+R320K,A339S+Q169E+R458K,A339S+Q169E+S323T ,A339S+Q169E+V206L,A339S+Q169E+Y295F,A339S+Q169E+Q172K,A339S+Q169E+Q299Y

24 Mar 2026
2026202266

,A339S+Q169E+Q345R,A339S+Q169E+Q365S,A339S+Q169E+R320K,A339S+Q169E+R458K,A339S+Q169E+S323T,A339S+Q169E+V206L,A339S+Q169E+Y295F,A339S+Q172K+Q299Y,A339S+Q172K+Q345R,A339S+Q172K+Q365S,A339S+Q172K+R320K,A339S+Q172K+R458K,A339S+Q172K+S323T,A339S+Q172K+V206L,A339S+Q172K+Y295F,A339S+Q299Y+Q345R,A339S+Q299Y+Q365S,A339S+Q299Y+R320K,A339S+Q299Y+R458K,A339S+Q299Y+S323T,A339S+Q299Y+V206L,A339S+Q299Y+Y295F,A339S+Q345R+Q365S,A339S+Q345R+R320K,A339S+Q345R+R458K,A339S+Q345R+S323T,A339S+Q345R+V206L,A339S+Q345R+Y295F,A339S+Q365S+R320K,A339S+Q365S+R458K,A339S+Q365S+S323T,A339S+Q365S+V206L,A339S+Q365S+Y295F,A339S+R320K+R458K,A339S+R320K+S323T,A339S+R320K+V206L,A339S+R320K+Y295F,A339S+R458K+S323T,A339S+R458K+V206L,A339S+R458K+Y295F,A339S+S323T+V206L,A339S+S323T+Y295F,A339S+V206L+Y295F,G109A+G149A+G182T, G109A+G149A+H1*, G109A+G149A+I9M, G109A+G149A+K391A, G109A+G149A+M202L, G109A+G149A+N16Y, G109A+G149A+N195F, G109A+G149A+N54S, G109A+G149A+Q169E, G109A+G149A+Q169E,G109A+G149A+Q172K,G109A+G149A+Q299Y,G109A+G149A+Q345R,G109A+G149A+Q365S,G109A+G149A+R320K,G109A+G149A+R458K,G109A+G149A+S323T, G109A+G149A+V206L, G109A+G149A+Y295F, G109A+G182T+H1*, G109A+G182T+I9M, G109A+G182T+K391A,G109A+G182T+M202L, G109A+G182T+N16Y, G109A+G182T+N195F, G109A+G182T+N54S,G109A+G182T+Q169E,G109A+G182T+Q169E, G109A+G182T+Q172K, G109A+G182T+Q299Y,G109A+G182T+Q345R,G109A+G182T+Q365S,G109A+G182T+R320K,G109A+G182T+R458K,G109A+G182T+S323T,G109A+G182T+V206L,G109A+G182T+Y295F,G109A+H1*+I9M,G109A+H1*+K391A,G109A+H1*+M202L,G109A+H1*+N16Y,G109A+H1*+N195F, G109A+H1*+N54S, G109A+H1*+Q169E, G109A+H1*+Q169E, G109A+H1*+Q172K, G109A+H1*+Q299Y,G109A+H1*+Q345R,G109A+H1*+Q365S,G109A+H1*+R320K,G109A+H1*+R458K, G109A+H1*+S323T, G109A+H1*+V206L, G109A+H1*+Y295F, G109A+I9M+K391A, G109A+I9M+M202L,G109A+I9M+N16Y,G109A+I9M+N195F,G109A+I9M+N54S,G109A+I9M+Q169E, G109A+I9M+Q169E, G109A+I9M+Q172K, G109A+I9M+Q299Y, G109A+I9M+Q345R, G109A+I9M+Q365S,G109A+I9M+R320K,G109A+I9M+R458K,G109A+I9M+S323T,G109A+I9M+V206L,G109A+I9M+Y295F,G109A+K391A+M202L,G109A+K391A+N16Y,G109A+K391A+N195F,G109A+K391A+N54S,G109A+K391A+Q169E,G109A+K391A+Q169E,G109A+K391A+Q172K,G109A+K391A+Q299Y,G109A+K391A+Q345R,G109A+K391A+Q365S,G109A+K391A+R320K,G109A+K391A+R458K,G109A+K391A+S323T,G109A+K391A+V206L,G109A+K391A+Y295F,G109A+M202L+N16Y,G109A+M202L+N195F,G109A+M202L+N54S,G109A+M202L+Q169E,G109A+M202L+Q169E,G109A+M202L+Q172K,G109A+M202L+Q299Y,G109A+M202L+Q345R,G109A+M202L+Q365S,G109A+M202L+R320K,G109A+M202L+R458K,G109A+M202L+S323T,G109A+M202L+V206L,G109A+M202L+Y295F,G109A+N16Y+N195F,G109A+N16Y+N54S,G109A+N16Y+Q169E,G109A+N16Y+Q169E,G109A+N16Y+Q172K, G109A+N16Y+Q299Y,

24 Mar 2026
2026202266

G109A+N16Y+Q345R, G109A+N16Y+Q365S, G109A+N16Y+R320K, G109A+N16Y+R458K, G109A+N16Y+S323T, G109A+N16Y+V206L, G109A+N16Y+Y295F, G109A+N195F+N54S, G109A+N195F+Q169E,G109A+N195F+Q169E,G109A+N195F+Q172K,G109A+N195F+Q299Y ,G109A+N195F+Q345R,G109A+N195F+Q365S,G109A+N195F+R320K,G109A+N195F+R458 K,G109A+N195F+S323T,G109A+N195F+V206L,G109A+N195F+Y295F,G109A+N54S+Q169E , G109A+N54S+Q169E, G109A+N54S+Q172K, G109A+N54S+Q299Y, G109A+N54S+Q345R, G109A+N54S+Q365S, G109A+N54S+R320K, G109A+N54S+R458K, G109A+N54S+S323T, G109A+N54S+V206L, G109A+N54S+Y295F, G109A+Q169E+Q169E, G109A+Q169E+Q172K, G109A+Q169E+Q299Y,G109A+Q169E+Q345R,G109A+Q169E+Q365S,G109A+Q169E+R320 K,G109A+Q169E+R458K,G109A+Q169E+S323T,G109A+Q169E+V206L,G109A+Q169E+Y29 5F,G109A+Q169E+Q172K,G109A+Q169E+Q299Y,G109A+Q169E+Q345R,G109A+Q169E+Q 365S,G109A+Q169E+R320K,G109A+Q169E+R458K,G109A+Q169E+S323T,G109A+Q169E+ V206L,G109A+Q169E+Y295F,G109A+Q172K+Q299Y,G109A+Q172K+Q345R,G109A+Q172K +Q365S,G109A+Q172K+R320K,G109A+Q172K+R458K,G109A+Q172K+S323T,G109A+Q172 K+V206L,G109A+Q172K+Y295F,G109A+Q299Y+Q345R,G109A+Q299Y+Q365S,G109A+Q29 9Y+R320K,G109A+Q299Y+R458K,G109A+Q299Y+S323T,G109A+Q299Y+V206L,G109A+Q2 99Y+Y295F,G109A+Q345R+Q365S,G109A+Q345R+R320K,G109A+Q345R+R458K,G109A+Q 345R+S323T,G109A+Q345R+V206L,G109A+Q345R+Y295F,G109A+Q365S+R320K,G109A+ Q365S+R458K,G109A+Q365S+S323T,G109A+Q365S+V206L,G109A+Q365S+Y295F,G109A +R320K+R458K,G109A+R320K+S323T,G109A+R320K+V206L,G109A+R320K+Y295F,G109A +R458K+S323T,G109A+R458K+V206L, G109A+R458K+Y295F, G109A+S323T+V206L, G109A+S323T+Y295F, G109A+V206L+Y295F, G149A+G182T+H1*,G149A+G182T+I9M, G149A+G182T+K391A,G149A+G182T+M202L, G149A+G182T+N16Y, G149A+G182T+N195F, G149A+G182T+N54S,G149A+G182T+Q169E,G149A+G182T+Q169E, G149A+G182T+Q172K, G149A+G182T+Q299Y,G149A+G182T+Q345R,G149A+G182T+Q365S,G149A+G182T+R320 K,G149A+G182T+R458K,G149A+G182T+S323T,G149A+G182T+V206L,G149A+G182T+Y295 F,G149A+H1*+I9M,G149A+H1*+K391A,G149A+H1*+M202L,G149A+H1*+N16Y,G149A+H1*+ N195F,G149A+H1*+N54S,G149A+H1*+Q169E,G149A+H1*+Q169E,G149A+H1*+Q172K,G149 A+H1*+Q299Y,G149A+H1*+Q345R,G149A+H1*+Q365S,G149A+H1*+R320K,G149A+H1*+R4 58K,G149A+H1*+S323T,G149A+H1*+V206L,G149A+H1*+Y295F,G149A+I9M+K391A,G149A+ I9M+M202L,G149A+I9M+N16Y,G149A+I9M+N195F,G149A+I9M+N54S,G149A+I9M+Q169E,G 149A+I9M+Q169E,G149A+I9M+Q172K,G149A+I9M+Q299Y,G149A+I9M+Q345R,G149A+I9M +Q365S,G149A+I9M+R320K,G149A+I9M+R458K,G149A+I9M+S323T,G149A+I9M+V206L,G1 49A+I9M+Y295F,G149A+K391A+M202L,G149A+K391A+N16Y,G149A+K391A+N195F,G149A +K391A+N54S,G149A+K391A+Q169E,G149A+K391A+Q169E,G149A+K391A+Q172K, G149A+K391A+Q299Y,G149A+K391A+Q345R,G149A+K391A+Q365S,G149A+K391A+R320K

24 Mar 2026
2026202266

,G149A+K391A+R458K,G149A+K391A+S323T,G149A+K391A+V206L,G149A+K391A+Y295F,
G149A+M202L+N16Y,G149A+M202L+N195F,G149A+M202L+N54S,G149A+M202L+Q169E,G
149A+M202L+Q169E,G149A+M202L+Q172K,G149A+M202L+Q299Y, G149A+M202L+Q345R,
G149A+M202L+Q365S,G149A+M202L+R320K,G149A+M202L+R458K,G149A+M202L+S323T
,G149A+M202L+V206L,G149A+M202L+Y295F,G149A+N16Y+N195F,G149A+N16Y+N54S,
G149A+N16Y+Q169E,G149A+N16Y+Q169E,G149A+N16Y+Q172K,G149A+N16Y+Q299Y,G1
49A+N16Y+Q345R,G149A+N16Y+Q365S,G149A+N16Y+R320K,G149A+N16Y+R458K,G149A
+N16Y+S323T,G149A+N16Y+V206L,G149A+N16Y+Y295F,G149A+N195F+N54S,G149A+N19
5F+Q169E,G149A+N195F+Q169E,G149A+N195F+Q172K,G149A+N195F+Q299Y,G149A+N1
95F+Q345R,G149A+N195F+Q365S,G149A+N195F+R320K,G149A+N195F+R458K,G149A+N
195F+S323T,G149A+N195F+V206L,G149A+N195F+Y295F,G149A+N54S+Q169E,G149A+N5
4S+Q169E,G149A+N54S+Q172K,G149A+N54S+Q299Y,G149A+N54S+Q345R,G149A+N54S
+Q365S,G149A+N54S+R320K,G149A+N54S+R458K,G149A+N54S+S323T,G149A+N54S+V2
06L,G149A+N54S+Y295F,G149A+Q169E+Q169E,G149A+Q169E+Q172K,G149A+Q169E+Q2
99Y,G149A+Q169E+Q345R,G149A+Q169E+Q365S,G149A+Q169E+R320K,G149A+Q169E+
R458K,G149A+Q169E+S323T,G149A+Q169E+V206L,G149A+Q169E+Y295F,G149A+Q169E
+Q172K,G149A+Q169E+Q299Y,G149A+Q169E+Q345R,G149A+Q169E+Q365S,G149A+Q16
9E+R320K,G149A+Q169E+R458K,G149A+Q169E+S323T,G149A+Q169E+V206L,G149A+Q1
69E+Y295F,G149A+Q172K+Q299Y,G149A+Q172K+Q345R,G149A+Q172K+Q365S,G149A+Q
172K+R320K,G149A+Q172K+R458K,G149A+Q172K+S323T,G149A+Q172K+V206L,G149A+
Q172K+Y295F,G149A+Q299Y+Q345R,G149A+Q299Y+Q365S,G149A+Q299Y+R320K,G149A
+Q299Y+R458K,G149A+Q299Y+S323T,G149A+Q299Y+V206L,G149A+Q299Y+Y295F,G149
A+Q345R+Q365S,G149A+Q345R+R320K,G149A+Q345R+R458K,G149A+Q345R+S323T,
G149A+Q345R+V206L,G149A+Q345R+Y295F,G149A+Q365S+R320K,G149A+Q365S+R458K
,G149A+Q365S+S323T,G149A+Q365S+V206L,G149A+Q365S+Y295F,G149A+R320K+R458K
,G149A+R320K+S323T,G149A+R320K+V206L,G149A+R320K+Y295F,G149A+R458K+S323T,
G149A+R458K+V206L, G149A+R458K+Y295F,G149A+S323T+V206L, G149A+S323T+Y295F,
G149A+V206L+Y295F,G182T+H1*+I9M,G182T+H1*+K391A,G182T+H1*+M202L,G182T+H1*
+N16Y,G182T+H1*+N195F,G182T+H1*+N54S,G182T+H1*+Q169E,G182T+H1*+Q169E,G182
T+H1*+Q172K,G182T+H1*+Q299Y,G182T+H1*+Q345R,G182T+H1*+Q365S,G182T+H1*+R32
0K,G182T+H1*+R458K,G182T+H1*+S323T,G182T+H1*+V206L,G182T+H1*+Y295F,G182T+I9
M+K391A,G182T+I9M+M202L,G182T+I9M+N16Y,G182T+I9M+N195F,G182T+I9M+N54S,G18
2T+I9M+Q169E,G182T+I9M+Q169E,G182T+I9M+Q172K,G182T+I9M+Q299Y,G182T+I9M+Q3
45R,G182T+I9M+Q365S,G182T+I9M+R320K,G182T+I9M+R458K,G182T+I9M+S323T,G182T
+I9M+V206L,G182T+I9M+Y295F,G182T+K391A+M202L,G182T+K391A+N16Y,G182T+K391A
+N195F,G182T+K391A+N54S,G182T+K391A+Q169E,G182T+K391A+Q169E,G182T+K391A+

24 Mar 2026
2026202266

Q172K,G182T+K391A+Q299Y,G182T+K391A+Q345R,G182T+K391A+Q365S,G182T+K391A+R320K,G182T+K391A+R458K,G182T+K391A+S323T,G182T+K391A+V206L,G182T+K391A+Y295F,G182T+M202L+N16Y,G182T+M202L+N195F,G182T+M202L+N54S,G182T+M202L+Q169E,G182T+M202L+Q169E,G182T+M202L+Q172K,G182T+M202L+Q299Y,G182T+M202L+Q345R,G182T+M202L+Q365S,G182T+M202L+R320K,G182T+M202L+R458K,G182T+M202L+S323T,G182T+M202L+V206L,G182T+M202L+Y295F,G182T+N16Y+N195F,G182T+N16Y+N54S,G182T+N16Y+Q169E,G182T+N16Y+Q169E,G182T+N16Y+Q172K,G182T+N16Y+Q299Y,G182T+N16Y+Q345R,G182T+N16Y+Q365S,G182T+N16Y+R320K,G182T+N16Y+R458K,G182T+N16Y+S323T,G182T+N16Y+V206L,G182T+N16Y+Y295F,G182T+N195F+N54S,G182T+N195F+Q169E,G182T+N195F+Q169E,G182T+N195F+Q172K,G182T+N195F+Q299Y,G182T+N195F+Q345R,G182T+N195F+Q365S,G182T+N195F+R320K,G182T+N195F+R458K,G182T+N195F+S323T,G182T+N195F+V206L,G182T+N195F+Y295F,G182T+N54S+Q169E,G182T+N54S+Q169E,G182T+N54S+Q172K,G182T+N54S+Q299Y,G182T+N54S+Q345R,G182T+N54S+Q365S,G182T+N54S+R320K,G182T+N54S+R458K,G182T+N54S+S323T,G182T+N54S+V206L,G182T+N54S+Y295F,G182T+Q169E+Q169E,G182T+Q169E+Q172K,G182T+Q169E+Q299Y,G182T+Q169E+Q345R,G182T+Q169E+Q365S,G182T+Q169E+R320K,G182T+Q169E+R458K,G182T+Q169E+S323T,G182T+Q169E+V206L,G182T+Q169E+Q172K,G182T+Q169E+Q299Y,G182T+Q169E+Q345R,G182T+Q169E+Q365S,G182T+Q169E+R320K,G182T+Q169E+R458K,G182T+Q169E+S323T,G182T+Q169E+V206L,G182T+Q169E+Y295F,G182T+Q172K+Q299Y,G182T+Q172K+Q345R,G182T+Q172K+Q365S,G182T+Q172K+R320K,G182T+Q172K+R458K,G182T+Q172K+S323T,G182T+Q172K+V206L,G182T+Q172K+Y295F,G182T+Q299Y+Q345R,G182T+Q299Y+Q365S,G182T+Q299Y+R320K,G182T+Q299Y+R458K,G182T+Q299Y+S323T,G182T+Q299Y+V206L,G182T+Q299Y+Y295F,G182T+Q345R+Q365S,G182T+Q345R+R320K,G182T+Q345R+R458K,G182T+Q345R+S323T,G182T+Q345R+V206L,G182T+Q345R+Y295F,G182T+Q365S+R320K,G182T+Q365S+R458K,G182T+Q365S+S323T,G182T+Q365S+V206L,G182T+Q365S+Y295F,G182T+R320K+R458K,G182T+R320K+S323T,G182T+R320K+V206L,G182T+R320K+Y295F,G182T+R458K+S323T,G182T+R458K+V206L,G182T+R458K+Y295F,G182T+S323T+V206L,G182T+S323T+Y295F,G182T+V206L+Y295F,H1*+I9M+K391A,H1*+I9M+M202L,H1*+I9M+N16Y,H1*+I9M+N195F,H1*+I9M+N54S,H1*+I9M+Q169E,H1*+I9M+Q169E,H1*+I9M+Q172K,H1*+I9M+Q299Y,H1*+I9M+Q345R,H1*+I9M+Q365S,H1*+I9M+R320K,H1*+I9M+R458K,H1*+I9M+S323T,H1*+I9M+V206L,H1*+I9M+Y295F,H1*+K391A+M202L,H1*+K391A+N16Y,H1*+K391A+N195F,H1*+K391A+N54S,H1*+K391A+Q169E,H1*+K391A+Q169E,H1*+K391A+Q172K,H1*+K391A+Q299Y,H1*+K391A+Q345R,H1*+K391A+Q365S,H1*+K391A+R320K,H1*+K391A+R458K,H1*+K391A+S323T,H1*+K391A+V206L,H1*+K391A+Y295F,H1*+M202L+N16Y,H1*+M202L+N195F,H1*+M202L+N54S,H1*+M202L+Q169E,H1*+M202L+Q169E,H1*+M202L+Q172K,H1*+M202L+Q299Y,H1*+M202L+Q345

24 Mar 2026
2026202266

R,H1*+M202L+Q365S,H1*+M202L+R320K,H1*+M202L+R458K,H1*+M202L+S323T,H1*+M20
2L+V206L,H1*+M202L+Y295F,H1*+N16Y+N195F,H1*+N16Y+N54S,H1*+N16Y+Q169E,H1*+N
16Y+Q169E,H1*+N16Y+Q172K,H1*+N16Y+Q299Y,H1*+N16Y+Q345R,H1*+N16Y+Q365S,H1*
+N16Y+R320K, H1*+N16Y+R458K,H1*+N16Y+S323T, H1*+N16Y+V206L, H1*+N16Y+Y295F,
H1*+N195F+N54S,H1*+N195F+Q169E,H1*+N195F+Q169E,H1*+N195F+Q172K,H1*+N195F+
Q299Y,H1*+N195F+Q345R,H1*+N195F+Q365S,H1*+N195F+R320K,H1*+N195F+R458K,H1*+
N195F+S323T,H1*+N195F+V206L,H1*+N195F+Y295F,H1*+N54S+Q169E,H1*+N54S+Q169E,
H1*+N54S+Q172K,H1*+N54S+Q299Y,H1*+N54S+Q345R,H1*+N54S+Q365S,H1*+N54S+R32
0K,H1*+N54S+R458K,H1*+N54S+S323T,H1*+N54S+V206L,H1*+N54S+Y295F,H1*+Q169E+
Q169E,H1*+Q169E+Q172K,H1*+Q169E+Q299Y,H1*+Q169E+Q345R,H1*+Q169E+Q365S,
H1*+Q169E+R320K,H1*+Q169E+R458K,H1*+Q169E+S323T,H1*+Q169E+V206L,H1*+Q169E
+Y295F,H1*+Q169E+Q172K, H1*+Q169E+Q299Y,H1*+Q169E+Q345R, H1*+Q169E+Q365S,
H1*+Q169E+R320K,H1*+Q169E+R458K,H1*+Q169E+S323T,H1*+Q169E+V206L,H1*+Q169E
+Y295F, H1*+Q172K+Q299Y, H1*+Q172K+Q345R, H1*+Q172K+Q365S, H1*+Q172K+R320K,
H1*+Q172K+R458K,H1*+Q172K+S323T,H1*+Q172K+V206L,H1*+Q172K+Y295F,H1*+Q299Y
+Q345R,H1*+Q299Y+Q365S,H1*+Q299Y+R320K,H1*+Q299Y+R458K, H1*+Q299Y+S323T,
H1*+Q299Y+V206L,H1*+Q299Y+Y295F,H1*+Q345R+Q365S,H1*+Q345R+R320K,H1*+Q345R
+R458K,H1*+Q345R+S323T,H1*+Q345R+V206L,H1*+Q345R+Y295F,H1*+Q365S+R320K,
H1*+Q365S+R458K,H1*+Q365S+S323T,H1*+Q365S+V206L,H1*+Q365S+Y295F,H1*+R320K
+R458K, H1*+R320K+S323T, H1*+R320K+V206L, H1*+R320K+Y295F,H1*+R458K+S323T,
H1*+R458K+V206L,H1*+R458K+Y295F,H1*+S323T+V206L,H1*+S323T+Y295F,H1*+V206L+
Y295F,I9M+K391A+M202L,I9M+K391A+N16Y,I9M+K391A+N195F,I9M+K391A+N54S,I9M+K3
91A+Q169E,I9M+K391A+Q169E,I9M+K391A+Q172K,I9M+K391A+Q299Y,
I9M+K391A+Q345R,I9M+K391A+Q365S,I9M+K391A+R320K,I9M+K391A+R458K,I9M+K391A
+S323T,I9M+K391A+V206L,I9M+K391A+Y295F,I9M+M202L+N16Y,I9M+M202L+N195F,I9M+
M202L+N54S,I9M+M202L+Q169E,I9M+M202L+Q169E,I9M+M202L+Q172K,I9M+M202L+Q29
9Y,I9M+M202L+Q345R,I9M+M202L+Q365S,I9M+M202L+R320K,I9M+M202L+R458K,I9M+M2
02L+S323T,I9M+M202L+V206L,I9M+M202L+Y295F,I9M+N16Y+N195F,I9M+N16Y+N54S,I9M
+N16Y+Q169E,I9M+N16Y+Q169E,I9M+N16Y+Q172K,I9M+N16Y+Q299Y,I9M+N16Y+Q345R,I
9M+N16Y+Q365S,I9M+N16Y+R320K,I9M+N16Y+R458K,I9M+N16Y+S323T,I9M+N16Y+V206
L,I9M+N16Y+Y295F,I9M+N195F+N54S,I9M+N195F+Q169E,I9M+N195F+Q169E,I9M+N195F+
Q172K,I9M+N195F+Q299Y,I9M+N195F+Q345R,I9M+N195F+Q365S,I9M+N195F+R320K,I9M
+N195F+R458K,I9M+N195F+S323T,I9M+N195F+V206L,I9M+N195F+Y295F,I9M+N54S+Q169
E,I9M+N54S+Q169E,I9M+N54S+Q172K,I9M+N54S+Q299Y,I9M+N54S+Q345R,I9M+N54S+Q
365S,I9M+N54S+R320K,I9M+N54S+R458K,I9M+N54S+S323T,I9M+N54S+V206L,I9M+N54S+
Y295F, I9M+Q169E+Q169E, I9M+Q169E+Q172K, I9M+Q169E+Q299Y, I9M+Q169E+Q345R,

24 Mar 2026
2026202266

I9M+Q169E+Q365S, I9M+Q169E+R320K, I9M+Q169E+R458K, I9M+Q169E+S323T, I9M+Q169E+V206L, I9M+Q169E+Y295F, I9M+Q169E+Q172K, I9M+Q169E+Q299Y, I9M+Q169E+Q345R, I9M+Q169E+Q365S, I9M+Q169E+R320K, I9M+Q169E+R458K, I9M+Q169E+S323T, I9M+Q169E+V206L, I9M+Q169E+Y295F, I9M+Q172K+Q299Y, I9M+Q172K+Q345R, I9M+Q172K+Q365S, I9M+Q172K+R320K, I9M+Q172K+R458K, I9M+Q172K+S323T, I9M+Q172K+V206L, I9M+Q172K+Y295F, I9M+Q299Y+Q345R, I9M+Q299Y+Q365S, I9M+Q299Y+R320K, I9M+Q299Y+R458K, I9M+Q299Y+S323T, I9M+Q299Y+V206L, I9M+Q299Y+Y295F, I9M+Q345R+Q365S, I9M+Q345R+R320K, I9M+Q345R+R458K, I9M+Q345R+S323T, I9M+Q345R+V206L, I9M+Q345R+Y295F, I9M+Q365S+R320K, I9M+Q365S+R458K, I9M+Q365S+S323T, I9M+Q365S+V206L, I9M+Q365S+Y295F, I9M+R320K+R458K, I9M+R320K+S323T, I9M+R320K+V206L, I9M+R320K+Y295F, I9M+R458K+S323T, I9M+R458K+V206L, I9M+R458K+Y295F, I9M+S323T+V206L, I9M+S323T+Y295F, I9M+V206L+Y295F, K391A+M202L+N16Y, K391A+M202L+N195F, K391A+M202L+N54S, K391A+M202L+Q169E, K391A+M202L+Q169E, K391A+M202L+Q172K, K391A+M202L+Q299Y, K391A+M202L+Q345R, K391A+M202L+Q365S, K391A+M202L+R320K, K391A+M202L+R458K, K391A+M202L+S323T, K391A+M202L+V206L, K391A+M202L+Y295F, K391A+N16Y+N195F, K391A+N16Y+N54S, K391A+N16Y+Q169E, K391A+N16Y+Q169E, K391A+N16Y+Q172K, K391A+N16Y+Q299Y, K391A+N16Y+Q345R, K391A+N16Y+Q365S, K391A+N16Y+R320K, K391A+N16Y+R458K, K391A+N16Y+S323T, K391A+N16Y+V206L, K391A+N16Y+Y295F, K391A+N195F+N54S, K391A+N195F+Q169E, K391A+N195F+Q169E, K391A+N195F+Q172K, K391A+N195F+Q299Y, K391A+N195F+Q345R, K391A+N195F+Q365S, K391A+N195F+R320K, K391A+N195F+R458K, K391A+N195F+S323T, K391A+N195F+V206L, K391A+N195F+Y295F, K391A+N54S+Q169E, K391A+N54S+Q169E, K391A+N54S+Q172K, K391A+N54S+Q299Y, K391A+N54S+Q345R, K391A+N54S+Q365S, K391A+N54S+R320K, K391A+N54S+R458K, K391A+N54S+S323T, K391A+N54S+V206L, K391A+N54S+Y295F, K391A+Q169E+Q169E,K391A+Q169E+Q172K,K391A+Q169E+Q299Y,K391A+Q169E+Q345R ,K391A+Q169E+Q365S,K391A+Q169E+R320K,K391A+Q169E+R458K,K391A+Q169E+S323T ,K391A+Q169E+V206L,K391A+Q169E+Y295F,K391A+Q169E+Q172K,K391A+Q169E+Q299Y ,K391A+Q169E+Q345R,K391A+Q169E+Q365S,K391A+Q169E+R320K,K391A+Q169E+R458 K,K391A+Q169E+S323T,K391A+Q169E+V206L,K391A+Q169E+Y295F,K391A+Q172K+Q299 Y,K391A+Q172K+Q345R,K391A+Q172K+Q365S,K391A+Q172K+R320K,K391A+Q172K+R45 8K,K391A+Q172K+S323T,K391A+Q172K+V206L,K391A+Q172K+Y295F,K391A+Q299Y+Q34 5R,K391A+Q299Y+Q365S,K391A+Q299Y+R320K,K391A+Q299Y+R458K,K391A+Q299Y+S3 23T,K391A+Q299Y+V206L,K391A+Q299Y+Y295F,K391A+Q345R+Q365S,K391A+Q345R+R3 20K,K391A+Q345R+R458K,K391A+Q345R+S323T,K391A+Q345R+V206L,K391A+Q345R+Y2

24 Mar 2026
2026202266

95F,K391A+Q365S+R320K,K391A+Q365S+R458K,K391A+Q365S+S323T,K391A+Q365S+V206L,K391A+Q365S+Y295F,K391A+R320K+R458K,K391A+R320K+S323T,K391A+R320K+V206L,K391A+R320K+Y295F,K391A+R458K+S323T,K391A+R458K+V206L,K391A+R458K+Y295F,K391A+S323T+V206L,K391A+S323T+Y295F,K391A+V206L+Y295F,M202L+N16Y+N195F,M202L+N16Y+N54S,M202L+N16Y+Q169E,M202L+N16Y+Q169E,M202L+N16Y+Q172K,M202L+N16Y+Q299Y,M202L+N16Y+Q345RM202L+N16Y+Q365S,M202L+N16Y+R320K,M202L+N16Y+R458K,M202L+N16Y+S323T,M202L+N16Y+V206L,M202L+N16Y+Y295F,M202L+N195F+N54S,M202L+N195F+Q169E,M202L+N195F+Q169E,M202L+N195F+Q172K,M202L+N195F+Q299Y,M202L+N195F+Q345R,M202L+N195F+Q365S,M202L+N195F+R320K,M202L+N195F+R458K,M202L+N195F+S323T,M202L+N195F+V206L,M202L+N195F+Y295F,M202L+N54S+Q169E,M202L+N54S+Q169E,M202L+N54S+Q172K,M202L+N54S+Q299Y,M202L+N54S+Q345R,M202L+N54S+Q365S,M202L+N54S+R320K,M202L+N54S+R458K,M202L+N54S+S323T,M202L+N54S+V206L,M202L+N54S+Y295F,M202L+Q169E+Q169E,M202L+Q169E+Q172K,M202L+Q169E+Q299Y,M202L+Q169E+Q345R,M202L+Q169E+Q365S,M202L+Q169E+R320K,M202L+Q169E+R458K,M202L+Q169E+S323T,M202L+Q169E+V206L,M202L+Q169E+Y295F,M202L+Q172K+Q299Y,M202L+Q172K+Q345R,M202L+Q172K+Q365S,M202L+Q172K+R320K,M202L+Q172K+R458K,M202L+Q172K+S323T,M202L+Q172K+V206L,M202L+Q172K+Y295F,M202L+Q299Y+Q345R,M202L+Q299Y+Q365S,M202L+Q299Y+R320K,M202L+Q299Y+R458K,M202L+Q299Y+S323T,M202L+Q299Y+V206L,M202L+Q299Y+Y295F,M202L+Q345R+Q365S,M202L+Q345R+R320K,M202L+Q345R+R458K,M202L+Q345R+S323T,M202L+Q345R+V206L,M202L+Q345R+Y295F,M202L+Q365S+R320K,M202L+Q365S+R458K,M202L+Q365S+S323T,M202L+Q365S+V206L,M202L+Q365S+Y295F,M202L+R320K+R458K,M202L+R320K+S323T,M202L+R320K+V206L,M202L+R320K+Y295F,M202L+R458K+S323T,M202L+R458K+V206L,M202L+R458K+Y295F,M202L+S323T+V206L,M202L+S323T+Y295F,M202L+V206L+Y295F,N16Y+N195F+N54S,N16Y+N195F+Q169E,N16Y+N195F+Q169E,N16Y+N195F+Q172K,N16Y+N195F+Q299Y,N16Y+N195F+Q345R,N16Y+N195F+Q365S,N16Y+N195F+R320K,N16Y+N195F+R458K,N16Y+N195F+S323T,N16Y+N195F+V206L,N16Y+N195F+Y295F,N16Y+N54S+Q169E,N16Y+N54S+Q169E,N16Y+N54S+Q172K,N16Y+N54S+Q299Y,N16Y+N54S+Q345R,N16Y+N54S+Q365S,N16Y+N54S+R320K,N16Y+N54S+R458K,N16Y+N54S+S323T,N16Y+N54S+V206L,N16Y+N54S+Y295F,N16Y+Q169E+Q169E,N16Y+Q169E+Q172K,N16Y+Q169E+Q299Y,N16Y+Q169E+Q345R,N16Y+Q169E+Q365S,N16Y+Q169E+R320K,N16Y+Q169E+R458K,N16Y+Q169E+S323T,N16Y+Q169E+V206L,N16Y+Q169E+Y295F,N16Y+Q169E+Q172K,N16Y+Q169E+Q299Y,N16Y+Q169E+Q345R,N16Y+Q169E+Q365S,N16Y+Q169E+R320K,N16Y+Q169E+R458K,N16Y+Q169E+S323T,N16Y+Q169E+V206L,N16Y+Q1

24 Mar 2026
2026202266

69E+Y295F,N16Y+Q172K+Q299Y,N16Y+Q172K+Q345R,N16Y+Q172K+Q365S,N16Y+Q172K
+R320K,N16Y+Q172K+R458K,N16Y+Q172K+S323T,N16Y+Q172K+V206L,N16Y+Q172K+Y2
95F,N16Y+Q299Y+Q345R,N16Y+Q299Y+Q365S,N16Y+Q299Y+R320K,N16Y+Q299Y+R458K
,N16Y+Q299Y+S323T,N16Y+Q299Y+V206L,N16Y+Q299Y+Y295F,N16Y+Q345R+Q365S,N16
Y+Q345R+R320K,N16Y+Q345R+R458K,N16Y+Q345R+S323T,N16Y+Q345R+V206L,N16Y+Q
345R+Y295F,N16Y+Q365S+R320K,N16Y+Q365S+R458K,N16Y+Q365S+S323T,N16Y+Q365
S+V206L,N16Y+Q365S+Y295F,N16Y+R320K+R458K,N16Y+R320K+S323T,N16Y+R320K+V2
06L,N16Y+R320K+Y295F,N16Y+R458K+S323T,N16Y+R458K+V206L,N16Y+R458K+Y295F,N
16Y+S323T+V206L,N16Y+S323T+Y295F,N16Y+V206L+Y295F,N195F+N54S+Q169E,N195F+
N54S+Q169E,N195F+N54S+Q172K,N195F+N54S+Q299Y,N195F+N54S+Q345R,N195F+N54
S+Q365S,N195F+N54S+R320K,N195F+N54S+R458K,N195F+N54S+S323T,N195F+N54S+V2
06L,N195F+N54S+Y295F,N195F+Q169E+Q169E,N195F+Q169E+Q172K,N195F+Q169E+Q29
9Y,N195F+Q169E+Q345R,N195F+Q169E+Q365S,N195F+Q169E+R320K,N195F+Q169E+R4
58K,N195F+Q169E+S323T,N195F+Q169E+V206L,N195F+Q169E+Y295F,N195F+Q169E+Q1
72K,N195F+Q169E+Q299Y,N195F+Q169E+Q345R,N195F+Q169E+Q365S,N195F+Q169E+R
320K,N195F+Q169E+R458K,N195F+Q169E+S323T,N195F+Q169E+V206L,N195F+Q169E+Y
295F,N195F+Q172K+Q299Y,N195F+Q172K+Q345R,N195F+Q172K+Q365S,N195F+Q172K+
R320K,N195F+Q172K+R458K,N195F+Q172K+S323T,N195F+Q172K+V206L,N195F+Q172K+
Y295F,N195F+Q299Y+Q345R,N195F+Q299Y+Q365S,N195F+Q299Y+R320K,N195F+Q299Y
+R458K,N195F+Q299Y+S323T,N195F+Q299Y+V206L,N195F+Q299Y+Y295F,N195F+Q345R
+Q365S,N195F+Q345R+R320K,N195F+Q345R+R458K,N195F+Q345R+S323T,N195F+Q345
R+V206L,N195F+Q345R+Y295F,N195F+Q365S+R320K,N195F+Q365S+R458K,N195F+Q365
S+S323T,N195F+Q365S+V206LN195F+Q365S+Y295F,N195F+R320K+R458K,N195F+R320K
+S323T,N195F+R320K+V206L,N195F+R320K+Y295F,N195F+R458K+S323T,N195F+R458K+
V206L,N195F+R458K+Y295F,N195F+S323T+V206L,N195F+S323T+Y295F,N195F+V206L+Y
295F,N54S+Q169E+Q169E,N54S+Q169E+Q172K,N54S+Q169E+Q299Y,N54S+Q169E+Q345
R,N54S+Q169E+Q365S,N54S+Q169E+R320K,N54S+Q169E+R458K,N54S+Q169E+S323T,N
54S+Q169E+V206L,N54S+Q169E+Y295F,N54S+Q169E+Q172K,N54S+Q169E+Q299Y,N54S
+Q169E+Q345R,N54S+Q169E+Q365S,N54S+Q169E+R320K,N54S+Q169E+R458K,N54S+Q
169E+S323T,N54S+Q169E+V206L,N54S+Q169E+Y295F,N54S+Q172K+Q299Y,N54S+Q172K
+Q345R,N54S+Q172K+Q365S,N54S+Q172K+R320K,N54S+Q172K+R458K,N54S+Q172K+S3
23T,N54S+Q172K+V206L,N54S+Q172K+Y295F,N54S+Q299Y+Q345R,N54S+Q299Y+Q365S,
N54S+Q299Y+R320K,N54S+Q299Y+R458K,N54S+Q299Y+S323T,N54S+Q299Y+V206L,N54
S+Q299Y+Y295F,N54S+Q345R+Q365S,N54S+Q345R+R320K,N54S+Q345R+R458K,N54S+
Q345R+S323T,N54S+Q345R+V206L,N54S+Q345R+Y295F,N54S+Q365S+R320K,N54S+Q36
5S+R458K,N54S+Q365S+S323T,N54S+Q365S+V206L,N54S+Q365S+Y295F,N54S+R320K+

24 Mar 2026
2026202266

R458K,N54S+R320K+S323T,N54S+R320K+V206L,N54S+R320K+Y295F,N54S+R458K+S323T,N54S+R458K+V206L,N54S+R458K+Y295F,N54S+S323T+V206L,N54S+S323T+Y295F,N54S+V206L+Y295F,Q169E+Q169E+Q172K,Q169E+Q169E+Q299Y,Q169E+Q169E+Q345R,Q169E+Q169E+Q365S,Q169E+Q169E+R320K,Q169E+Q169E+R458K,Q169E+Q169E+S323T,Q169E+Q169E+V206L,Q169E+Q169E+Y295F,Q169E+Q172K+Q299Y,Q169E+Q172K+Q345R,Q169E+Q172K+Q365S,Q169E+Q172K+R320K,Q169E+Q172K+R458K,Q169E+Q172K+S323T,Q169E+Q172K+V206L,Q169E+Q172K+Y295F,Q169E+Q299Y+Q345R,Q169E+Q299Y+Q365S,Q169E+Q299Y+R320K,Q169E+Q299Y+R458K,Q169E+Q299Y+S323T,Q169E+Q299Y+V206L,Q169E+Q299Y+Y295F,Q169E+Q345R+Q365S,Q169E+Q345R+R320K,Q169E+Q345R+R458K,Q169E+Q345R+S323T,Q169E+Q345R+V206L,Q169E+Q345R+Y295F,Q169E+Q365S+R320K,Q169E+Q365S+R458K,Q169E+Q365S+S323T,Q169E+Q365S+V206L,Q169E+Q365S+Y295F,Q169E+R320K+R458K,Q169E+R320K+S323T,Q169E+R320K+V206L,Q169E+R320K+Y295F,Q169E+R458K+S323T,Q169E+R458K+V206L,Q169E+R458K+Y295F,Q169E+S323T+V206L,Q169E+S323T+Y295F,Q169E+V206L+Y295F,Q169E+Q172K+Q299Y,Q169E+Q172K+Q345R,Q169E+Q172K+Q365S,Q169E+Q172K+R320K,Q169E+Q172K+R458K,Q169E+Q172K+S323T,Q169E+Q172K+V206L,Q169E+Q172K+Y295F,Q169E+Q299Y+Q345R,Q169E+Q299Y+Q365S,Q169E+Q299Y+R320K,Q169E+Q299Y+R458K,Q169E+Q299Y+S323T,Q169E+Q299Y+V206L,Q169E+Q299Y+Y295F,Q169E+Q345R+Q365S,Q169E+Q345R+R320K,Q169E+Q345R+R458K,Q169E+Q345R+S323T,Q169E+Q345R+V206L,Q169E+Q345R+Y295F,Q169E+Q365S+R320K,Q169E+Q365S+R458K,Q169E+Q365S+S323T,Q169E+Q365S+V206L,Q169E+Q365S+Y295F,Q169E+R320K+R458K,Q169E+R320K+S323T,Q169E+R320K+V206L,Q169E+R320K+Y295F,Q169E+R458K+S323T,Q169E+R458K+V206L,Q169E+R458K+Y295F,Q169E+S323T+V206L,Q169E+S323T+Y295F,Q169E+V206L+Y295F,Q172K+Q299Y+Q345R,Q172K+Q299Y+Q365S,Q172K+Q299Y+R320K,Q172K+Q299Y+R458K,Q172K+Q299Y+S323T,Q172K+Q299Y+V206L,Q172K+Q299Y+Y295F,Q172K+Q345R+Q365S,Q172K+Q345R+R320K,Q172K+Q345R+R458K,Q172K+Q345R+S323T,Q172K+Q345R+V206L,Q172K+Q345R+Y295F,Q172K+Q365S+R320K,Q172K+Q365S+R458K,Q172K+Q365S+S323T,Q172K+Q365S+V206L,Q172K+Q365S+Y295F,Q172K+R320K+R458K,Q172K+R320K+S323T,Q172K+R320K+V206L,Q172K+R320K+Y295F,Q172K+R458K+S323T,Q172K+R458K+V206L,Q172K+R458K+Y295F,Q172K+S323T+V206L,Q172K+S323T+Y295F,Q172K+V206L+Y295F,Q299Y+Q345R+Q365S,Q299Y+Q345R+R320K,Q299Y+Q345R+R458K,Q299Y+Q345R+S323T,Q299Y+Q345R+V206L,Q299Y+Q345R+Y295F,Q299Y+Q365S+R320K,Q299Y+Q365S+R458K,Q299Y+Q365S+S323T,Q299Y+Q365S+V206L,Q299Y+Q365S+Y295F,Q299Y+R320K+R458K,Q299Y+R320K+S323T,Q299Y+R320K+V206L,Q299Y+R320K+Y295F,Q299Y+R458K+S323T,Q299Y+R458K+V206L,Q299Y+R458K+Y295F,Q299Y+S323T+V206L,Q299Y+S323T+Y295F,Q299Y+V206L+Y295F,Q345R+Q365S+R320K,Q345R+Q365S+R458K,Q345R+Q365S+S323T,Q345R+Q365S+V206

24 Mar 2026
2026202266

L,Q345R+Q365S+Y295F,Q345R+R320K+R458K,Q345R+R320K+S323T,Q345R+R320K+V206L,Q345R+R320K+Y295F,Q345R+R458K+S323T,Q345R+R458K+V206L,Q345R+R458K+Y295F,Q345R+S323T+V206L,Q345R+S323T+Y295F,Q345R+V206L+Y295F,Q365S+R320K+R458K,Q365S+R320K+S323T,Q365S+R320K+V206L,Q365S+R320K+Y295F,Q365S+R458K+S323T,Q365S+R458K+V206L,Q365S+R458K+Y295F,Q365S+S323T+V206L,Q365S+S323T+Y295F,Q365S+V206L+Y295F,R320K+R458K+S323T,R320K+R458K+V206L,R320K+R458K+Y295F,R320K+S323T+V206L, R320K+S323T+Y295F, R320K+V206L+Y295F, R458K+S323T+V206L, R458K+S323T+Y295F, R458K+V206L+Y295F, S323T+V206L+Y295F, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID Nos; 1-17. In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions:

A174*+A339S+G109A+G149A,A174*+A339S+G109A+G182T,A174*+A339S+G109A+H1*,A174*+A339S+G109A+I9M,A174*+A339S+G109A+K391A,A174*+A339S+G109A+M202L,A174*+A339S+G109A+N16Y,A174*+A339S+G109A+N195F,A174*+A339S+G109A+N54S,A174*+A339S+G109A+Q169E,A174*+A339S+G109A+Q169E,A174*+A339S+G109A+Q172K,A174*+A339S+G109A+Q299Y,A174*+A339S+G109A+Q345R,A174*+A339S+G109A+Q365S,A174*+A339S+G109A+R320K,A174*+A339S+G109A+R458K,A174*+A339S+G109A+S323T,A174*+A339S+G109A+V206L,A174*+A339S+G109A+Y295F,A174*+A339S+G149A+G182T,A174*+A339S+G149A+H1*,A174*+A339S+G149A+I9M,A174*+A339S+G149A+K391A,A174*+A339S+G149A+M202L,A174*+A339S+G149A+N16Y,A174*+A339S+G149A+N195F,A174*+A339S+G149A+N54S,A174*+A339S+G149A+Q169E,A174*+A339S+G149A+Q169E,A174*+A339S+G149A+Q172K,A174*+A339S+G149A+Q299Y,A174*+A339S+G149A+Q345R,A174*+A339S+G149A+Q365S,A174*+A339S+G149A+R320K,A174*+A339S+G149A+R458K,A174*+A339S+G149A+S323T,A174*+A339S+G149A+V206L,A174*+A339S+G149A+Y295F,A174*+A339S+G182T+H1*,A174*+A339S+G182T+I9M,A174*+A339S+G182T+K391A,A174*+A339S+G182T+M202L,A174*+A339S+G182T+N16Y,A174*+A339S+G182T+N195F,A174*+A339S+G182T+N54S,A174*+A339S+G182T+Q169E,A174*+A339S+G182T+Q169E,A174*+A339S+G182T+Q172K,A174*+A339S+G182T+Q299Y,A174*+A339S+G182T+Q345R,A174*+A339S+G182T+Q365S,A174*+A339S+G182T+R320K,A174*+A339S+G182T+R458K,A174*+A339S+G182T+S323T,A174*+A339S+G182T+V206L,A174*+A339S+G182T+Y295F,A174*+A339S+H1*+I9M,A174*+A339S+H1*+K391A,A174*+A339S+H1*+M202L,A174*+A339S+H1*+N16Y,A174*+A339S+H1*+N195F,A174*+A339S+H1*+N54S,A174*+A339S+H1*+Q169E,A174*+A339S+H1*+Q169E,A174*+A339S+H1*+Q172K,A174*+A339S+H1*+Q299Y,A174*+A339S+H1*+Q345R,A174*+A339S+H1*+Q365S,A174*+A339S+H1*+R320K,A174*+A339S+H1*+R458K,A174*+A339S+H1*+S323T,A174*+A339

24 Mar 2026
2026202266

S+H1*+V206L,A174*+A339S+H1*+Y295F,A174*+A339S+I9M+K391A,A174*+A339S+I9M+M2
02L,A174*+A339S+I9M+N16Y,A174*+A339S+I9M+N195F,A174*+A339S+I9M+N54S,A174*+A
339S+I9M+Q169E,A174*+A339S+I9M+Q169E,A174*+A339S+I9M+Q172K,A174*+A339S+I9M
+Q299Y,A174*+A339S+I9M+Q345R,A174*+A339S+I9M+Q365S,A174*+A339S+I9M+R320K,A
174*+A339S+I9M+R458K,A174*+A339S+I9M+S323T,A174*+A339S+I9M+V206L,A174*+A339
S+I9M+Y295F,A174*+A339S+K391A+M202L,A174*+A339S+K391A+N16Y,A174*+A339S+K39
1A+N195F,A174*+A339S+K391A+N54S,A174*+A339S+K391A+Q169E,A174*+A339S+K391A
+Q169E,A174*+A339S+K391A+Q172K,A174*+A339S+K391A+Q299Y,A174*+A339S+K391A+
Q345R,A174*+A339S+K391A+Q365S,A174*+A339S+K391A+R320K,A174*+A339S+K391A+R
458K,A174*+A339S+K391A+S323T,A174*+A339S+K391A+V206L,A174*+A339S+K391A+Y29
5F,A174*+A339S+M202L+N16Y,A174*+A339S+M202L+N195F,A174*+A339S+M202L+N54S,
A174*+A339S+M202L+Q169E,A174*+A339S+M202L+Q169E,A174*+A339S+M202L+Q172K,A
174*+A339S+M202L+Q299Y,A174*+A339S+M202L+Q345R,A174*+A339S+M202L+Q365S,A1
74*+A339S+M202L+R320K,A174*+A339S+M202L+R458K,A174*+A339S+M202L+S323T,A17
4*+A339S+M202L+V206L,A174*+A339S+M202L+Y295F,A174*+A339S+N16Y+N195F,A174*+
A339S+N16Y+N54S,A174*+A339S+N16Y+Q169E,A174*+A339S+N16Y+Q169E,A174*+A339S
+N16Y+Q172K,A174*+A339S+N16Y+Q299Y,A174*+A339S+N16Y+Q345R,A174*+A339S+N1
6Y+Q365S,A174*+A339S+N16Y+R320K,A174*+A339S+N16Y+R458K,A174*+A339S+N16Y+S
323T,A174*+A339S+N16Y+V206L,A174*+A339S+N16Y+Y295F,A174*+A339S+N195F+N54S,
A174*+A339S+N195F+Q169E,A174*+A339S+N195F+Q169E,A174*+A339S+N195F+Q172K,A
174*+A339S+N195F+Q299Y,A174*+A339S+N195F+Q345R,A174*+A339S+N195F+Q365S,A1
74*+A339S+N195F+R320K,A174*+A339S+N195F+R458K,A174*+A339S+N195F+S323T,A174
+A339S+N195F+V206L,A174+A339S+N195F+Y295F,A174*+A339S+N54S+Q169E,A174*+A
339S+N54S+Q169E,A174*+A339S+N54S+Q172K,A174*+A339S+N54S+Q299Y,A174*+A339S
+N54S+Q345R,A174*+A339S+N54S+Q365S,A174*+A339S+N54S+R320K,A174*+A339S+N5
4S+R458K,A174*+A339S+N54S+S323T,A174*+A339S+N54S+V206L,A174*+A339S+N54S+Y
295F,A174*+A339S+Q169E+Q169E,A174*+A339S+Q169E+Q172K,A174*+A339S+Q169E+Q2
99Y,A174*+A339S+Q169E+Q345R,A174*+A339S+Q169E+Q365S,A174*+A339S+Q169E+R32
0K,A174*+A339S+Q169E+R458K,A174*+A339S+Q169E+S323T,A174*+A339S+Q169E+V206
L,A174*+A339S+Q169E+Y295F,A174*+A339S+Q169E+Q172K,A174*+A339S+Q169E+Q299Y
,A174*+A339S+Q169E+Q345R,A174*+A339S+Q169E+Q365S,A174*+A339S+Q169E+R320K,
A174*+A339S+Q169E+R458K,A174*+A339S+Q169E+S323T,A174*+A339S+Q169E+V206L,A
174*+A339S+Q169E+Y295F,A174*+A339S+Q172K+Q299Y,A174*+A339S+Q172K+Q345R,A1
74*+A339S+Q172K+Q365S,A174*+A339S+Q172K+R320K,A174*+A339S+Q172K+R458K,A17
4*+A339S+Q172K+S323T,A174*+A339S+Q172K+V206L,A174*+A339S+Q172K+Y295F,A174*
+A339S+Q299Y+Q345R,A174*+A339S+Q299Y+Q365S,A174*+A339S+Q299Y+R320K,A174*

24 Mar 2026
2026202266

+A339S+Q299Y+R458K,A174*+A339S+Q299Y+S323T,A174*+A339S+Q299Y+V206L,A174*+A339S+Q299Y+Y295F,A174*+A339S+Q345R+Q365S,A174*+A339S+Q345R+R320K,A174*+A339S+Q345R+R458K,A174*+A339S+Q345R+S323T,A174*+A339S+Q345R+V206L,A174*+A339S+Q345R+Y295F,A174*+A339S+Q365S+R320K,A174*+A339S+Q365S+R458K,A174*+A339S+Q365S+S323T,A174*+A339S+Q365S+V206L,A174*+A339S+Q365S+Y295F,A174*+A339S+R320K+R458K,A174*+A339S+R320K+S323T,A174*+A339S+R320K+V206L,A174*+A339S+R320K+Y295F,A174*+A339S+R458K+S323T,A174*+A339S+R458K+V206L,A174*+A339S+R458K+Y295F,A174*+A339S+S323T+V206L,A174*+A339S+S323T+Y295F,A174*+A339S+V206L+Y295F,A174*+G109A+G149A+G182T,A174*+G109A+G149A+H1*,A174*+G109A+G149A+I9M,A174*+G109A+G149A+K391A,A174*+G109A+G149A+M202L,A174*+G109A+G149A+N16Y,A174*+G109A+G149A+N195F,A174*+G109A+G149A+N54S,A174*+G109A+G149A+Q169E,A174*+G109A+G149A+Q169E,A174*+G109A+G149A+Q172K,A174*+G109A+G149A+Q299Y,A174*+G109A+G149A+Q345R,A174*+G109A+G149A+Q365S,A174*+G109A+G149A+R320K,A174*+G109A+G149A+R458K,A174*+G109A+G149A+S323T,A174*+G109A+G149A+V206L,A174*+G109A+G149A+Y295F,A174*+G109A+G182T+H1*,A174*+G109A+G182T+I9M,A174*+G109A+G182T+K391A,A174*+G109A+G182T+M202L,A174*+G109A+G182T+N16Y,A174*+G109A+G182T+N195F,A174*+G109A+G182T+N54S,A174*+G109A+G182T+Q169E,A174*+G109A+G182T+Q169E,A174*+G109A+G182T+Q172K,A174*+G109A+G182T+Q299Y,A174*+G109A+G182T+Q345R,A174*+G109A+G182T+Q365S,A174*+G109A+G182T+R320K,A174*+G109A+G182T+R458K,A174*+G109A+G182T+S323T,A174*+G109A+G182T+V206L,A174*+G109A+G182T+Y295F,A174*+G109A+H1*+I9M,A174*+G109A+H1*+K391A,A174*+G109A+H1*+M202L,A174*+G109A+H1*+N16Y,A174*+G109A+H1*+N195F,A174*+G109A+H1*+N54S,A174*+G109A+H1*+Q169E,A174*+G109A+H1*+Q169E,A174*+G109A+H1*+Q172K,A174*+G109A+H1*+Q299Y,A174*+G109A+H1*+Q345R,A174*+G109A+H1*+Q365S,A174*+G109A+H1*+R320K,A174*+G109A+H1*+R458K,A174*+G109A+H1*+S323T,A174*+G109A+H1*+V206L,A174*+G109A+H1*+Y295F,A174*+G109A+I9M+K391A,A174*+G109A+I9M+M202L,A174*+G109A+I9M+N16Y,A174*+G109A+I9M+N195F,A174*+G109A+I9M+N54S,A174*+G109A+I9M+Q169E,A174*+G109A+I9M+Q169E,A174*+G109A+I9M+Q172K,A174*+G109A+I9M+Q299Y,A174*+G109A+I9M+Q345R,A174*+G109A+I9M+Q365S,A174*+G109A+I9M+R320K,A174*+G109A+I9M+R458K,A174*+G109A+I9M+S323T,A174*+G109A+I9M+V206L,A174*+G109A+I9M+Y295F,A174*+G109A+K391A+M202L,A174*+G109A+K391A+N16Y,A174*+G109A+K391A+N195F,A174*+G109A+K391A+N54S,A174*+G109A+K391A+Q169E,A174*+G109A+K391A+Q169E,A174*+G109A+K391A+Q172K,A174*+G109A+K391A+Q299Y,A174*+G109A+K391A+Q345R,A174*+G109A+K391A+Q365S,A174*+G109A+K391A+R320K,A174*+G109A+K391A+R458K,A174*+G109A+K391A+S323T,A174*+G109A+K391A+V206L,A174*+G109A+K391A+Y295F,A174*+G109A+M202L+N16Y,A174*+G109A+M202L+N195F,A174*+G109A+M202L+N54S,A174*+G109

24 Mar 2026
2026202266

A+M202L+Q169E,A174*+G109A+M202L+Q169E,A174*+G109A+M202L+Q172K,A174*+G109A+M202L+Q299Y,A174*+G109A+M202L+Q345R,A174*+G109A+M202L+Q365S,A174*+G109A+M202L+R320K,A174*+G109A+M202L+R458K,A174*+G109A+M202L+S323T,A174*+G109A+M202L+V206L,A174*+G109A+M202L+Y295F,A174*+G109A+N16Y+N195F,A174*+G109A+N16Y+N54S,A174*+G109A+N16Y+Q169E,A174*+G109A+N16Y+Q169E,A174*+G109A+N16Y+Q172K,A174*+G109A+N16Y+Q299Y,A174*+G109A+N16Y+Q345R,A174*+G109A+N16Y+Q365S,A174*+G109A+N16Y+R320K,A174*+G109A+N16Y+R458K,A174*+G109A+N16Y+S323T,A174*+G109A+N16Y+V206L,A174*+G109A+N16Y+Y295F,A174*+G109A+N195F+N54S,A174*+G109A+N195F+Q169E,A174*+G109A+N195F+Q169E,A174*+G109A+N195F+Q172K,A174*+G109A+N195F+Q299Y,A174*+G109A+N195F+Q345R,A174*+G109A+N195F+Q365S,A174*+G109A+N195F+R320K,A174*+G109A+N195F+R458K,A174*+G109A+N195F+S323T,A174*+G109A+N195F+V206L,A174*+G109A+N195F+Y295F,A174*+G109A+N54S+Q169E,A174*+G109A+N54S+Q169E,A174*+G109A+N54S+Q172K,A174*+G109A+N54S+Q299Y,A174*+G109A+N54S+Q345R,A174*+G109A+N54S+Q365S,A174*+G109A+N54S+R320K,A174*+G109A+N54S+R458K,A174*+G109A+N54S+S323T,A174*+G109A+N54S+V206L,A174*+G109A+N54S+Y295F,A174*+G109A+Q169E+Q169E,A174*+G109A+Q169E+Q172K,A174*+G109A+Q169E+Q299Y,A174*+G109A+Q169E+Q345R,A174*+G109A+Q169E+Q365S,A174*+G109A+Q169E+R320K,A174*+G109A+Q169E+R458K,A174*+G109A+Q169E+S323T,A174*+G109A+Q169E+V206L,A174*+G109A+Q169E+Y295F,A174*+G109A+Q172K+Q299Y,A174*+G109A+Q172K+Q345R,A174*+G109A+Q172K+Q365S,A174*+G109A+Q172K+R320K,A174*+G109A+Q172K+R458K,A174*+G109A+Q172K+S323T,A174*+G109A+Q172K+V206L,A174*+G109A+Q172K+Y295F,A174*+G109A+Q299Y+Q345R,A174*+G109A+Q299Y+Q365S,A174*+G109A+Q299Y+R320K,A174*+G109A+Q299Y+R458K,A174*+G109A+Q299Y+S323T,A174*+G109A+Q299Y+V206L,A174*+G109A+Q299Y+Y295F,A174*+G109A+Q345R+Q365S,A174*+G109A+Q345R+R320K,A174*+G109A+Q345R+R458K,A174*+G109A+Q345R+S323T,A174*+G109A+Q345R+V206L,A174*+G109A+Q345R+Y295F,A174*+G109A+Q365S+R320K,A174*+G109A+Q365S+R458K,A174*+G109A+Q365S+S323T,A174*+G109A+Q365S+V206L,A174*+G109A+Q365S+Y295F,A174*+G109A+R320K+R458K,A174*+G109A+R320K+S323T,A174*+G109A+R320K+V206L,A174*+G109A+R320K+Y295F,A174*+G109A+R458K+S323T,A174*+G109A+R458K+V206L,A174*+G109A+R458K+Y295F,A174*+G109A+S323T+V206L,A174*+G109A+S323T+Y295F,A174*+G109A+V206L+Y295F,A174*+G149A+G182T+H1*,A174*+G149A+G182T+I9M,A174*+G149A+G182T+K391A,A174*+G149A+G182T+M202L,A174*+G149A+G182T+N16Y,A174*+G149A+G182T+N195F,A174*+G149A+G182T+N54S,A174*+G149A+G182T+Q169E,A174*+G149A+

24 Mar 2026
2026202266

G182T+Q169E,A174*+G149A+G182T+Q172K,A174*+G149A+G182T+Q299Y,A174*+G149A+G182T+Q345R,A174*+G149A+G182T+Q365S,A174*+G149A+G182T+R320K,A174*+G149A+G182T+R458K,A174*+G149A+G182T+S323T,A174*+G149A+G182T+V206L,A174*+G149A+G182T+Y295F,A174*+G149A+H1*+I9M,A174*+G149A+H1*+K391A,A174*+G149A+H1*+M202L,A174*+G149A+H1*+N16Y,A174*+G149A+H1*+N195F,A174*+G149A+H1*+N54S,A174*+G149A+H1*+Q169E,A174*+G149A+H1*+Q169E,A174*+G149A+H1*+Q172K,A174*+G149A+H1*+Q299Y,A174*+G149A+H1*+Q345R,A174*+G149A+H1*+Q365S,A174*+G149A+H1*+R320K,A174*+G149A+H1*+R458K,A174*+G149A+H1*+S323T,A174*+G149A+H1*+V206L,A174*+G149A+H1*+Y295F,A174*+G149A+I9M+K391A,A174*+G149A+I9M+M202L,A174*+G149A+I9M+N16Y,A174*+G149A+I9M+N195F,A174*+G149A+I9M+N54S,A174*+G149A+I9M+Q169E,A174*+G149A+I9M+Q169E,A174*+G149A+I9M+Q172K,A174*+G149A+I9M+Q299Y,A174*+G149A+I9M+Q345R,A174*+G149A+I9M+Q365S,A174*+G149A+I9M+R320K,A174*+G149A+I9M+R458K,A174*+G149A+I9M+S323T,A174*+G149A+I9M+V206L,A174*+G149A+I9M+Y295F,A174*+G149A+K391A+M202L,A174*+G149A+K391A+N16Y,A174*+G149A+K391A+N195F,A174*+G149A+K391A+N54S,A174*+G149A+K391A+Q169E,A174*+G149A+K391A+Q169E,A174*+G149A+K391A+Q172K,A174*+G149A+K391A+Q299Y,A174*+G149A+K391A+Q345R,A174*+G149A+K391A+Q365S,A174*+G149A+K391A+R320K,A174*+G149A+K391A+R458K,A174*+G149A+K391A+S323T,A174*+G149A+K391A+V206L,A174*+G149A+K391A+Y295F,A174*+G149A+M202L+N16Y,A174*+G149A+M202L+N195F,A174*+G149A+M202L+N54S,A174*+G149A+M202L+Q169E,A174*+G149A+M202L+Q169E,A174*+G149A+M202L+Q172K,A174*+G149A+M202L+Q299Y,A174*+G149A+M202L+Q345R,A174*+G149A+M202L+Q365S,A174*+G149A+M202L+R320K,A174*+G149A+M202L+R458K,A174*+G149A+M202L+S323T,A174*+G149A+M202L+V206L,A174*+G149A+M202L+Y295F,A174*+G149A+N16Y+N195F,A174*+G149A+N16Y+N54S,A174*+G149A+N16Y+Q169E,A174*+G149A+N16Y+Q169E,A174*+G149A+N16Y+Q172K,A174*+G149A+N16Y+Q299Y,A174*+G149A+N16Y+Q345R,A174*+G149A+N16Y+Q365S,A174*+G149A+N16Y+R320K,A174*+G149A+N16Y+R458K,A174*+G149A+N16Y+S323T,A174*+G149A+N16Y+V206L,A174*+G149A+N16Y+Y295F,A174*+G149A+N195F+N54S,A174*+G149A+N195F+Q169E,A174*+G149A+N195F+Q169E,A174*+G149A+N195F+Q172K,A174*+G149A+N195F+Q299Y,A174*+G149A+N195F+Q345R,A174*+G149A+N195F+Q365S,A174*+G149A+N195F+R320K,A174*+G149A+N195F+R458K,A174*+G149A+N195F+S323T,A174*+G149A+N195F+V206L,A174*+G149A+N195F+Y295F,A174*+G149A+N54S+Q169E,A174*+G149A+N54S+Q169E,A174*+G149A+N54S+Q172K,A174*+G149A+N54S+Q299Y,A174*+G149A+N54S+Q345R,A174*+G149A+N54S+Q365S,A174*+G149A+N54S+R320K,A174*+G149A+N54S+R458K,A174*+G149A+N54S+S323T,A174*+G149A+N54S+V206L,A174*+G149A+N54S+Y295F,A174*+G149A+Q169E+Q169E,A174*+G149A+Q169E+Q172K,A174*+G149A+Q169E+Q299Y,A174*+G149A+Q169E+Q345R,A174*+G149A+Q169E+Q365S,A174*+G149A+Q169E+R320K,A

24 Mar 2026
2026202266

174*+G149A+Q169E+R458K,A174*+G149A+Q169E+S323T,A174*+G149A+Q169E+V206L,A1
74*+G149A+Q169E+Y295F,A174*+G149A+Q169E+Q172K,A174*+G149A+Q169E+Q299Y,A1
74*+G149A+Q169E+Q345R,A174*+G149A+Q169E+Q365S,A174*+G149A+Q169E+R320K,A1
74*+G149A+Q169E+R458K,A174*+G149A+Q169E+S323T,A174*+G149A+Q169E+V206L,A17
4*+G149A+Q169E+Y295F,A174*+G149A+Q172K+Q299Y,A174*+G149A+Q172K+Q345R,A17
4*+G149A+Q172K+Q365S,A174*+G149A+Q172K+R320K,A174*+G149A+Q172K+R458K,A17
4*+G149A+Q172K+S323T,A174*+G149A+Q172K+V206L,A174*+G149A+Q172K+Y295F,A174
+G149A+Q299Y+Q345R,A174+G149A+Q299Y+Q365S,A174*+G149A+Q299Y+R320K,A174
+G149A+Q299Y+R458K,A174+G149A+Q299Y+S323T,A174*+G149A+Q299Y+V206L,A174*
+G149A+Q299Y+Y295F,A174*+G149A+Q345R+Q365S,A174*+G149A+Q345R+R320K,A174*
+G149A+Q345R+R458K,A174*+G149A+Q345R+S323T,A174*+G149A+Q345R+V206L,A174*
+G149A+Q345R+Y295F,A174*+G149A+Q365S+R320K,A174*+G149A+Q365S+R458K,A174*
+G149A+Q365S+S323T,A174*+G149A+Q365S+V206L,A174*+G149A+Q365S+Y295F,A174*+
G149A+R320K+R458K,A174*+G149A+R320K+S323T,A174*+G149A+R320K+V206L,A174*+G
149A+R320K+Y295F,A174*+G149A+R458K+S323T,A174*+G149A+R458K+V206L,A174*+G1
49A+R458K+Y295F,A174*+G149A+S323T+V206L,A174*+G149A+S323T+Y295F,A174*+G149
A+V206L+Y295F,A174*+G182T+H1*+I9M,A174*+G182T+H1*+K391A,A174*+G182T+H1*+M2
02L,A174*+G182T+H1*+N16Y,A174*+G182T+H1*+N195F,A174*+G182T+H1*+N54S,A174*+G
182T+H1*+Q169E,A174*+G182T+H1*+Q169E,A174*+G182T+H1*+Q172K,A174*+G182T+H1*
+Q299Y,A174*+G182T+H1*+Q345R,A174*+G182T+H1*+Q365S,A174*+G182T+H1*+R320K,A
174*+G182T+H1*+R458K,A174*+G182T+H1*+S323T,A174*+G182T+H1*+V206L,A174*+G182
T+H1*+Y295F,A174*+G182T+I9M+K391A,A174*+G182T+I9M+M202L,A174*+G182T+I9M+N1
6Y,A174*+G182T+I9M+N195F,A174*+G182T+I9M+N54S,A174*+G182T+I9M+Q169E,A174*+
G182T+I9M+Q169E,A174*+G182T+I9M+Q172K,A174*+G182T+I9M+Q299Y,A174*+G182T+I9
M+Q345R,A174*+G182T+I9M+Q365S,A174*+G182T+I9M+R320K,A174*+G182T+I9M+R458K
,A174*+G182T+I9M+S323T,A174*+G182T+I9M+V206L,A174*+G182T+I9M+Y295F,A174*+G1
82T+K391A+M202L,A174*+G182T+K391A+N16Y,A174*+G182T+K391A+N195F,A174*+G182
T+K391A+N54S,A174*+G182T+K391A+Q169E,A174*+G182T+K391A+Q169E,A174*+G182T+
K391A+Q172K,A174*+G182T+K391A+Q299Y,A174*+G182T+K391A+Q345R,A174*+G182T+K
391A+Q365S,A174*+G182T+K391A+R320K,A174*+G182T+K391A+R458K,A174*+G182T+K3
91A+S323T,A174*+G182T+K391A+V206L,A174*+G182T+K391A+Y295F,A174*+G182T+M202
L+N16Y,A174*+G182T+M202L+N195F,A174*+G182T+M202L+N54S,A174*+G182T+M202L+
Q169E,A174*+G182T+M202L+Q169E,A174*+G182T+M202L+Q172K,A174*+G182T+M202L+
Q299Y,A174*+G182T+M202L+Q345R,A174*+G182T+M202L+Q365S,A174*+G182T+M202L+
R320K,A174*+G182T+M202L+R458K,A174*+G182T+M202L+S323T,A174*+G182T+M202L+V
206L,A174*+G182T+M202L+Y295F,A174*+G182T+N16Y+N195F,A174*+G182T+N16Y+N54S,

24 Mar 2026
2026202266

A174*+G182T+N16Y+Q169E,A174*+G182T+N16Y+Q169E,A174*+G182T+N16Y+Q172K,A17
4*+G182T+N16Y+Q299Y,A174*+G182T+N16Y+Q345R,A174*+G182T+N16Y+Q365S,A174*+
G182T+N16Y+R320K,A174*+G182T+N16Y+R458K,A174*+G182T+N16Y+S323T,A174*+G182
T+N16Y+V206L,A174*+G182T+N16Y+Y295F,A174*+G182T+N195F+N54S,A174*+G182T+N1
95F+Q169E,A174*+G182T+N195F+Q169E,A174*+G182T+N195F+Q172K,A174*+G182T+N19
5F+Q299Y,A174*+G182T+N195F+Q345R,A174*+G182T+N195F+Q365S,A174*+G182T+N195
F+R320K,A174*+G182T+N195F+R458K,A174*+G182T+N195F+S323T,A174*+G182T+N195F
+V206L,A174*+G182T+N195F+Y295F,A174*+G182T+N54S+Q169E,A174*+G182T+N54S+Q1
69E,A174*+G182T+N54S+Q172K,A174*+G182T+N54S+Q299Y,A174*+G182T+N54S+Q345R,
A174*+G182T+N54S+Q365S,A174*+G182T+N54S+R320K,A174*+G182T+N54S+R458K,A174
+G182T+N54S+S323T,A174+G182T+N54S+V206L,A174*+G182T+N54S+Y295F,A174*+G1
82T+Q169E+Q169E,A174*+G182T+Q169E+Q172K,A174*+G182T+Q169E+Q299Y,A174*+G1
82T+Q169E+Q345R,A174*+G182T+Q169E+Q365S,A174*+G182T+Q169E+R320K,A174*+G1
82T+Q169E+R458K,A174*+G182T+Q169E+S323T,A174*+G182T+Q169E+V206L,A174*+G18
2T+Q169E+Y295F,A174*+G182T+Q169E+Q172K,A174*+G182T+Q169E+Q299Y,A174*+G182
T+Q169E+Q345R,A174*+G182T+Q169E+Q365S,A174*+G182T+Q169E+R320K,A174*+G182
T+Q169E+R458K,A174*+G182T+Q169E+S323T,A174*+G182T+Q169E+V206L,A174*+G182T
+Q169E+Y295F,A174*+G182T+Q172K+Q299Y,A174*+G182T+Q172K+Q345R,A174*+G182T
+Q172K+Q365S,A174*+G182T+Q172K+R320K,A174*+G182T+Q172K+R458K,A174*+G182T
+Q172K+S323T,A174*+G182T+Q172K+V206L,A174*+G182T+Q172K+Y295F,A174*+G182T+
Q299Y+Q345R,A174*+G182T+Q299Y+Q365S,A174*+G182T+Q299Y+R320K,A174*+G182T+
Q299Y+R458K,A174*+G182T+Q299Y+S323T,A174*+G182T+Q299Y+V206L,A174*+G182T+Q
299Y+Y295F,A174*+G182T+Q345R+Q365S,A174*+G182T+Q345R+R320K,A174*+G182T+Q
345R+R458K,A174*+G182T+Q345R+S323T,A174*+G182T+Q345R+V206L,A174*+G182T+Q3
45R+Y295F,A174*+G182T+Q365S+R320K,A174*+G182T+Q365S+R458K,A174*+G182T+Q36
5S+S323T,A174*+G182T+Q365S+V206L,A174*+G182T+Q365S+Y295F,A174*+G182T+R320
K+R458K,A174*+G182T+R320K+S323T,A174*+G182T+R320K+V206L,A174*+G182T+R320K
+Y295F,A174*+G182T+R458K+S323T,A174*+G182T+R458K+V206L,A174*+G182T+R458K+
Y295F,A174*+G182T+S323T+V206L,A174*+G182T+S323T+Y295F,A174*+G182T+V206L+Y2
95F,A174*+H1*+I9M+K391A,A174*+H1*+I9M+M202L,A174*+H1*+I9M+N16Y,A174*+H1*+I9M
+N195F,A174*+H1*+I9M+N54S,A174*+H1*+I9M+Q169E,A174*+H1*+I9M+Q169E,A174*+H1*+
I9M+Q172K,A174*+H1*+I9M+Q299Y,A174*+H1*+I9M+Q345R,A174*+H1*+I9M+Q365S,A174*
+H1*+I9M+R320K,A174*+H1*+I9M+R458K,A174*+H1*+I9M+S323T,A174*+H1*+I9M+V206L,A
174*+H1*+I9M+Y295F,A174*+H1*+K391A+M202L,A174*+H1*+K391A+N16Y,A174*+H1*+K39
1A+N195F,A174*+H1*+K391A+N54S,A174*+H1*+K391A+Q169E,A174*+H1*+K391A+Q169E,
A174*+H1*+K391A+Q172K,A174*+H1*+K391A+Q299Y,A174*+H1*+K391A+Q345R,A174*+H1

24 Mar 2026
2026202266

+K391A+Q365S,A174+H1*+K391A+R320K,A174*+H1*+K391A+R458K,A174*+H1*+K391A+S323T,A174*+H1*+K391A+V206L,A174*+H1*+K391A+Y295F,A174*+H1*+M202L+N16Y,A174*+H1*+M202L+N195F,A174*+H1*+M202L+N54S,A174*+H1*+M202L+Q169E,A174*+H1*+M202L+Q169E,A174*+H1*+M202L+Q172K,A174*+H1*+M202L+Q299Y,A174*+H1*+M202L+Q345R,A174*+H1*+M202L+Q365S,A174*+H1*+M202L+R320K,A174*+H1*+M202L+R458K,A174*+H1*+M202L+S323T,A174*+H1*+M202L+V206L,A174*+H1*+M202L+Y295F,A174*+H1*+N16Y+N195F,A174*+H1*+N16Y+N54S,A174*+H1*+N16Y+Q169E,A174*+H1*+N16Y+Q169E,A174*+H1*+N16Y+Q172K,A174*+H1*+N16Y+Q299Y,A174*+H1*+N16Y+Q345R,A174*+H1*+N16Y+Q365S,A174*+H1*+N16Y+R320K,A174*+H1*+N16Y+R458K,A174*+H1*+N16Y+S323T,A174*+H1*+N16Y+V206L,A174*+H1*+N16Y+Y295F,A174*+H1*+N195F+N54S,A174*+H1*+N195F+Q169E,A174*+H1*+N195F+Q169E,A174*+H1*+N195F+Q172K,A174*+H1*+N195F+Q299Y,A174*+H1*+N195F+Q345R,A174*+H1*+N195F+Q365S,A174*+H1*+N195F+R320K,A174*+H1*+N195F+R458K,A174*+H1*+N195F+S323T,A174*+H1*+N195F+V206L,A174*+H1*+N195F+Y295F,A174*+H1*+N54S+Q169E,A174*+H1*+N54S+Q169E,A174*+H1*+N54S+Q172K,A174*+H1*+N54S+Q299Y,A174*+H1*+N54S+Q345R,A174*+H1*+N54S+Q365S,A174*+H1*+N54S+R320K,A174*+H1*+N54S+R458K,A174*+H1*+N54S+S323T,A174*+H1*+N54S+V206L,A174*+H1*+N54S+Y295F,A174*+H1*+Q169E+Q169E,A174*+H1*+Q169E+Q172K,A174*+H1*+Q169E+Q299Y,A174*+H1*+Q169E+Q345R,A174*+H1*+Q169E+Q365S,A174*+H1*+Q169E+R320K,A174*+H1*+Q169E+R458K,A174*+H1*+Q169E+S323T,A174*+H1*+Q169E+V206L,A174*+H1*+Q169E+Y295F,A174*+H1*+Q169E+Q172K,A174*+H1*+Q169E+Q299Y,A174*+H1*+Q169E+Q345R,A174*+H1*+Q169E+Q365S,A174*+H1*+Q169E+R320K,A174*+H1*+Q169E+R458K,A174*+H1*+Q169E+S323T,A174*+H1*+Q169E+V206L,A174*+H1*+Q169E+Y295F,A174*+H1*+Q172K+Q299Y,A174*+H1*+Q172K+Q345R,A174*+H1*+Q172K+Q365S,A174*+H1*+Q172K+R320K,A174*+H1*+Q172K+R458K,A174*+H1*+Q172K+S323T,A174*+H1*+Q172K+V206L,A174*+H1*+Q172K+Y295F,A174*+H1*+Q299Y+Q345R,A174*+H1*+Q299Y+Q365S,A174*+H1*+Q299Y+R320K,A174*+H1*+Q299Y+R458K,A174*+H1*+Q299Y+S323T,A174*+H1*+Q299Y+V206L,A174*+H1*+Q299Y+Y295F,A174*+H1*+Q345R+Q365S,A174*+H1*+Q345R+R320K,A174*+H1*+Q345R+R458K,A174*+H1*+Q345R+S323T,A174*+H1*+Q345R+V206L,A174*+H1*+Q345R+Y295F,A174*+H1*+Q365S+R320K,A174*+H1*+Q365S+R458K,A174*+H1*+Q365S+S323T,A174*+H1*+Q365S+V206L,A174*+H1*+Q365S+Y295F,A174*+H1*+R320K+R458K,A174*+H1*+R320K+S323T,A174*+H1*+R320K+V206L,A174*+H1*+R320K+Y295F,A174*+H1*+R458K+S323T,A174*+H1*+R458K+V206L,A174*+H1*+R458K+Y295F,A174*+H1*+S323T+V206L,A174*+H1*+S323T+Y295F,A174*+H1*+V206L+Y295F,A174*+I9M+K391A+M202L,A174*+I9M+K391A+N16Y,A174*+I9M+K391A+N195F,A174*+I9M+K391A+N54S,A174*+I9M+K391A+Q169E,A174*+I9M+K391A+Q169E,A174*+I9M+K391A+Q172K,A174*+I9M+K391A+Q299Y,A174*+I9M+K391A+Q345R,A174*+I9M+K391A+Q365S,A174*+I9M+K391A+R320K,A174*+I9M+K391A+R45

24 Mar 2026
2026202266

8K,A174*+I9M+K391A+S323T,A174*+I9M+K391A+V206L,A174*+I9M+K391A+Y295F,A174*+I9M+M202L+N16Y,A174*+I9M+M202L+N195F,A174*+I9M+M202L+N54S,A174*+I9M+M202L+Q169E,A174*+I9M+M202L+Q169E,A174*+I9M+M202L+Q172K,A174*+I9M+M202L+Q299Y,A174*+I9M+M202L+Q345R,A174*+I9M+M202L+Q365S,A174*+I9M+M202L+R320K,A174*+I9M+M202L+R458K,A174*+I9M+M202L+S323T,A174*+I9M+M202L+V206L,A174*+I9M+M202L+Y295F,A174*+I9M+N16Y+N195F,A174*+I9M+N16Y+N54S,A174*+I9M+N16Y+Q169E,A174*+I9M+N16Y+Q169E,A174*+I9M+N16Y+Q172K,A174*+I9M+N16Y+Q299Y,A174*+I9M+N16Y+Q345R,A174*+I9M+N16Y+Q365S,A174*+I9M+N16Y+R320K,A174*+I9M+N16Y+R458K,A174*+I9M+N16Y+S323T,A174*+I9M+N16Y+V206L,A174*+I9M+N16Y+Y295F,A174*+I9M+N195F+N54S,A174*+I9M+N195F+Q169E,A174*+I9M+N195F+Q169E,A174*+I9M+N195F+Q172K,A174*+I9M+N195F+Q299Y,A174*+I9M+N195F+Q345R,A174*+I9M+N195F+Q365S,A174*+I9M+N195F+R320K,A174*+I9M+N195F+R458K,A174*+I9M+N195F+S323T,A174*+I9M+N195F+V206L,A174*+I9M+N195F+Y295F,A174*+I9M+N54S+Q169E,A174*+I9M+N54S+Q169E,A174*+I9M+N54S+Q172K,A174*+I9M+N54S+Q299Y,A174*+I9M+N54S+Q345R,A174*+I9M+N54S+Q365S,A174*+I9M+N54S+R320K,A174*+I9M+N54S+R458K,A174*+I9M+N54S+S323T,A174*+I9M+N54S+V206L,A174*+I9M+N54S+Y295F,A174*+I9M+Q169E+Q169E,A174*+I9M+Q169E+Q172K,A174*+I9M+Q169E+Q299Y,A174*+I9M+Q169E+Q345R,A174*+I9M+Q169E+Q365S,A174*+I9M+Q169E+R320K,A174*+I9M+Q169E+R458K,A174*+I9M+Q169E+S323T,A174*+I9M+Q169E+V206L,A174*+I9M+Q169E+Y295F,A174*+I9M+Q169E+Q172K,A174*+I9M+Q169E+Q299Y,A174*+I9M+Q169E+Q345R,A174*+I9M+Q169E+Q365S,A174*+I9M+Q169E+R320K,A174*+I9M+Q169E+R458K,A174*+I9M+Q169E+S323T,A174*+I9M+Q169E+V206L,A174*+I9M+Q169E+Y295F,A174*+I9M+Q172K+Q299Y,A174*+I9M+Q172K+Q345R,A174*+I9M+Q172K+Q365S,A174*+I9M+Q172K+R320K,A174*+I9M+Q172K+R458K,A174*+I9M+Q172K+S323T,A174*+I9M+Q172K+V206L,A174*+I9M+Q172K+Y295F,A174*+I9M+Q299Y+Q345R,A174*+I9M+Q299Y+Q365S,A174*+I9M+Q299Y+R320K,A174*+I9M+Q299Y+R458K,A174*+I9M+Q299Y+S323T,A174*+I9M+Q299Y+V206L,A174*+I9M+Q299Y+Y295F,A174*+I9M+Q345R+Q365S,A174*+I9M+Q345R+R320K,A174*+I9M+Q345R+R458K,A174*+I9M+Q345R+S323T,A174*+I9M+Q345R+V206L,A174*+I9M+Q345R+Y295F,A174*+I9M+Q365S+R320K,A174*+I9M+Q365S+R458K,A174*+I9M+Q365S+S323T,A174*+I9M+Q365S+V206L,A174*+I9M+Q365S+Y295F,A174*+I9M+R320K+R458K,A174*+I9M+R320K+S323T,A174*+I9M+R320K+V206L,A174*+I9M+R320K+Y295F,A174*+I9M+R458K+S323T,A174*+I9M+R458K+V206L,A174*+I9M+R458K+Y295F,A174*+I9M+S323T+V206L,A174*+I9M+S323T+Y295F,A174*+I9M+V206L+Y295F,A174*+K391A+M202L+N16Y,A174*+K391A+M202L+N195F,A174*+K391A+M202L+N54S,A174*+K391A+M202L+Q169E,A174*+K391A+M202L+Q169E,A174*+K391A+M202L+Q172K,A174*+K391A+M202L+Q299Y,A174*+K391A+M202L+Q345R,A174*+K391A+M202L+Q365S,A174*+K391A+M202L+R320K,A174*+K391A+M202L+R458K,A174*+K391A+M202L+S323T,A174*+K391A+M202L+V206L,A174

24 Mar 2026
2026202266

+K391A+M202L+Y295F,A174+K391A+N16Y+N195F,A174*+K391A+N16Y+N54S,A174*+K3
91A+N16Y+Q169E,A174*+K391A+N16Y+Q169E,A174*+K391A+N16Y+Q172K,A174*+K391A+
N16Y+Q299Y,A174*+K391A+N16Y+Q345R,A174*+K391A+N16Y+Q365S,A174*+K391A+N16
Y+R320K,A174*+K391A+N16Y+R458K,A174*+K391A+N16Y+S323T,A174*+K391A+N16Y+V2
06L,A174*+K391A+N16Y+Y295F,A174*+K391A+N195F+N54S,A174*+K391A+N195F+Q169E,
A174*+K391A+N195F+Q169E,A174*+K391A+N195F+Q172K,A174*+K391A+N195F+Q299Y,A
174*+K391A+N195F+Q345R,A174*+K391A+N195F+Q365S,A174*+K391A+N195F+R320K,A1
74*+K391A+N195F+R458K,A174*+K391A+N195F+S323T,A174*+K391A+N195F+V206L,A174
+K391A+N195F+Y295F,A174+K391A+N54S+Q169E,A174*+K391A+N54S+Q169E,A174*+K
391A+N54S+Q172K,A174*+K391A+N54S+Q299Y,A174*+K391A+N54S+Q345R,A174*+K391A
+N54S+Q365S,A174*+K391A+N54S+R320K,A174*+K391A+N54S+R458K,A174*+K391A+N54
S+S323T,A174*+K391A+N54S+V206L,A174*+K391A+N54S+Y295F,A174*+K391A+Q169E+Q
169E,A174*+K391A+Q169E+Q172K,A174*+K391A+Q169E+Q299Y,A174*+K391A+Q169E+Q3
45R,A174*+K391A+Q169E+Q365S,A174*+K391A+Q169E+R320K,A174*+K391A+Q169E+R45
8K,A174*+K391A+Q169E+S323T,A174*+K391A+Q169E+V206L,A174*+K391A+Q169E+Y295
F,A174*+K391A+Q169E+Q172K,A174*+K391A+Q169E+Q299Y,A174*+K391A+Q169E+Q345
R,A174*+K391A+Q169E+Q365S,A174*+K391A+Q169E+R320K,A174*+K391A+Q169E+R458
K,A174*+K391A+Q169E+S323T,A174*+K391A+Q169E+V206L,A174*+K391A+Q169E+Y295F,
A174*+K391A+Q172K+Q299Y,A174*+K391A+Q172K+Q345R,A174*+K391A+Q172K+Q365S,
A174*+K391A+Q172K+R320K,A174*+K391A+Q172K+R458K,A174*+K391A+Q172K+S323T,A
174*+K391A+Q172K+V206L,A174*+K391A+Q172K+Y295F,A174*+K391A+Q299Y+Q345R,A1
74*+K391A+Q299Y+Q365S,A174*+K391A+Q299Y+R320K,A174*+K391A+Q299Y+R458K,A17
4*+K391A+Q299Y+S323T,A174*+K391A+Q299Y+V206L,A174*+K391A+Q299Y+Y295F,A174*
+K391A+Q345R+Q365S,A174*+K391A+Q345R+R320K,A174*+K391A+Q345R+R458K,A174*
+K391A+Q345R+S323T,A174*+K391A+Q345R+V206L,A174*+K391A+Q345R+Y295F,A174*+
K391A+Q365S+R320K,A174*+K391A+Q365S+R458K,A174*+K391A+Q365S+S323T,A174*+K
391A+Q365S+V206L,A174*+K391A+Q365S+Y295F,A174*+K391A+R320K+R458K,A174*+K3
91A+R320K+S323T,A174*+K391A+R320K+V206L,A174*+K391A+R320K+Y295F,A174*+K391
A+R458K+S323T,A174*+K391A+R458K+V206L,A174*+K391A+R458K+Y295F,A174*+K391A+
S323T+V206L,A174*+K391A+S323T+Y295F,A174*+K391A+V206L+Y295F,A174*+M202L+N1
6Y+N195F,A174*+M202L+N16Y+N54S,A174*+M202L+N16Y+Q169E,A174*+M202L+N16Y+Q
169E,A174*+M202L+N16Y+Q172K,A174*+M202L+N16Y+Q299Y,A174*+M202L+N16Y+Q345
R,A174*+M202L+N16Y+Q365S,A174*+M202L+N16Y+R320K,A174*+M202L+N16Y+R458K,A1
74*+M202L+N16Y+S323T,A174*+M202L+N16Y+V206L,A174*+M202L+N16Y+Y295F,A174*+
M202L+N195F+N54S,A174*+M202L+N195F+Q169E,A174*+M202L+N195F+Q169E,A174*+M
202L+N195F+Q172K,A174*+M202L+N195F+Q299Y,A174*+M202L+N195F+Q345R,A174*+M2

24 Mar 2026
2026202266

02L+N195F+Q365S,A174*+M202L+N195F+R320K,A174*+M202L+N195F+R458K,A174*+M20
2L+N195F+S323T,A174*+M202L+N195F+V206L,A174*+M202L+N195F+Y295F,A174*+M202L
+N54S+Q169E,A174*+M202L+N54S+Q169E,A174*+M202L+N54S+Q172K,A174*+M202L+N5
4S+Q299Y,A174*+M202L+N54S+Q345R,A174*+M202L+N54S+Q365S,A174*+M202L+N54S+
R320K,A174*+M202L+N54S+R458K,A174*+M202L+N54S+S323T,A174*+M202L+N54S+V206
L,A174*+M202L+N54S+Y295F,A174*+M202L+Q169E+Q169E,A174*+M202L+Q169E+Q172K,
A174*+M202L+Q169E+Q299Y,A174*+M202L+Q169E+Q345R,A174*+M202L+Q169E+Q365S,
A174*+M202L+Q169E+R320K,A174*+M202L+Q169E+R458K,A174*+M202L+Q169E+S323T,A
174*+M202L+Q169E+V206L,A174*+M202L+Q169E+Y295F,A174*+M202L+Q169E+Q172K,A1
74*+M202L+Q169E+Q299Y,A174*+M202L+Q169E+Q345R,A174*+M202L+Q169E+Q365S,A1
74*+M202L+Q169E+R320K,A174*+M202L+Q169E+R458K,A174*+M202L+Q169E+S323T,A17
4*+M202L+Q169E+V206L,A174*+M202L+Q169E+Y295F,A174*+M202L+Q172K+Q299Y,A174
+M202L+Q172K+Q345R,A174+M202L+Q172K+Q365S,A174*+M202L+Q172K+R320K,A174*
+M202L+Q172K+R458K,A174*+M202L+Q172K+S323T,A174*+M202L+Q172K+V206L,A174*+
M202L+Q172K+Y295F,A174*+M202L+Q299Y+Q345R,A174*+M202L+Q299Y+Q365S,A174*+
M202L+Q299Y+R320K,A174*+M202L+Q299Y+R458K,A174*+M202L+Q299Y+S323T,A174*+
M202L+Q299Y+V206L,A174*+M202L+Q299Y+Y295F,A174*+M202L+Q345R+Q365S,A174*+
M202L+Q345R+R320K,A174*+M202L+Q345R+R458K,A174*+M202L+Q345R+S323T,A174*+
M202L+Q345R+V206L,A174*+M202L+Q345R+Y295F,A174*+M202L+Q365S+R320K,A174*+
M202L+Q365S+R458K,A174*+M202L+Q365S+S323T,A174*+M202L+Q365S+V206L,A174*+M
202L+Q365S+Y295F,A174*+M202L+R320K+R458K,A174*+M202L+R320K+S323T,A174*+M2
02L+R320K+V206L,A174*+M202L+R320K+Y295F,A174*+M202L+R458K+S323T,A174*+M202
L+R458K+V206L,A174*+M202L+R458K+Y295F,A174*+M202L+S323T+V206L,A174*+M202L+
S323T+Y295F,A174*+M202L+V206L+Y295F,A174*+N16Y+N195F+N54S,A174*+N16Y+N195
F+Q169E,A174*+N16Y+N195F+Q169E,A174*+N16Y+N195F+Q172K,A174*+N16Y+N195F+Q
299Y,A174*+N16Y+N195F+Q345R,A174*+N16Y+N195F+Q365S,A174*+N16Y+N195F+R320K
,A174*+N16Y+N195F+R458K,A174*+N16Y+N195F+S323T,A174*+N16Y+N195F+V206L,A174
+N16Y+N195F+Y295F,A174+N16Y+N54S+Q169E,A174*+N16Y+N54S+Q169E,A174*+N16Y
+N54S+Q172K,A174*+N16Y+N54S+Q299Y,A174*+N16Y+N54S+Q345R,A174*+N16Y+N54S+
Q365S,A174*+N16Y+N54S+R320K,A174*+N16Y+N54S+R458K,A174*+N16Y+N54S+S323T,A
174*+N16Y+N54S+V206L,A174*+N16Y+N54S+Y295F,A174*+N16Y+Q169E+Q169E,A174*+N
16Y+Q169E+Q172K,A174*+N16Y+Q169E+Q299Y,A174*+N16Y+Q169E+Q345R,A174*+N16Y
+Q169E+Q365S,A174*+N16Y+Q169E+R320K,A174*+N16Y+Q169E+R458K,A174*+N16Y+Q1
69E+S323T,A174*+N16Y+Q169E+V206L,A174*+N16Y+Q169E+Y295F,A174*+N16Y+Q169E+
Q172K,A174*+N16Y+Q169E+Q299Y,A174*+N16Y+Q169E+Q345R,A174*+N16Y+Q169E+Q36
5S,A174*+N16Y+Q169E+R320K,A174*+N16Y+Q169E+R458K,A174*+N16Y+Q169E+S323T,A

24 Mar 2026
2026202266

174*+N16Y+Q169E+V206L,A174*+N16Y+Q169E+Y295F,A174*+N16Y+Q172K+Q299Y,A174*+N16Y+Q172K+Q345R,A174*+N16Y+Q172K+Q365S,A174*+N16Y+Q172K+R320K,A174*+N16Y+Q172K+R458K,A174*+N16Y+Q172K+S323T,A174*+N16Y+Q172K+V206L,A174*+N16Y+Q172K+Y295F,A174*+N16Y+Q299Y+Q345R,A174*+N16Y+Q299Y+Q365S,A174*+N16Y+Q299Y+R320K,A174*+N16Y+Q299Y+R458K,A174*+N16Y+Q299Y+S323T,A174*+N16Y+Q299Y+V206L,A174*+N16Y+Q299Y+Y295F,A174*+N16Y+Q345R+Q365S,A174*+N16Y+Q345R+R320K,A174*+N16Y+Q345R+R458K,A174*+N16Y+Q345R+S323T,A174*+N16Y+Q345R+V206L,A174*+N16Y+Q345R+Y295F,A174*+N16Y+Q365S+R320K,A174*+N16Y+Q365S+R458K,A174*+N16Y+Q365S+S323T,A174*+N16Y+Q365S+V206L,A174*+N16Y+Q365S+Y295F,A174*+N16Y+R320K+R458K,A174*+N16Y+R320K+S323T,A174*+N16Y+R320K+V206L,A174*+N16Y+R320K+Y295F,A174*+N16Y+R458K+S323T,A174*+N16Y+R458K+V206L,A174*+N16Y+R458K+Y295F,A174*+N16Y+S323T+V206L,A174*+N16Y+S323T+Y295F,A174*+N16Y+V206L+Y295F,A174*+N195F+N54S+Q169E,A174*+N195F+N54S+Q169E,A174*+N195F+N54S+Q172K,A174*+N195F+N54S+Q299Y,A174*+N195F+N54S+Q345R,A174*+N195F+N54S+Q365S,A174*+N195F+N54S+R320K,A174*+N195F+N54S+R458K,A174*+N195F+N54S+S323T,A174*+N195F+N54S+V206L,A174*+N195F+N54S+Y295F,A174*+N195F+Q169E+Q169E,A174*+N195F+Q169E+Q172K,A174*+N195F+Q169E+Q299Y,A174*+N195F+Q169E+Q345R,A174*+N195F+Q169E+Q365S,A174*+N195F+Q169E+R320K,A174*+N195F+Q169E+R458K,A174*+N195F+Q169E+S323T,A174*+N195F+Q169E+V206L,A174*+N195F+Q169E+Y295F,A174*+N195F+Q169E+Q172K,A174*+N195F+Q169E+Q299Y,A174*+N195F+Q169E+Q345R,A174*+N195F+Q169E+Q365S,A174*+N195F+Q169E+R320K,A174*+N195F+Q169E+R458K,A174*+N195F+Q169E+S323T,A174*+N195F+Q169E+V206L,A174*+N195F+Q169E+Y295F,A174*+N195F+Q172K+Q299Y,A174*+N195F+Q172K+Q345R,A174*+N195F+Q172K+Q365S,A174*+N195F+Q172K+R320K,A174*+N195F+Q172K+R458K,A174*+N195F+Q172K+S323T,A174*+N195F+Q172K+V206L,A174*+N195F+Q172K+Y295F,A174*+N195F+Q299Y+Q345R,A174*+N195F+Q299Y+Q365S,A174*+N195F+Q299Y+R320K,A174*+N195F+Q299Y+R458K,A174*+N195F+Q299Y+S323T,A174*+N195F+Q299Y+V206L,A174*+N195F+Q299Y+Y295F,A174*+N195F+Q345R+Q365S,A174*+N195F+Q345R+R320K,A174*+N195F+Q345R+R458K,A174*+N195F+Q345R+S323T,A174*+N195F+Q345R+V206L,A174*+N195F+Q345R+Y295F,A174*+N195F+Q365S+R320K,A174*+N195F+Q365S+R458K,A174*+N195F+Q365S+S323T,A174*+N195F+Q365S+V206L,A174*+N195F+Q365S+Y295F,A174*+N195F+R320K+R458K,A174*+N195F+R320K+S323T,A174*+N195F+R320K+V206L,A174*+N195F+R320K+Y295F,A174*+N195F+R458K+S323T,A174*+N195F+R458K+V206L,A174*+N195F+R458K+Y295F,A174*+N195F+S323T+V206L,A174*+N195F+S323T+Y295F,A174*+N195F+V206L+Y295F,A174*+N54S+Q169E+Q169E,A174*+N54S+Q169E+Q172K,A174*+N54S+Q169E+Q299Y,A174*+N54S+Q169E+Q345R,A174*+N54S+Q169E+Q365S,A174*+N54S+Q169E+R320K,A174*+N54S+Q169E+R458K,A174*+N54S+Q16

24 Mar 2026
2026202266

9E+S323T,A174*+N54S+Q169E+V206L,A174*+N54S+Q169E+Y295F,A174*+N54S+Q169E+Q172K,A174*+N54S+Q169E+Q299Y,A174*+N54S+Q169E+Q345R,A174*+N54S+Q169E+Q365S,A174*+N54S+Q169E+R320K,A174*+N54S+Q169E+R458K,A174*+N54S+Q169E+S323T,A174*+N54S+Q169E+V206L,A174*+N54S+Q169E+Y295F,A174*+N54S+Q172K+Q299Y,A174*+N54S+Q172K+Q345R,A174*+N54S+Q172K+Q365S,A174*+N54S+Q172K+R320K,A174*+N54S+Q172K+R458K,A174*+N54S+Q172K+S323T,A174*+N54S+Q172K+V206L,A174*+N54S+Q172K+Y295F,A174*+N54S+Q299Y+Q345R,A174*+N54S+Q299Y+Q365S,A174*+N54S+Q299Y+R320K,A174*+N54S+Q299Y+R458K,A174*+N54S+Q299Y+S323T,A174*+N54S+Q299Y+V206L,A174*+N54S+Q299Y+Y295F,A174*+N54S+Q345R+Q365S,A174*+N54S+Q345R+R320K,A174*+N54S+Q345R+R458K,A174*+N54S+Q345R+S323T,A174*+N54S+Q345R+V206L,A174*+N54S+Q345R+Y295F,A174*+N54S+Q365S+R320K,A174*+N54S+Q365S+R458K,A174*+N54S+Q365S+S323T,A174*+N54S+Q365S+V206L,A174*+N54S+Q365S+Y295F,A174*+N54S+R320K+R458K,A174*+N54S+R320K+S323T,A174*+N54S+R320K+V206L,A174*+N54S+R320K+Y295F,A174*+N54S+R458K+S323T,A174*+N54S+R458K+V206L,A174*+N54S+R458K+Y295F,A174*+N54S+S323T+V206L,A174*+N54S+S323T+Y295F,A174*+N54S+V206L+Y295F,A174*+Q169E+Q169E+Q172K,A174*+Q169E+Q169E+Q299Y,A174*+Q169E+Q169E+Q345R,A174*+Q169E+Q169E+Q365S,A174*+Q169E+Q169E+R320K,A174*+Q169E+Q169E+R458K,A174*+Q169E+Q169E+S323T,A174*+Q169E+Q169E+V206L,A174*+Q169E+Q169E+Y295F,A174*+Q169E+Q172K+Q299Y,A174*+Q169E+Q172K+Q345R,A174*+Q169E+Q172K+Q365S,A174*+Q169E+Q172K+R320K,A174*+Q169E+Q172K+R458K,A174*+Q169E+Q172K+S323T,A174*+Q169E+Q172K+V206L,A174*+Q169E+Q172K+Y295F,A174*+Q169E+Q299Y+Q345R,A174*+Q169E+Q299Y+Q365S,A174*+Q169E+Q299Y+R320K,A174*+Q169E+Q299Y+R458K,A174*+Q169E+Q299Y+S323T,A174*+Q169E+Q299Y+V206L,A174*+Q169E+Q299Y+Y295F,A174*+Q169E+Q345R+Q365S,A174*+Q169E+Q345R+R320K,A174*+Q169E+Q345R+R458K,A174*+Q169E+Q345R+S323T,A174*+Q169E+Q345R+V206L,A174*+Q169E+Q345R+Y295F,A174*+Q169E+Q365S+R320K,A174*+Q169E+Q365S+R458K,A174*+Q169E+Q365S+S323T,A174*+Q169E+Q365S+V206L,A174*+Q169E+Q365S+Y295F,A174*+Q169E+R320K+R458K,A174*+Q169E+R320K+S323T,A174*+Q169E+R320K+V206L,A174*+Q169E+R320K+Y295F,A174*+Q169E+R458K+S323T,A174*+Q169E+R458K+V206L,A174*+Q169E+R458K+Y295F,A174*+Q169E+S323T+V206L,A174*+Q169E+S323T+Y295F,A174*+Q169E+V206L+Y295F,A174*+Q169E+Q172K+Q299Y,A174*+Q169E+Q172K+Q345R,A174*+Q169E+Q172K+Q365S,A174*+Q169E+Q172K+R320K,A174*+Q169E+Q172K+R458K,A174*+Q169E+Q172K+S323T,A174*+Q169E+Q172K+V206L,A174*+Q169E+Q172K+Y295F,A174*+Q169E+Q299Y+Q345R,A174*+Q169E+Q299Y+Q365S,A174*+Q169E+Q299Y+R320K,A174*+Q169E+Q299Y+R458K,A174*+Q169E+Q299Y+S323T,A174*+Q169E+Q299Y+V206L,A174*+Q169E+Q299Y+Y295F,A174*+Q169E+Q345R+Q365S,A174*+Q169E+Q345R+R320K,A174*+Q169E+Q345R+R458K,A174*+Q169E

24 Mar 2026
2026202266

+Q345R+S323T,A174*+Q169E+Q345R+V206L,A174*+Q169E+Q345R+Y295F,A174*+Q169E+Q365S+R320K,A174*+Q169E+Q365S+R458K,A174*+Q169E+Q365S+S323T,A174*+Q169E+Q365S+V206L,A174*+Q169E+Q365S+Y295F,A174*+Q169E+R320K+R458K,A174*+Q169E+R320K+S323T,A174*+Q169E+R320K+V206L,A174*+Q169E+R320K+Y295F,A174*+Q169E+R458K+S323T,A174*+Q169E+R458K+V206L,A174*+Q169E+R458K+Y295F,A174*+Q169E+S323T+V206L,A174*+Q169E+S323T+Y295F,A174*+Q169E+V206L+Y295F,A174*+Q172K+Q299Y+Q345R,A174*+Q172K+Q299Y+Q365S,A174*+Q172K+Q299Y+R320K,A174*+Q172K+Q299Y+R458K,A174*+Q172K+Q299Y+S323T,A174*+Q172K+Q299Y+V206L,A174*+Q172K+Q299Y+Y295F,A174*+Q172K+Q345R+Q365S,A174*+Q172K+Q345R+R320K,A174*+Q172K+Q345R+R458K,A174*+Q172K+Q345R+S323T,A174*+Q172K+Q345R+V206L,A174*+Q172K+Q345R+Y295F,A174*+Q172K+Q365S+R320K,A174*+Q172K+Q365S+R458K,A174*+Q172K+Q365S+S323T,A174*+Q172K+Q365S+V206L,A174*+Q172K+Q365S+Y295F,A174*+Q172K+R320K+R458K,A174*+Q172K+R320K+S323T,A174*+Q172K+R320K+V206L,A174*+Q172K+R320K+Y295F,A174*+Q172K+R458K+S323T,A174*+Q172K+R458K+V206L,A174*+Q172K+R458K+Y295F,A174*+Q172K+S323T+V206L,A174*+Q172K+S323T+Y295F,A174*+Q172K+V206L+Y295F,A174*+Q299Y+Q345R+Q365S,A174*+Q299Y+Q345R+R320K,A174*+Q299Y+Q345R+R458K,A174*+Q299Y+Q345R+S323T,A174*+Q299Y+Q345R+V206L,A174*+Q299Y+Q345R+Y295F,A174*+Q299Y+Q365S+R320K,A174*+Q299Y+Q365S+R458K,A174*+Q299Y+Q365S+S323T,A174*+Q299Y+Q365S+V206L,A174*+Q299Y+Q365S+Y295F,A174*+Q299Y+R320K+R458K,A174*+Q299Y+R320K+S323T,A174*+Q299Y+R320K+V206L,A174*+Q299Y+R320K+Y295F,A174*+Q299Y+R458K+S323T,A174*+Q299Y+R458K+V206L,A174*+Q299Y+R458K+Y295F,A174*+Q299Y+S323T+V206L,A174*+Q299Y+S323T+Y295F,A174*+Q299Y+V206L+Y295F,A174*+Q345R+Q365S+R320K,A174*+Q345R+Q365S+R458K,A174*+Q345R+Q365S+S323T,A174*+Q345R+Q365S+V206L,A174*+Q345R+Q365S+Y295F,A174*+Q345R+R320K+R458K,A174*+Q345R+R320K+S323T,A174*+Q345R+R320K+V206L,A174*+Q345R+R320K+Y295F,A174*+Q345R+R458K+S323T,A174*+Q345R+R458K+V206L,A174*+Q345R+R458K+Y295F,A174*+Q345R+S323T+V206L,A174*+Q345R+S323T+Y295F,A174*+Q345R+V206L+Y295F,A174*+Q365S+R320K+R458K,A174*+Q365S+R320K+S323T,A174*+Q365S+R320K+V206L,A174*+Q365S+R320K+Y295F,A174*+Q365S+R458K+S323T,A174*+Q365S+R458K+V206L,A174*+Q365S+R458K+Y295F,A174*+Q365S+S323T+V206L,A174*+Q365S+S323T+Y295F,A174*+Q365S+V206L+Y295F,A174*+R320K+R458K+S323T,A174*+R320K+R458K+V206L,A174*+R320K+R458K+Y295F,A174*+R320K+S323T+V206L,A174*+R320K+S323T+Y295F,A174*+R320K+V206L+Y295F,A174*+R458K+S323T+V206L,A174*+R458K+S323T+Y295F,A174*+R458K+V206L+Y295F,A174*+S323T+V206L+Y295F,A339S+G109A+G149A+G182T,A339S+G109A+G149A+H1*,A339S+G109A+G149A+I9M,A339S+G109A+G149A+K391A,A339S+G109A+G149A+M202L,A339S+G109A+G149A+N16Y,A339S+G109A+G149A+N195F,A339S+G109A+G149A+N54

24 Mar 2026
2026202266

S,A339S+G109A+G149A+Q169E,A339S+G109A+G149A+Q169E,A339S+G109A+G149A+Q1
72K,A339S+G109A+G149A+Q299Y,A339S+G109A+G149A+Q345R,A339S+G109A+G149A+
Q365S,A339S+G109A+G149A+R320K,A339S+G109A+G149A+R458K,A339S+G109A+G149A
+S323T,A339S+G109A+G149A+V206L,A339S+G109A+G149A+Y295F,A339S+G109A+G182T
+H1*,A339S+G109A+G182T+I9M,A339S+G109A+G182T+K391A,A339S+G109A+G182T+M20
2L,A339S+G109A+G182T+N16Y,A339S+G109A+G182T+N195F,A339S+G109A+G182T+N54
S,A339S+G109A+G182T+Q169E,A339S+G109A+G182T+Q169E,A339S+G109A+G182T+Q17
2K,A339S+G109A+G182T+Q299Y,A339S+G109A+G182T+Q345R,A339S+G109A+G182T+Q3
65S,A339S+G109A+G182T+R320K,A339S+G109A+G182T+R458K,A339S+G109A+G182T+S
323T,A339S+G109A+G182T+V206L,A339S+G109A+G182T+Y295F,A339S+G109A+H1*+I9M,
A339S+G109A+H1*+K391A,A339S+G109A+H1*+M202L,A339S+G109A+H1*+N16Y,A339S+G
109A+H1*+N195F,A339S+G109A+H1*+N54S,A339S+G109A+H1*+Q169E,A339S+G109A+H1
+Q169E,A339S+G109A+H1+Q172K,A339S+G109A+H1*+Q299Y,A339S+G109A+H1*+Q345
R,A339S+G109A+H1*+Q365S,A339S+G109A+H1*+R320K,A339S+G109A+H1*+R458K,A339
S+G109A+H1*+S323T,A339S+G109A+H1*+V206L,A339S+G109A+H1*+Y295F,A339S+G109
A+I9M+K391A,A339S+G109A+I9M+M202L,A339S+G109A+I9M+N16Y,A339S+G109A+I9M+N
195F,A339S+G109A+I9M+N54S,A339S+G109A+I9M+Q169E,A339S+G109A+I9M+Q169E,A33
9S+G109A+I9M+Q172K,A339S+G109A+I9M+Q299Y,A339S+G109A+I9M+Q345R,A339S+G1
09A+I9M+Q365S,A339S+G109A+I9M+R320K,A339S+G109A+I9M+R458K,A339S+G109A+I9
M+S323T,A339S+G109A+I9M+V206L,A339S+G109A+I9M+Y295F,A339S+G109A+K391A+M2
02L,A339S+G109A+K391A+N16Y,A339S+G109A+K391A+N195F,A339S+G109A+K391A+N54
S,A339S+G109A+K391A+Q169E,A339S+G109A+K391A+Q169E,A339S+G109A+K391A+Q17
2K,A339S+G109A+K391A+Q299Y,A339S+G109A+K391A+Q345R,A339S+G109A+K391A+Q3
65S,A339S+G109A+K391A+R320K,A339S+G109A+K391A+R458K,A339S+G109A+K391A+S
323T,A339S+G109A+K391A+V206L,A339S+G109A+K391A+Y295F,A339S+G109A+M202L+N
16Y,A339S+G109A+M202L+N195F,A339S+G109A+M202L+N54S,A339S+G109A+M202L+Q1
69E,A339S+G109A+M202L+Q169E,A339S+G109A+M202L+Q172K,A339S+G109A+M202L+Q
299Y,A339S+G109A+M202L+Q345R,A339S+G109A+M202L+Q365S,A339S+G109A+M202L+
R320K,A339S+G109A+M202L+R458K,A339S+G109A+M202L+S323T,A339S+G109A+M202L
+V206L,A339S+G109A+M202L+Y295F,A339S+G109A+N16Y+N195F,A339S+G109A+N16Y+
N54S,A339S+G109A+N16Y+Q169E,A339S+G109A+N16Y+Q169E,A339S+G109A+N16Y+Q1
72K,A339S+G109A+N16Y+Q299Y,A339S+G109A+N16Y+Q345R,A339S+G109A+N16Y+Q365
S,A339S+G109A+N16Y+R320K,A339S+G109A+N16Y+R458K,A339S+G109A+N16Y+S323T,
A339S+G109A+N16Y+V206L,A339S+G109A+N16Y+Y295F,A339S+G109A+N195F+N54S,A3
39S+G109A+N195F+Q169E,A339S+G109A+N195F+Q169E,A339S+G109A+N195F+Q172K,A
339S+G109A+N195F+Q299Y,A339S+G109A+N195F+Q345R,A339S+G109A+N195F+Q365S,

24 Mar 2026
2026202266

A339S+G109A+N195F+R320K,A339S+G109A+N195F+R458K,A339S+G109A+N195F+S323T,
A339S+G109A+N195F+V206L,A339S+G109A+N195F+Y295F,A339S+G109A+N54S+Q169E,
A339S+G109A+N54S+Q169E,A339S+G109A+N54S+Q172K,A339S+G109A+N54S+Q299Y,A3
39S+G109A+N54S+Q345R,A339S+G109A+N54S+Q365S,A339S+G109A+N54S+R320K,A339
S+G109A+N54S+R458K,A339S+G109A+N54S+S323T,A339S+G109A+N54S+V206L,A339S+
G109A+N54S+Y295F,A339S+G109A+Q169E+Q169E,A339S+G109A+Q169E+Q172K,A339S+
G109A+Q169E+Q299Y,A339S+G109A+Q169E+Q345R,A339S+G109A+Q169E+Q365S,A339
S+G109A+Q169E+R320K,A339S+G109A+Q169E+R458K,A339S+G109A+Q169E+S323T,A33
9S+G109A+Q169E+V206L,A339S+G109A+Q169E+Y295F,A339S+G109A+Q169E+Q172K,A3
39S+G109A+Q169E+Q299Y,A339S+G109A+Q169E+Q345R,A339S+G109A+Q169E+Q365S,
A339S+G109A+Q169E+R320K,A339S+G109A+Q169E+R458K,A339S+G109A+Q169E+S323
T,A339S+G109A+Q169E+V206L,A339S+G109A+Q169E+Y295F,A339S+G109A+Q172K+Q29
9Y,A339S+G109A+Q172K+Q345R,A339S+G109A+Q172K+Q365S,A339S+G109A+Q172K+R
320K,A339S+G109A+Q172K+R458K,A339S+G109A+Q172K+S323T,A339S+G109A+Q172K+
V206L,A339S+G109A+Q172K+Y295F,A339S+G109A+Q299Y+Q345R,A339S+G109A+Q299Y
+Q365S,A339S+G109A+Q299Y+R320K,A339S+G109A+Q299Y+R458K,A339S+G109A+Q299
Y+S323T,A339S+G109A+Q299Y+V206L,A339S+G109A+Q299Y+Y295F,A339S+G109A+Q34
5R+Q365S,A339S+G109A+Q345R+R320K,A339S+G109A+Q345R+R458K,A339S+G109A+Q
345R+S323T,A339S+G109A+Q345R+V206L,A339S+G109A+Q345R+Y295F,A339S+G109A+
Q365S+R320K,A339S+G109A+Q365S+R458K,A339S+G109A+Q365S+S323T,A339S+G109A
+Q365S+V206L,A339S+G109A+Q365S+Y295F,A339S+G109A+R320K+R458K,A339S+G109
A+R320K+S323T,A339S+G109A+R320K+V206L,A339S+G109A+R320K+Y295F,A339S+G109
A+R458K+S323T,A339S+G109A+R458K+V206L,A339S+G109A+R458K+Y295F,A339S+G109
A+S323T+V206L,A339S+G109A+S323T+Y295F,A339S+G109A+V206L+Y295F,A339S+G149
A+G182T+H1*,A339S+G149A+G182T+I9M,A339S+G149A+G182T+K391A,A339S+G149A+G
182T+M202L,A339S+G149A+G182T+N16Y,A339S+G149A+G182T+N195F,A339S+G149A+G
182T+N54S,A339S+G149A+G182T+Q169E,A339S+G149A+G182T+Q169E,A339S+G149A+G
182T+Q172K,A339S+G149A+G182T+Q299Y,A339S+G149A+G182T+Q345R,A339S+G149A+
G182T+Q365S,A339S+G149A+G182T+R320K,A339S+G149A+G182T+R458K,A339S+G149A
+G182T+S323T,A339S+G149A+G182T+V206L,A339S+G149A+G182T+Y295F,A339S+G149A
+H1*+I9M,A339S+G149A+H1*+K391A,A339S+G149A+H1*+M202L,A339S+G149A+H1*+N16Y
,A339S+G149A+H1*+N195F,A339S+G149A+H1*+N54S,A339S+G149A+H1*+Q169E,A339S+
G149A+H1*+Q169E,A339S+G149A+H1*+Q172K,A339S+G149A+H1*+Q299Y,A339S+G149A+
H1*+Q345R,A339S+G149A+H1*+Q365S,A339S+G149A+H1*+R320K,A339S+G149A+H1*+R4
58K,A339S+G149A+H1*+S323T,A339S+G149A+H1*+V206L,A339S+G149A+H1*+Y295F,A33
9S+G149A+I9M+K391A,A339S+G149A+I9M+M202L,A339S+G149A+I9M+N16Y,A339S+G149

24 Mar 2026
2026202266

A+I9M+N195F,A339S+G149A+I9M+N54S,A339S+G149A+I9M+Q169E,A339S+G149A+I9M+Q169E,A339S+G149A+I9M+Q172K,A339S+G149A+I9M+Q299Y,A339S+G149A+I9M+Q345R,A339S+G149A+I9M+Q365S,A339S+G149A+I9M+R320K,A339S+G149A+I9M+R458K,A339S+G149A+I9M+S323T,A339S+G149A+I9M+V206L,A339S+G149A+I9M+Y295F,A339S+G149A+K391A+M202L,A339S+G149A+K391A+N16Y,A339S+G149A+K391A+N195F,A339S+G149A+K391A+N54S,A339S+G149A+K391A+Q169E,A339S+G149A+K391A+Q169E,A339S+G149A+K391A+Q172K,A339S+G149A+K391A+Q299Y,A339S+G149A+K391A+Q345R,A339S+G149A+K391A+Q365S,A339S+G149A+K391A+R320K,A339S+G149A+K391A+R458K,A339S+G149A+K391A+S323T,A339S+G149A+K391A+V206L,A339S+G149A+K391A+Y295F,A339S+G149A+M202L+N16Y,A339S+G149A+M202L+N195F,A339S+G149A+M202L+N54S,A339S+G149A+M202L+Q169E,A339S+G149A+M202L+Q169E,A339S+G149A+M202L+Q172K,A339S+G149A+M202L+Q299Y,A339S+G149A+M202L+Q345R,A339S+G149A+M202L+Q365S,A339S+G149A+M202L+R320K,A339S+G149A+M202L+R458K,A339S+G149A+M202L+S323T,A339S+G149A+M202L+V206L,A339S+G149A+M202L+Y295F,A339S+G149A+N16Y+N195F,A339S+G149A+N16Y+N54S,A339S+G149A+N16Y+Q169E,A339S+G149A+N16Y+Q169E,A339S+G149A+N16Y+Q172K,A339S+G149A+N16Y+Q299Y,A339S+G149A+N16Y+Q345R,A339S+G149A+N16Y+Q365S,A339S+G149A+N16Y+R320K,A339S+G149A+N16Y+R458K,A339S+G149A+N16Y+S323T,A339S+G149A+N16Y+V206L,A339S+G149A+N16Y+Y295F,A339S+G149A+N195F+N54S,A339S+G149A+N195F+Q169E,A339S+G149A+N195F+Q169E,A339S+G149A+N195F+Q172K,A339S+G149A+N195F+Q299Y,A339S+G149A+N195F+Q345R,A339S+G149A+N195F+Q365S,A339S+G149A+N195F+R320K,A339S+G149A+N195F+R458K,A339S+G149A+N195F+S323T,A339S+G149A+N195F+V206L,A339S+G149A+N195F+Y295F,A339S+G149A+N54S+Q169E,A339S+G149A+N54S+Q169E,A339S+G149A+N54S+Q172K,A339S+G149A+N54S+Q299Y,A339S+G149A+N54S+Q345R,A339S+G149A+N54S+Q365S,A339S+G149A+N54S+R320K,A339S+G149A+N54S+R458K,A339S+G149A+N54S+S323T,A339S+G149A+N54S+V206L,A339S+G149A+N54S+Y295F,A339S+G149A+Q169E+Q169E,A339S+G149A+Q169E+Q172K,A339S+G149A+Q169E+Q299Y,A339S+G149A+Q169E+Q345R,A339S+G149A+Q169E+Q365S,A339S+G149A+Q169E+R320K,A339S+G149A+Q169E+R458K,A339S+G149A+Q169E+S323T,A339S+G149A+Q169E+V206L,A339S+G149A+Q169E+Y295F,A339S+G149A+Q169E+Q172K,A339S+G149A+Q169E+Q299Y,A339S+G149A+Q169E+Q345R,A339S+G149A+Q169E+Q365S,A339S+G149A+Q169E+R320K,A339S+G149A+Q169E+R458K,A339S+G149A+Q169E+S323T,A339S+G149A+Q169E+V206L,A339S+G149A+Q169E+Y295F,A339S+G149A+Q172K+Q299Y,A339S+G149A+Q172K+Q345R,A339S+G149A+Q172K+Q365S,A339S+G149A+Q172K+R320K,A339S+G149A+Q172K+R458K,A339S+G149A+Q172K+S323T,A339S+G149A+Q172K+V206L,A339S+G149A+Q172K+Y295F,A339S+G149A+Q299Y+Q345R,A339S+G149A+Q299Y+Q365S,A339S+G149A+Q299Y+R320K,A339S+G149A+Q299Y+R458K,A339S+G14

24 Mar 2026
2026202266

9A+Q299Y+S323T,A339S+G149A+Q299Y+V206L,A339S+G149A+Q299Y+Y295F,A339S+G1
49A+Q345R+Q365S,A339S+G149A+Q345R+R320K,A339S+G149A+Q345R+R458K,A339S+
G149A+Q345R+S323T,A339S+G149A+Q345R+V206L,A339S+G149A+Q345R+Y295F,A339S
+G149A+Q365S+R320K,A339S+G149A+Q365S+R458K,A339S+G149A+Q365S+S323T,A339
S+G149A+Q365S+V206L,A339S+G149A+Q365S+Y295F,A339S+G149A+R320K+R458K,A33
9S+G149A+R320K+S323T,A339S+G149A+R320K+V206L,A339S+G149A+R320K+Y295F,A33
9S+G149A+R458K+S323T,A339S+G149A+R458K+V206L,A339S+G149A+R458K+Y295F,A33
9S+G149A+S323T+V206L,A339S+G149A+S323T+Y295F,A339S+G149A+V206L+Y295F,A33
9S+G182T+H1*+I9M,A339S+G182T+H1*+K391A,A339S+G182T+H1*+M202L,A339S+G182T+
H1*+N16Y,A339S+G182T+H1*+N195F,A339S+G182T+H1*+N54S,A339S+G182T+H1*+Q169
E,A339S+G182T+H1*+Q169E,A339S+G182T+H1*+Q172K,A339S+G182T+H1*+Q299Y,A339
S+G182T+H1*+Q345R,A339S+G182T+H1*+Q365S,A339S+G182T+H1*+R320K,A339S+G182
T+H1*+R458K,A339S+G182T+H1*+S323T,A339S+G182T+H1*+V206L,A339S+G182T+H1*+Y
295F,A339S+G182T+I9M+K391A,A339S+G182T+I9M+M202L,A339S+G182T+I9M+N16Y,A33
9S+G182T+I9M+N195F,A339S+G182T+I9M+N54S,A339S+G182T+I9M+Q169E,A339S+G182
T+I9M+Q169E,A339S+G182T+I9M+Q172K,A339S+G182T+I9M+Q299Y,A339S+G182T+I9M+
Q345R,A339S+G182T+I9M+Q365S,A339S+G182T+I9M+R320K,A339S+G182T+I9M+R458K,
A339S+G182T+I9M+S323T,A339S+G182T+I9M+V206L,A339S+G182T+I9M+Y295F,A339S+G
182T+K391A+M202L,A339S+G182T+K391A+N16Y,A339S+G182T+K391A+N195F,A339S+G1
82T+K391A+N54S,A339S+G182T+K391A+Q169E,A339S+G182T+K391A+Q169E,A339S+G1
82T+K391A+Q172K,A339S+G182T+K391A+Q299Y,A339S+G182T+K391A+Q345R,A339S+G
182T+K391A+Q365S,A339S+G182T+K391A+R320K,A339S+G182T+K391A+R458K,A339S+G
182T+K391A+S323T,A339S+G182T+K391A+V206L,A339S+G182T+K391A+Y295F,A339S+G
182T+M202L+N16Y,A339S+G182T+M202L+N195F,A339S+G182T+M202L+N54S,A339S+G1
82T+M202L+Q169E,A339S+G182T+M202L+Q169E,A339S+G182T+M202L+Q172K,A339S+G
182T+M202L+Q299Y,A339S+G182T+M202L+Q345R,A339S+G182T+M202L+Q365S,A339S+
G182T+M202L+R320K,A339S+G182T+M202L+R458K,A339S+G182T+M202L+S323T,A339S+
G182T+M202L+V206L,A339S+G182T+M202L+Y295F,A339S+G182T+N16Y+N195F,A339S+G
182T+N16Y+N54S,A339S+G182T+N16Y+Q169E,A339S+G182T+N16Y+Q169E,A339S+G182
T+N16Y+Q172K,A339S+G182T+N16Y+Q299Y,A339S+G182T+N16Y+Q345R,A339S+G182T+
N16Y+Q365S,A339S+G182T+N16Y+R320K,A339S+G182T+N16Y+R458K,A339S+G182T+N1
6Y+S323T,A339S+G182T+N16Y+V206L,A339S+G182T+N16Y+Y295F,A339S+G182T+N195F
+N54S,A339S+G182T+N195F+Q169E,A339S+G182T+N195F+Q169E,A339S+G182T+N195F
+Q172K,A339S+G182T+N195F+Q299Y,A339S+G182T+N195F+Q345R,A339S+G182T+N195
F+Q365S,A339S+G182T+N195F+R320K,A339S+G182T+N195F+R458K,A339S+G182T+N195
F+S323T,A339S+G182T+N195F+V206L,A339S+G182T+N195F+Y295F,A339S+G182T+N54S

24 Mar 2026
2026202266

+Q169E,A339S+G182T+N54S+Q169E,A339S+G182T+N54S+Q172K,A339S+G182T+N54S+Q299Y,A339S+G182T+N54S+Q345R,A339S+G182T+N54S+Q365S,A339S+G182T+N54S+R320K,A339S+G182T+N54S+R458K,A339S+G182T+N54S+S323T,A339S+G182T+N54S+V206L,A339S+G182T+N54S+Y295F,A339S+G182T+Q169E+Q169E,A339S+G182T+Q169E+Q172K,A339S+G182T+Q169E+Q299Y,A339S+G182T+Q169E+Q345R,A339S+G182T+Q169E+Q365S,A339S+G182T+Q169E+R320K,A339S+G182T+Q169E+R458K,A339S+G182T+Q169E+S323T,A339S+G182T+Q169E+V206L,A339S+G182T+Q169E+Y295F,A339S+G182T+Q169E+Q172K,A339S+G182T+Q169E+Q299Y,A339S+G182T+Q169E+Q345R,A339S+G182T+Q169E+Q365S,A339S+G182T+Q169E+R320K,A339S+G182T+Q169E+R458K,A339S+G182T+Q169E+S323T,A339S+G182T+Q169E+V206L,A339S+G182T+Q169E+Y295F,A339S+G182T+Q172K+Q299Y,A339S+G182T+Q172K+Q345R,A339S+G182T+Q172K+Q365S,A339S+G182T+Q172K+R320K,A339S+G182T+Q172K+R458K,A339S+G182T+Q172K+S323T,A339S+G182T+Q172K+V206L,A339S+G182T+Q172K+Y295F,A339S+G182T+Q299Y+Q345R,A339S+G182T+Q299Y+Q365S,A339S+G182T+Q299Y+R320K,A339S+G182T+Q299Y+R458K,A339S+G182T+Q299Y+S323T,A339S+G182T+Q299Y+V206L,A339S+G182T+Q299Y+Y295F,A339S+G182T+Q345R+Q365S,A339S+G182T+Q345R+R320K,A339S+G182T+Q345R+R458K,A339S+G182T+Q345R+S323T,A339S+G182T+Q345R+V206L,A339S+G182T+Q345R+Y295F,A339S+G182T+Q365S+R320K,A339S+G182T+Q365S+R458K,A339S+G182T+Q365S+S323T,A339S+G182T+Q365S+V206L,A339S+G182T+Q365S+Y295F,A339S+G182T+R320K+R458K,A339S+G182T+R320K+S323T,A339S+G182T+R320K+V206L,A339S+G182T+R320K+Y295F,A339S+G182T+R458K+S323T,A339S+G182T+R458K+V206L,A339S+G182T+R458K+Y295F,A339S+G182T+S323T+V206L,A339S+G182T+S323T+Y295F,A339S+G182T+V206L+Y295F,A339S+H1*+I9M+K391A,A339S+H1*+I9M+M202L,A339S+H1*+I9M+N16Y,A339S+H1*+I9M+N195F,A339S+H1*+I9M+N54S,A339S+H1*+I9M+Q169E,A339S+H1*+I9M+Q169E,A339S+H1*+I9M+Q172K,A339S+H1*+I9M+Q299Y,A339S+H1*+I9M+Q345R,A339S+H1*+I9M+Q365S,A339S+H1*+I9M+R320K,A339S+H1*+I9M+R458K,A339S+H1*+I9M+S323T,A339S+H1*+I9M+V206L,A339S+H1*+I9M+Y295F,A339S+H1*+K391A+M202L,A339S+H1*+K391A+N16Y,A339S+H1*+K391A+N195F,A339S+H1*+K391A+N54S,A339S+H1*+K391A+Q169E,A339S+H1*+K391A+Q169E,A339S+H1*+K391A+Q172K,A339S+H1*+K391A+Q299Y,A339S+H1*+K391A+Q345R,A339S+H1*+K391A+Q365S,A339S+H1*+K391A+R320K,A339S+H1*+K391A+R458K,A339S+H1*+K391A+S323T,A339S+H1*+K391A+V206L,A339S+H1*+K391A+Y295F,A339S+H1*+M202L+N16Y,A339S+H1*+M202L+N195F,A339S+H1*+M202L+N54S,A339S+H1*+M202L+Q169E,A339S+H1*+M202L+Q169E,A339S+H1*+M202L+Q172K,A339S+H1*+M202L+Q299Y,A339S+H1*+M202L+Q345R,A339S+H1*+M202L+Q365S,A339S+H1*+M202L+R320K,A339S+H1*+M202L+R458K,A339S+H1*+M202L+S323T,A339S+H1*+M202L+V206L,A339S+H1*+M202L+Y295F,A339S+H1*+N16Y+N195F,A339S+H1*+N16Y+N54S,A339S+H1*+N16Y+Q169E,A339S+H1*+N16Y+Q169E

24 Mar 2026
2026202266

,A339S+H1*+N16Y+Q172K,A339S+H1*+N16Y+Q299Y,A339S+H1*+N16Y+Q345R,A339S+H1*+N16Y+Q365S,A339S+H1*+N16Y+R320K,A339S+H1*+N16Y+R458K,A339S+H1*+N16Y+S323T,A339S+H1*+N16Y+V206L,A339S+H1*+N16Y+Y295F,A339S+H1*+N195F+N54S,A339S+H1*+N195F+Q169E,A339S+H1*+N195F+Q169E,A339S+H1*+N195F+Q172K,A339S+H1*+N195F+Q299Y,A339S+H1*+N195F+Q345R,A339S+H1*+N195F+Q365S,A339S+H1*+N195F+R320K,A339S+H1*+N195F+R458K,A339S+H1*+N195F+S323T,A339S+H1*+N195F+V206L,A339S+H1*+N195F+Y295F,A339S+H1*+N54S+Q169E,A339S+H1*+N54S+Q169E,A339S+H1*+N54S+Q172K,A339S+H1*+N54S+Q299Y,A339S+H1*+N54S+Q345R,A339S+H1*+N54S+Q365S,A339S+H1*+N54S+R320K,A339S+H1*+N54S+R458K,A339S+H1*+N54S+S323T,A339S+H1*+N54S+V206L,A339S+H1*+N54S+Y295F,A339S+H1*+Q169E+Q169E,A339S+H1*+Q169E+Q172K,A339S+H1*+Q169E+Q299Y,A339S+H1*+Q169E+Q345R,A339S+H1*+Q169E+Q365S,A339S+H1*+Q169E+R320K,A339S+H1*+Q169E+R458K,A339S+H1*+Q169E+S323T,A339S+H1*+Q169E+V206L,A339S+H1*+Q169E+Y295F,A339S+H1*+Q172K+Q299Y,A339S+H1*+Q172K+Q345R,A339S+H1*+Q172K+Q365S,A339S+H1*+Q172K+R320K,A339S+H1*+Q172K+R458K,A339S+H1*+Q172K+S323T,A339S+H1*+Q172K+V206L,A339S+H1*+Q172K+Y295F,A339S+H1*+Q299Y+Q345R,A339S+H1*+Q299Y+Q365S,A339S+H1*+Q299Y+R320K,A339S+H1*+Q299Y+R458K,A339S+H1*+Q299Y+S323T,A339S+H1*+Q299Y+V206L,A339S+H1*+Q299Y+Y295F,A339S+H1*+Q345R+Q365S,A339S+H1*+Q345R+R320K,A339S+H1*+Q345R+R458K,A339S+H1*+Q345R+S323T,A339S+H1*+Q345R+V206L,A339S+H1*+Q345R+Y295F,A339S+H1*+Q365S+R320K,A339S+H1*+Q365S+R458K,A339S+H1*+Q365S+S323T,A339S+H1*+Q365S+V206L,A339S+H1*+Q365S+Y295F,A339S+H1*+R320K+R458K,A339S+H1*+R320K+S323T,A339S+H1*+R320K+V206L,A339S+H1*+R320K+Y295F,A339S+H1*+R458K+S323T,A339S+H1*+R458K+V206L,A339S+H1*+R458K+Y295F,A339S+H1*+S323T+V206L,A339S+H1*+S323T+Y295F,A339S+H1*+V206L+Y295F,A339S+I9M+K391A+M202L,A339S+I9M+K391A+N16Y,A339S+I9M+K391A+N195F,A339S+I9M+K391A+N54S,A339S+I9M+K391A+Q169E,A339S+I9M+K391A+Q169E,A339S+I9M+K391A+Q172K,A339S+I9M+K391A+Q299Y,A339S+I9M+K391A+Q345R,A339S+I9M+K391A+Q365S,A339S+I9M+K391A+R320K,A339S+I9M+K391A+R458K,A339S+I9M+K391A+S323T,A339S+I9M+K391A+V206L,A339S+I9M+K391A+Y295F,A339S+I9M+M202L+N16Y,A339S+I9M+M202L+N195F,A339S+I9M+M202L+N54S,A339S+I9M+M202L+Q169E,A339S+I9M+M202L+Q169E,A339S+I9M+M202L+Q172K,A339S+I9M+M202L+Q299Y,A339S+I9M+M202L+Q345R,A339S+I9M+M202L+Q365S,A339S+I9M+M202L+R320K,A339S+I9M+M202L+R458K,A339S+I9M+M202L+S323T,A339S+I9M+M202L+V206L,A339S+I9M+M202L+Y295F,A339S+I9M+N16Y+N195F,A339S+I9M+N16Y+N54S,A339S+I9M+N16Y+Q169E,A339S+I9M+N16Y+Q169E,A

24 Mar 2026
2026202266

339S+I9M+N16Y+Q172K,A339S+I9M+N16Y+Q299Y,A339S+I9M+N16Y+Q345R,A339S+I9M+N16Y+Q365S,A339S+I9M+N16Y+R320K,A339S+I9M+N16Y+R458K,A339S+I9M+N16Y+S323T,A339S+I9M+N16Y+V206L,A339S+I9M+N16Y+Y295F,A339S+I9M+N195F+N54S,A339S+I9M+N195F+Q169E,A339S+I9M+N195F+Q169E,A339S+I9M+N195F+Q172K,A339S+I9M+N195F+Q299Y,A339S+I9M+N195F+Q345R,A339S+I9M+N195F+Q365S,A339S+I9M+N195F+R320K,A339S+I9M+N195F+R458K,A339S+I9M+N195F+S323T,A339S+I9M+N195F+V206L,A339S+I9M+N195F+Y295F,A339S+I9M+N54S+Q169E,A339S+I9M+N54S+Q169E,A339S+I9M+N54S+Q172K,A339S+I9M+N54S+Q299Y,A339S+I9M+N54S+Q345R,A339S+I9M+N54S+Q365S,A339S+I9M+N54S+R320K,A339S+I9M+N54S+R458K,A339S+I9M+N54S+S323T,A339S+I9M+N54S+V206L,A339S+I9M+N54S+Y295F,A339S+I9M+Q169E+Q169E,A339S+I9M+Q169E+Q172K,A339S+I9M+Q169E+Q299Y,A339S+I9M+Q169E+Q345R,A339S+I9M+Q169E+Q365S,A339S+I9M+Q169E+R320K,A339S+I9M+Q169E+R458K,A339S+I9M+Q169E+S323T,A339S+I9M+Q169E+V206L,A339S+I9M+Q169E+Y295F,A339S+I9M+Q169E+Q172K,A339S+I9M+Q169E+Q299Y,A339S+I9M+Q169E+Q345R,A339S+I9M+Q169E+Q365S,A339S+I9M+Q169E+R320K,A339S+I9M+Q169E+R458K,A339S+I9M+Q169E+S323T,A339S+I9M+Q169E+V206L,A339S+I9M+Q169E+Y295F,A339S+I9M+Q172K+Q299Y,A339S+I9M+Q172K+Q345R,A339S+I9M+Q172K+Q365S,A339S+I9M+Q172K+R320K,A339S+I9M+Q172K+R458K,A339S+I9M+Q172K+S323T,A339S+I9M+Q172K+V206L,A339S+I9M+Q172K+Y295F,A339S+I9M+Q299Y+Q345R,A339S+I9M+Q299Y+Q365S,A339S+I9M+Q299Y+R320K,A339S+I9M+Q299Y+R458K,A339S+I9M+Q299Y+S323T,A339S+I9M+Q299Y+V206L,A339S+I9M+Q299Y+Y295F,A339S+I9M+Q345R+Q365S,A339S+I9M+Q345R+R320K,A339S+I9M+Q345R+R458K,A339S+I9M+Q345R+S323T,A339S+I9M+Q345R+V206L,A339S+I9M+Q345R+Y295F,A339S+I9M+Q365S+R320K,A339S+I9M+Q365S+R458K,A339S+I9M+Q365S+S323T,A339S+I9M+Q365S+V206L,A339S+I9M+Q365S+Y295F,A339S+I9M+R320K+R458K,A339S+I9M+R320K+S323T,A339S+I9M+R320K+V206L,A339S+I9M+R320K+Y295F,A339S+I9M+R458K+S323T,A339S+I9M+R458K+V206L,A339S+I9M+R458K+Y295F,A339S+I9M+S323T+V206L,A339S+I9M+S323T+Y295F,A339S+I9M+V206L+Y295F,A339S+K391A+M202L+N16Y,A339S+K391A+M202L+N195F,A339S+K391A+M202L+N54S,A339S+K391A+M202L+Q169E,A339S+K391A+M202L+Q169E,A339S+K391A+M202L+Q172K,A339S+K391A+M202L+Q299Y,A339S+K391A+M202L+Q345R,A339S+K391A+M202L+Q365S,A339S+K391A+M202L+R320K,A339S+K391A+M202L+R458K,A339S+K391A+M202L+S323T,A339S+K391A+M202L+V206L,A339S+K391A+M202L+Y295F,A339S+K391A+N16Y+N195F,A339S+K391A+N16Y+N54S,A339S+K391A+N16Y+Q169E,A339S+K391A+N16Y+Q169E,A339S+K391A+N16Y+Q172K,A339S+K391A+N16Y+Q299Y,A339S+K391A+N16Y+Q345R,A339S+K391A+N16Y+Q365S,A339S+K391A+N16Y+R320K,A339S+K391A+N16Y+R458K,A339S+K391A+N16Y+S323T,A339S+K391A+N16Y+V206L,A339S+K391A+N16Y+Y295F,A339S+K391A+N195F+N54S,A339S+K391A+N195F+Q169E,A339S+K391A+N195F+Q169E,A339

24 Mar 2026
2026202266

S+K391A+N195F+Q172K,A339S+K391A+N195F+Q299Y,A339S+K391A+N195F+Q345R,A339S+K391A+N195F+Q365S,A339S+K391A+N195F+R320K,A339S+K391A+N195F+R458K,A339S+K391A+N195F+S323T,A339S+K391A+N195F+V206L,A339S+K391A+N195F+Y295F,A339S+K391A+N54S+Q169E,A339S+K391A+N54S+Q169E,A339S+K391A+N54S+Q172K,A339S+K391A+N54S+Q299Y,A339S+K391A+N54S+Q345R,A339S+K391A+N54S+Q365S,A339S+K391A+N54S+R320K,A339S+K391A+N54S+R458K,A339S+K391A+N54S+S323T,A339S+K391A+N54S+V206L,A339S+K391A+N54S+Y295F,A339S+K391A+Q169E+Q169E,A339S+K391A+Q169E+Q172K,A339S+K391A+Q169E+Q299Y,A339S+K391A+Q169E+Q345R,A339S+K391A+Q169E+Q365S,A339S+K391A+Q169E+R320K,A339S+K391A+Q169E+R458K,A339S+K391A+Q169E+S323T,A339S+K391A+Q169E+V206L,A339S+K391A+Q169E+Y295F,A339S+K391A+Q169E+Q172K,A339S+K391A+Q169E+Q299Y,A339S+K391A+Q169E+Q345R,A339S+K391A+Q169E+Q365S,A339S+K391A+Q169E+R320K,A339S+K391A+Q169E+R458K,A339S+K391A+Q169E+S323T,A339S+K391A+Q169E+V206L,A339S+K391A+Q169E+Y295F,A339S+K391A+Q172K+Q299Y,A339S+K391A+Q172K+Q345R,A339S+K391A+Q172K+Q365S,A339S+K391A+Q172K+R320K,A339S+K391A+Q172K+R458K,A339S+K391A+Q172K+S323T,A339S+K391A+Q172K+V206L,A339S+K391A+Q172K+Y295F,A339S+K391A+Q299Y+Q345R,A339S+K391A+Q299Y+Q365S,A339S+K391A+Q299Y+R320K,A339S+K391A+Q299Y+R458K,A339S+K391A+Q299Y+S323T,A339S+K391A+Q299Y+V206L,A339S+K391A+Q299Y+Y295F,A339S+K391A+Q345R+Q365S,A339S+K391A+Q345R+R320K,A339S+K391A+Q345R+R458K,A339S+K391A+Q345R+S323T,A339S+K391A+Q345R+V206L,A339S+K391A+Q345R+Y295F,A339S+K391A+Q365S+R320K,A339S+K391A+Q365S+R458K,A339S+K391A+Q365S+S323T,A339S+K391A+Q365S+V206L,A339S+K391A+Q365S+Y295F,A339S+K391A+R320K+R458K,A339S+K391A+R320K+S323T,A339S+K391A+R320K+V206L,A339S+K391A+R320K+Y295F,A339S+K391A+R458K+S323T,A339S+K391A+R458K+V206L,A339S+K391A+R458K+Y295F,A339S+K391A+S323T+V206L,A339S+K391A+S323T+Y295F,A339S+K391A+V206L+Y295F,A339S+M202L+N16Y+N195F,A339S+M202L+N16Y+N54S,A339S+M202L+N16Y+Q169E,A339S+M202L+N16Y+Q169E,A339S+M202L+N16Y+Q172K,A339S+M202L+N16Y+Q299Y,A339S+M202L+N16Y+Q345R,A339S+M202L+N16Y+Q365S,A339S+M202L+N16Y+R320K,A339S+M202L+N16Y+R458K,A339S+M202L+N16Y+S323T,A339S+M202L+N16Y+V206L,A339S+M202L+N16Y+Y295F,A339S+M202L+N195F+N54S,A339S+M202L+N195F+Q169E,A339S+M202L+N195F+Q169E,A339S+M202L+N195F+Q172K,A339S+M202L+N195F+Q299Y,A339S+M202L+N195F+Q345R,A339S+M202L+N195F+Q365S,A339S+M202L+N195F+R320K,A339S+M202L+N195F+R458K,A339S+M202L+N195F+S323T,A339S+M202L+N195F+V206L,A339S+M202L+N195F+Y295F,A339S+M202L+N54S+Q169E,A339S+M202L+N54S+Q169E,A339S+M202L+N54S+Q172K,A339S+M202L+N54S+Q299Y,A339S+M202L+N54S+Q345R,A339S+M202L+N54S+Q365S,A339S+M202L+N54S+R320K,A339S+M202L+N54S+R458K,A339S+M202L+N54S+S323

24 Mar 2026
2026202266

T,A339S+M202L+N54S+V206L,A339S+M202L+N54S+Y295F,A339S+M202L+Q169E+Q169E,
A339S+M202L+Q169E+Q172K,A339S+M202L+Q169E+Q299Y,A339S+M202L+Q169E+Q345
R,A339S+M202L+Q169E+Q365S,A339S+M202L+Q169E+R320K,A339S+M202L+Q169E+R45
8K,A339S+M202L+Q169E+S323T,A339S+M202L+Q169E+V206L,A339S+M202L+Q169E+Y29
5F,A339S+M202L+Q169E+Q172K,A339S+M202L+Q169E+Q299Y,A339S+M202L+Q169E+Q3
45R,A339S+M202L+Q169E+Q365S,A339S+M202L+Q169E+R320K,A339S+M202L+Q169E+R
458K,A339S+M202L+Q169E+S323T,A339S+M202L+Q169E+V206L,A339S+M202L+Q169E+Y
295F,A339S+M202L+Q172K+Q299Y,A339S+M202L+Q172K+Q345R,A339S+M202L+Q172K+
Q365S,A339S+M202L+Q172K+R320K,A339S+M202L+Q172K+R458K,A339S+M202L+Q172K
+S323T,A339S+M202L+Q172K+V206L,A339S+M202L+Q172K+Y295F,A339S+M202L+Q299Y
+Q345R,A339S+M202L+Q299Y+Q365S,A339S+M202L+Q299Y+R320K,A339S+M202L+Q299
Y+R458K,A339S+M202L+Q299Y+S323T,A339S+M202L+Q299Y+V206L,A339S+M202L+Q299
Y+Y295F,A339S+M202L+Q345R+Q365S,A339S+M202L+Q345R+R320K,A339S+M202L+Q34
5R+R458K,A339S+M202L+Q345R+S323T,A339S+M202L+Q345R+V206L,A339S+M202L+Q3
45R+Y295F,A339S+M202L+Q365S+R320K,A339S+M202L+Q365S+R458K,A339S+M202L+Q
365S+S323T,A339S+M202L+Q365S+V206L,A339S+M202L+Q365S+Y295F,A339S+M202L+R
320K+R458K,A339S+M202L+R320K+S323T,A339S+M202L+R320K+V206L,A339S+M202L+R
320K+Y295F,A339S+M202L+R458K+S323T,A339S+M202L+R458K+V206L,A339S+M202L+R
458K+Y295F,A339S+M202L+S323T+V206L,A339S+M202L+S323T+Y295F,A339S+M202L+V2
06L+Y295F,A339S+N16Y+N195F+N54S,A339S+N16Y+N195F+Q169E,A339S+N16Y+N195F+
Q169E,A339S+N16Y+N195F+Q172K,A339S+N16Y+N195F+Q299Y,A339S+N16Y+N195F+Q3
45R,A339S+N16Y+N195F+Q365S,A339S+N16Y+N195F+R320K,A339S+N16Y+N195F+R458
K,A339S+N16Y+N195F+S323T,A339S+N16Y+N195F+V206L,A339S+N16Y+N195F+Y295F,A
339S+N16Y+N54S+Q169E,A339S+N16Y+N54S+Q169E,A339S+N16Y+N54S+Q172K,A339S+
N16Y+N54S+Q299Y,A339S+N16Y+N54S+Q345R,A339S+N16Y+N54S+Q365S,A339S+N16Y
+N54S+R320K,A339S+N16Y+N54S+R458K,A339S+N16Y+N54S+S323T,A339S+N16Y+N54S
+V206L,A339S+N16Y+N54S+Y295F,A339S+N16Y+Q169E+Q169E,A339S+N16Y+Q169E+Q1
72K,A339S+N16Y+Q169E+Q299Y,A339S+N16Y+Q169E+Q345R,A339S+N16Y+Q169E+Q365
S,A339S+N16Y+Q169E+R320K,A339S+N16Y+Q169E+R458K,A339S+N16Y+Q169E+S323T,
A339S+N16Y+Q169E+V206L,A339S+N16Y+Q169E+Y295F,A339S+N16Y+Q169E+Q172K,A3
39S+N16Y+Q169E+Q299Y,A339S+N16Y+Q169E+Q345R,A339S+N16Y+Q169E+Q365S,A339
S+N16Y+Q169E+R320K,A339S+N16Y+Q169E+R458K,A339S+N16Y+Q169E+S323T,A339S+
N16Y+Q169E+V206L,A339S+N16Y+Q169E+Y295F,A339S+N16Y+Q172K+Q299Y,A339S+N1
6Y+Q172K+Q345R,A339S+N16Y+Q172K+Q365S,A339S+N16Y+Q172K+R320K,A339S+N16Y
+Q172K+R458K,A339S+N16Y+Q172K+S323T,A339S+N16Y+Q172K+V206L,A339S+N16Y+Q
172K+Y295F,A339S+N16Y+Q299Y+Q345R,A339S+N16Y+Q299Y+Q365S,A339S+N16Y+Q29

24 Mar 2026
2026202266

9Y+R320K,A339S+N16Y+Q299Y+R458K,A339S+N16Y+Q299Y+S323T,A339S+N16Y+Q299Y
+V206L,A339S+N16Y+Q299Y+Y295F,A339S+N16Y+Q345R+Q365S,A339S+N16Y+Q345R+R
320K,A339S+N16Y+Q345R+R458K,A339S+N16Y+Q345R+S323T,A339S+N16Y+Q345R+V20
6L,A339S+N16Y+Q345R+Y295F,A339S+N16Y+Q365S+R320K,A339S+N16Y+Q365S+R458K,
A339S+N16Y+Q365S+S323T,A339S+N16Y+Q365S+V206L,A339S+N16Y+Q365S+Y295F,A33
9S+N16Y+R320K+R458K,A339S+N16Y+R320K+S323T,A339S+N16Y+R320K+V206L,A339S+
N16Y+R320K+Y295F,A339S+N16Y+R458K+S323T,A339S+N16Y+R458K+V206L,A339S+N16
Y+R458K+Y295F,A339S+N16Y+S323T+V206L,A339S+N16Y+S323T+Y295F,A339S+N16Y+V
206L+Y295F,A339S+N195F+N54S+Q169E,A339S+N195F+N54S+Q169E,A339S+N195F+N54
S+Q172K,A339S+N195F+N54S+Q299Y,A339S+N195F+N54S+Q345R,A339S+N195F+N54S+
Q365S,A339S+N195F+N54S+R320K,A339S+N195F+N54S+R458K,A339S+N195F+N54S+S3
23T,A339S+N195F+N54S+V206L,A339S+N195F+N54S+Y295F,A339S+N195F+Q169E+Q169
E,A339S+N195F+Q169E+Q172K,A339S+N195F+Q169E+Q299Y,A339S+N195F+Q169E+Q34
5R,A339S+N195F+Q169E+Q365S,A339S+N195F+Q169E+R320K,A339S+N195F+Q169E+R4
58K,A339S+N195F+Q169E+S323T,A339S+N195F+Q169E+V206L,A339S+N195F+Q169E+Y2
95F,A339S+N195F+Q169E+Q172K,A339S+N195F+Q169E+Q299Y,A339S+N195F+Q169E+Q
345R,A339S+N195F+Q169E+Q365S,A339S+N195F+Q169E+R320K,A339S+N195F+Q169E+
R458K,A339S+N195F+Q169E+S323T,A339S+N195F+Q169E+V206L,A339S+N195F+Q169E+
Y295F,A339S+N195F+Q172K+Q299Y,A339S+N195F+Q172K+Q345R,A339S+N195F+Q172K
+Q365S,A339S+N195F+Q172K+R320K,A339S+N195F+Q172K+R458K,A339S+N195F+Q172
K+S323T,A339S+N195F+Q172K+V206L,A339S+N195F+Q172K+Y295F,A339S+N195F+Q299
Y+Q345R,A339S+N195F+Q299Y+Q365S,A339S+N195F+Q299Y+R320K,A339S+N195F+Q29
9Y+R458K,A339S+N195F+Q299Y+S323T,A339S+N195F+Q299Y+V206L,A339S+N195F+Q29
9Y+Y295F,A339S+N195F+Q345R+Q365S,A339S+N195F+Q345R+R320K,A339S+N195F+Q3
45R+R458K,A339S+N195F+Q345R+S323T,A339S+N195F+Q345R+V206L,A339S+N195F+Q3
45R+Y295F,A339S+N195F+Q365S+R320K,A339S+N195F+Q365S+R458K,A339S+N195F+Q
365S+S323T,A339S+N195F+Q365S+V206L,A339S+N195F+Q365S+Y295F,A339S+N195F+R
320K+R458K,A339S+N195F+R320K+S323T,A339S+N195F+R320K+V206L,A339S+N195F+R
320K+Y295F,A339S+N195F+R458K+S323T,A339S+N195F+R458K+V206L,A339S+N195F+R
458K+Y295F,A339S+N195F+S323T+V206L,A339S+N195F+S323T+Y295F,A339S+N195F+V2
06L+Y295F,A339S+N54S+Q169E+Q169E,A339S+N54S+Q169E+Q172K,A339S+N54S+Q169
E+Q299Y,A339S+N54S+Q169E+Q345R,A339S+N54S+Q169E+Q365S,A339S+N54S+Q169E
+R320K,A339S+N54S+Q169E+R458K,A339S+N54S+Q169E+S323T,A339S+N54S+Q169E+V
206L,A339S+N54S+Q169E+Y295F,A339S+N54S+Q169E+Q172K,A339S+N54S+Q169E+Q29
9Y,A339S+N54S+Q169E+Q345R,A339S+N54S+Q169E+Q365S,A339S+N54S+Q169E+R320K
,A339S+N54S+Q169E+R458K,A339S+N54S+Q169E+S323T,A339S+N54S+Q169E+V206L,A3

24 Mar 2026
2026202266

39S+N54S+Q169E+Y295F,A339S+N54S+Q172K+Q299Y,A339S+N54S+Q172K+Q345R,A339S+N54S+Q172K+Q365S,A339S+N54S+Q172K+R320K,A339S+N54S+Q172K+R458K,A339S+N54S+Q172K+S323T,A339S+N54S+Q172K+V206L,A339S+N54S+Q172K+Y295F,A339S+N54S+Q299Y+Q345R,A339S+N54S+Q299Y+Q365S,A339S+N54S+Q299Y+R320K,A339S+N54S+Q299Y+R458K,A339S+N54S+Q299Y+S323T,A339S+N54S+Q299Y+V206L,A339S+N54S+Q299Y+Y295F,A339S+N54S+Q345R+Q365S,A339S+N54S+Q345R+R320K,A339S+N54S+Q345R+R458K,A339S+N54S+Q345R+S323T,A339S+N54S+Q345R+V206L,A339S+N54S+Q345R+Y295F,A339S+N54S+Q365S+R320K,A339S+N54S+Q365S+R458K,A339S+N54S+Q365S+S323T,A339S+N54S+Q365S+V206L,A339S+N54S+Q365S+Y295F,A339S+N54S+R320K+R458K,A339S+N54S+R320K+S323T,A339S+N54S+R320K+V206L,A339S+N54S+R320K+Y295F,A339S+N54S+R458K+S323T,A339S+N54S+R458K+V206L,A339S+N54S+R458K+Y295F,A339S+N54S+S323T+V206L,A339S+N54S+S323T+Y295F,A339S+N54S+V206L+Y295F,A339S+Q169E+Q169E+Q172K,A339S+Q169E+Q169E+Q299Y,A339S+Q169E+Q169E+Q345R,A339S+Q169E+Q169E+Q365S,A339S+Q169E+Q169E+R320K,A339S+Q169E+Q169E+R458K,A339S+Q169E+Q169E+S323T,A339S+Q169E+Q169E+V206L,A339S+Q169E+Q169E+Y295F,A339S+Q169E+Q172K+Q299Y,A339S+Q169E+Q172K+Q345R,A339S+Q169E+Q172K+Q365S,A339S+Q169E+Q172K+R320K,A339S+Q169E+Q172K+R458K,A339S+Q169E+Q172K+S323T,A339S+Q169E+Q172K+V206L,A339S+Q169E+Q172K+Y295F,A339S+Q169E+Q299Y+Q345R,A339S+Q169E+Q299Y+Q365S,A339S+Q169E+Q299Y+R320K,A339S+Q169E+Q299Y+R458K,A339S+Q169E+Q299Y+S323T,A339S+Q169E+Q299Y+V206L,A339S+Q169E+Q299Y+Y295F,A339S+Q169E+Q345R+Q365S,A339S+Q169E+Q345R+R320K,A339S+Q169E+Q345R+R458K,A339S+Q169E+Q345R+S323T,A339S+Q169E+Q345R+V206L,A339S+Q169E+Q345R+Y295F,A339S+Q169E+Q365S+R320K,A339S+Q169E+Q365S+R458K,A339S+Q169E+Q365S+S323T,A339S+Q169E+Q365S+V206L,A339S+Q169E+Q365S+Y295F,A339S+Q169E+R320K+R458K,A339S+Q169E+R320K+S323T,A339S+Q169E+R320K+V206L,A339S+Q169E+R320K+Y295F,A339S+Q169E+R458K+S323T,A339S+Q169E+R458K+V206L,A339S+Q169E+R458K+Y295F,A339S+Q169E+S323T+V206L,A339S+Q169E+S323T+Y295F,A339S+Q169E+V206L+Y295F,A339S+Q169E+Q172K+Q299Y,A339S+Q169E+Q172K+Q345R,A339S+Q169E+Q172K+Q365S,A339S+Q169E+Q172K+R320K,A339S+Q169E+Q172K+R458K,A339S+Q169E+Q172K+S323T,A339S+Q169E+Q172K+V206L,A339S+Q169E+Q172K+Y295F,A339S+Q169E+Q299Y+Q345R,A339S+Q169E+Q299Y+Q365S,A339S+Q169E+Q299Y+R320K,A339S+Q169E+Q299Y+R458K,A339S+Q169E+Q299Y+S323T,A339S+Q169E+Q299Y+V206L,A339S+Q169E+Q299Y+Y295F,A339S+Q169E+Q345R+Q365S,A339S+Q169E+Q345R+R320K,A339S+Q169E+Q345R+R458K,A339S+Q169E+Q345R+S323T,A339S+Q169E+Q345R+V206L,A339S+Q169E+Q345R+Y295F,A339S+Q169E+Q365S+R320K,A339S+Q169E+Q365S+R458K,A339S+Q169E+Q365S+S323T,A339S+Q169E+Q365S+V206L,A339S+Q169E+Q365S+Y295F,A339S+Q

24 Mar 2026
2026202266

169E+R320K+R458K,A339S+Q169E+R320K+S323T,A339S+Q169E+R320K+V206L,A339S+Q169E+R320K+Y295F,A339S+Q169E+R458K+S323T,A339S+Q169E+R458K+V206L,A339S+Q169E+R458K+Y295F,A339S+Q169E+S323T+V206L,A339S+Q169E+S323T+Y295F,A339S+Q169E+V206L+Y295F,A339S+Q172K+Q299Y+Q345R,A339S+Q172K+Q299Y+Q365S,A339S+Q172K+Q299Y+R320K,A339S+Q172K+Q299Y+R458K,A339S+Q172K+Q299Y+S323T,A339S+Q172K+Q299Y+V206L,A339S+Q172K+Q299Y+Y295F,A339S+Q172K+Q345R+Q365S,A339S+Q172K+Q345R+R320K,A339S+Q172K+Q345R+R458K,A339S+Q172K+Q345R+S323T,A339S+Q172K+Q345R+V206L,A339S+Q172K+Q345R+Y295F,A339S+Q172K+Q365S+R320K,A339S+Q172K+Q365S+R458K,A339S+Q172K+Q365S+S323T,A339S+Q172K+Q365S+V206L,A339S+Q172K+Q365S+Y295F,A339S+Q172K+R320K+R458K,A339S+Q172K+R320K+S323T,A339S+Q172K+R320K+V206L,A339S+Q172K+R320K+Y295F,A339S+Q172K+R458K+S323T,A339S+Q172K+R458K+V206L,A339S+Q172K+R458K+Y295F,A339S+Q172K+S323T+V206L,A339S+Q172K+S323T+Y295F,A339S+Q172K+V206L+Y295F,A339S+Q299Y+Q345R+Q365S,A339S+Q299Y+Q345R+R320K,A339S+Q299Y+Q345R+R458K,A339S+Q299Y+Q345R+S323T,A339S+Q299Y+Q345R+V206L,A339S+Q299Y+Q345R+Y295F,A339S+Q299Y+Q365S+R320K,A339S+Q299Y+Q365S+R458K,A339S+Q299Y+Q365S+S323T,A339S+Q299Y+Q365S+V206L,A339S+Q299Y+Q365S+Y295F,A339S+Q299Y+R320K+R458K,A339S+Q299Y+R320K+S323T,A339S+Q299Y+R320K+V206L,A339S+Q299Y+R320K+Y295F,A339S+Q299Y+R458K+S323T,A339S+Q299Y+R458K+V206L,A339S+Q299Y+R458K+Y295F,A339S+Q299Y+S323T+V206L,A339S+Q299Y+S323T+Y295F,A339S+Q299Y+V206L+Y295F,A339S+Q345R+Q365S+R320K,A339S+Q345R+Q365S+R458K,A339S+Q345R+Q365S+S323T,A339S+Q345R+Q365S+V206L,A339S+Q345R+Q365S+Y295F,A339S+Q345R+R320K+R458K,A339S+Q345R+R320K+S323T,A339S+Q345R+R320K+V206L,A339S+Q345R+R320K+Y295F,A339S+Q345R+R458K+S323T,A339S+Q345R+R458K+V206L,A339S+Q345R+R458K+Y295F,A339S+Q345R+S323T+V206L,A339S+Q345R+S323T+Y295F,A339S+Q345R+V206L+Y295F,A339S+Q365S+R320K+R458K,A339S+Q365S+R320K+S323T,A339S+Q365S+R320K+V206L,A339S+Q365S+R320K+Y295F,A339S+Q365S+R458K+S323T,A339S+Q365S+R458K+V206L,A339S+Q365S+R458K+Y295F,A339S+Q365S+S323T+V206L,A339S+Q365S+S323T+Y295F,A339S+Q365S+V206L+Y295F,A339S+R320K+R458K+S323T,A339S+R320K+R458K+V206L,A339S+R320K+R458K+Y295F,A339S+R320K+S323T+V206L,A339S+R320K+S323T+Y295F,A339S+R320K+V206L+Y295F,A339S+R458K+S323T+V206L,A339S+R458K+S323T+Y295F,A339S+R458K+V206L+Y295F,A339S+S323T+V206L+Y295F,G109A+G149A+G182T+H1*,G109A+G149A+G182T+I9M,G109A+G149A+G182T+K391A,G109A+G149A+G182T+M202L,G109A+G149A+G182T+N16Y,G109A+G149A+G182T+N195F,G109A+G149A+G182T+N54S,G109A+G149A+G182T+Q169E,G109A+G149A+G182T+Q169E,G109A+G149A+G182T+Q172K,G109A+G149A+G182T+Q299Y,G109A+G149A+G182T+Q345R,G109A+G149A+G182T+Q365S,G109A+G149A+G182

24 Mar 2026
2026202266

T+R320K,G109A+G149A+G182T+R458K,G109A+G149A+G182T+S323T,G109A+G149A+G18
2T+V206L,G109A+G149A+G182T+Y295F,G109A+G149A+H1*+I9M,G109A+G149A+H1*+K39
1A,G109A+G149A+H1*+M202L,G109A+G149A+H1*+N16Y,G109A+G149A+H1*+N195F,G109
A+G149A+H1*+N54S,G109A+G149A+H1*+Q169E,G109A+G149A+H1*+Q169E,G109A+G149
A+H1*+Q172K,G109A+G149A+H1*+Q299Y,G109A+G149A+H1*+Q345R,G109A+G149A+H1*
+Q365S,G109A+G149A+H1*+R320K,G109A+G149A+H1*+R458K,G109A+G149A+H1*+S323
T,G109A+G149A+H1*+V206L,G109A+G149A+H1*+Y295F,G109A+G149A+I9M+K391A,G109
A+G149A+I9M+M202L,G109A+G149A+I9M+N16Y,G109A+G149A+I9M+N195F,G109A+G149
A+I9M+N54S,G109A+G149A+I9M+Q169E,G109A+G149A+I9M+Q169E,G109A+G149A+I9M+
Q172K,G109A+G149A+I9M+Q299Y,G109A+G149A+I9M+Q345R,G109A+G149A+I9M+Q365S
,G109A+G149A+I9M+R320K,G109A+G149A+I9M+R458K,G109A+G149A+I9M+S323T,G109A
+G149A+I9M+V206L,G109A+G149A+I9M+Y295F,G109A+G149A+K391A+M202L,G109A+G14
9A+K391A+N16Y,G109A+G149A+K391A+N195F,G109A+G149A+K391A+N54S,G109A+G149
A+K391A+Q169E,G109A+G149A+K391A+Q169E,G109A+G149A+K391A+Q172K,G109A+G1
49A+K391A+Q299Y,G109A+G149A+K391A+Q345R,G109A+G149A+K391A+Q365S,G109A+
G149A+K391A+R320K,G109A+G149A+K391A+R458K,G109A+G149A+K391A+S323T,G109A
+G149A+K391A+V206L,G109A+G149A+K391A+Y295F,G109A+G149A+M202L+N16Y,G109A
+G149A+M202L+N195F,G109A+G149A+M202L+N54S,G109A+G149A+M202L+Q169E,G109
A+G149A+M202L+Q169E,G109A+G149A+M202L+Q172K,G109A+G149A+M202L+Q299Y,G1
09A+G149A+M202L+Q345R,G109A+G149A+M202L+Q365S,G109A+G149A+M202L+R320K,
G109A+G149A+M202L+R458K,G109A+G149A+M202L+S323T,G109A+G149A+M202L+V206
L,G109A+G149A+M202L+Y295F,G109A+G149A+N16Y+N195F,G109A+G149A+N16Y+N54S,
G109A+G149A+N16Y+Q169E,G109A+G149A+N16Y+Q169E,G109A+G149A+N16Y+Q172K,G
109A+G149A+N16Y+Q299Y,G109A+G149A+N16Y+Q345R,G109A+G149A+N16Y+Q365S,G1
09A+G149A+N16Y+R320K,G109A+G149A+N16Y+R458K,G109A+G149A+N16Y+S323T,G109
A+G149A+N16Y+V206L,G109A+G149A+N16Y+Y295F,G109A+G149A+N195F+N54S,G109A+
G149A+N195F+Q169E,G109A+G149A+N195F+Q169E,G109A+G149A+N195F+Q172K,G109
A+G149A+N195F+Q299Y,G109A+G149A+N195F+Q345R,G109A+G149A+N195F+Q365S,G1
09A+G149A+N195F+R320K,G109A+G149A+N195F+R458K,G109A+G149A+N195F+S323T,G
109A+G149A+N195F+V206L,G109A+G149A+N195F+Y295F,G109A+G149A+N54S+Q169E,G
109A+G149A+N54S+Q169E,G109A+G149A+N54S+Q172K,G109A+G149A+N54S+Q299Y,G1
09A+G149A+N54S+Q345R,G109A+G149A+N54S+Q365S,G109A+G149A+N54S+R320K,G10
9A+G149A+N54S+R458K,G109A+G149A+N54S+S323T,G109A+G149A+N54S+V206L,G109A
+G149A+N54S+Y295F,G109A+G149A+Q169E+Q169E,G109A+G149A+Q169E+Q172K,G109
A+G149A+Q169E+Q299Y,G109A+G149A+Q169E+Q345R,G109A+G149A+Q169E+Q365S,G1
09A+G149A+Q169E+R320K,G109A+G149A+Q169E+R458K,G109A+G149A+Q169E+S323T,

24 Mar 2026
2026202266

G109A+G149A+Q169E+V206L,G109A+G149A+Q169E+Y295F,G109A+G149A+Q169E+Q172K,G109A+G149A+Q169E+Q299Y,G109A+G149A+Q169E+Q345R,G109A+G149A+Q169E+Q365S,G109A+G149A+Q169E+R320K,G109A+G149A+Q169E+R458K,G109A+G149A+Q169E+S323T,G109A+G149A+Q169E+V206L,G109A+G149A+Q169E+Y295F,G109A+G149A+Q172K+Q299Y,G109A+G149A+Q172K+Q345R,G109A+G149A+Q172K+Q365S,G109A+G149A+Q172K+R320K,G109A+G149A+Q172K+R458K,G109A+G149A+Q172K+S323T,G109A+G149A+Q172K+V206L,G109A+G149A+Q172K+Y295F,G109A+G149A+Q299Y+Q345R,G109A+G149A+Q299Y+Q365S,G109A+G149A+Q299Y+R320K,G109A+G149A+Q299Y+R458K,G109A+G149A+Q299Y+S323T,G109A+G149A+Q299Y+V206L,G109A+G149A+Q299Y+Y295F,G109A+G149A+Q345R+Q365S,G109A+G149A+Q345R+R320K,G109A+G149A+Q345R+R458K,G109A+G149A+Q345R+S323T,G109A+G149A+Q345R+V206L,G109A+G149A+Q345R+Y295F,G109A+G149A+Q365S+R320K,G109A+G149A+Q365S+R458K,G109A+G149A+Q365S+S323T,G109A+G149A+Q365S+V206L,G109A+G149A+Q365S+Y295F,G109A+G149A+R320K+R458K,G109A+G149A+R320K+S323T,G109A+G149A+R320K+V206L,G109A+G149A+R320K+Y295F,G109A+G149A+R458K+S323T,G109A+G149A+R458K+V206L,G109A+G149A+R458K+Y295F,G109A+G149A+S323T+V206L,G109A+G149A+S323T+Y295F,G109A+G149A+V206L+Y295F,G109A+G182T+H1*+I9M,G109A+G182T+H1*+K391A,G109A+G182T+H1*+M202L,G109A+G182T+H1*+N16Y,G109A+G182T+H1*+N195F,G109A+G182T+H1*+N54S,G109A+G182T+H1*+Q169E,G109A+G182T+H1*+Q169E,G109A+G182T+H1*+Q172K,G109A+G182T+H1*+Q299Y,G109A+G182T+H1*+Q345R,G109A+G182T+H1*+Q365S,G109A+G182T+H1*+R320K,G109A+G182T+H1*+R458K,G109A+G182T+H1*+S323T,G109A+G182T+H1*+V206L,G109A+G182T+H1*+Y295F,G109A+G182T+I9M+K391A,G109A+G182T+I9M+M202L,G109A+G182T+I9M+N16Y,G109A+G182T+I9M+N195F,G109A+G182T+I9M+N54S,G109A+G182T+I9M+Q169E,G109A+G182T+I9M+Q169E,G109A+G182T+I9M+Q172K,G109A+G182T+I9M+Q299Y,G109A+G182T+I9M+Q345R,G109A+G182T+I9M+Q365S,G109A+G182T+I9M+R320K,G109A+G182T+I9M+R458K,G109A+G182T+I9M+S323T,G109A+G182T+I9M+V206L,G109A+G182T+I9M+Y295F,G109A+G182T+K391A+M202L,G109A+G182T+K391A+N16Y,G109A+G182T+K391A+N195F,G109A+G182T+K391A+N54S,G109A+G182T+K391A+Q169E,G109A+G182T+K391A+Q169E,G109A+G182T+K391A+Q172K,G109A+G182T+K391A+Q299Y,G109A+G182T+K391A+Q345R,G109A+G182T+K391A+Q365S,G109A+G182T+K391A+R320K,G109A+G182T+K391A+R458K,G109A+G182T+K391A+S323T,G109A+G182T+K391A+V206L,G109A+G182T+K391A+Y295F,G109A+G182T+M202L+N16Y,G109A+G182T+M202L+N195F,G109A+G182T+M202L+N54S,G109A+G182T+M202L+Q169E,G109A+G182T+M202L+Q169E,G109A+G182T+M202L+Q172K,G109A+G182T+M202L+Q299Y,G109A+G182T+M202L+Q345R,G109A+G182T+M202L+Q365S,G109A+G182T+M202L+R320K,G109A+G182T+M202L+R458K,G109A+G182T+M202L+S323T,G109A+G182T+M202L+V206L,G109A+G182T+M202L+Y295F,G109A+G182T+N16Y

24 Mar 2026
2026202266

+N195F,G109A+G182T+N16Y+N54S,G109A+G182T+N16Y+Q169E,G109A+G182T+N16Y+Q
169E,G109A+G182T+N16Y+Q172K,G109A+G182T+N16Y+Q299Y,G109A+G182T+N16Y+Q3
45R,G109A+G182T+N16Y+Q365S,G109A+G182T+N16Y+R320K,G109A+G182T+N16Y+R458
K,G109A+G182T+N16Y+S323T,G109A+G182T+N16Y+V206L,G109A+G182T+N16Y+Y295F,
G109A+G182T+N195F+N54S,G109A+G182T+N195F+Q169E,G109A+G182T+N195F+Q169E,
G109A+G182T+N195F+Q172K,G109A+G182T+N195F+Q299Y,G109A+G182T+N195F+Q345
R,G109A+G182T+N195F+Q365S,G109A+G182T+N195F+R320K,G109A+G182T+N195F+R45
8K,G109A+G182T+N195F+S323T,G109A+G182T+N195F+V206L,G109A+G182T+N195F+Y29
5F,G109A+G182T+N54S+Q169E,G109A+G182T+N54S+Q169E,G109A+G182T+N54S+Q172
K,G109A+G182T+N54S+Q299Y,G109A+G182T+N54S+Q345R,G109A+G182T+N54S+Q365S,
G109A+G182T+N54S+R320K,G109A+G182T+N54S+R458K,G109A+G182T+N54S+S323T,G1
09A+G182T+N54S+V206L,G109A+G182T+N54S+Y295F,G109A+G182T+Q169E+Q169E,G10
9A+G182T+Q169E+Q172K,G109A+G182T+Q169E+Q299Y,G109A+G182T+Q169E+Q345R,G
109A+G182T+Q169E+Q365S,G109A+G182T+Q169E+R320K,G109A+G182T+Q169E+R458K,
G109A+G182T+Q169E+S323T,G109A+G182T+Q169E+V206L,G109A+G182T+Q169E+Y295F
,G109A+G182T+Q169E+Q172K,G109A+G182T+Q169E+Q299Y,G109A+G182T+Q169E+Q34
5R,G109A+G182T+Q169E+Q365S,G109A+G182T+Q169E+R320K,G109A+G182T+Q169E+R
458K,G109A+G182T+Q169E+S323T,G109A+G182T+Q169E+V206L,G109A+G182T+Q169E+
Y295F,G109A+G182T+Q172K+Q299Y,G109A+G182T+Q172K+Q345R,G109A+G182T+Q172
K+Q365S,G109A+G182T+Q172K+R320K,G109A+G182T+Q172K+R458K,G109A+G182T+Q1
72K+S323T,G109A+G182T+Q172K+V206L,G109A+G182T+Q172K+Y295F,G109A+G182T+Q
299Y+Q345R,G109A+G182T+Q299Y+Q365S,G109A+G182T+Q299Y+R320K,G109A+G182T+
Q299Y+R458K,G109A+G182T+Q299Y+S323T,G109A+G182T+Q299Y+V206L,G109A+G182T
+Q299Y+Y295F,G109A+G182T+Q345R+Q365S,G109A+G182T+Q345R+R320K,G109A+G18
2T+Q345R+R458K,G109A+G182T+Q345R+S323T,G109A+G182T+Q345R+V206L,G109A+G1
82T+Q345R+Y295F,G109A+G182T+Q365S+R320K,G109A+G182T+Q365S+R458K,G109A+G
182T+Q365S+S323T,G109A+G182T+Q365S+V206L,G109A+G182T+Q365S+Y295F,G109A+
G182T+R320K+R458K,G109A+G182T+R320K+S323T,G109A+G182T+R320K+V206L,G109A
+G182T+R320K+Y295F,G109A+G182T+R458K+S323T,G109A+G182T+R458K+V206L,G109
A+G182T+R458K+Y295F,G109A+G182T+S323T+V206L,G109A+G182T+S323T+Y295F,G109
A+G182T+V206L+Y295F,G109A+H1*+I9M+K391A,G109A+H1*+I9M+M202L,G109A+H1*+I9M
+N16Y,G109A+H1*+I9M+N195F,G109A+H1*+I9M+N54S,G109A+H1*+I9M+Q169E,G109A+H1
+I9M+Q169E,G109A+H1+I9M+Q172K,G109A+H1*+I9M+Q299Y,G109A+H1*+I9M+Q345R,G
109A+H1*+I9M+Q365S,G109A+H1*+I9M+R320K,G109A+H1*+I9M+R458K,G109A+H1*+I9M+
S323T,G109A+H1*+I9M+V206L,G109A+H1*+I9M+Y295F,G109A+H1*+K391A+M202L,G109A
+H1*+K391A+N16Y,G109A+H1*+K391A+N195F,G109A+H1*+K391A+N54S,G109A+H1*+K39

24 Mar 2026
2026202266

1A+Q169E,G109A+H1*+K391A+Q169E,G109A+H1*+K391A+Q172K,G109A+H1*+K391A+Q29
9Y,G109A+H1*+K391A+Q345R,G109A+H1*+K391A+Q365S,G109A+H1*+K391A+R320K,G10
9A+H1*+K391A+R458K,G109A+H1*+K391A+S323T,G109A+H1*+K391A+V206L,G109A+H1*+
K391A+Y295F,G109A+H1*+M202L+N16Y,G109A+H1*+M202L+N195F,G109A+H1*+M202L+N
54S,G109A+H1*+M202L+Q169E,G109A+H1*+M202L+Q169E,G109A+H1*+M202L+Q172K,G1
09A+H1*+M202L+Q299Y,G109A+H1*+M202L+Q345R,G109A+H1*+M202L+Q365S,G109A+H
1*+M202L+R320K,G109A+H1*+M202L+R458K,G109A+H1*+M202L+S323T,G109A+H1*+M20
2L+V206L,G109A+H1*+M202L+Y295F,G109A+H1*+N16Y+N195F,G109A+H1*+N16Y+N54S,
G109A+H1*+N16Y+Q169E,G109A+H1*+N16Y+Q169E,G109A+H1*+N16Y+Q172K,G109A+H1
+N16Y+Q299Y,G109A+H1+N16Y+Q345R,G109A+H1*+N16Y+Q365S,G109A+H1*+N16Y+R
320K,G109A+H1*+N16Y+R458K,G109A+H1*+N16Y+S323T,G109A+H1*+N16Y+V206L,G109
A+H1*+N16Y+Y295F,G109A+H1*+N195F+N54S,G109A+H1*+N195F+Q169E,G109A+H1*+N1
95F+Q169E,G109A+H1*+N195F+Q172K,G109A+H1*+N195F+Q299Y,G109A+H1*+N195F+Q3
45R,G109A+H1*+N195F+Q365S,G109A+H1*+N195F+R320K,G109A+H1*+N195F+R458K,G1
09A+H1*+N195F+S323T,G109A+H1*+N195F+V206L,G109A+H1*+N195F+Y295F,G109A+H1*
+N54S+Q169E,G109A+H1*+N54S+Q169E,G109A+H1*+N54S+Q172K,G109A+H1*+N54S+Q2
99Y,G109A+H1*+N54S+Q345R,G109A+H1*+N54S+Q365S,G109A+H1*+N54S+R320K,G109A
+H1*+N54S+R458K,G109A+H1*+N54S+S323T,G109A+H1*+N54S+V206L,G109A+H1*+N54S
+Y295F,G109A+H1*+Q169E+Q169E,G109A+H1*+Q169E+Q172K,G109A+H1*+Q169E+Q299
Y,G109A+H1*+Q169E+Q345R,G109A+H1*+Q169E+Q365S,G109A+H1*+Q169E+R320K,G109
A+H1*+Q169E+R458K,G109A+H1*+Q169E+S323T,G109A+H1*+Q169E+V206L,G109A+H1*+
Q169E+Y295F,G109A+H1*+Q169E+Q172K,G109A+H1*+Q169E+Q299Y,G109A+H1*+Q169E
+Q345R,G109A+H1*+Q169E+Q365S,G109A+H1*+Q169E+R320K,G109A+H1*+Q169E+R458
K,G109A+H1*+Q169E+S323T,G109A+H1*+Q169E+V206L,G109A+H1*+Q169E+Y295F,G109
A+H1*+Q172K+Q299Y,G109A+H1*+Q172K+Q345R,G109A+H1*+Q172K+Q365S,G109A+H1*
+Q172K+R320K,G109A+H1*+Q172K+R458K,G109A+H1*+Q172K+S323T,G109A+H1*+Q172
K+V206L,G109A+H1*+Q172K+Y295F,G109A+H1*+Q299Y+Q345R,G109A+H1*+Q299Y+Q365
S,G109A+H1*+Q299Y+R320K,G109A+H1*+Q299Y+R458K,G109A+H1*+Q299Y+S323T,G109
A+H1*+Q299Y+V206L,G109A+H1*+Q299Y+Y295F,G109A+H1*+Q345R+Q365S,G109A+H1*+
Q345R+R320K,G109A+H1*+Q345R+R458K,G109A+H1*+Q345R+S323T,G109A+H1*+Q345R
+V206L,G109A+H1*+Q345R+Y295F,G109A+H1*+Q365S+R320K,G109A+H1*+Q365S+R458K
,G109A+H1*+Q365S+S323T,G109A+H1*+Q365S+V206L,G109A+H1*+Q365S+Y295F,G109A
+H1*+R320K+R458K,G109A+H1*+R320K+S323T,G109A+H1*+R320K+V206L,G109A+H1*+R
320K+Y295F,G109A+H1*+R458K+S323T,G109A+H1*+R458K+V206L,G109A+H1*+R458K+Y
295F,G109A+H1*+S323T+V206L,G109A+H1*+S323T+Y295F,G109A+H1*+V206L+Y295F,G10
9A+I9M+K391A+M202L,G109A+I9M+K391A+N16Y,G109A+I9M+K391A+N195F,G109A+I9M+

24 Mar 2026
2026202266

K391A+N54S,G109A+I9M+K391A+Q169E,G109A+I9M+K391A+Q169E,G109A+I9M+K391A+Q172K,G109A+I9M+K391A+Q299Y,G109A+I9M+K391A+Q345R,G109A+I9M+K391A+Q365S,G109A+I9M+K391A+R320K,G109A+I9M+K391A+R458K,G109A+I9M+K391A+S323T,G109A+I9M+K391A+V206L,G109A+I9M+K391A+Y295F,G109A+I9M+M202L+N16Y,G109A+I9M+M202L+N195F,G109A+I9M+M202L+N54S,G109A+I9M+M202L+Q169E,G109A+I9M+M202L+Q169E,G109A+I9M+M202L+Q172K,G109A+I9M+M202L+Q299Y,G109A+I9M+M202L+Q345R,G109A+I9M+M202L+Q365S,G109A+I9M+M202L+R320K,G109A+I9M+M202L+R458K,G109A+I9M+M202L+S323T,G109A+I9M+M202L+V206L,G109A+I9M+M202L+Y295F,G109A+I9M+N16Y+N195F,G109A+I9M+N16Y+N54S,G109A+I9M+N16Y+Q169E,G109A+I9M+N16Y+Q169E,G109A+I9M+N16Y+Q172K,G109A+I9M+N16Y+Q299Y,G109A+I9M+N16Y+Q345R,G109A+I9M+N16Y+Q365S,G109A+I9M+N16Y+R320K,G109A+I9M+N16Y+R458K,G109A+I9M+N16Y+S323T,G109A+I9M+N16Y+V206L,G109A+I9M+N16Y+Y295F,G109A+I9M+N195F+N54S,G109A+I9M+N195F+Q169E,G109A+I9M+N195F+Q169E,G109A+I9M+N195F+Q172K,G109A+I9M+N195F+Q299Y,G109A+I9M+N195F+Q345R,G109A+I9M+N195F+Q365S,G109A+I9M+N195F+R320K,G109A+I9M+N195F+R458K,G109A+I9M+N195F+S323T,G109A+I9M+N195F+V206L,G109A+I9M+N195F+Y295F,G109A+I9M+N54S+Q169E,G109A+I9M+N54S+Q169E,G109A+I9M+N54S+Q172K,G109A+I9M+N54S+Q299Y,G109A+I9M+N54S+Q345R,G109A+I9M+N54S+Q365S,G109A+I9M+N54S+R320K,G109A+I9M+N54S+R458K,G109A+I9M+N54S+S323T,G109A+I9M+N54S+V206L,G109A+I9M+N54S+Y295F,G109A+I9M+Q169E+Q169E,G109A+I9M+Q169E+Q172K,G109A+I9M+Q169E+Q299Y,G109A+I9M+Q169E+Q345R,G109A+I9M+Q169E+Q365S,G109A+I9M+Q169E+R320K,G109A+I9M+Q169E+R458K,G109A+I9M+Q169E+S323T,G109A+I9M+Q169E+V206L,G109A+I9M+Q169E+Y295F,G109A+I9M+Q172K+Q299Y,G109A+I9M+Q172K+Q345R,G109A+I9M+Q172K+Q365S,G109A+I9M+Q172K+R320K,G109A+I9M+Q172K+R458K,G109A+I9M+Q172K+S323T,G109A+I9M+Q172K+V206L,G109A+I9M+Q172K+Y295F,G109A+I9M+Q299Y+Q345R,G109A+I9M+Q299Y+Q365S,G109A+I9M+Q299Y+R320K,G109A+I9M+Q299Y+R458K,G109A+I9M+Q299Y+S323T,G109A+I9M+Q299Y+V206L,G109A+I9M+Q299Y+Y295F,G109A+I9M+Q345R+Q365S,G109A+I9M+Q345R+R320K,G109A+I9M+Q345R+R458K,G109A+I9M+Q345R+S323T,G109A+I9M+Q345R+V206L,G109A+I9M+Q345R+Y295F,G109A+I9M+Q365S+R320K,G109A+I9M+Q365S+R458K,G109A+I9M+Q365S+S323T,G109A+I9M+Q365S+V206L,G109A+I9M+Q365S+Y295F,G109A+I9M+R320K+R458K,G109A+I9M+R320K+S323T,G109A+I9M+R320K+V206L,G109A+I9M+R320K+Y295F,G109A+I9M+R458K+S323T,G109A+I9M+R458K+V206L,G109A+I9M+R458K+Y295F,G109A+I9M+S323T+V206L,G109A+I9M+S323T+Y295F,G109A+I9M+V206L+Y295F,G109A+K391A+M202L+N16Y,G109A+K391A+M202L+N195F,G109A+

24 Mar 2026
2026202266

K391A+M202L+N54S,G109A+K391A+M202L+Q169E,G109A+K391A+M202L+Q169E,G109A+K391A+M202L+Q172K,G109A+K391A+M202L+Q299Y,G109A+K391A+M202L+Q345R,G109A+K391A+M202L+Q365S,G109A+K391A+M202L+R320K,G109A+K391A+M202L+R458K,G109A+K391A+M202L+S323T,G109A+K391A+M202L+V206L,G109A+K391A+M202L+Y295F,G109A+K391A+N16Y+N195F,G109A+K391A+N16Y+N54S,G109A+K391A+N16Y+Q169E,G109A+K391A+N16Y+Q169E,G109A+K391A+N16Y+Q172K,G109A+K391A+N16Y+Q299Y,G109A+K391A+N16Y+Q345R,G109A+K391A+N16Y+Q365S,G109A+K391A+N16Y+R320K,G109A+K391A+N16Y+R458K,G109A+K391A+N16Y+S323T,G109A+K391A+N16Y+V206L,G109A+K391A+N16Y+Y295F,G109A+K391A+N195F+N54S,G109A+K391A+N195F+Q169E,G109A+K391A+N195F+Q169E,G109A+K391A+N195F+Q172K,G109A+K391A+N195F+Q299Y,G109A+K391A+N195F+Q345R,G109A+K391A+N195F+Q365S,G109A+K391A+N195F+R320K,G109A+K391A+N195F+R458K,G109A+K391A+N195F+S323T,G109A+K391A+N195F+V206L,G109A+K391A+N195F+Y295F,G109A+K391A+N54S+Q169E,G109A+K391A+N54S+Q169E,G109A+K391A+N54S+Q172K,G109A+K391A+N54S+Q299Y,G109A+K391A+N54S+Q345R,G109A+K391A+N54S+Q365S,G109A+K391A+N54S+R320K,G109A+K391A+N54S+R458K,G109A+K391A+N54S+S323T,G109A+K391A+N54S+V206L,G109A+K391A+N54S+Y295F,G109A+K391A+Q169E+Q169E,G109A+K391A+Q169E+Q172K,G109A+K391A+Q169E+Q299Y,G109A+K391A+Q169E+Q345R,G109A+K391A+Q169E+Q365S,G109A+K391A+Q169E+R320K,G109A+K391A+Q169E+R458K,G109A+K391A+Q169E+S323T,G109A+K391A+Q169E+V206L,G109A+K391A+Q169E+Y295F,G109A+K391A+Q169E+Q172K,G109A+K391A+Q169E+Q299Y,G109A+K391A+Q169E+Q345R,G109A+K391A+Q169E+Q365S,G109A+K391A+Q169E+R320K,G109A+K391A+Q169E+R458K,G109A+K391A+Q169E+S323T,G109A+K391A+Q169E+V206L,G109A+K391A+Q169E+Y295F,G109A+K391A+Q172K+Q299Y,G109A+K391A+Q172K+Q345R,G109A+K391A+Q172K+Q365S,G109A+K391A+Q172K+R320K,G109A+K391A+Q172K+R458K,G109A+K391A+Q172K+S323T,G109A+K391A+Q172K+V206L,G109A+K391A+Q172K+Y295F,G109A+K391A+Q299Y+Q345R,G109A+K391A+Q299Y+Q365S,G109A+K391A+Q299Y+R320K,G109A+K391A+Q299Y+R458K,G109A+K391A+Q299Y+S323T,G109A+K391A+Q299Y+V206L,G109A+K391A+Q299Y+Y295F,G109A+K391A+Q345R+Q365S,G109A+K391A+Q345R+R320K,G109A+K391A+Q345R+R458K,G109A+K391A+Q345R+S323T,G109A+K391A+Q345R+V206L,G109A+K391A+Q345R+Y295F,G109A+K391A+Q365S+R320K,G109A+K391A+Q365S+R458K,G109A+K391A+Q365S+S323T,G109A+K391A+Q365S+V206L,G109A+K391A+Q365S+Y295F,G109A+K391A+R320K+R458K,G109A+K391A+R320K+S323T,G109A+K391A+R320K+V206L,G109A+K391A+R320K+Y295F,G109A+K391A+R458K+S323T,G109A+K391A+R458K+V206L,G109A+K391A+R458K+Y295F,G109A+K391A+S323T+V206L,G109A+K391A+S323T+Y295F,G109A+K391A+V206L+Y295F,G109A+M202L+N16Y+N195F,G109A+M202L+N16Y+N54S,G109A+M202L+N16Y+Q169E,G109A+M202L+N16Y+Q169E,G109A+M202L+N16Y+Q172K,G109

24 Mar 2026
2026202266

A+M202L+N16Y+Q299Y,G109A+M202L+N16Y+Q345R,G109A+M202L+N16Y+Q365S,G109A+M202L+N16Y+R320K,G109A+M202L+N16Y+R458K,G109A+M202L+N16Y+S323T,G109A+M202L+N16Y+V206L,G109A+M202L+N16Y+Y295F,G109A+M202L+N195F+N54S,G109A+M202L+N195F+Q169E,G109A+M202L+N195F+Q169E,G109A+M202L+N195F+Q172K,G109A+M202L+N195F+Q299Y,G109A+M202L+N195F+Q345R,G109A+M202L+N195F+Q365S,G109A+M202L+N195F+R320K,G109A+M202L+N195F+R458K,G109A+M202L+N195F+S323T,G109A+M202L+N195F+V206L,G109A+M202L+N195F+Y295F,G109A+M202L+N54S+Q169E,G109A+M202L+N54S+Q169E,G109A+M202L+N54S+Q172K,G109A+M202L+N54S+Q299Y,G109A+M202L+N54S+Q345R,G109A+M202L+N54S+Q365S,G109A+M202L+N54S+R320K,G109A+M202L+N54S+R458K,G109A+M202L+N54S+S323T,G109A+M202L+N54S+V206L,G109A+M202L+N54S+Y295F,G109A+M202L+Q169E+Q169E,G109A+M202L+Q169E+Q172K,G109A+M202L+Q169E+Q299Y,G109A+M202L+Q169E+Q345R,G109A+M202L+Q169E+Q365S,G109A+M202L+Q169E+R320K,G109A+M202L+Q169E+R458K,G109A+M202L+Q169E+S323T,G109A+M202L+Q169E+V206L,G109A+M202L+Q169E+Y295F,G109A+M202L+Q169E+Q172K,G109A+M202L+Q169E+Q299Y,G109A+M202L+Q169E+Q345R,G109A+M202L+Q169E+Q365S,G109A+M202L+Q169E+R320K,G109A+M202L+Q169E+R458K,G109A+M202L+Q169E+S323T,G109A+M202L+Q169E+V206L,G109A+M202L+Q169E+Y295F,G109A+M202L+Q172K+Q299Y,G109A+M202L+Q172K+Q345R,G109A+M202L+Q172K+Q365S,G109A+M202L+Q172K+R320K,G109A+M202L+Q172K+R458K,G109A+M202L+Q172K+S323T,G109A+M202L+Q172K+V206L,G109A+M202L+Q172K+Y295F,G109A+M202L+Q299Y+Q345R,G109A+M202L+Q299Y+Q365S,G109A+M202L+Q299Y+R320K,G109A+M202L+Q299Y+R458K,G109A+M202L+Q299Y+S323T,G109A+M202L+Q299Y+V206L,G109A+M202L+Q299Y+Y295F,G109A+M202L+Q345R+Q365S,G109A+M202L+Q345R+R320K,G109A+M202L+Q345R+R458K,G109A+M202L+Q345R+S323T,G109A+M202L+Q345R+V206L,G109A+M202L+Q345R+Y295F,G109A+M202L+Q365S+R320K,G109A+M202L+Q365S+R458K,G109A+M202L+Q365S+S323T,G109A+M202L+Q365S+V206L,G109A+M202L+Q365S+Y295F,G109A+M202L+R320K+R458K,G109A+M202L+R320K+S323T,G109A+M202L+R320K+V206L,G109A+M202L+R320K+Y295F,G109A+M202L+R458K+S323T,G109A+M202L+R458K+V206L,G109A+M202L+R458K+Y295F,G109A+M202L+S323T+V206L,G109A+M202L+S323T+Y295F,G109A+M202L+V206L+Y295F,G109A+N16Y+N195F+N54S,G109A+N16Y+N195F+Q169E,G109A+N16Y+N195F+Q169E,G109A+N16Y+N195F+Q172K,G109A+N16Y+N195F+Q299Y,G109A+N16Y+N195F+Q345R,G109A+N16Y+N195F+Q365S,G109A+N16Y+N195F+R320K,G109A+N16Y+N195F+R458K,G109A+N16Y+N195F+S323T,G109A+N16Y+N195F+V206L,G109A+N16Y+N195F+Y295F,G109A+N16Y+N54S+Q169E,G109A+N16Y+N54S+Q169E,G109A+N16Y+N54S+Q172K,G109A+N16Y+N54S+Q299Y,G109A+N16Y+N54S+Q345R,G109A+N16Y+N54S+Q365S,G109A+N16Y+N54S+R320K,G109A+N16Y+N54S+R458K,G109A+N16Y+N54S+S323T,G109A+N16Y+N54S+V206L,G109A+N16Y+N5

24 Mar 2026
2026202266

4S+Y295F,G109A+N16Y+Q169E+Q169E,G109A+N16Y+Q169E+Q172K,G109A+N16Y+Q169E+Q299Y,G109A+N16Y+Q169E+Q345R,G109A+N16Y+Q169E+Q365S,G109A+N16Y+Q169E+R320K,G109A+N16Y+Q169E+R458K,G109A+N16Y+Q169E+S323T,G109A+N16Y+Q169E+V206L,G109A+N16Y+Q169E+Y295F,G109A+N16Y+Q169E+Q172K,G109A+N16Y+Q169E+Q299Y,G109A+N16Y+Q169E+Q345R,G109A+N16Y+Q169E+Q365S,G109A+N16Y+Q169E+R320K,G109A+N16Y+Q169E+R458K,G109A+N16Y+Q169E+S323T,G109A+N16Y+Q169E+V206L,G109A+N16Y+Q169E+Y295F,G109A+N16Y+Q172K+Q299Y,G109A+N16Y+Q172K+Q345R,G109A+N16Y+Q172K+Q365S,G109A+N16Y+Q172K+R320K,G109A+N16Y+Q172K+R458K,G109A+N16Y+Q172K+S323T,G109A+N16Y+Q172K+V206L,G109A+N16Y+Q172K+Y295F,G109A+N16Y+Q299Y+Q345R,G109A+N16Y+Q299Y+Q365S,G109A+N16Y+Q299Y+R320K,G109A+N16Y+Q299Y+R458K,G109A+N16Y+Q299Y+S323T,G109A+N16Y+Q299Y+V206L,G109A+N16Y+Q299Y+Y295F,G109A+N16Y+Q345R+Q365S,G109A+N16Y+Q345R+R320K,G109A+N16Y+Q345R+R458K,G109A+N16Y+Q345R+S323T,G109A+N16Y+Q345R+V206L,G109A+N16Y+Q345R+Y295F,G109A+N16Y+Q365S+R320K,G109A+N16Y+Q365S+R458K,G109A+N16Y+Q365S+S323T,G109A+N16Y+Q365S+V206L,G109A+N16Y+Q365S+Y295F,G109A+N16Y+R320K+R458K,G109A+N16Y+R320K+S323T,G109A+N16Y+R320K+V206L,G109A+N16Y+R320K+Y295F,G109A+N16Y+R458K+S323T,G109A+N16Y+R458K+V206L,G109A+N16Y+R458K+Y295F,G109A+N16Y+S323T+V206L,G109A+N16Y+S323T+Y295F,G109A+N16Y+V206L+Y295F,G109A+N195F+N54S+Q169E,G109A+N195F+N54S+Q169E,G109A+N195F+N54S+Q172K,G109A+N195F+N54S+Q299Y,G109A+N195F+N54S+Q345R,G109A+N195F+N54S+Q365S,G109A+N195F+N54S+R320K,G109A+N195F+N54S+R458K,G109A+N195F+N54S+S323T,G109A+N195F+N54S+V206L,G109A+N195F+N54S+Y295F,G109A+N195F+Q169E+Q169E,G109A+N195F+Q169E+Q172K,G109A+N195F+Q169E+Q299Y,G109A+N195F+Q169E+Q345R,G109A+N195F+Q169E+Q365S,G109A+N195F+Q169E+R320K,G109A+N195F+Q169E+R458K,G109A+N195F+Q169E+S323T,G109A+N195F+Q169E+V206L,G109A+N195F+Q169E+Y295F,G109A+N195F+Q169E+Q172K,G109A+N195F+Q169E+Q299Y,G109A+N195F+Q169E+Q345R,G109A+N195F+Q169E+Q365S,G109A+N195F+Q169E+R320K,G109A+N195F+Q169E+R458K,G109A+N195F+Q169E+S323T,G109A+N195F+Q169E+V206L,G109A+N195F+Q169E+Y295F,G109A+N195F+Q172K+Q299Y,G109A+N195F+Q172K+Q345R,G109A+N195F+Q172K+Q365S,G109A+N195F+Q172K+R320K,G109A+N195F+Q172K+R458K,G109A+N195F+Q172K+S323T,G109A+N195F+Q172K+V206L,G109A+N195F+Q172K+Y295F,G109A+N195F+Q299Y+Q345R,G109A+N195F+Q299Y+Q365S,G109A+N195F+Q299Y+R320K,G109A+N195F+Q299Y+R458K,G109A+N195F+Q299Y+S323T,G109A+N195F+Q299Y+V206L,G109A+N195F+Q299Y+Y295F,G109A+N195F+Q345R+Q365S,G109A+N195F+Q345R+R320K,G109A+N195F+Q345R+R458K,G109A+N195F+Q345R+S323T,G109A+N195F+Q345R+V206L,G109A+N195F+Q345R+Y295F,G109A+N195F+Q365S+R320K,G109A+N195F+Q365S+R458K,G109A+N195

24 Mar 2026
2026202266

F+Q365S+S323T,G109A+N195F+Q365S+V206L,G109A+N195F+Q365S+Y295F,G109A+N19
5F+R320K+R458K,G109A+N195F+R320K+S323T,G109A+N195F+R320K+V206L,G109A+N19
5F+R320K+Y295F,G109A+N195F+R458K+S323T,G109A+N195F+R458K+V206L,G109A+N19
5F+R458K+Y295F,G109A+N195F+S323T+V206L,G109A+N195F+S323T+Y295F,G109A+N19
5F+V206L+Y295F,G109A+N54S+Q169E+Q169E,G109A+N54S+Q169E+Q172K,G109A+N54S
+Q169E+Q299Y,G109A+N54S+Q169E+Q345R,G109A+N54S+Q169E+Q365S,G109A+N54S+
Q169E+R320K,G109A+N54S+Q169E+R458K,G109A+N54S+Q169E+S323T,G109A+N54S+Q
169E+V206L,G109A+N54S+Q169E+Y295F,G109A+N54S+Q169E+Q172K,G109A+N54S+Q16
9E+Q299Y,G109A+N54S+Q169E+Q345R,G109A+N54S+Q169E+Q365S,G109A+N54S+Q169
E+R320K,G109A+N54S+Q169E+R458K,G109A+N54S+Q169E+S323T,G109A+N54S+Q169E
+V206L,G109A+N54S+Q169E+Y295F,G109A+N54S+Q172K+Q299Y,G109A+N54S+Q172K+
Q345R,G109A+N54S+Q172K+Q365S,G109A+N54S+Q172K+R320K,G109A+N54S+Q172K+R
458K,G109A+N54S+Q172K+S323T,G109A+N54S+Q172K+V206L,G109A+N54S+Q172K+Y29
5F,G109A+N54S+Q299Y+Q345R,G109A+N54S+Q299Y+Q365S,G109A+N54S+Q299Y+R320
K,G109A+N54S+Q299Y+R458K,G109A+N54S+Q299Y+S323T,G109A+N54S+Q299Y+V206L,
G109A+N54S+Q299Y+Y295F,G109A+N54S+Q345R+Q365S,G109A+N54S+Q345R+R320K,G
109A+N54S+Q345R+R458K,G109A+N54S+Q345R+S323T,G109A+N54S+Q345R+V206L,G10
9A+N54S+Q345R+Y295F,G109A+N54S+Q365S+R320K,G109A+N54S+Q365S+R458K,G109
A+N54S+Q365S+S323T,G109A+N54S+Q365S+V206L,G109A+N54S+Q365S+Y295F,G109A+
N54S+R320K+R458K,G109A+N54S+R320K+S323T,G109A+N54S+R320K+V206L,G109A+N5
4S+R320K+Y295F,G109A+N54S+R458K+S323T,G109A+N54S+R458K+V206L,G109A+N54S
+R458K+Y295F,G109A+N54S+S323T+V206L,G109A+N54S+S323T+Y295F,G109A+N54S+V2
06L+Y295F,G109A+Q169E+Q169E+Q172K,G109A+Q169E+Q169E+Q299Y,G109A+Q169E+
Q169E+Q345R,G109A+Q169E+Q169E+Q365S,G109A+Q169E+Q169E+R320K,G109A+Q169
E+Q169E+R458K,G109A+Q169E+Q169E+S323T,G109A+Q169E+Q169E+V206L,G109A+Q16
9E+Q169E+Y295F,G109A+Q169E+Q172K+Q299Y,G109A+Q169E+Q172K+Q345R,G109A+Q
169E+Q172K+Q365S,G109A+Q169E+Q172K+R320K,G109A+Q169E+Q172K+R458K,G109A
+Q169E+Q172K+S323T,G109A+Q169E+Q172K+V206L,G109A+Q169E+Q172K+Y295F,G109
A+Q169E+Q299Y+Q345R,G109A+Q169E+Q299Y+Q365S,G109A+Q169E+Q299Y+R320K,G1
09A+Q169E+Q299Y+R458K,G109A+Q169E+Q299Y+S323T,G109A+Q169E+Q299Y+V206L,G
109A+Q169E+Q299Y+Y295F,G109A+Q169E+Q345R+Q365S,G109A+Q169E+Q345R+R320K
,G109A+Q169E+Q345R+R458K,G109A+Q169E+Q345R+S323T,G109A+Q169E+Q345R+V20
6L,G109A+Q169E+Q345R+Y295F,G109A+Q169E+Q365S+R320K,G109A+Q169E+Q365S+R
458K,G109A+Q169E+Q365S+S323T,G109A+Q169E+Q365S+V206L,G109A+Q169E+Q365S+
Y295F,G109A+Q169E+R320K+R458K,G109A+Q169E+R320K+S323T,G109A+Q169E+R320K
+V206L,G109A+Q169E+R320K+Y295F,G109A+Q169E+R458K+S323T,G109A+Q169E+R458

24 Mar 2026
2026202266

K+V206L,G109A+Q169E+R458K+Y295F,G109A+Q169E+S323T+V206L,G109A+Q169E+S323T+Y295F,G109A+Q169E+V206L+Y295F,G109A+Q169E+Q172K+Q299Y,G109A+Q169E+Q172K+Q345R,G109A+Q169E+Q172K+Q365S,G109A+Q169E+Q172K+R320K,G109A+Q169E+Q172K+R458K,G109A+Q169E+Q172K+S323T,G109A+Q169E+Q172K+V206L,G109A+Q169E+Q172K+Y295F,G109A+Q169E+Q299Y+Q345R,G109A+Q169E+Q299Y+Q365S,G109A+Q169E+Q299Y+R320K,G109A+Q169E+Q299Y+R458K,G109A+Q169E+Q299Y+S323T,G109A+Q169E+Q299Y+V206L,G109A+Q169E+Q299Y+Y295F,G109A+Q169E+Q345R+Q365S,G109A+Q169E+Q345R+R320K,G109A+Q169E+Q345R+R458K,G109A+Q169E+Q345R+S323T,G109A+Q169E+Q345R+V206L,G109A+Q169E+Q345R+Y295F,G109A+Q169E+Q365S+R320K,G109A+Q169E+Q365S+R458K,G109A+Q169E+Q365S+S323T,G109A+Q169E+Q365S+V206L,G109A+Q169E+Q365S+Y295F,G109A+Q169E+R320K+R458K,G109A+Q169E+R320K+S323T,G109A+Q169E+R320K+V206L,G109A+Q169E+R320K+Y295F,G109A+Q169E+R458K+S323T,G109A+Q169E+R458K+V206L,G109A+Q169E+R458K+Y295F,G109A+Q169E+S323T+V206L,G109A+Q169E+S323T+Y295F,G109A+Q169E+V206L+Y295F,G109A+Q172K+Q299Y+Q345R,G109A+Q172K+Q299Y+Q365S,G109A+Q172K+Q299Y+R320K,G109A+Q172K+Q299Y+R458K,G109A+Q172K+Q299Y+S323T,G109A+Q172K+Q299Y+V206L,G109A+Q172K+Q299Y+Y295F,G109A+Q172K+Q345R+Q365S,G109A+Q172K+Q345R+R320K,G109A+Q172K+Q345R+R458K,G109A+Q172K+Q345R+S323T,G109A+Q172K+Q345R+V206L,G109A+Q172K+Q345R+Y295F,G109A+Q172K+Q365S+R320K,G109A+Q172K+Q365S+R458K,G109A+Q172K+Q365S+S323T,G109A+Q172K+Q365S+V206L,G109A+Q172K+Q365S+Y295F,G109A+Q172K+R320K+R458K,G109A+Q172K+R320K+S323T,G109A+Q172K+R320K+V206L,G109A+Q172K+R320K+Y295F,G109A+Q172K+R458K+S323T,G109A+Q172K+R458K+V206L,G109A+Q172K+R458K+Y295F,G109A+Q172K+S323T+V206L,G109A+Q172K+S323T+Y295F,G109A+Q172K+V206L+Y295F,G109A+Q299Y+Q345R+Q365S,G109A+Q299Y+Q345R+R320K,G109A+Q299Y+Q345R+R458K,G109A+Q299Y+Q345R+S323T,G109A+Q299Y+Q345R+V206L,G109A+Q299Y+Q345R+Y295F,G109A+Q299Y+Q365S+R320K,G109A+Q299Y+Q365S+R458K,G109A+Q299Y+Q365S+S323T,G109A+Q299Y+Q365S+V206L,G109A+Q299Y+Q365S+Y295F,G109A+Q299Y+R320K+R458K,G109A+Q299Y+R320K+S323T,G109A+Q299Y+R320K+V206L,G109A+Q299Y+R320K+Y295F,G109A+Q299Y+R458K+S323T,G109A+Q299Y+R458K+V206L,G109A+Q299Y+R458K+Y295F,G109A+Q299Y+S323T+V206L,G109A+Q299Y+S323T+Y295F,G109A+Q299Y+V206L+Y295F,G109A+Q345R+Q365S+R320K,G109A+Q345R+Q365S+R458K,G109A+Q345R+Q365S+S323T,G109A+Q345R+Q365S+V206L,G109A+Q345R+Q365S+Y295F,G109A+Q345R+R320K+R458K,G109A+Q345R+R320K+S323T,G109A+Q345R+R320K+V206L,G109A+Q345R+R320K+Y295F,G109A+Q345R+R458K+S323T,G109A+Q345R+R458K+V206L,G109A+Q345R+R458K+Y295F,G109A+Q345R+S323T+V206L,G109A+Q345R+S323T+Y295F,G109A+Q345R+V206L+Y295F,G109A+Q365S+R320K+R458K,G109A+Q365S+R320K+

24 Mar 2026
2026202266

S323T,G109A+Q365S+R320K+V206L,G109A+Q365S+R320K+Y295F,G109A+Q365S+R458K
+S323T,G109A+Q365S+R458K+V206L,G109A+Q365S+R458K+Y295F,G109A+Q365S+S323
T+V206L,G109A+Q365S+S323T+Y295F,G109A+Q365S+V206L+Y295F,G109A+R320K+R458
K+S323T,G109A+R320K+R458K+V206L,G109A+R320K+R458K+Y295F,G109A+R320K+S323
T+V206L,G109A+R320K+S323T+Y295F,G109A+R320K+V206L+Y295F,G109A+R458K+S323
T+V206L,G109A+R458K+S323T+Y295F,G109A+R458K+V206L+Y295F,G109A+S323T+V206
L+Y295F,G149A+G182T+H1*+I9M,G149A+G182T+H1*+K391A,G149A+G182T+H1*+M202L,G
149A+G182T+H1*+N16Y,G149A+G182T+H1*+N195F,G149A+G182T+H1*+N54S,G149A+G18
2T+H1*+Q169E,G149A+G182T+H1*+Q169E,G149A+G182T+H1*+Q172K,G149A+G182T+H1*
+Q299Y,G149A+G182T+H1*+Q345R,G149A+G182T+H1*+Q365S,G149A+G182T+H1*+R320
K,G149A+G182T+H1*+R458K,G149A+G182T+H1*+S323T,G149A+G182T+H1*+V206L,G149
A+G182T+H1*+Y295F,G149A+G182T+I9M+K391A,G149A+G182T+I9M+M202L,G149A+G182
T+I9M+N16Y,G149A+G182T+I9M+N195F,G149A+G182T+I9M+N54S,G149A+G182T+I9M+Q1
69E,G149A+G182T+I9M+Q169E,G149A+G182T+I9M+Q172K,G149A+G182T+I9M+Q299Y,G1
49A+G182T+I9M+Q345R,G149A+G182T+I9M+Q365S,G149A+G182T+I9M+R320K,G149A+G
182T+I9M+R458K,G149A+G182T+I9M+S323T,G149A+G182T+I9M+V206L,G149A+G182T+I9
M+Y295F,G149A+G182T+K391A+M202L,G149A+G182T+K391A+N16Y,G149A+G182T+K391
A+N195F,G149A+G182T+K391A+N54S,G149A+G182T+K391A+Q169E,G149A+G182T+K391
A+Q169E,G149A+G182T+K391A+Q172K,G149A+G182T+K391A+Q299Y,G149A+G182T+K39
1A+Q345R,G149A+G182T+K391A+Q365S,G149A+G182T+K391A+R320K,G149A+G182T+K3
91A+R458K,G149A+G182T+K391A+S323T,G149A+G182T+K391A+V206L,G149A+G182T+K3
91A+Y295F,G149A+G182T+M202L+N16Y,G149A+G182T+M202L+N195F,G149A+G182T+M2
02L+N54S,G149A+G182T+M202L+Q169E,G149A+G182T+M202L+Q169E,G149A+G182T+M2
02L+Q172K,G149A+G182T+M202L+Q299Y,G149A+G182T+M202L+Q345R,G149A+G182T+
M202L+Q365S,G149A+G182T+M202L+R320K,G149A+G182T+M202L+R458K,G149A+G182T
+M202L+S323T,G149A+G182T+M202L+V206L,G149A+G182T+M202L+Y295F,G149A+G182
T+N16Y+N195F,G149A+G182T+N16Y+N54S,G149A+G182T+N16Y+Q169E,G149A+G182T+
N16Y+Q169E,G149A+G182T+N16Y+Q172K,G149A+G182T+N16Y+Q299Y,G149A+G182T+N
16Y+Q345R,G149A+G182T+N16Y+Q365S,G149A+G182T+N16Y+R320K,G149A+G182T+N1
6Y+R458K,G149A+G182T+N16Y+S323T,G149A+G182T+N16Y+V206L,G149A+G182T+N16Y
+Y295F,G149A+G182T+N195F+N54S,G149A+G182T+N195F+Q169E,G149A+G182T+N195F
+Q169E,G149A+G182T+N195F+Q172K,G149A+G182T+N195F+Q299Y,G149A+G182T+N195
F+Q345R,G149A+G182T+N195F+Q365S,G149A+G182T+N195F+R320K,G149A+G182T+N19
5F+R458K,G149A+G182T+N195F+S323T,G149A+G182T+N195F+V206L,G149A+G182T+N19
5F+Y295F,G149A+G182T+N54S+Q169E,G149A+G182T+N54S+Q169E,G149A+G182T+N54S
+Q172K,G149A+G182T+N54S+Q299Y,G149A+G182T+N54S+Q345R,G149A+G182T+N54S+

24 Mar 2026
2026202266

Q365S,G149A+G182T+N54S+R320K,G149A+G182T+N54S+R458K,G149A+G182T+N54S+S323T,G149A+G182T+N54S+V206L,G149A+G182T+N54S+Y295F,G149A+G182T+Q169E+Q169E,G149A+G182T+Q169E+Q172K,G149A+G182T+Q169E+Q299Y,G149A+G182T+Q169E+Q345R,G149A+G182T+Q169E+Q365S,G149A+G182T+Q169E+R320K,G149A+G182T+Q169E+R458K,G149A+G182T+Q169E+S323T,G149A+G182T+Q169E+V206L,G149A+G182T+Q169E+Y295F,G149A+G182T+Q169E+Q172K,G149A+G182T+Q169E+Q299Y,G149A+G182T+Q169E+Q345R,G149A+G182T+Q169E+Q365S,G149A+G182T+Q169E+R320K,G149A+G182T+Q169E+R458K,G149A+G182T+Q169E+S323T,G149A+G182T+Q169E+V206L,G149A+G182T+Q169E+Y295F,G149A+G182T+Q172K+Q299Y,G149A+G182T+Q172K+Q345R,G149A+G182T+Q172K+Q365S,G149A+G182T+Q172K+R320K,G149A+G182T+Q172K+R458K,G149A+G182T+Q172K+S323T,G149A+G182T+Q172K+V206L,G149A+G182T+Q172K+Y295F,G149A+G182T+Q299Y+Q345R,G149A+G182T+Q299Y+Q365S,G149A+G182T+Q299Y+R320K,G149A+G182T+Q299Y+R458K,G149A+G182T+Q299Y+S323T,G149A+G182T+Q299Y+V206L,G149A+G182T+Q299Y+Y295F,G149A+G182T+Q345R+Q365S,G149A+G182T+Q345R+R320K,G149A+G182T+Q345R+R458K,G149A+G182T+Q345R+S323T,G149A+G182T+Q345R+V206L,G149A+G182T+Q345R+Y295F,G149A+G182T+Q365S+R320K,G149A+G182T+Q365S+R458K,G149A+G182T+Q365S+S323T,G149A+G182T+Q365S+V206L,G149A+G182T+Q365S+Y295F,G149A+G182T+R320K+R458K,G149A+G182T+R320K+S323T,G149A+G182T+R320K+V206L,G149A+G182T+R320K+Y295F,G149A+G182T+R458K+S323T,G149A+G182T+R458K+V206L,G149A+G182T+R458K+Y295F,G149A+G182T+S323T+V206L,G149A+G182T+S323T+Y295F,G149A+G182T+V206L+Y295F,G149A+H1*+I9M+K391A,G149A+H1*+I9M+M202L,G149A+H1*+I9M+N16Y,G149A+H1*+I9M+N195F,G149A+H1*+I9M+N54S,G149A+H1*+I9M+Q169E,G149A+H1*+I9M+Q169E,G149A+H1*+I9M+Q172K,G149A+H1*+I9M+Q299Y,G149A+H1*+I9M+Q345R,G149A+H1*+I9M+Q365S,G149A+H1*+I9M+R320K,G149A+H1*+I9M+R458K,G149A+H1*+I9M+S323T,G149A+H1*+I9M+V206L,G149A+H1*+I9M+Y295F,G149A+H1*+K391A+M202L,G149A+H1*+K391A+N16Y,G149A+H1*+K391A+N195F,G149A+H1*+K391A+N54S,G149A+H1*+K391A+Q169E,G149A+H1*+K391A+Q169E,G149A+H1*+K391A+Q172K,G149A+H1*+K391A+Q299Y,G149A+H1*+K391A+Q345R,G149A+H1*+K391A+Q365S,G149A+H1*+K391A+R320K,G149A+H1*+K391A+R458K,G149A+H1*+K391A+S323T,G149A+H1*+K391A+V206L,G149A+H1*+K391A+Y295F,G149A+H1*+M202L+N16Y,G149A+H1*+M202L+N195F,G149A+H1*+M202L+N54S,G149A+H1*+M202L+Q169E,G149A+H1*+M202L+Q169E,G149A+H1*+M202L+Q172K,G149A+H1*+M202L+Q299Y,G149A+H1*+M202L+Q345R,G149A+H1*+M202L+Q365S,G149A+H1*+M202L+R320K,G149A+H1*+M202L+R458K,G149A+H1*+M202L+S323T,G149A+H1*+M202L+V206L,G149A+H1*+M202L+Y295F,G149A+H1*+N16Y+N195F,G149A+H1*+N16Y+N54S,G149A+H1*+N16Y+Q169E,G149A+H1*+N16Y+Q169E,G149A+H1*+N16Y+Q172K,G149A+H1*+N16Y+Q299Y,G149A+H1*+N16Y+Q345R,G149A+H1*+N16Y+Q365S,G149A+H1

24 Mar 2026
2026202266

+N16Y+R320K,G149A+H1+N16Y+R458K,G149A+H1*+N16Y+S323T,G149A+H1*+N16Y+V206L,G149A+H1*+N16Y+Y295F,G149A+H1*+N195F+N54S,G149A+H1*+N195F+Q169E,G149A+H1*+N195F+Q169E,G149A+H1*+N195F+Q172K,G149A+H1*+N195F+Q299Y,G149A+H1*+N195F+Q345R,G149A+H1*+N195F+Q365S,G149A+H1*+N195F+R320K,G149A+H1*+N195F+R458K,G149A+H1*+N195F+S323T,G149A+H1*+N195F+V206L,G149A+H1*+N195F+Y295F,G149A+H1*+N54S+Q169E,G149A+H1*+N54S+Q169E,G149A+H1*+N54S+Q172K,G149A+H1*+N54S+Q299Y,G149A+H1*+N54S+Q345R,G149A+H1*+N54S+Q365S,G149A+H1*+N54S+R320K,G149A+H1*+N54S+R458K,G149A+H1*+N54S+S323T,G149A+H1*+N54S+V206L,G149A+H1*+N54S+Y295F,G149A+H1*+Q169E+Q169E,G149A+H1*+Q169E+Q172K,G149A+H1*+Q169E+Q299Y,G149A+H1*+Q169E+Q345R,G149A+H1*+Q169E+Q365S,G149A+H1*+Q169E+R320K,G149A+H1*+Q169E+R458K,G149A+H1*+Q169E+S323T,G149A+H1*+Q169E+V206L,G149A+H1*+Q169E+Y295F,G149A+H1*+Q169E+Q172K,G149A+H1*+Q169E+Q299Y,G149A+H1*+Q169E+Q345R,G149A+H1*+Q169E+Q365S,G149A+H1*+Q169E+R320K,G149A+H1*+Q169E+R458K,G149A+H1*+Q169E+S323T,G149A+H1*+Q169E+V206L,G149A+H1*+Q169E+Y295F,G149A+H1*+Q172K+Q299Y,G149A+H1*+Q172K+Q345R,G149A+H1*+Q172K+Q365S,G149A+H1*+Q172K+R320K,G149A+H1*+Q172K+R458K,G149A+H1*+Q172K+S323T,G149A+H1*+Q172K+V206L,G149A+H1*+Q172K+Y295F,G149A+H1*+Q299Y+Q345R,G149A+H1*+Q299Y+Q365S,G149A+H1*+Q299Y+R320K,G149A+H1*+Q299Y+R458K,G149A+H1*+Q299Y+S323T,G149A+H1*+Q299Y+V206L,G149A+H1*+Q299Y+Y295F,G149A+H1*+Q345R+Q365S,G149A+H1*+Q345R+R320K,G149A+H1*+Q345R+R458K,G149A+H1*+Q345R+S323T,G149A+H1*+Q345R+V206L,G149A+H1*+Q345R+Y295F,G149A+H1*+Q365S+R320K,G149A+H1*+Q365S+R458K,G149A+H1*+Q365S+S323T,G149A+H1*+Q365S+V206L,G149A+H1*+Q365S+Y295F,G149A+H1*+R320K+R458K,G149A+H1*+R320K+S323T,G149A+H1*+R320K+V206L,G149A+H1*+R320K+Y295F,G149A+H1*+R458K+S323T,G149A+H1*+R458K+V206L,G149A+H1*+R458K+Y295F,G149A+H1*+S323T+V206L,G149A+H1*+S323T+Y295F,G149A+H1*+V206L+Y295F,G149A+I9M+K391A+M202L,G149A+I9M+K391A+N16Y,G149A+I9M+K391A+N195F,G149A+I9M+K391A+N54S,G149A+I9M+K391A+Q169E,G149A+I9M+K391A+Q169E,G149A+I9M+K391A+Q172K,G149A+I9M+K391A+Q299Y,G149A+I9M+K391A+Q345R,G149A+I9M+K391A+Q365S,G149A+I9M+K391A+R320K,G149A+I9M+K391A+R458K,G149A+I9M+K391A+S323T,G149A+I9M+K391A+V206L,G149A+I9M+K391A+Y295F,G149A+I9M+M202L+N16Y,G149A+I9M+M202L+N195F,G149A+I9M+M202L+N54S,G149A+I9M+M202L+Q169E,G149A+I9M+M202L+Q169E,G149A+I9M+M202L+Q172K,G149A+I9M+M202L+Q299Y,G149A+I9M+M202L+Q345R,G149A+I9M+M202L+Q365S,G149A+I9M+M202L+R320K,G149A+I9M+M202L+R458K,G149A+I9M+M202L+S323T,G149A+I9M+M202L+V206L,G149A+I9M+M202L+Y295F,G149A+I9M+N16Y+N195F,G149A+I9M+N16Y+N54S,G149A+I9M+N16Y+Q169E,G149A+I9M+N16Y+Q169E,G149A+I9M+N16Y+Q172K,G149A+I9M+N16Y+Q299Y,G149A+I9M+N16Y+Q345R,G149A+I9

24 Mar 2026
2026202266

M+N16Y+Q365S,G149A+I9M+N16Y+R320K,G149A+I9M+N16Y+R458K,G149A+I9M+N16Y+S323T,G149A+I9M+N16Y+V206L,G149A+I9M+N16Y+Y295F,G149A+I9M+N195F+N54S,G149A+I9M+N195F+Q169E,G149A+I9M+N195F+Q169E,G149A+I9M+N195F+Q172K,G149A+I9M+N195F+Q299Y,G149A+I9M+N195F+Q345R,G149A+I9M+N195F+Q365S,G149A+I9M+N195F+R320K,G149A+I9M+N195F+R458K,G149A+I9M+N195F+S323T,G149A+I9M+N195F+V206L,G149A+I9M+N195F+Y295F,G149A+I9M+N54S+Q169E,G149A+I9M+N54S+Q169E,G149A+I9M+N54S+Q172K,G149A+I9M+N54S+Q299Y,G149A+I9M+N54S+Q345R,G149A+I9M+N54S+Q365S,G149A+I9M+N54S+R320K,G149A+I9M+N54S+R458K,G149A+I9M+N54S+S323T,G149A+I9M+N54S+V206L,G149A+I9M+N54S+Y295F,G149A+I9M+Q169E+Q169E,G149A+I9M+Q169E+Q172K,G149A+I9M+Q169E+Q299Y,G149A+I9M+Q169E+Q345R,G149A+I9M+Q169E+Q365S,G149A+I9M+Q169E+R320K,G149A+I9M+Q169E+R458K,G149A+I9M+Q169E+S323T,G149A+I9M+Q169E+V206L,G149A+I9M+Q169E+Y295F,G149A+I9M+Q172K+Q299Y,G149A+I9M+Q172K+Q345R,G149A+I9M+Q172K+Q365S,G149A+I9M+Q172K+R320K,G149A+I9M+Q172K+R458K,G149A+I9M+Q172K+S323T,G149A+I9M+Q172K+V206L,G149A+I9M+Q172K+Y295F,G149A+I9M+Q299Y+Q345R,G149A+I9M+Q299Y+Q365S,G149A+I9M+Q299Y+R320K,G149A+I9M+Q299Y+R458K,G149A+I9M+Q299Y+S323T,G149A+I9M+Q299Y+V206L,G149A+I9M+Q299Y+Y295F,G149A+I9M+Q345R+Q365S,G149A+I9M+Q345R+R320K,G149A+I9M+Q345R+R458K,G149A+I9M+Q345R+S323T,G149A+I9M+Q345R+V206L,G149A+I9M+Q345R+Y295F,G149A+I9M+Q365S+R320K,G149A+I9M+Q365S+R458K,G149A+I9M+Q365S+S323T,G149A+I9M+Q365S+V206L,G149A+I9M+Q365S+Y295F,G149A+I9M+R320K+R458K,G149A+I9M+R320K+S323T,G149A+I9M+R320K+V206L,G149A+I9M+R320K+Y295F,G149A+I9M+R458K+S323T,G149A+I9M+R458K+V206L,G149A+I9M+R458K+Y295F,G149A+I9M+S323T+V206L,G149A+I9M+S323T+Y295F,G149A+I9M+V206L+Y295F,G149A+K391A+M202L+N16Y,G149A+K391A+M202L+N195F,G149A+K391A+M202L+N54S,G149A+K391A+M202L+Q169E,G149A+K391A+M202L+Q169E,G149A+K391A+M202L+Q172K,G149A+K391A+M202L+Q299Y,G149A+K391A+M202L+Q345R,G149A+K391A+M202L+Q365S,G149A+K391A+M202L+R320K,G149A+K391A+M202L+R458K,G149A+K391A+M202L+S323T,G149A+K391A+M202L+V206L,G149A+K391A+M202L+Y295F,G149A+K391A+N16Y+N195F,G149A+K391A+N16Y+N54S,G149A+K391A+N16Y+Q169E,G149A+K391A+N16Y+Q169E,G149A+K391A+N16Y+Q172K,G149A+K391A+N16Y+Q299Y,G149A+K391A+N16Y+Q345R,G149A+K391A+N16Y+Q365S,G149A+K391A+N16Y+R320K,G149A+K391A+N16Y+R458K,G149A+K391A+N16Y+S323T,G149A+K391A+N16Y+V206L,G149A+K391A+N16Y+Y295F,G149A+K391A+N195F+N54S,G149A+K391A+N195F+Q169E,G149A+K391A+N195F+Q169E,G149A+K391A+N195F+Q172K,G149A+K391A+N195F+Q299Y,G149A+K3

24 Mar 2026
2026202266

91A+N195F+Q345R,G149A+K391A+N195F+Q365S,G149A+K391A+N195F+R320K,G149A+K391A+N195F+R458K,G149A+K391A+N195F+S323T,G149A+K391A+N195F+V206L,G149A+K391A+N195F+Y295F,G149A+K391A+N54S+Q169E,G149A+K391A+N54S+Q169E,G149A+K391A+N54S+Q172K,G149A+K391A+N54S+Q299Y,G149A+K391A+N54S+Q345R,G149A+K391A+N54S+Q365S,G149A+K391A+N54S+R320K,G149A+K391A+N54S+R458K,G149A+K391A+N54S+S323T,G149A+K391A+N54S+V206L,G149A+K391A+N54S+Y295F,G149A+K391A+Q169E+Q169E,G149A+K391A+Q169E+Q172K,G149A+K391A+Q169E+Q299Y,G149A+K391A+Q169E+Q345R,G149A+K391A+Q169E+Q365S,G149A+K391A+Q169E+R320K,G149A+K391A+Q169E+R458K,G149A+K391A+Q169E+S323T,G149A+K391A+Q169E+V206L,G149A+K391A+Q169E+Y295F,G149A+K391A+Q172K+Q299Y,G149A+K391A+Q172K+Q345R,G149A+K391A+Q172K+Q365S,G149A+K391A+Q172K+R320K,G149A+K391A+Q172K+R458K,G149A+K391A+Q172K+S323T,G149A+K391A+Q172K+V206L,G149A+K391A+Q172K+Y295F,G149A+K391A+Q299Y+Q345R,G149A+K391A+Q299Y+Q365S,G149A+K391A+Q299Y+R320K,G149A+K391A+Q299Y+R458K,G149A+K391A+Q299Y+S323T,G149A+K391A+Q299Y+V206L,G149A+K391A+Q299Y+Y295F,G149A+K391A+Q345R+Q365S,G149A+K391A+Q345R+R320K,G149A+K391A+Q345R+R458K,G149A+K391A+Q345R+S323T,G149A+K391A+Q345R+V206L,G149A+K391A+Q345R+Y295F,G149A+K391A+Q365S+R320K,G149A+K391A+Q365S+R458K,G149A+K391A+Q365S+S323T,G149A+K391A+Q365S+V206L,G149A+K391A+Q365S+Y295F,G149A+K391A+R320K+R458K,G149A+K391A+R320K+S323T,G149A+K391A+R320K+V206L,G149A+K391A+R320K+Y295F,G149A+K391A+R458K+S323T,G149A+K391A+R458K+V206L,G149A+K391A+R458K+Y295F,G149A+K391A+S323T+V206L,G149A+K391A+S323T+Y295F,G149A+K391A+V206L+Y295F,G149A+M202L+N16Y+N195F,G149A+M202L+N16Y+N54S,G149A+M202L+N16Y+Q169E,G149A+M202L+N16Y+Q169E,G149A+M202L+N16Y+Q172K,G149A+M202L+N16Y+Q299Y,G149A+M202L+N16Y+Q345R,G149A+M202L+N16Y+Q365S,G149A+M202L+N16Y+R320K,G149A+M202L+N16Y+R458K,G149A+M202L+N16Y+S323T,G149A+M202L+N16Y+V206L,G149A+M202L+N16Y+Y295F,G149A+M202L+N195F+N54S,G149A+M202L+N195F+Q169E,G149A+M202L+N195F+Q169E,G149A+M202L+N195F+Q172K,G149A+M202L+N195F+Q299Y,G149A+M202L+N195F+Q345R,G149A+M202L+N195F+Q365S,G149A+M202L+N195F+R320K,G149A+M202L+N195F+R458K,G149A+M202L+N195F+S323T,G149A+M202L+N195F+V206L,G149A+M202L+N195F+Y295F,G149A+M202L+N54S+Q169E,G149A+M202L+N54S+Q169E,G149A+M202L+N54S+Q172K,G149A+M202L+N54S+Q299Y,G149A+M202L+N54S+Q345R,G149A+M202L+N54S+Q365S,G149A+M202L+N54S+R320K,G149A+M202L+N54S+R458K,G149A+M202L+N54S+S323T,G149A+M202L+N54S+V206L,G149

24 Mar 2026
2026202266

A+M202L+N54S+Y295F,G149A+M202L+Q169E+Q169E,G149A+M202L+Q169E+Q172K,G149A+M202L+Q169E+Q299Y,G149A+M202L+Q169E+Q345R,G149A+M202L+Q169E+Q365S,G149A+M202L+Q169E+R320K,G149A+M202L+Q169E+R458K,G149A+M202L+Q169E+S323T,G149A+M202L+Q169E+V206L,G149A+M202L+Q169E+Y295F,G149A+M202L+Q169E+Q172K,G149A+M202L+Q169E+Q299Y,G149A+M202L+Q169E+Q345R,G149A+M202L+Q169E+Q365S,G149A+M202L+Q169E+R320K,G149A+M202L+Q169E+R458K,G149A+M202L+Q169E+S323T,G149A+M202L+Q169E+V206L,G149A+M202L+Q169E+Y295F,G149A+M202L+Q172K+Q299Y,G149A+M202L+Q172K+Q345R,G149A+M202L+Q172K+Q365S,G149A+M202L+Q172K+R320K,G149A+M202L+Q172K+R458K,G149A+M202L+Q172K+S323T,G149A+M202L+Q172K+V206L,G149A+M202L+Q172K+Y295F,G149A+M202L+Q299Y+Q345R,G149A+M202L+Q299Y+Q365S,G149A+M202L+Q299Y+R320K,G149A+M202L+Q299Y+R458K,G149A+M202L+Q299Y+S323T,G149A+M202L+Q299Y+V206L,G149A+M202L+Q299Y+Y295F,G149A+M202L+Q345R+Q365S,G149A+M202L+Q345R+R320K,G149A+M202L+Q345R+R458K,G149A+M202L+Q345R+S323T,G149A+M202L+Q345R+V206L,G149A+M202L+Q345R+Y295F,G149A+M202L+Q365S+R320K,G149A+M202L+Q365S+R458K,G149A+M202L+Q365S+S323T,G149A+M202L+Q365S+V206L,G149A+M202L+Q365S+Y295F,G149A+M202L+R320K+R458K,G149A+M202L+R320K+S323T,G149A+M202L+R320K+V206L,G149A+M202L+R320K+Y295F,G149A+M202L+R458K+S323T,G149A+M202L+R458K+V206L,G149A+M202L+R458K+Y295F,G149A+M202L+S323T+V206L,G149A+M202L+S323T+Y295F,G149A+M202L+V206L+Y295F,G149A+N16Y+N195F+N54S,G149A+N16Y+N195F+Q169E,G149A+N16Y+N195F+Q169E,G149A+N16Y+N195F+Q172K,G149A+N16Y+N195F+Q299Y,G149A+N16Y+N195F+Q345R,G149A+N16Y+N195F+Q365S,G149A+N16Y+N195F+R320K,G149A+N16Y+N195F+R458K,G149A+N16Y+N195F+S323T,G149A+N16Y+N195F+V206L,G149A+N16Y+N195F+Y295F,G149A+N16Y+N54S+Q169E,G149A+N16Y+N54S+Q169E,G149A+N16Y+N54S+Q172K,G149A+N16Y+N54S+Q299Y,G149A+N16Y+N54S+Q345R,G149A+N16Y+N54S+Q365S,G149A+N16Y+N54S+R320K,G149A+N16Y+N54S+R458K,G149A+N16Y+N54S+S323T,G149A+N16Y+N54S+V206L,G149A+N16Y+N54S+Y295F,G149A+N16Y+Q169E+Q169E,G149A+N16Y+Q169E+Q172K,G149A+N16Y+Q169E+Q299Y,G149A+N16Y+Q169E+Q345R,G149A+N16Y+Q169E+Q365S,G149A+N16Y+Q169E+R320K,G149A+N16Y+Q169E+R458K,G149A+N16Y+Q169E+S323T,G149A+N16Y+Q169E+V206L,G149A+N16Y+Q169E+Y295F,G149A+N16Y+Q172K+Q299Y,G149A+N16Y+Q172K+Q345R,G149A+N16Y+Q172K+Q365S,G149A+N16Y+Q172K+R320K,G149A+N16Y+Q172K+R458K,G149A+N16Y+Q172K+S323T,G149A+N16Y+Q172K+V206L,G149A+N16Y+Q172K+Y295F,G149A+N16Y+Q299Y+Q345R,G149A+N16Y+Q299Y+Q365S,G149A+N16Y+Q299Y+R32

24 Mar 2026
2026202266

0K,G149A+N16Y+Q299Y+R458K,G149A+N16Y+Q299Y+S323T,G149A+N16Y+Q299Y+V206L
,G149A+N16Y+Q299Y+Y295F,G149A+N16Y+Q345R+Q365S,G149A+N16Y+Q345R+R320K,
G149A+N16Y+Q345R+R458K,G149A+N16Y+Q345R+S323T,G149A+N16Y+Q345R+V206L,G
149A+N16Y+Q345R+Y295F,G149A+N16Y+Q365S+R320K,G149A+N16Y+Q365S+R458K,G14
9A+N16Y+Q365S+S323T,G149A+N16Y+Q365S+V206L,G149A+N16Y+Q365S+Y295F,G149A
+N16Y+R320K+R458K,G149A+N16Y+R320K+S323T,G149A+N16Y+R320K+V206L,G149A+N
16Y+R320K+Y295F,G149A+N16Y+R458K+S323T,G149A+N16Y+R458K+V206L,G149A+N16
Y+R458K+Y295F,G149A+N16Y+S323T+V206L,G149A+N16Y+S323T+Y295F,G149A+N16Y+
V206L+Y295F,G149A+N195F+N54S+Q169E,G149A+N195F+N54S+Q169E,G149A+N195F+N
54S+Q172K,G149A+N195F+N54S+Q299Y,G149A+N195F+N54S+Q345R,G149A+N195F+N54
S+Q365S,G149A+N195F+N54S+R320K,G149A+N195F+N54S+R458K,G149A+N195F+N54S+
S323T,G149A+N195F+N54S+V206L,G149A+N195F+N54S+Y295F,G149A+N195F+Q169E+Q
169E,G149A+N195F+Q169E+Q172K,G149A+N195F+Q169E+Q299Y,G149A+N195F+Q169E+
Q345R,G149A+N195F+Q169E+Q365S,G149A+N195F+Q169E+R320K,G149A+N195F+Q169
E+R458K,G149A+N195F+Q169E+S323T,G149A+N195F+Q169E+V206L,G149A+N195F+Q16
9E+Y295F,G149A+N195F+Q169E+Q172K,G149A+N195F+Q169E+Q299Y,G149A+N195F+Q1
69E+Q345R,G149A+N195F+Q169E+Q365S,G149A+N195F+Q169E+R320K,G149A+N195F+
Q169E+R458K,G149A+N195F+Q169E+S323T,G149A+N195F+Q169E+V206L,G149A+N195F
+Q169E+Y295F,G149A+N195F+Q172K+Q299Y,G149A+N195F+Q172K+Q345R,G149A+N195
F+Q172K+Q365S,G149A+N195F+Q172K+R320K,G149A+N195F+Q172K+R458K,G149A+N19
5F+Q172K+S323T,G149A+N195F+Q172K+V206L,G149A+N195F+Q172K+Y295F,G149A+N1
95F+Q299Y+Q345R,G149A+N195F+Q299Y+Q365S,G149A+N195F+Q299Y+R320K,G149A+
N195F+Q299Y+R458K,G149A+N195F+Q299Y+S323T,G149A+N195F+Q299Y+V206L,G149A
+N195F+Q299Y+Y295F,G149A+N195F+Q345R+Q365S,G149A+N195F+Q345R+R320K,G149
A+N195F+Q345R+R458K,G149A+N195F+Q345R+S323T,G149A+N195F+Q345R+V206L,G14
9A+N195F+Q345R+Y295F,G149A+N195F+Q365S+R320K,G149A+N195F+Q365S+R458K,G1
49A+N195F+Q365S+S323T,G149A+N195F+Q365S+V206L,G149A+N195F+Q365S+Y295F,G
149A+N195F+R320K+R458K,G149A+N195F+R320K+S323T,G149A+N195F+R320K+V206L,G
149A+N195F+R320K+Y295F,G149A+N195F+R458K+S323T,G149A+N195F+R458K+V206L,G
149A+N195F+R458K+Y295F,G149A+N195F+S323T+V206L,G149A+N195F+S323T+Y295F,G
149A+N195F+V206L+Y295F,G149A+N54S+Q169E+Q169E,G149A+N54S+Q169E+Q172K,G1
49A+N54S+Q169E+Q299Y,G149A+N54S+Q169E+Q345R,G149A+N54S+Q169E+Q365S,G14
9A+N54S+Q169E+R320K,G149A+N54S+Q169E+R458K,G149A+N54S+Q169E+S323T,G149
A+N54S+Q169E+V206L,G149A+N54S+Q169E+Y295F,G149A+N54S+Q169E+Q172K,G149A+
N54S+Q169E+Q299Y,G149A+N54S+Q169E+Q345R,G149A+N54S+Q169E+Q365S,G149A+N
54S+Q169E+R320K,G149A+N54S+Q169E+R458K,G149A+N54S+Q169E+S323T,G149A+N54

24 Mar 2026
2026202266

S+Q169E+V206L,G149A+N54S+Q169E+Y295F,G149A+N54S+Q172K+Q299Y,G149A+N54S+Q172K+Q345R,G149A+N54S+Q172K+Q365S,G149A+N54S+Q172K+R320K,G149A+N54S+Q172K+R458K,G149A+N54S+Q172K+S323T,G149A+N54S+Q172K+V206L,G149A+N54S+Q172K+Y295F,G149A+N54S+Q299Y+Q345R,G149A+N54S+Q299Y+Q365S,G149A+N54S+Q299Y+R320K,G149A+N54S+Q299Y+R458K,G149A+N54S+Q299Y+S323T,G149A+N54S+Q299Y+V206L,G149A+N54S+Q299Y+Y295F,G149A+N54S+Q345R+Q365S,G149A+N54S+Q345R+R320K,G149A+N54S+Q345R+R458K,G149A+N54S+Q345R+S323T,G149A+N54S+Q345R+V206L,G149A+N54S+Q345R+Y295F,G149A+N54S+Q365S+R320K,G149A+N54S+Q365S+R458K,G149A+N54S+Q365S+S323T,G149A+N54S+Q365S+V206L,G149A+N54S+Q365S+Y295F,G149A+N54S+R320K+R458K,G149A+N54S+R320K+S323T,G149A+N54S+R320K+V206L,G149A+N54S+R320K+Y295F,G149A+N54S+R458K+S323T,G149A+N54S+R458K+V206L,G149A+N54S+R458K+Y295F,G149A+N54S+S323T+V206L,G149A+N54S+S323T+Y295F,G149A+N54S+V206L+Y295F,G149A+Q169E+Q169E+Q172K,G149A+Q169E+Q169E+Q299Y,G149A+Q169E+Q169E+Q345R,G149A+Q169E+Q169E+Q365S,G149A+Q169E+Q169E+R320K,G149A+Q169E+Q169E+R458K,G149A+Q169E+Q169E+S323T,G149A+Q169E+Q169E+V206L,G149A+Q169E+Q169E+Y295F,G149A+Q169E+Q172K+Q299Y,G149A+Q169E+Q172K+Q345R,G149A+Q169E+Q172K+Q365S,G149A+Q169E+Q172K+R320K,G149A+Q169E+Q172K+R458K,G149A+Q169E+Q172K+S323T,G149A+Q169E+Q172K+V206L,G149A+Q169E+Q172K+Y295F,G149A+Q169E+Q299Y+Q345R,G149A+Q169E+Q299Y+Q365S,G149A+Q169E+Q299Y+R320K,G149A+Q169E+Q299Y+R458K,G149A+Q169E+Q299Y+S323T,G149A+Q169E+Q299Y+V206L,G149A+Q169E+Q299Y+Y295F,G149A+Q169E+Q345R+Q365S,G149A+Q169E+Q345R+R320K,G149A+Q169E+Q345R+R458K,G149A+Q169E+Q345R+S323T,G149A+Q169E+Q345R+V206L,G149A+Q169E+Q345R+Y295F,G149A+Q169E+Q365S+R320K,G149A+Q169E+Q365S+R458K,G149A+Q169E+Q365S+S323T,G149A+Q169E+Q365S+V206L,G149A+Q169E+Q365S+Y295F,G149A+Q169E+R320K+R458K,G149A+Q169E+R320K+S323T,G149A+Q169E+R320K+V206L,G149A+Q169E+R320K+Y295F,G149A+Q169E+R458K+S323T,G149A+Q169E+R458K+V206L,G149A+Q169E+R458K+Y295F,G149A+Q169E+S323T+V206L,G149A+Q169E+S323T+Y295F,G149A+Q169E+V206L+Y295F,G149A+Q169E+Q172K+Q299Y,G149A+Q169E+Q172K+Q345R,G149A+Q169E+Q172K+Q365S,G149A+Q169E+Q172K+R320K,G149A+Q169E+Q172K+R458K,G149A+Q169E+Q172K+S323T,G149A+Q169E+Q172K+V206L,G149A+Q169E+Q172K+Y295F,G149A+Q169E+Q299Y+Q345R,G149A+Q169E+Q299Y+Q365S,G149A+Q169E+Q299Y+R320K,G149A+Q169E+Q299Y+R458K,G149A+Q169E+Q299Y+S323T,G149A+Q169E+Q299Y+V206L,G149A+Q169E+Q299Y+Y295F,G149A+Q169E+Q345R+Q365S,G149A+Q169E+Q345R+R320K,G149A+Q169E+Q345R+R458K,G149A+Q169E+Q345R+S323T,G149A+Q169E+Q345R+V206L,G149A+Q169E+Q345R+Y295F,G149A+Q169E+Q365S+R320K,G149A+Q169E+Q365S+R458K,G149A+Q169E+Q365S+S323T,G149A+Q169E+Q365S+

24 Mar 2026
2026202266

V206L,G149A+Q169E+Q365S+Y295F,G149A+Q169E+R320K+R458K,G149A+Q169E+R320K+S323T,G149A+Q169E+R320K+V206L,G149A+Q169E+R320K+Y295F,G149A+Q169E+R458K+S323T,G149A+Q169E+R458K+V206L,G149A+Q169E+R458K+Y295F,G149A+Q169E+S323T+V206L,G149A+Q169E+S323T+Y295F,G149A+Q169E+V206L+Y295F,G149A+Q172K+Q299Y+Q345R,G149A+Q172K+Q299Y+Q365S,G149A+Q172K+Q299Y+R320K,G149A+Q172K+Q299Y+R458K,G149A+Q172K+Q299Y+S323T,G149A+Q172K+Q299Y+V206L,G149A+Q172K+Q299Y+Y295F,G149A+Q172K+Q345R+Q365S,G149A+Q172K+Q345R+R320K,G149A+Q172K+Q345R+R458K,G149A+Q172K+Q345R+S323T,G149A+Q172K+Q345R+V206L,G149A+Q172K+Q345R+Y295F,G149A+Q172K+Q365S+R320K,G149A+Q172K+Q365S+R458K,G149A+Q172K+Q365S+S323T,G149A+Q172K+Q365S+V206L,G149A+Q172K+Q365S+Y295F,G149A+Q172K+R320K+R458K,G149A+Q172K+R320K+S323T,G149A+Q172K+R320K+V206L,G149A+Q172K+R320K+Y295F,G149A+Q172K+R458K+S323T,G149A+Q172K+R458K+V206L,G149A+Q172K+R458K+Y295F,G149A+Q172K+S323T+V206L,G149A+Q172K+S323T+Y295F,G149A+Q172K+V206L+Y295F,G149A+Q299Y+Q345R+Q365S,G149A+Q299Y+Q345R+R320K,G149A+Q299Y+Q345R+R458K,G149A+Q299Y+Q345R+S323T,G149A+Q299Y+Q345R+V206L,G149A+Q299Y+Q345R+Y295F,G149A+Q299Y+Q365S+R320K,G149A+Q299Y+Q365S+R458K,G149A+Q299Y+Q365S+S323T,G149A+Q299Y+Q365S+V206L,G149A+Q299Y+Q365S+Y295F,G149A+Q299Y+R320K+R458K,G149A+Q299Y+R320K+S323T,G149A+Q299Y+R320K+V206L,G149A+Q299Y+R320K+Y295F,G149A+Q299Y+R458K+S323T,G149A+Q299Y+R458K+V206L,G149A+Q299Y+R458K+Y295F,G149A+Q299Y+S323T+V206L,G149A+Q299Y+S323T+Y295F,G149A+Q299Y+V206L+Y295F,G149A+Q345R+Q365S+R320K,G149A+Q345R+Q365S+R458K,G149A+Q345R+Q365S+S323T,G149A+Q345R+Q365S+V206L,G149A+Q345R+Q365S+Y295F,G149A+Q345R+R320K+R458K,G149A+Q345R+R320K+S323T,G149A+Q345R+R320K+V206L,G149A+Q345R+R320K+Y295F,G149A+Q345R+R458K+S323T,G149A+Q345R+R458K+V206L,G149A+Q345R+R458K+Y295F,G149A+Q345R+S323T+V206L,G149A+Q345R+S323T+Y295F,G149A+Q345R+V206L+Y295F,G149A+Q365S+R320K+R458K,G149A+Q365S+R320K+S323T,G149A+Q365S+R320K+V206L,G149A+Q365S+R320K+Y295F,G149A+Q365S+R458K+S323T,G149A+Q365S+R458K+V206L,G149A+Q365S+R458K+Y295F,G149A+Q365S+S323T+V206L,G149A+Q365S+S323T+Y295F,G149A+Q365S+V206L+Y295F,G149A+R320K+R458K+S323T,G149A+R320K+R458K+V206L,G149A+R320K+R458K+Y295F,G149A+R320K+S323T+V206L,G149A+R320K+S323T+Y295F,G149A+R320K+V206L+Y295F,G149A+R458K+S323T+V206L,G149A+R458K+S323T+Y295F,G149A+R458K+V206L+Y295F,G149A+S323T+V206L+Y295F,G182T+H1*+I9M+K391A,G182T+H1*+I9M+M202L,G182T+H1*+I9M+N16Y,G182T+H1*+I9M+N195F,G182T+H1*+I9M+N54S,G182T+H1*+I9M+Q169E,G182T+H1*+I9M+Q169E,G182T+H1*+I9M+Q172K,G182T+H1*+I9M+Q299Y,G182T+H1*+I9M+Q345R,G182T+H1*+I9M+Q365S,G182T+H1*+I9M+R320K,G182T+H1*+I9M+R458K,G182T+H1*+I9M+S323T,G

24 Mar 2026
2026202266

182T+H1*+I9M+V206L,G182T+H1*+I9M+Y295F,G182T+H1*+K391A+M202L,G182T+H1*+K391A+N16Y,G182T+H1*+K391A+N195F,G182T+H1*+K391A+N54S,G182T+H1*+K391A+Q169E,G182T+H1*+K391A+Q169E,G182T+H1*+K391A+Q172K,G182T+H1*+K391A+Q299Y,G182T+H1*+K391A+Q345R,G182T+H1*+K391A+Q365S,G182T+H1*+K391A+R320K,G182T+H1*+K391A+R458K,G182T+H1*+K391A+S323T,G182T+H1*+K391A+V206L,G182T+H1*+K391A+Y295F,G182T+H1*+M202L+N16Y,G182T+H1*+M202L+N195F,G182T+H1*+M202L+N54S,G182T+H1*+M202L+Q169E,G182T+H1*+M202L+Q169E,G182T+H1*+M202L+Q172K,G182T+H1*+M202L+Q299Y,G182T+H1*+M202L+Q345R,G182T+H1*+M202L+Q365S,G182T+H1*+M202L+R320K,G182T+H1*+M202L+R458K,G182T+H1*+M202L+S323T,G182T+H1*+M202L+V206L,G182T+H1*+M202L+Y295F,G182T+H1*+N16Y+N195F,G182T+H1*+N16Y+N54S,G182T+H1*+N16Y+Q169E,G182T+H1*+N16Y+Q169E,G182T+H1*+N16Y+Q172K,G182T+H1*+N16Y+Q299Y,G182T+H1*+N16Y+Q345R,G182T+H1*+N16Y+Q365S,G182T+H1*+N16Y+R320K,G182T+H1*+N16Y+R458K,G182T+H1*+N16Y+S323T,G182T+H1*+N16Y+V206L,G182T+H1*+N16Y+Y295F,G182T+H1*+N195F+N54S,G182T+H1*+N195F+Q169E,G182T+H1*+N195F+Q169E,G182T+H1*+N195F+Q172K,G182T+H1*+N195F+Q299Y,G182T+H1*+N195F+Q345R,G182T+H1*+N195F+Q365S,G182T+H1*+N195F+R320K,G182T+H1*+N195F+R458K,G182T+H1*+N195F+S323T,G182T+H1*+N195F+V206L,G182T+H1*+N195F+Y295F,G182T+H1*+N54S+Q169E,G182T+H1*+N54S+Q169E,G182T+H1*+N54S+Q172K,G182T+H1*+N54S+Q299Y,G182T+H1*+N54S+Q345R,G182T+H1*+N54S+Q365S,G182T+H1*+N54S+R320K,G182T+H1*+N54S+R458K,G182T+H1*+N54S+S323T,G182T+H1*+N54S+V206L,G182T+H1*+N54S+Y295F,G182T+H1*+Q169E+Q169E,G182T+H1*+Q169E+Q172K,G182T+H1*+Q169E+Q299Y,G182T+H1*+Q169E+Q345R,G182T+H1*+Q169E+Q365S,G182T+H1*+Q169E+R320K,G182T+H1*+Q169E+R458K,G182T+H1*+Q169E+S323T,G182T+H1*+Q169E+V206L,G182T+H1*+Q169E+Y295F,G182T+H1*+Q169E+Q172K,G182T+H1*+Q169E+Q299Y,G182T+H1*+Q169E+Q345R,G182T+H1*+Q169E+Q365S,G182T+H1*+Q169E+R320K,G182T+H1*+Q169E+R458K,G182T+H1*+Q169E+S323T,G182T+H1*+Q169E+V206L,G182T+H1*+Q169E+Y295F,G182T+H1*+Q172K+Q299Y,G182T+H1*+Q172K+Q345R,G182T+H1*+Q172K+Q365S,G182T+H1*+Q172K+R320K,G182T+H1*+Q172K+R458K,G182T+H1*+Q172K+S323T,G182T+H1*+Q172K+V206L,G182T+H1*+Q172K+Y295F,G182T+H1*+Q299Y+Q345R,G182T+H1*+Q299Y+Q365S,G182T+H1*+Q299Y+R320K,G182T+H1*+Q299Y+R458K,G182T+H1*+Q299Y+S323T,G182T+H1*+Q299Y+V206L,G182T+H1*+Q299Y+Y295F,G182T+H1*+Q345R+Q365S,G182T+H1*+Q345R+R320K,G182T+H1*+Q345R+R458K,G182T+H1*+Q345R+S323T,G182T+H1*+Q345R+V206L,G182T+H1*+Q345R+Y295F,G182T+H1*+Q365S+R320K,G182T+H1*+Q365S+R458K,G182T+H1*+Q365S+S323T,G182T+H1*+Q365S+V206L,G182T+H1*+Q365S+Y295F,G182T+H1*+R320K+R458K,G182T+H1*+R320K+S323T,G182T+H1*+R320K+V206L,G182T+H1*+R320K+Y295F,G182T+H1*+R458K+S323T,G182T+H1*+R458K+V206L,G182T+H1*+R458K+Y295F,G182T+H1*+S323T+V20

24 Mar 2026
2026202266

6L,G182T+H1*+S323T+Y295F,G182T+H1*+V206L+Y295F,G182T+I9M+K391A+M202L,G182T+I9M+K391A+N16Y,G182T+I9M+K391A+N195F,G182T+I9M+K391A+N54S,G182T+I9M+K391A+Q169E,G182T+I9M+K391A+Q169E,G182T+I9M+K391A+Q172K,G182T+I9M+K391A+Q299Y,G182T+I9M+K391A+Q345R,G182T+I9M+K391A+Q365S,G182T+I9M+K391A+R320K,G182T+I9M+K391A+R458K,G182T+I9M+K391A+S323T,G182T+I9M+K391A+V206L,G182T+I9M+K391A+Y295F,G182T+I9M+M202L+N16Y,G182T+I9M+M202L+N195F,G182T+I9M+M202L+N54S,G182T+I9M+M202L+Q169E,G182T+I9M+M202L+Q169E,G182T+I9M+M202L+Q172K,G182T+I9M+M202L+Q299Y,G182T+I9M+M202L+Q345R,G182T+I9M+M202L+Q365S,G182T+I9M+M202L+R320K,G182T+I9M+M202L+R458K,G182T+I9M+M202L+S323T,G182T+I9M+M202L+V206L,G182T+I9M+M202L+Y295F,G182T+I9M+N16Y+N195F,G182T+I9M+N16Y+N54S,G182T+I9M+N16Y+Q169E,G182T+I9M+N16Y+Q169E,G182T+I9M+N16Y+Q172K,G182T+I9M+N16Y+Q299Y,G182T+I9M+N16Y+Q345R,G182T+I9M+N16Y+Q365S,G182T+I9M+N16Y+R320K,G182T+I9M+N16Y+R458K,G182T+I9M+N16Y+S323T,G182T+I9M+N16Y+V206L,G182T+I9M+N16Y+Y295F,G182T+I9M+N195F+N54S,G182T+I9M+N195F+Q169E,G182T+I9M+N195F+Q169E,G182T+I9M+N195F+Q172K,G182T+I9M+N195F+Q299Y,G182T+I9M+N195F+Q345R,G182T+I9M+N195F+Q365S,G182T+I9M+N195F+R320K,G182T+I9M+N195F+R458K,G182T+I9M+N195F+S323T,G182T+I9M+N195F+V206L,G182T+I9M+N195F+Y295F,G182T+I9M+N54S+Q169E,G182T+I9M+N54S+Q169E,G182T+I9M+N54S+Q172K,G182T+I9M+N54S+Q299Y,G182T+I9M+N54S+Q345R,G182T+I9M+N54S+Q365S,G182T+I9M+N54S+R320K,G182T+I9M+N54S+R458K,G182T+I9M+N54S+S323T,G182T+I9M+N54S+V206L,G182T+I9M+N54S+Y295F,G182T+I9M+Q169E+Q169E,G182T+I9M+Q169E+Q172K,G182T+I9M+Q169E+Q299Y,G182T+I9M+Q169E+Q345R,G182T+I9M+Q169E+Q365S,G182T+I9M+Q169E+R320K,G182T+I9M+Q169E+R458K,G182T+I9M+Q169E+S323T,G182T+I9M+Q169E+V206L,G182T+I9M+Q169E+Y295F,G182T+I9M+Q169E+Q172K,G182T+I9M+Q169E+Q299Y,G182T+I9M+Q169E+Q345R,G182T+I9M+Q169E+Q365S,G182T+I9M+Q169E+R320K,G182T+I9M+Q169E+R458K,G182T+I9M+Q169E+S323T,G182T+I9M+Q169E+V206L,G182T+I9M+Q169E+Y295F,G182T+I9M+Q172K+Q299Y,G182T+I9M+Q172K+Q345R,G182T+I9M+Q172K+Q365S,G182T+I9M+Q172K+R320K,G182T+I9M+Q172K+R458K,G182T+I9M+Q172K+S323T,G182T+I9M+Q172K+V206L,G182T+I9M+Q172K+Y295F,G182T+I9M+Q299Y+Q345R,G182T+I9M+Q299Y+Q365S,G182T+I9M+Q299Y+R320K,G182T+I9M+Q299Y+R458K,G182T+I9M+Q299Y+S323T,G182T+I9M+Q299Y+V206L,G182T+I9M+Q299Y+Y295F,G182T+I9M+Q345R+Q365S,G182T+I9M+Q345R+R320K,G182T+I9M+Q345R+R458K,G182T+I9M+Q345R+S323T,G182T+I9M+Q345R+V206L,G182T+I9M+Q345R+Y295F,G182T+I9M+Q365S+R320K,G182T+I9M+Q365S+R458K,G182T+I9M+Q365S+S323T,G182T+I9M+Q365S+V206L,G182T+I9M+Q365S+Y295F,G182T+I9M+R320K+R458K,G182T+I9M+R320K+S323T,G182T+I9M+R320K+V206L,G182T+I9M+R320K+Y295F,G182T+I9M+R458K+S323T,G182T+I9M+R458K+V206L,G182T+I9M+R458K+Y295F,G182T+I

24 Mar 2026
2026202266

9M+S323T+V206L,G182T+I9M+S323T+Y295F,G182T+I9M+V206L+Y295F,G182T+K391A+M202L+N16Y,G182T+K391A+M202L+N195F,G182T+K391A+M202L+N54S,G182T+K391A+M202L+Q169E,G182T+K391A+M202L+Q169E,G182T+K391A+M202L+Q172K,G182T+K391A+M202L+Q299Y,G182T+K391A+M202L+Q345R,G182T+K391A+M202L+Q365S,G182T+K391A+M202L+R320K,G182T+K391A+M202L+R458K,G182T+K391A+M202L+S323T,G182T+K391A+M202L+V206L,G182T+K391A+M202L+Y295F,G182T+K391A+N16Y+N195F,G182T+K391A+N16Y+N54S,G182T+K391A+N16Y+Q169E,G182T+K391A+N16Y+Q169E,G182T+K391A+N16Y+Q172K,G182T+K391A+N16Y+Q299Y,G182T+K391A+N16Y+Q345R,G182T+K391A+N16Y+Q365S,G182T+K391A+N16Y+R320K,G182T+K391A+N16Y+R458K,G182T+K391A+N16Y+S323T,G182T+K391A+N16Y+V206L,G182T+K391A+N16Y+Y295F,G182T+K391A+N195F+N54S,G182T+K391A+N195F+Q169E,G182T+K391A+N195F+Q169E,G182T+K391A+N195F+Q172K,G182T+K391A+N195F+Q299Y,G182T+K391A+N195F+Q345R,G182T+K391A+N195F+Q365S,G182T+K391A+N195F+R320K,G182T+K391A+N195F+R458K,G182T+K391A+N195F+S323T,G182T+K391A+N195F+V206L,G182T+K391A+N195F+Y295F,G182T+K391A+N54S+Q169E,G182T+K391A+N54S+Q169E,G182T+K391A+N54S+Q172K,G182T+K391A+N54S+Q299Y,G182T+K391A+N54S+Q345R,G182T+K391A+N54S+Q365S,G182T+K391A+N54S+R320K,G182T+K391A+N54S+R458K,G182T+K391A+N54S+S323T,G182T+K391A+N54S+V206L,G182T+K391A+N54S+Y295F,G182T+K391A+Q169E+Q169E,G182T+K391A+Q169E+Q172K,G182T+K391A+Q169E+Q299Y,G182T+K391A+Q169E+Q345R,G182T+K391A+Q169E+Q365S,G182T+K391A+Q169E+R320K,G182T+K391A+Q169E+R458K,G182T+K391A+Q169E+S323T,G182T+K391A+Q169E+V206L,G182T+K391A+Q169E+Y295F,G182T+K391A+Q172K+Q299Y,G182T+K391A+Q172K+Q345R,G182T+K391A+Q172K+Q365S,G182T+K391A+Q172K+R320K,G182T+K391A+Q172K+R458K,G182T+K391A+Q172K+S323T,G182T+K391A+Q172K+V206L,G182T+K391A+Q172K+Y295F,G182T+K391A+Q299Y+Q345R,G182T+K391A+Q299Y+Q365S,G182T+K391A+Q299Y+R320K,G182T+K391A+Q299Y+R458K,G182T+K391A+Q299Y+S323T,G182T+K391A+Q299Y+V206L,G182T+K391A+Q299Y+Y295F,G182T+K391A+Q345R+Q365S,G182T+K391A+Q345R+R320K,G182T+K391A+Q345R+R458K,G182T+K391A+Q345R+S323T,G182T+K391A+Q345R+V206L,G182T+K391A+Q345R+Y295F,G182T+K391A+Q365S+R320K,G182T+K391A+Q365S+R458K,G182T+K391A+Q365S+S323T,G182T+K391A+Q365S+V206L,G182T+K391A+Q365S+Y295F,G182T+K391A+R320K+R458K,G182T+K391A+R320K+S323T,G182T+K391A+R320K+V206L,G182T+K391A+R320K+Y295F,G182T+K391A+R458K+S323T,G182T+K391A+R458K+V206L,G182T+K391A+R458K+Y295F,G182T+K391A+S323T+V206L,G182T+K391A+S323T+Y295F,G182T+K391A+V206L+Y295F,G182T+M202L+N16Y

24 Mar 2026
2026202266

+N195F,G182T+M202L+N16Y+N54S,G182T+M202L+N16Y+Q169E,G182T+M202L+N16Y+Q169E,G182T+M202L+N16Y+Q172K,G182T+M202L+N16Y+Q299Y,G182T+M202L+N16Y+Q345R,G182T+M202L+N16Y+Q365S,G182T+M202L+N16Y+R320K,G182T+M202L+N16Y+R458K,G182T+M202L+N16Y+S323T,G182T+M202L+N16Y+V206L,G182T+M202L+N16Y+Y295F,G182T+M202L+N195F+N54S,G182T+M202L+N195F+Q169E,G182T+M202L+N195F+Q169E,G182T+M202L+N195F+Q172K,G182T+M202L+N195F+Q299Y,G182T+M202L+N195F+Q345R,G182T+M202L+N195F+Q365S,G182T+M202L+N195F+R320K,G182T+M202L+N195F+R458K,G182T+M202L+N195F+S323T,G182T+M202L+N195F+V206L,G182T+M202L+N195F+Y295F,G182T+M202L+N54S+Q169E,G182T+M202L+N54S+Q169E,G182T+M202L+N54S+Q172K,G182T+M202L+N54S+Q299Y,G182T+M202L+N54S+Q345R,G182T+M202L+N54S+Q365S,G182T+M202L+N54S+R320K,G182T+M202L+N54S+R458K,G182T+M202L+N54S+S323T,G182T+M202L+N54S+V206L,G182T+M202L+N54S+Y295F,G182T+M202L+Q169E+Q169E,G182T+M202L+Q169E+Q172K,G182T+M202L+Q169E+Q299Y,G182T+M202L+Q169E+Q345R,G182T+M202L+Q169E+Q365S,G182T+M202L+Q169E+R320K,G182T+M202L+Q169E+R458K,G182T+M202L+Q169E+S323T,G182T+M202L+Q169E+V206L,G182T+M202L+Q169E+Y295F,G182T+M202L+Q172K,G182T+M202L+Q169E+Q299Y,G182T+M202L+Q169E+Q345R,G182T+M202L+Q169E+Q365S,G182T+M202L+Q169E+R320K,G182T+M202L+Q169E+R458K,G182T+M202L+Q169E+S323T,G182T+M202L+Q169E+V206L,G182T+M202L+Q169E+Y295F,G182T+M202L+Q172K+Q299Y,G182T+M202L+Q172K+Q345R,G182T+M202L+Q172K+Q365S,G182T+M202L+Q172K+R320K,G182T+M202L+Q172K+R458K,G182T+M202L+Q172K+S323T,G182T+M202L+Q172K+V206L,G182T+M202L+Q172K+Y295F,G182T+M202L+Q299Y+Q345R,G182T+M202L+Q299Y+Q365S,G182T+M202L+Q299Y+R320K,G182T+M202L+Q299Y+R458K,G182T+M202L+Q299Y+S323T,G182T+M202L+Q299Y+V206L,G182T+M202L+Q299Y+Y295F,G182T+M202L+Q345R+Q365S,G182T+M202L+Q345R+R320K,G182T+M202L+Q345R+R458K,G182T+M202L+Q345R+S323T,G182T+M202L+Q345R+V206L,G182T+M202L+Q345R+Y295F,G182T+M202L+Q365S+R320K,G182T+M202L+Q365S+R458K,G182T+M202L+Q365S+S323T,G182T+M202L+Q365S+V206L,G182T+M202L+Q365S+Y295F,G182T+M202L+R320K+R458K,G182T+M202L+R320K+S323T,G182T+M202L+R320K+V206L,G182T+M202L+R320K+Y295F,G182T+M202L+R458K+S323T,G182T+M202L+R458K+V206L,G182T+M202L+R458K+Y295F,G182T+M202L+S323T+V206L,G182T+M202L+S323T+Y295F,G182T+M202L+V206L+Y295F,G182T+N16Y+N195F+N54S,G182T+N16Y+N195F+Q169E,G182T+N16Y+N195F+Q169E,G182T+N16Y+N195F+Q172K,G182T+N16Y+N195F+Q299Y,G182T+N16Y+N195F+Q345R,G182T+N16Y+N195F+Q365S,G182T+N16Y+N195F+R320K,G182T+N16Y+N195F+R458K,G182T+N16Y+N195F+S323T,G182T+N16Y+N195F+V206L,G182T+N16Y+N195F+Y295F,G182T+N16Y+N54S+Q169E,G182T+N16Y+N54S+Q169E,G182T+N16Y+N54S+Q172K,G182T+N16Y+N54S+Q299Y,G182T+N16Y+N54S+Q345R,G182T+N16Y+N54S+Q365S,G182T+

24 Mar 2026
2026202266

N16Y+N54S+R320K,G182T+N16Y+N54S+R458K,G182T+N16Y+N54S+S323T,G182T+N16Y+N54S+V206L,G182T+N16Y+N54S+Y295F,G182T+N16Y+Q169E+Q169E,G182T+N16Y+Q169E+Q172K,G182T+N16Y+Q169E+Q299Y,G182T+N16Y+Q169E+Q345R,G182T+N16Y+Q169E+Q365S,G182T+N16Y+Q169E+R320K,G182T+N16Y+Q169E+R458K,G182T+N16Y+Q169E+S323T,G182T+N16Y+Q169E+V206L,G182T+N16Y+Q169E+Y295F,G182T+N16Y+Q169E+Q172K,G182T+N16Y+Q169E+Q299Y,G182T+N16Y+Q169E+Q345R,G182T+N16Y+Q169E+Q365S,G182T+N16Y+Q169E+R320K,G182T+N16Y+Q169E+R458K,G182T+N16Y+Q169E+S323T,G182T+N16Y+Q169E+V206L,G182T+N16Y+Q169E+Y295F,G182T+N16Y+Q172K+Q299Y,G182T+N16Y+Q172K+Q345R,G182T+N16Y+Q172K+Q365S,G182T+N16Y+Q172K+R320K,G182T+N16Y+Q172K+R458K,G182T+N16Y+Q172K+S323T,G182T+N16Y+Q172K+V206L,G182T+N16Y+Q172K+Y295F,G182T+N16Y+Q299Y+Q345R,G182T+N16Y+Q299Y+Q365S,G182T+N16Y+Q299Y+R320K,G182T+N16Y+Q299Y+R458K,G182T+N16Y+Q299Y+S323T,G182T+N16Y+Q299Y+V206L,G182T+N16Y+Q299Y+Y295F,G182T+N16Y+Q345R+Q365S,G182T+N16Y+Q345R+R320K,G182T+N16Y+Q345R+R458K,G182T+N16Y+Q345R+S323T,G182T+N16Y+Q345R+V206L,G182T+N16Y+Q345R+Y295F,G182T+N16Y+Q365S+R320K,G182T+N16Y+Q365S+R458K,G182T+N16Y+Q365S+S323T,G182T+N16Y+Q365S+V206L,G182T+N16Y+Q365S+Y295F,G182T+N16Y+R320K+R458K,G182T+N16Y+R320K+S323T,G182T+N16Y+R320K+V206L,G182T+N16Y+R320K+Y295F,G182T+N16Y+R458K+S323T,G182T+N16Y+R458K+V206L,G182T+N16Y+R458K+Y295F,G182T+N16Y+S323T+V206L,G182T+N16Y+S323T+Y295F,G182T+N16Y+V206L+Y295F,G182T+N195F+N54S+Q169E,G182T+N195F+N54S+Q169E,G182T+N195F+N54S+Q172K,G182T+N195F+N54S+Q299Y,G182T+N195F+N54S+Q345R,G182T+N195F+N54S+Q365S,G182T+N195F+N54S+R320K,G182T+N195F+N54S+R458K,G182T+N195F+N54S+S323T,G182T+N195F+N54S+V206L,G182T+N195F+N54S+Y295F,G182T+N195F+Q169E+Q169E,G182T+N195F+Q169E+Q172K,G182T+N195F+Q169E+Q299Y,G182T+N195F+Q169E+Q345R,G182T+N195F+Q169E+Q365S,G182T+N195F+Q169E+R320K,G182T+N195F+Q169E+R458K,G182T+N195F+Q169E+S323T,G182T+N195F+Q169E+V206L,G182T+N195F+Q169E+Y295F,G182T+N195F+Q172K+Q299Y,G182T+N195F+Q172K+Q345R,G182T+N195F+Q172K+Q365S,G182T+N195F+Q172K+R320K,G182T+N195F+Q172K+R458K,G182T+N195F+Q172K+S323T,G182T+N195F+Q172K+V206L,G182T+N195F+Q172K+Y295F,G182T+N195F+Q299Y+Q345R,G182T+N195F+Q299Y+Q365S,G182T+N195F+Q299Y+R320K,G182T+N195F+Q299Y+R458K,G182T+N195F+Q299Y+S323T,G182T+N195F+Q299Y+V206L,G182T+N195F+Q299Y+Y295F,G182T+N195F+Q345R+Q365S,G182T+N195F+Q345R+R320K,G182T+N195F+Q345R+R458K,G182T+N195F+Q345R+S323T,G182T+N195F+Q345R+V206L

24 Mar 2026
2026202266

,G182T+N195F+Q345R+Y295F,G182T+N195F+Q365S+R320K,G182T+N195F+Q365S+R458K,G182T+N195F+Q365S+S323T,G182T+N195F+Q365S+V206L,G182T+N195F+Q365S+Y295F,G182T+N195F+R320K+R458K,G182T+N195F+R320K+S323T,G182T+N195F+R320K+V206L,G182T+N195F+R320K+Y295F,G182T+N195F+R458K+S323T,G182T+N195F+R458K+V206L,G182T+N195F+R458K+Y295F,G182T+N195F+S323T+V206L,G182T+N195F+S323T+Y295F,G182T+N195F+V206L+Y295F,G182T+N54S+Q169E+Q169E,G182T+N54S+Q169E+Q172K,G182T+N54S+Q169E+Q299Y,G182T+N54S+Q169E+Q345R,G182T+N54S+Q169E+Q365S,G182T+N54S+Q169E+R320K,G182T+N54S+Q169E+R458K,G182T+N54S+Q169E+S323T,G182T+N54S+Q169E+V206L,G182T+N54S+Q169E+Y295F,G182T+N54S+Q169E+Q172K,G182T+N54S+Q169E+Q299Y,G182T+N54S+Q169E+Q345R,G182T+N54S+Q169E+Q365S,G182T+N54S+Q169E+R320K,G182T+N54S+Q169E+R458K,G182T+N54S+Q169E+S323T,G182T+N54S+Q169E+V206L,G182T+N54S+Q169E+Y295F,G182T+N54S+Q172K+Q299Y,G182T+N54S+Q172K+Q345R,G182T+N54S+Q172K+Q365S,G182T+N54S+Q172K+R320K,G182T+N54S+Q172K+R458K,G182T+N54S+Q172K+S323T,G182T+N54S+Q172K+V206L,G182T+N54S+Q172K+Y295F,G182T+N54S+Q299Y+Q345R,G182T+N54S+Q299Y+Q365S,G182T+N54S+Q299Y+R320K,G182T+N54S+Q299Y+R458K,G182T+N54S+Q299Y+S323T,G182T+N54S+Q299Y+V206L,G182T+N54S+Q299Y+Y295F,G182T+N54S+Q345R+Q365S,G182T+N54S+Q345R+R320K,G182T+N54S+Q345R+R458K,G182T+N54S+Q345R+S323T,G182T+N54S+Q345R+V206L,G182T+N54S+Q345R+Y295F,G182T+N54S+Q365S+R320K,G182T+N54S+Q365S+R458K,G182T+N54S+Q365S+S323T,G182T+N54S+Q365S+V206L,G182T+N54S+Q365S+Y295F,G182T+N54S+R320K+R458K,G182T+N54S+R320K+S323T,G182T+N54S+R320K+V206L,G182T+N54S+R320K+Y295F,G182T+N54S+R458K+S323T,G182T+N54S+R458K+V206L,G182T+N54S+R458K+Y295F,G182T+N54S+S323T+V206L,G182T+N54S+S323T+Y295F,G182T+N54S+V206L+Y295F,G182T+Q169E+Q169E+Q172K,G182T+Q169E+Q169E+Q299Y,G182T+Q169E+Q169E+Q345R,G182T+Q169E+Q169E+Q365S,G182T+Q169E+Q169E+R320K,G182T+Q169E+Q169E+R458K,G182T+Q169E+Q169E+S323T,G182T+Q169E+Q169E+V206L,G182T+Q169E+Q169E+Y295F,G182T+Q169E+Q172K+Q299Y,G182T+Q169E+Q172K+Q345R,G182T+Q169E+Q172K+Q365S,G182T+Q169E+Q172K+R320K,G182T+Q169E+Q172K+R458K,G182T+Q169E+Q172K+S323T,G182T+Q169E+Q172K+V206L,G182T+Q169E+Q172K+Y295F,G182T+Q169E+Q299Y+Q345R,G182T+Q169E+Q299Y+Q365S,G182T+Q169E+Q299Y+R320K,G182T+Q169E+Q299Y+R458K,G182T+Q169E+Q299Y+S323T,G182T+Q169E+Q299Y+V206L,G182T+Q169E+Q299Y+Y295F,G182T+Q169E+Q345R+Q365S,G182T+Q169E+Q345R+R320K,G182T+Q169E+Q345R+R458K,G182T+Q169E+Q345R+S323T,G182T+Q169E+Q345R+V206L,G182T+Q169E+Q345R+Y295F,G182T+Q169E+Q365S+R320K,G182T+Q169E+Q365S+R458K,G182T+Q169E+Q365S+S323T,G182T+Q169E+Q365S+V206L,G182T+Q169E+Q365S+Y295F,G182T+Q169E+R320K+R458K,G182T+Q169E+R320K+S323T,G182T+Q169E+R320

24 Mar 2026
2026202266

K+V206L,G182T+Q169E+R320K+Y295F,G182T+Q169E+R458K+S323T,G182T+Q169E+R45
8K+V206L,G182T+Q169E+R458K+Y295F,G182T+Q169E+S323T+V206L,G182T+Q169E+S32
3T+Y295F,G182T+Q169E+V206L+Y295F,G182T+Q169E+Q172K+Q299Y,G182T+Q169E+Q1
72K+Q345R,G182T+Q169E+Q172K+Q365S,G182T+Q169E+Q172K+R320K,G182T+Q169E+
Q172K+R458K,G182T+Q169E+Q172K+S323T,G182T+Q169E+Q172K+V206L,G182T+Q169E
+Q172K+Y295F,G182T+Q169E+Q299Y+Q345R,G182T+Q169E+Q299Y+Q365S,G182T+Q169
E+Q299Y+R320K,G182T+Q169E+Q299Y+R458K,G182T+Q169E+Q299Y+S323T,G182T+Q16
9E+Q299Y+V206L,G182T+Q169E+Q299Y+Y295F,G182T+Q169E+Q345R+Q365S,G182T+Q1
69E+Q345R+R320K,G182T+Q169E+Q345R+R458K,G182T+Q169E+Q345R+S323T,G182T+
Q169E+Q345R+V206L,G182T+Q169E+Q345R+Y295F,G182T+Q169E+Q365S+R320K,G182T
+Q169E+Q365S+R458K,G182T+Q169E+Q365S+S323T,G182T+Q169E+Q365S+V206L,G182
T+Q169E+Q365S+Y295F,G182T+Q169E+R320K+R458K,G182T+Q169E+R320K+S323T,G18
2T+Q169E+R320K+V206L,G182T+Q169E+R320K+Y295F,G182T+Q169E+R458K+S323T,G1
82T+Q169E+R458K+V206L,G182T+Q169E+R458K+Y295F,G182T+Q169E+S323T+V206L,G1
82T+Q169E+S323T+Y295F,G182T+Q169E+V206L+Y295F,G182T+Q172K+Q299Y+Q345R,G
182T+Q172K+Q299Y+Q365S,G182T+Q172K+Q299Y+R320K,G182T+Q172K+Q299Y+R458K,
G182T+Q172K+Q299Y+S323T,G182T+Q172K+Q299Y+V206L,G182T+Q172K+Q299Y+Y295F
,G182T+Q172K+Q345R+Q365S,G182T+Q172K+Q345R+R320K,G182T+Q172K+Q345R+R45
8K,G182T+Q172K+Q345R+S323T,G182T+Q172K+Q345R+V206L,G182T+Q172K+Q345R+Y2
95F,G182T+Q172K+Q365S+R320K,G182T+Q172K+Q365S+R458K,G182T+Q172K+Q365S+S
323T,G182T+Q172K+Q365S+V206L,G182T+Q172K+Q365S+Y295F,G182T+Q172K+R320K+
R458K,G182T+Q172K+R320K+S323T,G182T+Q172K+R320K+V206L,G182T+Q172K+R320K
+Y295F,G182T+Q172K+R458K+S323T,G182T+Q172K+R458K+V206L,G182T+Q172K+R458
K+Y295F,G182T+Q172K+S323T+V206L,G182T+Q172K+S323T+Y295F,G182T+Q172K+V206
L+Y295F,G182T+Q299Y+Q345R+Q365S,G182T+Q299Y+Q345R+R320K,G182T+Q299Y+Q34
5R+R458K,G182T+Q299Y+Q345R+S323T,G182T+Q299Y+Q345R+V206L,G182T+Q299Y+Q3
45R+Y295F,G182T+Q299Y+Q365S+R320K,G182T+Q299Y+Q365S+R458K,G182T+Q299Y+Q
365S+S323T,G182T+Q299Y+Q365S+V206L,G182T+Q299Y+Q365S+Y295F,G182T+Q299Y+
R320K+R458K,G182T+Q299Y+R320K+S323T,G182T+Q299Y+R320K+V206L,G182T+Q299Y
+R320K+Y295F,G182T+Q299Y+R458K+S323T,G182T+Q299Y+R458K+V206L,G182T+Q299
Y+R458K+Y295F,G182T+Q299Y+S323T+V206L,G182T+Q299Y+S323T+Y295F,G182T+Q299
Y+V206L+Y295F,G182T+Q345R+Q365S+R320K,G182T+Q345R+Q365S+R458K,G182T+Q34
5R+Q365S+S323T,G182T+Q345R+Q365S+V206L,G182T+Q345R+Q365S+Y295F,G182T+Q3
45R+R320K+R458K,G182T+Q345R+R320K+S323T,G182T+Q345R+R320K+V206L,G182T+Q
345R+R320K+Y295F,G182T+Q345R+R458K+S323T,G182T+Q345R+R458K+V206L,G182T+
Q345R+R458K+Y295F,G182T+Q345R+S323T+V206L,G182T+Q345R+S323T+Y295F,G182T+

24 Mar 2026
2026202266

Q345R+V206L+Y295F,G182T+Q365S+R320K+R458K,G182T+Q365S+R320K+S323T,G182T+Q365S+R320K+V206L,G182T+Q365S+R320K+Y295F,G182T+Q365S+R458K+S323T,G182T+Q365S+R458K+V206L,G182T+Q365S+R458K+Y295F,G182T+Q365S+S323T+V206L,G182T+Q365S+S323T+Y295F,G182T+Q365S+V206L+Y295F,G182T+R320K+R458K+S323T,G182T+R320K+R458K+V206L,G182T+R320K+R458K+Y295F,G182T+R320K+S323T+V206L,G182T+R320K+S323T+Y295F,G182T+R320K+V206L+Y295F,G182T+R458K+S323T+V206L,G182T+R458K+S323T+Y295F,G182T+R458K+V206L+Y295F,G182T+S323T+V206L+Y295F,H1*+I9M+K391A+M202L,H1*+I9M+K391A+N16Y,H1*+I9M+K391A+N195F,H1*+I9M+K391A+N54S,H1*+I9M+K391A+Q169E,H1*+I9M+K391A+Q169E,H1*+I9M+K391A+Q172K,H1*+I9M+K391A+Q299Y,H1*+I9M+K391A+Q345R,H1*+I9M+K391A+Q365S,H1*+I9M+K391A+R320K,H1*+I9M+K391A+R458K,H1*+I9M+K391A+S323T,H1*+I9M+K391A+V206L,H1*+I9M+K391A+Y295F,H1*+I9M+M202L+N16Y,H1*+I9M+M202L+N195F,H1*+I9M+M202L+N54S,H1*+I9M+M202L+Q169E,H1*+I9M+M202L+Q169E,H1*+I9M+M202L+Q172K,H1*+I9M+M202L+Q299Y,H1*+I9M+M202L+Q345R,H1*+I9M+M202L+Q365S,H1*+I9M+M202L+R320K,H1*+I9M+M202L+R458K,H1*+I9M+M202L+S323T,H1*+I9M+M202L+V206L,H1*+I9M+M202L+Y295F,H1*+I9M+N16Y+N195F,H1*+I9M+N16Y+N54S,H1*+I9M+N16Y+Q169E,H1*+I9M+N16Y+Q169E,H1*+I9M+N16Y+Q172K,H1*+I9M+N16Y+Q299Y,H1*+I9M+N16Y+Q345R,H1*+I9M+N16Y+Q365S,H1*+I9M+N16Y+R320K,H1*+I9M+N16Y+R458K,H1*+I9M+N16Y+S323T,H1*+I9M+N16Y+V206L,H1*+I9M+N16Y+Y295F,H1*+I9M+N195F+N54S,H1*+I9M+N195F+Q169E,H1*+I9M+N195F+Q169E,H1*+I9M+N195F+Q172K,H1*+I9M+N195F+Q299Y,H1*+I9M+N195F+Q345R,H1*+I9M+N195F+Q365S,H1*+I9M+N195F+R320K,H1*+I9M+N195F+R458K,H1*+I9M+N195F+S323T,H1*+I9M+N195F+V206L,H1*+I9M+N195F+Y295F,H1*+I9M+N54S+Q169E,H1*+I9M+N54S+Q169E,H1*+I9M+N54S+Q172K,H1*+I9M+N54S+Q299Y,H1*+I9M+N54S+Q345R,H1*+I9M+N54S+Q365S,H1*+I9M+N54S+R320K,H1*+I9M+N54S+R458K,H1*+I9M+N54S+S323T,H1*+I9M+N54S+V206L,H1*+I9M+N54S+Y295F,H1*+I9M+Q169E+Q169E,H1*+I9M+Q169E+Q172K,H1*+I9M+Q169E+Q299Y,H1*+I9M+Q169E+Q345R,H1*+I9M+Q169E+Q365S,H1*+I9M+Q169E+R320K,H1*+I9M+Q169E+R458K,H1*+I9M+Q169E+S323T,H1*+I9M+Q169E+V206L,H1*+I9M+Q169E+Y295F,H1*+I9M+Q169E+Q172K,H1*+I9M+Q169E+Q299Y,H1*+I9M+Q169E+Q345R,H1*+I9M+Q169E+Q365S,H1*+I9M+Q169E+R320K,H1*+I9M+Q169E+R458K,H1*+I9M+Q169E+S323T,H1*+I9M+Q169E+V206L,H1*+I9M+Q169E+Y295F,H1*+I9M+Q172K+Q299Y,H1*+I9M+Q172K+Q345R,H1*+I9M+Q172K+Q365S,H1*+I9M+Q172K+R320K,H1*+I9M+Q172K+R458K,H1*+I9M+Q172K+S323T,H1*+I9M+Q172K+V206L,H1*+I9M+Q172K+Y295F,H1*+I9M+Q299Y+Q345R,H1*+I9M+Q299Y+Q365S,H1*+I9M+Q299Y+R320K,H1*+I9M+Q299Y+R458K,H1*+I9M+Q299Y+S323T,H1*+I9M+Q299Y+V206L,H1*+I9M+Q299Y+Y295F,H1*+I9M+Q345R+Q365S,H1*+I9M+Q345R+R320K,H1*+I9M+Q345R+R458K,H1*+I9M+Q345R+S323T,H1*+I9M+Q345R+V206L,H1*+I9M+Q345R+Y295F,H1*+I9M+Q365S+R320K,H1*+I9M+Q365S+R458K,H1*+I9M+Q365S+S323T,H1*+I

24 Mar 2026
2026202266

9M+Q365S+V206L,H1*+I9M+Q365S+Y295F,H1*+I9M+R320K+R458K,H1*+I9M+R320K+S323T,H1*+I9M+R320K+V206L,H1*+I9M+R320K+Y295F,H1*+I9M+R458K+S323T,H1*+I9M+R458K+V206L,H1*+I9M+R458K+Y295F,H1*+I9M+S323T+V206L,H1*+I9M+S323T+Y295F,H1*+I9M+V206L+Y295F,H1*+K391A+M202L+N16Y,H1*+K391A+M202L+N195F,H1*+K391A+M202L+N54S,H1*+K391A+M202L+Q169E,H1*+K391A+M202L+Q169E,H1*+K391A+M202L+Q172K,H1*+K391A+M202L+Q299Y,H1*+K391A+M202L+Q345R,H1*+K391A+M202L+Q365S,H1*+K391A+M202L+R320K,H1*+K391A+M202L+R458K,H1*+K391A+M202L+S323T,H1*+K391A+M202L+V206L,H1*+K391A+M202L+Y295F,H1*+K391A+N16Y+N195F,H1*+K391A+N16Y+N54S,H1*+K391A+N16Y+Q169E,H1*+K391A+N16Y+Q169E,H1*+K391A+N16Y+Q172K,H1*+K391A+N16Y+Q299Y,H1*+K391A+N16Y+Q345R,H1*+K391A+N16Y+Q365S,H1*+K391A+N16Y+R320K,H1*+K391A+N16Y+R458K,H1*+K391A+N16Y+S323T,H1*+K391A+N16Y+V206L,H1*+K391A+N16Y+Y295F,H1*+K391A+N195F+N54S,H1*+K391A+N195F+Q169E,H1*+K391A+N195F+Q169E,H1*+K391A+N195F+Q172K,H1*+K391A+N195F+Q299Y,H1*+K391A+N195F+Q345R,H1*+K391A+N195F+Q365S,H1*+K391A+N195F+R320K,H1*+K391A+N195F+R458K,H1*+K391A+N195F+S323T,H1*+K391A+N195F+V206L,H1*+K391A+N195F+Y295F,H1*+K391A+N54S+Q169E,H1*+K391A+N54S+Q169E,H1*+K391A+N54S+Q172K,H1*+K391A+N54S+Q299Y,H1*+K391A+N54S+Q345R,H1*+K391A+N54S+Q365S,H1*+K391A+N54S+R320K,H1*+K391A+N54S+R458K,H1*+K391A+N54S+S323T,H1*+K391A+N54S+V206L,H1*+K391A+N54S+Y295F,H1*+K391A+Q169E+Q169E,H1*+K391A+Q169E+Q172K,H1*+K391A+Q169E+Q299Y,H1*+K391A+Q169E+Q345R,H1*+K391A+Q169E+Q365S,H1*+K391A+Q169E+R320K,H1*+K391A+Q169E+R458K,H1*+K391A+Q169E+S323T,H1*+K391A+Q169E+V206L,H1*+K391A+Q169E+Y295F,H1*+K391A+Q172K+Q299Y,H1*+K391A+Q172K+Q345R,H1*+K391A+Q172K+Q365S,H1*+K391A+Q172K+R320K,H1*+K391A+Q172K+R458K,H1*+K391A+Q172K+S323T,H1*+K391A+Q172K+V206L,H1*+K391A+Q172K+Y295F,H1*+K391A+Q299Y+Q345R,H1*+K391A+Q299Y+Q365S,H1*+K391A+Q299Y+R320K,H1*+K391A+Q299Y+R458K,H1*+K391A+Q299Y+S323T,H1*+K391A+Q299Y+V206L,H1*+K391A+Q299Y+Y295F,H1*+K391A+Q345R+Q365S,H1*+K391A+Q345R+R320K,H1*+K391A+Q345R+R458K,H1*+K391A+Q345R+S323T,H1*+K391A+Q345R+V206L,H1*+K391A+Q345R+Y295F,H1*+K391A+Q365S+R320K,H1*+K391A+Q365S+R458K,H1*+K391A+Q365S+S323T,H1*+K391A+Q365S+V206L,H1*+K391A+Q365S+Y295F,H1*+K391A+R320K+R458K,H1*+K391A+R320K+S323T,H1*+K391A+R320K+V206L,H1*+K391A+R320K+Y295F,H1*+K391A+R458K+S323T,H1*+K391A+R458K+V206L,H1*+K391A+R458K+Y295F,H1*+K391A+S323T+V206L,H1*+K391A+S323T+Y295F,H1*+K391A+V206L+Y295F,H1*+M202L+N16Y+N195F,H1*+M202L+N16Y+N54S,H1*+M202L+N16Y+Q169E,H1*+M202L+N16Y+Q169E,H1*+M202L+N16Y+

24 Mar 2026
2026202266

Q172K,H1*+M202L+N16Y+Q299Y,H1*+M202L+N16Y+Q345R,H1*+M202L+N16Y+Q365S,H1*+M202L+N16Y+R320K,H1*+M202L+N16Y+R458K,H1*+M202L+N16Y+S323T,H1*+M202L+N16Y+V206L,H1*+M202L+N16Y+Y295F,H1*+M202L+N195F+N54S,H1*+M202L+N195F+Q169E,H1*+M202L+N195F+Q169E,H1*+M202L+N195F+Q172K,H1*+M202L+N195F+Q299Y,H1*+M202L+N195F+Q345R,H1*+M202L+N195F+Q365S,H1*+M202L+N195F+R320K,H1*+M202L+N195F+R458K,H1*+M202L+N195F+S323T,H1*+M202L+N195F+V206L,H1*+M202L+N195F+Y295F,H1*+M202L+N54S+Q169E,H1*+M202L+N54S+Q169E,H1*+M202L+N54S+Q172K,H1*+M202L+N54S+Q299Y,H1*+M202L+N54S+Q345R,H1*+M202L+N54S+Q365S,H1*+M202L+N54S+R320K,H1*+M202L+N54S+R458K,H1*+M202L+N54S+S323T,H1*+M202L+N54S+V206L,H1*+M202L+N54S+Y295F,H1*+M202L+Q169E+Q169E,H1*+M202L+Q169E+Q172K,H1*+M202L+Q169E+Q299Y,H1*+M202L+Q169E+Q345R,H1*+M202L+Q169E+Q365S,H1*+M202L+Q169E+R320K,H1*+M202L+Q169E+R458K,H1*+M202L+Q169E+S323T,H1*+M202L+Q169E+V206L,H1*+M202L+Q169E+Y295F,H1*+M202L+Q172K+Q299Y,H1*+M202L+Q172K+Q345R,H1*+M202L+Q172K+Q365S,H1*+M202L+Q172K+R320K,H1*+M202L+Q172K+R458K,H1*+M202L+Q172K+S323T,H1*+M202L+Q172K+V206L,H1*+M202L+Q172K+Y295F,H1*+M202L+Q299Y+Q345R,H1*+M202L+Q299Y+Q365S,H1*+M202L+Q299Y+R320K,H1*+M202L+Q299Y+R458K,H1*+M202L+Q299Y+S323T,H1*+M202L+Q299Y+V206L,H1*+M202L+Q299Y+Y295F,H1*+M202L+Q345R+Q365S,H1*+M202L+Q345R+R320K,H1*+M202L+Q345R+R458K,H1*+M202L+Q345R+S323T,H1*+M202L+Q345R+V206L,H1*+M202L+Q345R+Y295F,H1*+M202L+Q365S+R320K,H1*+M202L+Q365S+R458K,H1*+M202L+Q365S+S323T,H1*+M202L+Q365S+V206L,H1*+M202L+Q365S+Y295F,H1*+M202L+R320K+R458K,H1*+M202L+R320K+S323T,H1*+M202L+R320K+V206L,H1*+M202L+R320K+Y295F,H1*+M202L+R458K+S323T,H1*+M202L+R458K+V206L,H1*+M202L+R458K+Y295F,H1*+M202L+S323T+V206L,H1*+M202L+S323T+Y295F,H1*+M202L+V206L+Y295F,H1*+N16Y+N195F+N54S,H1*+N16Y+N195F+Q169E,H1*+N16Y+N195F+Q169E,H1*+N16Y+N195F+Q172K,H1*+N16Y+N195F+Q299Y,H1*+N16Y+N195F+Q345R,H1*+N16Y+N195F+Q365S,H1*+N16Y+N195F+R320K,H1*+N16Y+N195F+R458K,H1*+N16Y+N195F+S323T,H1*+N16Y+N195F+V206L,H1*+N16Y+N195F+Y295F,H1*+N16Y+N54S+Q169E,H1*+N16Y+N54S+Q169E,H1*+N16Y+N54S+Q172K,H1*+N16Y+N54S+Q299Y,H1*+N16Y+N54S+Q345R,H1*+N16Y+N54S+Q365S,H1*+N16Y+N54S+R320K,H1*+N16Y+N54S+R458K,H1*+N16Y+N54S+S323T,H1*+N16Y+N54S+V206L,H1*+N16Y+N54S+Y295F,H1*+N16Y+Q169E+Q169E,H1*+N16Y+Q169E+Q172K,H1*+N16Y+Q169E+Q299Y,H1*+N16Y+Q169E+Q345R,H1*+N16Y+Q169E+Q365S,H1*+N16Y+Q169E+R320K,H1*+N16Y+Q169E+R458K,H1*+N16Y+Q169E+S323T,H1*+N16Y+Q169E+V206L,H1*+N16Y+Q169E+Y295F,H1*+N16Y+Q169E+Q172K,H1*+N16Y+Q169E+Q299

24 Mar 2026
2026202266

Y,H1*+N16Y+Q169E+Q345R,H1*+N16Y+Q169E+Q365S,H1*+N16Y+Q169E+R320K,H1*+N16Y+Q169E+R458K,H1*+N16Y+Q169E+S323T,H1*+N16Y+Q169E+V206L,H1*+N16Y+Q169E+Y295F,H1*+N16Y+Q172K+Q299Y,H1*+N16Y+Q172K+Q345R,H1*+N16Y+Q172K+Q365S,H1*+N16Y+Q172K+R320K,H1*+N16Y+Q172K+R458K,H1*+N16Y+Q172K+S323T,H1*+N16Y+Q172K+V206L,H1*+N16Y+Q172K+Y295F,H1*+N16Y+Q299Y+Q345R,H1*+N16Y+Q299Y+Q365S,H1*+N16Y+Q299Y+R320K,H1*+N16Y+Q299Y+R458K,H1*+N16Y+Q299Y+S323T,H1*+N16Y+Q299Y+V206L,H1*+N16Y+Q299Y+Y295F,H1*+N16Y+Q345R+Q365S,H1*+N16Y+Q345R+R320K,H1*+N16Y+Q345R+R458K,H1*+N16Y+Q345R+S323T,H1*+N16Y+Q345R+V206L,H1*+N16Y+Q345R+Y295F,H1*+N16Y+Q365S+R320K,H1*+N16Y+Q365S+R458K,H1*+N16Y+Q365S+S323T,H1*+N16Y+Q365S+V206L,H1*+N16Y+Q365S+Y295F,H1*+N16Y+R320K+R458K,H1*+N16Y+R320K+S323T,H1*+N16Y+R320K+V206L,H1*+N16Y+R320K+Y295F,H1*+N16Y+R458K+S323T,H1*+N16Y+R458K+V206L,H1*+N16Y+R458K+Y295F,H1*+N16Y+S323T+V206L,H1*+N16Y+S323T+Y295F,H1*+N16Y+V206L+Y295F,H1*+N195F+N54S+Q169E,H1*+N195F+N54S+Q169E,H1*+N195F+N54S+Q172K,H1*+N195F+N54S+Q299Y,H1*+N195F+N54S+Q345R,H1*+N195F+N54S+Q365S,H1*+N195F+N54S+R320K,H1*+N195F+N54S+R458K,H1*+N195F+N54S+S323T,H1*+N195F+N54S+V206L,H1*+N195F+N54S+Y295F,H1*+N195F+Q169E+Q169E,H1*+N195F+Q169E+Q172K,H1*+N195F+Q169E+Q299Y,H1*+N195F+Q169E+Q345R,H1*+N195F+Q169E+Q365S,H1*+N195F+Q169E+R320K,H1*+N195F+Q169E+R458K,H1*+N195F+Q169E+S323T,H1*+N195F+Q169E+V206L,H1*+N195F+Q169E+Y295F,H1*+N195F+Q169E+Q172K,H1*+N195F+Q169E+Q299Y,H1*+N195F+Q169E+Q345R,H1*+N195F+Q169E+Q365S,H1*+N195F+Q169E+R320K,H1*+N195F+Q169E+R458K,H1*+N195F+Q169E+S323T,H1*+N195F+Q169E+V206L,H1*+N195F+Q169E+Y295F,H1*+N195F+Q172K+Q299Y,H1*+N195F+Q172K+Q345R,H1*+N195F+Q172K+Q365S,H1*+N195F+Q172K+R320K,H1*+N195F+Q172K+R458K,H1*+N195F+Q172K+S323T,H1*+N195F+Q172K+V206L,H1*+N195F+Q172K+Y295F,H1*+N195F+Q299Y+Q345R,H1*+N195F+Q299Y+Q365S,H1*+N195F+Q299Y+R320K,H1*+N195F+Q299Y+R458K,H1*+N195F+Q299Y+S323T,H1*+N195F+Q299Y+V206L,H1*+N195F+Q299Y+Y295F,H1*+N195F+Q345R+Q365S,H1*+N195F+Q345R+R320K,H1*+N195F+Q345R+R458K,H1*+N195F+Q345R+S323T,H1*+N195F+Q345R+V206L,H1*+N195F+Q345R+Y295F,H1*+N195F+Q365S+R320K,H1*+N195F+Q365S+R458K,H1*+N195F+Q365S+S323T,H1*+N195F+Q365S+V206L,H1*+N195F+Q365S+Y295F,H1*+N195F+R320K+R458K,H1*+N195F+R320K+S323T,H1*+N195F+R320K+V206L,H1*+N195F+R320K+Y295F, H1*+N195F+R458K+S323T, H1*+N195F+R458K+V206L, H1*+N195F+R458K+Y295F, H1*+N195F+S323T+V206L,H1*+N195F+S323T+Y295F,H1*+N195F+V206L+Y295F,H1*+N54S+Q169E+Q169E,H1*+N54S+Q169E+Q172K,H1*+N54S+Q169E+Q299Y,H1*+N54S+Q169E+Q345R,H1*+N54S+Q169E+Q365S, H1*+N54S+Q169E+R320K, H1*+N54S+Q169E+R458K, H1*+N54S+Q169E+S323T,

24 Mar 2026
2026202266

H1*+N54S+Q169E+V206L,H1*+N54S+Q169E+Y295F,H1*+N54S+Q169E+Q172K,H1*+N54S+Q169E+Q299Y,H1*+N54S+Q169E+Q345R,H1*+N54S+Q169E+Q365S,H1*+N54S+Q169E+R320K,H1*+N54S+Q169E+R458K, H1*+N54S+Q169E+S323T, H1*+N54S+Q169E+V206L, H1*+N54S+Q169E+Y295F,

H1*+N54S+Q172K+Q299Y,H1*+N54S+Q172K+Q345R,H1*+N54S+Q172K+Q365S,H1*+N54S+Q172K+R320K,H1*+N54S+Q172K+R458K,H1*+N54S+Q172K+S323T,H1*+N54S+Q172K+V206L,H1*+N54S+Q172K+Y295F,H1*+N54S+Q299Y+Q345R,H1*+N54S+Q299Y+Q365S,H1*+N54S+Q299Y+R320K,H1*+N54S+Q299Y+R458K,H1*+N54S+Q299Y+S323T,H1*+N54S+Q299Y+V206L,H1*+N54S+Q299Y+Y295F,H1*+N54S+Q345R+Q365S,H1*+N54S+Q345R+R320K,H1*+N54S+Q345R+R458K,H1*+N54S+Q345R+S323T,H1*+N54S+Q345R+V206L,H1*+N54S+Q345R+Y295F,H1*+N54S+Q365S+R320K,H1*+N54S+Q365S+R458K,H1*+N54S+Q365S+S323T,H1*+N54S+Q365S+V206L,H1*+N54S+Q365S+Y295F,H1*+N54S+R320K+R458K,H1*+N54S+R320K+S323T,H1*+N54S+R320K+V206L,H1*+N54S+R320K+Y295F,H1*+N54S+R458K+S323T,H1*+N54S+R458K+V206L,H1*+N54S+R458K+Y295F,H1*+N54S+S323T+V206L,H1*+N54S+S323T+Y295F,H1*+N54S+V206L+Y295F,H1*+Q169E+Q169E+Q172K,H1*+Q169E+Q169E+Q299Y,H1*+Q169E+Q169E+Q345R,H1*+Q169E+Q169E+Q365S,H1*+Q169E+Q169E+R320K,

H1*+Q169E+Q169E+R458K,H1*+Q169E+Q169E+S323T,H1*+Q169E+Q169E+V206L,H1*+Q169E+Q169E+Y295F, H1*+Q169E+Q172K+Q299Y, H1*+Q169E+Q172K+Q345R,

H1*+Q169E+Q172K+Q365S,

H1*+Q169E+Q172K+R320K,H1*+Q169E+Q172K+R458K,H1*+Q169E+Q172K+S323T,H1*+Q169E+Q172K+V206L,H1*+Q169E+Q172K+Y295F,H1*+Q169E+Q299Y+Q345R,H1*+Q169E+Q299Y+Q365S,H1*+Q169E+Q299Y+R320K,H1*+Q169E+Q299Y+R458K,H1*+Q169E+Q299Y+S323T,H1*+Q169E+Q299Y+V206L,H1*+Q169E+Q299Y+Y295F,H1*+Q169E+Q345R+Q365S,H1*+Q169E+Q345R+R320K,H1*+Q169E+Q345R+R458K,H1*+Q169E+Q345R+S323T,H1*+Q169E+Q345R+V206L,H1*+Q169E+Q345R+Y295F,H1*+Q169E+Q365S+R320K,H1*+Q169E+Q365S+R458K,H1*+Q169E+Q365S+S323T,H1*+Q169E+Q365S+V206L,H1*+Q169E+Q365S+Y295F,H1*+Q169E+R320K+R458K,H1*+Q169E+R320K+S323T,H1*+Q169E+R320K+V206L,H1*+Q169E+R320K+Y295F,H1*+Q169E+R458K+S323T,H1*+Q169E+R458K+V206L,H1*+Q169E+R458K+Y295F,H1*+Q169E+S323T+V206L,H1*+Q169E+S323T+Y295F,H1*+Q169E+V206L+Y295F,H1*+Q169E+Q172K+Q299Y,H1*+Q169E+Q172K+Q345R,H1*+Q169E+Q172K+Q365S,H1*+Q169E+Q172K+R320K,H1*+Q169E+Q172K+R458K,H1*+Q169E+Q172K+S323T,H1*+Q169E+Q172K+V206L,H1*+Q169E+Q172K+Y295F,H1*+Q169E+Q299Y+Q345R,H1*+Q169E+Q299Y+Q365S,H1*+Q169E+Q299Y+R320K,H1*+Q169E+Q299Y+R458K,H1*+Q169E+Q299Y+S323T,H1*+Q169E+Q299Y+V206L,H1*+Q169E+Q299Y+Y295F,H1*+Q169E+Q345R+Q365S,H1*+Q169E+Q345R+R320K,H1*+Q169E+Q345R+R458K,H1*+Q169E+Q345R+S323T,H1*+Q169

24 Mar 2026
2026202266

E+Q345R+V206L,H1*+Q169E+Q345R+Y295F,H1*+Q169E+Q365S+R320K,H1*+Q169E+Q365S+R458K,H1*+Q169E+Q365S+S323T,H1*+Q169E+Q365S+V206L,H1*+Q169E+Q365S+Y295F,H1*+Q169E+R320K+R458K,H1*+Q169E+R320K+S323T,H1*+Q169E+R320K+V206L,H1*+Q169E+R320K+Y295F,H1*+Q169E+R458K+S323T,H1*+Q169E+R458K+V206L,H1*+Q169E+R458K+Y295F,H1*+Q169E+S323T+V206L,H1*+Q169E+S323T+Y295F,H1*+Q169E+V206L+Y295F,H1*+Q172K+Q299Y+Q345R,H1*+Q172K+Q299Y+Q365S,H1*+Q172K+Q299Y+R320K,H1*+Q172K+Q299Y+R458K,H1*+Q172K+Q299Y+S323T,H1*+Q172K+Q299Y+V206L,H1*+Q172K+Q299Y+Y295F,H1*+Q172K+Q345R+Q365S,H1*+Q172K+Q345R+R320K,H1*+Q172K+Q345R+R458K,H1*+Q172K+Q345R+S323T,H1*+Q172K+Q345R+V206L,H1*+Q172K+Q345R+Y295F,H1*+Q172K+Q365S+R320K,H1*+Q172K+Q365S+R458K,H1*+Q172K+Q365S+S323T,H1*+Q172K+Q365S+V206L,H1*+Q172K+Q365S+Y295F,H1*+Q172K+R320K+R458K,H1*+Q172K+R320K+S323T,H1*+Q172K+R320K+V206L,H1*+Q172K+R320K+Y295F,H1*+Q172K+R458K+S323T,H1*+Q172K+R458K+V206L,H1*+Q172K+R458K+Y295F,H1*+Q172K+S323T+V206L,H1*+Q172K+S323T+Y295F,H1*+Q172K+V206L+Y295F,H1*+Q299Y+Q345R+Q365S,H1*+Q299Y+Q345R+R320K,H1*+Q299Y+Q345R+R458K,H1*+Q299Y+Q345R+S323T,H1*+Q299Y+Q345R+V206L,H1*+Q299Y+Q345R+Y295F,H1*+Q299Y+Q365S+R320K,H1*+Q299Y+Q365S+R458K,H1*+Q299Y+Q365S+S323T,H1*+Q299Y+Q365S+V206L,H1*+Q299Y+Q365S+Y295F,H1*+Q299Y+R320K+R458K,H1*+Q299Y+R320K+S323T,H1*+Q299Y+R320K+V206L,H1*+Q299Y+R320K+Y295F,H1*+Q299Y+R458K+S323T,H1*+Q299Y+R458K+V206L,H1*+Q299Y+R458K+Y295F,H1*+Q299Y+S323T+V206L,H1*+Q299Y+S323T+Y295F,H1*+Q299Y+V206L+Y295F,H1*+Q345R+Q365S+R320K,H1*+Q345R+Q365S+R458K,H1*+Q345R+Q365S+S323T,H1*+Q345R+Q365S+V206L,H1*+Q345R+Q365S+Y295F,H1*+Q345R+R320K+R458K,H1*+Q345R+R320K+S323T,H1*+Q345R+R320K+V206L,H1*+Q345R+R320K+Y295F,H1*+Q345R+R458K+S323T,H1*+Q345R+R458K+V206L,H1*+Q345R+R458K+Y295F,H1*+Q345R+S323T+V206L,H1*+Q345R+S323T+Y295F,H1*+Q345R+V206L+Y295F,H1*+Q365S+R320K+R458K,H1*+Q365S+R320K+S323T,H1*+Q365S+R320K+V206L,H1*+Q365S+R320K+Y295F,H1*+Q365S+R458K+S323T,H1*+Q365S+R458K+V206L,H1*+Q365S+R458K+Y295F,H1*+Q365S+S323T+V206L,H1*+Q365S+S323T+Y295F,H1*+Q365S+V206L+Y295F,H1*+R320K+R458K+S323T,H1*+R320K+R458K+V206L,H1*+R320K+R458K+Y295F,H1*+R320K+S323T+V206L,H1*+R320K+S323T+Y295F,H1*+R320K+V206L+Y295F,H1*+R458K+S323T+V206L,H1*+R458K+S323T+Y295F,H1*+R458K+V206L+Y295F,H1*+S323T+V206L+Y295F,I9M+K391A+M202L+N16Y,I9M+K391A+M202L+N195F,I9M+K391A+M202L+N54S,I9M+K391A+M202L+Q169E,I9M+K391A+M202L+Q169E,I9M+K391A+M202L+Q172K,I9M+K391A+M202L+Q299Y,I9M+K391A+M202L+Q345R,I9M+K391A+M202L+Q365S,I9M+K391A+M202L+R320K,I9M+K391A+M202L+R458K,I9M+K391A+M202L+S323T,I9M+K391A+M202L+V206L,I9M+K391A+M202L+Y295F,I9M+K391A+N16Y+N195F,I9M+K391A+N16Y+N54S,I9M+K391A+N16Y+Q169E,I9M+K391A+N16Y+Q

24 Mar 2026
2026202266

169E,I9M+K391A+N16Y+Q172K,I9M+K391A+N16Y+Q299Y, I9M+K391A+N16Y+Q345R, I9M+K391A+N16Y+Q365S, I9M+K391A+N16Y+R320K, I9M+K391A+N16Y+R458K, I9M+K391A+N16Y+S323T, I9M+K391A+N16Y+V206L, I9M+K391A+N16Y+Y295F,I9M+K391A+N195F+N54S,I9M+K391A+N195F+Q169E,I9M+K391A+N195F+Q169E,I9M+K391A+N195F+Q172K,I9M+K391A+N195F+Q299Y,I9M+K391A+N195F+Q345R,I9M+K391A+N195F+Q365S,I9M+K391A+N195F+R320K,I9M+K391A+N195F+R458K,I9M+K391A+N195F+S323T,I9M+K391A+N195F+V206L,I9M+K391A+N195F+Y295F,I9M+K391A+N54S+Q169E,I9M+K391A+N54S+Q169E,I9M+K391A+N54S+Q172K,I9M+K391A+N54S+Q299Y,I9M+K391A+N54S+Q345R,I9M+K391A+N54S+Q365S,I9M+K391A+N54S+R320K,I9M+K391A+N54S+R458K,I9M+K391A+N54S+S323T,I9M+K391A+N54S+V206L,I9M+K391A+N54S+Y295F,I9M+K391A+Q169E+Q169E,I9M+K391A+Q169E+Q172K,I9M+K391A+Q169E+Q299Y,I9M+K391A+Q169E+Q345R,I9M+K391A+Q169E+Q365S,I9M+K391A+Q169E+R320K,I9M+K391A+Q169E+R458K,I9M+K391A+Q169E+S323T,I9M+K391A+Q169E+V206L,I9M+K391A+Q169E+Y295F,I9M+K391A+Q169E+Q172K,I9M+K391A+Q169E+Q299Y,I9M+K391A+Q169E+Q345R,I9M+K391A+Q169E+Q365S,I9M+K391A+Q169E+R320K,I9M+K391A+Q169E+R458K,I9M+K391A+Q169E+S323T,I9M+K391A+Q169E+V206L,I9M+K391A+Q169E+Y295F,I9M+K391A+Q172K+Q299Y,I9M+K391A+Q172K+Q345R,I9M+K391A+Q172K+Q365S,I9M+K391A+Q172K+R320K,I9M+K391A+Q172K+R458K,I9M+K391A+Q172K+S323T,I9M+K391A+Q172K+V206L,I9M+K391A+Q172K+Y295F,I9M+K391A+Q299Y+Q345R,I9M+K391A+Q299Y+Q365S,I9M+K391A+Q299Y+R320K,I9M+K391A+Q299Y+R458K,I9M+K391A+Q299Y+S323T,I9M+K391A+Q299Y+V206L,I9M+K391A+Q299Y+Y295F,I9M+K391A+Q345R+Q365S,I9M+K391A+Q345R+R320K,I9M+K391A+Q345R+R458K,I9M+K391A+Q345R+S323T,I9M+K391A+Q345R+V206L,I9M+K391A+Q345R+Y295F,I9M+K391A+Q365S+R320K,I9M+K391A+Q365S+R458K,I9M+K391A+Q365S+S323T,I9M+K391A+Q365S+V206L,I9M+K391A+Q365S+Y295F,I9M+K391A+R320K+R458K,I9M+K391A+R320K+S323T,I9M+K391A+R320K+V206L,I9M+K391A+R320K+Y295F,I9M+K391A+R458K+S323T,I9M+K391A+R458K+V206L,I9M+K391A+R458K+Y295F,I9M+K391A+S323T+V206L,I9M+K391A+S323T+Y295F,I9M+K391A+V206L+Y295F,I9M+M202L+N16Y+N195F,I9M+M202L+N16Y+N54S,I9M+M202L+N16Y+Q169E,I9M+M202L+N16Y+Q169E,I9M+M202L+N16Y+Q172K,I9M+M202L+N16Y+Q299Y,I9M+M202L+N16Y+Q345R,I9M+M202L+N16Y+Q365S,I9M+M202L+N16Y+R320K,I9M+M202L+N16Y+R458K,I9M+M202L+N16Y+S323T,I9M+M202L+N16Y+V206L,I9M+M202L+N16Y+Y295F,I9M+M202L+N195F+N54S,I9M+M202L+N195F+Q169E,I9M+M202L+N195F+Q169E,I9M+M202L+N195F+Q172K,I9M+M202L+N195F+Q299Y,I9M+M202L+N195F+Q345R,I9M+M202L+N195F+Q365S,I9M+M202L+N195F+R320K,I9M+M202L+N195F+R458K,I9M+M202L+N195F+S323T,I9M+M202L+N195F+V206L,I9M+M202L+N195F+Y295F,I9M+M202L+N54S+Q169E,I9M+M202L+N54S+Q169E,I9M+M202L+N54S+Q172K,I9M+M202L+N54S+Q299Y,I9M+M202L+N54S+Q345R,

24 Mar 2026
2026202266

I9M+M202L+N54S+Q365S,I9M+M202L+N54S+R320K,I9M+M202L+N54S+R458K,I9M+M202L+N54S+S323T,I9M+M202L+N54S+V206L,I9M+M202L+N54S+Y295F,I9M+M202L+Q169E+Q169E,I9M+M202L+Q169E+Q172K,I9M+M202L+Q169E+Q299Y,I9M+M202L+Q169E+Q345R,I9M+M202L+Q169E+Q365S,I9M+M202L+Q169E+R320K,I9M+M202L+Q169E+R458K,I9M+M202L+Q169E+S323T,I9M+M202L+Q169E+V206L, I9M+M202L+Q169E+Y295F, I9M+M202L+Q169E+Q172K, I9M+M202L+Q169E+Q299Y, I9M+M202L+Q169E+Q345R,I9M+M202L+Q169E+Q365S,I9M+M202L+Q169E+R320K,I9M+M202L+Q169E+R458K,I9M+M202L+Q169E+S323T,I9M+M202L+Q169E+V206L,I9M+M202L+Q169E+Y295F,I9M+M202L+Q172K+Q299Y,I9M+M202L+Q172K+Q345R,I9M+M202L+Q172K+Q365S,I9M+M202L+Q172K+R320K,I9M+M202L+Q172K+R458K,I9M+M202L+Q172K+S323T,I9M+M202L+Q172K+V206L,I9M+M202L+Q172K+Y295F,I9M+M202L+Q299Y+Q345R,I9M+M202L+Q299Y+Q365S,I9M+M202L+Q299Y+R320K,I9M+M202L+Q299Y+R458K,I9M+M202L+Q299Y+S323T,I9M+M202L+Q299Y+V206L,I9M+M202L+Q299Y+Y295F,I9M+M202L+Q345R+Q365S,I9M+M202L+Q345R+R320K,I9M+M202L+Q345R+R458K,I9M+M202L+Q345R+S323T,I9M+M202L+Q345R+V206L,I9M+M202L+Q345R+Y295F,I9M+M202L+Q365S+R320K,I9M+M202L+Q365S+R458K,I9M+M202L+Q365S+S323T,I9M+M202L+Q365S+V206L,I9M+M202L+Q365S+Y295F,I9M+M202L+R320K+R458K,I9M+M202L+R320K+S323T,I9M+M202L+R320K+V206LI9M+M202L+R320K+Y295F, I9M+M202L+R458K+S323T, I9M+M202L+R458K+V206L, I9M+M202L+R458K+Y295F,I9M+M202L+S323T+V206L,I9M+M202L+S323T+Y295F,I9M+M202L+V206L+Y295F,I9M+N16Y+N195F+N54S,I9M+N16Y+N195F+Q169E,I9M+N16Y+N195F+Q169E,I9M+N16Y+N195F+Q172K, I9M+N16Y+N195F+Q299Y, I9M+N16Y+N195F+Q345R, I9M+N16Y+N195F+Q365S, I9M+N16Y+N195F+R320K, I9M+N16Y+N195F+R458K, I9M+N16Y+N195F+S323T, I9M+N16Y+N195F+V206L,I9M+N16Y+N195F+Y295F,I9M+N16Y+N54S+Q169E,I9M+N16Y+N54S+Q169E,I9M+N16Y+N54S+Q172K,I9M+N16Y+N54S+Q299Y,I9M+N16Y+N54S+Q345R,I9M+N16Y+N54S+Q365S,I9M+N16Y+N54S+R320K,I9M+N16Y+N54S+R458K,I9M+N16Y+N54S+S323T,I9M+N16Y+N54S+V206L,I9M+N16Y+N54S+Y295F,I9M+N16Y+Q169E+Q169E,I9M+N16Y+Q169E+Q172K,I9M+N16Y+Q169E+Q299Y,I9M+N16Y+Q169E+Q345R,I9M+N16Y+Q169E+Q365S,I9M+N16Y+Q169E+R320K,I9M+N16Y+Q169E+R458K,I9M+N16Y+Q169E+S323T,I9M+N16Y+Q169E+V206L,I9M+N16Y+Q169E+Y295F,I9M+N16Y+Q172K+Q299Y,I9M+N16Y+Q172K+Q345R,I9M+N16Y+Q172K+Q365S,I9M+N16Y+Q172K+R320K,I9M+N16Y+Q172K+R458K,I9M+N16Y+Q172K+S323T,I9M+N16Y+Q172K+V206L,I9M+N16Y+Q172K+Y295F,I9M+N16Y+Q299Y+Q345R,I9M+N16Y+Q299Y+Q365S,I9M+N16Y+Q299Y+R320K,I9M+N16Y+Q299Y+R458K,I9M+N16Y+Q299Y+S323T,I

24 Mar 2026
2026202266

9M+N16Y+Q299Y+V206L,I9M+N16Y+Q299Y+Y295F,I9M+N16Y+Q345R+Q365S,I9M+N16Y+Q345R+R320K,I9M+N16Y+Q345RR458K,I9M+N16Y+Q345R+S323T,I9M+N16Y+Q345R+V206L,I9M+N16Y+Q345R+Y295F,I9M+N16Y+Q365S+R320K,I9M+N16Y+Q365S+R458K,I9M+N16Y+Q365S+S323T,I9M+N16Y+Q365S+V206L,I9M+N16Y+Q365S+Y295F,I9M+N16Y+R320K+R458K,I9M+N16Y+R320K+S323T,I9M+N16Y+R320K+V206L,I9M+N16Y+R320K+Y295F,I9M+N16Y+R458K+S323T,I9M+N16Y+R458K+V206L,I9M+N16Y+R458K+Y295F,I9M+N16Y+S323T+V206L,I9M+N16Y+S323T+Y295F,I9M+N16Y+V206L+Y295F,I9M+N195F+N54S+Q169E,I9M+N195F+N54S+Q169E,I9M+N195F+N54S+Q172K,I9M+N195F+N54S+Q299Y,I9M+N195F+N54S+Q345R,I9M+N195F+N54S+Q365S,I9M+N195F+N54S+R320K,I9M+N195F+N54S+R458K,I9M+N195F+N54S+S323T,I9M+N195F+N54S+V206L,I9M+N195F+N54S+Y295F,I9M+N195F+Q169E+Q169E,I9M+N195F+Q169E+Q172K,I9M+N195F+Q169E+Q299Y,I9M+N195F+Q169E+Q345R,I9M+N195F+Q169E+Q365S,I9M+N195F+Q169E+R320K,I9M+N195F+Q169E+R458K,I9M+N195F+Q169E+S323T,I9M+N195F+Q169E+V206L,I9M+N195F+Q169E+Y295F,I9M+N195F+Q172K+Q299Y,I9M+N195F+Q172K+Q345R,I9M+N195F+Q172K+Q365S,I9M+N195F+Q172K+R320K,I9M+N195F+Q172K+R458K,I9M+N195F+Q172K+S323T,I9M+N195F+Q172K+V206L,I9M+N195F+Q172K+Y295F,I9M+N195F+Q299Y+Q345R,I9M+N195F+Q299Y+Q365S,I9M+N195F+Q299Y+R320K,I9M+N195F+Q299Y+R458K,I9M+N195F+Q299Y+S323T,I9M+N195F+Q299Y+V206L,I9M+N195F+Q299Y+Y295F,I9M+N195F+Q345R+Q365S,I9M+N195F+Q345R+R320K,I9M+N195F+Q345R+R458K,I9M+N195F+Q345R+S323T,I9M+N195F+Q345R+V206L,I9M+N195F+Q345R+Y295F,I9M+N195F+Q365S+R320K,I9M+N195F+Q365S+R458K,I9M+N195F+Q365S+S323T,I9M+N195F+Q365S+V206L,I9M+N195F+Q365S+Y295F,I9M+N195F+R320K+R458K,I9M+N195F+R320K+S323T,I9M+N195F+R320K+V206L,I9M+N195F+R320K+Y295F,I9M+N195F+R458K+S323T,I9M+N195F+R458K+V206L,I9M+N195F+R458K+Y295F,I9M+N195F+S323T+V206L,I9M+N195F+S323T+Y295F,I9M+N195F+V206L+Y295F,I9M+N54S+Q169E+Q169E,I9M+N54S+Q169E+Q172K,I9M+N54S+Q169E+Q299Y,I9M+N54S+Q169E+Q345R,I9M+N54S+Q169E+Q365S,I9M+N54S+Q169E+R320K,I9M+N54S+Q169E+R458K,I9M+N54S+Q169E+S323T,I9M+N54S+Q169E+V206L,I9M+N54S+Q169E+Y295F,I9M+N54S+Q172K,I9M+N54S+Q169E+Q299Y,I9M+N54S+Q169E+Q345R,I9M+N54S+Q169E+Q365S,I9M+N54S+Q169E+R320K,I9M+N54S+Q169E+R458K,I9M+N54S+Q169E+S323T,I9M+N54S+Q169E+V206L,I9M+N54S+Q169E+Y295F,I9M+N54S+Q172K+Q299Y,I9M+N54S+Q172K+Q345R,I9M+N54S+Q172K+Q365S,I9M+N54S+Q172K+R320K,I9M+N54S+Q172K+R458K,I9M+N54S+Q172K+S323T,I9M+N54S+Q172K+V206L,I9M+N54S+Q172K+Y295F,I9M+N54S+Q299Y+Q345R,I9M+N54S+Q299Y+Q365S,I9M+N54S+Q299Y+R320K,I9M+N54S+Q299Y+R458K,I9M+N54S+Q299Y+S323T,I9M+N

24 Mar 2026
2026202266

54S+Q299Y+V206L,I9M+N54S+Q299Y+Y295F,I9M+N54S+Q345R+Q365S,I9M+N54S+Q345R+R320K,I9M+N54S+Q345R+R458K,I9M+N54S+Q345R+S323T,I9M+N54S+Q345R+V206L,I9M+N54S+Q345R+Y295F,I9M+N54S+Q365S+R320K, I9M+N54S+Q365S+R458K, I9M+N54S+Q365S+S323T, I9M+N54S+Q365S+V206L, I9M+N54S+Q365S+Y295F,I9M+N54S+R320K+R458K,I9M+N54S+R320K+S323T,I9M+N54S+R320K+V206L, I9M+N54S+R320K+Y295F, I9M+N54S+R458K+S323T, I9M+N54S+R458K+V206L,I9M+N54S+R458K+Y295F,I9M+N54S+S323T+V206L,I9M+N54S+S323T+Y295F,I9M+N54S+V206L+Y295F,I9M+Q169E+Q169E+Q172K,I9M+Q169E+Q169E+Q299Y,I9M+Q169E+Q169E+Q345R,I9M+Q169E+Q169E+Q365S,I9M+Q169E+Q169E+R320K,I9M+Q169E+Q169E+R458K,I9M+Q169E+Q169E+S323T,I9M+Q169E+Q169E+V206L,I9M+Q169E+Q169E+Y295F,I9M+Q169E+Q172K+Q299Y,I9M+Q169E+Q172K+Q345R,I9M+Q169E+Q172K+Q365S,I9M+Q169E+Q172K+R320K,I9M+Q169E+Q172K+R458K,I9M+Q169E+Q172K+S323T,I9M+Q169E+Q172K+V206L,I9M+Q169E+Q172K+Y295FI9M+Q169E+Q299Y+Q345R,I9M+Q169E+Q299Y+Q365S,I9M+Q169E+Q299Y+R320K,I9M+Q169E+Q299Y+R458K,I9M+Q169E+Q299Y+S323T,I9M+Q169E+Q299Y+V206L,I9M+Q169E+Q299Y+Y295F,I9M+Q169E+Q345R+Q365S,I9M+Q169E+Q345R+R320K,I9M+Q169E+Q345R+R458K,I9M+Q169E+Q345R+S323T,I9M+Q169E+Q345R+V206L,I9M+Q169E+Q345R+Y295F,I9M+Q169E+Q365S+R320K,I9M+Q169E+Q365S+R458K,I9M+Q169E+Q365S+S323T,I9M+Q169E+Q365S+V206L,I9M+Q169E+Q365S+Y295F,I9M+Q169E+R320K+R458K,I9M+Q169E+R320K+S323T,I9M+Q169E+R320K+V206L,I9M+Q169E+R320K+Y295F,I9M+Q169E+R458K+S323T,I9M+Q169E+R458K+V206L,I9M+Q169E+R458K+Y295F,I9M+Q169E+S323T+V206L,I9M+Q169E+S323T+Y295F,I9M+Q169E+V206L+Y295F,I9M+Q169E+Q172K+Q299Y,I9M+Q169E+Q172K+Q345R,I9M+Q169E+Q172K+Q365S,I9M+Q169E+Q172K+R320K,I9M+Q169E+Q172K+R458K,I9M+Q169E+Q172K+S323T,I9M+Q169E+Q172K+V206L,I9M+Q169E+Q172K+Y295F,I9M+Q169E+Q299Y+Q345R,I9M+Q169E+Q299Y+Q365S,I9M+Q169E+Q299Y+R320K,I9M+Q169E+Q299Y+R458K,I9M+Q169E+Q299Y+S323T,I9M+Q169E+Q299Y+V206L,I9M+Q169E+Q299Y+Y295F,I9M+Q169E+Q345R+Q365S,I9M+Q169E+Q345R+R320K,I9M+Q169E+Q345R+R458K,I9M+Q169E+Q345R+S323T,I9M+Q169E+Q345R+V206L,I9M+Q169E+Q345R+Y295F,I9M+Q169E+Q365S+R320K,I9M+Q169E+Q365S+R458K,I9M+Q169E+Q365S+S323T,I9M+Q169E+Q365S+V206L,I9M+Q169E+Q365S+Y295F,I9M+Q169E+R320K+R458K,I9M+Q169E+R320K+S323T,I9M+Q169E+R320K+V206L,I9M+Q169E+R320K+Y295F,I9M+Q169E+R458K+S323T,I9M+Q169E+R458K+V206L,I9M+Q169E+R458K+Y295F,I9M+Q169E+S323T+V206L,I9M+Q169E+S323T+Y295F,I9M+Q169E+V206L+Y295F,I9M+Q172K+Q299Y+Q345R,I9M+Q172K+Q299Y+Q365S,I9M+Q172K+Q299Y+R320K,I9M+Q172K+Q299Y+R458K,I9M+Q172K+Q299Y+S323T,I9M+Q172K+Q299Y+V206L,I9M+Q172K+Q299Y+Y295F,I9M+Q172K+Q345R+Q365S,I9M+Q172K+Q345R+R320K,I9M+Q172K+Q345R+R458K,I9M+Q172K+Q345R+S323T,I9M+Q172K+Q345R+V206L,I9M+Q172K

24 Mar 2026
2026202266

+Q345R+Y295F,I9M+Q172K+Q365S+R320K,I9M+Q172K+Q365S+R458K,I9M+Q172K+Q365S+S323T,I9M+Q172K+Q365S+V206L,I9M+Q172K+Q365S+Y295F,I9M+Q172K+R320K+R458K,I9M+Q172K+R320K+S323T,I9M+Q172K+R320K+V206L,I9M+Q172K+R320K+Y295F,I9M+Q172K+R458K+S323T,I9M+Q172K+R458K+V206L,I9M+Q172K+R458K+Y295F,I9M+Q172K+S323T+V206L,I9M+Q172K+S323T+Y295F,I9M+Q172K+V206L+Y295F,I9M+Q299Y+Q345R+Q365S,I9M+Q299Y+Q345R+R320K,I9M+Q299Y+Q345R+R458K,I9M+Q299Y+Q345R+S323T,I9M+Q299Y+Q345R+V206L,I9M+Q299Y+Q345R+Y295F,I9M+Q299Y+Q365S+R320K,I9M+Q299Y+Q365S+R458K,I9M+Q299Y+Q365S+S323T,I9M+Q299Y+Q365S+V206L,I9M+Q299Y+Q365S+Y295F,I9M+Q299Y+R320K+R458K,I9M+Q299Y+R320K+S323T,I9M+Q299Y+R320K+V206L,I9M+Q299Y+R320K+Y295F,I9M+Q299Y+R458K+S323T,I9M+Q299Y+R458K+V206L,I9M+Q299Y+R458K+Y295F,I9M+Q299Y+S323T+V206L,I9M+Q299Y+S323T+Y295F,I9M+Q299Y+V206L+Y295F,I9M+Q345R+Q365S+R320K,I9M+Q345R+Q365S+R458K,I9M+Q345R+Q365S+S323T,I9M+Q345R+Q365S+V206L,I9M+Q345R+Q365S+Y295F,I9M+Q345R+R320K+R458K,I9M+Q345R+R320K+S323T,I9M+Q345R+R320K+V206L,I9M+Q345R+R320K+Y295F,I9M+Q345R+R458K+S323T,I9M+Q345R+R458K+V206L,I9M+Q345R+R458K+Y295F,I9M+Q345R+S323T+V206L,I9M+Q345R+S323T+Y295F,I9M+Q345R+V206L+Y295F,I9M+Q365S+R320K+R458K,I9M+Q365S+R320K+S323T,I9M+Q365S+R320K+V206L,I9M+Q365S+R320K+Y295F,I9M+Q365S+R458K+S323T,I9M+Q365S+R458K+V206L,I9M+Q365S+R458K+Y295F,I9M+Q365S+S323T+V206L,I9M+Q365S+S323T+Y295F,I9M+Q365S+V206L+Y295F,I9M+R320K+R458K+S323T,I9M+R320K+R458K+V206L,I9M+R320K+R458K+Y295F,I9M+R320K+S323T+V206L,I9M+R320K+S323T+Y295F,I9M+R320K+V206L+Y295F,I9M+R458K+S323T+V206L,I9M+R458K+S323T+Y295F,I9M+R458K+V206L+Y295F, I9M+S323T+V206L+Y295F,
K391A+M202L+N16Y+N195F, K391A+M202L+N16Y+N54S,
K391A+M202L+N16Y+Q169E,K391A+M202L+N16Y+Q169E,K391A+M202L+N16Y+Q172K,K391A+M202L+N16Y+Q299Y,K391A+M202L+N16Y+Q345R,K391A+M202L+N16Y+Q365S,K391A+M202L+N16Y+R320K,K391A+M202L+N16Y+R458K,K391A+M202L+N16Y+S323T,K391A+M202L+N16Y+V206L,K391A+M202L+N16Y+Y295F,K391A+M202L+N195F+N54S,K391A+M202L+N195F+Q169E,K391A+M202L+N195F+Q169E,K391A+M202L+N195F+Q172K,K391A+M202L+N195F+Q299Y,K391A+M202L+N195F+Q345R,K391A+M202L+N195F+Q365S,K391A+M202L+N195F+R320K,K391A+M202L+N195F+R458K,K391A+M202L+N195F+S323T,K391A+M202L+N195F+V206L,K391A+M202L+N195F+Y295F,K391A+M202L+N54S+Q169E,K391A+M202L+N54S+Q169E,K391A+M202L+N54S+Q172K,K391A+M202L+N54S+Q299Y,K391A+M202L+N54S+Q345R,K391A+M202L+N54S+Q365S,K391A+M202L+N54S+R320K,K391A+M202L+N54S+R458K,K391A+M202L+N54S+S323T,K391A+M202L+N54S+V206L,K391A+M202L+N54S+Y295F,K391A+M202L+Q169E+Q169E,K391A+M202L+Q169E+Q172K,K391A+M202L+Q169E+Q299Y,K391A+M202L+Q169E+Q345R,K391A+M202L+Q169E+Q365S,K391A+M202L

24 Mar 2026
2026202266

+Q169E+R320K,K391A+M202L+Q169E+R458K,K391A+M202L+Q169E+S323T,K391A+M202L+Q169E+V206L,K391A+M202L+Q169E+Y295F,K391A+M202L+Q169E+Q172K,K391A+M202L+Q169E+Q299Y,K391A+M202L+Q169E+Q345R,K391A+M202L+Q169E+Q365S,K391A+M202L+Q169E+R320K,K391A+M202L+Q169E+R458K,K391A+M202L+Q169E+S323T,K391A+M202L+Q169E+V206L,K391A+M202L+Q169E+Y295F,K391A+M202L+Q172K+Q299Y,K391A+M202L+Q172K+Q345R,K391A+M202L+Q172K+Q365S,K391A+M202L+Q172K+R320K,K391A+M202L+Q172K+R458K,K391A+M202L+Q172K+S323T,K391A+M202L+Q172K+V206L,K391A+M202L+Q172K+Y295F,K391A+M202L+Q299Y+Q345R,K391A+M202L+Q299Y+Q365S,K391A+M202L+Q299Y+R320K,K391A+M202L+Q299Y+R458K,K391A+M202L+Q299Y+S323T,K391A+M202L+Q299Y+V206L,K391A+M202L+Q299Y+Y295F,K391A+M202L+Q345R+Q365S,K391A+M202L+Q345R+R320K,K391A+M202L+Q345R+R458K,K391A+M202L+Q345R+S323T,K391A+M202L+Q345R+V206L,K391A+M202L+Q345R+Y295F,K391A+M202L+Q365S+R320K,K391A+M202L+Q365S+R458K,K391A+M202L+Q365S+S323T,K391A+M202L+Q365S+V206L,K391A+M202L+Q365S+Y295F,K391A+M202L+R320K+R458K,K391A+M202L+R320K+S323T,K391A+M202L+R320K+V206L,K391A+M202L+R320K+Y295F,K391A+M202L+R458K+S323T,K391A+M202L+R458K+V206L,K391A+M202L+R458K+Y295F,K391A+M202L+S323T+V206L,K391A+M202L+S323T+Y295F,K391A+M202L+V206L+Y295F,K391A+N16Y+N195F+N54S,K391A+N16Y+N195F+Q169E,K391A+N16Y+N195F+Q169E,K391A+N16Y+N195F+Q172K,K391A+N16Y+N195F+Q299Y,K391A+N16Y+N195F+Q345R,K391A+N16Y+N195F+Q365S,K391A+N16Y+N195F+R320K,K391A+N16Y+N195F+R458K,K391A+N16Y+N195F+S323T,K391A+N16Y+N195F+V206L,K391A+N16Y+N195F+Y295F,K391A+N16Y+N54S+Q169E,K391A+N16Y+N54S+Q169E,K391A+N16Y+N54S+Q172K,K391A+N16Y+N54S+Q299Y,K391A+N16Y+N54S+Q345R,K391A+N16Y+N54S+Q365S,K391A+N16Y+N54S+R320K,K391A+N16Y+N54S+R458K,K391A+N16Y+N54S+S323T,K391A+N16Y+N54S+V206L,K391A+N16Y+N54S+Y295F,K391A+N16Y+Q169E+Q169E,K391A+N16Y+Q169E+Q172K,K391A+N16Y+Q169E+Q299Y,K391A+N16Y+Q169E+Q345R,K391A+N16Y+Q169E+Q365S,K391A+N16Y+Q169E+R320K,K391A+N16Y+Q169E+R458K,K391A+N16Y+Q169E+S323T,K391A+N16Y+Q169E+V206L,K391A+N16Y+Q169E+Y295F,K391A+N16Y+Q172K+Q299Y,K391A+N16Y+Q172K+Q345R,K391A+N16Y+Q172K+Q365S,K391A+N16Y+Q172K+R320K,K391A+N16Y+Q172K+R458K,K391A+N16Y+Q172K+S323T,K391A+N16Y+Q172K+V206L,K391A+N16Y+Q172K+Y295F,K391A+N16Y+Q299Y+Q345R,K391A+N16Y+Q299Y+Q365S,K391A+N16Y+Q299Y+R320K,K391A+N16Y+Q299Y+R458K,K391A+N16Y+Q299Y+S323T,K391A+N16Y+Q299Y+V206L,K391A+N16Y+Q299Y+Y295F,K391A+N16Y+Q345R+Q365S,K391A+N16Y+Q345R+R320K,K391A+N16Y+Q345R+R458K,K391

24 Mar 2026
2026202266

A+N16Y+Q345R+S323T,K391A+N16Y+Q345R+V206L,K391A+N16Y+Q345R+Y295F,K391A+N16Y+Q365S+R320K,K391A+N16Y+Q365S+R458K,K391A+N16Y+Q365S+S323T,K391A+N16Y+Q365S+V206L,K391A+N16Y+Q365S+Y295F,K391A+N16Y+R320K+R458K,K391A+N16Y+R320K+S323T,K391A+N16Y+R320K+V206L,K391A+N16Y+R320K+Y295F,K391A+N16Y+R458K+S323T,K391A+N16Y+R458K+V206L,K391A+N16Y+R458K+Y295F,K391A+N16Y+S323T+V206L,K391A+N16Y+S323T+Y295F,K391A+N16Y+V206L+Y295F,K391A+N195F+N54S+Q169E,K391A+N195F+N54S+Q169E,K391A+N195F+N54S+Q172K,K391A+N195F+N54S+Q299Y,K391A+N195F+N54S+Q345R,K391A+N195F+N54S+Q365S,K391A+N195F+N54S+R320K,K391A+N195F+N54S+R458K,K391A+N195F+N54S+S323T,K391A+N195F+N54S+V206L,K391A+N195F+N54S+Y295F,K391A+N195F+Q169E+Q169E,K391A+N195F+Q169E+Q172K,K391A+N195F+Q169E+Q299Y,K391A+N195F+Q169E+Q345R,K391A+N195F+Q169E+Q365S,K391A+N195F+Q169E+R320K,K391A+N195F+Q169E+R458K,K391A+N195F+Q169E+S323T,K391A+N195F+Q169E+V206L,K391A+N195F+Q169E+Y295F,K391A+N195F+Q169E+Q172K,K391A+N195F+Q169E+Q299,K391A+N195F+Q169E+Q345R,K391A+N195F+Q169E+Q365S,K391A+N195F+Q169E+R320K,K391A+N195F+Q169E+R458K,K391A+N195F+Q169E+S323T,K391A+N195F+Q169E+V206L,K391A+N195F+Q169E+Y295F,K391A+N195F+Q172K+Q299Y,K391A+N195F+Q172K+Q345R,K391A+N195F+Q172K+Q365S,K391A+N195F+Q172K+R320K,K391A+N195F+Q172K+R458K,K391A+N195F+Q172K+S323,K391A+N195F+Q172K+V206L,K391A+N195F+Q172K+Y295F,K391A+N195F+Q299Y+Q345R,K391A+N195F+Q299Y+Q365S,K391A+N195F+Q299Y+R320K,K391A+N195F+Q299Y+R458K,K391A+N195F+Q299Y+S323T,K391A+N195F+Q299Y+V206L,K391A+N195F+Q299Y+Y295F,K391A+N195F+Q345R+Q365S,K391A+N195F+Q345R+R320K,K391A+N195F+Q345R+R458K,K391A+N195F+Q345R+S323T,K391A+N195F+Q345R+V206L,K391A+N195F+Q345R+Y295F,K391A+N195F+Q365S+R320K,K391A+N195F+Q365S+R458K,K391A+N195F+Q365S+S323T,K391A+N195F+Q365S+V206L,K391A+N195F+Q365S+Y295F,K391A+N195F+R320K+R458K,K391A+N195F+R320K+S323T,K391A+N195F+R320K+V206L,K391A+N195F+R320K+Y295F,K391A+N195F+R458K+S323T,K391A+N195F+R458K+V206L,K391A+N195F+R458K+Y295F,K391A+N195F+S323T+V206L,K391A+N195F+S323T+Y295F,K391A+N195F+V206L+Y295F,K391A+N54S+Q169E+Q169E,K391A+N54S+Q169E+Q172K,K391A+N54S+Q169E+Q299Y,K391A+N54S+Q169E+Q345R,K391A+N54S+Q169E+Q365S,K391A+N54S+Q169E+R320K,K391A+N54S+Q169E+R458K,K391A+N54S+Q169E+S323T,K391A+N54S+Q169E+V206L,K391A+N54S+Q169E+Y295F,K391A+N54S+Q169E+Q172K,K391A+N54S+Q169E+Q299Y,K391A+N54S+Q169E+Q345R,K391A+N54S+Q169E+Q365S,K391A+N54S+Q169E+R320K,K391A+N54S+Q169E+R458K,K391A+N54S+Q169E+S323T,K391A+N54S+Q169E+V206L,K391A+N54S+Q169E+Y295F,K391A+N54S+Q172K+Q299Y,K391A+N54S+Q172K+Q345R,K391A+N54S+Q172K+Q365S,K391A+N54S+Q172K+R320K,K391A+N54S+Q172K+R458K,K391A+N54S+Q172K+S323T,K391A+N54S+Q172K+

24 Mar 2026
2026202266

V206L,K391A+N54S+Q172K+Y295F,K391A+N54S+Q299Y+Q345R,K391A+N54S+Q299Y+Q365S,K391A+N54S+Q299Y+R320K,K391A+N54S+Q299Y+R458K,K391A+N54S+Q299Y+S323T,K391A+N54S+Q299Y+V206L,K391A+N54S+Q299Y+Y295F,K391A+N54S+Q345R+Q365S,K391A+N54S+Q345R+R320K,K391A+N54S+Q345R+R458K,K391A+N54S+Q345R+S323T,K391A+N54S+Q345R+V206L,K391A+N54S+Q345R+Y295F,K391A+N54S+Q365S+R320K,K391A+N54S+Q365S+R458K,K391A+N54S+Q365S+S323T,K391A+N54S+Q365S+V206L,K391A+N54S+Q365S+Y295F,K391A+N54S+R320K+R458K,K391A+N54S+R320K+S323T,K391A+N54S+R320K+V206L,K391A+N54S+R320K+Y295F,K391A+N54S+R458K+S323TK391A+N54S+R458K+V206L,K391A+N54S+R458K+Y295F,K391A+N54S+S323T+V206L,K391A+N54S+S323T+Y295F,K391A+N54S+V206L+Y295F,K391A+Q169E+Q169E+Q172K,K391A+Q169E+Q169E+Q299Y,K391A+Q169E+Q169E+Q345R,K391A+Q169E+Q169E+Q365S,K391A+Q169E+Q169E+R320K,K391A+Q169E+Q169E+R458K,K391A+Q169E+Q169E+S323T,K391A+Q169E+Q169E+V206L,K391A+Q169E+Q169E+Y295F,K391A+Q169E+Q172K+Q299Y,K391A+Q169E+Q172K+Q345R,K391A+Q169E+Q172K+Q365S,K391A+Q169E+Q172K+R320K,K391A+Q169E+Q172K+R458K,K391A+Q169E+Q172K+S323T,K391A+Q169E+Q172K+V206L,K391A+Q169E+Q172K+Y295F,K391A+Q169E+Q299Y+Q345R,K391A+Q169E+Q299Y+Q365S,K391A+Q169E+Q299Y+R320K,K391A+Q169E+Q299Y+R458K,K391A+Q169E+Q299Y+S323T,K391A+Q169E+Q299Y+V206L,K391A+Q169E+Q299Y+Y295F,K391A+Q169E+Q345R+Q365S,K391A+Q169E+Q345R+R320K,K391A+Q169E+Q345R+R458K,K391A+Q169E+Q345R+S323T,K391A+Q169E+Q345R+V206L,K391A+Q169E+Q345R+Y295F,K391A+Q169E+Q365S+R320K,K391A+Q169E+Q365S+R458K,K391A+Q169E+Q365S+S323T,K391A+Q169E+Q365S+V206L,K391A+Q169E+Q365S+Y295F,K391A+Q169E+R320K+R458K,K391A+Q169E+R320K+S323T,K391A+Q169E+R320K+V206L,K391A+Q169E+R320K+Y295F,K391A+Q169E+R458K+S323T,K391A+Q169E+R458K+V206L,K391A+Q169E+R458K+Y295F,K391A+Q169E+S323T+V206L,K391A+Q169E+S323T+Y295F,K391A+Q169E+V206L+Y295F,K391A+Q169E+Q172K+Q299Y,K391A+Q169E+Q172K+Q345R,K391A+Q169E+Q172K+Q365S,K391A+Q169E+Q172K+R320K,K391A+Q169E+Q172K+R458K,K391A+Q169E+Q172K+S323T,K391A+Q169E+Q172K+V206L,K391A+Q169E+Q172K+Y295F,K391A+Q169E+Q299Y+Q345R,K391A+Q169E+Q299Y+Q365S,K391A+Q169E+Q299Y+R320K,K391A+Q169E+Q299Y+R458K,K391A+Q169E+Q299Y+S323T,K391A+Q169E+Q299Y+V206L,K391A+Q169E+Q299Y+Y295F,K391A+Q169E+Q345R+Q365S,K391A+Q169E+Q345R+R320K,K391A+Q169E+Q345R+R458K,K391A+Q169E+Q345R+S323T,K391A+Q169E+Q345R+V206L,K391A+Q169E+Q345R+Y295F,K391A+Q169E+Q365S+R320K,K391A+Q169E+Q365S+R458K,K391A+Q169E+Q365S+S323T,K391A+Q169E+Q365S+V206L,K391A+Q169E+Q365S+Y295F,K391A+Q169E+R320K+R458K,K391A+Q169E+R320K+S323T,K391A+Q169E+R320K+V206L,K391A+Q169E+R320K+Y295F,K391A+Q169E+R458K+S323T,K391A+Q169E+R458K+V206L,K391A+Q169E+R458K+Y295F,K391A+Q169E+S323

24 Mar 2026
2026202266

T+V206L,K391A+Q169E+S323T+Y295F,K391A+Q169E+V206L+Y295F,K391A+Q172K+Q299Y+Q345R,K391A+Q172K+Q299Y+Q365S,K391A+Q172K+Q299Y+R320K,K391A+Q172K+Q299Y+R458K,K391A+Q172K+Q299Y+S323T,K391A+Q172K+Q299Y+V206L,K391A+Q172K+Q299Y+Y295F,K391A+Q172K+Q345R+Q365S,K391A+Q172K+Q345R+R320K,K391A+Q172K+Q345R+R458K,K391A+Q172K+Q345R+S323T,K391A+Q172K+Q345R+V206L,K391A+Q172K+Q345R+Y295F,K391A+Q172K+Q365S+R320K,K391A+Q172K+Q365S+R458K,K391A+Q172K+Q365S+S323T,K391A+Q172K+Q365S+V206L,K391A+Q172K+Q365S+Y295F,K391A+Q172K+R320K+R458K,K391A+Q172K+R320K+S323T,K391A+Q172K+R320K+V206L,K391A+Q172K+R320K+Y295F,K391A+Q172K+R458K+S323T,K391A+Q172K+R458K+V206L,K391A+Q172K+R458K+Y295F,K391A+Q172K+S323T+V206L,K391A+Q172K+S323T+Y295F,K391A+Q172K+V206L+Y295F,K391A+Q299Y+Q345R+Q365S,K391A+Q299Y+Q345R+R320K,K391A+Q299Y+Q345R+R458K,K391A+Q299Y+Q345R+S323T,K391A+Q299Y+Q345R+V206L,K391A+Q299Y+Q345R+Y295F,K391A+Q299Y+Q365S+R320K,K391A+Q299Y+Q365S+R458K,K391A+Q299Y+Q365S+S323T,K391A+Q299Y+Q365S+V206L,K391A+Q299Y+Q365S+Y295F,K391A+Q299Y+R320K+R458K,K391A+Q299Y+R320K+S323T,K391A+Q299Y+R320K+V206L,K391A+Q299Y+R320K+Y295F,K391A+Q299Y+R458K+S323T,K391A+Q299Y+R458K+V206L,K391A+Q299Y+R458K+Y295F,K391A+Q299Y+S323T+V206L,K391A+Q299Y+S323T+Y295F,K391A+Q299Y+V206L+Y295F,K391A+Q345R+Q365S+R320K,K391A+Q345R+Q365S+R458K,K391A+Q345R+Q365S+S323T,K391A+Q345R+Q365S+V206L,K391A+Q345R+Q365S+Y295F,K391A+Q345R+R320K+R458K,K391A+Q345R+R320K+S323T,K391A+Q345R+R320K+V206L,K391A+Q345R+R320K+Y295F,K391A+Q345R+R458K+S323T,K391A+Q345R+R458K+V206L,K391A+Q345R+R458K+Y295F,K391A+Q345R+S323T+V206L,K391A+Q345R+S323T+Y295F,K391A+Q345R+V206L+Y295F,K391A+Q365S+R320K+R458K,K391A+Q365S+R320K+S323T,K391A+Q365S+R320K+V206L,K391A+Q365S+R320K+Y295F,K391A+Q365S+R458K+S323T,K391A+Q365S+R458K+V206L,K391A+Q365S+R458K+Y295F,K391A+Q365S+S323T+V206L,K391A+Q365S+S323T+Y295F,K391A+Q365S+V206L+Y295F,K391A+R320K+R458K+S323T,K391A+R320K+R458K+V206L,K391A+R320K+R458K+Y295F,K391A+R320K+S323T+V206L,K391A+R320K+S323T+Y295F,K391A+R320K+V206L+Y295F,K391A+R458K+S323T+V206L,K391A+R458K+S323T+Y295F,K391A+R458K+V206L+Y295F,K391A+S323T+V206L+Y295F,M202L+N16Y+N195F+N54S,M202L+N16Y+N195F+Q169E,M202L+N16Y+N195F+Q169E,M202L+N16Y+N195F+Q172K,M202L+N16Y+N195F+Q299Y,M202L+N16Y+N195F+Q345R,M202L+N16Y+N195F+Q365S,M202L+N16Y+N195F+R320K,M202L+N16Y+N195F+R458K,M202L+N16Y+N195F+S323T,M202L+N16Y+N195F+V206L,M202L+N16Y+N195F+Y295F,M202L+N16Y+N54S+Q169E,M202L+N16Y+N54S+Q169E,M202L+N16Y+N54S+Q172K,M202L+N16Y+N54S+Q299Y,M202L+N16Y+N54S+Q345R,M202L+N16Y+N54S+Q365S,M202L+N16Y+N54S+R320K,M202L+N16Y+N54S+R458K,M202L+N16Y+N54S+S323T,M202L+N16Y+N54S+V206L,M202L

24 Mar 2026
2026202266

+N16Y+N54S+Y295F,M202L+N16Y+Q169E+Q169E,M202L+N16Y+Q169E+Q172K,M202L+N16Y+Q169E+Q299Y,M202L+N16Y+Q169E+Q345R,M202L+N16Y+Q169E+Q365S,M202L+N16Y+Q169E+R320K,M202L+N16Y+Q169E+R458K,M202L+N16Y+Q169E+S323T,M202L+N16Y+Q169E+V206L,M202L+N16Y+Q169E+Y295F,M202L+N16Y+Q169E+Q172K,M202L+N16Y+Q169E+Q299Y,M202L+N16Y+Q169E+Q345R,M202L+N16Y+Q169E+Q365S,M202L+N16Y+Q169E+R320K,M202L+N16Y+Q169E+R458K,M202L+N16Y+Q169E+S323T,M202L+N16Y+Q169E+V206L,M202L+N16Y+Q169E+Y295F,M202L+N16Y+Q172K+Q299Y,M202L+N16Y+Q172K+Q345R,M202L+N16Y+Q172K+Q365S,M202L+N16Y+Q172K+R320K,M202L+N16Y+Q172K+R458K,M202L+N16Y+Q172K+S323T,M202L+N16Y+Q172K+V206L,M202L+N16Y+Q172K+Y295F,M202L+N16Y+Q299Y+Q345R,M202L+N16Y+Q299Y+Q365S,M202L+N16Y+Q299Y+R320K,M202L+N16Y+Q299Y+R458K,M202L+N16Y+Q299Y+S323T,M202L+N16Y+Q299Y+V206L,M202L+N16Y+Q299Y+Y295F,M202L+N16Y+Q345R+Q365S,M202L+N16Y+Q345R+R320K,M202L+N16Y+Q345R+R458K,M202L+N16Y+Q345R+S323T,M202L+N16Y+Q345R+V206L,M202L+N16Y+Q345R+Y295F,M202L+N16Y+Q365S+R320K,M202L+N16Y+Q365S+R458K,M202L+N16Y+Q365S+S323T,M202L+N16Y+Q365S+V206L,M202L+N16Y+Q365S+Y295F,M202L+N16Y+R320K+R458K,M202L+N16Y+R320K+S323T,M202L+N16Y+R320K+V206L,M202L+N16Y+R320K+Y295F,M202L+N16Y+R458K+S323T,M202L+N16Y+R458K+V206L,M202L+N16Y+R458K+Y295F,M202L+N16Y+S323T+V206L,M202L+N16Y+S323T+Y295F,M202L+N16Y+V206L+Y295F,M202L+N195F+N54S+Q169E,M202L+N195F+N54S+Q169E,M202L+N195F+N54S+Q172K,M202L+N195F+N54S+Q299Y,M202L+N195F+N54S+Q345R,M202L+N195F+N54S+Q365S,M202L+N195F+N54S+R320K,M202L+N195F+N54S+R458K,M202L+N195F+N54S+S323T,M202L+N195F+N54S+V206L,M202L+N195F+N54S+Y295F,M202L+N195F+Q169E+Q169E,M202L+N195F+Q169E+Q172K,M202L+N195F+Q169E+Q299Y,M202L+N195F+Q169E+Q345R,M202L+N195F+Q169E+Q365S,M202L+N195F+Q169E+R320K,M202L+N195F+Q169E+R458K,M202L+N195F+Q169E+S323T,M202L+N195F+Q169E+V206L,M202L+N195F+Q169E+Y295F,M202L+N195F+Q172K+Q299Y,M202L+N195F+Q172K+Q345R,M202L+N195F+Q172K+Q365S,M202L+N195F+Q172K+R320K,M202L+N195F+Q172K+R458K,M202L+N195F+Q172K+S323T,M202L+N195F+Q172K+V206L,M202L+N195F+Q172K+Y295F,M202L+N195F+Q299Y+Q345R,M202L+N195F+Q299Y+Q365S,M202L+N195F+Q299Y+R320K,M202L+N195F+Q299Y+R458K,M202L+N195F+Q299Y+S323T,M202L+N195F+Q299Y+V206L,M202L+N195F+Q299Y+Y295F,M202L+N195F+Q345R+Q365S,M202L+N195F+Q345R+R320K,M202L+N195F+Q345R+R458K,M202L+N195F+Q345R+S323T,M202L+N195F+Q345R+V206L,M202L+N195F+Q345R+Y295F,M202L+N195F+Q365S+R320K,M202L+N195F+Q365S+R458K,M202L+N195F+

24 Mar 2026
2026202266

Q365S+S323T,M202L+N195F+Q365S+V206L,M202L+N195F+Q365S+Y295F,M202L+N195F+R320K+R458K,M202L+N195F+R320K+S323T,M202L+N195F+R320K+V206L,M202L+N195F+R320K+Y295F,M202L+N195F+R458K+S323T,M202L+N195F+R458K+V206L,M202L+N195F+R458K+Y295F,M202L+N195F+S323T+V206L,M202L+N195F+S323T+Y295F,M202L+N195F+V206L+Y295F,M202L+N54S+Q169E+Q169E,M202L+N54S+Q169E+Q172K,M202L+N54S+Q169E+Q299Y,M202L+N54S+Q169E+Q345R,M202L+N54S+Q169E+Q365S,M202L+N54S+Q169E+R320K,M202L+N54S+Q169E+R458K,M202L+N54S+Q169E+S323T,M202L+N54S+Q169E+V206L,M202L+N54S+Q169E+Y295F,M202L+N54S+Q169E+Q172K,M202L+N54S+Q169E+Q299Y,M202L+N54S+Q169E+Q345R,M202L+N54S+Q169E+Q365S,M202L+N54S+Q169E+R320K,M202L+N54S+Q169E+R458K,M202L+N54S+Q169E+S323T,M202L+N54S+Q169E+V206L,M202L+N54S+Q169E+Y295F,M202L+N54S+Q172K+Q299Y,M202L+N54S+Q172K+Q345R,M202L+N54S+Q172K+Q365S,M202L+N54S+Q172K+R320K,M202L+N54S+Q172K+R458K,M202L+N54S+Q172K+S323T,M202L+N54S+Q172K+V206L,M202L+N54S+Q172K+Y295F,M202L+N54S+Q299Y+Q345R,M202L+N54S+Q299Y+Q365S,M202L+N54S+Q299Y+R320K,M202L+N54S+Q299Y+R458K,M202L+N54S+Q299Y+S323T,M202L+N54S+Q299Y+V206L,M202L+N54S+Q299Y+Y295F,M202L+N54S+Q345R+Q365S,M202L+N54S+Q345R+R320K,M202L+N54S+Q345R+R458K,M202L+N54S+Q345R+S323T,M202L+N54S+Q345R+V206L,M202L+N54S+Q345R+Y295F,M202L+N54S+Q365S+R320K,M202L+N54S+Q365S+R458K,M202L+N54S+Q365S+S323T,M202L+N54S+Q365S+V206L,M202L+N54S+Q365S+Y295F,M202L+N54S+R320K+R458K,M202L+N54S+R320K+S323T,M202L+N54S+R320K+V206L,M202L+N54S+R320K+Y295F,M202L+N54S+R458K+S323T,M202L+N54S+R458K+V206L,M202L+N54S+R458K+Y295F,M202L+N54S+S323T+V206L,M202L+N54S+S323T+Y295F,M202L+N54S+V206L+Y295F,M202L+Q169E+Q169E+Q172K,M202L+Q169E+Q169E+Q299Y,M202L+Q169E+Q169E+Q345R,M202L+Q169E+Q169E+Q365S,M202L+Q169E+Q169E+R320K,M202L+Q169E+Q169E+R458K,M202L+Q169E+Q169E+S323T,M202L+Q169E+Q169E+V206L,M202L+Q169E+Q169E+Y295F,M202L+Q169E+Q172K+Q299Y,M202L+Q169E+Q172K+Q345R,M202L+Q169E+Q172K+Q365S,M202L+Q169E+Q172K+R320K,M202L+Q169E+Q172K+R458K,M202L+Q169E+Q172K+S323T,M202L+Q169E+Q172K+V206L,M202L+Q169E+Q172K+Y295F,M202L+Q169E+Q299Y+Q345R,M202L+Q169E+Q299Y+Q365S,M202L+Q169E+Q299Y+R320K,M202L+Q169E+Q299Y+R458K,M202L+Q169E+Q299Y+S323T,M202L+Q169E+Q299Y+V206L,M202L+Q169E+Q299Y+Y295F,M202L+Q169E+Q345R+Q365S,M202L+Q169E+Q345R+R320K,M202L+Q169E+Q345R+R458K,M202L+Q169E+Q345R+S323T,M202L+Q169E+Q345R+V206L,M202L+Q169E+Q345R+Y295F,M202L+Q169E+Q365S+R320K,M202L+Q169E+Q365S+R458K,M202L+Q169E+Q365S+S323T,M202L+Q169E+Q365S+V206L,M202L+Q169E+Q365S+Y295F,M202L+Q169E+R320K+R458K,M202L+Q169E+R320K+S323T,M202L+Q169E+R320K+V206L,M202L+Q169E+R320K+Y295F,M202L+Q169E+R458K+S323T,M202L+Q169E+R458K+V206L,M202L

24 Mar 2026
2026202266

+Q169E+R458K+Y295F,M202L+Q169E+S323T+V206L,M202L+Q169E+S323T+Y295F,M202L
+Q169E+V206L+Y295F,M202L+Q169E+Q172K+Q299Y,M202L+Q169E+Q172K+Q345R,M202
L+Q169E+Q172K+Q365S,M202L+Q169E+Q172K+R320K,M202L+Q169E+Q172K+R458K,M2
02L+Q169E+Q172K+S323T,M202L+Q169E+Q172K+V206L,M202L+Q169E+Q172K+Y295F,M
202L+Q169E+Q299Y+Q345R,M202L+Q169E+Q299Y+Q365S,M202L+Q169E+Q299Y+R320K,
M202L+Q169E+Q299Y+R458K,M202L+Q169E+Q299Y+S323T,M202L+Q169E+Q299Y+V206
L,M202L+Q169E+Q299Y+Y295F,M202L+Q169E+Q345R+Q365S,M202L+Q169E+Q345R+R32
0K,M202L+Q169E+Q345R+R458K,M202L+Q169E+Q345R+S323T,M202L+Q169E+Q345R+V
206L,M202L+Q169E+Q345R+Y295F,M202L+Q169E+Q365S+R320K,M202L+Q169E+Q365S+
R458K,M202L+Q169E+Q365S+S323T,M202L+Q169E+Q365S+V206L,M202L+Q169E+Q365S
+Y295F,M202L+Q169E+R320K+R458K,M202L+Q169E+R320K+S323T,M202L+Q169E+R320
K+V206L,M202L+Q169E+R320K+Y295F,M202L+Q169E+R458K+S323T,M202L+Q169E+R45
8K+V206L,M202L+Q169E+R458K+Y295F,M202L+Q169E+S323T+V206L,M202L+Q169E+S32
3T+Y295F,M202L+Q169E+V206L+Y295F,M202L+Q172K+Q299Y+Q345R,M202L+Q172K+Q2
99Y+Q365S,M202L+Q172K+Q299Y+R320K,M202L+Q172K+Q299Y+R458K,M202L+Q172K+
Q299Y+S323T,M202L+Q172K+Q299Y+V206L,M202L+Q172K+Q299Y+Y295F,M202L+Q172K
+Q345R+Q365S,M202L+Q172K+Q345R+R320K,M202L+Q172K+Q345R+R458K,M202L+Q17
2K+Q345R+S323T,M202L+Q172K+Q345R+V206L,M202L+Q172K+Q345R+Y295F,M202L+Q1
72K+Q365S+R320K,M202L+Q172K+Q365S+R458K,M202L+Q172K+Q365S+S323T,M202L+Q
172K+Q365S+V206L,M202L+Q172K+Q365S+Y295F,M202L+Q172K+R320K+R458K,M202L+
Q172K+R320K+S323T,M202L+Q172K+R320K+V206L,M202L+Q172K+R320K+Y295F,M202L
+Q172K+R458K+S323T,M202L+Q172K+R458K+V206L,M202L+Q172K+R458K+Y295F,M202
L+Q172K+S323T+V206L,M202L+Q172K+S323T+Y295F,M202L+Q172K+V206L+Y295F,M202
L+Q299Y+Q345R+Q365S,M202L+Q299Y+Q345R+R320K,M202L+Q299Y+Q345R+R458K,M2
02L+Q299Y+Q345R+S323T,M202L+Q299Y+Q345R+V206L,M202L+Q299Y+Q345R+Y295F,M
202L+Q299Y+Q365S+R320K,M202L+Q299Y+Q365S+R458K,M202L+Q299Y+Q365S+S323T,
M202L+Q299Y+Q365S+V206L,M202L+Q299Y+Q365S+Y295F,M202L+Q299Y+R320K+R458K
,M202L+Q299Y+R320K+S323T,M202L+Q299Y+R320K+V206L,M202L+Q299Y+R320K+Y295
F,M202L+Q299Y+R458K+S323T,
M202L+Q299Y+R458K+V206L,M202L+Q299Y+R458K+Y295F,M202L+Q299Y+S323T+V206L,
M202L+Q299Y+S323T+Y295F,M202L+Q299Y+V206L+Y295F,M202L+Q345R+Q365S+R320K
,M202L+Q345R+Q365S+R458K,M202L+Q345R+Q365S+S323T,M202L+Q345R+Q365S+V206
L,M202L+Q345R+Q365S+Y295F,M202L+Q345R+R320K+R458K,M202L+Q345R+R320K+S32
3T,M202L+Q345R+R320K+V206L,M202L+Q345R+R320K+Y295F,M202L+Q345R+R458K+S3
23T,M202L+Q345R+R458K+V206L,M202L+Q345R+R458K+Y295F,M202L+Q345R+S323T+V
206L,M202L+Q345R+S323T+Y295F,M202L+Q345R+V206L+Y295F,M202L+Q365S+R320K+R

24 Mar 2026
2026202266

458K,M202L+Q365S+R320K+S323T,M202L+Q365S+R320K+V206L,M202L+Q365S+R320K+Y295F,M202L+Q365S+R458K+S323T,M202L+Q365S+R458K+V206L,M202L+Q365S+R458K+Y295F,M202L+Q365S+S323T+V206L,M202L+Q365S+S323T+Y295F,M202L+Q365S+V206L+Y295F,M202L+R320K+R458K+S323T,M202L+R320K+R458K+V206L,M202L+R320K+R458K+Y295F,M202L+R320K+S323T+V206L,M202L+R320K+S323T+Y295F,M202L+R320K+V206L+Y295F,M202L+R458K+S323T+V206L,M202L+R458K+S323T+Y295F,M202L+R458K+V206L+Y295F,M202L+S323T+V206L+Y295F,N16Y+N195F+N54S+Q169E,N16Y+N195F+N54S+Q169E,N16Y+N195F+N54S+Q172K,N16Y+N195F+N54S+Q299Y,N16Y+N195F+N54S+Q345R,N16Y+N195F+N54S+Q365S,N16Y+N195F+N54S+R320K,N16Y+N195F+N54S+R458K,N16Y+N195F+N54S+S323T,N16Y+N195F+N54S+V206L,N16Y+N195F+N54S+Y295F,N16Y+N195F+Q169E+Q169E,N16Y+N195F+Q169E+Q172K,N16Y+N195F+Q169E+Q299Y,N16Y+N195F+Q169E+Q345R,N16Y+N195F+Q169E+Q365S,N16Y+N195F+Q169E+R320K,N16Y+N195F+Q169E+R458K,N16Y+N195F+Q169E+S323T,N16Y+N195F+Q169E+V206L,N16Y+N195F+Q169E+Y295F,N16Y+N195F+Q169E+Q172K,N16Y+N195F+Q169E+Q299Y,N16Y+N195F+Q169E+Q345R,N16Y+N195F+Q169E+Q365S,N16Y+N195F+Q169E+R320K,N16Y+N195F+Q169E+R458K,N16Y+N195F+Q169E+S323T,N16Y+N195F+Q169E+V206L,N16Y+N195F+Q169E+Y295F,N16Y+N195F+Q172K+Q299Y,N16Y+N195F+Q172K+Q345R,N16Y+N195F+Q172K+Q365S,N16Y+N195F+Q172K+R320K,N16Y+N195F+Q172K+R458K,N16Y+N195F+Q172K+S323T,N16Y+N195F+Q172K+V206L,N16Y+N195F+Q172K+Y295F,N16Y+N195F+Q299Y+Q345R,N16Y+N195F+Q299Y+Q365S,N16Y+N195F+Q299Y+R320K,N16Y+N195F+Q299Y+R458K,N16Y+N195F+Q299Y+S323T,N16Y+N195F+Q299Y+V206L,N16Y+N195F+Q299Y+Y295F,N16Y+N195F+Q345R+Q365S,N16Y+N195F+Q345R+R320K,N16Y+N195F+Q345R+R458K,N16Y+N195F+Q345R+S323T,N16Y+N195F+Q345R+V206L,N16Y+N195F+Q345R+Y295F,N16Y+N195F+Q365S+R320K,N16Y+N195F+Q365S+R458K,N16Y+N195F+Q365S+S323T,N16Y+N195F+Q365S+V206L,N16Y+N195F+Q365S+Y295F,N16Y+N195F+R320K+R458K,N16Y+N195F+R320K+S323T,N16Y+N195F+R320K+V206L,N16Y+N195F+R320K+Y295F,N16Y+N195F+R458K+S323T,N16Y+N195F+R458K+V206L,N16Y+N195F+R458K+Y295F,N16Y+N195F+S323T+V206L,N16Y+N195F+S323T+Y295F,N16Y+N195F+V206L+Y295F,N16Y+N54S+Q169E+Q169E,N16Y+N54S+Q169E+Q172K,N16Y+N54S+Q169E+Q299Y,N16Y+N54S+Q169E+Q345R,N16Y+N54S+Q169E+Q365S,N16Y+N54S+Q169E+R320K,N16Y+N54S+Q169E+R458K,N16Y+N54S+Q169E+S323T,N16Y+N54S+Q169E+V206L,N16Y+N54S+Q169E+Y295F,N16Y+N54S+Q172K+Q299Y,N16Y+N54S+Q172K+Q345R,N16Y+N54S+Q172K+Q365S,N16Y+N54S+Q172K+R320K,N16Y+N54S+Q172K+R458K,N16Y+N54S+Q172K+S323T,N16Y+N54S+Q172K+V206L,N16Y+N54S+Q172K+Y

24 Mar 2026
2026202266

295F,N16Y+N54S+Q299Y+Q345R,N16Y+N54S+Q299Y+Q365S,N16Y+N54S+Q299Y+R320K,
N16Y+N54S+Q299Y+R458K,N16Y+N54S+Q299Y+S323T,N16Y+N54S+Q299Y+V206L,N16Y+
N54S+Q299Y+Y295F,N16Y+N54S+Q345R+Q365S,N16Y+N54S+Q345R+R320K,N16Y+N54S
+Q345R+R458K,N16Y+N54S+Q345R+S323T,N16Y+N54S+Q345R+V206L,N16Y+N54S+Q34
5R+Y295F,N16Y+N54S+Q365S+R320K,N16Y+N54S+Q365S+R458K,N16Y+N54S+Q365S+S
323T,N16Y+N54S+Q365S+V206L,N16Y+N54S+Q365S+Y295F,N16Y+N54S+R320K+R458K,
N16Y+N54S+R320K+S323T,N16Y+N54S+R320K+V206L,N16Y+N54S+R320K+Y295F,N16Y+
N54S+R458K+S323T,N16Y+N54S+R458K+V206L,N16Y+N54S+R458K+Y295F,N16Y+N54S+
S323T+V206L,N16Y+N54S+S323T+Y295F,N16Y+N54S+V206L+Y295F,N16Y+Q169E+Q169E
+Q172K,N16Y+Q169E+Q169E+Q299Y,N16Y+Q169E+Q169E+Q345R,N16Y+Q169E+Q169E+
Q365S,N16Y+Q169E+Q169E+R320K,N16Y+Q169E+Q169E+R458K,N16Y+Q169E+Q169E+S
323T,N16Y+Q169E+Q169E+V206L,N16Y+Q169E+Q169E+Y295F,N16Y+Q169E+Q172K+Q29
9Y,N16Y+Q169E+Q172K+Q345R,N16Y+Q169E+Q172K+Q365S,N16Y+Q169E+Q172K+R320
K,N16Y+Q169E+Q172K+R458K,N16Y+Q169E+Q172K+S323T,N16Y+Q169E+Q172K+V206L,
N16Y+Q169E+Q172K+Y295F,N16Y+Q169E+Q299Y+Q345R,N16Y+Q169E+Q299Y+Q365S,
N16Y+Q169E+Q299Y+R320K,N16Y+Q169E+Q299Y+R458K,N16Y+Q169E+Q299Y+S323T,
N16Y+Q169E+Q299Y+V206L,N16Y+Q169E+Q299Y+Y295F,N16Y+Q169E+Q345R+Q365S,
N16Y+Q169E+Q345R+R320K,N16Y+Q169E+Q345R+R458K,N16Y+Q169E+Q345R+S323T,
N16Y+Q169E+Q345R+V206L,N16Y+Q169E+Q345R+Y295F,N16Y+Q169E+Q365S+R320K,
N16Y+Q169E+Q365S+R458K,N16Y+Q169E+Q365S+S323T,N16Y+Q169E+Q365S+V206L,
N16Y+Q169E+Q365S+Y295F,N16Y+Q169E+R320K+R458K,N16Y+Q169E+R320K+S323T,N1
6Y+Q169E+R320K+V206L,N16Y+Q169E+R320K+Y295F,N16Y+Q169E+R458K+S323T,N16Y
+Q169E+R458K+V206L,N16Y+Q169E+R458K+Y295F,N16Y+Q169E+S323T+V206L,N16Y+Q
169E+S323T+Y295F,N16Y+Q169E+V206L+Y295F,N16Y+Q169E+Q172K+Q299Y,N16Y+Q16
9E+Q172K+Q345R,N16Y+Q169E+Q172K+Q365S,N16Y+Q169E+Q172K+R320K,N16Y+Q169
E+Q172K+R458K,N16Y+Q169E+Q172K+S323T,N16Y+Q169E+Q172K+V206L,N16Y+Q169E+
Q172K+Y295F,N16Y+Q169E+Q299Y+Q345R,N16Y+Q169E+Q299Y+Q365S,N16Y+Q169E+Q
299Y+R320K,N16Y+Q169E+Q299Y+R458K,N16Y+Q169E+Q299Y+S323T,N16Y+Q169E+Q29
9Y+V206L,N16Y+Q169E+Q299Y+Y295F,N16Y+Q169E+Q345R+Q365S,N16Y+Q169E+Q345
R+R320K,N16Y+Q169E+Q345R+R458K,N16Y+Q169E+Q345R+S323T,N16Y+Q169E+Q345R
+V206L,N16Y+Q169E+Q345R+Y295F,N16Y+Q169E+Q365S+R320K,N16Y+Q169E+Q365S+
R458K,N16Y+Q169E+Q365S+S323T,N16Y+Q169E+Q365S+V206L,N16Y+Q169E+Q365S+Y2
95F,N16Y+Q169E+R320K+R458K,N16Y+Q169E+R320K+S323T,N16Y+Q169E+R320K+V206
L,N16Y+Q169E+R320K+Y295F,N16Y+Q169E+R458K+S323T,N16Y+Q169E+R458K+V206L,N
16Y+Q169E+R458K+Y295F,N16Y+Q169E+S323T+V206L,N16Y+Q169E+S323T+Y295F,N16Y
+Q169E+V206L+Y295F,N16Y+Q172K+Q299Y+Q345R,N16Y+Q172K+Q299Y+Q365S,N16Y+

24 Mar 2026
2026202266

Q172K+Q299Y+R320K,N16Y+Q172K+Q299Y+R458K,N16Y+Q172K+Q299Y+S323T,N16Y+Q172K+Q299Y+V206L,N16Y+Q172K+Q299Y+Y295F,N16Y+Q172K+Q345R+Q365S,N16Y+Q172K+Q345R+R320K,N16Y+Q172K+Q345R+R458K,N16Y+Q172K+Q345R+S323T,N16Y+Q172K+Q345R+V206L,N16Y+Q172K+Q345R+Y295F,N16Y+Q172K+Q365S+R320K,N16Y+Q172K+Q365S+R458K,N16Y+Q172K+Q365S+S323T,N16Y+Q172K+Q365S+V206L,N16Y+Q172K+Q365S+Y295F,N16Y+Q172K+R320K+R458K,N16Y+Q172K+R320K+S323T,N16Y+Q172K+R320K+V206L,N16Y+Q172K+R320K+Y295F,N16Y+Q172K+R458K+S323T,N16Y+Q172K+R458K+V206L,N16Y+Q172K+R458K+Y295F,N16Y+Q172K+S323T+V206L,N16Y+Q172K+S323T+Y295F,N16Y+Q172K+V206L+Y295F,N16Y+Q299Y+Q345R+Q365S,N16Y+Q299Y+Q345R+R320K,N16Y+Q299Y+Q345R+R458K,N16Y+Q299Y+Q345R+S323T,N16Y+Q299Y+Q345R+V206L,N16Y+Q299Y+Q345R+Y295F,N16Y+Q299Y+Q365S+R320K,N16Y+Q299Y+Q365S+R458K,N16Y+Q299Y+Q365S+S323T,N16Y+Q299Y+Q365S+V206L,N16Y+Q299Y+Q365S+Y295F,N16Y+Q299Y+R320K+R458K,N16Y+Q299Y+R320K+S323T,N16Y+Q299Y+R320K+V206L,N16Y+Q299Y+R320K+Y295F,N16Y+Q299Y+R458K+S323T,N16Y+Q299Y+R458K+V206L,N16Y+Q299Y+R458K+Y295F,N16Y+Q299Y+S323T+V206L,N16Y+Q299Y+S323T+Y295F,N16Y+Q299Y+V206L+Y295F,N16Y+Q345R+Q365S+R320K,N16Y+Q345R+Q365S+R458K,N16Y+Q345R+Q365S+S323T,N16Y+Q345R+Q365S+V206L,N16Y+Q345R+Q365S+Y295F,N16Y+Q345R+R320K+R458K,N16Y+Q345R+R320K+S323T,N16Y+Q345R+R320K+V206L,N16Y+Q345R+R320K+Y295F,N16Y+Q345R+R458K+S323T,N16Y+Q345R+R458K+V206L,N16Y+Q345R+R458K+Y295F,N16Y+Q345R+S323T+V206L,N16Y+Q345R+S323T+Y295F,N16Y+Q345R+V206L+Y295F,N16Y+Q365S+R320K+R458K,N16Y+Q365S+R320K+S323T,N16Y+Q365S+R320K+V206L,N16Y+Q365S+R320K+Y295F,N16Y+Q365S+R458K+S323T,N16Y+Q365S+R458K+V206L,N16Y+Q365S+R458K+Y295F,N16Y+Q365S+S323T+V206L,N16Y+Q365S+S323T+Y295F,N16Y+Q365S+V206L+Y295F,N16Y+R320K+R458K+S323T,N16Y+R320K+R458K+V206L,N16Y+R320K+R458K+Y295F,N16Y+R320K+S323T+V206L,N16Y+R320K+S323T+Y295F,N16Y+R320K+V206L+Y295F,N16Y+R458K+S323T+V206L,N16Y+R458K+S323T+Y295F,N16Y+R458K+V206L+Y295F,N16Y+S323T+V206L+Y295F,N195F+N54S+Q169E+Q169E,N195F+N54S+Q169E+Q172K,N195F+N54S+Q169E+Q299Y,N195F+N54S+Q169E+Q345R,N195F+N54S+Q169E+Q365S,N195F+N54S+Q169E+R320K,N195F+N54S+Q169E+R458K,N195F+N54S+Q169E+S323T,N195F+N54S+Q169E+V206L,N195F+N54S+Q169E+Y295F,N195F+N54S+Q172K+Q299Y,N195F+N54S+Q172K+Q345R,N195F+N54S+Q172K+Q365S,N195F+N54S+Q172K+R320K,N195F+N54S+Q172K+R458K,N195F+N54S+Q172K+S323T,N195F+N54S+Q172K+V206L,N195F+N54S+Q172K+Y295F,N195F+N54S+Q299Y+Q345R,N195F+N54S+Q299Y+Q365S,N195F+N5

24 Mar 2026
2026202266

4S+Q299Y+R320K,N195F+N54S+Q299Y+R458K,N195F+N54S+Q299Y+S323T,N195F+N54S
+Q299Y+V206L,N195F+N54S+Q299Y+Y295F,N195F+N54S+Q345R+Q365S,N195F+N54S+Q
345R+R320K,N195F+N54S+Q345R+R458K,N195F+N54S+Q345R+S323T,N195F+N54S+Q34
5R+V206L,N195F+N54S+Q345R+Y295F,N195F+N54S+Q365S+R320K,N195F+N54S+Q365S
+R458K,N195F+N54S+Q365S+S323T,N195F+N54S+Q365S+V206L,N195F+N54S+Q365S+Y
295F,N195F+N54S+R320K+R458K,N195F+N54S+R320K+S323T,N195F+N54S+R320K+V206
L,N195F+N54S+R320K+Y295F,N195F+N54S+R458K+S323T,N195F+N54S+R458K+V206L,N
195F+N54S+R458K+Y295F,N195F+N54S+S323T+V206L,N195F+N54S+S323T+Y295F,N195
F+N54S+V206L+Y295F,N195F+Q169E+Q169E+Q172K,N195F+Q169E+Q169E+Q299Y,N195
F+Q169E+Q169E+Q345R,N195F+Q169E+Q169E+Q365S,N195F+Q169E+Q169E+R320K,N1
95F+Q169E+Q169E+R458K,N195F+Q169E+Q169E+S323T,N195F+Q169E+Q169E+V206L,N
195F+Q169E+Q169E+Y295F,N195F+Q169E+Q172K+Q299Y,N195F+Q169E+Q172K+Q345R,
N195F+Q169E+Q172K+Q365S,N195F+Q169E+Q172K+R320K,N195F+Q169E+Q172K+R458
K,N195F+Q169E+Q172K+S323T,N195F+Q169E+Q172K+V206L,N195F+Q169E+Q172K+Y29
5F,N195F+Q169E+Q299Y+Q345R,N195F+Q169E+Q299Y+Q365S,N195F+Q169E+Q299Y+R3
20K,N195F+Q169E+Q299Y+R458K,N195F+Q169E+Q299Y+S323T,N195F+Q169E+Q299Y+V
206L,N195F+Q169E+Q299Y+Y295F,N195F+Q169E+Q345R+Q365S,N195F+Q169E+Q345R+
R320K,N195F+Q169E+Q345R+R458K,N195F+Q169E+Q345R+S323T,N195F+Q169E+Q345R
+V206L,N195F+Q169E+Q345R+Y295F,N195F+Q169E+Q365S+R320K,N195F+Q169E+Q365
S+R458K,N195F+Q169E+Q365S+S323T,N195F+Q169E+Q365S+V206L,N195F+Q169E+Q36
5S+Y295F,N195F+Q169E+R320K+R458K,N195F+Q169E+R320K+S323T,N195F+Q169E+R3
20K+V206L,N195F+Q169E+R320K+Y295F,N195F+Q169E+R458K+S323T,N195F+Q169E+R4
58K+V206L,N195F+Q169E+R458K+Y295F,N195F+Q169E+S323T+V206L,N195F+Q169E+S3
23T+Y295F,N195F+Q169E+V206L+Y295F,N195F+Q169E+Q172K+Q299Y,N195F+Q169E+Q1
72K+Q345R,N195F+Q169E+Q172K+Q365S,N195F+Q169E+Q172K+R320K,N195F+Q169E+
Q172K+R458K,N195F+Q169E+Q172K+S323T,N195F+Q169E+Q172K+V206L,N195F+Q169E
+Q172K+Y295F,N195F+Q169E+Q299Y+Q345R,N195F+Q169E+Q299Y+Q365S,N195F+Q169
E+Q299Y+R320K,N195F+Q169E+Q299Y+R458K,N195F+Q169E+Q299Y+S323T,N195F+Q16
9E+Q299Y+V206L,N195F+Q169E+Q299Y+Y295F,N195F+Q169E+Q345R+Q365S,N195F+Q1
69E+Q345R+R320K,N195F+Q169E+Q345R+R458K,N195F+Q169E+Q345R+S323T,N195F+Q
169E+Q345R+V206L,N195F+Q169E+Q345R+Y295F,N195F+Q169E+Q365S+R320K,N195F+
Q169E+Q365S+R458K,N195F+Q169E+Q365S+S323T,N195F+Q169E+Q365S+V206L,N195F
+Q169E+Q365S+Y295F,N195F+Q169E+R320K+R458K,N195F+Q169E+R320K+S323T,N195
F+Q169E+R320K+V206L,N195F+Q169E+R320K+Y295F,N195F+Q169E+R458K+S323T,N195
F+Q169E+R458K+V206L,N195F+Q169E+R458K+Y295F,N195F+Q169E+S323T+V206L,N195
F+Q169E+S323T+Y295F,N195F+Q169E+V206L+Y295F,N195F+Q172K+Q299Y+Q345R,N195

24 Mar 2026
2026202266

F+Q172K+Q299Y+Q365S,N195F+Q172K+Q299Y+R320K,N195F+Q172K+Q299Y+R458K,N19
5F+Q172K+Q299Y+S323T,N195F+Q172K+Q299Y+V206L,N195F+Q172K+Q299Y+Y295F,N1
95F+Q172K+Q345R+Q365S,N195F+Q172K+Q345R+R320K,N195F+Q172K+Q345R+R458K,
N195F+Q172K+Q345R+S323T,N195F+Q172K+Q345R+V206L,N195F+Q172K+Q345R+Y295F
,N195F+Q172K+Q365S+R320K,N195F+Q172K+Q365S+R458K,N195F+Q172K+Q365S+S323
T,N195F+Q172K+Q365S+V206L,N195F+Q172K+Q365S+Y295F,N195F+Q172K+R320K+R45
8K,N195F+Q172K+R320K+S323T,N195F+Q172K+R320K+V206L,N195F+Q172K+R320K+Y29
5F,N195F+Q172K+R458K+S323T,N195F+Q172K+R458K+V206L,N195F+Q172K+R458K+Y29
5F,N195F+Q172K+S323T+V206L,N195F+Q172K+S323T+Y295F,N195F+Q172K+V206L+Y29
5F,N195F+Q299Y+Q345R+Q365S,N195F+Q299Y+Q345R+R320K,N195F+Q299Y+Q345R+R
458K,N195F+Q299Y+Q345R+S323T,N195F+Q299Y+Q345R+V206L,N195F+Q299Y+Q345R+
Y295F,N195F+Q299Y+Q365S+R320K,N195F+Q299Y+Q365S+R458K,N195F+Q299Y+Q365S
+S323T,N195F+Q299Y+Q365S+V206L,N195F+Q299Y+Q365S+Y295F,N195F+Q299Y+R320K
+R458K,N195F+Q299Y+R320K+S323T,N195F+Q299Y+R320K+V206L,N195F+Q299Y+R320K
+Y295F,N195F+Q299Y+R458K+S323T,N195F+Q299Y+R458K+V206L,N195F+Q299Y+R458K
+Y295F,N195F+Q299Y+S323T+V206L,N195F+Q299Y+S323T+Y295F,N195F+Q299Y+V206L
+Y295F,N195F+Q345R+Q365S+R320K,N195F+Q345R+Q365S+R458K,N195F+Q345R+Q365
S+S323T,N195F+Q345R+Q365S+V206L,N195F+Q345R+Q365S+Y295F,N195F+Q345R+R32
0K+R458K,N195F+Q345R+R320K+S323T,N195F+Q345R+R320K+V206L,N195F+Q345R+R3
20K+Y295F,N195F+Q345R+R458K+S323T,N195F+Q345R+R458K+V206L,N195F+Q345R+R
458K+Y295F,N195F+Q345R+S323T+V206L,N195F+Q345R+S323T+Y295F,N195F+Q345R+V
206L+Y295F,N195F+Q365S+R320K+R458K,N195F+Q365S+R320K+S323T,N195F+Q365S+R
320K+V206L,N195F+Q365S+R320K+Y295F,N195F+Q365S+R458K+S323T,N195F+Q365S+R
458K+V206L,N195F+Q365S+R458K+Y295F,N195F+Q365S+S323T+V206L,N195F+Q365S+S
323T+Y295F,N195F+Q365S+V206L+Y295F,N195F+R320K+R458K+S323T,N195F+R320K+R
458K+V206L,N195F+R320K+R458K+Y295F,N195F+R320K+S323T+V206L,N195F+R320K+S
323T+Y295F,N195F+R320K+V206L+Y295F,N195F+R458K+S323T+V206L,N195F+R458K+S3
23T+Y295F,N195F+R458K+V206L+Y295F,N195F+S323T+V206L+Y295F,N54S+Q169E+Q169
E+Q172K,N54S+Q169E+Q169E+Q299Y,N54S+Q169E+Q169E+Q345R,N54S+Q169E+Q169E
+Q365S,N54S+Q169E+Q169E+R320K,N54S+Q169E+Q169E+R458K,N54S+Q169E+Q169E+
S323T,N54S+Q169E+Q169E+V206L,N54S+Q169E+Q169E+Y295F,N54S+Q169E+Q172K+Q2
99Y,N54S+Q169E+Q172K+Q345R,N54S+Q169E+Q172K+Q365S,N54S+Q169E+Q172K+R32
0K,N54S+Q169E+Q172K+R458K,N54S+Q169E+Q172K+S323T,N54S+Q169E+Q172K+V206L
,N54S+Q169E+Q172K+Y295F,N54S+Q169E+Q299Y+Q345R,N54S+Q169E+Q299Y+Q365S,N
54S+Q169E+Q299Y+R320K,N54S+Q169E+Q299Y+R458K,N54S+Q169E+Q299Y+S323T,N54
S+Q169E+Q299Y+V206L,N54S+Q169E+Q299Y+Y295F,N54S+Q169E+Q345R+Q365S,N54S

24 Mar 2026
2026202266

+Q169E+Q345R+R320K,N54S+Q169E+Q345R+R458K,N54S+Q169E+Q345R+S323T,N54S+Q169E+Q345R+V206L,N54S+Q169E+Q345R+Y295F,N54S+Q169E+Q365S+R320K,N54S+Q169E+Q365S+R458K,N54S+Q169E+Q365S+S323T,N54S+Q169E+Q365S+V206L,N54S+Q169E+Q365S+Y295F,N54S+Q169E+R320K+R458K,N54S+Q169E+R320K+S323T,N54S+Q169E+R320K+V206L,N54S+Q169E+R320K+Y295F,N54S+Q169E+R458K+S323T,N54S+Q169E+R458K+V206L,N54S+Q169E+R458K+Y295F,N54S+Q169E+S323T+V206L,N54S+Q169E+S323T+Y295F,N54S+Q169E+V206L+Y295F,N54S+Q169E+Q172K+Q299Y,N54S+Q169E+Q172K+Q345R,N54S+Q169E+Q172K+Q365S,N54S+Q169E+Q172K+R320K,N54S+Q169E+Q172K+R458K,N54S+Q169E+Q172K+S323T,N54S+Q169E+Q172K+V206L,N54S+Q169E+Q172K+Y295F,N54S+Q169E+Q299Y+Q345R,N54S+Q169E+Q299Y+Q365S,N54S+Q169E+Q299Y+R320K,N54S+Q169E+Q299Y+R458K,N54S+Q169E+Q299Y+S323T,N54S+Q169E+Q299Y+V206L,N54S+Q169E+Q299Y+Y295F,N54S+Q169E+Q345R+Q365S,N54S+Q169E+Q345R+R320K,N54S+Q169E+Q345R+R458K,N54S+Q169E+Q345R+S323T,N54S+Q169E+Q345R+V206L,N54S+Q169E+Q345R+Y295F,N54S+Q169E+Q365S+R320K,N54S+Q169E+Q365S+R458K,N54S+Q169E+Q365S+S323T,N54S+Q169E+Q365S+V206L,N54S+Q169E+Q365S+Y295F,N54S+Q169E+R320K+R458K,N54S+Q169E+R320K+S323T,N54S+Q169E+R320K+V206L,N54S+Q169E+R320K+Y295F,N54S+Q169E+R458K+S323T,N54S+Q169E+R458K+V206L,N54S+Q169E+R458K+Y295F,N54S+Q169E+S323T+V206L,N54S+Q169E+S323T+Y295F,N54S+Q169E+V206L+Y295F,N54S+Q172K+Q299Y+Q345R,N54S+Q172K+Q299Y+Q365S,N54S+Q172K+Q299Y+R320K,N54S+Q172K+Q299Y+R458K,N54S+Q172K+Q299Y+S323T,N54S+Q172K+Q299Y+V206L,N54S+Q172K+Q299Y+Y295F,N54S+Q172K+Q345R+Q365S,N54S+Q172K+Q345R+R320K,N54S+Q172K+Q345R+R458K,N54S+Q172K+Q345R+S323T,N54S+Q172K+Q345R+V206L,N54S+Q172K+Q345R+Y295F,N54S+Q172K+Q365S+R320K,N54S+Q172K+Q365S+R458K,N54S+Q172K+Q365S+S323T,N54S+Q172K+Q365S+V206L,N54S+Q172K+Q365S+Y295F,N54S+Q172K+R320K+R458K,N54S+Q172K+R320K+S323T,N54S+Q172K+R320K+V206L,N54S+Q172K+R320K+Y295F,N54S+Q172K+R458K+S323T,N54S+Q172K+R458K+V206L,N54S+Q172K+R458K+Y295F,N54S+Q172K+S323T+V206L,N54S+Q172K+S323T+Y295F,N54S+Q172K+V206L+Y295F,N54S+Q299Y+Q345R+Q365S,N54S+Q299Y+Q345R+R320K,N54S+Q299Y+Q345R+R458K,N54S+Q299Y+Q345R+S323T,N54S+Q299Y+Q345R+V206L,N54S+Q299Y+Q345R+Y295F,N54S+Q299Y+Q365S+R320K,N54S+Q299Y+Q365S+R458K,N54S+Q299Y+Q365S+S323T,N54S+Q299Y+Q365S+V206L,N54S+Q299Y+Q365S+Y295F,N54S+Q299Y+R320K+R458K,N54S+Q299Y+R320K+S323T,N54S+Q299Y+R320K+V206L,N54S+Q299Y+R320K+Y295F,N54S+Q299Y+R458K+S323T,N54S+Q299Y+R458K+V206L,N54S+Q299Y+R458K+Y295F,N54S+Q299Y+S323T+V206L,N54S+Q299Y+S323T+Y295F,N54S+Q299Y+V206L+Y295F,N54S+Q345R+Q365S+R320K,N54S+Q345R+Q365S+R458K,N54S+Q345R+Q365S+S323T,N54S+Q345R+Q365S+V206L,N54S+Q345R+Q365S+Y295F,N54S+Q345R+R320K+R458

24 Mar 2026
2026202266

K,N54S+Q345R+R320K+S323T,N54S+Q345R+R320K+V206L,N54S+Q345R+R320K+Y295F,
N54S+Q345R+R458K+S323T,N54S+Q345R+R458K+V206L,N54S+Q345R+R458K+Y295F,N5
4S+Q345R+S323T+V206L,N54S+Q345R+S323T+Y295F,N54S+Q345R+V206L+Y295F,N54S+
Q365S+R320K+R458K,N54S+Q365S+R320K+S323T,N54S+Q365S+R320K+V206L,N54S+Q3
65S+R320K+Y295F,N54S+Q365S+R458K+S323T,N54S+Q365S+R458K+V206L,N54S+Q365
S+R458K+Y295F,N54S+Q365S+S323T+V206L,N54S+Q365S+S323T+Y295F,N54S+Q365S+
V206L+Y295F,N54S+R320K+R458K+S323T,N54S+R320K+R458K+V206L,N54S+R320K+R45
8K+Y295F,N54S+R320K+S323T+V206L,N54S+R320K+S323T+Y295F,N54S+R320K+V206L+
Y295F,N54S+R458K+S323T+V206L,N54S+R458K+S323T+Y295F,N54S+R458K+V206L+Y29
5F,N54S+S323T+V206L+Y295F,Q169E+Q169E+Q172K+Q299Y,Q169E+Q169E+Q172K+Q34
5R,Q169E+Q169E+Q172K+Q365S,Q169E+Q169E+Q172K+R320K,Q169E+Q169E+Q172K+R
458K,Q169E+Q169E+Q172K+S323T,Q169E+Q169E+Q172K+V206L,Q169E+Q169E+Q172K+
Y295F,Q169E+Q169E+Q299Y+Q345R,Q169E+Q169E+Q299Y+Q365S,Q169E+Q169E+Q299
Y+R320K,Q169E+Q169E+Q299Y+R458K,Q169E+Q169E+Q299Y+S323T,Q169E+Q169E+Q2
99Y+V206L,Q169E+Q169E+Q299Y+Y295F,Q169E+Q169E+Q345R+Q365S,Q169E+Q169E+
Q345R+R320K,Q169E+Q169E+Q345R+R458K,Q169E+Q169E+Q345R+S323T,Q169E+Q169
E+Q345R+V206L,Q169E+Q169E+Q345R+Y295F,Q169E+Q169E+Q365S+R320K,Q169E+Q1
69E+Q365S+R458K,Q169E+Q169E+Q365S+S323T,Q169E+Q169E+Q365S+V206L,Q169E+Q
169E+Q365S+Y295F,Q169E+Q169E+R320K+R458K,Q169E+Q169E+R320K+S323T,Q169E+
Q169E+R320K+V206L,Q169E+Q169E+R320K+Y295F,Q169E+Q169E+R458K+S323T,Q169E
+Q169E+R458K+V206L,Q169E+Q169E+R458K+Y295F,Q169E+Q169E+S323T+V206L,Q169
E+Q169E+S323T+Y295F,Q169E+Q169E+V206L+Y295F,Q169E+Q172K+Q299Y+Q345R,Q16
9E+Q172K+Q299Y+Q365S,Q169E+Q172K+Q299Y+R320K,Q169E+Q172K+Q299Y+R458K,Q
169E+Q172K+Q299Y+S323T,Q169E+Q172K+Q299Y+V206L,Q169E+Q172K+Q299Y+Y295F,
Q169E+Q172K+Q345R+Q365S,Q169E+Q172K+Q345R+R320K,Q169E+Q172K+Q345R+R45
8K,Q169E+Q172K+Q345R+S323T,Q169E+Q172K+Q345R+V206L,Q169E+Q172K+Q345R+Y
295F,Q169E+Q172K+Q365S+R320K,Q169E+Q172K+Q365S+R458K,Q169E+Q172K+Q365S+
S323T,Q169E+Q172K+Q365S+V206L,Q169E+Q172K+Q365S+Y295F,Q169E+Q172K+R320K
+R458K,Q169E+Q172K+R320K+S323T,Q169E+Q172K+R320K+V206L,Q169E+Q172K+R320
K+Y295F,Q169E+Q172K+R458K+S323T,Q169E+Q172K+R458K+V206L,Q169E+Q172K+R45
8K+Y295F,Q169E+Q172K+S323T+V206L,Q169E+Q172K+S323T+Y295F,Q169E+Q172K+V20
6L+Y295F,Q169E+Q299Y+Q345R+Q365S,Q169E+Q299Y+Q345R+R320K,Q169E+Q299Y+Q
345R+R458K,Q169E+Q299Y+Q345R+S323T,Q169E+Q299Y+Q345R+V206L,Q169E+Q299Y+
Q345R+Y295F,Q169E+Q299Y+Q365S+R320K,Q169E+Q299Y+Q365S+R458K,Q169E+Q299
Y+Q365S+S323T,Q169E+Q299Y+Q365S+V206L,Q169E+Q299Y+Q365S+Y295F,Q169E+Q29
9Y+R320K+R458K,Q169E+Q299Y+R320K+S323T,Q169E+Q299Y+R320K+V206L,Q169E+Q2

24 Mar 2026
2026202266

99Y+R320K+Y295F,Q169E+Q299Y+R458K+S323T,Q169E+Q299Y+R458K+V206L,Q169E+Q299Y+R458K+Y295F,Q169E+Q299Y+S323T+V206L,Q169E+Q299Y+S323T+Y295F,Q169E+Q299Y+V206L+Y295F,Q169E+Q345R+Q365S+R320K,Q169E+Q345R+Q365S+R458K,Q169E+Q345R+Q365S+S323T,Q169E+Q345R+Q365S+V206L,Q169E+Q345R+Q365S+Y295F,Q169E+Q345R+R320K+R458K,Q169E+Q345R+R320K+S323T,Q169E+Q345R+R320K+V206L,Q169E+Q345R+R320K+Y295F,Q169E+Q345R+R458K+S323T,Q169E+Q345R+R458K+V206L,Q169E+Q345R+R458K+Y295F,Q169E+Q345R+S323T+V206L,Q169E+Q345R+S323T+Y295F,Q169E+Q345R+V206L+Y295F,Q169E+Q365S+R320K+R458K,Q169E+Q365S+R320K+S323T,Q169E+Q365S+R320K+V206L,Q169E+Q365S+R320K+Y295F,Q169E+Q365S+R458K+S323T,Q169E+Q365S+R458K+V206L,Q169E+Q365S+R458K+Y295F,Q169E+Q365S+S323T+V206L,Q169E+Q365S+S323T+Y295F,Q169E+Q365S+V206L+Y295F,Q169E+R320K+R458K+S323T,Q169E+R320K+R458K+V206L,Q169E+R320K+R458K+Y295F,Q169E+R320K+S323T+V206L,Q169E+R320K+S323T+Y295F,Q169E+R320K+V206L+Y295F,Q169E+R458K+S323T+V206L,Q169E+R458K+S323T+Y295F,Q169E+R458K+V206L+Y295F,Q169E+S323T+V206L+Y295F,Q169E+Q172K+Q299Y+Q345R,Q169E+Q172K+Q299Y+Q365S,Q169E+Q172K+Q299Y+R320K,Q169E+Q172K+Q299Y+R458K,Q169E+Q172K+Q299Y+S323T,Q169E+Q172K+Q299Y+V206L,Q169E+Q172K+Q299Y+Y295F,Q169E+Q172K+Q345R+Q365S,Q169E+Q172K+Q345R+R320K,Q169E+Q172K+Q345R+R458K,Q169E+Q172K+Q345R+S323T,Q169E+Q172K+Q345R+V206L,Q169E+Q172K+Q345R+Y295F,Q169E+Q172K+Q365S+R320K,Q169E+Q172K+Q365S+R458K,Q169E+Q172K+Q365S+S323T,Q169E+Q172K+Q365S+V206L,Q169E+Q172K+Q365S+Y295F,Q169E+Q172K+R320K+R458K,Q169E+Q172K+R320K+S323T,Q169E+Q172K+R320K+V206L,Q169E+Q172K+R320K+Y295F,Q169E+Q172K+R458K+S323T,Q169E+Q172K+R458K+V206L,Q169E+Q172K+R458K+Y295F,Q169E+Q172K+S323T+V206L,Q169E+Q172K+S323T+Y295F,Q169E+Q172K+V206L+Y295F,Q169E+Q299Y+Q345R+Q365S,Q169E+Q299Y+Q345R+R320K,Q169E+Q299Y+Q345R+R458K,Q169E+Q299Y+Q345R+S323T,Q169E+Q299Y+Q345R+V206L,Q169E+Q299Y+Q345R+Y295F,Q169E+Q299Y+Q365S+R320K,Q169E+Q299Y+Q365S+R458K,Q169E+Q299Y+Q365S+S323T,Q169E+Q299Y+Q365S+V206L,Q169E+Q299Y+Q365S+Y295F,Q169E+Q299Y+R320K+R458K,Q169E+Q299Y+R320K+S323T,Q169E+Q299Y+R320K+V206L,Q169E+Q299Y+R320K+Y295F,Q169E+Q299Y+R458K+S323T,Q169E+Q299Y+R458K+V206L,Q169E+Q299Y+R458K+Y295F,Q169E+Q299Y+S323T+V206L,Q169E+Q299Y+S323T+Y295F,Q169E+Q299Y+V206L+Y295F,Q169E+Q345R+Q365S+R320K,Q169E+Q345R+Q365S+R458K,Q169E+Q345R+Q365S+S323T,Q169E+Q345R+Q365S+V206L,Q169E+Q345R+Q365S+Y295F,Q169E+Q345R+R320K+R458K,Q169E+Q345R+R320K+S323T,Q169E+Q345R+R320K+V206L,Q169E+Q345R+R320K+Y295F,Q169E+Q345R+R458K+S323T,Q169E+Q345R+R458K+V206L,Q169E+Q345R+R458K+Y295F,Q169E+Q345R+S323T+V206L,Q169E+Q345R+S323T+Y295F,Q169E+Q345R+V206L+Y295F,Q169E+Q365S+R320K+R

24 Mar 2026
2026202266

458K,Q169E+Q365S+R320K+S323T,Q169E+Q365S+R320K+V206L,Q169E+Q365S+R320K+Y295F,Q169E+Q365S+R458K+S323T,Q169E+Q365S+R458K+V206L,Q169E+Q365S+R458K+Y295F,Q169E+Q365S+S323T+V206L,Q169E+Q365S+S323T+Y295F,Q169E+Q365S+V206L+Y295F,Q169E+R320K+R458K+S323T,Q169E+R320K+R458K+V206L,Q169E+R320K+R458K+Y295F,Q169E+R320K+S323T+V206L,Q169E+R320K+S323T+Y295F,Q169E+R320K+V206L+Y295F,Q169E+R458K+S323T+V206L,Q169E+R458K+S323T+Y295F,Q169E+R458K+V206L+Y295F,Q169E+S323T+V206L+Y295F,Q172K+Q299Y+Q345R+Q365S,Q172K+Q299Y+Q345R+R320K,Q172K+Q299Y+Q345R+R458K,Q172K+Q299Y+Q345R+S323T,Q172K+Q299Y+Q345R+V206L,Q172K+Q299Y+Q345R+Y295F,Q172K+Q299Y+Q365S+R320K,Q172K+Q299Y+Q365S+R458K,Q172K+Q299Y+Q365S+S323T,Q172K+Q299Y+Q365S+V206L,Q172K+Q299Y+Q365S+Y295F,Q172K+Q299Y+R320K+R458K,Q172K+Q299Y+R320K+S323T,Q172K+Q299Y+R320K+V206L,Q172K+Q299Y+R320K+Y295F,Q172K+Q299Y+R458K+S323T,Q172K+Q299Y+R458K+V206L,Q172K+Q299Y+R458K+Y295F,Q172K+Q299Y+S323T+V206L,Q172K+Q299Y+S323T+Y295F,Q172K+Q299Y+V206L+Y295F,Q172K+Q345R+Q365S+R320K,Q172K+Q345R+Q365S+R458K,Q172K+Q345R+Q365S+S323T,Q172K+Q345R+Q365S+V206L,Q172K+Q345R+Q365S+Y295F,Q172K+Q345R+R320K+R458K,Q172K+Q345R+R320K+S323T,Q172K+Q345R+R320K+V206L,Q172K+Q345R+R320K+Y295F,Q172K+Q345R+R458K+S323T,Q172K+Q345R+R458K+V206L,Q172K+Q345R+R458K+Y295F,Q172K+Q345R+S323T+V206L,Q172K+Q345R+S323T+Y295F,Q172K+Q345R+V206L+Y295F,Q172K+Q365S+R320K+R458K,Q172K+Q365S+R320K+S323T,Q172K+Q365S+R320K+V206L,Q172K+Q365S+R320K+Y295F,Q172K+Q365S+R458K+S323T,Q172K+Q365S+R458K+V206L,Q172K+Q365S+R458K+Y295F,Q172K+Q365S+S323T+V206L,Q172K+Q365S+S323T+Y295F,Q172K+Q365S+V206L+Y295F,Q172K+R320K+R458K+S323T,Q172K+R320K+R458K+V206L,Q172K+R320K+R458K+Y295F,Q172K+R320K+S323T+V206L,Q172K+R320K+S323T+Y295F,Q172K+R320K+V206L+Y295F,Q172K+R458K+S323T+V206L,Q172K+R458K+S323T+Y295F,Q172K+R458K+V206L+Y295F,Q172K+S323T+V206L+Y295F,Q299Y+Q345R+Q365S+R320K,Q299Y+Q345R+Q365S+R458K,Q299Y+Q345R+Q365S+S323T,Q299Y+Q345R+Q365S+V206L,Q299Y+Q345R+Q365S+Y295F,Q299Y+Q345R+R320K+R458K,Q299Y+Q345R+R320K+S323T,Q299Y+Q345R+R320K+V206L,Q299Y+Q345R+R320K+Y295F,Q299Y+Q345R+R458K+S323T,Q299Y+Q345R+R458K+V206L,Q299Y+Q345R+R458K+Y295F,Q299Y+Q345R+S323T+V206L,Q299Y+Q345R+S323T+Y295F,Q299Y+Q345R+V206L+Y295F,Q299Y+Q365S+R320K+R458K,Q299Y+Q365S+R320K+S323T,Q299Y+Q365S+R320K+V206L,Q299Y+Q365S+R320K+Y295F,Q299Y+Q365S+R458K+S323T,Q299Y+Q365S+R458K+V206L,Q299Y+Q365S+R458K+Y295F,Q299Y+Q365S+S323T+V206L,Q299Y+Q365S+S323T+Y295F,Q299Y+Q365S+V206L+Y295F,Q299Y+R320K+R458K+S323T,Q299Y+R320K+R458K+V206L,Q299Y+R320K+R458K+Y295F,Q299Y+R320K+S323T+V206L,Q299Y+R320K+S323T+Y295F,Q299Y+R320K+V206L+Y295F,

24 Mar 2026
2026202266

Q299Y+R458K+S323T+V206L,Q299Y+R458K+S323T+Y295F,Q299Y+R458K+V206L+Y295F,Q299Y+S323T+V206L+Y295F,Q345R+Q365S+R320K+R458K,Q345R+Q365S+R320K+S323T,Q345R+Q365S+R320K+V206L,Q345R+Q365S+R320K+Y295F,Q345R+Q365S+R458K+S323T,Q345R+Q365S+R458K+V206L,Q345R+Q365S+R458K+Y295F,Q345R+Q365S+S323T+V206L,Q345R+Q365S+S323T+Y295F,Q345R+Q365S+V206L+Y295F,Q345R+R320K+R458K+S323T,Q345R+R320K+R458K+V206L,Q345R+R320K+R458K+Y295F,Q345R+R320K+S323T+V206L,Q345R+R320K+S323T+Y295F,Q345R+R320K+V206L+Y295F,Q345R+R458K+S323T+V206L,Q345R+R458K+S323T+Y295F,Q345R+R458K+V206L+Y295F,Q345R+S323T+V206L+Y295F,Q365S+R320K+R458K+S323T,Q365S+R320K+R458K+V206L,Q365S+R320K+R458K+Y295F,Q365S+R320K+S323T+V206L,Q365S+R320K+S323T+Y295F,Q365S+R320K+V206L+Y295F,Q365S+R458K+S323T+V206L,Q365S+R458K+S323T+Y295F,Q365S+R458K+V206L+Y295F,Q365S+S323T+V206L+Y295F,R320K+R458K+S323T+V206L,R320K+R458K+S323T+Y295F,R320K+R458K+V206L+Y295F,R320K+S323T+V206L+Y295F,R458K+S323T+V206L+Y295F, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID Nos; 1-17.

In one aspect, the variant comprises one or more of the following modification at a position corresponding to positions: H1* + N16Y + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L + V206L + Q365S + K391A, H1* + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L + V206L + Q365S + K391A, H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has at least 60%, at least 65%, at least 70%, 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% sequence identity to the polypeptide of SEQ ID Nos; 1-17.

The inventors of the present invention have identified that these specific modification at these positions of the amino acid sequence as set forth in SEQ ID NO: 1 or 2, are particularly relevant for improving the performance of a variant alpha-amylase having at least 60% sequence identity to the parent polypeptide.

According to the present invention, a value of 1.0 corresponds to the performance observed for the parent polypeptide. A value above 1.0 indicates an improvement of performance of the variant tested compared to the parent polypeptide. Accordingly, any value of > 1.0 is indicative for improvement of property, such as performance, of the variant compared to the parent polypeptide.

24 Mar 2026
2026202266

According to the present invention, a variant showing improvement of property under at least one condition tested, is considered a variant having improved property as compared to the parent polypeptide.

As stated elsewhere herein, the parent polypeptide may be any polypeptide having alpha-amylase activity and at least 60% sequence identity to any one of the amino acid sequences as set forth in SEQ ID NO: 2.

As can be seen from the data obtained in Examples 3, 4 and 5, all tested variants have an Improvement Factor (IF) of at least 1.1, *i.e.* above the parent polypeptide having SEQ ID NO: 2, when tested in either

(i) a Model A detergent and an enzyme concentration of 0.1mg/L,

(ii) a ADW detergent Model at 45°C and an enzyme concentration of 0.35mg/L,

(iii) a ADW detergent Model at 40°C and an enzyme concentration of 1.5mg/L, or

(iv) a ADW detergent at 45°C and an enzyme concentration of 0.9mg/L.

In one embodiment, the variant has an improved wash performance, the enhanced wash performance corresponding to an Improvement Factor (IF) of at least 1.1, preferably at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 1.6, at least 1.7, at least 1.8, at least 1.9, at least 2.0, at least 2.2, at least 2.4, at least 2.6, at least 2.8, at least 3.0, at least 3.2, at least 3.4, at least 3.6, at least 3.8, or at least 4.0 when compared to said parent alpha-amylase having alpha-amylase activity wherein said IF is determined by using Model A detergent compostion and/or ADW detergent composition and wherein said parent alpha-amylase has amino acid sequence as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

In one aspect, the variant is selected from a group consisting of:

A60T

Y135H

Q169E

W48Y

A174*

M246L

R90Q

Y203L+V206L

Q169F+S170A

S132D+G133D

N195F+Q365C

N195F+Q365S

N195F+Q365M

R127L+Q365S

24 Mar 2026
2026202266

R127N+Q365S
R127L+Q365C
N195F+Q365K
I9M+N195F
R171H+Q365C
Y267F+Q365S
F328L+Q365S
R171L+Q365S
N195F+M286L
T134P+N195F
S170*+R171*+A174*
V264I+A265G+Y267F
Q169*+S170*+A174*
M246L+L275V+Q365S
V264I+V291I+Q365S
V264I+V291T+Q365K
V264I+F328L+Q365C
I9M+N195F+Q365C
Q11H+Y267F+Q365C
I9M +N195F+Q365S
V264I+Y267F+Q365K
R127L+M246V+Q365S
A60S+R171Y+Q365S
R127N+M246T+L275V
V104A+N195F+Q365S
V264I+F328L+Q365S
R171H+N302H+Q365S
V264I+Y267F+Q365S
A174*+N175*+Y178F
V264I+A265G+Q365C
R171L+N302H+Q365C
R171L+M246V+Q365C
R171Y+M246L+Q365S
V264T+Y267F+Q365S
I9M+Y160H+N195F+Q365S
I9M+R127N+N195F+Q365S

24 Mar 2026
2026202266

R127H+L235I+Q365S+G435C
I9M+R171H+N195F+Q365S
I9M+A186H+N195F+Q365S
I9M+R171L+N195F+Q365S
Q169*+S170*+R171*+A174*
M246L+L275V+Q365S+D406H
I9M+G184K+N195F+Q365S
R127N+M246L+L275V+Q365S
R171H+M246L+L275V+Q365S
R127H+M246I+Q365C+V481A
Y267F+V291A+F328L+Q365C
I9M+A186E+N195F+Q365S
E86L+R171L+N306R+Q365S
V264I+Y267F+F328L+Q365S
I9M+N195F+V291A+Q365S
R127L+L235I+M246I+Q365C
Y267F+V291A+F328L+Q365S
V264I+Y267F+F328L+Q365K
Q11H+V264I+A265G+Q365C
W187M+N195F+H210K+Q365S
R127H+M246T+L275A+Q365S
I9M+A111T+N195F+Q365S
I9M+Y58F+N195F+Q365S
V264T+V291A+F328L+Q365S
V264I+A265G+V291A+Q365C
V264I+A265G+Y267F+Q365C
V264I+Y267F+V291A+F328L+Q365S
R127N+R171H+M246L+L275V+Q365S
V264I+A265G+V291A+F328L+Q365S
R127N+M246I+A265G+Y267H+Q365S
E130I+T134A+R181N+N195F+Q365S
R127N+M246L+L275V+N306R+Q365S
I9M+N195F+V206L+D209N+Q365S
R116S+S132F+R181N+N195F+Q365S
E130T+T134Y+A186K+N195F+Q365S
A37V+V264I+Y267F+F328L+Q365C

24 Mar 2026
2026202266

Q11H+V264I+Y267F+F328L+Q365C
V264I+Y267F+V291T+F328L+Q365S
Q169*+R171*+Q172*+L173*+A174*
R116Y+S132P+Q136N+N195F+Q365S
N195F+G337D+Q365S+P375K+D377Y
V264I+A265G+Y267F+F328L+Q365S
I9M+N195F+K269Q+A274K+Q365S
E130D+T134Y+R181H+N195F+Q365S
R116N+S132M+Q136R+N195F+Q365S
N195F+G337D+Q365S+P375K+D377N
R127N+R171L+M246L+L275V+Q365S
N195F+G337E+Q365S+P375K+D377N
Q11H+V264I+A265G+Y267F+Q365C
R158Q+Y160N+W187M+N195F+Q365S
V264I+Y267F+Q365K+W408H+V410I
R127N+R171Y+M246L+L275V+Q365S
N54Q+F113T+R171H+N302A+Q365C
V264A+Y267F+V291T+F328L+Q365C
Q169*+S170*+R171*+Q172*+L173*+A174*
R116K+S132L+Q136R+R181C+N195F+Q365S
V264T+A265G+Y267F+V291A+F328L+Q365C
E130N+T134S+R181N+A186K+N195F+Q365S
E130V+T134N+R181Y+A186K+N195F+Q365S
E130D+T134W+R181KA186E+N195F+Q365S
R116N+S132A+Q136D+R181K+N195F+Q365S
E130S+T134E+R181S+A186T+N195F+Q365S
R116C+S132A+Q136S+R181A+N195F+Q365S
R116K+S132P+Q136D+R181Q+N195F+Q365S
R127H+R171H+M246L+L275V+N306R+Q365S
E130L+T134N+R181W+A186T+N195F+Q365S
R116C+S132M+Q136S+R181Q+N195F+Q365S
R116S+Y135H+Q136G+R181T+N195F+Q365S
R116S+S132L+Q136E+R181G+N195F+Q365S
N16E+N195F+G337E+Q365S+P375T+D377H
V264I+A265G+Y267F+V291I+F328L+Q365S
N16E+N195F+G337D+Q365S+P375K+D377N

24 Mar 2026
2026202266

V264I+A265G+Y267F+F328L+Q365S+Q395K
E130N+T134C+R181Q+A186N+N195F+Q365S
V264I+A265G+Y267F+V291A+F328L+Q365C
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S
A139T+R158S+Y160D+W187M+N195F+H210N+Q365S
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+Y58F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195H+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A
H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A

Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K

H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L

H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A

Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A

H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A

Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K

H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A

A139T +R158S +Y160D +W187M +N195F +H210N +Q365S

A186D +N195F

A60S +R171Y +Q365S

E130D +T134W +R181K +A186E +N195F +Q365S

E130D +T134Y +R181H +N195F +Q365S

E130D+T134W+R181K+A186E+N195F+Q365S

E130F +T134R +R181S +A186D +N195F +Q365S

E130I +T134A +R181N +N195F +Q365S

E130I+T134A+R181N+N195F+Q365S

E130L +T134N +R181W +A186T +N195F +Q365S

E130N +T134C +R181Q +A186N +N195F +Q365S

E130S +T134E +R181S +A186T +N195F +Q365S

E130T +T134Y +A186K +N195F +Q365S

E130V +T134N +R181Y +A186K +N195F +Q365S

E130Y +S132T +T134S +R181E +A186D +N195F +Q365S

E130Y+S132T+T134S+R181E+A186D+N195F+Q365S

E86L +R171L +N306R +Q365S

E86L +Y160H +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K

E86L+R171L+N306R+Q365S

F113Q +R116H

24 Mar 2026
2026202266

F113T +R171K +G273V

F328L +Q365S

G109A+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K

G7A+F113N+R116N+E276N+S304G+R320S+Q345N+W439R+N465G+Q466S+W469Y

H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S

H1* +I9M +N54S +V56T +G109A +F113G +R116H +D163H +Q169E +R171H +Q172K +A174S +G182T +N195F +M202L +V206L +M246L +L275V +A288V +L317V +Q319H +H324K +Q365S +K391A

H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K

H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A

H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A

H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A

H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +Q365S +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L+ V206L +W284Y +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +N306R +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +Q365S +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +V206L +K391A

H1* +N54S +V56T +G109A +R171H +N195F +V206L +K391A

H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A

H1*+I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K +A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S

H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A

H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A

H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A

H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K39

24 Mar 2026

2026202266

1A

H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Q125G+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D377H+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K269M+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L235I+V238A+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311K+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365H+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V238A+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A

H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F

H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Q172S+L173K+A174S+N175*+R176A+N195F+V206L+K391A

H1*+N54S+V56T+G109A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+R116H+Q169E+Q172K+A174*+N195F+V206L+N314Q+Q385L+K391A

H1*+N54S+V56T+G109A+R127F+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A

H1*+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K

I9M +A186E +N195F +Q365S

24 Mar 2026
2026202266

I9M +A186H +N195F +Q365S
I9M +G184K +N195F +Q365S
I9M +N195F +K269Q +A274K +Q365S
I9M +N195F +N270G +Q365S
I9M +N195F +N270P +Q365S
I9M +N195F +Q365C
I9M +N195F +V206L +D209N +Q365S
I9M +N195F +V291A +Q365S
I9M +R127N +N195F +Q365S
I9M +R171H +N195F +Q365S
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S
I9M +R171L +N195F +Q365S
I9M +Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K
I9M +Y160H +N195F +Q365S
I9M+A186E+N195F+Q365S
I9M+A186H+N195F+Q365S
I9M+G184K+N195F+Q365S
I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S
I9M+N195F+Q365C
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K
I9M+R127N+N195F+Q365S
I9M+R171H+N195F+Q365S
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S
I9M+R171L+N195F+Q365S
I9M+Y160H+N195F+Q365S
M202L
M246L +L275V +Q365S +D406H
M246L
M246L+ L275V +Q365S
M246L+L275V+Q365S+D406H
N16E +N195F +G337D +Q365S +P375K +D377N
N16E +N195F +G337E +Q365S +P375T +D377H

24 Mar 2026
2026202266

N16E+N195F+G337E+Q365S+P375T+D377H
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S
N195F +G337D +Q365S +P375K +D377N
N195F +G337D +Q365S +P375K +D377Y
N195F +G337E +Q365S +P375K +D377N
N195F+G337D+Q365S+P375K+D377Y
N195F+G337E+Q365S+P375K+D377N
N195F+Q365S
N54Q +F113T +R171H +N302A +Q365C
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Q11H +V264I +A265G +Q365C
Q11H +V264I +A265G +Y267F +Q365C
Q11H +V264I +Y267F +F328L +Q365C
Q11H +Y267F +Q365C
Q11H+V264I+A265G+Q365C
Q169* +S170* +A174*
Q169* +S170* +R171* +A174*
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P
R116K +S132L +Q136R +R181C +N195F +Q365S
R116K +S132P +Q136D +R181Q +N195F +A204V +Q365S
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S
R116N +S132A +Q136D +R181K +N195F +Q365S
R116N +S132M +Q136R +N195F +Q365S
R116N+S132A+Q136D+R181K+N195F+Q365S
R116S +S132F +R181N +N195F +Q365S
R116S +Y135H +Q136G +R181T +N195F +Q365S
R116Y +S132P +Q136N +N195F +Q365S
R127H+L235I+Q365S+G435C
R127L +M246V +Q365S
R127L +Q365C
R127L +Q365S
R127L
R127N +M246L +L275V +Q365S
R127N +Q365S
R127N +R171L +M246L +L275V +Q365S

24 Mar 2026
2026202266

R127N+R171H+M246L+L275V+Q365S
R171H + Q365C
R171H +M246L +L275V +Q365S
R171H +N302H +Q365S
R171H
R171H+Q365C
R171L +N302H +Q365C
R171L +Q365S
R171Y + +M246L +Q365S
R171Y +N306K
R181S +G184S
V104A +N195F +Q365S
V264A +Y267F +V291T +F328L +Q365C
V264I +A265G +V291A +F328L +Q365S
V264I +A265G +V291A +Q365C
V264I +A265G +Y267F +F328L +Q365S +Q395K
V264I +A265G +Y267F +F328L +Q365S
V264I +A265G +Y267F +V291I +F328L +Q365S
V264I +A265G +Y267F
V264I +F328L +Q365C
V264I +F328L +Q365S
V264I +L357F
V264I +Q365C
V264I +V291I +Q365S
V264I +V291T +Q365K
V264I +Y267F +F328L +Q365C
V264I +Y267F +F328L +Q365K
V264I +Y267F +F328L +Q365S
V264I +Y267F +Q365K +W408H +V410I
V264I +Y267F +Q365K
V264I +Y267F +Q365S
V264I +Y267F +V291A +F328L +Q365C
V264I +Y267F +V291A +F328L +Q365S
V264I +Y267F +V291T +F328L +Q365S
V264I+A265G+Y267F
V264I+F328L+Q365C

24 Mar 2026
2026202266

V264I+Y267F+F328L+Q365K
V264I+Y267F+V291T+F328L+Q365S
V264T +A265G +Y267F +V291A +F328L +Q365C
V264T +A265G +Y267L +F328L +Q365C
V264T +V291A +F328L +Q365S
V264T +Y267F +Q365S
V264T +Y267L +F328L +Q365C
V56T+Y160H+A174N+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
W187M +N195F +H210K +Q365S
Y160H +E212D +E276N +W284Y +R320S +Q365S +W408H +W439T +W469N +F473S +G476K
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473I +G476K
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K
Y160H+A174S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+E276N+W284Y+N306R+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+E276N+W284Y+N306Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+K259G+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+Q256N+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+M202L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473I+G476K
Y160H+N195F+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+N195Q+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+N195Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+Q169E+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+R171Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y267F +Q365S
Y267F +V291A +F328L +Q365C
Y267F +V291A +F328L +Q365S

24 Mar 2026

2026202266

Y267F+Q365S

Y267F+V291A+F328L+Q365S

Y295F, using SEQ ID NO: 1 for numbering and wherein said variant Improvement Factor (IF) of at least 1.1, preferably at least 1.2, such as at least 1.3, such as at least 1.4, such as at least 1.5, such as at least 1.6, such as at least 1.7, such as at least 1.8, such as at least 1.9, such as at least 2.0, such as at least 2.2, such as at least 2.4, such as at least 2.6, such as at least 2.8, such as at least 3.0, such as at least 3.2, such as at least 3.4, such as at least 3.6, such as at least 3.8, or such as at least 4.0 in Model A detergent composition and/or in ADW detergent composition with bleach when compared to said parent alpha-amylase and wherein said parent alpha-amylase has amino acid sequence as shown in SEQ ID NO: 2.

In one aspect, the variant is selected from a group consisting of:

A60T

Y135H

Q169E

W48Y

A174*

M246L

R90Q

Y203L+V206L

Q169F+S170A

S132D+G133D

N195F+Q365C

N195F+Q365S

N195F+Q365M

R127L+Q365S

R127N+Q365S

R127L+Q365C

N195F+Q365K

I9M+N195F

R171H+Q365C

Y267F+Q365S

F328L+Q365S

R171L+Q365S

N195F+M286L

T134P+N195F

24 Mar 2026
2026202266

S170*+R171*+A174*
V264I+A265G+Y267F
Q169*+S170*+A174*
M246L+L275V+Q365S
V264I+V291I+Q365S
V264I+V291T+Q365K
V264I+F328L+Q365C
I9M+N195F+Q365C
Q11H+Y267F+Q365C
I9M +N195F+Q365S
V264I+Y267F+Q365K
R127L+M246V+Q365S
A60S+R171Y+Q365S
R127N+M246T+L275V
V104A+N195F+Q365S
V264I+F328L+Q365S
R171H+N302H+Q365S
V264I+Y267F+Q365S
A174*+N175*+Y178F
V264I+A265G+Q365C
R171L+N302H+Q365C
R171L+M246V+Q365C
R171Y+M246L+Q365S
V264T+Y267F+Q365S
I9M+Y160H+N195F+Q365S
I9M+R127N+N195F+Q365S
R127H+L235I+Q365S+G435C
I9M+R171H+N195F+Q365S
I9M+A186H+N195F+Q365S
I9M+R171L+N195F+Q365S
Q169*+S170*+R171*+A174*
M246L+L275V+Q365S+D406H
I9M+G184K+N195F+Q365S
R127N+M246L+L275V+Q365S
R171H+M246L+L275V+Q365S
R127H+M246I+Q365C+V481A

24 Mar 2026
2026202266

Y267F+V291A+F328L+Q365C
I9M+A186E+N195F+Q365S
E86L+R171L+N306R+Q365S
V264I+Y267F+F328L+Q365S
I9M+N195F+V291A+Q365S
R127L+L235I+M246I+Q365C
Y267F+V291A+F328L+Q365S
V264I+Y267F+F328L+Q365K
Q11H+V264I+A265G+Q365C
W187M+N195F+H210K+Q365S
R127H+M246T+L275A+Q365S
I9M+A111T+N195F+Q365S
I9M+Y58F+N195F+Q365S
V264T+V291A+F328L+Q365S
V264I+A265G+V291A+Q365C
V264I+A265G+Y267F+Q365C
V264I+Y267F+V291A+F328L+Q365S
R127N+R171H+M246L+L275V+Q365S
V264I+A265G+V291A+F328L+Q365S
R127N+M246I+A265G+Y267H+Q365S
E130I+T134A+R181N+N195F+Q365S
R127N+M246L+L275V+N306R+Q365S
I9M+N195F+V206L+D209N+Q365S
R116S+S132F+R181N+N195F+Q365S
E130T+T134Y+A186K+N195F+Q365S
A37V+V264I+Y267F+F328L+Q365C
Q11H+V264I+Y267F+F328L+Q365C
V264I+Y267F+V291T+F328L+Q365S
Q169*+R171*+Q172*+L173*+A174*
R116Y+S132P+Q136N+N195F+Q365S
N195F+G337D+Q365S+P375K+D377Y
V264I+A265G+Y267F+F328L+Q365S
I9M+N195F+K269Q+A274K+Q365S
E130D+T134Y+R181H+N195F+Q365S
R116N+S132M+Q136R+N195F+Q365S
N195F+G337D+Q365S+P375K+D377N

24 Mar 2026
2026202266

R127N+R171L+M246L+L275V+Q365S
N195F+G337E+Q365S+P375K+D377N
Q11H+V264I+A265G+Y267F+Q365C
R158Q+Y160N+W187M+N195F+Q365S
V264I+Y267F+Q365K+W408H+V410I
R127N+R171Y+M246L+L275V+Q365S
N54Q+F113T+R171H+N302A+Q365C
V264A+Y267F+V291T+F328L+Q365C
Q169*+S170*+R171*+Q172*+L173*+A174*
R116K+S132L+Q136R+R181C+N195F+Q365S
V264T+A265G+Y267F+V291A+F328L+Q365C
E130N+T134S+R181N+A186K+N195F+Q365S
E130V+T134N+R181Y+A186K+N195F+Q365S
E130D+T134W+R181KA186E+N195F+Q365S
R116N+S132A+Q136D+R181K+N195F+Q365S
E130S+T134E+R181S+A186T+N195F+Q365S
R116C+S132A+Q136S+R181A+N195F+Q365S
R116K+S132P+Q136D+R181Q+N195F+Q365S
R127H+R171H+M246L+L275V+N306R+Q365S
E130L+T134N+R181W+A186T+N195F+Q365S
R116C+S132M+Q136S+R181Q+N195F+Q365S
R116S+Y135H+Q136G+R181T+N195F+Q365S
R116S+S132L+Q136E+R181G+N195F+Q365S
N16E+N195F+G337E+Q365S+P375T+D377H
V264I+A265G+Y267F+V291I+F328L+Q365S
N16E+N195F+G337D+Q365S+P375K+D377N
V264I+A265G+Y267F+F328L+Q365S+Q395K
E130N+T134C+R181Q+A186N+N195F+Q365S
V264I+A265G+Y267F+V291A+F328L+Q365C
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S
A139T+R158S+Y160D+W187M+N195F+H210N+Q365S

24 Mar 2026
2026202266

I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+Y58F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195H+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A

24 Mar 2026
2026202266

Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q125G+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311K+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K269M+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+K391A
Y160H+E212D+K259G+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+A174S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+N195Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+Q169E+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
Y160H+E212D+E276N+W284Y+N306Y+R320S+W408H+W439T+W469N+F473S+G476K
G7A+F113N+R116N+E276N+S304G+R320S+Q345N+W439R+N465G+Q466S+W469Y
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D377H+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V238A+K391A
Y160H+N195F+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+Q256N+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365H+K391A
Y160H+N195Q+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+R171Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
G109A+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
Y160H+E212D+E276N+W284Y+N306R+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+R127F+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S
+G476K
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F
Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L235I+V238A+K391A
H1*+N54S+V56T+G109A+Q172S+L173K+A174S+N175*+R176A+N195F+V206L+K391A
H1*+N54S+V56T+G109A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A
V56T+Y160H+A174N+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A
H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A
H1*+N54S+V56T+G109A+R116H+Q169E+Q172K+A174*+N195F+V206L+N314Q+Q385L+K391A
H1*+I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S, using SEQ ID NO: 1 for numbering and wherein said variant Improvement Factor (IF) of at least 1.1, preferably at least 1.2, such as at least 1.3, such as at least 1.4, such as at least 1.5, such as at least 1.6, such as at least 1.7, such as at least 1.8, such as at least 1.9, such as at least 2.0, such as at least 2.2, such as at least 2.4, such as at least 2.6, such as at least 2.8, such as at least 3.0, such as at least 3.2, such as at least 3.4, such as at least 3.6, such as at least 3.8, or such as at least 4.0 in Model A detergent composition when compared to said parent alpha-amylase and wherein said parent alpha-amylase has amino acid sequence as shown in SEQ ID NO: 2.

24 Mar 2026
2026202266

In one aspect, the variant is selected from a group consisting of:

A139T +R158S +Y160D +W187M +N195F +H210N +Q365S

A186D +N195F

A60S +R171Y +Q365S

E130D +T134W +R181K +A186E +N195F +Q365S

E130D +T134Y +R181H +N195F +Q365S

E130D+T134W+R181K+A186E+N195F+Q365S

E130F +T134R +R181S +A186D +N195F +Q365S

E130I +T134A +R181N +N195F +Q365S

E130I+T134A+R181N+N195F+Q365S

E130L +T134N +R181W +A186T +N195F +Q365S

E130N +T134C +R181Q +A186N +N195F +Q365S

E130S +T134E +R181S +A186T +N195F +Q365S

E130T +T134Y +A186K +N195F +Q365S

E130V +T134N +R181Y +A186K +N195F +Q365S

E130Y +S132T +T134S +R181E +A186D +N195F +Q365S

E130Y+S132T+T134S+R181E+A186D+N195F+Q365S

E86L +R171L +N306R +Q365S

E86L +Y160H +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K

E86L+R171L+N306R+Q365S

F113Q +R116H

F113T +R171K +G273V

F328L +Q365S

H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S

H1* +I9M +N54S +V56T +G109A +F113G +R116H +D163H +Q169E +R171H +Q172K +A174S +G182T +N195F +M202L +V206L +M246L +L275V +A288V +L317V +Q319H +H324K +Q365S +K391A

H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K

H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A

H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A

H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A

H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A

24 Mar 2026
2026202266

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +Q365S +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L+ V206L +W284Y +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +N306R +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +Q365S +K391A

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +V206L +K391A

H1* +N54S +V56T +G109A +R171H +N195F +V206L +K391A

H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A

H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A

H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A

H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A

I9M +A186E +N195F +Q365S

I9M +A186H +N195F +Q365S

I9M +G184K +N195F +Q365S

I9M +N195F +K269Q +A274K +Q365S

I9M +N195F +N270G +Q365S

I9M +N195F +N270P +Q365S

I9M +N195F +Q365C

I9M +N195F +V206L +D209N +Q365S

I9M +N195F +V291A +Q365S

I9M +R127N +N195F +Q365S

I9M +R171H +N195F +Q365S

I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S

I9M +R171L +N195F +Q365S

I9M +Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K

24 Mar 2026
2026202266

I9M +Y160H +N195F +Q365S

I9M+A186E+N195F+Q365S

I9M+A186H+N195F+Q365S

I9M+G184K+N195F+Q365S

I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S

I9M+N195F+Q365C

I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K

I9M+R127N+N195F+Q365S

I9M+R171H+N195F+Q365S

I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S

I9M+R171L+N195F+Q365S

I9M+Y160H+N195F+Q365S

M202L

M246L

M246L +L275V +Q365S +D406H

M246L+ L275V +Q365S

M246L+L275V+Q365S+D406H

N16E +N195F +G337D +Q365S +P375K +D377N

N16E +N195F +G337E +Q365S +P375T +D377H

N16E+N195F+G337E+Q365S+P375T+D377H

N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S

N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S

N195F +G337D +Q365S +P375K +D377N

N195F +G337D +Q365S +P375K +D377Y

N195F +G337E +Q365S +P375K +D377N

N195F+G337D+Q365S+P375K+D377Y

N195F+G337E+Q365S+P375K+D377N

N195F+Q365S

N54Q +F113T +R171H +N302A +Q365C

Q11H +V264I +A265G +Q365C

Q11H +V264I +A265G +Y267F +Q365C

Q11H +V264I +Y267F +F328L +Q365C

Q11H +Y267F +Q365C

24 Mar 2026
2026202266

Q11H+V264I+A265G+Q365C
Q169* +S170* +A174*
Q169* +S170* +R171* +A174*
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P
R116K +S132L +Q136R +R181C +N195F +Q365S
R116K +S132P +Q136D +R181Q +N195F +A204V +Q365S
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S
R116N +S132A +Q136D +R181K +N195F +Q365S
R116N +S132M +Q136R +N195F +Q365S
R116N+S132A+Q136D+R181K+N195F+Q365S
R116S +S132F +R181N +N195F +Q365S
R116S +Y135H +Q136G +R181T +N195F +Q365S
R116Y +S132P +Q136N +N195F +Q365S
R127H+L235I+Q365S+G435C
R127L
R127L +M246V +Q365S
R127L +Q365C
R127L +Q365S
R127N +M246L +L275V +Q365S
R127N +Q365S
R127N +R171L +M246L +L275V +Q365S
R127N+R171H+M246L+L275V+Q365S
R171H
R171H + Q365C
R171H +M246L +L275V +Q365S
R171H +N302H +Q365S
R171H+Q365C
R171L +N302H +Q365C
R171L +Q365S
R171Y + +M246L +Q365S
R171Y +N306K
*
R181S +G184S
V104A +N195F +Q365S
V264A +Y267F +V291T +F328L +Q365C
V264I +A265G +V291A +F328L +Q365S

24 Mar 2026
2026202266

V264I +A265G +V291A +Q365C
V264I +A265G +Y267F
V264I +A265G +Y267F +F328L +Q365S
V264I +A265G +Y267F +F328L +Q365S +Q395K
V264I +A265G +Y267F +V291I +F328L +Q365S
V264I +F328L +Q365C
V264I +F328L +Q365S
V264I +L357F
V264I +Q365C
V264I +V291I +Q365S
V264I +V291T +Q365K
V264I +Y267F +F328L +Q365C
V264I +Y267F +F328L +Q365K
V264I +Y267F +F328L +Q365S
V264I +Y267F +Q365K
V264I +Y267F +Q365K +W408H +V410I
V264I +Y267F +Q365S
V264I +Y267F +V291A +F328L +Q365C
V264I +Y267F +V291A +F328L +Q365S
V264I +Y267F +V291T +F328L +Q365S
V264I+A265G+Y267F
V264I+F328L+Q365C
V264I+Y267F+F328L+Q365K
V264I+Y267F+V291T+F328L+Q365S
V264T +A265G +Y267F +V291A +F328L +Q365C
V264T +A265G +Y267L +F328L +Q365C
V264T +V291A +F328L +Q365S
V264T +Y267F +Q365S
V264T +Y267L +F328L +Q365C
W187M +N195F +H210K +Q365S
Y160H +E212D +E276N +W284Y +R320S +Q365S +W408H +W439T +W469N +F473S +G476K
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473I +G476K
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K
Y160H+M202L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473I+G476K
Y267F +Q365S

24 Mar 2026
2026202266

Y267F +V291A +F328L +Q365C
Y267F +V291A +F328L +Q365S
Y267F+Q365S
Y267F+V291A+F328L+Q365S
Y295F, using SEQ ID NO: 1 for numbering and wherein said variant Improvement Factor (IF) of at least 1.1, preferably at least 1.2, such as at least 1.3, such as at least 1.4, such as at least 1.5, such as at least 1.6, such as at least 1.7, such as at least 1.8, such as at least 1.9, such as at least 2.0, such as at least 2.2, such as at least 2.4, such as at least 2.6, such as at least 2.8, such as at least 3.0, such as at least 3.2, such as at least 3.4, such as at least 3.6, such as at least 3.8, or such as at least 4.0 in ADW detergent with bleach when compared to said parent alpha-amylase and wherein said parent alpha-amylase has amino acid sequence as shown in SEQ ID NO: 2.

In one aspect, the variant is selected from the group consisting of:
A60T,
Y135H,
Q169E,
W48Y,
A174*,
M246L,
R90Q,
Y203L+V206L,
Q169F+S170A,
S132D+G133D,
N195F+Q365C,
N195F+Q365S,
N195F+Q365M,
N195F+Q365K,
R127L+Q365S,
R127N+Q365S,
R127L+Q365C,
R171L+Q365S,
R171H+Q365C,
Y267F+Q365S,
F328L+Q365S,
I9M+N195F,
N195F+M286L,

24 Mar 2026
2026202266

T134P+N195F,
S170*+R171*+A174*,
V264I+A265G+Y267F,
Q169*+S170*+A174*,
M246L+L275V+Q365S,
V264I+V291I+Q365S,
V264I+V291T+Q365K,
V264I+F328L+Q365C,
I9M+N195F+Q365C,
Q11H+Y267F+Q365C,
I9M +N195F+Q365S,
V264I+Y267F+Q365K,
R127L+M246V+Q365S,
A60S+R171Y+Q365S,
R127N+M246T+L275V,
V104A+N195F+Q365S,
V264I+F328L+Q365S,
R171H+N302H+Q365S,
V264I+Y267F+Q365S,
A174*+N175*+Y178F,
V264I+A265G+Q365C,
R171L+N302H+Q365C,
R171L+M246V+Q365C,
R171Y+M246L+Q365S,
V264T+Y267F+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127N+M246L+L275V+Q365S,

24 Mar 2026
2026202266

R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
R127N+M246L+L275V+Q365S,
Y267F+V291A+F328L+Q365C,
I9M+A186E+N195F+Q365S,
E86L+R171L+N306R+Q365S,
V264I+Y267F+F328L+Q365S,
I9M+N195F+V291A+Q365S,
R127L+L235I+M246I+Q365C,
Y267F+V291A+F328L+Q365S,
V264I+Y267F+F328L+Q365K,
Q11H+V264I+A265G+Q365C,
I9M+R171H+N195F+Q365S,
W187M+N195F+H210K+Q365S,
R127H+M246T+L275A+Q365S,
I9M+A111T+N195F+Q365S,
I9M+Y58F+N195F+Q365S,
V264T+V291A+F328L+Q365S,
V264I+A265G+V291A+Q365C,
V264I+A265G+Y267F+Q365C,
V264I+Y267F+V291A+F328L+Q365S,
R127N+R171H+M246L+L275V+Q365S,
V264I+A265G+V291A+F328L+Q365S,
R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
R116S+S132F+R181N+N195F+Q365S,
E130T+T134Y+A186K+N195F+Q365S,
A37V+V264I+Y267F+F328L+Q365C,
Q11H+V264I+Y267F+F328L+Q365C,
V264I+Y267F+V291T+F328L+Q365S,
Q169*+R171*+Q172*+L173*+A174*,
R116Y+S132P+Q136N+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377Y,
V264I+A265G+Y267F+F328L+Q365S,

24 Mar 2026
2026202266

I9M+N195F+K269Q+A274K+Q365S,
E130D+T134Y+R181H+N195F+Q365S,
R116N+S132M+Q136R+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377N,
R127N+R171L+M246L+L275V+Q365S,
N195F+G337E+Q365S+P375K+D377N,
Q11H+V264I+A265G+Y267F+Q365C,
R158Q+Y160N+W187M+N195F+Q365S,
V264I+Y267F+Q365K+W408H+V410I,
R127N+R171Y+M246L+L275V+Q365S,
N54Q+F113T+R171H+N302A+Q365C,
V264A+Y267F+V291T+F328L+Q365C,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,
E130D+T134W+R181KA186E+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
E130S+T134E+R181S+A186T+N195F+Q365S,
R116C+S132A+Q136S+R181A+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+Q365S,
R127H+R171H+M246L+L275V+N306R+Q365S,
E130L+T134N+R181W+A186T+N195F+Q365S,
R116C+S132M+Q136S+R181Q+N195F+Q365S,
R116S+Y135H+Q136G+R181T+N195F+Q365S,
R116S+S132L+Q136E+R181G+N195F+Q365S,
N16E+N195F+G337E+Q365S+P375T+D377H,
V264I+A265G+Y267F+V291I+F328L+Q365S,
N16E+N195F+G337D+Q365S+P375K+D377N,
V264I+A265G+Y267F+F328L+Q365S+Q395K,
E130N+T134C+R181Q+A186N+N195F+Q365S,
V264I+A265G+Y267F+V291A+F328L+Q365C,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,

24 Mar 2026
2026202266

N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
A139T+R158S+Y160D+W187M+N195F+H210N+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*,
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+Y58F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195H+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A,
H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A,
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A,
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A,
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A,
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,

24 Mar 2026
2026202266

H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A,
Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A,
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A,
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q125G+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K269M+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+K391A,
Y160H+E212D+K259G+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+A174S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+N195Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q169E+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,

24 Mar 2026
2026202266

G7A+F113N+R116N+E276N+S304G+R320S+Q345N+W439R+N465G+Q466S+W469Y,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D377H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V238A+K391A,
Y160H+N195F+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256N+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365H+K391A,
Y160H+N195Q+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+R171Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
G109A+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R127F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A,
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A,
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F,
Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L235I+V238A+K391A,
H1*+N54S+V56T+G109A+Q172S+L173K+A174S+N175*+R176A+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
V56T+Y160H+A174N+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,
H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026

2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A,

H1*+N54S+V56T+G109A+R116H+Q169E+Q172K+A174*+N195F+V206L+N314Q+Q385L+K391A,

H1*+I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S, using SEQ ID NO: 1 for numbering and wherein said variant has an improved relative specific activity of at least ≥1.1 in Model A detergent composition as a measure of wash performance compared to parent alpha-amylase of SEQ ID NO: 2.

In one aspect, the variant is selected from the group consisting of:

M246L,

N195F+Q365C,

N195F+Q365S,

N195F+Q365M,

N195F+Q365K,

R127L+Q365S,

R127N+Q365S,

R127L+Q365C,

R171H+Q365C,

Y267F+Q365S,

F328L+Q365S,

I9M+N195F,

S170*+R171*+A174*,

V264I+A265G+Y267F,

Q169*+S170*+A174*,

M246L+L275V+Q365S,

V264I+V291I+Q365S,

V264I+V291T+Q365K,

V264I+F328L+Q365C,

I9M+N195F+Q365C,

Q11H+Y267F+Q365C,

I9M +N195F+Q365S,

V264I+Y267F+Q365K,

R127L+M246V+Q365S,

I9M+Y160H+N195F+Q365S,

I9M+R127N+N195F+Q365S,

24 Mar 2026
2026202266

R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127N+M246L+L275V+Q365S,
R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
R127N+M246L+L275V+Q365S,
Y267F+V291A+F328L+Q365C,
I9M+A186E+N195F+Q365S,
E86L+R171L+N306R+Q365S,
V264I+Y267F+F328L+Q365S,
I9M+N195F+V291A+Q365S,
R127L+L235I+M246I+Q365C,
Y267F+V291A+F328L+Q365S,
V264I+Y267F+F328L+Q365K,
Q11H+V264I+A265G+Q365C,
V264I+Y267F+V291A+F328L+Q365S,
V264I+A265G+V291A+F328L+Q365S,
R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
R116S+S132F+R181N+N195F+Q365S,
E130T+T134Y+A186K+N195F+Q365S,
A37V+V264I+Y267F+F328L+Q365C,
Q11H+V264I+Y267F+F328L+Q365C,
V264I+Y267F+V291T+F328L+Q365S,
Q169*+R171*+Q172*+L173*+A174*,
R116Y+S132P+Q136N+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377Y,
V264I+A265G+Y267F+F328L+Q365S,

24 Mar 2026
2026202266

I9M+N195F+K269Q+A274K+Q365S,
E130D+T134Y+R181H+N195F+Q365S,
R116N+S132M+Q136R+N195F+Q365S,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,
E130D+T134W+R181KA186E+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
E130S+T134E+R181S+A186T+N195F+Q365S,
R116C+S132A+Q136S+R181A+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+Q365S,
R127H+R171H+M246L+L275V+N306R+Q365S,
E130L+T134N+R181W+A186T+N195F+Q365S,
R116C+S132M+Q136S+R181Q+N195F+Q365S,
R116S+Y135H+Q136G+R181T+N195F+Q365S,
R116S+S132L+Q136E+R181G+N195F+Q365S,
N16E+N195F+G337E+Q365S+P375T+D377H,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*,
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026
2026202266

H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A,
H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A,
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A,
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A,
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A,
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A,
Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A,
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A,
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,

24 Mar 2026
2026202266

H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A,
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A,
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F,
Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,
H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A, using SEQ ID NO: 1 for numbering and wherein said variant has an improved relative specific activity of at least ≥1.5 in Model A detergent composition as measure of wash performance compared to parent alpha-amylase of SEQ ID NO: 2.

In one aspect, variant is selected from the group consisting of:

N195F+Q365C,
N195F+Q365S,
N195F+Q365M,
R127L+Q365S,
R127N+Q365S,
S170*+R171*+A174*,
V264I+A265G+Y267F,
Q169*+S170*+A174*,
V264I+V291I+Q365S,

24 Mar 2026
2026202266

V264I+V291T+Q365K,
V264I+F328L+Q365C,
I9M+Y160H+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127N+M246L+L275V+Q365S,
R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
R127N+M246L+L275V+Q365S,
Y267F+V291A+F328L+Q365C,
V264I+Y267F+V291A+F328L+Q365S,
V264I+A265G+V291A+F328L+Q365S,
R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,
using SEQ ID NO: 1 for numbering and wherein said variant has an improved relative specific activity of at least ≥ 2.0 in Model A detergent composition as a measure of wash performance compared to parent alpha-amylase of SEQ ID NO: 2.

In one aspect, variant is selected from the group consisting of:
N195F+Q365C,
S170*+R171*+A174*,
I9M+Y160H+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
V264I+Y267F+V291A+F328L+Q365S,
Q169*+S170*+R171*+Q172*+L173*+A174*,

24 Mar 2026
2026202266

W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
using SEQ ID NO: 1 for numbering and wherein said variant has an improved relative specific activity of at least ≥ 2.5 in Model A detergent composition as a measure of wash performance compared to parent alpha-amylase of SEQ ID NO: 2.

In one embodiment, the variant has an improved wash performance, the enhanced wash performance corresponding to an Improvement Factor (IF) in ADW detergent with bleach is assessed using an Automatic Mechanical Stress Assay (AMSA) of at least 1.1, preferably at least 1.2, such as at least 1.3, such as at least 1.4, such as at least 1.5, such as at least 1.6, such as at least 1.7, such as at least 1.8, such as at least 1.9, such as at least 2.0, such as at least 2.2, such as at least 2.4, such as at least 2.6, such as at least 2.8, such as at least 3.0, such as at least 3.2, such as at least 3.4, such as at least 3.6, such as at least 3.8, or such as at least 4.0 when compared to said parent alpha-amylase and wherein said parent alpha-amylase has amino acid sequence as shown in SEQ ID NO: 2.

In one aspect, the variant is selected from the group consisting of:
Y295F,
M246L,
M202L,
R181S +G184S,
F113Q +R116H,
V264I +L357F,
Y267F +Q365S,
R171H,
R171Y +N306K,
R171H + Q365C,
R171L +Q365S,
R171H +N302H +Q365S,
R171L +N302H +Q365C,
R171Y + +M246L +Q365S,
F328L +Q365S,
R127L,
R127N +Q365S,

24 Mar 2026
2026202266

R127L +Q365C,
R127L +Q365S,
R127L +M246V +Q365S,
A186D +N195F,
V264I +Q365C,
I9M +N195F +Q365C,
V264I +A265G +Y267F,
V264I +V291T +Q365K,
A60S +R171Y +Q365S,
V264I +Y267F +Q365K,
V264I +F328L +Q365C,
M246L+ L275V +Q365S,
V264T +Y267F +Q365S,
V264I +F328L +Q365S,
Q11H +Y267F +Q365C,
V104A +N195F +Q365S,
V264I +V291I +Q365S,
V264I +Y267F +Q365S,
F113T +R171K +G273V,
Q169* +S170* +A174*,
I9M +R171H +N195F +Q365S,
I9M +R127N +N195F +Q365S,
E86L +R171L +N306R +Q365S,
I9M +A186E +N195F +Q365S,
I9M +Y160H +N195F +Q365S,
I9M +A186H +N195F +Q365S,
R171H +M246L +L275V +Q365S,
I9M +N195F +V291A +Q365S,
I9M +G184K +N195F +Q365S,
M246L +L275V +Q365S +D406H,
Y267F +V291A +F328L +Q365S,
Y267F +V291A +F328L +Q365C,
V264I +Y267F +F328L +Q365K,
I9M +R171L +N195F +Q365S,
Q11H +V264I +A265G +Q365C,
V264T +V291A +F328L +Q365S,

24 Mar 2026
2026202266

V264I +Y267F +F328L +Q365S,
R127N +M246L +L275V +Q365S,
I9M +N195F +N270G +Q365S,
I9M +N195F +N270P +Q365S,
V264T +Y267L +F328L +Q365C,
V264I +A265G +V291A +Q365C,
W187M +N195F +H210K +Q365S,
V264I +Y267F +F328L +Q365C,
Q169* +S170* +R171* +A174*,
I9M +N195F +V206L +D209N +Q365S,
N195F +G337D +Q365S +P375K +D377N,
V264I +Y267F +V291T +F328L +Q365S,
N195F +G337E +Q365S +P375K +D377N,
N195F +G337D +Q365S +P375K +D377Y,
V264I +A265G +V291A +F328L +Q365S,
I9M +N195F +K269Q +A274K +Q365S,
V264I +Y267F +Q365K +W408H +V410I,
E130D +T134Y +R181H +N195F +Q365S,
V264I +Y267F +V291A +F328L +Q365S,
E130I +T134A +R181N +N195F +Q365S,
R116Y +S132P +Q136N +N195F +Q365S,
R116N +S132M +Q136R +N195F +Q365S,
V264I +A265G +Y267F +F328L +Q365S,
Q11H +V264I +Y267F +F328L +Q365C,
Q11H +V264I +A265G +Y267F +Q365C,
E130T +T134Y +A186K +N195F +Q365S,
R116S +S132F +R181N +N195F +Q365S,
V264A +Y267F +V291T +F328L +Q365C,
N54Q +F113T +R171H +N302A +Q365C,
R127N +R171L +M246L +L275V +Q365S,
V264T +A265G +Y267L +F328L +Q365C,
V264I +Y267F +V291A +F328L +Q365C,
N16E +N195F +G337E +Q365S +P375T +D377H,
E130D +T134W +R181K +A186E +N195F +Q365S,
E130F +T134R +R181S +A186D +N195F +Q365S,
V264T +A265G +Y267F +V291A +F328L +Q365C,

24 Mar 2026
2026202266

E130V +T134N +R181Y +A186K +N195F +Q365S,
R116N +S132A +Q136D +R181K +N195F +Q365S,
E130L +T134N +R181W +A186T +N195F +Q365S,
V264I +A265G +Y267F +F328L +Q365S +Q395K,
N16E +N195F +G337D +Q365S +P375K +D377N,
E130N +T134C +R181Q +A186N +N195F +Q365S,
R116S +Y135H +Q136G +R181T +N195F +Q365S,
R116K +S132L +Q136R +R181C +N195F +Q365S,
V264I +A265G +Y267F +V291I +F328L +Q365S,
E130S +T134E +R181S +A186T +N195F +Q365S,
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S,
A139T +R158S +Y160D +W187M +N195F +H210N +Q365S,
R116K +S132P +Q136D +R181Q +N195F +A204V +Q365S,
E130Y +S132T +T134S +R181E +A186D +N195F +Q365S,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P,
H1* +N54S +V56T +G109A +R171H +N195F +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473I +G476K,
Y160H +E212D +E276N +W284Y +R320S +Q365S +W408H +W439T +W469N +F473S +G476K,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +Q365S +K391A,
E86L +Y160H +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +N306R +K391A,
H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
I9M +Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S

24 Mar 2026
2026202266

+G476K,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +Q365S +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L+ V206L +W284Y +K391A,

H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,

H1* +I9M +N54S +V56T +G109A +F113G +R116H +D163H +Q169E +R171H +Q172K +A174S +G182T +N195F +M202L +V206L +M246L +L275V +A288V +L317V +Q319H +H324K +Q365S +K391A,

H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.1 in ADW detergent composition with bleach assessed using AMSA.

In one aspect, the variant is selected from the group consisting of:

Y295F,

M246L,

M202L,

R181S +G184S,

F113Q +R116H,

Y267F +Q365S,

R171H,

R171H + Q365C,

R171L +Q365S,

R171H +N302H +Q365S,

R171L +N302H +Q365C,

R171Y + +M246L +Q365S,

F328L +Q365S,

I9M +N195F +Q365C,

V264I +A265G +Y267F,

V264I +V291T +Q365K,

A60S +R171Y +Q365S,

V264I +Y267F +Q365K,

V264I +F328L +Q365C,

M246L+ L275V +Q365S,

24 Mar 2026
2026202266

V264T +Y267F +Q365S,
V264I +F328L +Q365S,
Q11H +Y267F +Q365C,
I9M +R171H +N195F +Q365S,
I9M +R127N +N195F +Q365S,
E86L +R171L +N306R +Q365S,
I9M +A186E +N195F +Q365S,
I9M +Y160H +N195F +Q365S,
I9M +A186H +N195F +Q365S,
I9M +N195F +V291A +Q365S,
I9M +G184K +N195F +Q365S,
M246L +L275V +Q365S +D406H,
Y267F +V291A +F328L +Q365S,
Y267F +V291A +F328L +Q365C,
V264I +Y267F +F328L +Q365K,
I9M +R171L +N195F +Q365S,
Q11H +V264I +A265G +Q365C,
I9M +N195F +V206L +D209N +Q365S,
N195F +G337D +Q365S +P375K +D377N,
V264I +Y267F +V291T +F328L +Q365S,
N195F +G337E +Q365S +P375K +D377N,
N195F +G337D +Q365S +P375K +D377Y,
V264I +A265G +V291A +F328L +Q365S,
I9M +N195F +K269Q +A274K +Q365S,
V264I +Y267F +Q365K +W408H +V410I,
E130D +T134Y +R181H +N195F +Q365S,
V264I +Y267F +V291A +F328L +Q365S,
E130I +T134A +R181N +N195F +Q365S,
R116Y +S132P +Q136N +N195F +Q365S,
R116N +S132M +Q136R +N195F +Q365S,
N16E +N195F +G337E +Q365S +P375T +D377H,
E130D +T134W +R181K +A186E +N195F +Q365S,
E130F +T134R +R181S +A186D +N195F +Q365S,
V264T +A265G +Y267F +V291A +F328L +Q365C,
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,

24 Mar 2026
2026202266

Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,
H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.5 in ADW detergent composition with bleach assessed using AMSA.

In one aspect, the variant is selected from the group consisting of:

M202L,
R171H + Q365C,
R171L +Q365S,
R171H +N302H +Q365S,
R171L +N302H +Q365C,
I9M +N195F +Q365C,
V264I +A265G +Y267F,
E86L +R171L +N306R +Q365S,
I9M +A186E +N195F +Q365S,
I9M +Y160H +N195F +Q365S,
I9M +A186H +N195F +Q365S,
I9M +N195F +V206L +D209N +Q365S,
N195F +G337D +Q365S +P375K +D377N,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,

24 Mar 2026
2026202266

H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,

H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,

H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,

H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.0 in ADW detergent composition with bleach assessed using AMSA.

In one aspect, the variant is selected from the group consisting of:

M202L,

R171H + Q365C,

I9M +N195F +Q365C,

H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A, Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.5 in ADW detergent composition with bleach assessed using AMSA.

In one aspect, the variant is selected from the group consisting of:

H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A, Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.5 in ADW detergent composition with bleach assessed using AMSA.

In one aspect, the variant is selected from the group consisting of:

V264I+A265G+Y267F,

R171L+Q365S,

Y267F+Q365S,

R127L+Q365S,

V264I+F328L+Q365C,

M246L+L275V+Q365S+D406H,

Q11H+V264I+A265G+Q365C,

R127N+R171H+M246L+L275V+Q365S,

V264I+Y267F+V291T+F328L+Q365S,

Y267F+V291A+F328L+Q365S,

24 Mar 2026
2026202266

V264I+Y267F+F328L+Q365K,
R127H+L235I+Q365S+G435C,
N195F+Q365S,
I9M+N195F+Q365C,
I9M+R127N+N195F+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+A186E+N195F+Q365S,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+G184K+N195F+Q365S,
N195F+G337E+Q365S+P375K+D377N,
N195F+G337D+Q365S+P375K+D377Y,
E130I+T134A+R181N+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
N16E+N195F+G337E+Q365S+P375T+D377H,
E130D+T134W+R181K+A186E+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
Y160H+M202L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473I+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y2
95F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,

24 Mar 2026

2026202266

I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S,

H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.1 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

In one aspect, the variant is selected from the group consisting of:

V264I+A265G+Y267F,

R127N+R171H+M246L+L275V+Q365S,

V264I+Y267F+V291T+F328L+Q365S,

I9M+N195F+Q365C,

I9M+R127N+N195F+Q365S,

I9M+Y160H+N195F+Q365S,

I9M+A186E+N195F+Q365S,

N195F+G337E+Q365S+P375K+D377N,

N16E+N195F+G337E+Q365S+P375T+D377H,

E130D+T134W+R181K+A186E+N195F+Q365S,

E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,

R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,

N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,

H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,

Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,

H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,

I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+

24 Mar 2026
2026202266

Q445S+Q466S,

H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 1.5 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

In one aspect, the variant is selected from the group consisting of:

N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,

Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,

H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,

I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S,

H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.0 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

In one aspect, the variant is selected from the group consisting of:

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,

H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,

H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L +

24 Mar 2026
2026202266

Q365S + K391A, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.5 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

In one aspect, the variant is selected from the group consisting of:

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 3.0 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

In one aspect, the variant is selected from the group consisting of:

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 3.5 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

In one aspect, the variant is selected from the group consisting of:

Y295F,
M246L,
N195F+Q365S,
R171H+Q365C,
V264I+A265G+Y267F,
E86L+R171L+N306R+Q365S,
V264I+Y267F+V291T+F328L+Q365S,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
I9M+R127N+N195F+Q365S,
I9M+R171L+N195F+Q365S,
N195F+G337E+Q365S+P375K+D377N,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 1.1 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

In one aspect, the variant is selected from the group consisting of:
V264I+A265G+Y267F,
E86L+R171L+N306R+Q365S,
V264I+Y267F+V291T+F328L+Q365S,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
N195F+Q365S,
I9M+R127N+N195F+Q365S,
I9M+R171L+N195F+Q365S,
N195F+G337E+Q365S+P375K+D377N,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 1.2 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

In one aspect, the variant is selected from the group consisting of:
N195F+Q365S,
V264I+A265G+Y267F,
E86L+R171L+N306R+Q365S,
V264I+Y267F+V291T+F328L+Q365S,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,

24 Mar 2026
2026202266

I9M+R127N+N195F+Q365S,
I9M+R171L+N195F+Q365S,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 1.3 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

In one aspect, the variant is selected from the group consisting of:
V264I+A265G+Y267F
V264I+Y267F+V291T+F328L+Q365S
I9M+R171L+N195F+Q365S
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.5 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

In one aspect, the variant is selected from the group consisting of:
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A +

24 Mar 2026
2026202266

R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.0 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

In one aspect, the variant is selected from the group consisting of:

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,

H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 3.0 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

The variants according to the present invention may further comprise one or more additional alterations than those described above 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, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, and Asp/Gly.

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.

Essential amino acids in a polypeptide may 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

24 Mar 2026
2026202266

introduced at every residue in the molecule, and the resultant mutant molecules are tested for alpha-amylase 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.

The variants according to the present invention may consist of 400 to 485 amino acids, *e.g.*, 410 to 485, 425 to 485, and 440 to 485 amino acids.

Parent Alpha-amylases

The parent alpha-amylase may be a polypeptide with at least 60% sequence identity with any one of the polypeptides of SEQ ID Nos: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16 or 17.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 1 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 1.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 1. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 1. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 1.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 2 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 2.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 2. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 2. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 2.

24 Mar 2026
2026202266

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 3 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 3.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 3. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 3. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 3.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 4 of at least 60% *e.g.,* at least 65%, at least 70%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 4.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 4. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 4. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 4.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 5 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 5.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 5. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 5. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 5.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 6 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 6.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 6. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 6. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 6.

24 Mar 2026
2026202266

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 7 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 7.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 7. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 7. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 7.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 8 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 8.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 8. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 8. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 8.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 9 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 9.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 9. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 9. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 9.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 10 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 10.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 10. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 10. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO:10.

24 Mar 2026

2026202266

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 11 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 11.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 11. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 11. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 11.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 12 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 12.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 12. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 12. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 12.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 13 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 13.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 13. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 13. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 13.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 14 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 14.

24 Mar 2026
2026202266

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 14. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 14. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 14.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 15 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 15.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 15. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 15. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 15.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 16 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 16.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 16. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 16. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 16.

In one embodiment, the parent has a sequence identity to the polypeptide of SEQ ID NO: 17 of at least 60% *e.g.,* at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 87%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have alpha-amylase activity. In one embodiment, the amino acid sequence of the parent differs by no more than ten amino acids, *e.g.*, by five amino acids, by four amino acids, by three amino acids, by two amino acids, and by one amino acid from the polypeptide of SEQ ID NO: 17.

The parent preferably comprises or consists of the amino acid sequence of SEQ ID NO: 17. In one embodiment the parent comprises or consists of the polypeptide of SEQ ID NO: 17. In another embodiment, the parent is an allelic variant of the polypeptide of SEQ ID NO: 17.

The amino acid sequence of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, or an active 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

24 Mar 2026
2026202266

genomic or cDNA of the genus or species 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 14, *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 or at least 200 nucleotides in length., 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}P, ^{3}H, ^{35}S, biotin, or avidin). Such probes are encompassed by the present invention.

A genomic DNA or cDNA library prepared from such other organisms may be screened for DNA that hybridizes with the probes described above and encodes a parent. Genomic or other DNA from such other organisms 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, which is used in a Southern blot.

For purposes of the present invention, hybridization indicates that the polynucleotide hybridizes to a labeled nucleotide probe corresponding to a polynucleotide encoding SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, or a subsequence thereof, under low to very high stringency conditions. Molecules to which the probe hybridizes 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 a polynucleotide that encodes the polypeptide of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17, or an active fragment thereof.

For long probes of at least 100 nucleotides in length, very low to very high stringency conditions are defined as prehybridization and hybridization at 42°C in 5X SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and either 25% formamide for very low and low stringencies, 35% formamide for medium and medium-high stringencies, or 50% formamide for high and very high stringencies, following standard Southern blotting procedures for 12 to 24 hours optimally. The carrier material is finally washed three times each for 15 minutes using 2X SSC, 0.2% SDS at 45°C (very low stringency), 50°C (low stringency), 55°C (medium stringency), 60°C (medium-high stringency), 65°C (high stringency), or 70°C (very high stringency).

24 Mar 2026
2026202266

For short probes that are about 15 nucleotides to about 70 nucleotides in length, stringency conditions are defined as prehybridization and hybridization at about 5°C to about 10°C below the calculated T_m using the calculation according to Bolton and McCarthy (1962, *Proc. Natl. Acad. Sci. USA* 48: 1390) in 0.9 M NaCl, 0.09 M Tris-HCl pH 7.6, 6 mM EDTA, 0.5% NP-40, 1X Denhardt's solution, 1 mM sodium pyrophosphate, 1 mM sodium monobasic phosphate, 0.1 mM ATP, and 0.2 mg of yeast RNA per ml following standard Southern blotting procedures for 12 to 24 hours optimally. The carrier material is finally washed once in 6X SCC plus 0.1% SDS for 15 minutes and twice each for 15 minutes using 6X SSC at 5°C to 10°C below the calculated T_m.

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

The parent may be a bacterial alpha-amylase. 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* alpha-amylase, or a gram-negative bacterial polypeptide such as a *Campylobacter*, *E. coli*, *Flavobacterium*, *Fusobacterium*, *Helicobacter*, *Ilyobacter*, *Neisseria*, *Pseudomonas*, *Salmonella*, or *Ureaplasma* alpha-amylase.

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* alpha-amylase.

In another aspect, the parent is a *Streptococcus equisimilis*, *Streptococcus pyogenes*, *Streptococcus uberis*, or *Streptococcus equi* subsp. *Zooepidemicus* alpha-amylase.

In another aspect, the parent is a *Streptomyces achromogenes*, *Streptomyces avermitilis*, *Streptomyces coelicolor*, *Streptomyces griseus*, or *Streptomyces lividans* alpha-amylase.

The parent may be a fungal alpha-amylase. For example, the parent may be a yeast alpha-amylase such as a *Candida*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* alpha-amylase. For example, the parent may be a filamentous fungal alpha-amylase such as an *Acremonium*, *Agaricus*, *Alternaria*, *Aspergillus*, *Aureobasidium*, *Botryospaeria*, *Ceriporiopsis*, *Chaetomidium*, *Chrysosporium*, *Claviceps*, *Cochliobolus*, *Coprinopsis*, *Coptotermes*, *Corynascus*, *Cryphonectria*, *Cryptococcus*, *Diplodia*, *Exidia*, *Filibasidium*, *Fusarium*, *Gibberella*, *Holomastigotoides*, *Humicola*, *Irpex*, *Lentinula*, *Leptospaeria*, *Magnaporthe*, *Melanocarpus*, *Meripilus*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Piromyces*, *Poitrasia*, *Pseudoplectania*,

24 Mar 2026
2026202266

Pseudotrichonympha, *Rhizomucor*, *Schizophyllum*, *Scytalidium*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, *Trichoderma*, *Trichophaea*, *Verticillium*, *Volvariella*, or *Xylaria* alpha-amylase.

In another aspect, the parent is a *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis*, or *Saccharomyces oviformis* alpha-amylase.

In another aspect, the parent is an *Acremonium cellulolyticus*, *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus fumigatus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, *Chrysosporium inops*, *Chrysosporium keratinophilum*, *Chrysosporium lucknowense*, *Chrysosporium merdarium*, *Chrysosporium pannicola*, *Chrysosporium queenslandicum*, *Chrysosporium tropicum*, *Chrysosporium zonatum*, *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecioides*, *Fusarium venenatum*, *Humicola grisea*, *Humicola insolens*, *Humicola lanuginosa*, *Irpex lacteus*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium funiculosum*, *Penicillium purpurogenum*, *Phanerochaete chrysosporium*, *Thielavia achromatica*, *Thielavia albomyces*, *Thielavia albopilosa*, *Thielavia australeinsis*, *Thielavia fimeti*, *Thielavia microspora*, *Thielavia ovispora*, *Thielavia peruviana*, *Thielavia setosa*, *Thielavia spededonium*, *Thielavia subthermophila*, *Thielavia terrestris*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* alpha-amylase.

In another aspect, the parent is a *Bacillus* sp. alpha-amylase, *e.g.*, the alpha-amylase of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16, SEQ ID NO: 17.

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

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

24 Mar 2026
2026202266

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. The polynucleotide encoding a parent may then be derived by similarly screening a genomic or cDNA library of another microorganism or mixed DNA sample. Once a polynucleotide encoding a parent has been detected with a probe(s), the polynucleotide may 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*).

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

The parent may also be a fused polypeptide or cleavable fusion polypeptide in which one polypeptide is fused at the N-terminus or the C-terminus of another polypeptide. A fused polypeptide is produced by fusing a polynucleotide encoding one polypeptide to a polynucleotide encoding another polypeptide. 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 fused polypeptide is under control of the same promoter(s) and terminator. Fusion proteins may also be constructed using intein technology in which fusions 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.

Polynucleotides

The present invention also relates to polynucleotides encoding a variant of the present invention. Thus, in particular, the present invention relates to a polynucleotide encoding a variant comprising a modification at one or more positions corresponding to postions: H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136,

24 Mar 2026
2026202266

A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering.

The term "polynucleotides encoding" as used herein, refers to a polynucleotide that encodes a polypeptide having alpha-amylase having alpha-amylase activity. In one aspect, the polypeptide coding sequence is the nucleotide sequence set forth in SEQ ID NO: 18.

In one embodiment, the polynucleotide encoding a variant according to the present invention as at least 60%, such as at least 65%, such as at least 70%, such as at least 75%, such as at least 80%, such as at least 85%, such as at least 90%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, such as at least 99% but less than 100% sequence identity to the polynucleotide of SEQ ID NO: 18.

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. Thus, in particular, the present invention relates to a nucleic acid construct comprising a polynucleotide encoding a variant comprising a modification at one or more positions corresponding to positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481A, using SEQ ID NO: 1 for numbering.

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

24 Mar 2026
2026202266

The term "operably linked" as used herein, refers to a configuration in which a control sequence is placed at an appropriate position relative to the coding sequence of a polynucleotide such that the control sequence directs expression of the coding sequence.

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 comprises 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.

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. Thus, the present invention relates to an expression vector, optionally recombinant, comprising a polynucleotide encoding a variant comprising a modification at one or more positions corresponding to positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering, a promotor, and transcriptional and translational stop signals.

The term "expression vector" as used herein, refers to a linear or circular DNA molecule that comprises a polynucleotide encoding a variant and is operably linked to control sequences that provide for its expression.

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,

24 Mar 2026
2026202266

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.

The skilled person would know which expression vector is the most suitable for specific expression systems. Thus, the present invention is not limited to any specific expression vector, but any expression vector comprising the polynucleotide encoding a variant according to the invention is considered part of the present invention.

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. Thus, the present invention relates to a host cell, optionally a recombinant host cell, comprising a polynucleotide encoding a variant comprising a modification at one or more positions corresponding to positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210,

24 Mar 2026
2026202266

E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering operably linked to one or more control sequences that direct the production of the variant.

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

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 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*.

Preparation of Variants

The present invention also relates to methods for obtaining a variant having alpha-amylase activity, comprising: (a) introducing into a parent alpha-amylase of SEQ ID NO: 2 a modification at one or more positions corresponding to positions: H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering and the variant has alpha-

24 Mar 2026
2026202266

amylase activity; and (b) recovering the variant.

The present invention also relates to methods for obtaining a variant having alpha-amylase activity, comprising: (a) introducing into a parent alpha-amylase of SEQ ID NO: 2 a modification at one or more positions corresponding to position: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; Y160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q385L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481, using SEQ ID NO: 1 for numbering.

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

Site-directed mutagenesis is a technique in which one or more (several) modifications are created 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 modification. Site-directed mutagenesis can also be performed *in vitro* by cassette mutagenesis involving the cleavage by a restriction enzyme at

24 Mar 2026
2026202266

a site in the plasmid comprising a polynucleotide encoding the parent and subsequent ligation of an oligonucleotide containing the modification in the polynucleotide. Usually the restriction enzyme that digests at the plasmid and the oligonucleotide is the same, permitting sticky ends of the plasmid and 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 olgionucleotides are synthesized and assembled upon photo-programable 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; U.S. Patent No. 5,223,409; WO 92/06204) and region-directed mutagenesis (Derbyshire *et al.*, 1986, *Gene* 46: 145; Ner *et al.*, 1988, *DNA* 7: 127).

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

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 constuction 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,

24 Mar 2026
2026202266

while yet other regions may be subjected to error-prone PCR or non-error prone PCR ampflication. Polynucleotide subsequences may then be shuffled.

Methods of Production

The present invention also relates to methods of producing an alpha-amylase variant, comprising: (a) cultivating a host cell of the present invention under conditions suitable for the 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 polypeptide to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (*e.g.*, in catalogues of the American Type Culture Collection). If the 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. These detection methods may include 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 by 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*, J.-C. Janson and Lars Ryden, editors, VCH Publishers, New York, 1989) to obtain substantially pure variants.

Alternatively, the variant is not recovered, but rather a host cell of the present invention expressing a variant is used as a source of the variant.

Fermentation Broth Formulations or Cell Compositions

The present invention also relates to a fermentation broth formulation or a cell composition comprising a polypeptide of the present invention. Thus, in one embodiment, the fermentation broth formulation or the cell composition comprises a polynucleotide encoding a variant

24 Mar 2026
2026202266

comprising a modification in one or more positions corresponding to the positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481 and wherein the positions correspond to amino acid positions in the amino acid sequence set forth in SEQ ID NO: 2, a nucleic acid construct encoding a variant comprising an modification in one or more positions corresponding to the positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481 and wherein the positions correspond to amino acid positions in the amino acid sequence set forth in SEQ ID NO: 2, or an expression vector encoding a variant comprising an modification in one or more positions corresponding to the positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476, and V481 and wherein the positions correspond to amino acid positions in the amino acid sequence set forth in SEQ ID NO: 2. The fermentation broth product may further comprise additional ingredients used in the fermentation process, such as, for example, cells (including, the host cells containing the gene encoding the polypeptide of the present invention which are used to produce the

24 Mar 2026
2026202266

polypeptide of interest), cell debris, biomass, fermentation media and/or fermentation products. In some embodiments, the composition is a cell-killed whole broth containing organic acid(s), killed cells and/or cell debris, and culture medium.

The term "fermentation broth" as used herein refers to a preparation produced by cellular fermentation that undergoes no or minimal recovery and/or purification. For example, fermentation broths are produced when microbial cultures are grown to saturation, incubated under carbon-limiting conditions to allow protein synthesis (e.g., expression of enzymes by host cells) and secretion into cell culture medium. The fermentation broth can contain unfractionated or fractionated contents of the fermentation materials derived at the end of the fermentation. Typically, the fermentation broth is unfractionated and comprises the spent culture medium and cell debris present after the microbial cells (e.g., filamentous fungal cells) are removed, e.g., by centrifugation. In some embodiments, the fermentation broth contains spent cell culture medium, extracellular enzymes, and viable and/or nonviable microbial cells.

In one embodiment, the fermentation broth formulation and cell compositions comprise a first organic acid component comprising at least one 1-5 carbon organic acid and/or a salt thereof and a second organic acid component comprising at least one 6 or more carbon organic acid and/or a salt thereof. In a particular embodiment, the first organic acid component is acetic acid, formic acid, propionic acid, a salt thereof, or a mixture of two or more of the foregoing and the second organic acid component is benzoic acid, cyclohexanecarboxylic acid, 4-methylvaleric acid, phenylacetic acid, a salt thereof, or a mixture of two or more of the foregoing.

In one embodiment, the composition contains an organic acid(s), and optionally further contains killed cells and/or cell debris. In one embodiment, the killed cells and/or cell debris are removed from a cell-killed whole broth to provide a composition that is free of these components.

The fermentation broth formulations or cell compositions may further comprise a preservative and/or anti-microbial (*e.g.*, bacteriostatic) agent, including, but not limited to, sorbitol, sodium chloride, potassium sorbate, and others known in the art.

The cell-killed whole broth or composition may comprise the unfractionated contents of the fermentation materials derived at the end of the fermentation. Typically, the cell-killed whole broth or composition comprises the spent culture medium and cell debris present after the microbial cells (*e.g.*, filamentous fungal cells) are grown to saturation, incubated under carbon-limiting conditions to allow protein synthesis. In some embodiments, the cell-killed whole broth or composition comprises the spent cell culture medium, extracellular enzymes, and killed filamentous fungal cells. In some embodiments, the microbial cells present in the cell-killed whole broth or composition may be permeabilized and/or lysed using methods known in the art.

A whole broth or cell composition as described herein is typically a liquid, but may comprise insoluble components, such as killed cells, cell debris, culture media components,

24 Mar 2026
2026202266

and/or insoluble enzyme(s). In some embodiments, insoluble components may be removed to provide a clarified liquid composition.

The whole broth formulations and cell compositions of the present invention may be produced by a method described in WO 90/15861 or WO 2010/096673.

Compositions

The present invention also relates to composition comprising a variant of the present invention. Accordingly, the present invention relates to compositions comprising a variant having a modification at one or more positions corresponding to positions: H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481 and wherein the positions correspond to amino acid positions in the amino acid sequence set forth in SEQ ID NO: 2.

In one embodiment, the composition comprises a variant comprising

a) a deletion and/or a substitution at two or more positions corresponding to positions R181, G182, D183, and G184 of the amino acid sequence as set forth in SEQ ID NO: 2, and

b) an modification at one or more positions corresponding to positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481 of the amino acid sequence as set forth in SEQ ID NO : 2.

Preferably, the compositions are enriched in such a variant. The term "enriched" means that the alpha-amylase activity of the composition has been increased, *e.g.*, with an enrichment factor of 1.1.

24 Mar 2026
2026202266

In one embodiment, the invention is directed to compositions comprising a variant of the present invention in combination with one or more 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.

In one embodiment, the present invention relates to a composition comprising one or more additional components selected from the group consisting of one or more enzymes, oxidizing agents, bleach activators, bleach catalysts, chelating agents, bulking agents, builders, buffering agents, structurants, sequestrants, optical brighteners, antifoaming agents, enzymes, fragrances, anti-redeposition agents, skin conditioning agents, softness extenders, emulsifiers, crystal growth inhibitors, metal care agents, glass care agents and colorants.

In one embodiment, the present invention relates to a composition comprises a surfactant.

In one embodiment, the present invention relates to a composition wherein the surfactant is one or more surfactants selected from the group consisting of an anionic surfactant, a cationic surfactant, a non-ionic surfactant, zwitterionic surfactant, and amphoteric surfactants or any mixtures thereof.

In one embodiment, the present invention relates to a composition wherein the composition is a detergent composition.

In one embodiment, the composition is a liquid laundry or liquid dish wash composition, such as an Automatic Dish Wash (ADW) liquid detergent composition, or a powder laundry, such as a soap bar, or powder dish wash composition, such as an ADW unit dose detergent composition and such as a Hand Dish Wash (HDW) detergent composition.

In one embodiment, the present invention relates to a composition wherein the composition comprises one or more additional enzymes.

The composition may comprise a variant as the major enzymatic component, *e.g.*, a mono-component composition. Alternatively, the composition may comprise multiple enzymatic activities, such as an proteases, amylases, phospho- lipases, esterases,lipases, cutinases, cellulases, endoglucanases, xyloglucanases, xylanases, pectinases, hemicellulases pectin lyases, xanthanases, peroxidases, keratinases haloperoxygenases, catalases, mannanases, lechinase, RNase, DNAse, reductases, oxidases, phenoloxidases, lipoxygenases, ligninases, pullulanases, tannases, pento-sanases, malanases, β-glucanases, arabinosidases, hyaluronidase, chondroitinase, and laccase or any mixture thereof.

The additional enzyme(s) may be produced, for example, by a microorganism belonging to the genus *Bacillus, e.g. Bacillus licheniformis and Bacillus subtilis,* or the genus *Aspergillus*, *e.g.*, *Aspergillus aculeatus*, *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus fumigatus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, or *Aspergillus oryzae*; *Fusarium*, *e.g.*, *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*,

24 Mar 2026
2026202266

Fusarium graminearum, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sulphureum*, *Fusarium toruloseum*, *Fusarium trichothecioides*, or *Fusarium venenatum*; *Humicola*, *e.g.*, *Humicola insolens* or *Humicola lanuginosa*; or *Trichoderma*, *e.g.*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* or any other host cell herein described.

The compositions may be prepared in accordance with methods known in the art and may be in the form of a liquid or a dry composition. For instance, the composition may be in the form of a granulate or a microgranulate. The variant may be stabilized in accordance with methods known in the art.

Such compositions comprise a cleaning/detergent components, preferably a mixture of components. Typically, the cleaning components will be present in the composition in an amount from 0.001 to 99.9 wt%, more typically from 0.01 to 80 wt% cleaning component.

In another preferred aspect the composition comprises one or more surfactants, which may be non-ionic including semi-polar and/or anionic and/or cationic and/or zwitterionic and/or ampholytic and/or semi-polar nonionic and/or mixtures thereof. The surfactants are typically present at a level of from 0.1% to 60% by weight or from 0.5 to 50 wt% or 1 to 40 wt% of the composition.

In one embodiment of the present invention, the variant 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 term “protein” in this context is contemplated to be understood to include a variant according to the present invention.

A composition for use in automatic dish wash (ADW), for example, may include 0.0001%-50%, such as 0.001%-20%, such as 0.01%-10%, such as 0.05-5% of enzyme protein by weight of the composition.

A composition for use in laundry granulation, for example, may include 0.0001%-50%, such as 0.001%-20%, such as 0.01%-10%, such as 0.05%-5% of enzyme protein by weight of the composition.

A composition for use in laundry liquid, for example, may include 0.0001%-10%, such as 0.001-7%, such as 0.1%-5% of enzyme protein by weight of the composition.

The variants of the invention as well as the further active components, such as additional enzymes, may be stabilized using conventional stabilizing agents, e.g., a polyol such as propylene glycol or glycerol, a sugar or sugar alcohol, lactic acid, boric acid, or a boric acid derivative, e.g., an aromatic borate ester, or a phenyl boronic acid derivative such as 4-formylphenyl boronic acid,

24 Mar 2026
2026202266

and the composition may be formulated as described in, for example, WO92/19709 and WO92/19708.

In certain markets different wash conditions and, as such, different types of detergents are used. This is disclosed in e.g. EP 1 025 240. For example, In Asia (Japan) a low detergent concentration system is used, while the United States uses a medium detergent concentration system, and Europe uses a high detergent concentration system.

A low detergent concentration system includes detergents where less than about 800 ppm of detergent components are present in the wash water. Japanese detergents are typically considered low detergent concentration system as they have approximately 667 ppm of detergent components present in the wash water.

A medium detergent concentration includes detergents where between about 800 ppm and about 2000ppm of detergent components are present in the wash water. North American detergents are generally considered to be medium detergent concentration systems as they have approximately 975 ppm of detergent components present in the wash water.

A high detergent concentration system includes detergents where greater than about 2000 ppm of detergent components are present in the wash water. European detergents are generally considered to be high detergent concentration systems as they have approximately 4500-5000 ppm of detergent components in the wash water.

Latin American detergents are generally high suds phosphate builder detergents and the range of detergents used in Latin America can fall in both the medium and high detergent concentrations as they range from 1500 ppm to 6000 ppm of detergent components in the wash water. Such detergent compositions are all embodiments of the invention.

A variant of the present invention may also be incorporated in the detergent formulations disclosed in WO97/07202, which is hereby incorporated by reference.

Examples are given herein of preferred uses of the compositions of the present invention. The dosage of the composition and other conditions under which the composition is used may be determined on the basis of methods known in the art.

In particular, a composition according to the present invention further comprises a chelator.

The term “chelator” as used herein, refers to chemicals which form molecules with certain metal ions, inactivating the ions so that they cannot react with other elements. Thus, a chelator may be defined as a binding agent that suppresses chemical activity by forming chelates. Chelation is the formation or presence of two or more separate bindings between a ligand and a single central atom. The ligand may be any organic compound, a silicate or a phosphate. In the present context the term “chelating agents” comprises chelants, chelating agent, chelating agents, complexing agents, or sequestering agents that forms water-soluble complexes with

24 Mar 2026
2026202266

metal ions such as calcium and magnesium. The chelate effect describes the enhanced affinity of chelating ligands for a metal ion compared to the affinity of a collection of similar nonchelating ligands for the same metal. Chelating agents having binding capacity with metal ions, in particular calcium (Ca2+) ions, and has been used widely in detergents and compositions in general for wash, such as laundry or dish wash. Chelating agents have however shown themselves to inhibit enzymatic activity. The term chelating agent is used in the present application interchangeably with “complexing agent” or “chelating agent” or “chelant”.

Since most alpha-amylases are calcium sensitive the presence of chelating agents these may impair the enzyme activity. The calcium sensitivity of alpha-amylases can be determined by incubating a given alpha-amylase in the presence of a strong chelating agent and analyze the impact of this incubation on the activity of the alpha-amylase in question. A calcium sensitive alpha-amylase will lose a major part or all of its activity during the incubation. Chelating agent may be present in the composition in an amount from 0.0001 wt% to 20wt%, preferably from 0.01 to 10 wt%, more preferably from 0.1 to 5wt%.

Non-limiting examples of chelating agents are; EDTA, DTMPA, HEDP, and citrate. Thus, in one embodiment, the composition comprises a variant according to the invention and a chelating agent, such as EDTA, DTMPA, HEDP or citrate.

The term “EDTA” as used herein, refers to ethylene-diamine-tetra-acetic acid which falls under the definition of “strong chelating agents”.

The term “DTMPA” as used herein, refers to diethylenetriamine penta(methylene phosphonic acid). DTMPA can inhibit the scale formation of carbonate, sulfate and phosphate.

The term “HEDP” as used herein, refers to hydroxy-ethane diphosphonic acid, which falls under the definition of “strong chelating agents”.

The chelate effect or the chelating effect describes the enhanced affinity of chelating ligands for a metal ion compared to the affinity of a collection of similar nonchelating ligands for the same metal. However, the strength of this chelate effect can be determined by various types of assays or measure methods thereby differentiating or ranking the chelating agents according to their chelating effect (or strength).

In an assay the chelating agents may be characterized by their ability to reduce the concentration of free calcium ions (Ca2+) from 2.0 mM to 0.10 mM or less at pH 8.0, e.g. by using a test based on the method described by M.K.Nagarajan et al., JAOCS, Vol. 61, no. 9 (September 1984), pp. 1475-1478.

For reference, a chelator having the same ability to reduce the concentration of free calcium ions (Ca2+) from 2.0 mM to 0.10 mM at pH as EDTA at equal concentrations of the chelator are said to be strong chelators.

24 Mar 2026
2026202266

The composition of the present invention may be in any convenient form, e.g., a bar, a homogenous tablet, a tablet having two or more layers, a pouch having one or more compartments, a regular or compact powder, a granule, a paste, a gel, or a regular, compact or concentrated liquid. There are a number of detergent formulation forms such as layers (same or different phases), pouches, as well as 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 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 may be separated physically from each other by compartments in water dissolvable pouches or in different layers of tablets. Thereby negative storage interaction between components may be avoided. Different dissolution profiles of each of the compartments can also give rise to delayed dissolution of selected components in the wash solution.

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

Another form of composition is in the form of a soap bar, such as a laundry soap bar, and may be used for hand washing laundry, fabrics and/or textiles. The term “soap bar” as used herein, refers to includes laundry bars, soap bars, combo bars, syndet bars and detergent bars.

24 Mar 2026
2026202266

The types of bar usually differ in the type of surfactant they contain, and the term laundry soap bar includes those containing soaps from fatty acids and/or synthetic soaps. The laundry soap bar has a physical form which is solid and not a liquid, gel or a powder at room temperature. The term "solid" as used herein, refers to a physical form which does not significantly change over time, i.e. if a solid object (e.g. laundry soap bar) is placed inside a container, the solid object does not change to fill the container it is placed in. The bar is a solid typically in bar form but can be in other solid shapes such as round or oval.

The soap bar may also comprise complexing agents like EDTA and HEDP, perfumes and/or different type of fillers, surfactants e.g. anionic synthetic surfactants, builders, polymeric soil release agents, detergent chelators, stabilizing agents, fillers, dyes, colorants, dye transfer inhibitors, alkoxylated polycarbonates, suds suppressers, structurants, binders, leaching agents, bleaching activators, clay soil removal agents, anti-redeposition agents, polymeric dispersing agents, brighteners, fabric softeners, perfumes and/or other compounds known in the art.

The soap bar may be processed in conventional laundry soap bar making equipment such as but not limited to: mixers, plodders, e.g. a two stage vacuum plodder, extruders, cutters, logo-stampers, cooling tunnels and wrappers. The invention is not limited to preparing the soap bars by any single method. The premix of the invention may be added to the soap at different stages of the process. For example, the premix comprising a soap, an enzyme, optionally one or more additional enzymes, a protease inhibitor, and a salt of a monovalent cation and an organic anion may be prepared and the mixture may then plodded. The enzyme and optional additional enzymes may be added at the same time as an enzyme inhibitor, e.g. a protease inhibitor, for example in liquid form. Besides the mixing step and the plodding step, the process may further comprise the steps of milling, extruding, cutting, stamping, cooling and/or wrapping.

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

24 Mar 2026
2026202266

sulfates and sulfonates, in particular, linear alkylbenzenesulfonates (LAS), isomers of LAS, branched alkylbenzenesulfonates (BABS), phenylalkanesulfonates, alpha-olefinsulfonates (AOS), olefin sulfonates, alkene sulfonates, alkane-2,3-diylbis(sulfates), hydroxyalkanesulfonates and disulfonates, alkyl sulfates (AS) such as sodium dodecyl sulfate (SDS), fatty alcohol sulfates (FAS), primary alcohol sulfates (PAS), alcohol ethersulfates (AES or AEOS or FES, also known as alcohol ethoxysulfates or fatty alcohol ether sulfates), secondary alkanesulfonates (SAS), paraffin sulfonates (PS), ester sulfonates, sulfonated fatty acid glycerol esters, alpha-sulfo fatty acid methyl esters (alpha-SFMe or SES) including methyl ester sulfonate (MES), alkyl- or alkenylsuccinic acid, dodecenyl/tetradecenyl succinic acid (DTSA), fatty acid derivatives of amino acids, diesters and monoesters of sulfo-succinic acid or soap, and combinations thereof.

When included therein the detergent will usually contain from about 0 % to about 40% by weight of a cationic surfactant. Non-limiting examples of cationic surfactants include alklydimethylethanolamine quat (ADMEAQ), cetyltrimethylammonium bromide (CTAB), dimethyldistearylammonium chloride (DSDMAC), and alkylbenzyldimethylammonium, alkyl quaternary ammonium compounds, alkoxylated quaternary ammonium (AQA) compounds, and combinations thereof.

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), epoxy-capped poly(oxyalkylated) alcohols, alkoxylated fatty acid alkyl esters, such as ethoxylated and/or propoxylated fatty acid alkyl esters, alkylphenol ethoxylates (APE), nonylphenol ethoxylates (NPE), alkylpolyglycosides (APG), alkoxylated amines, fatty acid monoethanolamides (FAM), fatty acid diethanolamides (FADA), ethoxylated fatty acid monoethanolamides (EFAM), propoxylated fatty acid monoethanolamides (PFAM), 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 0 % 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 0% to about 40% by weight of a zwitterionic surfactant. Non-limiting examples of zwitterionic surfactants include betaine, alkyldimethylbetaine, sulfobetaine, and combinations thereof.

24 Mar 2026
2026202266

The detergent composition may also comprise one or more isoprenoid surfactants as disclosed in US 20130072416 or US 20130072415.

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 miceller, 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 sulfonate (STS), sodium xylene sulfonate (SXS), sodium cumene sulfonate (SCS), sodium cymene sulfonate, amine oxides, alcohols and polyglycolethers, sodium hydroxynaphthoate, sodium hydroxynaphthalene sulfonate, sodium ethylhexyl sulfate, and combinations thereof.

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/hard surface cleaning detergents may be utilized. Non-limiting examples of builders include zeolites, diphosphates (pyrophosphates), triphosphates such as sodium triphosphate (STP or STPP), carbonates such as sodium carbonate, soluble silicates such as sodium metasilicate, layered silicates (*e.g.*, SKS-6 from Hoechst), ethanolamines such as 2-aminoethan-1-ol (MEA), diethanolamine (DEA, also known as 2,2'-iminodiethan-1-ol),

24 Mar 2026
2026202266

triethanolamine (TEA, also known as 2,2',2"-nitrilotriethan-1-ol), and (carboxymethyl)inulin (CMI), and combinations thereof.

The detergent composition may also contain 0-50% by weight, such as about 5% to about 30%, of a detergent co-builder. The detergent composition may include a co-builder alone, or in combination with a builder, for example a zeolite builder. Non-limiting examples of co-builders include homopolymers of polyacrylates or copolymers thereof, such as poly(acrylic acid) (PAA) or copoly(acrylic acid/maleic acid) (PAA/PMA). Further non-limiting examples include citrate, chelators such as aminocarboxylates, aminopolycarboxylates and phosphonates, and alkyl- or alkenylsuccinic acid. Additional specific examples include 2,2',2"-nitrilotriacetic acid (NTA), ethylenediaminetetraacetic acid (EDTA), diethylenetriaminepentaacetic acid (DTPA), iminodisuccinic acid (IDS), ethylenediamine-*N*,*N*'-disuccinic acid (EDDS), methylglycinediacetic acid (MGDA), glutamic acid-*N*,*N*-diacetic acid (GLDA), 1-hydroxyethane-1,1-diphosphonic acid (HEDP), ethylenediaminetetra(methylenephosphonic acid) (EDTMPA), diethylenetriaminepentakis(methylenephosphonic acid) (DTMPA or DTPMPA), *N*-(2-hydroxyethyl)iminodiacetic acid (EDG), aspartic acid-*N*-monoacetic acid (ASMA), aspartic acid-*N*,*N*-diacetic acid (ASDA), aspartic acid-*N*-monopropionic acid (ASMP), iminodisuccinic acid (IDA), *N*-(2-sulfomethyl)-aspartic acid (SMAS), *N*-(2-sulfoethyl)-aspartic acid (SEAS), *N*-(2-sulfomethyl)-glutamic acid (SMGL), *N*-(2-sulfoethyl)-glutamic acid (SEGL), *N*-methyliminodiacetic acid (MIDA), α-alanine-*N*,*N*-diacetic acid (α-ALDA), serine-*N*,*N*-diacetic acid (SEDA), isoserine-*N*,*N*-diacetic acid (ISDA), phenylalanine-*N*,*N*-diacetic acid (PHDA), anthranilic acid-*N*,*N*-diacetic acid (ANDA), sulfanilic acid-*N*,*N*-diacetic acid (SLDA) , taurine-*N*,*N*-diacetic acid (TUDA) and sulfomethyl-*N*,*N*-diacetic acid (SMDA), *N*-(2-hydroxyethyl)ethylenediamine-*N*,*N'*,*N''*-triacetic acid (HEDTA), diethanolglycine (DEG), diethylenetriamine penta(methylenephosphonic acid) (DTPMP), aminotris(methylenephosphonic acid) (ATMP), and combinations and salts thereof. Further exemplary builders and/or co-builders are described in, e.g., WO 09/102854, US 5977053

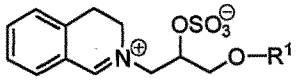
Bleaching Systems

The detergent may contain 0-30% by weight, such as about 1% to about 20%, of a bleaching system. Any bleaching system known in the art for use in laundry/ADW/hard surface cleaning detergents may be utilized. Suitable bleaching system components include bleaching catalysts, photobleaches, bleach activators, sources of hydrogen peroxide such as sodium percarbonate, sodium perborates and hydrogen peroxide—urea (1:1), preformed peracids and mixtures thereof. Suitable preformed peracids include, but are not limited to, peroxycarboxylic acids and salts, diperoxydicarboxylic acids, 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

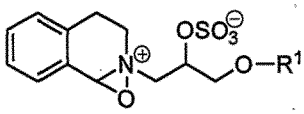
24 Mar 2026
2026202266

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. The term bleach activator is meant herein as a compound which reacts with hydrogen peroxide to form a peracid via perhydrolysis. 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 tetraacetylethylenediamine (TAED), acylated triazine derivatives, in particular 1,5-diacetyl-2,4-dioxohexahydro-1,3,5-triazine (DADHT), acylated glycolurils, in particular tetraacetylglycoluril (TAGU). N-acylimides, in particular N-nonanoylsuccinimide (NOSI), sodium 4-[(3,5,5-trimethylhexanoyl)oxy]benzene-1-sulfonate (ISONOBS), 4-(dodecanoyloxy)benzene-1-sulfonate (LOBS), 4-(decanoyloxy)benzene-1-sulfonate, 4-(decanoyloxy)benzoate (DOBS or DOBA), 4-(nonanoyloxy)benzene-1-sulfonate (NOBS), and/or those disclosed in WO98/17767. A particular family of bleach activators of interest was disclosed in EP624154 and particulary preferred in that family is acetyl triethyl citrate (ATC). ATC or a short chain triglyceride like triacetin has the advantage that it is environmentally friendly Furthermore acetyl triethyl citrate and triacetin have good hydrolytical stability in the product upon storage and are efficient bleach activators. Finally ATC is multifunctional, as the citrate released in the perhydrolysis reaction may function as a builder. 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-(phthalimido)peroxyhexanoic acid (PAP). The bleaching system may also include a bleach catalyst, for example manganese triazacyclononane, manganese oxalate, Co, Cu, Mn and Fe bispyridylamine and pentamine acetate cobalt(III). In some embodiments the bleach component may be an organic catalyst selected from the group consisting of organic catalysts having the following formulae:

(i)



(ii)



(iii) and mixtures thereof;

wherein each R^1 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^1 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^1 is independently selected from the group consisting of 2-propylheptyl, 2-butyloctyl, 2-pentylnonyl, 2-hexyldecyl, dodecyl, tetradecyl, hexadecyl, octadecyl, isononyl, isodecyl, isotridecyl and isopentadecyl. Other exemplary bleaching systems are described, e.g. in WO2007/087258, WO2007/087244, WO2007/087259, EP1867708 (Vitamin K)

24 Mar 2026

2026202266

and WO2007/087242. Suitable photobleaches may for example be sulfonated zinc or aluminium phthalocyanines.

Preferably the bleach component comprises a source of peracid in addition to bleach catalyst, particularly organic bleach catalyst. The source of peracid may be selected from (a) pre-formed peracid; (b) percarbonate, perborate or persulfate salt (hydrogen peroxide source) preferably in combination with a bleach activator; and (c) perhydrolase enzyme and an ester for forming peracid in situ in the presence of water in a textile or hard surface treatment step.

Polymers

The detergent may contain 0-10% by weight, such as 0.5-5%, 2-5%, 0.5-2% or 0.2-1% of a polymer. Any polymer known in the art for use in detergents may be utilized. The polymer may function as a co-builder as mentioned above, or may provide antiredeposition, fiber protection, soil release, dye transfer inhibition, grease cleaning and/or anti-foaming properties. Some polymers may have more than one of the above-mentioned properties and/or more than one of the below-mentioned motifs. Exemplary polymers include (carboxymethyl)cellulose (CMC), poly(vinyl alcohol) (PVA), poly(vinylpyrrolidone) (PVP), poly(ethyleneglycol) or poly(ethylene oxide) (PEG), ethoxylated poly(ethyleneimine), carboxymethyl inulin (CMI), and polycarboxylates such as PAA, PAA/PMA, poly-aspartic acid, and lauryl methacrylate/acrylic acid copolymers , hydrophobically modified CMC (HM-CMC) and silicones, copolymers of terephthalic acid and oligomeric glycols, copolymers of poly(ethylene terephthalate) and poly(oxyethene terephthalate) (PET-POET), PVP, poly(vinylimidazole) (PVI), poly(vinylpyridine-*N*-oxide) (PVPO or PVPNO) and polyvinylpyrrolidone-vinylimidazole (PVPVI). 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 of the present invention may also include fabric hueing agents such as dyes or pigments, which when formulated in detergent compositions can deposit onto a fabric when said fabric is contacted with a wash liquor comprising said detergent compositions and thus altering the tint of said fabric through absorption/reflection of visible light. Fluorescent whitening agents emit at least some visible light. In contrast, fabric hueing agents alter the tint of a surface as they absorb at least a portion of the visible light spectrum. Suitable fabric hueing agents include dyes and dye-clay conjugates, and may also include pigments. Suitable dyes include small molecule dyes and polymeric dyes. Suitable small molecule dyes include small molecule dyes selected from the group consisting of dyes falling into the Colour

24 Mar 2026
2026202266

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

Adjunct materials

Any detergent components known in the art for use in laundry, ADW or hard surface cleaning 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, metal care agents, glass care agents, 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, ADW or hard surface cleaning detergents may be utilized. The choice of such ingredients is well within the skill of the artisan.

Dispersants

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

Dye Transfer Inhibiting Agents

The detergent compositions of the present invention may also include one or more dye transfer inhibiting agents. Suitable polymeric dye transfer inhibiting agents include, but are not limited to, polyvinylpyrrolidone polymers, polyamine *N*-oxide polymers, copolymers of *N*-vinylpyrrolidone and *N*-vinylimidazole, polyvinyloxazolidones and polyvinylimidazoles or mixtures thereof. When present in a subject composition, the dye transfer inhibiting agents may be present

24 Mar 2026
2026202266

at levels from about 0.0001 % to about 10%, from about 0.01% to about 5% or even from about 0.1% to about 3% by weight of the composition.

Fluorescent whitening agent

The detergent compositions of the present invention will preferably also contain additional components that may tint articles being cleaned, such as fluorescent whitening agent or optical brighteners. Where present the brightener is preferably at a level of about 0.01% to about 0.5%. Any fluorescent whitening agent suitable for use in a laundry detergent composition may be used in the composition of the present invention. The most commonly used fluorescent whitening agents are those belonging to the classes of diaminostilbene-sulfonic acid derivatives, diarylpyrazoline derivatives and bisphenyl-distyryl derivatives. Examples of the diaminostilbene-sulfonic acid derivative type of fluorescent whitening agents include the sodium salts of: 4,4'-bis-(2-diethanolamino-4-anilino-s-triazin-6-ylamino) stilbene-2,2'-disulfonate, 4,4'-bis-(2,4-dianilino-s-triazin-6-ylamino) stilbene-2.2'-disulfonate, 4,4'-bis-(2-anilino-4-(*N*-methyl-*N*-2-hydroxy-ethylamino)-s-triazin-6-ylamino) stilbene-2,2'-disulfonate, 4,4'-bis-(4-phenyl-1,2,3-triazol-2-yl)stilbene-2,2'-disulfonate and sodium 5-(2*H*-naphtho[1,2-*d*][1,2,3]triazol-2-yl)-2-[(*E*)-2-phenylvinyl]benzenesulfonate. Preferred fluorescent whitening agents are Tinopal DMS and Tinopal CBS available from Ciba-Geigy AG, Basel, Switzerland. Tinopal DMS is the disodium salt of 4,4'-bis-(2-morpholino-4-anilino-s-triazin-6-ylamino) stilbene-2,2'-disulfonate. Tinopal CBS is the disodium salt of 2,2'-bis-(phenyl-styryl)-disulfonate. Also preferred are fluorescent whitening agents is the commercially available Parawhite KX, supplied by Paramount Minerals and Chemicals, Mumbai, India. Other fluorescers suitable for use in the invention include the 1-3-diaryl pyrazolines and the 7-alkylaminocoumarins.

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

Soil release polymers

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

2026202266 24 Mar 2026

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 deriviatives such as those described in EP 1867808 or WO 2003/040279 (both are hereby incorporated by reference). Suitable cellulosic polymers include cellulose, cellulose ethers, cellulose esters, cellulose amides and mixtures thereof. Suitable cellulosic polymers include anionically modified cellulose, nonionically modified cellulose, cationically modified cellulose, zwitterionically modified cellulose, and mixtures thereof. Suitable cellulosic polymers include methyl cellulose, carboxy methyl cellulose, ethyl cellulose, hydroxyl ethyl cellulose, hydroxyl propyl methyl cellulose, ester carboxy methyl cellulose, and mixtures thereof.

Anti-redeposition agents

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

Rheology Modifiers

The detergent compositions of the present invention may also include one or more rheology modifiers, structurants or thickeners, as distinct from viscosity reducing agents. The rheology modifiers are selected from the group consisting of non-polymeric crystalline, hydroxy-functional materials, polymeric rheology modifiers which impart shear thinning characteristics to the aqueous liquid matrix of a liquid detergent composition. The rheology and viscosity of the detergent can be modified and adjusted by methods known in the art, for example as shown in EP 2169040.

Other suitable 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, and structurants for liquid detergents and/or structure elasticizing agents.

24 Mar 2026
2026202266

Enzymes

In one embodiment, the composition according to the invention comprises one or more further enzymes, such as at least two enzymes, more preferred at least three, four or five enzymes. Preferably, the enzymes of the detergent composition have different substrate specificity, *e.g.,* proteolytic activity, amylolytic activity, lipolytic activity, cellulytic activity, hemicellulytic activity, oxidative activity, RNAse activity, DNAse activity or pectolytic activity.

The composition according to the invention may comprise one or more additional enzymes selected from proteases, second amylases, lipases, cutinases, cellulases, endoglucanases, lechinase, xyloglucanases, pectinases, pectin lyases, xanthanases, peroxidases, haloperoxygenases, catalases, mannanases, or any mixture thereof. Other suitable enzymes include carbohydrate-active enzymes like carbohydrase, arabinase, galactanase, xylanase; or oxidases, *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

24 Mar 2026
2026202266

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

Peroxidases/Oxidases:

A peroxidase according to the invention is a peroxidase enzyme comprised by the enzyme classification EC 1.11.1.7, as set out by the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB), or any fragment derived therefrom, exhibiting peroxidase activity.

Suitable peroxidases include those of plant, bacterial or fungal origin. Chemically modified or protein engineered mutants are included. Examples of useful peroxidases include peroxidases from Coprinopsis, e.g., from C. cinerea (EP 179,486), and variants thereof as those described in WO 93/24618, WO 95/10602, and WO 98/15257. Commercially available peroxidases include Guardzyme™ (Novozymes A/S).

A peroxidase according to the invention also include a haloperoxidase enzyme, such as chloroperoxidase, bromoperoxidase and compounds exhibiting chloroperoxidase or bromoperoxidase activity. Haloperoxidases are classified according to their specificity for halide ions. Chloroperoxidases (E.C. 1.11.1.10) catalyze formation of hypochlorite from chloride ions.

In an embodiment, the haloperoxidase of the invention is a chloroperoxidase. Preferably, the haloperoxidase is a vanadium haloperoxidase, *i.e.*, a vanadate-containing haloperoxidase. In a preferred method of the present invention the vanadate-containing haloperoxidase is combined with a source of chloride ion.

Haloperoxidases have been isolated from many different fungi, in particular from the fungus group dematiaceous hyphomycetes, such as *Caldariomyces*, *e.g.*, *C. fumago*, *Alternaria*, *Curvularia*, *e.g.*, *C. verruculosa* and *C. inaequalis*, *Drechslera*, *Ulocladium* and *Botrytis*.

Haloperoxidases have also been isolated from bacteria such as *Pseudomonas*, *e.g.*, *P. pyrrocinia* and *Streptomyces*, *e.g.*, *S. aureofaciens*.

In an preferred embodiment, the haloperoxidase is derivable from *Curvularia* sp., in particular *Curvularia verruculosa* or *Curvularia inaequalis*, such as *C. inaequalis* CBS 102.42 as described in WO 95/27046; or *C. verruculosa* CBS 147.63 or *C. verruculosa* CBS 444.70 as described in WO 97/04102; or from *Drechslera hartlebii* as described in WO 01/79459, *Dendryphiella salina* as described in WO 01/79458, *Phaeotrichoconis crotalarie* as described in WO 01/79461, or *Geniculosporium* sp. as described in WO 01/79460.

An oxidase according to the invention include, in particular, any laccase enzyme comprised by the enzyme classification EC 1.10.3.2, or any fragment derived therefrom exhibiting

24 Mar 2026
2026202266

laccase activity, or a compound exhibiting a similar activity, such as a catechol oxidase (EC 1.10.3.1), an o-aminophenol oxidase (EC 1.10.3.4), or a bilirubin oxidase (EC 1.3.3.5).

Preferred laccase enzymes are enzymes of microbial origin. The enzymes may be derived from plants, bacteria or fungi (including filamentous fungi and yeasts).

Suitable examples from fungi include a laccase derivable from a strain of *Aspergillus, Neurospora*, *e.g.*, *N. crassa*, *Podospora*, *Botrytis*, *Collybia*, *Fomes*, *Lentinus*, *Pleurotus*, *Trametes*, *e.g.*, *T. villosa* and *T. versicolor*, *Rhizoctonia*, *e.g.*, *R. solani*, *Coprinopsis*, *e.g.*, *C. cinerea*, *C. comatus*, *C. friesii*, and *C. plicatilis*, *Psathyrella*, *e.g.*, *P. condelleana*, *Panaeolus*, *e.g.*, *P. papilionaceus*, *Myceliophthora*, *e.g.*, *M. thermophila*, *Schytalidium*, *e.g.*, *S. thermophilum*, *Polyporus*, *e.g.*, *P. pinsitus*, *Phlebia*, *e.g.*, *P. radiata* (WO 92/01046), or *Coriolus*, *e.g.*, *C. hirsutus* (JP 2238885).

Suitable examples from bacteria include a laccase derivable from a strain of *Bacillus*.

A laccase derived from *Coprinopsis* or *Myceliophthora* is preferred; in particular a laccase derived from *Coprinopsis cinerea*, as disclosed in WO 97/08325; or from *Myceliophthora thermophila*, as disclosed in WO 95/33836.

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, Bacillus alkalophilus, Bacillus subtilis, Bacillus amyloliquefaciens, Bacillus pumilus* and *Bacillus gibsonii* described in; US7262042 and WO09/021867, and *Subtilisin lentus*, *Subtilisin* Novo, *subtilisin* Carlsberg, *Bacillus licheniformis*, *subtilisin* BPN', *subtilisin* 309, *subtilisin* 147 and *subtilisin* 168 and e.g. protease PD138 described in (WO93/18140). Other useful proteases may be those described in WO01/016285 and WO02/016547. Examples of trypsin-like proteases are trypsin (e.g. of porcine or bovine origin) and the *Fusarium* protease described in WO94/25583 and

24 Mar 2026
2026202266

WO05/040372, and the chymotrypsin proteases derived from *Cellumonas* described in WO05/052161 and WO05/052146.

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

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

Examples of useful proteases are the variants described in: WO89/06279 WO92/19729, WO96/034946, WO98/20115, WO98/20116, WO99/011768, WO01/44452, WO03/006602, WO04/03186, WO04/041979, WO07/006305, WO11/036263, WO11/036264, especially the variants with substitutions in one or more of the following positions: 3, 4, 9, 15, 24, 27, 42, 55, 59, 60, 66, 74, 85, 96, 97, 98, 99, 100, 101, 102, 104, 116, 118, 121, 126, 127, 128, 154, 156, 157, 158, 161, 164, 176, 179, 182, 185, 188, 189, 193, 198, 199, 200, 203, 206, 211, 212, 216, 218, 226, 229, 230, 239, 246, 255, 256, 268 and 269 wherein the positions correspond to the positions of the *Bacillus lentus* protease shown in SEQ ID NO 1 of WO 2016/001449. More preferred the protease variants may comprise one or more of the mutations selected from the group consisting of: S3T, V4I, S9R, S9E, A15T, S24G, S24R, K27R, N42R, S55P, G59E, G59D, N60D, N60E, V66A, N74D, S85R, A96S, S97G, S97D, S97A, S99E, S99D, S99G, S99M, S99N, S99R, S99H, S101A, V102I, V102Y, V102N, S104A, G116V, G116R, H118D, H118N, A120S, S126L, P127Q, S128A, S154D, A156E, G157D, G157P, S158E, Y161A, R164S, Q176E, N179E, S182E, Q185N, A188P, G189E, V193M, N198D, V199I, Y203W, S206G, L211Q, L211D, N212D, N212S, M216S, A226V, K229L, Q230H, Q239R, N246K, N255W, N255D, N255E, L256E, L256D T268A and R269H. The protease variants are preferably variants of the *Bacillus lentus* protease shown in SEQ ID NO 1 of WO2016/001449, the *Bacillus amylolichenifaciens* protease (BPN') shown in SEQ ID NO 2 of WO2016/001449. The protease variants preferably have at least 80% sequence identity to SEQ ID NO 1 or SEQ ID NO 2 of WO 2016/001449.

A protease variant comprising a substitution at one or more positions corresponding to positions 171, 173, 175, 179, or 180 of SEQ ID NO: 1 of WO2004/067737, wherein said protease variant has a sequence identity of at least 75% but less than 100% to SEQ ID NO: 1 of WO2004/067737.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutation S99D, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19

24 Mar 2026
2026202266

with the mutation S99D.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutation S99E, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19 with the mutation S99E.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutations Y167A+R170S+A194P, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19 with the mutations Y167A+R170S+A194P.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutations S9E+N43R+N76D+V205I+Q206L+Y209W+S259D+N261W+L262E, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at least 80%, at least 85%, at least 90% or at least 95% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19 with the mutations S9E+N43R+N76D+V205I+Q206L+Y209W+S259D+N261W+L262E.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutations S3T+V4I+S99D+S101R+S103A+V104I+G160S+V199M+V205I+L217D, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at least 80%, at least 85%, at least 90% or at least 95% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19 with the mutations S3T+V4I+S99D+S101R+S103A+V104I+G160S+V199M+V205I+L217D.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutations S3T+V4I+S99D+S101E+S103A+V104I+G160S+V205I, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at least 80%, at least 85%, at least 90% or at least 95% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19 with the mutations S3T+V4I+S99D+S101E+S103A+V104I+ G160S+V205I.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutations S99D+S101E+S103A+V104I+G160S, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at

24 Mar 2026
2026202266

least 80%, at least 85%, at least 90%, at least 95% or at least 96% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19 with the mutations S99D+S101E+S103A+V104I+G160S.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutations S99D+S101E+S103A+V104I+S156D+G160S+L262E, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at least 80%, at least 85%, at least 90% or at least 95% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19 with the mutations S99D+S101E+S103A+V104I+S156D+G160S+L262E.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 19 comprising the mutations S87N+S101G+V104N, wherein position numbers correspond to positions of the polypeptide of SEQ ID NO: 20, for example a variant having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to SEQ ID NO: 19. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 19 with the mutations S87N+S101G+V104N.

In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 20.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 20 comprising the mutation Y217L, for example a variant having at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97% or at least 98% sequence identity to SEQ ID NO: 20. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 20 with the mutation Y217L.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 20 comprising the mutations S24G+S53G+S78N+S101N+G128S+Y217Q, for example a variant having at least 80%, at least 85%, at least 90%, at least 95% or at least 96% sequence identity to SEQ ID NO: 20. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 20 with the mutations S24G+S53G+S78N+S101N+G128S+Y217Q.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 20 comprising the mutations S24G+S53G+S78N+S101N+G128A+Y217Q, for example a variant having at least 80%, at least 85%, at least 90%, at least 95% or at least 96% sequence identity to SEQ ID NO: 20. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 20 with the mutations S24G+S53G+S78N+S101N+G128A+Y217Q.

In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 21.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 21 having at least 80%, at least 85%, at least 90% or at least 95% sequence identity to SEQ ID NO: 21. The

24 Mar 2026
2026202266

protease may e.g. be a variant of the polypeptide of SEQ ID NO: 21 comprising one or more mutations selected from the group consisting of S27K, N109K, S111E, S171E, S173P, G174K, S175P, F180Y, G182A, L184F, Q198E, N199K and T297P, for example 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12 or all of said mutations.

In one embodiment, the protease is a variant of the polypeptide of SEQ ID NO: 21 comprising the mutations S27K+N109K+S111E+S171E+S173P+G174K+S175P+F180Y+ G182A+L184F+Q198E+ N199K+T297P, for example a variant having at least 80%, at least 85%, at least 90% or at least 95% sequence identity to SEQ ID NO: 21. In one embodiment, the protease comprises or consists of the polypeptide of SEQ ID NO: 21 with the mutations S27K+N109K+S111E+S171E+S173P+G174K+S175P+F180Y+G182A+L184F+Q198E+ N199K+T297P.

Suitable commercially available protease enzymes include those sold under the trade names Alcalase®, Duralase™, Durazym™, Relase®, Relase® Ultra, Savinase®, Savinase® Ultra, Primase®, Polarzyme®, Kannase®, Liquanase®, Liquanase® Ultra, Ovozyme®, Coronase®, Coronase® Ultra, Blaze®, Blaze Evity® 100T, Blaze Evity® 125T, Blaze Evity® 150T, Neutrase®, Everlase®, Esperase®, Novozymes Progress®, Novozymes Progress® Uno and Novozymes Progress®Excel (Novozymes A/S), those sold under the tradename Maxatase®, Maxacal®, Maxapem®, Purafect Ox®, Purafect OxP®, Puramax®, FN2®, FN3®, FN4®, Excellase®, Excellenz P1000™, Excellenz P1250™, Eraser®, Preferenz P100™, Purafect Prime®, Preferenz P110™, Effectenz P1000™, Purafect®™, Effectenz P1050™, Purafect Ox®™, Effectenz P2000™, Purafast®, Properase®, Opticlean® and Optimase® (Danisco/DuPont), Axapem™ (Gist-Brocases N.V.), BLAP (sequence shown in Figure 29 of US5352604) and variants hereof (Henkel AG) and KAP (*Bacillus alkalophilus* subtilisin) from Kao.

Nucleases

Suitable nucleases include deoxyribonucleases (DNases) and ribonucleases (RNases) which are any enzyme that catalyzes the hydrolytic cleavage of phosphodiester linkages in the DNA or RNA backbone respectively, thus degrading DNA and RNA. There are two primary classifications based on the locus of activity. Exonucleases digest nucleic acids from the ends. Endonucleases act on regions in the middle of target molecules. The nuclease is preferably a DNase, which is preferable is obtainable from a microorganism, preferably a fungi or bacterium. In particular, a DNase which is obtainable from a species of Bacillus is preferred; in particular a DNase which is obtainable from Bacillus cibi, Bacillus subtilis or Bacillus licheniformis is preferred. Examples of such DNases are described in WO 2011/098579, WO2014/087011 and WO2017/060475. Particularly preferred is also a DNase obtainable from a species of Aspergillus; in particular a DNase which is obtainable from Aspergillus oryzae, such as a DNase described in WO 2015/155350.The detergent enzyme(s) may be included in a detergent composition by

24 Mar 2026
2026202266

adding separate additives containing one or more enzymes, or by adding a combined additive comprising all of these enzymes. A detergent additive of the invention, 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 as described above, liquids, in particular stabilized liquids, or slurries.

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 compositions 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-

24 Mar 2026
2026202266

amylases obtained from *Bacillus*, *e.g.*, a special strain of *Bacillus licheniformis*, described in more detail in GB 1,296,839.

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

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

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

M197T;

H156Y+A181T+N190F+A209V+Q264S; or

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

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

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

24 Mar 2026
2026202266

184, such as 181 and 182, 182 and 183, or positions 183 and 184. Most preferred amylase variants of SEQ ID NO: 1, SEQ ID NO: 2 or SEQ ID NO: 7 are those having a deletion in positions 183 and 184 and a substitution in one or more of positions 140, 195, 206, 243, 260, 304 and 476.

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

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

N128C+K178L+T182G+Y305R+G475K;

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

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

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

Further suitable amylases are amylases having SEQ ID NO: 1 of WO13184577 or variants having 90% sequence identity to SEQ ID NO: 1 thereof. Preferred variants of SEQ ID NO: 1 are those having a substitution, a deletion or an insertion in one of more of the following positions: K176, R178, G179, T180, G181, E187, N192, M199, I203, S241, R458, T459, D460, G476 and G477. More preferred variants of SEQ ID NO: 1 are those having the substitution in one of more of the following positions: K176L, E187P, N192FYH, M199L, I203YF, S241QADN, R458N, T459S, D460T, G476K and G477K and/or deletion in position R178 and/or S179 or of T180 and/or G181. Most preferred amylase variants of SEQ ID NO: 1 are those having the substitutions:

E187P+I203Y+G476K

E187P+I203Y+R458N+T459S+D460T+G476K

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

24 Mar 2026
2026202266

at position 178 and/or position 179.

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

N21D+D97N+V128I

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

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

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

Commercially available amylases are Amplify Prime™, Atlantic™, Arctic™, Everest™, 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).

The detergent enzyme(s) may be included in the detergent composition according to the invention 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, may 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

24 Mar 2026
2026202266

US 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.

Microorgansims

The detergent additive as well as the detergent composition may also comprise one or more microorganisms, such as one or more fungi, yeast, or bacteria.

In an embodiment, the one or more microorganisms are dehydrated (for example by lyophilization) bacteria or yeast, such as a strain of *Lactobacillus*.

In another embodiment, the microrganisms are one or more microbial spores (as opposed to vegetative cells), such as bacterial spores; or fungal spores, conidia, hypha. Preferably, the one or more spores are *Bacillus* endospores; even more preferably the one or more spores are endospores of *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, or *Bacillus megaterium*.

The microrganisms may be included in the detergent composition or additive in the same way as enzymes (see above).

It is at present contemplated that in the detergent compositions any enzyme, in particular the alpha amylase polypeptides of the invention, may be added in an amount corresponding to 0.01-100 mg of enzyme protein per liter of wash liquor, preferably 0.05 - 5 mg of enzyme protein per liter of wash liquor, in particular 0.1-1 mg of enzyme protein per liter of wash liquor.

The alpha amylase polypeptides of the invention may additionally be incorporated in the detergent formulations disclosed in WO 2006/002643, which is hereby incorporated as reference.

Formulation of detergent products

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

A detergent composition according to the invention 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

24 Mar 2026
2026202266

formulated as a detergent composition for use in general household hard surface cleaning operations, or be formulated for hand or machine dishwashing operations.

Thus, in one embodiment, the detergent composition according to the present invention is a liquid laundry detergent composition, a powder laundry detergent composition, a liquid dishwash detergent composition, or a powder dishwash detergent composition. In an embodiment, the composition is a liquid or powder automatic dishwashing (ADW) detergent composition; or a liquid manual dishwashing detergent composition.

Pouches can be configured as single or multicompartments. It can be of any form, shape and material which is suitable for hold the composition, e.g. without allowing the release of the composition to release of the composition from the pouch prior to water contact. The pouch is made from water soluble film which encloses an inner volume. Said inner volume can be divided into compartments of the pouch. Preferred films are polymeric materials preferably polymers which are formed into a film or sheet. Preferred polymers, copolymers or derivates thereof are selected polyacrylates, and water soluble acrylate copolymers, methyl cellulose, carboxy methyl cellulose, sodium dextrin, ethyl cellulose, hydroxyethyl cellulose, hydroxypropyl methyl cellulose, malto dextrin, poly methacrylates, most preferably polyvinyl alcohol copolymers and, hydroxypropyl methyl cellulose (HPMC). Preferably the level of polymer in the film for example PVA is at least about 60%. Preferred average molecular weight will typically be about 20,000 to about 150,000. Films can also be of blended compositions comprising hydrolytically degradable and water soluble polymer blends such as polylactide and polyvinyl alcohol (known under the Trade reference M8630 as sold by MonoSol LLC, Indiana, USA) plus plasticisers like glycerol, ethylene glycerol, propylene glycol, sorbitol and mixtures thereof. The pouches can comprise a solid laundry cleaning composition or part components and/or a liquid cleaning composition or part components separated by the water soluble film. The compartment for liquid components can be different in composition than compartments containing solids: US2009/0011970 A1.

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

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

A liquid or gel detergent may be non-aqueous.

24 Mar 2026
2026202266

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.

Formulation of enzyme in co-granule

The enzyme of the invention may be formulated as a granule for example as a co-granule that combines one or more enzymes. Each enzyme will then be present in more granules securing a more uniform distribution of enzymes in the detergent. This also reduces the physical segregation of different enzymes due to different particle sizes. Methods for producing multi-enzyme co-granulates for the detergent industry are disclosed in the IP.com disclosure IPCOM000200739D.

Another example of formulation of enzymes by the use of co-granulates are disclosed in WO 2013/188331, which relates to a detergent composition comprising (a) a multi-enzyme co-granule; (b) less than 10 wt zeolite (anhydrous basis); and (c) less than 10 wt phosphate salt (anhydrous basis), wherein said enzyme co-granule comprises from 10 to 98 wt% moisture sink

24 Mar 2026
2026202266

component and the composition additionally comprises from 20 to 80 wt% detergent moisture sink component.

WO 2013/188331 also relates to a method of treating and/or cleaning a surface, preferably a fabric surface comprising the steps of (i) contacting said surface with the detergent composition as claimed and described herein in an aqueous wash liquor, (ii) rinsing and/or drying the surface.

The multi-enzyme co-granule may comprise an enzyme of the invention and (a) one or more enzymes selected from the group consisting of lipases, cellulases, xyloglucanases, perhydrolases, peroxidases, lipoxygenases, laccases, hemicellulases, proteases, cellobiose dehydrogenases, xylanases, phospholipases, esterases, cutinases, pectinases, mannanases, pectate lyases, keratinases, reductases, oxidases, phenoloxidases, ligninases, pullulanases, tannases, pentosanases, lichenases glucanases, arabinosidases, hyaluronidase, chondroitinase, second amylases, and mixtures thereof.

Uses

The present invention is also directed to methods for using the alpha-amylase variants. The alpha-amylase variants of the invention are useful in detergent compositions, laundry washing, dishwashing and/or cleaning processes.

In one embodiment, the invention relates the use of variants of the present invention in detergent compositions, for use in cleaning hard-surfaces, such as dish wash, or in laundering or for stain removal. In another embodiment, the invention relates to the use of an alpha-amylase variant according to the invention in a cleaning process such as laundry or hard surface cleaning including, but not limited to, dish wash and industrial cleaning. Thus, in one embodiment, the invention relates to the use of a variant comprising an modification in one or more positions corresponding to the positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481 of SEQ ID NO: 2 in a cleaning process such as laundry or hard surface cleaning including dish wash and industrial cleaning.

In a particular embodiment, the invention relates to the use of a variant comprising a) a substitution and/or deletion of two or more positions in the parent alpha-amylase said positions

24 Mar 2026
2026202266

corresponding to positions R181, G182, D183, and G184 of the polypeptide of SEQ ID NO: 2; and

b) an modification at one or more positions corresponding to positions H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481 of SEQ ID NO: 2, in a cleaning process such as laundry or hard surface cleaning including dish wash and industrial cleaning.

The soils and stains that are important for cleaning are composed of many different substances, and a range of different enzymes, all with different substrate specificities, have been developed for use in detergents both in relation to laundry and hard surface cleaning, such as dishwashing. These enzymes are considered to provide an enzyme detergency benefit, since they specifically improve stain removal in the cleaning process that they are used in, compared to the same process without enzymes. Stain removing enzymes that are known in the art include enzymes such as proteases, second amylases, lipases, cutinases, cellulases, endoglucanases, xyloglucanases, pectinases, pectin lyases, xanthanases, peroxidaes, haloperoxygenases, catalases and mannanases.

In one aspect, the present invention relates to the use of a variant as described herein, or to the use of a composition comprising the variant, in a domestic or industrial cleaning process.

In one aspect, the present invention relates to the use of a variant as described herein, or to the use of a composition comprising the variant for cleaning of fabric, for example laundry.

In one aspect, the present invention relates to the use of a variant as described herein, or to the use of a composition comprising the variant for cleaning of ceramic, plastic or glass material, for example dishwashing.

In one aspect, the invention relates to a laundering process which may be for household laundering as well as industrial laundering. Furthermore, the invention relates to a process for the laundering of textiles (e.g. fabrics, garments, cloths etc.) where the process comprises treating the textile with a washing solution containing a detergent composition of the present invention. The laundering can for example be carried out using a household or an industrial washing machine or be carried out by hand using a detergent composition of the invention.

In one aspect, the invention relates to a dish wash process, including ADW; or hard

24 Mar 2026
2026202266

surface cleaning, which may be for household cleaning as well as industrial cleaning. Furthermore, the invention relates to a process for dish wash or hard surface cleaning, where the process comprises treating the dishes or hard surfaces with a washing solution comprising a detergent composition of the present invention. The dish wash or hard surface cleaning can for example be carried out using a household dish washing machine or be carried out by hand using a detergent composition of the invention.

Methods of Use

The invention provides a use of a detergent composition in a domestic or industrial cleaning process. A cleaning process may for example be a dishwashing process, such as automated dishwashing; a laundry process; or cleaning of hard surfaces such as bathroom tiles, floors, table tops, drains, sinks and washbasins.

Dishwashing

An automated dishwashing process may comprise the following steps:

a. Exposing dishware to an aqueous wash liquor comprising a detergent composition;

b. Completing at least one wash cycle; and

c. Optionally rinsing and drying the dishware.

Thus, the invention provides a method of dishwashing in an automatic dishwashing machine using a detergent composition as described herein, comprising the steps of adding said detergent composition in a detergent composition compartment in said automatic dishwashing machine, and releasing said detergent composition during a main-wash cycle.

The compositions may be employed at concentrations from about 1000 - 8000 ppm in the wash liquor, such as 2000-6000 ppm in the wash liquor. The hardness of the wash liquor may be 3-30 °dH. The pH of the wash liquor may be 3-11, such as 7-11.

The temperature of the wash liquor when used may be in the range of 10-70°C. For example the temperature of the wash liquor can be in the range of 15-60°C, in the range of 20-50°C, in the range of 25-50°C, in the range of 30-45°C, in the range of 35-40°C, in the range of 35-55°C, or in the range of 40-50°C.

The temperature may vary throughout the wash program. One enzyme may be activated at one active temperature range and other enzymes may be activated at another active temperature range differing from the active temperature range of the first enzyme. For example, one or more wash cycles may be carried out at a temperature of 32-38°C and other wash cycles may be carried out at a temperature of 45-55°C. The advantage of this is that the single enzymes are allowed to work at their optimal temperature. The optimal temperature of the enzymes of a detergent composition may vary but is typically in the range of 65-70°C for proteases and in the range of 55-65°C for amylases. The optimal temperature may be determined by different assays,

24 Mar 2026
2026202266

such as comparing the activity over a 15 min period of time in a buffered solution at different temperatures.

During or after completion of a wash cycle the dishware can be rinsed with water or with water comprising a rinsing aid. The effectiveness of the cleaning can be further improved if an acidic rinsing aid is used. The rinsing aid should be capable of lowering the pH below 4 during at least a period of the rinsing step. The pH may be even further lowered e.g. to below pH 3.5, such as below pH 3, below pH 2.5 or below pH 2. The period of lowering the pH may be at least 1 minute, such as at least 2 minutes, at least 3 minutes, at least 4 minutes, at least 5 minutes, at least 6 minutes or at least 7 minutes. The period of lowering the pH may even be as long as the time period for the full rinsing step.

The ability of lowering the pH during the rinsing step is due to a buffering agent. A buffer with strong buffer capacity at low pH, from pH 4 and below should be selected. The buffer capacity should correspond to the same effect as the pH drop was done with 15 ml 4M HCL/rinse cycle. The ability of lowering the pH during the rinsing step is due to a buffering agent selected from the group consisting of citric acid, acetic acid, potassium dihydrogen phosphate, boric acid, diethyl barbituric acid, Carmody buffer and Britton-Robinson buffer.

The rinsing aid can further improve the cleaning of the dishware by rinsing away any soil released from the dishware during the washing cycle. In addition, the acidic rinsing aid prevents precipitation of calcium on the dishware.

Laundering

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 as described herein. 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 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 cellulosics, including cotton, flax, linen, jute, ramie, sisal or coir or manmade cellulosics (*e.g.*, originating from wood pulp) including viscose/rayon, ramie, cellulose acetate fibres (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 fibres.

In one aspect, the present invention relates to a method of laundering in an automatic

24 Mar 2026
2026202266

laundering machine using a detergent composition as described herein, comprising the steps of adding said detergent composition in a detergent composition compartment in said automatic laundering machine, and releasing said detergent composition during a main wash cycle. In another aspect, the present invention relates to a method of laundering, comprising laundering a garment with a detergent composition as described herein, preferably at a temperature of 50°C or less, or more preferably at a temperature of 45°C or less, or even more preferably at a temperature of 40°C or less even more preferably at a temperature of 35°C or less or even more preferably at a temperature of 30°C or less, even more preferably at a temperature of 25°C or less or even more preferably at a temperature of 20°C or less.

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 5ºC to about 95ºC, including about 10ºC, about 15ºC, about 20ºC, about 25ºC, about 30ºC, about 35ºC, about 40ºC, about 45ºC, about 50ºC, about 55ºC, about 60ºC, about 65ºC, about 70ºC, about 75ºC, about 80ºC, about 85ºC and about 90ºC. 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 degree of hardness of from about 0°dH to 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 alpha-amylase variants of this invention possess valuable properties allowing for a variety of other industrial applications. For example, alpha-amylase polypeptides of the invention may be used for starch processes, in particular starch conversion, especially liquefaction of starch (see, *e.g.*, US 3,912,590, EP patent application nos. 252 730 and 63 909, WO 99/19467, and WO 96/28567 all references hereby incorporated by reference). Also contemplated are compositions for starch conversion purposes, which may beside the variant of the invention also comprise a glucoamylase, pullulanase, and other alpha-amylases.

Furthermore, alpha-amylase variants of this invention are also particularly useful in the production of sweeteners and ethanol (see, e.g., US patent no. 5,231,017 hereby incorporated by reference), such as fuel, drinking and industrial ethanol, from starch or whole grains.

Alpha-amylase variants of the invention may also be useful for desizing of textiles, fabrics and garments (see, e.g., WO 95/21247, US patent 4,643,736, EP 119,920 hereby in corporate by reference), beer making or brewing, in pulp and paper production.

Starch Conversion

24 Mar 2026
2026202266

Conventional starch-conversion processes, such as liquefaction and saccharification processes are described, *e.g.,* in US Patent No. 3,912,590 and EP patent publications Nos. 252,730 and 63,909, hereby incorporated by reference.

In an embodiment the starch conversion process degrading starch to lower molecular weight carbohydrate components such as sugars or fat replacers includes a debranching step.

In the case of converting starch into a sugar, the starch is depolymerized. Such depolymerization processes may consist of a pre-treatment step and two or three consecutive process steps, viz. a liquefaction process, a saccharification process and dependent on the desired end product optionally an isomerization process.

(i) Pre-treatment of native starch

Native starch consists of microscopic granules, which are insoluble in water at room temperature. When an aqueous starch slurry is heated, the granules swell and eventually burst, dispersing the starch molecules into the solution. During this "gelatinization" process there is a dramatic increase in viscosity. As the solids level is 30-40% in a typically industrial process, the starch has to be thinned or "liquefied" so that it can be handled. This reduction in viscosity is today mostly obtained by enzymatic degradation.

(ii) Liquefaction

During the liquefaction step, the long chained starch is degraded into branched and linear shorter units (maltodextrins) by an alpha-amylase. The liquefaction process is carried out at 105-110°C for 5 to 10 minutes followed by 1-2 hours at 95°C. The pH lies between 5.5 and 6.2. In order to ensure optimal enzyme stability under these conditions, 1 mM of calcium is added (40 ppm free calcium ions). After this treatment the liquefied starch will have a "dextrose equivalent" (DE) of 10-15.

(iii) Saccharification

After the liquefaction process the maltodextrins are converted into dextrose by addition of a glucoamylase (*e.g.*, AMG) and a debranching enzyme, such as an isoamylase (US patent no. 4,335,208) or a pullulanase (*e.g.*, Promozyme™) (US patent no. 4,560,651). Before this step the pH is reduced to a value below 4.5, maintaining the high temperature (above 95°C) to inactivate the liquefying alpha-amylase to reduce the formation of short oligosaccharide called "panose precursors" which cannot be hydrolyzed properly by the debranching enzyme.

The temperature is lowered to 60°C, and glucoamylase and debranching enzyme are added. The saccharification process proceeds for 24-72 hours.

24 Mar 2026
2026202266

Normally, when denaturing the α-amylase after the liquefaction step about 0.2-0.5% of the saccharification product is the branched trisaccharide 6<2>-alpha-glucosyl maltose (panose) which cannot be degraded by a pullulanase. If active amylase from the liquefaction step is present during saccharification (i.e., no denaturing), this level can be as high as 1-2%, which is highly undesirable as it lowers the saccharification yield significantly.

(iv) Isomerization

When the desired final sugar product is, *e.g.,* high fructose syrup the dextrose syrup may be converted into fructose. After the saccharification process the pH is increased to a value in the range of 6-8, preferably pH 7.5, and the calcium is removed by ion exchange. The dextrose syrup is then converted into high fructose syrup using, *e.g.,* an immmobilized glucoseisomerase (such as Sweetzyme<™> IT).

Ethanol production

In general alcohol production (ethanol) from whole grain can be separated into 4 main steps

- Milling
- Liquefaction
- Saccharification
- Fermentation

(i) Milling

The grain is milled in order to open up the structure and allowing for further processing. Two processes are used wet or dry milling. In dry milling the whole kernel is milled and used in the remaining part of the process. Wet milling gives a very good separation of germ and meal (starch granules and protein) and is with a few exceptions applied at locations where there is a parallel production of syrups.

(ii) Liquefaction

In the liquefaction process the starch granules are solubilized by hydrolysis to maltodextrins mostly of a DP higher than 4. The hydrolysis may be carried out by acid treatment or enzymatically by alpha-amylase. Acid hydrolysis is used on a limited basis. The raw material can be milled whole grain or a side stream from starch processing.

Enzymatic liquefaction is typically carried out as a three-step hot slurry process. The slurry is heated to between 60-95°C, preferably 80-85°C, and the enzyme(s) is (are) added. Then the slurry is jet-cooked at between 95-140°C, preferably 105-125°C, cooled to 60-95°C and more

24 Mar 2026
2026202266

enzyme(s) is (are) added to obtain the final hydrolysis. The liquefaction process is carried out at pH 4.5-6.5, typically at a pH between 5 and 6. Milled and liquefied grain is also known as mash.

(iii) Saccharification

To produce low molecular sugars DP1-3 that can be metabolized by yeast, the maltodextrin from the liquefaction must be further hydrolyzed. The hydrolysis is typically done enzymatically by glucoamylases, alternatively alpha-glucosidases or acid alpha-amylases can be used. A full saccharification step may last up to 72 hours, however, it is common only to do a pre-saccharification of typically 40-90 minutes and then complete saccharification during fermentation (SSF). Saccharification is typically carried out at temperatures from 30-65ºC, typically around 60ºC, and at pH 4.5.

(iv) Fermentation

Yeast typically from Saccharomyces spp. is added to the mash and the fermentation is ongoing for 24-96 hours, such as typically 35-60 hours. The temperature is between 26-34°C, typically at about 32°C, and the pH is from pH 3-6, preferably around pH 4-5.

Note that the most widely used process is a simultaneous saccharification and fermentation (SSF) process where there is no holding stage for the saccharification, meaning that yeast and enzyme is added together. When doing SSF it is common to introduce a pre-saccharification step at a temperature above 50°C, just prior to the fermentation.

(v) Distillation

Following the fermentation the mash is distilled to extract the ethanol.

The ethanol obtained according to the process of the invention may be used as, e.g., fuel ethanol; drinking ethanol, i.e., potable neutral spirits; or industrial ethanol.

(vi) By-products

Left over from the fermentation is the grain, which is typically used for animal feed either in liquid form or dried.

Further details on how to carry out liquefaction, saccharification, fermentation, distillation, and recovering of ethanol are well known to the skilled person.

According to the process of the invention the saccharification and fermentation may be carried out simultaneously or separately.

Pulp and Paper Production

Alkaline alpha-amylase polypeptides of the invention may also be used in the production of lignocellulosic materials, such as pulp, paper and cardboard, from starch reinforced waste

24 Mar 2026
2026202266

paper and cardboard, especially where re-pulping occurs at pH above 7 and where amylases facilitate the disintegration of the waste material through degradation of the reinforcing starch. The alpha-amylase of the invention is especially useful in a process for producing a papermaking pulp from starch-coated printed-paper. The process may be performed as described in WO 95/14807, comprising the following steps:

a) disintegrating the paper to produce a pulp,
b) treating with a starch-degrading enzyme before, during or after step a), and
c) separating ink particles from the pulp after steps a) and b).

The alpha-amylases of the invention may also be very useful in modifying starch where enzymatically modified starch is used in papermaking together with alkaline fillers such as calcium carbonate, kaolin and clays. With the alkaline alpha-amylases of the invention it becomes possible to modify the starch in the presence of the filler thus allowing for a simpler integrated process.

Desizing of Textiles, Fabrics and Garments

An alpha-amylase of the invention may also be very useful in textile, fabric or garment desizing. In the textile processing industry, alpha-amylases are traditionally used as auxiliaries in the desizing process to facilitate the removal of starch-containing size, which has served as a protective coating on weft yarns during weaving. Complete removal of the size coating after weaving is important to ensure optimum results in the subsequent processes, in which the fabric is scoured, bleached and dyed. Enzymatic starch breakdown is preferred because it does not involve any harmful effect on the fiber material. In order to reduce processing cost and increase mill throughput, the desizing processing is sometimes combined with the scouring and bleaching steps. In such cases, non-enzymatic auxiliaries such as alkali or oxidation agents are typically used to break down the starch, because traditional alpha-amylases are not very compatible with high pH levels and bleaching agents. The non-enzymatic breakdown of the starch size does lead to some fiber damage because of the rather aggressive chemicals used. Accordingly, it would be desirable to use the alpha-amylases of the invention as they have an improved performance in alkaline solutions. The alpha-amylases may be used alone or in combination with a cellulase when desizing cellulose-containing fabric or textile.

Desizing and bleaching processes are well known in the art. For instance, such processes are described in WO 95/21247, US patent 4,643,736, EP 119,920 hereby in corporate by reference.

Commercially available products for desizing include AQUAZYME® and AQUAZYME® ULTRA from Novozymes A/S.

24 Mar 2026
2026202266

Beer making

The alpha-amylases of the invention may also be very useful in a beer-making process; the alpha-amylases will typically be added during the mashing process.

The invention is further described in the following paragraphs.

1. An alpha-amylase variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17, and wherein said variant has alpha-amylase activity.

2. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 1, and wherein said variant has alpha-amylase activity.

3. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase

24 Mar 2026
2026202266

comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 2, and wherein said variant has alpha-amylase activity.

4. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 3, and wherein said variant has alpha-amylase activity.

5. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357,

24 Mar 2026

2026202266

365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 4, and wherein said variant has alpha-amylase activity.

6. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 5, and wherein said variant has alpha-amylase activity.

7. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 6, and wherein said variant has alpha-

24 Mar 2026
2026202266

amylase activity.

8. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 7, and wherein said variant has alpha-amylase activity.

9. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 8, and wherein said variant has alpha-amylase activity.

10. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173,

24 Mar 2026
2026202266

174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 9, and wherein said variant has alpha-amylase activity.

11. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 10, and wherein said variant has alpha-amylase activity.

12. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%,

24 Mar 2026
2026202266

e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 11, and wherein said variant has alpha-amylase activity.

13. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 12, and wherein said variant has alpha-amylase activity.

14. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 13, and wherein said variant has alpha-amylase activity.

15. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase

24 Mar 2026
2026202266

comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 14, and wherein said variant has alpha-amylase activity.

16. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 15, and wherein said variant has alpha-amylase activity.

17. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357,

24 Mar 2026

2026202266

365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 16, and wherein said variant has alpha-amylase activity.

18. The alpha-amylase variant of paragraph 1, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NO: 17, and wherein said variant has alpha-amylase activity.

19. The alpha-amylase variant according to any one of the preceding paragraphs, wherein said variant of a parent alpha-amylase comprises a modification at one or more positions corresponding to position: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering; and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID

24 Mar 2026
2026202266

NOs: 1-17, and wherein said variant has alpha-amylase activity and wherein said variant has Improvement Factor (IF) >1.0 for a measure of wash performance when compared to said parent polypeptide having alpha-amylase activity as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

20. The alpha-amylase variant according to any one of the preceding paragraphs, wherein said modifications at one or more positions corresponding to positions: H1, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering, and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17, and wherein said variant has alpha-amylase activity and wherein said variant has an Improvement Factor (IF) of >1.0 for a measure of wash performance when compared to said parent alpha-amylase as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

21. The variant according to any one of the preceding paragraphs, wherein the number of substitutions and/or deletion is 1 to 20, *e.g.*, 1 to 10 and 1 to 5, such as 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10 substitutions and/or deletions.

22. The variant according to any one of the preceding paragraphs, wherein said variant comprises a deletion in two or more positions corresponding to positions R181, G182, D183, and G184, using SEQ ID NO: 1 for numbering.

23. The variant according to paragraph 22, wherein said variant comprises a deletion in the positions corresponding to the positions R181+G182; R181+D183; R181+G184; G182+D183; G182+G184; or D183+G184, using SEQ ID NO: 1 for numbering.

24 Mar 2026

2026202266

24. The variant according to any one of the preceding paragraphs, wherein said variant has an Improvement Factor (IF) of at least 1.1, at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 1.6, at least 1.7, at least 1.8, at least 1.9, at least 2.0, at least 2.2, at least 2.4, at least 2.6, at least 2.8, at least 3.0, at least 3.2, at least 3.4, at least 3.6, at least 3.8, or at least 4.0 for a measure of wash performance when compared to said parent alpha-amylase as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

25. The variant according to any one of the preceding paragraphs, wherein said variant has an Improvement Factor (IF) of at least 1.1, at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 1.6, at least 1.7, at least 1.8, at least 1.9, at least 2.0, at least 2.2, at least 2.4, at least 2.6, at least 2.8, at least 3.0, at least 3.2, at least 3.4, at least 3.6, at least 3.8, or at least 4.0 for a measure of wash performance in Model A detergent composition when compared to said parent alpha-amylase as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

26. The variant according to any one of the preceding paragraphs, wherein said variant has an Improvement Factor (IF) of at least 1.1, at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 1.6, at least 1.7, at least 1.8, at least 1.9, at least 2.0, at least 2.2, at least 2.4, at least 2.6, at least 2.8, at least 3.0, at least 3.2, at least 3.4, at least 3.6, at least 3.8, or at least 4.0 for a measure of wash performance in ADW detergent composition with bleach when compared to said parent alpha-amylase as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

27. The variant according to any one of the preceding paragraphs, wherein said variant has an Improvement Factor (IF) of at least 1.1, at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 1.6, at least 1.7, at least 1.8, at least 1.9, at least 2.0, at least 2.2, at least 2.4, at least 2.6, at least 2.8, at least 3.0, at least 3.2, at least 3.4, at least 3.6, at least 3.8, or at least 4.0 for a measure of wash performance in Model A detergent composition and/or ADW detergent composition with bleach when compared to said parent alpha-amylase as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

28. The variant according to any one of the preceding paragraphs, wherein said variant has an Improvement Factor (IF) of at least 1.1, at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 1.6, at least 1.7, at least 1.8, at least 1.9, at least 2.0, at least 2.2, at least 2.4, at least 2.6, at least 2.8, at least 3.0, at least 3.2, at least 3.4, at least 3.6, at least 3.8, or at least 4.0 for a measure of wash performance in ADW detergent composition with bleach assessed using an Automatic Mechanical Stress Assay (AMSA) when compared to said parent alpha-amylase as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

24 Mar 2026

2026202266

29. The variant according to any one of the preceding paragraphs, wherein said variant has an Improvement Factor (IF) of at least 1.1, at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 1.6, at least 1.7, at least 1.8, at least 1.9, at least 2.0, at least 2.2, at least 2.4, at least 2.6, at least 2.8, at least 3.0, at least 3.2, at least 3.4, at least 3.6, at least 3.8, or at least 4.0 for a measure of wash performance in ADW detergent composition with bleach assessed using an a full scale automatic dishwash (ADW) when compared to said parent having alpha-amylase activity as shown in SEQ ID NO: 1 or SEQ ID NO: 2.

30. The alpha-amylase variant according to preceding paragraphs, wherein the parent polypeptide has at least 59%, e.g. at least 60%, e.g., at least 62%, at least 63%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% sequence identity to the polypeptide of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16 or SEQ ID NO: 17.

31. The alpha-amylase variant according to paragraph 11, wherein the parent polypeptide comprises or consists of the polypeptide of SEQ ID NO: 1, SEQ ID NO: 2, SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9, SEQ ID NO: 10, SEQ ID NO: 11, SEQ ID NO: 12, SEQ ID NO: 13, SEQ ID NO: 14, SEQ ID NO: 15, SEQ ID NO: 16 or SEQ ID NO: 17.

32. The alpha-amylase variant according to any one of the preceding paragraphs, which has at least 60%, *e.g.*, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95% identity, at least 96%, at least 97%, at least 98%, or at least 99%, but less than 100%, sequence identity to the amino acid sequence of the parent polypeptide.

33. The alpha-amylase variant according to any one of the preceding paragraphs, wherein said variant comprises a) a deletion and/or a substitution at two or more positions corresponding to positions R181, G182, D183, and G184, using SEQ ID NO: 1 for numbering and b) a modification at one or more positions corresponding to positions H1, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246,

24 Mar 2026
2026202266

Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering.

34. The alpha-amylase variant according to any one of the preceding paragraphs, wherein said variant comprises one or more of the following modifications: H1*; G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering.

34. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
A60T,

24 Mar 2026
2026202266

Y135H,
Q169E,
W48Y,
A174*,
M246L,
R90Q,
Y203L+V206L,
Q169F+S170A,
S132D+G133D,
N195F+Q365C,
N195F+Q365S,
N195F+Q365M,
R127L+Q365S,
R127N+Q365S,
R127L+Q365C,
N195F+Q365K,
I9M+N195F,
R171H+Q365C,
Y267F+Q365S,
F328L+Q365S,
R171L+Q365S,
N195F+M286L,
T134P+N195F,
S170*+R171*+A174*,
V264I+A265G+Y267F,
Q169*+S170*+A174*,
M246L+L275V+Q365S,
V264I+V291I+Q365S,
V264I+V291T+Q365K,
V264I+F328L+Q365C,
I9M+N195F+Q365C,
Q11H+Y267F+Q365C,
I9M +N195F+Q365S,
V264I+Y267F+Q365K,
R127L+M246V+Q365S,
A60S+R171Y+Q365S,

24 Mar 2026
2026202266

R127N+M246T+L275V,
V104A+N195F+Q365S,
V264I+F328L+Q365S,
R171H+N302H+Q365S,
V264I+Y267F+Q365S,
A174*+N175*+Y178F,
V264I+A265G+Q365C,
R171L+N302H+Q365C,
R171L+M246V+Q365C,
R171Y+M246L+Q365S,
V264T+Y267F+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
R127N+M246L+L275V+Q365S,
R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
Y267F+V291A+F328L+Q365C,
I9M+A186E+N195F+Q365S,
E86L+R171L+N306R+Q365S,
V264I+Y267F+F328L+Q365S,
I9M+N195F+V291A+Q365S,
R127L+L235I+M246I+Q365C,
Y267F+V291A+F328L+Q365S,
V264I+Y267F+F328L+Q365K,
Q11H+V264I+A265G+Q365C,
W187M+N195F+H210K+Q365S,
R127H+M246T+L275A+Q365S,
I9M+A111T+N195F+Q365S,
I9M+Y58F+N195F+Q365S,

24 Mar 2026
2026202266

V264T+V291A+F328L+Q365S,
V264I+A265G+V291A+Q365C,
V264I+A265G+Y267F+Q365C,
V264I+Y267F+V291A+F328L+Q365S,
R127N+R171H+M246L+L275V+Q365S,
V264I+A265G+V291A+F328L+Q365S,
R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
R116S+S132F+R181N+N195F+Q365S,
E130T+T134Y+A186K+N195F+Q365S,
A37V+V264I+Y267F+F328L+Q365C,
Q11H+V264I+Y267F+F328L+Q365C,
V264I+Y267F+V291T+F328L+Q365S,
Q169*+R171*+Q172*+L173*+A174*,
R116Y+S132P+Q136N+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377Y,
V264I+A265G+Y267F+F328L+Q365S,
I9M+N195F+K269Q+A274K+Q365S,
E130D+T134Y+R181H+N195F+Q365S,
R116N+S132M+Q136R+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377N,
R127N+R171L+M246L+L275V+Q365S,
N195F+G337E+Q365S+P375K+D377N,
Q11H+V264I+A265G+Y267F+Q365C,
R158Q+Y160N+W187M+N195F+Q365S,
V264I+Y267F+Q365K+W408H+V410I,
R127N+R171Y+M246L+L275V+Q365S,
N54Q+F113T+R171H+N302A+Q365C,
V264A+Y267F+V291T+F328L+Q365C,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,

24 Mar 2026
2026202266

E130D+T134W+R181KA186E+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
E130S+T134E+R181S+A186T+N195F+Q365S,
R116C+S132A+Q136S+R181A+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+Q365S,
R127H+R171H+M246L+L275V+N306R+Q365S,
E130L+T134N+R181W+A186T+N195F+Q365S,
R116C+S132M+Q136S+R181Q+N195F+Q365S,
R116S+Y135H+Q136G+R181T+N195F+Q365S,
R116S+S132L+Q136E+R181G+N195F+Q365S,
N16E+N195F+G337E+Q365S+P375T+D377H,
V264I+A265G+Y267F+V291I+F328L+Q365S,
N16E+N195F+G337D+Q365S+P375K+D377N,
V264I+A265G+Y267F+F328L+Q365S+Q395K,
E130N+T134C+R181Q+A186N+N195F+Q365S,
V264I+A265G+Y267F+V291A+F328L+Q365C,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
A139T+R158S+Y160D+W187M+N195F+H210N+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*,
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+Y58F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195H+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A,
H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A,
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A,
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A,
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A,
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A,
Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A,
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A,
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A139T +R158S +Y160D +W187M +N195F +H210N +Q365S,
A186D +N195F,
A60S +R171Y +Q365S,
E130D +T134W +R181K +A186E +N195F +Q365S,
E130D +T134Y +R181H +N195F +Q365S,
E130D+T134W+R181K+A186E+N195F+Q365S,
E130F +T134R +R181S +A186D +N195F +Q365S,

24 Mar 2026
2026202266

E130I +T134A +R181N +N195F +Q365S,
E130I+T134A+R181N+N195F+Q365S,
E130L +T134N +R181W +A186T +N195F +Q365S,
E130N +T134C +R181Q +A186N +N195F +Q365S,
E130S +T134E +R181S +A186T +N195F +Q365S,
E130T +T134Y +A186K +N195F +Q365S,
E130V +T134N +R181Y +A186K +N195F +Q365S,
E130Y +S132T +T134S +R181E +A186D +N195F +Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
E86L +R171L +N306R +Q365S,
E86L +Y160H +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
E86L+R171L+N306R+Q365S,
F113Q +R116H,
F113T +R171K +G273V,
F328L +Q365S,
G109A+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
G7A+F113N+R116N+E276N+S304G+R320S+Q345N+W439R+N465G+Q466S+W469Y,
H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S,
H1* +I9M +N54S +V56T +G109A +F113G +R116H +D163H +Q169E +R171H +Q172K +A174S +G182T +N195F +M202L +V206L +M246L +L275V +A288V +L317V +Q319H +H324K +Q365S +K391A,
H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,
H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +Q365S +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L+ V206L +W284Y +K391A,

24 Mar 2026
2026202266

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +N306R +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +Q365S +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +V206L +K391A,
H1* +N54S +V56T +G109A +R171H +N195F +V206L +K391A,
H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1*+I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K +A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R44 4T+Q445S+Q466S,
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A,
H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K39 1A,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q125G+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D377H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K269M+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L235I+V238A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V238A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K39

24 Mar 2026
2026202266

1A,
H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F,
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q172S+L173K+A174S+N175*+R176A+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R116H+Q169E+Q172K+A174*+N195F+V206L+N314Q+Q385L+K391A,
H1*+N54S+V56T+G109A+R127F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
I9M +A186E +N195F +Q365S,
I9M +A186H +N195F +Q365S,
I9M +G184K +N195F +Q365S,
I9M +N195F +K269Q +A274K +Q365S,
I9M +N195F +N270G +Q365S,
I9M +N195F +N270P +Q365S,
I9M +N195F +Q365C,
I9M +N195F +V206L +D209N +Q365S,
I9M +N195F +V291A +Q365S,
I9M +R127N +N195F +Q365S
I9M +R171H +N195F +Q365S,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,
I9M +R171L +N195F +Q365S,
I9M +Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
I9M +Y160H +N195F +Q365S,
I9M+A186E+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+G184K+N195F+Q365S,
I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+

24 Mar 2026
2026202266

Q445S+Q466S,
I9M+N195F+Q365C,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
I9M+R127N+N195F+Q365S,
I9M+R171H+N195F+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
I9M+R171L+N195F+Q365S,
I9M+Y160H+N195F+Q365S,
M202L,
M246L +L275V +Q365S +D406H,
M246L,
M246L+ L275V +Q365S,
M246L+L275V+Q365S+D406H,
N16E +N195F +G337D +Q365S +P375K +D377N,
N16E +N195F +G337E +Q365S +P375T +D377H,
N16E+N195F+G337E+Q365S+P375T+D377H,
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
N195F +G337D +Q365S +P375K +D377N,
N195F +G337D +Q365S +P375K +D377Y,
N195F +G337E +Q365S +P375K +D377N,
N195F+G337D+Q365S+P375K+D377Y,
N195F+G337E+Q365S+P375K+D377N,
N195F+Q365S,
N54Q +F113T +R171H +N302A +Q365C,
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Q11H +V264I +A265G +Q365C,
Q11H +V264I +A265G +Y267F +Q365C,
Q11H +V264I +Y267F +F328L +Q365C,
Q11H +Y267F +Q365C,
Q11H+V264I+A265G+Q365C,
Q169* +S170* +A174*,
Q169* +S170* +R171* +A174*,
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P,
R116K +S132L +Q136R +R181C +N195F +Q365S,

24 Mar 2026
2026202266

R116K +S132P +Q136D +R181Q +N195F +A204V +Q365S,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
R116N +S132A +Q136D +R181K +N195F +Q365S,
R116N +S132M +Q136R +N195F +Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
R116S +S132F +R181N +N195F +Q365S,
R116S +Y135H +Q136G +R181T +N195F +Q365S,
R116Y +S132P +Q136N +N195F +Q365S,
R127H+L235I+Q365S+G435C,
R127L +M246V +Q365S,
R127L +Q365C,
R127L +Q365S,
R127L,
R127N +M246L +L275V +Q365S,
R127N +Q365S,
R127N +R171L +M246L +L275V +Q365S,
R127N+R171H+M246L+L275V+Q365S,
R171H + Q365C,
R171H +M246L +L275V +Q365S,
R171H +N302H +Q365S,
R171H,
R171H+Q365C,
R171L +N302H +Q365C,
R171L +Q365S,
R171Y + +M246L +Q365S,
R171Y +N306K,
R181S +G184S,
V104A +N195F +Q365S,
V264A +Y267F +V291T +F328L +Q365C,
V264I +A265G +V291A +F328L +Q365S,
V264I +A265G +V291A +Q365C,
V264I +A265G +Y267F +F328L +Q365S +Q395K,
V264I +A265G +Y267F +F328L +Q365S,
V264I +A265G +Y267F +V291I +F328L +Q365S,
V264I +A265G +Y267F,
V264I +F328L +Q365C,

24 Mar 2026
2026202266

V264I +F328L +Q365S,
V264I +L357F,
V264I +Q365C,
V264I +V291I +Q365S,
V264I +V291T +Q365K,
V264I +Y267F +F328L +Q365C,
V264I +Y267F +F328L +Q365K,
V264I +Y267F +F328L +Q365S,
V264I +Y267F +Q365K +W408H +V410I,
V264I +Y267F +Q365K,
V264I +Y267F +Q365S,
V264I +Y267F +V291A +F328L +Q365C,
V264I +Y267F +V291A +F328L +Q365S,
V264I +Y267F +V291T +F328L +Q365S,
V264I+A265G+Y267F,
V264I+F328L+Q365C,
V264I+Y267F+F328L+Q365K,
V264I+Y267F+V291T+F328L+Q365S,
V264T +A265G +Y267F +V291A +F328L +Q365C,
V264T +A265G +Y267L +F328L +Q365C,
V264T +V291A +F328L +Q365S,
V264T +Y267F +Q365S,
V264T +Y267L +F328L +Q365C,
V56T+Y160H+A174N+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
W187M +N195F +H210K +Q365S,
Y160H +E212D +E276N +W284Y +R320S +Q365S +W408H +W439T +W469N +F473S +G476K,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473I +G476K,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
Y160H+A174S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,

24 Mar 2026
2026202266

Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+K259G+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256N+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+M202L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473I+G476K,
Y160H+N195F+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+N195Q+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+N195Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q169E+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+R171Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y267F +Q365S,
Y267F +V291A +F328L +Q365C,
Y267F +V291A +F328L +Q365S,
Y267F+Q365S,
Y267F+V291A+F328L+Q365S,
Y295F, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.1 in Model A detergent composition as measure of wash performance and/or ADW detergent composition with bleach.

35. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
A60T,
Y135H,
Q169E,
W48Y,
A174*,
M246L,
R90Q,
Y203L+V206L,
Q169F+S170A,
S132D+G133D,

24 Mar 2026
2026202266

N195F+Q365C,
N195F+Q365S,
N195F+Q365M,
N195F+Q365K,
R127L+Q365S,
R127N+Q365S,
R127L+Q365C,
R171L+Q365S,
R171H+Q365C,
Y267F+Q365S,
F328L+Q365S,
I9M+N195F,
N195F+M286L,
T134P+N195F,
S170*+R171*+A174*,
V264I+A265G+Y267F,
Q169*+S170*+A174*,
M246L+L275V+Q365S,
V264I+V291I+Q365S,
V264I+V291T+Q365K,
V264I+F328L+Q365C,
I9M+N195F+Q365C,
Q11H+Y267F+Q365C,
I9M +N195F+Q365S,
V264I+Y267F+Q365K,
R127L+M246V+Q365S,
A60S+R171Y+Q365S,
R127N+M246T+L275V,
V104A+N195F+Q365S,
V264I+F328L+Q365S,
R171H+N302H+Q365S,
V264I+Y267F+Q365S,
A174*+N175*+Y178F,
V264I+A265G+Q365C,
R171L+N302H+Q365C,
R171L+M246V+Q365C,

24 Mar 2026
2026202266

R171Y+M246L+Q365S,
V264T+Y267F+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127N+M246L+L275V+Q365S,
R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
R127N+M246L+L275V+Q365S,
Y267F+V291A+F328L+Q365C,
I9M+A186E+N195F+Q365S,
E86L+R171L+N306R+Q365S,
V264I+Y267F+F328L+Q365S,
I9M+N195F+V291A+Q365S,
R127L+L235I+M246I+Q365C,
Y267F+V291A+F328L+Q365S,
V264I+Y267F+F328L+Q365K,
Q11H+V264I+A265G+Q365C,
I9M+R171H+N195F+Q365S,
W187M+N195F+H210K+Q365S,
R127H+M246T+L275A+Q365S,
I9M+A111T+N195F+Q365S,
I9M+Y58F+N195F+Q365S,
V264T+V291A+F328L+Q365S,
V264I+A265G+V291A+Q365C,
V264I+A265G+Y267F+Q365C,
V264I+Y267F+V291A+F328L+Q365S,
R127N+R171H+M246L+L275V+Q365S,
V264I+A265G+V291A+F328L+Q365S,

24 Mar 2026
2026202266

R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
R116S+S132F+R181N+N195F+Q365S,
E130T+T134Y+A186K+N195F+Q365S,
A37V+V264I+Y267F+F328L+Q365C,
Q11H+V264I+Y267F+F328L+Q365C,
V264I+Y267F+V291T+F328L+Q365S,
Q169*+R171*+Q172*+L173*+A174*,
R116Y+S132P+Q136N+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377Y,
V264I+A265G+Y267F+F328L+Q365S,
I9M+N195F+K269Q+A274K+Q365S,
E130D+T134Y+R181H+N195F+Q365S,
R116N+S132M+Q136R+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377N,
R127N+R171L+M246L+L275V+Q365S,
N195F+G337E+Q365S+P375K+D377N,
Q11H+V264I+A265G+Y267F+Q365C,
R158Q+Y160N+W187M+N195F+Q365S,
V264I+Y267F+Q365K+W408H+V410I,
R127N+R171Y+M246L+L275V+Q365S,
N54Q+F113T+R171H+N302A+Q365C,
V264A+Y267F+V291T+F328L+Q365C,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,
E130D+T134W+R181KA186E+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
E130S+T134E+R181S+A186T+N195F+Q365S,
R116C+S132A+Q136S+R181A+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+Q365S,
R127H+R171H+M246L+L275V+N306R+Q365S,

24 Mar 2026
2026202266

E130L+T134N+R181W+A186T+N195F+Q365S,
R116C+S132M+Q136S+R181Q+N195F+Q365S,
R116S+Y135H+Q136G+R181T+N195F+Q365S,
R116S+S132L+Q136E+R181G+N195F+Q365S,
N16E+N195F+G337E+Q365S+P375T+D377H,
V264I+A265G+Y267F+V291I+F328L+Q365S,
N16E+N195F+G337D+Q365S+P375K+D377N,
V264I+A265G+Y267F+F328L+Q365S+Q395K,
E130N+T134C+R181Q+A186N+N195F+Q365S,
V264I+A265G+Y267F+V291A+F328L+Q365C,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
A139T+R158S+Y160D+W187M+N195F+H210N+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*,
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+Y58F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195H+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A,
H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A,
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A,
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A,
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A,

2026202266 24 Mar 2026

A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A,
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A,
Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A,
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A,
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q125G+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026
2026202266

H1*+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K269M+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+K391A,
Y160H+E212D+K259G+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+A174S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+N195Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q169E+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
G7A+F113N+R116N+E276N+S304G+R320S+Q345N+W439R+N465G+Q466S+W469Y,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D377H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V238A+K391A,
Y160H+N195F+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256N+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365H+K391A,
Y160H+N195Q+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+R171Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
G109A+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R127F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A,
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A,
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F, Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L235I+V238A+K391A,
H1*+N54S+V56T+G109A+Q172S+L173K+A174S+N175*+R176A+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
V56T+Y160H+A174N+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,
H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A,
H1*+N54S+V56T+G109A+R116H+Q169E+Q172K+A174*+N195F+V206L+N314Q+Q385L+K391A,
H1*+I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S, using SEQ ID NO: 1 for numbering and wherein said variant has an improved relative specific activity of at least ≥1.1 in Model A detergent composition as a measure of wash performance compared to parent alpha-amylase of SEQ ID NO: 2.

36. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
M246L,
N195F+Q365C,
N195F+Q365S,
N195F+Q365M,
N195F+Q365K,
R127L+Q365S,
R127N+Q365S,
R127L+Q365C,
R171H+Q365C,
Y267F+Q365S,
F328L+Q365S,

24 Mar 2026
2026202266

I9M+N195F,
S170*+R171*+A174*,
V264I+A265G+Y267F,
Q169*+S170*+A174*,
M246L+L275V+Q365S,
V264I+V291I+Q365S,
V264I+V291T+Q365K,
V264I+F328L+Q365C,
I9M+N195F+Q365C,
Q11H+Y267F+Q365C,
I9M +N195F+Q365S,
V264I+Y267F+Q365K,
R127L+M246V+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127N+M246L+L275V+Q365S,
R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
R127N+M246L+L275V+Q365S,
Y267F+V291A+F328L+Q365C,
I9M+A186E+N195F+Q365S,
E86L+R171L+N306R+Q365S,
V264I+Y267F+F328L+Q365S,
I9M+N195F+V291A+Q365S,
R127L+L235I+M246I+Q365C,
Y267F+V291A+F328L+Q365S,
V264I+Y267F+F328L+Q365K,
Q11H+V264I+A265G+Q365C,

24 Mar 2026
2026202266

V264I+Y267F+V291A+F328L+Q365S,
V264I+A265G+V291A+F328L+Q365S,
R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
R116S+S132F+R181N+N195F+Q365S,
E130T+T134Y+A186K+N195F+Q365S,
A37V+V264I+Y267F+F328L+Q365C,
Q11H+V264I+Y267F+F328L+Q365C,
V264I+Y267F+V291T+F328L+Q365S,
Q169*+R171*+Q172*+L173*+A174*,
R116Y+S132P+Q136N+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377Y,
V264I+A265G+Y267F+F328L+Q365S,
I9M+N195F+K269Q+A274K+Q365S,
E130D+T134Y+R181H+N195F+Q365S,
R116N+S132M+Q136R+N195F+Q365S,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,
E130D+T134W+R181KA186E+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
E130S+T134E+R181S+A186T+N195F+Q365S,
R116C+S132A+Q136S+R181A+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+Q365S,
R127H+R171H+M246L+L275V+N306R+Q365S,
E130L+T134N+R181W+A186T+N195F+Q365S,
R116C+S132M+Q136S+R181Q+N195F+Q365S,
R116S+Y135H+Q136G+R181T+N195F+Q365S,
R116S+S132L+Q136E+R181G+N195F+Q365S,
N16E+N195F+G337E+Q365S+P375T+D377H,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,

24 Mar 2026
2026202266

N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*,
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A,
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A,
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A,
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A,
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A,
Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A,
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A,
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A,
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A,
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F,
Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,
H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K39

24 Mar 2026

2026202266

1A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A, using SEQ ID NO: 1 for numbering and wherein said variant has an improved relative specific activity of at least ≥1.5 in Model A detergent composition as a measure of wash performance compared to parent alpha-amylase of SEQ ID NO: 2.

37. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
N195F+Q365C,
N195F+Q365S,
N195F+Q365M,
R127L+Q365S,
R127N+Q365S,
S170*+R171*+A174*,
V264I+A265G+Y267F,
Q169*+S170*+A174*,
V264I+V291I+Q365S,
V264I+V291T+Q365K,
V264I+F328L+Q365C,
I9M+Y160H+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127N+M246L+L275V+Q365S,
R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
R127N+M246L+L275V+Q365S,
Y267F+V291A+F328L+Q365C,
V264I+Y267F+V291A+F328L+Q365S,
V264I+A265G+V291A+F328L+Q365S,

24 Mar 2026
2026202266

R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,

24 Mar 2026
2026202266

Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,
using SEQ ID NO: 1 for numbering and wherein said variant has an improved relative specific activity of at least ≥ 2.0 in Model A detergent composition as a measure of wash performance compared to parent alpha-amylase of SEQ ID NO: 2.

38. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
N195F+Q365C,
S170*+R171*+A174*,
I9M+Y160H+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
V264I+Y267F+V291A+F328L+Q365S,
Q169*+S170*+R171*+Q172*+L173*+A174*,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
using SEQ ID NO: 1 for numbering and wherein said variant has an improved relative specific activity of at least ≥ 2.5 in Model A detergent composition as a measure of wash performance compared to parent alpha-amylase of SEQ ID NO: 2.

39. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
Y295F,
M246L,
M202L,
R181S +G184S,
F113Q +R116H,

24 Mar 2026
2026202266

V264I +L357F,
Y267F +Q365S,
R171H,
R171Y +N306K,
R171H + Q365C,
R171L +Q365S,
R171H +N302H +Q365S,
R171L +N302H +Q365C,
R171Y + +M246L +Q365S,
F328L +Q365S,
R127L,
R127N +Q365S,
R127L +Q365C,
R127L +Q365S,
R127L +M246V +Q365S,
A186D +N195F,
V264I +Q365C,
I9M +N195F +Q365C,
V264I +A265G +Y267F,
V264I +V291T +Q365K,
A60S +R171Y +Q365S,
V264I +Y267F +Q365K,
V264I +F328L +Q365C,
M246L+ L275V +Q365S,
V264T +Y267F +Q365S,
V264I +F328L +Q365S,
Q11H +Y267F +Q365C,
V104A +N195F +Q365S,
V264I +V291I +Q365S,
V264I +Y267F +Q365S,
F113T +R171K +G273V,
Q169* +S170* +A174*,
I9M +R171H +N195F +Q365S,
I9M +R127N +N195F +Q365S,
E86L +R171L +N306R +Q365S,
I9M +A186E +N195F +Q365S,

24 Mar 2026
2026202266

I9M +Y160H +N195F +Q365S,
I9M +A186H +N195F +Q365S,
R171H +M246L +L275V +Q365S,
I9M +N195F +V291A +Q365S,
I9M +G184K +N195F +Q365S,
M246L +L275V +Q365S +D406H,
Y267F +V291A +F328L +Q365S,
Y267F +V291A +F328L +Q365C,
V264I +Y267F +F328L +Q365K,
I9M +R171L +N195F +Q365S,
Q11H +V264I +A265G +Q365C,
V264T +V291A +F328L +Q365S,
V264I +Y267F +F328L +Q365S,
R127N +M246L +L275V +Q365S,
I9M +N195F +N270G +Q365S,
I9M +N195F +N270P +Q365S,
V264T +Y267L +F328L +Q365C,
V264I +A265G +V291A +Q365C,
W187M +N195F +H210K +Q365S,
V264I +Y267F +F328L +Q365C,
Q169* +S170* +R171* +A174*,
I9M +N195F +V206L +D209N +Q365S,
N195F +G337D +Q365S +P375K +D377N,
V264I +Y267F +V291T +F328L +Q365S,
N195F +G337E +Q365S +P375K +D377N,
N195F +G337D +Q365S +P375K +D377Y,
V264I +A265G +V291A +F328L +Q365S,
I9M +N195F +K269Q +A274K +Q365S,
V264I +Y267F +Q365K +W408H +V410I,
E130D +T134Y +R181H +N195F +Q365S,
V264I +Y267F +V291A +F328L +Q365S,
E130I +T134A +R181N +N195F +Q365S,
R116Y +S132P +Q136N +N195F +Q365S,
R116N +S132M +Q136R +N195F +Q365S,
V264I +A265G +Y267F +F328L +Q365S,
Q11H +V264I +Y267F +F328L +Q365C,

24 Mar 2026
2026202266

Q11H +V264I +A265G +Y267F +Q365C,
E130T +T134Y +A186K +N195F +Q365S,
R116S +S132F +R181N +N195F +Q365S,
V264A +Y267F +V291T +F328L +Q365C,
N54Q +F113T +R171H +N302A +Q365C,
R127N +R171L +M246L +L275V +Q365S,
V264T +A265G +Y267L +F328L +Q365C,
V264I +Y267F +V291A +F328L +Q365C,
N16E +N195F +G337E +Q365S +P375T +D377H,
E130D +T134W +R181K +A186E +N195F +Q365S,
E130F +T134R +R181S +A186D +N195F +Q365S,
V264T +A265G +Y267F +V291A +F328L +Q365C,
E130V +T134N +R181Y +A186K +N195F +Q365S,
R116N +S132A +Q136D +R181K +N195F +Q365S,
E130L +T134N +R181W +A186T +N195F +Q365S,
V264I +A265G +Y267F +F328L +Q365S +Q395K,
N16E +N195F +G337D +Q365S +P375K +D377N,
E130N +T134C +R181Q +A186N +N195F +Q365S,
R116S +Y135H +Q136G +R181T +N195F +Q365S,
R116K +S132L +Q136R +R181C +N195F +Q365S,
V264I +A265G +Y267F +V291I +F328L +Q365S,
E130S +T134E +R181S +A186T +N195F +Q365S,
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S,
A139T +R158S +Y160D +W187M +N195F +H210N +Q365S,
R116K +S132P +Q136D +R181Q +N195F +A204V +Q365S,
E130Y +S132T +T134S +R181E +A186D +N195F +Q365S,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P,
H1* +N54S +V56T +G109A +R171H +N195F +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473I +G476K,
Y160H +E212D +E276N +W284Y +R320S +Q365S +W408H +W439T +W469N +F473S

24 Mar 2026
2026202266

+G476K,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +Q365S +K391A,
E86L +Y160H +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +N306R +K391A,
H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
I9M +Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +Q365S +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L+ V206L +W284Y +K391A,
H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,
H1* +I9M +N54S +V56T +G109A +F113G +R116H +D163H +Q169E +R171H +Q172K +A174S +G182T +N195F +M202L +V206L +M246L +L275V +A288V +L317V +Q319H +H324K +Q365S +K391A,
H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.1 in ADW detergent composition with bleach assessed using AMSA.

40. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
Y295F,
M246L,
M202L,
R181S +G184S,
F113Q +R116H,
Y267F +Q365S,

24 Mar 2026
2026202266

R171H,
R171H + Q365C,
R171L +Q365S,
R171H +N302H +Q365S,
R171L +N302H +Q365C,
R171Y + +M246L +Q365S,
F328L +Q365S,
I9M +N195F +Q365C,
V264I +A265G +Y267F,
V264I +V291T +Q365K,
A60S +R171Y +Q365S,
V264I +Y267F +Q365K,
V264I +F328L +Q365C,
M246L+ L275V +Q365S,
V264T +Y267F +Q365S,
V264I +F328L +Q365S,
Q11H +Y267F +Q365C,
I9M +R171H +N195F +Q365S,
I9M +R127N +N195F +Q365S,
E86L +R171L +N306R +Q365S,
I9M +A186E +N195F +Q365S,
I9M +Y160H +N195F +Q365S,
I9M +A186H +N195F +Q365S,
I9M +N195F +V291A +Q365S,
I9M +G184K +N195F +Q365S,
M246L +L275V +Q365S +D406H,
Y267F +V291A +F328L +Q365S,
Y267F +V291A +F328L +Q365C,
V264I +Y267F +F328L +Q365K,
I9M +R171L +N195F +Q365S,
Q11H +V264I +A265G +Q365C,
I9M +N195F +V206L +D209N +Q365S,
N195F +G337D +Q365S +P375K +D377N,
V264I +Y267F +V291T +F328L +Q365S,
N195F +G337E +Q365S +P375K +D377N,
N195F +G337D +Q365S +P375K +D377Y,

24 Mar 2026
2026202266

V264I +A265G +V291A +F328L +Q365S,
I9M +N195F +K269Q +A274K +Q365S,
V264I +Y267F +Q365K +W408H +V410I,
E130D +T134Y +R181H +N195F +Q365S,
V264I +Y267F +V291A +F328L +Q365S,
E130I +T134A +R181N +N195F +Q365S,
R116Y +S132P +Q136N +N195F +Q365S,
R116N +S132M +Q136R +N195F +Q365S,
N16E +N195F +G337E +Q365S +P375T +D377H,
E130D +T134W +R181K +A186E +N195F +Q365S,
E130F +T134R +R181S +A186D +N195F +Q365S,
V264T +A265G +Y267F +V291A +F328L +Q365C,
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,
H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.5 in ADW detergent composition with bleach assessed using AMSA.

41. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
M202L,

24 Mar 2026
2026202266

R171H + Q365C,
R171L +Q365S,
R171H +N302H +Q365S,
R171L +N302H +Q365C,
I9M +N195F +Q365C,
V264I +A265G +Y267F,
E86L +R171L +N306R +Q365S,
I9M +A186E +N195F +Q365S,
I9M +Y160H +N195F +Q365S,
I9M +A186H +N195F +Q365S,
I9M +N195F +V206L +D209N +Q365S,
N195F +G337D +Q365S +P375K +D377N,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,
H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.0 in ADW detergent composition with bleach assessed using AMSA.

42. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
M202L,
R171H + Q365C,
I9M +N195F +Q365C,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S

24 Mar 2026
2026202266

+G476K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.5 in ADW detergent composition with bleach assessed using AMSA.

43. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.5 in ADW detergent composition with bleach assessed using AMSA.

44. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
V264I+A265G+Y267F,
R171L+Q365S,
Y267F+Q365S,
R127L+Q365S,
V264I+F328L+Q365C,
M246L+L275V+Q365S+D406H,
Q11H+V264I+A265G+Q365C,
R127N+R171H+M246L+L275V+Q365S,
V264I+Y267F+V291T+F328L+Q365S,
Y267F+V291A+F328L+Q365S,
V264I+Y267F+F328L+Q365K,
R127H+L235I+Q365S+G435C,
N195F+Q365S,
I9M+N195F+Q365C,
I9M+R127N+N195F+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+A186E+N195F+Q365S,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+G184K+N195F+Q365S,
N195F+G337E+Q365S+P375K+D377N,
N195F+G337D+Q365S+P375K+D377Y,
E130I+T134A+R181N+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,

24 Mar 2026
2026202266

N16E+N195F+G337E+Q365S+P375T+D377H,
E130D+T134W+R181K+A186E+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
Y160H+M202L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473I+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y2
95F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A1
74*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+
Q445S+Q466S,
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.1 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

45. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
V264I+A265G+Y267F,
R127N+R171H+M246L+L275V+Q365S,
V264I+Y267F+V291T+F328L+Q365S,
I9M+N195F+Q365C,

24 Mar 2026
2026202266

I9M+R127N+N195F+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+A186E+N195F+Q365S,
N195F+G337E+Q365S+P375K+D377N,
N16E+N195F+G337E+Q365S+P375T+D377H,
E130D+T134W+R181K+A186E+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S,
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 1.5 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

46. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026
2026202266

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S,
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.0 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

47. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.5 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

48. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 3.0 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

48. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 3.5 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 40 °C.

49. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
Y295F,
M246L,
N195F+Q365S,
R171H+Q365C,
V264I+A265G+Y267F,
E86L+R171L+N306R+Q365S,
V264I+Y267F+V291T+F328L+Q365S,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
I9M+R127N+N195F+Q365S,
I9M+R171L+N195F+Q365S,
N195F+G337E+Q365S+P375K+D377N,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,

24 Mar 2026

2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 1.1 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

50. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
V264I+A265G+Y267F,
E86L+R171L+N306R+Q365S,
V264I+Y267F+V291T+F328L+Q365S,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
N195F+Q365S,
I9M+R127N+N195F+Q365S,
I9M+R171L+N195F+Q365S,
N195F+G337E+Q365S+P375K+D377N,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 1.2 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

51. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
N195F+Q365S,
V264I+A265G+Y267F,
E86L+R171L+N306R+Q365S,

24 Mar 2026
2026202266

V264I+Y267F+V291T+F328L+Q365S,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
I9M+R127N+N195F+Q365S,
I9M+R171L+N195F+Q365S,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 1.3 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

52. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of: V264I+A265G+Y267F
V264I+Y267F+V291T+F328L+Q365S
I9M+R171L+N195F+Q365S
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥1.5 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

53. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 2.0 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

54. The variant according to any one of the preceding paragraphs, wherein said variant is selected from the group consisting of:
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K, using SEQ ID NO: 1 for numbering and wherein said variant has an Improvement Factor (IF) of at least ≥ 3.0 in ADW detergent composition with bleach assessed using a full scale automatic dishwash (ADW) at 45 °C.

55. A polynucleotide encoding said variant according to any one of paragraphs 1 to 54.

56. A nucleic acid construct comprising said polynucleotide according to paragraph 55.

57. An expression vector comprising said polynucleotide according to paragraph 55.

58. A host cell comprising said polynucleotide according to paragraph 55, said nucleic acid construct according to paragraph 56, or said expression vector according to paragraph 57.

59. A method of producing an alpha-amylase variant, comprising: cultivating said host cell according to paragraph 58 under conditions suitable for expression of said variant; and (b) recovering said variant.

60. A composition comprising the variant according to any one of paragraphs 1 to 54 and at least one additional active component.

24 Mar 2026
2026202266

61. The composition according to paragraph 60, wherein one or more additional active component is selected from the group consisting of one or more enzymes, oxidizing agents, bleach activators, bleach catalysts, chelating agents, bulking agents, builders, buffering agents, structurants, sequestrants, optical brighteners, antifoaming agents, enzymes, fragrances, anti-redeposition agents, crystal growth inhibitors, metal care agents, glass care agents, skin conditioning agents, softness extenders, emulsifiers, and colorants.

62. The composition according to paragraphs 60-61, wherein the additional enzyme is selected from the group consisting of proteases, amylases, phospho- lipases, esterases, lipases, cutinases, cellulases, endoglucanases, xyloglucanases, xylanases, pectinases, hemicellulases pectin lyases, xanthanases, peroxidases, keratinases haloperoxygenases, catalases, mannanases, lechinase, RNase, DNAse, reductases, oxidases, phenoloxidases, lipoxygenases, ligninases, pullulanases, tannases, pento-sanases, malanases, β-glucanases, arabinosidases, hyaluronidase, chondroitinase, and laccase or any mixture thereof.

63. The composition according to paragraphs 60-62, further comprising a surfactant, wherein the surfactant is one or more surfactants selected from the group consisting of an anionic surfactant, a cationic surfactant, a non-ionic surfactant, zwitterionic surfactant, and amphoteric surfactants or any mixtures thereof.

64. The composition according to any one of paragraphs 60-63, wherein said composition is a detergent composition.

65. The composition according to paragraphs 60-64, wherein the detergent composition is a liquid laundry detergent composition, a powder laundry detergent composition, a liquid dishwash detergent composition, or a powder dishwash detergent composition.

66. The composition according to paragraphs 60-65, wherein said composition is a liquid or powder laundry detergent composition.

67. The composition according to paragraphs 60-66, wherein said composition is a liquid or powder automatic dishwashing (ADW) detergent composition.

68. The composition according to any one of paragraphs 60-67, wherein said composition is a liquid manual dishwashing detergent composition.

24 Mar 2026
2026202266

69. Use of a variant according to any one of paragraphs 1 to 54, or of a composition according to any one of paragraphs 60-68, in a domestic or industrial cleaning process.

70. Use according to paragraph 69 for cleaning of fabric, for example laundry.

71. Use according to paragraph 70 for hard surface cleaning, cleaning of ceramic, metal, plastic or glass material, for example dishwashing.

72. A method for removal of soils from fabric or hard surfaces comprising contacting the fabric or hard surfaces contaminated with soils with a composition according to any one of paragraphs 60-68.

73. A method according to paragraph 72 for cleaning of fabric, for example laundry.

74. A method according to paragraph 72 for hard surface cleaning, for example dishwashing.

75. A method according to paragraph 74 wherein the method is performed using an automated dishwasher.

76. A method of dishwashing in an automatic dishwashing machine using a composition according to any one of paragraphs 60-68 comprising the steps of adding said detergent composition in a detergent composition compartment in said automatic dishwashing machine, and releasing said detergent composition during a main-wash cycle.

77. A method of laundering in an automatic laundering machine using a composition according to any one of paragraphs 60-68, comprising the steps of adding said detergent composition in a detergent composition compartment in said automatic laundering machine, and releasing said detergent composition during a main wash cycle.

78. A method of improving the performance, such as wash performance, of a parent alpha-amylase having the amino acid sequence of SEQ ID NO: 2, or having at least 59% sequence identity hereto, said method comprising the steps of *a)* introducing a substitution and/or deletion at two or more positions corresponding to positions R181, G182, D183, and G184, using SEQ ID NO: 1 for numbering; and *b)* introducing a deletion and/or substitution at one or more positions selected from the group consisting of: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139,

24 Mar 2026
2026202266

142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and/or 481, using SEQ ID NO: 1; said method thereby providing an alpha-amylase variant of said parent alpha-amylase, wherein said variant has at least 59%, such as at least 60%, such as at least 65%, such as at least 70%, such as at least 75%, such as at least 80%,such as at least 85%, such as at least 90%, such as at least 95%, such as at least 97%, such as at least 99%, but less than 100%, sequence identity to the amino acid sequence as set forth in SEQ ID NOs: 1-17, and wherein said variant has alpha-amylase activity and improved performance as compared to said parent alpha-amylase having alpha-amylase activity as shown in SEQ ID NO: 2.

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

Materials and Method

Strains

The DNA encoding the GH13_5 alpha-amylase was isolated from *Bacillus sp* isolated from soil samples collected in Denmark and sequenced as described in WO 2000/060058.

Chemicals used as buffers and substrates were commercial products of at least reagent grade.

CS-28 swatch-DM-277 (double soiled Mix starch) was purchased from Center for Testmaterials BV, Stoomloggerweg 11, 3133 KT Vlaardingen, the Netherlands.

Assays for alpha-amylase activity

1. *PNP-G7 assay*

The alpha-amylase activity was determined by employing the pNP-G7 substrate (PNP-G7 the abbreviation for 4,6-ethylidene(G7)-p-nitrophenyl(G1)-α,D-maltoheptaoside, a blocked oligosaccharide which is cleaved by an endo-amylase, such as an alpha-amylase).

An antibody was diluted in Phosphate buffered saline (PBS) (0.010 M Phosphate buffer pH7.4, 0.0027M KCl, 0.14M NaCl) buffer to concentration of 10µg/ml. A maxisorp microtiter plate was coated with antibody by adding 100µl diluted antibody (10µg/ml) to each well and incubated for 1h at room temperature (RT) and mixing at 800 rpm. After incubation the microtiter plate was washed (using Bio-Tek ELx405 ELISA washer) with 3x 200µl Phosphate buffered saline with 0.05% Tween (PBST) (0.010 M Phosphate buffer pH7.4, 0.0027M KCl, 0.14M NaCl, 0.05%

24 Mar 2026
2026202266

Tween 20) buffer.

Microtiter plates with the alpha-amylase variants culture broths were spun down and supernatants transferred to new microtiter plates and diluted 4x in PBST buffer. 100µl diluted supernatant was transferred to antibody coated maxisorp microtiter plate and incubated for 1h at RT and mixing at 800rpm. After incubation microtiter plates were washed in PBST buffer (3x 200µl, ELISA washer).

Upon the cleavage of the pNP-G7 substrate, the alpha-Glucosidase included in the kit used is digested and the hydrolysed substrate liberates a free pNP molecule which has a yellow color and thus can be measured by visible spectophometry at Abs=405nm (400-420 nm.). Kits containing pNP-G7 substrate and alpha-Glucosidase are manufactured by Roche/Hitachi (cat. No.11876473). 100µl pNP-G7 substrate was added to all wells and mixed for 1 minute before measuring absorbance at 405nm. The slope (absorbance per minute) is determined and only the linear range of curve is used.

The slope of the time dependent absorption-curve is directly proportional to the activity of the alpha-amylase in question under the given set of conditions.

The specific alpha-amylase activity may also be determined by other activity assays, such as amylazyme activity assay, Phadebas activity assay, or reducing sugar activity assay as described below.

2. Amylazyme activity assay

Amylazyme activity assay (from Megazyme, Ireland): An Amylazyme tablet includes interlinked amylose polymers that are in the form of globular microspheres that are insoluble in water. A blue dye is covalently bound to these microspheres. The interlinked amylose polymers in the microsphere are degraded at a speed that is proportional to the alpha-amylase activity. When the alpha-amylase degrades the amylose polymers, the released blue dye is water soluble and concentration of dye can be determined by measuring absorbance at 650nm. The concentration of blue is proportional to the alpha-amylase activity in the sample.

The amylase sample to be analysed is diluted in activity buffer with the desired pH. One substrate tablet is suspended in 5mL activity buffer and mixed on magnetic stirrer. During mixing of substrate transfer 150µl to microtiter plate (MTP). Add 30µl diluted amylase sample to 150µl substrate and mix. Incubate for 15 minutes at 37°C. The reaction is stopped by adding 30µl 1M NaOH and mix. Centrifuge MTP for 5 minutes at 4000xg. Transfer 100µl to new MTP and measure absorbance at 620nm.

The amylase sample should be diluted so that the absorbance at 650nm is between 0 and 2.2, and is within the linear range of the activity assay.

24 Mar 2026
2026202266

3. Phadebas assay

A Phadebas tablet (from for example Magle Life Sciences, Lund, Sweden) includes interlinked starch polymers that are in the form of globular microspheres that are insoluble in water. A blue dye is covalently bound to these microspheres. The interlinked starch polymers in the microsphere are degraded at a speed that is proportional to the alpha-amylase activity. When the alpha-amylase degrades the starch polymers, the released blue dye is water soluble and concentration of dye can be determined by measuring absorbance at 650nm. The concentration of blue is proportional to the alpha-amylase activity in the sample.

The amylase sample to be analysed is diluted in activity buffer with the desired pH. One substrate tablet is suspended in 5mL activity buffer and mixed on magnetic stirrer. During mixing of substrate transfer 150µl to microtiter plate (MTP). Add 30µl diluted amylase sample to 150µl substrate and mix. Incubate for 15 minutes at 37°C. The reaction is stopped by adding 30µl 1M NaOH and mix. Centrifuge MTP for 5 minutes at 4000xg. Transfer 100µl to new MTP and measure absorbance at 620nm.

The measured absorbance is directly proportional to the specific activity (activity/mg of pure alpha-amylase protein) of the alpha-amylase in question under the given set of conditions.

4. Reducing sugar activity assay

Number of reducing ends formed by the alpha-amylase hydrolysing the alpha-1,4-glycosidic linkages in starch is determined by reaction with p-Hydroxybenzoic acid hydrazide (PHBAH). After reaction with PHBAH the number of reducing ends can be measured by absorbance at 405nm and the concentration of reducing ends is proportional to the alpha-amylase activity in the sample.

The corns starch substrate (3mg/ml) is solubilised by cooking for 5 minutes in milliQ water and cooled down before assay. For the stop solution prepare a Ka-Na-tartrate/NaOH solution (K-Na-tartrate (Merck 8087) 50g/l, NaOH 20g/l) and prepare freshly the stop solution by adding p-Hydroxybenzoic acid hydrazide (PHBAH, Sigma H9882) to Ka-Na-tartrate/NaOH solution to 15mg/ml.

In PCR-MTP 50µl activity buffer is mixed with 50µl substrate. Add 50µl diluted enzyme and mix. Incubate at the desired temperature in PCR machine for 5 minutes. Reaction is stopped by adding 75µl stop solution (Ka-Na-tartrate/NaOH/PHBAH). Incubate in PCR machine for 10 minutes at 95°C. Transfer 150µl to new MTP and measure absorbance at 405nm.

The measured absorbance is directly proportional to the specific activity (activity/mg of pure alpha-amylase protein) of the alpha-amylase in question under the given set of conditions.

24 Mar 2026
2026202266

EXAMPLES

Example 1: Construction of the parent polypeptide as set forth in SEQ ID NO: 2

Construction of a polypeptide having the amino acid sequence set forth in SEQ ID NO: 2 (the parent polypeptide). The polypeptide is a modified alpha-amylase (EC 3.2.1.1) belonging to the glycoside hydrolase GH13 Family, Subfamily 5.

Example 2: Generation of variants

Using the parent alpha-amylase having the amino acid sequence as set forth in SEQ ID NO: 2, the variants of the present invention were constructed. The variants were prepared by standard procedures, which in brief is; introducing an amino acid substitution in SEQ ID NO: 2 by site-directed mutagenesis into the gene, transforming *Bacillus subtilis* host cells with the mutated gene, fermenting the transformed cells (*e.g.* as described in Example 1 of WO 2004/111220), and purifying the variants from the fermentation broth. The reference amylase, *i.e.* the parent alpha-amylase, having the amino acid sequence as set forth in SEQ ID NO: 2, were produced recombinantly in *Bacillus subtilis* in a similar manner.

A library of variants were generated where different combinations of modifications in the following positions were made: H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering.

The generated variants are listed in the following examples.

Example 3: Amylase activity assay with CS-28 swatches

Purified amylase variants were initially diluted to 0.1 mg/ml (concentrations based on absorbance at 280 nm) with 0.01% Triton X-100, 1 mM $CaCl_2$. Further enzyme dilutions are in 0.01% Triton X-100.

In microtiter plates containing a CS-28 rice starch substrate swatch in each of the 96 wells, 50 µl diluted amylase (final concentrations in wells of 0.04, 0.02 and 0.01 ppm) was mixed with 150 µl Model A wash solution (final concentration in well of 3.45 g/l Model A detergent, 21°dH

24 Mar 2026
2026202266

water hardness (molar ratio Ca:Mg:HCO3 = 4:1:10)). After 10-15 min incubation at room temperature with agitation, 20 µl supernatant was transferred to another 96 well microtiter plate to determine solubilized amount of starch fragments. To hydrolyze the starch fragments to glucose, 10 µl 0.5 mg/ml glucoamylase was added and the plate was incubated 10 min at room temperature with agitation. Then 140 µl GOD-Perid reagent (0.1 M potassium phosphate, pH 7, 0.6 g/l glucose oxidase (Sigma G6125), 20 mg/l peroxidase (Sigma P8125), 1 g/l ABTS (Roche 102946)) was added, and glucose concentration was assumed to be proportional to absorbance read in a plate reader at 420 nm after 15 min incubation. For each sample duplicates of 3 concentrations (0.04, 0.02 and 0.01 ppm) are tested. A reference sample (SEQ ID NO: 2) was included on all plates. A dose-response curve was fitted (least squares method) for each sample to a 4-parameter logistic expression:

A420 = A420min + (A420max - A420min) / (1 + (C / C50) ^ Slope)

where A420 is measured absorbance, A420min is a minimum absorbance, A420max is a maximum absorbance, C is the amylase concentration, C50 is the amylase concentration giving an absorbance of 0.5 * (A420min + A420max), and Slope is a steepness parameter. A420min, A420max and Slope are assumed to be identical for all samples on a plate, whereas C50 is fitted for each sample. Dose Improvement Factor (Dose IF) for a sample is calculated as:

Dose IF(sample) = C50(reference)/C50(sample)

Table 1: Model A detergent (percentages given in w/w)

Compound	Content ingredients	Fraction active component
MGDA- H_3 (Trilon M Granules SG)	33%	59%
Sodium citrate	20%	100%
Sodium carbonate	20%	100%
Sodium silicate	6%	80%
Sodium sulfate	12%	100%
Acusol 588G	5%	92%
Non-ionic surfactant (Surfac 23-6.5 (added as liquid)	5%	100%

24 Mar 2026
2026202266

Dose IF of the variants according to the invention obtained by the method described above are shown in Table 2 below. The test results clearly demonstrate that the variants have improved relative activity to the reference amylase, *i.e.* the parent alpha-amylase.

Table 2: Relative specific activity of variants

Modifications in SEQ ID NO: 2	IF
SEQ ID NO: 2	1.0
A60T	1.4
Y135H	1.4
Q169E	1.4
W48Y	1.3
A174*	1.1
M246L	1.5
R90Q	1.4
Y203L+V206L	1.3
Q169F+S170A	1.1
S132D+G133D	1.1
N195F+Q365C	2.6
N195F+Q365S	2.1
N195F+Q365M	2.1
N195F+Q365K	1.8
R127L+Q365S	2.0
R127N+Q365S	2.0
R127L+Q365C	1.9
R171L+Q365S	1.4
R171H+Q365C	1.6
Y267F+Q365S	1.5
F328L+Q365S	1.5
I9M+N195F	1.7
N195F+M286L	1.1
T134P+N195F	1.1
S170*+R171*+A174*	2.6
V264I+A265G+Y267F	2.3
Q169*+S170*+A174*	2.2
M246L+L275V+Q365S	1.5

2026202266 24 Mar 2026

V264I+V291I+Q365S	2.1
V264I+V291T+Q365K	2.1
V264I+F328L+Q365C	2.0
I9M+N195F+Q365C	1.9
Q11H+Y267F+Q365C	1.7
I9M +N195F+Q365S	1.7
V264I+Y267F+Q365K	1.6
R127L+M246V+Q365S	1.6
A60S+R171Y+Q365S	1.4
R127N+M246T+L275V	1.4
V104A+N195F+Q365S	1.4
V264I+F328L+Q365S	1.4
R171H+N302H+Q365S	1.4
V264I+Y267F+Q365S	1.3
A174*+N175*+Y178F	1.3
V264I+A265G+Q365C	1.3
R171L+N302H+Q365C	1.1
R171L+M246V+Q365C	1.1
R171Y+M246L+Q365S	1.1
V264T+Y267F+Q365S	1.1
I9M+Y160H+N195F+Q365S	2.7
I9M+R127N+N195F+Q365S	2.1
R127H+L235I+Q365S+G435C	2.5
I9M+R171H+N195F+Q365S	2.5
I9M+A186H+N195F+Q365S	2.4
I9M+R171L+N195F+Q365S	2.3
Q169*+S170*+R171*+A174*	2.3
M246L+L275V+Q365S+D406H	2.3
I9M+G184K+N195F+Q365S	2.2
I9M+R127N+N195F+Q365S	2.2
R127N+M246L+L275V+Q365S	2.2
R171H+M246L+L275V+Q365S	2.1
R127H+M246I+Q365C+V481A	2.0
R127N+M246L+L275V+Q365S	2.0
Y267F+V291A+F328L+Q365C	2.0

2026202266 24 Mar 2026

I9M+A186E+N195F+Q365S	1.9
E86L+R171L+N306R+Q365S	1.8
V264I+Y267F+F328L+Q365S	1.7
I9M+N195F+V291A+Q365S	1.7
R127L+L235I+M246I+Q365C	1.7
Y267F+V291A+F328L+Q365S	1.6
V264I+Y267F+F328L+Q365K	1.6
Q11H+V264I+A265G+Q365C	1.5
I9M+R171H+N195F+Q365S	1.4
W187M+N195F+H210K+Q365S	1.4
R127H+M246T+L275A+Q365S	1.4
I9M+A111T+N195F+Q365S	1.3
I9M+Y58F+N195F+Q365S	1.3
V264T+V291A+F328L+Q365S	1.2
V264I+A265G+V291A+Q365C	1.1
V264I+A265G+Y267F+Q365C	1.1
V264I+Y267F+V291A+F328L+Q365S	2.5
R127N+R171H+M246L+L275V+Q365S	1.3
V264I+A265G+V291A+F328L+Q365S	2.4
R127N+M246I+A265G+Y267H+Q365S	2.3
E130I+T134A+R181N+N195F+Q365S	2.2
R127N+M246L+L275V+N306R+Q365S	2.0
I9M+N195F+V206L+D209N+Q365S	2.0
R116S+S132F+R181N+N195F+Q365S	1.9
E130T+T134Y+A186K+N195F+Q365S	1.9
A37V+V264I+Y267F+F328L+Q365C	1.8
Q11H+V264I+Y267F+F328L+Q365C	1.8
V264I+Y267F+V291T+F328L+Q365S	1.8
Q169*+R171*+Q172*+L173*+A174*	1.8
R116Y+S132P+Q136N+N195F+Q365S	1.8
N195F+G337D+Q365S+P375K+D377Y	1.7
V264I+A265G+Y267F+F328L+Q365S	1.7
I9M+N195F+K269Q+A274K+Q365S	1.7
E130D+T134Y+R181H+N195F+Q365S	1.6
R116N+S132M+Q136R+N195F+Q365S	1.5

2026202266 24 Mar 2026

N195F+G337D+Q365S+P375K+D377N	1.4
R127N+R171L+M246L+L275V+Q365S	1.2
N195F+G337E+Q365S+P375K+D377N	1.3
Q11H+V264I+A265G+Y267F+Q365C	1.3
R158Q+Y160N+W187M+N195F+Q365S	1.3
V264I+Y267F+Q365K+W408H+V410I	1.2
R127N+R171Y+M246L+L275V+Q365S	1.2
N54Q+F113T+R171H+N302A+Q365C	1.2
V264A+Y267F+V291T+F328L+Q365C	1.1
Q169*+S170*+R171*+Q172*+L173*+A174*	2.6
R116K+S132L+Q136R+R181C+N195F+Q365S	2.3
V264T+A265G+Y267F+V291A+F328L+Q365C	2.2
E130N+T134S+R181N+A186K+N195F+Q365S	2.0
E130V+T134N+R181Y+A186K+N195F+Q365S	2.0
E130D+T134W+R181KA186E+N195F+Q365S	1.9
R116N+S132A+Q136D+R181K+N195F+Q365S	1.9
E130S+T134E+R181S+A186T+N195F+Q365S	1.9
R116C+S132A+Q136S+R181A+N195F+Q365S	1.8
R116K+S132P+Q136D+R181Q+N195F+Q365S	1.8
R127H+R171H+M246L+L275V+N306R+Q365S	1.8
E130L+T134N+R181W+A186T+N195F+Q365S	1.8
R116C+S132M+Q136S+R181Q+N195F+Q365S	1.7
R116S+Y135H+Q136G+R181T+N195F+Q365S	1.7
R116S+S132L+Q136E+R181G+N195F+Q365S	1.6
N16E+N195F+G337E+Q365S+P375T+D377H	1.5
V264I+A265G+Y267F+V291I+F328L+Q365S	1.4
N16E+N195F+G337D+Q365S+P375K+D377N	1.3
V264I+A265G+Y267F+F328L+Q365S+Q395K	1.2
E130N+T134C+R181Q+A186N+N195F+Q365S	1.2
V264I+A265G+Y267F+V291A+F328L+Q365C	1.1
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*	3.2
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*	1.1
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S	2.8
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S	2.6
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S	2.5

2026202266 24 Mar 2026

E130Y+S132T+T134S+R181E+A186D+N195F+Q365S	2.0
A139T+R158S+Y160D+W187M+N195F+H210N+Q365S	1.2
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S	1.6
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A	1.3
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*	1.8
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.7
H1*+Y58F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.3
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A	1.9
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.5
N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.4
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195H+V206L+K391A	1.3
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A	2.8
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S +G476K	2.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A	2.4
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A	2.3
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.3
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.2
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A	2.2
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A	2.2
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A	2.1
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.1
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A	2.1
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A	2.1
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.1
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+ G476K	2.1
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A	2.0
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A	2.0
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.0
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.0
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.0
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A	1.9

2026202266 24 Mar 2026

H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.0
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A	2.0
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.9
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A	1.9
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A	1.9
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A	1.9
H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A	1.9
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L	1.9
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A	1.9
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.9
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A	1.9
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A	1.7
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.9
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.8
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A	1.8
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A+	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A	1.8
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A	1.8
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.8
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A	1.7
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A	1.7
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A	1.7
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.7

2026202266 24 Mar 2026

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A	1.7
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A	1.7
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A	1.7
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A	1.7
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A	1.7
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A	1.7
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S +G476K	1.7
H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L	1.7
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A	1.6
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A	1.6
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A	1.6
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A	1.6
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A	1.6
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A	1.6
Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S +G476K	1.6
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A	1.6
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.6
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A	1.6
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A	1.5
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A	1.5
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S +G476K	1.5
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.5
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A	1.5
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A	1.5
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A	1.5
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+ G476K	1.5
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+ G476K	1.5
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.5
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S +G476K	1.5

2026202266 24 Mar 2026

H1*+N54S+V56T+G109A+Q125G+Q169E+Q172K+A174*+N195F+V206L+K391A	1.4
H1*+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.4
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A	1.4
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311K+K391A	1.4
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K269M+K391A	1.4
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+K391A	1.4
Y160H+E212D+K259G+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.4
Y160H+A174S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.3
Y160H+N195Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.3
Y160H+Q169E+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.3
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.3
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.3
Y160H+E212D+E276N+W284Y+N306Y+R320S+W408H+W439T+W469N+F473S+G476K	1.3
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A	1.2
G7A+F113N+R116N+E276N+S304G+R320S+Q345N+W439R+N465G+Q466S+W469Y	1.2
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D377H+K391A	1.2
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V238A+K391A	1.2
Y160H+N195F+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.2
Y160H+E212D+Q256N+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.2
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365H+K391A	1.2
Y160H+N195Q+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.2
Y160H+R171Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.2

2026202266 24 Mar 2026

G109A+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.2
Y160H+E212D+E276N+W284Y+N306R+R320S+W408H+W439T+W469N+F473S+G476K	1.2
H1*+N54S+V56T+G109A+R127F+Q169E+Q172K+A174*+N195F+V206L+K391A	1.1
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A	2.2
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K	2.2
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A	2.0
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A	1.9
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A	1.9
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A	1.8
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A	1.8
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.6
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A	1.6
H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F	1.5
Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K	1.5
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L235I+V238A+K391A	1.4
H1*+N54S+V56T+G109A+Q172S+L173K+A174S+N175*+R176A+N195F+V206L+K391A	1.4
H1*+N54S+V56T+G109A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A	1.3

2026202266 24 Mar 2026

V56T+Y160H+A174N+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K	1.2
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A	2.1
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A	2.1
H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A	1.5
H1*+N54S+V56T+G109A+R116H+Q169E+Q172K+A174*+N195F+V206L+N314Q+Q385L+K391A	1.4
H1*+I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S	1.3

Example 4: Assessment of wash performance of alpha-amylase variants using Automatic Mechanical Stress Assay (AMSA) for Automatic Dish Wash

Washing experiments are performed in order to assess the wash performance of selected alpha-amylase variants in dishwash detergent compositions. The alpha-amylase variants of the present application may be tested using the Automatic Mechanical Stress Assay (AMSA). With the AMSA, the wash performance of many small volume enzyme-detergent solutions can be examined. The AMSA plate has a number of slots for test solutions and a lid that firmly squeezes the dish wash monitor to be washed against the slot openings. During the wash, the plate, test solutions, dishwash monitor and lid are vigorously shaken to bring the test solution in contact with the soiled dishwash monitor and apply mechanical stress in a regular, periodic oscillating manner. For further description see WO 02/42740 especially the paragraph "Special method embodiments" at page 23-24.

The experiment may be conducted under the experimental conditions as specified in the Table 3 below:

Table 3: Experimental condition

Detergent	ADW model detergent with bleach (Table 5)
Detergent dosage	3.94 g/L
Test solution volume	160 micro L

24 Mar 2026
2026202266

pH	As is
Wash time	20 minutes
Temperature	45°C
Water hardness	21°dH (ratio Ca:Mg:HCO3 = 4:1:10)
Enzyme concentration in test solution	0.35 mg enzyme protein/L
Test material	DM-277 (double soiled Mix starch)

Water hardness was adjusted to 21°dH by addition of $CaCl_2$, $MgCl_2$, and $NaHCO_3$ (Ca^{2+}:Mg^{2+}:HCO_3^- = 4:1:10) to Milli-Q water.

The wash performance is measured as the brightness of the color of the dish wash monitor. 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.

Color measurements are made with a professional flatbed scanner, 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:

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

General wash performance description

A test solution comprising water hardness adjusted water (21°dH, ratio Ca:Mg:HCO3 = 4:1:10), 3.94 g/L detergent, as described below, and the enzyme of the invention, e.g. at concentration of 0.35 mg enzyme protein/L, was prepared. Melamine tiles stained with starch (e.g. DM-277 (double soiled Mix starch) from Center For Testmaterials BV, P.O. Box 120, 3133 KT, Vlaardingen, The Netherlands), used as dishwash monitors, were added to the AMSA plate and washed for 20 minutes at 45°C. After thorough rinse under cold running tap water and drying in the dark, the light intensity of the stained tiles was subsequently measured as a measure for wash performance using a professional flatbed scanner (Kodak iQsmart, Kodak, Midtager 29, DK-2605 Brøndby, Denmark).

The wash performance was compared to that of the parent alpha-amylase, with the performance result of the parent alpha-amylase is assigned the value of 1.0 and the results of the variants are compared to this value (improvement Factor (IF) value).

The wash performance of the variants according to the invention obtained by AMSA are

2026202266 24 Mar 2026

the following:

Table 4: AMSA Performance Improvement Factor (IF) Dataset I

Modifications in SEQ ID NO: 2	IF
SEQ ID NO: 2	1.0
Y295F	1.9
M246L	1.5
M202L	2.5
R181S +G184S	1.5
F113Q +R116H	1.5
V264I +L357F	1.3
Y267F +Q365S	1.8
R171H	1.6
R171Y +N306K	1.2
R171H + Q365C	2.5
R171L +Q365S	2.1
R171H +N302H +Q365S	2.1
R171L +N302H +Q365C	2.0
R171Y + +M246L +Q365S	1.7
F328L +Q365S	1.6
R127L	1.1
R127N +Q365S	1.2
R127L +Q365C	1.3
R127L +Q365S	1.2
R127L +M246V +Q365S	1.3
A186D +N195F	1.2
V264I +Q365C	1.1
I9M +N195F +Q365C	2.7
V264I +A265G +Y267F	2.1
V264I +V291T +Q365K	1.8
A60S +R171Y +Q365S	1.8
V264I +Y267F +Q365K	1.7
V264I +F328L +Q365C	1.7
M246L+ L275V +Q365S	1.7
V264T +Y267F +Q365S	1.7
V264I +F328L +Q365S	1.6

2026202266 24 Mar 2026

Q11H +Y267F +Q365C	1.5
V104A +N195F +Q365S	1.3
V264I +V291I +Q365S	1.3
V264I +Y267F +Q365S	1.3
F113T +R171K +G273V	1.1
Q169* +S170* +A174*	1.1
I9M +R171H +N195F +Q365S	1.6
I9M +R127N +N195F +Q365S	1.6
E86L +R171L +N306R +Q365S	2.3
I9M +A186E +N195F +Q365S	2.3
I9M +Y160H +N195F +Q365S	2.1
I9M +A186H +N195F +Q365S	2.1
R171H +M246L +L275V +Q365S	1.4
I9M +N195F +V291A +Q365S	1.9
I9M +G184K +N195F +Q365S	1.8
M246L +L275V +Q365S +D406H	1.8
Y267F +V291A +F328L +Q365S	1.8
Y267F +V291A +F328L +Q365C	1.7
V264I +Y267F +F328L +Q365K	1.7
I9M +R171L +N195F +Q365S	1.6
Q11H +V264I +A265G +Q365C	1.6
V264T +V291A +F328L +Q365S	1.4
V264I +Y267F +F328L +Q365S	1.3
R127N +M246L +L275V +Q365S	1.3
I9M +N195F +N270G +Q365S	1.2
I9M +N195F +N270P +Q365S	1.2
V264T +Y267L +F328L +Q365C	1.2
V264I +A265G +V291A +Q365C	1.2
W187M +N195F +H210K +Q365S	1.2
V264I +Y267F +F328L +Q365C	1.1
Q169* +S170* +R171* +A174*	1.1
I9M +N195F +V206L +D209N +Q365S	2.3
N195F +G337D +Q365S +P375K +D377N	2.0
V264I +Y267F +V291T +F328L +Q365S	1.9
N195F +G337E +Q365S +P375K +D377N	1.8

2026202266 24 Mar 2026

N195F +G337D +Q365S +P375K +D377Y	1.7
V264I +A265G +V291A +F328L +Q365S	1.7
I9M +N195F +K269Q +A274K +Q365S	1.7
V264I +Y267F +Q365K +W408H +V410I	1.6
E130D +T134Y +R181H +N195F +Q365S	1.6
V264I +Y267F +V291A +F328L +Q365S	1.6
E130I +T134A +R181N +N195F +Q365S	1.5
R116Y +S132P +Q136N +N195F +Q365S	1.5
R116N +S132M +Q136R +N195F +Q365S	1.5
V264I +A265G +Y267F +F328L +Q365S	1.4
Q11H +V264I +Y267F +F328L +Q365C	1.4
Q11H +V264I +A265G +Y267F +Q365C	1.4
E130T +T134Y +A186K +N195F +Q365S	1.3
R116S +S132F +R181N +N195F +Q365S	1.2
V264A +Y267F +V291T +F328L +Q365C	1.2
N54Q +F113T +R171H +N302A +Q365C	1.2
R127N +R171L +M246L +L275V +Q365S	1.2
V264T +A265G +Y267L +F328L +Q365C	1.1
V264I +Y267F +V291A +F328L +Q365C	1.1
N16E +N195F +G337E +Q365S +P375T +D377H	1.9
E130D +T134W +R181K +A186E +N195F +Q365S	1.7
E130F +T134R +R181S +A186D +N195F +Q365S	1.5
V264T +A265G +Y267F +V291A +F328L +Q365C	1.5
E130V +T134N +R181Y +A186K +N195F +Q365S	1.4
R116N +S132A +Q136D +R181K +N195F +Q365S	1.4
E130L +T134N +R181W +A186T +N195F +Q365S	1.3
V264I +A265G +Y267F +F328L +Q365S +Q395K	1.3
N16E +N195F +G337D +Q365S +P375K +D377N	1.3
E130N +T134C +R181Q +A186N +N195F +Q365S	1.2
R116S +Y135H +Q136G +R181T +N195F +Q365S	1.2
R116K +S132L +Q136R +R181C +N195F +Q365S	1.2
V264I +A265G +Y267F +V291I +F328L +Q365S	1.2
E130S +T134E +R181S +A186T +N195F +Q365S	1.1
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S	1.6
A139T +R158S +Y160D +W187M +N195F +H210N +Q365S	1.2

2026202266 24 Mar 2026

R116K +S132P +Q136D +R181Q +N195F +A204V +Q365S	1.2
E130Y +S132T +T134S +R181E +A186D +N195F +Q365S	1.2
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S	2.3
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P	1.5
H1* +N54S +V56T +G109A +R171H +N195F +V206L +K391A	1.1
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +V206L +K391A	1.3
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A	1.8
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A	3.4
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K	3.3
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473I +G476K	1.1
Y160H +E212D +E276N +W284Y +R320S +Q365S +W408H +W439T +W469N +F473S +G476K	1.4
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +Q365S +K391A	1.4
E86L +Y160H +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K	1.1
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A	1.1
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +N306R +K391A	1.1
H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A	2.3
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A	2.2
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A	2.2
H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A	1.5
I9M +Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K	1.2

2026202266 24 Mar 2026

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +Q365S +K391A	1.1
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L+ V206L +W284Y +K391A	1.1
H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K	2.3
H1* +I9M +N54S +V56T +G109A +F113G +R116H +D163H +Q169E +R171H +Q172K +A174S +G182T +N195F +M202L +V206L +M246L +L275V +A288V +L317V +Q319H +H324K +Q365S +K391A	1.2
H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S	2.0

Example 5: Assessment of wash performance of alpha-amylase variants using Automatic Dish Wash (ADW)

In order to assess the wash performance of the alpha-amylase variants of the present invention in a detergent base composition, washing experiments may be performed using full scale Automatic Dish Wash (ADW). The full scale ADW setup is used for testing the wash performance of polypeptides in test conditions mimicking a regular consumer setup.

In the present study, 40°C and 45°C wash programs using a Miele GSL2 dishwasher were used.

General wash performance description.

Melamine tiles stained with starch (DM-277) (from Center For Test materials BV, P.O. Box 120, 3133 KT, Vlaardingen, The Netherlands) were used as test material and washed at “R40°C/8min/KI55°C” and “R45°C/8min/KI55°C” program in presence of 50 g of IKW Ballast soil using water with 21 °dH, as specified below (see Tables 5 and 6). Two tiles of each stain type were added to each automatic dishwasher. Four replicates were carried out and an average for each test condition was calculated.

After approximately 2 minutes of running the machine program (when the detergent dispenser opened), the detergent and the amylase polypeptide of the invention were added. The full-scale wash performance experiments were conducted under the experimental conditions specified below:

2026202266 24 Mar 2026

Table 5: Experimental conditions

Detergent	**ADW model detergent (with bleach) (see Table 6)**
Detergent dosage	21.27g/wash
pH	As is
Wash program	40°C/8/KI55C or 45°C/8/KI55C
Water hardness	21 °dH
Amylase concentration in test	As described below. Typically, 0.9 mg polypeptide/wash using program 45°C/8/KI55C or 1.5 mg polypeptide/wash using program 40°C/8/KI55C
Test material	Melamine plates (Mixed Starch) DM-277

Table 6: ADW model detergent (with bleach) (percentages given in w/w)

Compound	Content ingredients	Fraction active component
MGDA-H_3 (Trilon M Granules SG)	29%	59%
Sodium citrate	17%	100%
Sodium carbonate	17%	100%
Sodium percarbonate	10%	88%
Sodium silicate	5%	80%
Sodium sulfate	10%	100%
Acusol 588G	5%	92%
TAED	3%	92%
Non-ionic surfactant (Surfac 23-6.5 (added as liquid)	4%	100%

The wash performance was measured as difference in remission for the melamine tiles. The remission measurements were made with a Color-Eye 7000 (CE7000) used for taking spectra and performing calculations of remission and/or colour difference. The remission was measured at 460 nm with no UV light in the illuminant.

The term “improved wash performance” of the present experiment was defined as displaying an alteration of the wash performance of a variant of the present invention relative to

24 Mar 2026

2026202266

the wash performance of the polypeptide having an amino acid sequence as set forth in SEQ ID NO: 2. The alteration may *e.g.* be seen as increased stain removal. Improved wash performance was determined as described above. The wash performance was considered to be improved if the Improvement Factor (IF) was at least 1.1, preferably at least 1.2 in one or more of the conditions listed above; *i.e.* either at 40C/8/KI55C or 45C/8/KI55C.

The wash performance of the variants according to the invention obtained by full scale wash are the following:

Table 7: FSW dataset I (40°C/8/KI55C-1.5 mg protein/wash)

Modifications in SEQ ID NO: 2	**IF**
SEQ ID NO: 2	1.0
V264I+A265G+Y267F	1.6
R171L+Q365S	1.4
Y267F+Q365S	1.3
R127L+Q365S	1.2
V264I+F328L+Q365C	1.2
M246L+L275V+Q365S+D406H	1.2
Q11H+V264I+A265G+Q365C	1.1
R127N+R171H+M246L+L275V+Q365S	1.8
V264I+Y267F+V291T+F328L+Q365S	1.8
Y267F+V291A+F328L+Q365S	1.4
V264I+Y267F+F328L+Q365K	1.4
R127H+L235I+Q365S+G435C	1.2
N195F+Q365S	1.3
I9M+N195F+Q365C	1.5
I9M+R127N+N195F+Q365S	1.6

2026202266 24 Mar 2026

I9M+Y160H+N195F+Q365S	1.6
I9M+A186E+N195F+Q365S	1.5
I9M+R171H+N195F+Q365S	1.4
I9M+A186H+N195F+Q365S	1.2
I9M+G184K+N195F+Q365S	1.4
N195F+G337E+Q365S+P375K+D377N	1.5
N195F+G337D+Q365S+P375K+D377Y	1.4
E130I+T134A+R181N+N195F+Q365S	1.3
R116N+S132A+Q136D+R181K+N195F+Q365S	1.1
N16E+N195F+G337E+Q365S+P375T+D377H	1.7
E130D+T134W+R181K+A186E+N195F+Q365S	1.6
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S	1.5
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S	1.8
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S	2.1
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S	1.4
Y160H+M202L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473I+G476K	1.4
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A	2.0
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.6
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K	2.0
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A	1.4
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A	2.3

2026202266 24 Mar 2026

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	2.4
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A	2.5
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A	1.3
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A	4.0
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206LK+391[a]	3.4
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A	3.1
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A	3.0
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A	2.8
I9M+ N54S+ V56T+ G109A+ G149A+ Q169E+ Q172K+ A174*+ G182T+ N195F+ M202L+ V206L+ Y295F+ Q299Y+ R320K+ S323T+ A339S+ Q345R+ Q365S+ K391A+ R458K	3.1
I9M+ N16Y+ N54S+ V56T+ G109A+ R116Y+ Q118T+ Q125S+ Q136E+ Y160H+ Q169E+ Q172K+ A174*+ R181H+ N195F+ M202L+ V206L+ R310N+ R320Q+ Q365S+ K391A+ R400S+ W408H+ R444T+ Q445S+ Q466S	2.0
H1* + I9M + N54S + V56T + G109A + Q169E + Q172K + A174* + N195F + M202L+ V206L + Q365S + K391A	4.2

Table 8: FSW dataset II (45°C/8/KI55C-0.9 mg protein/wash)

Modifications in SEQ ID NO: 2	**IF**
SEQ ID NO: 2	1.0
Y295F	1.1
M246L	1.1
N195F+Q365S	1.4
R171H+Q365C	1.1
V264I+A265G+Y267F	1.8
E86L+R171L+N306R+Q365S	1.3
V264I+Y267F+V291T+F328L+Q365S	1.6
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G4	1.3

2026202266 24 Mar 2026

76K	
I9M+R127N+N195F+Q365S	1.3
I9M+R171L+N195F+Q365S	1.9
N195F+G337E+Q365S+P375K+D377N	1.2
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A	1.1
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A	1.9
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A	3.4
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A	1.8
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A	3.3
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A	1.3
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A	2.2
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A	3.7
H1* + I9M + N54S + V56T + G109A + G149A + Q169E + Q172K + A174* + G182T + N195F + M202L + V206L + Y295F + Q299Y + R320K + S323T + A339S + Q345R + Q365S + K391A + R458K	3.3

The invention described and claimed herein is not to be limited in scope by the specific aspects herein disclosed, since these aspects are intended as illustrations of several aspects of the invention. Any equivalent aspects are intended to be within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. In the case of conflict, the present disclosure including definitions will control.

24 Mar 2026
2026202266

CLAIMS

1. An alpha-amylase variant of a parent alpha-amylase polypeptide comprises a modification in one or more position corresponding to position: 1, 2, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and 481, using SEQ ID NO: 1 for numbering and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17 and wherein said variant has alpha-amylase activity.

2. The alpha-amylase variant of claim 1, wherein said modification in one or more positions correspond to the following: H1, H2, G7, I9, Q11, N16, N19, N25, A37, W43, W48, N54, V56, Y58, G59, A60, L63, T81, E84, E86, R90, Q98, V104, G109, A111, F113, R116, Q118, Q125, R127, E130, S132, G133, T134, Y135, Q136, A139, G142, N144, G149, R158, Y160, D163, W167, Q169, S170, R171, Q172, L173, A174, N175, R176, Y178, R181, G182, A186, W187, N195, M202, Y203, A204, V206, D209, H210, E212, T227, L235, V238, M246, Q256, K259, V264, A265, E266, Y267, K269, N270, L272, G273, A274, L275, E276, W284, M286, V291, L293, Y295, Y298, Q299, N302, S303, S304, N306, R310, N311, N314, G315, L317, Q319, R320, S323, F328, G337, A339, Q345, D357, Q365, P377, D375, Q385, K391, Q395, R400, D406, W408, V410, S431, G435, W439, R444, Q445, R458, N465, Q466, W469, F473, G476 and V481, using SEQ ID NO: 1 for numbering and wherein each modification is independently a substitution, insertion, or deletion, and wherein said variant has at least 59%, e.g. at least 60%, e.g. at least 65%, e.g., at least 70%, 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% sequence identity to the polypeptide of SEQ ID NOs: 1-17, and wherein said variant has alpha-amylase activity and wherein said variant having an Improvement Factor (IF) of >1.0 for a measure of wash performance when compared to said parent polypeptide having alpha-amylase activity of SEQ ID NO: 1 or SEQ ID NO: 2.

24 Mar 2026
2026202266

3. The alpha-amylase variant according to claims 1-2, wherein said variant comprises a deletion in two or more positions corresponding to positions R181, G182, D183, and G184, using SEQ ID NO: 1 for numbering.

4. The alpha-amylase variant according to any one of the preceding claims, wherein said variant comprises one or more of the following modifications: H1*; H2*, G7A; I9M; Q11H; N16E; N16H; N16Y; N19D; N25K; N25M; N25T; A37V; W43Y; W48Y; N54Q; N54S; V56I; V56T; Y58F; G59A; A60S; A60T; L63F; T81A; E84Q; E86L; R90H; R90N; R90Q; Q98N; V104A; G109A; A111T; F113A; F113G; F113N; F113Q; F113T; F113Y; R116C; R116D; R116F; R116H; R116K; R116N; R116S; R116Y; Q118N; Q118T; Q125G; Q125S; R127A; R127F; R127H; R127L; R127N; R127T; E130D; E130F; E130I; E130K; E130L; E130N; E130S; E130T; E130V; S132A; S132D; S132F; S132L; S132M; S132P; S132T; G133D; T134C; T134E; T134N; T134P; T134R; T134S; T134W; T134Y; T134A; Y135H; Q136D; Q136E; Q136G; Q136N; Q136R; Q136S; A139T; G142H; N144H; G149A; R158C; R158H; R158K; R158Q; R158S; Y160D; Y160F; T160H; Y160N; D163H; W167*; Q169*; Q169E; Q169F; S170*; S170A; R171*; R171H; R171K; R171L; R171Y; Q172*; Q172K; Q172N; Q172S; L173*; L173K; A174*; A174N; A174S; N175*; N175S; R176*; R176A; Y178F; R181*; R181A; R181C; R181E; R181G; R181H; R181K; R181N; R181Q; G182*; G182T; A186D; A186E; A186H; A186K; A186N; A186T; W187M; N195D; N195F; N195H; N195Q; N195Y; M202L; Y203L; A204V; V206L; D209N; H210K; H210N; E212D; T227K; T227N; L235I; V238A; M246I; M246L; M246T; M246V; Q256H; Q256N; K259G; K259H; V264A; V246I; V264T; A265G; E266V; Y267F; Y267H; Y267L; K269M; K269Q; K269R; N270G; N270P; L272I; G273V; A274K; A274S; L275A; L275I; L275V; E276N; W284R; W284Y; M286L; V291A; V291I; V291T; L293I; L293V; Y295F; Y298E; Y298N; Q299N; Q299Y; N302A; N302H; N302K; N302Q; S303G; S304G; S304Q; N306H; N306K; N306Q; N306R; N306Y; R310N; R310S; R310Q; N311K; N311R; N314Q; G315N; L317V; Q319H; R320K; R320Q; R320S; S323T; H323K; F328L; G337D; G337E; A339S; Q345N; Q345R; L357F; Q365A; Q365C; Q365E; Q365H; Q365K; Q365M; Q365S; P377K; P377T; D375H; D375N; D375Y; Q386L; K391A; Q395K; R400S; D406H; W408H; V410I; S431F; G435C; W439R; W439T; R444T; Q445S; R458K; N465G; Q466S; W469N; W469Y; F473I; F473P; F473S; G476K; and V481A, using SEQ ID NO: 1 for numbering.

5. The variant according to any one of the preceding claims, wherein said variant is selected from the group consisting of:
A60T,
Y135H,
Q169E,

24 Mar 2026
2026202266

W48Y,
A174*,
M246L,
R90Q,
Y203L+V206L,
Q169F+S170A,
S132D+G133D,
N195F+Q365C,
N195F+Q365S,
N195F+Q365M,
R127L+Q365S,
R127N+Q365S,
R127L+Q365C,
N195F+Q365K,
I9M+N195F,
R171H+Q365C,
Y267F+Q365S,
F328L+Q365S,
R171L+Q365S,
N195F+M286L,
T134P+N195F,
S170*+R171*+A174*,
V264I+A265G+Y267F,
Q169*+S170*+A174*,
M246L+L275V+Q365S,
V264I+V291I+Q365S,
V264I+V291T+Q365K,
V264I+F328L+Q365C,
I9M+N195F+Q365C,
Q11H+Y267F+Q365C,
I9M +N195F+Q365S,
V264I+Y267F+Q365K,
R127L+M246V+Q365S,
A60S+R171Y+Q365S,
R127N+M246T+L275V,
V104A+N195F+Q365S,

24 Mar 2026
2026202266

V264I+F328L+Q365S,
R171H+N302H+Q365S,
V264I+Y267F+Q365S,
A174*+N175*+Y178F,
V264I+A265G+Q365C,
R171L+N302H+Q365C,
R171L+M246V+Q365C,
R171Y+M246L+Q365S,
V264T+Y267F+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
R127N+M246L+L275V+Q365S,
R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
Y267F+V291A+F328L+Q365C,
I9M+A186E+N195F+Q365S,
E86L+R171L+N306R+Q365S,
V264I+Y267F+F328L+Q365S,
I9M+N195F+V291A+Q365S,
R127L+L235I+M246I+Q365C,
Y267F+V291A+F328L+Q365S,
V264I+Y267F+F328L+Q365K,
Q11H+V264I+A265G+Q365C,
W187M+N195F+H210K+Q365S,
R127H+M246T+L275A+Q365S,
I9M+A111T+N195F+Q365S,
I9M+Y58F+N195F+Q365S,
V264T+V291A+F328L+Q365S,
V264I+A265G+V291A+Q365C,

24 Mar 2026
2026202266

V264I+A265G+Y267F+Q365C,
V264I+Y267F+V291A+F328L+Q365S,
R127N+R171H+M246L+L275V+Q365S,
V264I+A265G+V291A+F328L+Q365S,
R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
R116S+S132F+R181N+N195F+Q365S,
E130T+T134Y+A186K+N195F+Q365S,
A37V+V264I+Y267F+F328L+Q365C,
Q11H+V264I+Y267F+F328L+Q365C,
V264I+Y267F+V291T+F328L+Q365S,
Q169*+R171*+Q172*+L173*+A174*,
R116Y+S132P+Q136N+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377Y,
V264I+A265G+Y267F+F328L+Q365S,
I9M+N195F+K269Q+A274K+Q365S,
E130D+T134Y+R181H+N195F+Q365S,
R116N+S132M+Q136R+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377N,
R127N+R171L+M246L+L275V+Q365S,
N195F+G337E+Q365S+P375K+D377N,
Q11H+V264I+A265G+Y267F+Q365C,
R158Q+Y160N+W187M+N195F+Q365S,
V264I+Y267F+Q365K+W408H+V410I,
R127N+R171Y+M246L+L275V+Q365S,
N54Q+F113T+R171H+N302A+Q365C,
V264A+Y267F+V291T+F328L+Q365C,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,
E130D+T134W+R181KA186E+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,

24 Mar 2026
2026202266

E130S+T134E+R181S+A186T+N195F+Q365S,
R116C+S132A+Q136S+R181A+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+Q365S,
R127H+R171H+M246L+L275V+N306R+Q365S,
E130L+T134N+R181W+A186T+N195F+Q365S,
R116C+S132M+Q136S+R181Q+N195F+Q365S,
R116S+Y135H+Q136G+R181T+N195F+Q365S,
R116S+S132L+Q136E+R181G+N195F+Q365S,
N16E+N195F+G337E+Q365S+P375T+D377H,
V264I+A265G+Y267F+V291I+F328L+Q365S,
N16E+N195F+G337D+Q365S+P375K+D377N,
V264I+A265G+Y267F+F328L+Q365S+Q395K,
E130N+T134C+R181Q+A186N+N195F+Q365S,
V264I+A265G+Y267F+V291A+F328L+Q365C,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
A139T+R158S+Y160D+W187M+N195F+H210N+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*,
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+Y58F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195H+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,

24 Mar 2026
2026202266

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,
H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A,
H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A,
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A,
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A,
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A,
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A,
Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A,
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A,
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A139T +R158S +Y160D +W187M +N195F +H210N +Q365S,
A186D +N195F,
A60S +R171Y +Q365S,
E130D +T134W +R181K +A186E +N195F +Q365S,
E130D +T134Y +R181H +N195F +Q365S,
E130D+T134W+R181K+A186E+N195F+Q365S,
E130F +T134R +R181S +A186D +N195F +Q365S,
E130I +T134A +R181N +N195F +Q365S,
E130I+T134A+R181N+N195F+Q365S,

24 Mar 2026
2026202266

E130L +T134N +R181W +A186T +N195F +Q365S,
E130N +T134C +R181Q +A186N +N195F +Q365S,
E130S +T134E +R181S +A186T +N195F +Q365S,
E130T +T134Y +A186K +N195F +Q365S,
E130V +T134N +R181Y +A186K +N195F +Q365S,
E130Y +S132T +T134S +R181E +A186D +N195F +Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
E86L +R171L +N306R +Q365S,
E86L +Y160H +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
E86L+R171L+N306R+Q365S,
F113Q +R116H,
F113T +R171K +G273V,
F328L +Q365S,
G109A+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
G7A+F113N+R116N+E276N+S304G+R320S+Q345N+W439R+N465G+Q466S+W469Y,
H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S,
H1* +I9M +N54S +V56T +G109A +F113G +R116H +D163H +Q169E +R171H +Q172K +A174S +G182T +N195F +M202L +V206L +M246L +L275V +A288V +L317V +Q319H +H324K +Q365S +K391A,
H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,
H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +Q365S +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L+ V206L +W284Y +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +N306R +K391A,
H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +Q365S +K391A,

24 Mar 2026
2026202266

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +V206L +K391A,
H1* +N54S +V56T +G109A +R171H +N195F +V206L +K391A,
H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,
H1*+I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K +A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S,
H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A,
H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q125G+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D377H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K269M+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L235I+V238A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V238A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q172S+L173K+A174S+N175*+R176A+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R116H+Q169E+Q172K+A174*+N195F+V206L+N314Q+Q385L+K391A,
H1*+N54S+V56T+G109A+R127F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
I9M +A186E +N195F +Q365S,
I9M +A186H +N195F +Q365S,
I9M +G184K +N195F +Q365S,
I9M +N195F +K269Q +A274K +Q365S,
I9M +N195F +N270G +Q365S,
I9M +N195F +N270P +Q365S,
I9M +N195F +Q365C,
I9M +N195F +V206L +D209N +Q365S,
I9M +N195F +V291A +Q365S,
I9M +R127N +N195F +Q365S
I9M +R171H +N195F +Q365S,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,
I9M +R171L +N195F +Q365S,
I9M +Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
I9M +Y160H +N195F +Q365S,
I9M+A186E+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+G184K+N195F+Q365S,
I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S,
I9M+N195F+Q365C,

24 Mar 2026
2026202266

I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
I9M+R127N+N195F+Q365S,
I9M+R171H+N195F+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
I9M+R171L+N195F+Q365S,
I9M+Y160H+N195F+Q365S,
M202L,
M246L +L275V +Q365S +D406H,
M246L,
M246L+ L275V +Q365S,
M246L+L275V+Q365S+D406H,
N16E +N195F +G337D +Q365S +P375K +D377N,
N16E +N195F +G337E +Q365S +P375T +D377H,
N16E+N195F+G337E+Q365S+P375T+D377H,
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
N195F +G337D +Q365S +P375K +D377N,
N195F +G337D +Q365S +P375K +D377Y,
N195F +G337E +Q365S +P375K +D377N,
N195F+G337D+Q365S+P375K+D377Y,
N195F+G337E+Q365S+P375K+D377N,
N195F+Q365S,
N54Q +F113T +R171H +N302A +Q365C,
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Q11H +V264I +A265G +Q365C,
Q11H +V264I +A265G +Y267F +Q365C,
Q11H +V264I +Y267F +F328L +Q365C,
Q11H +Y267F +Q365C,
Q11H+V264I+A265G+Q365C,
Q169* +S170* +A174*,
Q169* +S170* +R171* +A174*,
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P,
R116K +S132L +Q136R +R181C +N195F +Q365S,
R116K +S132P +Q136D +R181Q +N195F +A204V +Q365S,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,

24 Mar 2026
2026202266

R116N +S132A +Q136D +R181K +N195F +Q365S,
R116N +S132M +Q136R +N195F +Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
R116S +S132F +R181N +N195F +Q365S,
R116S +Y135H +Q136G +R181T +N195F +Q365S,
R116Y +S132P +Q136N +N195F +Q365S,
R127H+L235I+Q365S+G435C,
R127L +M246V +Q365S,
R127L +Q365C,
R127L +Q365S,
R127L,
R127N +M246L +L275V +Q365S,
R127N +Q365S,
R127N +R171L +M246L +L275V +Q365S,
R127N+R171H+M246L+L275V+Q365S,
R171H + Q365C,
R171H +M246L +L275V +Q365S,
R171H +N302H +Q365S,
R171H,
R171H+Q365C,
R171L +N302H +Q365C,
R171L +Q365S,
R171Y + +M246L +Q365S,
R171Y +N306K,
R181S +G184S,
V104A +N195F +Q365S,
V264A +Y267F +V291T +F328L +Q365C,
V264I +A265G +V291A +F328L +Q365S,
V264I +A265G +V291A +Q365C,
V264I +A265G +Y267F +F328L +Q365S +Q395K,
V264I +A265G +Y267F +F328L +Q365S,
V264I +A265G +Y267F +V291I +F328L +Q365S,
V264I +A265G +Y267F,
V264I +F328L +Q365C,
V264I +F328L +Q365S,
V264I +L357F,

24 Mar 2026
2026202266

V264I +Q365C,
V264I +V291I +Q365S,
V264I +V291T +Q365K,
V264I +Y267F +F328L +Q365C,
V264I +Y267F +F328L +Q365K,
V264I +Y267F +F328L +Q365S,
V264I +Y267F +Q365K +W408H +V410I,
V264I +Y267F +Q365K,
V264I +Y267F +Q365S,
V264I +Y267F +V291A +F328L +Q365C,
V264I +Y267F +V291A +F328L +Q365S,
V264I +Y267F +V291T +F328L +Q365S,
V264I+A265G+Y267F,
V264I+F328L+Q365C,
V264I+Y267F+F328L+Q365K,
V264I+Y267F+V291T+F328L+Q365S,
V264T +A265G +Y267F +V291A +F328L +Q365C,
V264T +A265G +Y267L +F328L +Q365C,
V264T +V291A +F328L +Q365S,
V264T +Y267F +Q365S,
V264T +Y267L +F328L +Q365C,
V56T+Y160H+A174N+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
W187M +N195F +H210K +Q365S,
Y160H +E212D +E276N +W284Y +R320S +Q365S +W408H +W439T +W469N +F473S +G476K,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473I +G476K,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
Y160H+A174S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,

24 Mar 2026
2026202266

Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+K259G+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256N+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+M202L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473I+G476K,
Y160H+N195F+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+N195Q+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+N195Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q169E+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+R171Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y267F +Q365S,
Y267F +V291A +F328L +Q365C,
Y267F +V291A +F328L +Q365S,
Y267F+Q365S,
Y267F+V291A+F328L+Q365S,
Y295F, using SEQ ID NO: 1 for numbering and wherein said variant Improvement Factor (IF) of at least 1.1, preferably at least 1.2, such as at least 1.3, such as at least 1.4, such as at least 1.5, such as at least 1.6, such as at least 1.7, such as at least 1.8, such as at least 1.9, such as at least 2.0, such as at least 2.2, such as at least 2.4, such as at least 2.6, such as at least 2.8, such as at least 3.0, such as at least 3.2, such as at least 3.4, such as at least 3.6, such as at least 3.8, or such as at least 4.0 in Model A detergent compositon and/or ADW detergent composition with bleach when compared to said parent alpha-amylase and wherein said parent alpha-amylase has amino acid sequence as shown in SEQ ID NO: 2.

6. The variant according to any one of the preceding claims, wherein said variant is selected from the group consisting of:
A60T,
Y135H,
Q169E,
W48Y,
A174*,
M246L,
R90Q,

24 Mar 2026
2026202266

Y203L+V206L,
Q169F+S170A,
S132D+G133D,
N195F+Q365C,
N195F+Q365S,
N195F+Q365M,
R127L+Q365S,
R127N+Q365S,
R127L+Q365C,
N195F+Q365K,
I9M+N195F,
R171H+Q365C,
Y267F+Q365S,
F328L+Q365S,
R171L+Q365S,
N195F+M286L,
T134P+N195F,
S170*+R171*+A174*,
V264I+A265G+Y267F,
Q169*+S170*+A174*,
M246L+L275V+Q365S,
V264I+V291I+Q365S,
V264I+V291T+Q365K,
V264I+F328L+Q365C,
I9M+N195F+Q365C,
Q11H+Y267F+Q365C,
I9M +N195F+Q365S,
V264I+Y267F+Q365K,
R127L+M246V+Q365S,
A60S+R171Y+Q365S,
R127N+M246T+L275V,
V104A+N195F+Q365S,
V264I+F328L+Q365S,
R171H+N302H+Q365S,
V264I+Y267F+Q365S,
A174*+N175*+Y178F,

24 Mar 2026
2026202266

V264I+A265G+Q365C,
R171L+N302H+Q365C,
R171L+M246V+Q365C,
R171Y+M246L+Q365S,
V264T+Y267F+Q365S,
I9M+Y160H+N195F+Q365S,
I9M+R127N+N195F+Q365S,
R127H+L235I+Q365S+G435C,
I9M+R171H+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+R171L+N195F+Q365S,
Q169*+S170*+R171*+A174*,
M246L+L275V+Q365S+D406H,
I9M+G184K+N195F+Q365S,
R127N+M246L+L275V+Q365S,
R171H+M246L+L275V+Q365S,
R127H+M246I+Q365C+V481A,
Y267F+V291A+F328L+Q365C,
I9M+A186E+N195F+Q365S,
E86L+R171L+N306R+Q365S,
V264I+Y267F+F328L+Q365S,
I9M+N195F+V291A+Q365S,
R127L+L235I+M246I+Q365C,
Y267F+V291A+F328L+Q365S,
V264I+Y267F+F328L+Q365K,
Q11H+V264I+A265G+Q365C,
W187M+N195F+H210K+Q365S,
R127H+M246T+L275A+Q365S,
I9M+A111T+N195F+Q365S
I9M+Y58F+N195F+Q365S,
V264T+V291A+F328L+Q365S,
V264I+A265G+V291A+Q365C,
V264I+A265G+Y267F+Q365C,
V264I+Y267F+V291A+F328L+Q365S,
R127N+R171H+M246L+L275V+Q365S,
V264I+A265G+V291A+F328L+Q365S,

24 Mar 2026
2026202266

R127N+M246I+A265G+Y267H+Q365S,
E130I+T134A+R181N+N195F+Q365S,
R127N+M246L+L275V+N306R+Q365S,
I9M+N195F+V206L+D209N+Q365S,
R116S+S132F+R181N+N195F+Q365S,
E130T+T134Y+A186K+N195F+Q365S,
A37V+V264I+Y267F+F328L+Q365C,
Q11H+V264I+Y267F+F328L+Q365C,
V264I+Y267F+V291T+F328L+Q365S,
Q169*+R171*+Q172*+L173*+A174*,
R116Y+S132P+Q136N+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377Y,
V264I+A265G+Y267F+F328L+Q365S,
I9M+N195F+K269Q+A274K+Q365S,
E130D+T134Y+R181H+N195F+Q365S,
R116N+S132M+Q136R+N195F+Q365S,
N195F+G337D+Q365S+P375K+D377N,
R127N+R171L+M246L+L275V+Q365S,
N195F+G337E+Q365S+P375K+D377N,
Q11H+V264I+A265G+Y267F+Q365C,
R158Q+Y160N+W187M+N195F+Q365S,
V264I+Y267F+Q365K+W408H+V410I,
R127N+R171Y+M246L+L275V+Q365S,
N54Q+F113T+R171H+N302A+Q365C,
V264A+Y267F+V291T+F328L+Q365C,
Q169*+S170*+R171*+Q172*+L173*+A174*,
R116K+S132L+Q136R+R181C+N195F+Q365S,
V264T+A265G+Y267F+V291A+F328L+Q365C,
E130N+T134S+R181N+A186K+N195F+Q365S,
E130V+T134N+R181Y+A186K+N195F+Q365S,
E130D+T134W+R181KA186E+N195F+Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
E130S+T134E+R181S+A186T+N195F+Q365S,
R116C+S132A+Q136S+R181A+N195F+Q365S,
R116K+S132P+Q136D+R181Q+N195F+Q365S,
R127H+R171H+M246L+L275V+N306R+Q365S,

24 Mar 2026
2026202266

E130L+T134N+R181W+A186T+N195F+Q365S,
R116C+S132M+Q136S+R181Q+N195F+Q365S,
R116S+Y135H+Q136G+R181T+N195F+Q365S,
R116S+S132L+Q136E+R181G+N195F+Q365S,
N16E+N195F+G337E+Q365S+P375T+D377H,
V264I+A265G+Y267F+V291I+F328L+Q365S,
N16E+N195F+G337D+Q365S+P375K+D377N,
V264I+A265G+Y267F+F328L+Q365S+Q395K,
E130N+T134C+R181Q+A186N+N195F+Q365S,
V264I+A265G+Y267F+V291A+F328L+Q365C,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
E130K+S132T+T134Y+R181T+A186K+N195F+Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
A139T+R158S+Y160D+W187M+N195F+H210N+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
W167*+Q169*+S170*+R171*+Q172*+L173*+A174*+N175*+R176*,
H1*+G59A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+Y58F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+G109A+Q169E+Q172K+A174*+N195F+V206L+L293I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+D209N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195D+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195H+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275I+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337E+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25K+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R127T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D209N+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+R127N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+L63F+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L275V+K391A,
H1*+N19D+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
A60S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+R171L+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G337D+K391A,
H1*+N25M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+T81A+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N25T+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+R90N+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
E86L+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R158C+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L293V+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L272I+K391A,
H1*+N54S+V56T+G109A+R158H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+G109A+K391A+N16Y+N54S+V56T+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+R158S+Q169E+Q172K+A174*+N195F+V206L+K391A,
R127N+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+A274S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186E+N195F+V206L+K391A,
H1*+N54S+V56T+R90H+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
I9M+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q172S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365C+K391A,
H1*+N54S+V56T+G109A+R116N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302H+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365E+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+A186H+N195F+V206L+K391A,
H1*+N54S+V56T+A60S+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+R181S+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172S+A174*+N175S+N195F+V206L+K391A,
H1*+N54S+V56T+E86L+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302K+K391A,
H1*+N54S+V56T+G109A+R127L+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+R171Y+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V291A+K391A,
H1*+N54S+V56T+G109A+R116F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+K391A,
Y160H+R171L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+G109A+K391A+N54S+V56T+Y160H+Q169E+Q172K+A174*+N195F+V206L,
H1*+N54S+V56T+G109A+Q118N+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+T134P+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*N195F+V206L+Q299Y+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365A+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q299N+K391A,
Y160H+E212D+L275V+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306Q+K391A,
H1*+W43Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311R+K391A,
Y160H+E212D+M246L+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+E84Q+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R158K+Q169E+Q172K+A174*+N195F+V206L+K391A,
V56T+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
N54S+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q125G+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N311K+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K269M+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+K391A,
Y160H+E212D+K259G+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+A174S+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+N195Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+Q169E+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,

24 Mar 2026
2026202266

H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
G7A+F113N+R116N+E276N+S304G+R320S+Q345N+W439R+N465G+Q466S+W469Y,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+D377H+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+V238A+K391A,
Y160H+N195F+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+Q256N+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365H+K391A,
Y160H+N195Q+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+R171Y+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
G109A+Y160H+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
Y160H+E212D+E276N+W284Y+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+R127F+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+L173K+A174*+N175S+N195F+V206L+K391A,
Y160H+E212D+E276N+W284Y+S304G+N306R+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+G142H+N144H+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N302Q+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+N306R+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+T227K+K269R+K391A,
H1*+N54S+V56I+G109A+R127A+Q169E+Q172K+A174*+N195F+V206L+Q385L+K391A,
Y160H+E212D+Q256H+K259H+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+G315N+Q385L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172N+A174*+N175S+N195F+V206L+K391A+S431F,
Y160H+E212D+E276N+W284Y+S304G+N306Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+L235I+V238A+K391A,
H1*+N54S+V56T+G109A+Q172S+L173K+A174S+N175*+R176A+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
V56T+Y160H+A174N+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473S+G476K,
H1*+N54S+V56T+R90Q+G109A+Q169E+Q172K+A174*+N195F+V206L+E266V+Q385L+K391A,
H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V20+6L+Q385L+K391A,

24 Mar 2026
2026202266

H1*+N54S+V56T+G109A+F113A+R116D+Q118T+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Y298E+N302K+S303G+K391A,
H1*+N54S+V56T+G109A+R116H+Q169E+Q172K+A174*+N195F+V206L+N314Q+Q385L+K391A,
H1*+I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S, using SEQ ID NO: 1 for numbering and wherein said variant Improvement Factor (IF) of at least 1.1, preferably at least 1.2, such as at least 1.3, such as at least 1.4, such as at least 1.5, such as at least 1.6, such as at least 1.7, such as at least 1.8, such as at least 1.9, such as at least 2.0, such as at least 2.2, such as at least 2.4, such as at least 2.6, such as at least 2.8, such as at least 3.0, such as at least 3.2, such as at least 3.4, such as at least 3.6, such as at least 3.8, or such as at least 4.0 in Model A detergent composition when compared to said parent alpha-amylase and wherein said parent alpha-amylase has amino acid sequence as shown in SEQ ID NO: 2.

7. The variant according to any one of the preceding claims, wherein said variant is selected from the group consisting of:

A139T +R158S +Y160D +W187M +N195F +H210N +Q365S,
A186D +N195F,
A60S +R171Y +Q365S,
E130D +T134W +R181K +A186E +N195F +Q365S,
E130D +T134Y +R181H +N195F +Q365S,
E130D+T134W+R181K+A186E+N195F+Q365S,
E130F +T134R +R181S +A186D +N195F +Q365S,
E130I +T134A +R181N +N195F +Q365S,
E130I+T134A+R181N+N195F+Q365S,
E130L +T134N +R181W +A186T +N195F +Q365S,
E130N +T134C +R181Q +A186N +N195F +Q365S,
E130S +T134E +R181S +A186T +N195F +Q365S,
E130T +T134Y +A186K +N195F +Q365S,
E130V +T134N +R181Y +A186K +N195F +Q365S,
E130Y +S132T +T134S +R181E +A186D +N195F +Q365S,
E130Y+S132T+T134S+R181E+A186D+N195F+Q365S,
E86L +R171L +N306R +Q365S,

24 Mar 2026
2026202266

E86L +Y160H +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,

E86L+R171L+N306R+Q365S,

F113Q +R116H,

F113T +R171K +G273V,

F328L +Q365S,

H1* +I9M +N16Y +N54S +V56T +G109A +R116Y +Q118T +Q125S +Q136E +Y160H +Q169E +Q172K +A174* +R181H +N195F +M202L +V206L +R310N +R320Q +Q365S +K391A +R400S +W408H +R444T +Q445S +Q466S,

H1* +I9M +N54S +V56T +G109A +F113G +R116H +D163H +Q169E +R171H +Q172K +A174S +G182T +N195F +M202L +V206L +M246L +L275V +A288V +L317V +Q319H +H324K +Q365S +K391A,

H1* +I9M +N54S +V56T +G109A +G149A +Q169E +Q172K +A174* +G182T +N195F +M202L+V206L +Y295F +Q299Y +R320K +S323T +A339S +Q345R +Q365S +K391A +R458K,

H1* +I9M +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,

H1* +N16H +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,

H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,

H1* +N16Y +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +Q365S +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L +V206L +R320S +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +M202L+ V206L +W284Y +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +N306R +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +N195F +V206L +Q365S +K391A,

H1* +N54S +V56T +G109A +Q169E +Q172K +A174* +V206L +K391A,

H1* +N54S +V56T +G109A +R171H +N195F +V206L +K391A,

H1* +N54S +V56T +G109A +Y160H +Q169E +Q172K +A174* +N195F +M202L +V206L +K391A,

H1*+I9M+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,

H1*+N16H+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,

24 Mar 2026
2026202266

H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N16Y+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+G184K+N195F+V206L+T227N+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+M202L+V206L+R320S+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+M246L+K391A,
H1*+N54S+V56T+G109A+Q169E+Q172K+A174*+N195F+V206L+Q365S+K391A,
H1*+N54S+V56T+G109A+R171H+N195F+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+M202L+V206L+K391A,
H1*+N54S+V56T+G109A+Y160H+Q169E+Q172K+A174*+N195F+V206L+K391A,
I9M +A186E +N195F +Q365S,
I9M +A186H +N195F +Q365S,
I9M +G184K +N195F +Q365S,
I9M +N195F +K269Q +A274K +Q365S,
I9M +N195F +N270G +Q365S,
I9M +N195F +N270P +Q365S,
I9M +N195F +Q365C,
I9M +N195F +V206L +D209N +Q365S,
I9M +N195F +V291A +Q365S,
I9M +R127N +N195F +Q365S
I9M +R171H +N195F +Q365S,
I9M +R171L +N195F +M246L +K269M +W284R +Y298N +Q365S,
I9M +R171L +N195F +Q365S,
I9M +Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
I9M +Y160H +N195F +Q365S,
I9M+A186E+N195F+Q365S,
I9M+A186H+N195F+Q365S,
I9M+G184K+N195F+Q365S,
I9M+N16Y+N54S+V56T+G109A+R116Y+Q118T+Q125S+Q136E+Y160H+Q169E+Q172K+A174*+R181H+N195F+M202L+V206L+R310N+R320Q+Q365S+K391A+R400S+W408H+R444T+Q445S+Q466S,
I9M+N195F+Q365C,
I9M+N54S+V56T+G109A+G149A+Q169E+Q172K+A174*+G182T+N195F+M202L+V206L+Y295F+Q299Y+R320K+S323T+A339S+Q345R+Q365S+K391A+R458K,
I9M+R127N+N195F+Q365S,

24 Mar 2026
2026202266

I9M+R171H+N195F+Q365S,
I9M+R171L+N195F+M246L+K269M+W284R+Y298N+Q365S,
I9M+R171L+N195F+Q365S,
I9M+Y160H+N195F+Q365S,
M202L,
M246L,
M246L +L275V +Q365S +D406H,
M246L+ L275V +Q365S,
M246L+L275V+Q365S+D406H,
N16E +N195F +G337D +Q365S +P375K +D377N,
N16E +N195F +G337E +Q365S +P375T +D377H,
N16E+N195F+G337E+Q365S+P375T+D377H,
N16Y +Y160H +N195F +L275I +S304G +G337E +Q365S,
N16Y+Y160H+N195F+L275I+S304G+G337E+Q365S,
N195F +G337D +Q365S +P375K +D377N,
N195F +G337D +Q365S +P375K +D377Y,
N195F +G337E +Q365S +P375K +D377N,
N195F+G337D+Q365S+P375K+D377Y,
N195F+G337E+Q365S+P375K+D377N,
N195F+Q365S,
N54Q +F113T +R171H +N302A +Q365C,
Q11H +V264I +A265G +Q365C,
Q11H +V264I +A265G +Y267F +Q365C,
Q11H +V264I +Y267F +F328L +Q365C,
Q11H +Y267F +Q365C,
Q11H+V264I+A265G+Q365C,
Q169* +S170* +A174*,
Q169* +S170* +R171* +A174* ,
Q98N +F113Y +R158Q +Y160F +S304Q +R320S +W439R +F473P,
R116K +S132L +Q136R +R181C +N195F +Q365S,
R116K +S132P +Q136D +R181Q +N195F +A204V +Q365S,
R116K+S132P+Q136D+R181Q+N195F+A204V+Q365S,
R116N +S132A +Q136D +R181K +N195F +Q365S,
R116N +S132M +Q136R +N195F +Q365S,
R116N+S132A+Q136D+R181K+N195F+Q365S,
R116S +S132F +R181N +N195F +Q365S,

24 Mar 2026
2026202266

R116S +Y135H +Q136G +R181T +N195F +Q365S,
R116Y +S132P +Q136N +N195F +Q365S,
R127H+L235I+Q365S+G435C,
R127L,
R127L +M246V +Q365S,
R127L +Q365C,
R127L +Q365S,
R127N +M246L +L275V +Q365S,
R127N +Q365S,
R127N +R171L +M246L +L275V +Q365S,
R127N+R171H+M246L+L275V+Q365S,
R171H,
R171H + Q365C,
R171H +M246L +L275V +Q365S,
R171H +N302H +Q365S,
R171H+Q365C,
R171L +N302H +Q365C,
R171L +Q365S,
R171Y + +M246L +Q365S,
R171Y +N306K,
R181S +G184S,
V104A +N195F +Q365S,
V264A +Y267F +V291T +F328L +Q365C,
V264I +A265G +V291A +F328L +Q365S,
V264I +A265G +V291A +Q365C,
V264I +A265G +Y267F,
V264I +A265G +Y267F +F328L +Q365S,
V264I +A265G +Y267F +F328L +Q365S +Q395K,
V264I +A265G +Y267F +V291I +F328L +Q365S,
V264I +F328L +Q365C,
V264I +F328L +Q365S,
V264I +L357F,
V264I +Q365C,
V264I +V291I +Q365S,
V264I +V291T +Q365K,
V264I +Y267F +F328L +Q365C,

24 Mar 2026
2026202266

V264I +Y267F +F328L +Q365K,
V264I +Y267F +F328L +Q365S,
V264I +Y267F +Q365K,
V264I +Y267F +Q365K +W408H +V410I,
V264I +Y267F +Q365S,
V264I +Y267F +V291A +F328L +Q365C,
V264I +Y267F +V291A +F328L +Q365S,
V264I +Y267F +V291T +F328L +Q365S,
V264I+A265G+Y267F,
V264I+F328L+Q365C,
V264I+Y267F+F328L+Q365K,
V264I+Y267F+V291T+F328L+Q365S,
V264T +A265G +Y267F +V291A +F328L +Q365C,
V264T +A265G +Y267L +F328L +Q365C,
V264T +V291A +F328L +Q365S,
V264T +Y267F +Q365S,
V264T +Y267L +F328L +Q365C,
W187M +N195F +H210K +Q365S,
Y160H +E212D +E276N +W284Y +R320S +Q365S +W408H +W439T +W469N +F473S +G476K,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473I +G476K,
Y160H +M202L +E212D +E276N +W284Y +R320S +W408H +W439T +W469N +F473S +G476K,
Y160H+E212D+E276N+W284Y+R320S+Q365S+W408H+W439T+W469N+F473S+G476K,
Y160H+M202L+E212D+E276N+W284Y+R320S+W408H+W439T+W469N+F473I+G476K,
Y267F +Q365S,
Y267F +V291A +F328L +Q365C,
Y267F +V291A +F328L +Q365S,
Y267F+Q365S,
Y267F+V291A+F328L+Q365S,
Y295F, using SEQ ID NO: 1 for numbering and wherein said variant Improvement Factor (IF) of at least 1.1, preferably at least 1.2, such as at least 1.3, such as at least 1.4, such as at least 1.5, such as at least 1.6, such as at least 1.7, such as at least 1.8, such as at least 1.9, such as at least 2.0, such as at least 2.2, such as at least 2.4, such as at least 2.6, such as at least 2.8, such as at least 3.0, such as at least 3.2, such as at least 3.4, such as at least 3.6,

24 Mar 2026
2026202266

such as at least 3.8, or such as at least 4.0 in ADW detergent composition with bleach when compared to said parent alpha-amylase and wherein said parent alpha-amylase has amino acid sequence as shown in SEQ ID NO: 2.

8. A composition comprising the variant according to any one of claims 1 to 7 and at least one additional active component.

9. The composition according to claim 8, wherein the composition is a detergent and wherein the detergent composition is a liquid laundry detergent composition, a powder laundry detergent composition, a liquid dishwash detergent composition, or a powder dishwash detergent composition.

10. The composition according to claims 8-9, wherein said composition is a liquid or powder automatic dishwashing (ADW) detergent composition.

11. Use of a variant according to any one of claims 1 to 7, or of a composition according to any one of claims 8-10, in a domestic or industrial cleaning process.

12. A method for removal of soils from fabric or hard surfaces comprising contacting the fabric or hard surfaces contaminated with soils with a composition according to any one of claims 8-10.

13. A method of dishwashing in an automatic dishwashing machine using a composition according to any one of claims 8-10 comprising the steps of adding said detergent composition in a detergent composition compartment in said automatic dishwashing machine, and releasing said detergent composition during a main-wash cycle.

14. A method of laundering in an automatic laundering machine using a composition according to any one of claims 8-10, comprising the steps of adding said detergent composition in a detergent composition compartment in said automatic laundering machine, and releasing said detergent composition during a main wash cycle.

15. A method of improving the performance, such as wash performance, of a parent alpha-amylase having the amino acid sequence of SEQ ID NO: 2, or having at least 59% sequence identity hereto, said method comprising the steps of *a)* introducing a substitution and/or deletion at two or more positions corresponding to positions R181, G182, D183, and G184,

24 Mar 2026
2026202266

using SEQ ID NO: 1 for numbering; and *b)* introducing a deletion and/or substitution at one or more positions selected from the group consisting of: 1, 7, 9, 11, 16, 19, 25, 37, 43, 48, 54, 56, 58, 59, 60, 63, 81, 84, 86, 90, 98, 104, 109, 111, 113, 116, 118, 125, 127, 130, 132, 133, 134, 135, 136, 139, 142, 144, 149, 158, 160, 163, 167, 169, 170, 171, 172, 173, 174, 175, 176, 178, 181, 182, 186, 187, 195, 202, 203, 204, 206, 209, 210, 212, T227, 235, 238, 246, 256, 259, 264, 265, 266, 267, 269, 270, 272, 273, 274, 275, 276, 284, 286, 291, 293, 295, 298, 299, 302, 303, 304, 306, 310, 311, 314, 315, 317, 319, 320, 323, 328, 337, 339, 345, 357, 365, 377, 375, 385, 391, 395, 400, 406, 408, 410, 431, 435, 439, 444, 445, 458, 465, 466, 469, 473, 476 and/or 481; using SEQ ID NO: 1 for numbering and said method thereby providing an alpha-amylase variant of said parent alpha-amylase, wherein said variant has at least 59%, such as at least 60%, such as at least 65%, such as at least 70%, such as at least 75%, such as at least 80%,such as at least 85%, such as at least 90%, such as at least 95%, such as at least 97%, such as at least 99%, but less than 100%, sequence identity to the amino acid sequence as set forth in SEQ ID NOs: 1-17, and wherein said variant has alpha-amylase activity and improved performance as compared to said parent alpha-amylase.

24 Mar 2026
2026202266

Sequence Listing

1	**Sequence Listing Information**	
1-1	File Name	113956AUP00D1 ST.26 Sequence Listing (10Mar2026).xml
1-2	DTD Version	V1_3
1-3	Software Name	WIPO Sequence
1-4	Software Version	2.3.0
1-5	Production Date	2026-03-10
1-6	Original free text language code	
1-7	Non English free text language code	
2	**General Information**	
2-1	Current application: IP Office	
2-2	Current application: Application number	
2-3	Current application: Filing date	
2-4	Current application: Applicant file reference	113956AUP00D1
2-5	Earliest priority application: IP Office	EP
2-6	Earliest priority application: Application number	EP19164228.9
2-7	Earliest priority application: Filing date	2019-03-21
2-8en	Applicant name	NOVOZYMES A/S
2-8	Applicant name: Name Latin	
2-9en	Inventor name	
2-9	Inventor name: Name Latin	
2-10en	Invention title	ALPHA-AMYLASE VARIANTS AND POLYNUCLEOTIDES ENCODING SAME
2-11	Sequence Total Quantity	21

2026202266 24 Mar 2026

3-1	**Sequences**	
3-1-1	Sequence Number [ID]	1
3-1-2	Molecule Type	AA
3-1-3	Length	485
3-1-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus sp.
	NonEnglishQualifier Value	
3-1-5	Residues	HHDGTNGTIM QYFEWNVPND GQHWNRLHNN AQNLKNAGIT AIWIPPAWKG TSQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TKAELERAIR SLKANGIQVY GDVVMNHKGG ADFTERVQAV 120 EVNPQNRNQE VSGTYQIEAW TGFNFPGRGN QHSSFKWRWY HFDGTDWDQS RQLANRIYKF 180 RGDGKAWDWE VDTENGNYDY LMYADVDMDH PEVINELNRW GVWYANTLNL DGFRLDAVKH 240 IKFSFMRDWL GHVRGQTGKN LFAVAEYWKN DLGALENYLS KTNWTMSAFD VPLHYNLYQA 300 SNSSGNYDMR NLLNGTLVQR HPSHAVTFVD NHDTQPGEAL ESFVQGWFKP LAYATILTRE 360 QGYPQVFYGD YYGIPSDGVP SYRQQIDPLL KARQQYAYGR QHDYFDHWDV IGWTREGNAS 420 HPNSGLATIM SDGPGGSKWM YVGRQKAGEV WHDMTGNRSG TVTINQDGWG HFFVNGGSVS 480 VWVKR 485
3-2	**Sequences**	
3-2-1	Sequence Number [ID]	2
3-2-2	Molecule Type	AA
3-2-3	Length	483
3-2-4	Features	**source 1..483**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus sp.
	NonEnglishQualifier Value	
3-2-5	Residues	HHDGTNGTIM QYFEWNVPND GQHWNRLHNN AQNLKNAGIT AIWIPPAWKG TSQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TKAELERAIR SLKANGIQVY GDVVMNHKGG ADFTERVQAV 120 EVNPQNRNQE VSGTYQIEAW TGFNFPGRGN QHSSFKWRWY HFDGTDWDQS RQLANRIYKF 180 RGKAWDWEVD TENGNYDYLM YADVDMDHPE VINELNRWGV WYANTLNLDG FRLDAVKHIK 240 FSFMRDWLGH VRGQTGKNLF AVAEYWKNDL GALENYLSKT NWTMSAFDVP LHYNLYQASN 300 SSGNYDMRNL LNGTLVQRHP SHAVTFVDNH DTQPGEALES FVQGWFKPLA YATILTREQG 360 YPQVFYGDYY GIPSDGVPSY RQQIDPLLKA RQQYAYGRQH DYFDHWDVIG WTREGNASHP 420 NSGLATIMSD GPGGSKWMYV GRQKAGEVWH DMTGNRSGTV TINQDGWGHF FVNGGSVSVW 480 VKR 483
3-3	**Sequences**	
3-3-1	Sequence Number [ID]	3
3-3-2	Molecule Type	AA
3-3-3	Length	483
3-3-4	Features	**source 1..483**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus halmapalus
	NonEnglishQualifier Value	
3-3-5	Residues	HHNGTNGTMM QYFEWHLPND GNHWNRLRDD ASNLRNRGIT AIWIPPAWKG TSQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TRSQLESAIH ALKNNGVQVY GDVVMNHKGG ADATENVLAV 120 EVNPNNRNQE ISGDYTIEAY TKFDFPGRGN TYSDFKWRWY HFDGVDWDQS RQFQNRIYKF 180 RGKAWDWEVD SEFGNYDYLM YADYDMDHPE VVNELRRWGE WYTNTLNLDG FRIDAVKHIK 240 FSFTRDWLTH VRNATGKGMF AVAEFWKNDL GALENYLNKT NWNHSVFDVP LHYNLYNASN 300 SRGNYDMAKL LNGTVVQKHP MHAVTFVDNH DSQPGESLES FVQEWFKPLA YALILTREQG 360 YPSVFYGDYY GIPTHSVPAM KAKIDPILEA RQNFAYGTQH DYFDHHNIIG WTREGNTTHP 420 NSGLATIMSD GPGGEKWMYV GQNKAGQVWH DITGNKPGTV TINADGWANF SVNKGSVSIW 480 VKR 483
3-4	**Sequences**	
3-4-1	Sequence Number [ID]	4
3-4-2	Molecule Type	AA
3-4-3	Length	485
3-4-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus halmapalus
	NonEnglishQualifier Value	
3-4-5	Residues	HHNGTNGTMM QYFEWHLPND GNHWNRLRDD ASNLRNRGIT AIWIPPAWKG TSQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TRSQLESAIH ALKNNGVQVY GDVVMNHKGG ADATENVLAV 120 EVNPNNRNQE ISGDYTIEAW TKFDFPGRGN TYSDFKWRWY HFDGVDWDQS RQFQNRIYKF 180 RGDGKAWDWE VDSENGNYDY LMYADVDMDH PEVVNELRRW GEWYTNTLNL DGFRIDAVKH 240 IKYSFTRDWL THVRNATGKE MFAVAEFWKN DLGALENYLN KTNWNHSVFD VPLHYNLYNA 300 SNSGGNYDMA KLLNGTVVQK HPMHAVTFVD NHDSQPGESL ESFVQEWFKP LAYALILTRE 360 QGYPSVFYGD YYGIPTHSVP AMKAKIDPIL EARQNFAYGT QHDYFDHHNI IGWTREGNTT 420 HPNSGLATIM SDGPGGEKWM YVGQNKAGQV WHDITGNKPG TVTINADGWA NFSVNGGSVS 480 IWVKR 485
3-5	**Sequences**	
3-5-1	Sequence Number [ID]	5
3-5-2	Molecule Type	AA
3-5-3	Length	485

2026202266 24 Mar 2026

3-5-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus halmapalus
	NonEnglishQualifier Value	
3-5-5	Residues	HHNGTNGTMM QYFEWHLPND GNHWNRLRDD ASNLRNRGIT AIWIPPAWKG TSQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TRSQLESAIH ALKNNGVQVY GDVVMNHKGG ADATENVLAV 120 EVNPNNRNQE ISGDYTIEAW TKFDFPGRGN TYSDFKWRWY HFDGVDWDQS RQFQNRIYKF 180 RGDGKAWDWE VDSENGNYDY LMYADVDMDH PEVVNELRRW GEWYTNTLNL DGFRIDAVKH 240 IKYSFTRDWL THVRNATGKE MFAVAEFWKN DLGALENYLN KTNWNHSVFD VPLHYNLYNA 300 SNSGGNYDMA KLLNGTVVQK HPMHAVTFVD NHDSQPGESL ESFVQEWFKP LAYALILTRE 360 QGYPSVFYGD YYGIPTHSVP AMKAKIDPIL EARQNFAYGT QHDYFDHHNI IGWTREGNTT 420 HPNSGLATIM SDGPGGEKWM YVGQNKAGQV WHDITGNKPG TVTINADGWA NFSVNGGSVS 480 IWVKR 485
3-6	**Sequences**	
3-6-1	Sequence Number [ID]	6
3-6-2	Molecule Type	AA
3-6-3	Length	485
3-6-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus sp.
	NonEnglishQualifier Value	
3-6-5	Residues	HHNGTNGTMM QYFEWYLPND GNHWNRLRSD ASNLKDKGIS AVWIPPAWKG ASQNDVGYGA 60 YDLYDLGEFN QKGTIRTKYG TRNQLQAAVN ALKSNGIQVY GDVVMNHKGG ADATEMVRAV 120 EVNPNNRNQE VSGEYTIEAW TKFDFPGRGN THSNFKWRWY HFDGVDWDQS RKLNNRIYKF 180 RGDGKGWDWE VDTENGNYDY LMYADIDMDH PEVVNELRNW GVWYTNTLGL DGFRIDAVKH 240 IKYSFTRDWI NHVRSATGKN MFAVAEFWKN DLGAIENYLN KTNWNHSVFD VPLHYNLYNA 300 SKSGGNYDMR QIFNGTVVQR HPMHAVTFVD NHDSQPEEAL ESFVEEWFKP LAYALTLTRE 360 QGYPSVFYGD YYGIPTHGVP AMKSKIDPIL EARQKYAYGR QNDYLDHHNI IGWTREGNTA 420 HPNSGLATIM SDGAGGNKWM FVGRNKAGQV WTDITGNRAG TVTINADGWG NFSVNGGSVS 480 IWVNK 485
3-7	**Sequences**	
3-7-1	Sequence Number [ID]	7
3-7-2	Molecule Type	AA
3-7-3	Length	484
3-7-4	Features	**source 1..484**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus sp
	NonEnglishQualifier Value	
3-7-5	Residues	NTAPINETMM QYFEWDLPND GTLWTKVKNE AANLSSLGIT ALWLPPAYKG TSQSDVGYGV 60 YDLYDLGEFN QKGTIRTKYG TKTQYIQAIQ AAKAAGMQVY ADVVFNHKAG ADGTEFVDAV 120 EVDPSNRNQE TSGTYQIQAW TKFDFPGRGN TYSSFKWRWY HFDGTDWDES RKLNRIYKFR 180 STGKAWDWEV DTENGNYDYL MFADLDMDHP EVVTELKNWG TWYVNTTNID GFRLDAVKHI 240 KYTFFPDWLT YVRNQTGKNL FAVGEFWSYD VNKLHNYITK TNGSMSLFDA PLHNNFYTAS 300 KSSGYFDMRY LLNNTLMKDQ PSLAVTLVDN HDTQPGQSLQ SWVEPWFKPL AYAFILTRQE 360 GYPCVFYGDY YGIPKYNIPG LKSKIDPLLI ARRDYAYGTQ RDYIDHQDII GWTREGIDTK 420 PNSGLAALIT DGPGGSKWMY VGKKHAGKVF YDLTGNRSDT VTINADGWGE FKVNGGSVSI 480 WVAK 484
3-8	**Sequences**	
3-8-1	Sequence Number [ID]	8
3-8-2	Molecule Type	AA
3-8-3	Length	485
3-8-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein
		organism=Cytophaga sp.
	NonEnglishQualifier Value	
3-8-5	Residues	AATNGTMMQY FEWYVPNDGQ QWNRLRTDAP YLSSVGITAV WTPPAYKGTS QADVGYGPYD 60 LYDLGEFNQK GTVRTKYGTK GELKSAVNTL HSNGIQVYGD VVMNHKAGAD YTENVTAVEV 120 NPSNRNQETS GEYNIQAWTG FNFPGRGTTY SNFKWQWFHF DGTDWDQSRS LSRIFKFRGT 180 GKAWDWEVSS ENGNYDYLMY ADIDYDHPDV VNEMKKWGVW YANEVGLDGY RLDAVKHIKF 240 SFLKDWVDNA RAATGKEMFT VGEYWQNDLG ALNNYLAKVN YNQSLFDAPL HYNFYAASTG 300 GGYYDMRNIL NNTLVASNPT KAVTLVENHD TQPGQSLEST VQPWFKPLAY AFILTRSGGY 360 PSVFYGDMYG TKGTTTREIP ALKSKIEPLL KARKDYAYGT QRDYIDNPDV IGWTREGDST 420 KAKSGLATVI TDGPGGSKRM YVGTSNAGEI WYDLTGNRTD KITIGSDGYA TFPVNGGSVS 480 VWVQQ 485
3-9	**Sequences**	
3-9-1	Sequence Number [ID]	9
3-9-2	Molecule Type	AA
3-9-3	Length	485
3-9-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein
		organism=Bacillius sp
	NonEnglishQualifier Value	

2026202266 24 Mar 2026

3-9-5	Residues	HHNGTNGTMM QYFEWYLPND GNHWNRLNSD ASNLKSKGIT AVWIPPAWKG ASQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TRSQLQAAVT SLKNNGIQVY GDVVMNHKGG ADATEMVRAV 120 EVNPNNRNQE VTGEYTIEAW TRFDFPGRGN THSSFKWRWY HFDGVDWDQS RRLNNRIYKF 180 RGHGKAWDWE VDTENGNYDY LMYADIDMDH PEVVNELRNW GVWYTNTLGL DGFRIDAVKH 240 IKYSFTRDWI NHVRSATGKN MFAVAEFWKN DLGAIENYLQ KTNWNHSVFD VPLHYNLYNA 300 SKSGGNYDMR NIFNGTVVQR HPSHAVTFVD NHDSQPEEAL ESFVEEWFKP LAYALTLTRE 360 QGYPSVFYGD YYGIPTHGVP AMRSKIDPIL EARQKYAYGK QNDYLDHHNI IGWTREGNTA 420 HPNSGLATIM SDGAGGSKWM FVGRNKAGQV WSDITGNRTG TVTINADGWG NFSVNGGSVS 480 IWVNK 485
3-10	**Sequences**	
3-10-1	Sequence Number [ID]	10
3-10-2	Molecule Type	AA
3-10-3	Length	483
3-10-4	Features	**source 1..483**
	Location/Qualifiers	mol_type=protein organism=Bacillus sp
	NonEnglishQualifier Value	
3-10-5	Residues	HHNGTNGTMM QYFEWYLPND GNHWNRLNSD ASNLKSKGIT AVWIPPAWKG ASQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TRSQLQAAVT SLKNNGIQVY GDVVMNHKGG ADATEMVRAV 120 EVNPNNRNQE VTGEYTIEAW TRFDFPGRGN THSSFKWRWY HFDGVDWDQS RRLNNRIYKF 180 RGKAWDWEVD TENGNYDYLM YADIDMDHPE VVNELRNWGV WYTNTLGLDG FRIDAVKHIK 240 YSFTRDWINH VRSATGKNMF AVAEFWKNDL GAIENYLQKT NWNHSVFDVP LHYNLYNASK 300 SGGNYDMRNI FNGTVVQRHP SHAVTFVDNH DSQPEEALES FVEEWFKPLA YALTLTREQG 360 YPSVFYGDYY GIPTHGVPAM RSKIDPILEA RQKYAYGPQH DYLDHPDVIG WTREGDSSHP 420 KSGLATLITD GPGGSKRMYA GLKNAGETWY DITGNRSDTV KIGSDGWGEF HVNDGSVSIY 480 VQK 483
3-11	**Sequences**	
3-11-1	Sequence Number [ID]	11
3-11-2	Molecule Type	AA
3-11-3	Length	485
3-11-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein organism=Bacillus sp
	NonEnglishQualifier Value	
3-11-5	Residues	HHNGTNGTMM QYFEWYLPND GNHWNRLRSD ASNLKDKGIT AVWIPPAWKG ASQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TRNQLQAAVT ALKSNGIQVY GDVVMNHKGG ADATEWVRAV 120 EVNPSNRNQE VSGDYTIEAW TKFDFPGRGN THSNFKWRWY HFDGVDWDQS RQLQNRIYKF 180 RGDGKGWDWE VDTENGNYDY LMYADIDMDH PEVVNELRNW GVWYTNTLGL DGFRIDAVKH 240 IKYSFTRDWL THVRNTTGKN MFAVAEFWKN DIGAIENYLS KTNWNHSVFD VPLHYNLYNA 300 SRSGGNYDMR QIFNGTVVQR HPTHAVTFVD NHDSQPEEAL ESFVEEWFKP LACALTLTRD 360 QGYPSVFYGD YYGIPTHGVP AMKSKIDPIL EARQKYAYGK QNDYLDHHNM IGWTREGNTA 420 HPNSGLATIM SDGPGGNKWM YVGRNKAGQV WRDITGNRSG TVTINADGWG NFSVNGGSVS 480 IWVNN 485
3-12	**Sequences**	
3-12-1	Sequence Number [ID]	12
3-12-2	Molecule Type	AA
3-12-3	Length	483
3-12-4	Features	**source 1..483**
	Location/Qualifiers	mol_type=protein organism=Bacillus licheniformis
	NonEnglishQualifier Value	
3-12-5	Residues	ANLNGTLMQY FEWYMPNDGQ HWRRLQNDSA YLAEHGITAV WIPPAYKGTS QADVGYGAYD 60 LYDLGEFHQK GTVRTKYGTK GELQSAIKSL HSRDINVYGD VVINHKGGAD ATEDVTAVEV 120 DPADRNRVIS GEHLIKAWTH FHFPGRGSTY SDFKWHWYHF DGTDWDESRK LNRIYKFQGK 180 AWDWEVSNEN GNYDYLMYAD IDYDHPDVAA EIKRWGTWYA NELQLDGFRL DAVKHIKFSF 240 LRDWVNHVRE KTGKEMFTVA EYWQNDLGAL ENYLNKTNFN HSVFDVPLHY QFHAASTQGG 300 GYDMRKLLNG TVVSKHPLKS VTFVDNHDTQ PGQSLESTVQ TWFKPLAYAF ILTRESGYPQ 360 VFYGDMYGTK GDSQREIPAL KHKIEPILKA RKQYAYGAQH DYFDHHDIVG WTREGDSSVA 420 NSGLAALITD GPGGAKRMYV GRQNAGETWH DITGNRSEPV VINSEGWGEF HVNGGSVSIY 480 VQR 483
3-13	**Sequences**	
3-13-1	Sequence Number [ID]	13
3-13-2	Molecule Type	AA
3-13-3	Length	481
3-13-4	Features	**source 1..481**
	Location/Qualifiers	mol_type=protein organism=Artifical
	NonEnglishQualifier Value	
3-13-5	Residues	VNGTLMQYFE WYTPNDGQHW KRLQNDAEHL SDIGITAVWI PPAYKGTSQA DVGYGAYDLY 60 DLGEFHQKGT VRTKYGTKGE LQSAIKSLHS RDINVYGDVV INHKGGADAT EDVTAVEVDP 120 ADRNRVISGE HLIKAWTHFH FPGRGSTYSD FKWHWYHFDG TDWDESRKLN RIYKFQGKAW 180 DWEVSNENGN YDYLMYADID YDHPDVAAEI KRWGTWYANE LQLDGFRLDA VKHIKFSFLR 240

2026202266 24 Mar 2026

		DWVNHVREKT GKEMFTVAEY WQNDLGALEN YLNKTNFNHS VFDVPLHYQF HAASTQGGGY 300 DMRKLLNGTV VSKHPLKSVT FVDNHDTQPG QSLESTVQTW FKPLAYAFIL TRESGYPQVF 360 YGDMYGTKGD SQREIPALKH KIEPILKARK QYAYGAQHDY FDHHDIVGWT REGDSSVANS 420 GLAALITDGP GGAKRMYVGR QNAGETWHDI TGNRSEPVVI NSEGWGEFHV NGGSVSIYVQ 480 R 481
3-14	**Sequences**	
3-14-1	Sequence Number [ID]	14
3-14-2	Molecule Type	AA
3-14-3	Length	485
3-14-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein organism=Artifical
	NonEnglishQualifier Value	
3-14-5	Residues	HHDGTNGTIM QYFEWNVPND GQHWNRLHNN AQNLKNAGIT AIWIPPAWKG TSQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TKAELERAIR SLKANGIQVY GDVVMNHKGG ADFTERVQAV 120 EVNPQNRNQE VSGTYQIEAW TGFNFPGRGN QHSSFKWRWY HFDGTDWDQS RQLANRIYKF 180 RGDGKAWDWE VDTENGNYDY LMYADVDMDH PEVINELNRW GVWYANTLNL DGFRLDAVKH 240 IKFSFMRDWL GHVRGQTGKN LFAVAEYWKN DLGALENYLS KTNWTMSAFD VPLHYNLYQA 300 SNSSGNYDMR NLLNGTLVQR HPSHAVTFVD NHDTQPGEAL ESFVQGWFKP LAYATILTRE 360 QGYPQVFYGD YYGIPSDGVP SYRQQIDPLL KARQQYAYGT QHDYLDNQDV IGWTREGDSA 420 HAGSGLATVM SDGPGGSKTM YVGTAHAGQV FKDITGNRTD TVTINSAGNG TFPCNGGSVS 480 IWVKQ 485
3-15	**Sequences**	
3-15-1	Sequence Number [ID]	15
3-15-2	Molecule Type	AA
3-15-3	Length	485
3-15-4	Features	**source 1..485**
	Location/Qualifiers	mol_type=protein organism=Bacillus sp
	NonEnglishQualifier Value	
3-15-5	Residues	HHNGTNGTMM QYFEWHLPND GNHWNRLRDD AANLKSKGIT AVWIPPAWKG TSQNDVGYGA 60 YDLYDLGEFN QKGTVRTKYG TRSQLQGAVT SLKNNGIQVY GDVVMNHKGG ADGTEMVNAV 120 EVNRSNRNQE ISGEYTIEAW TKFDFPGRGN THSNFKWRWY HFDGTDWDQS RQLQNKIYKF 180 RGTGKAWDWE VDIENGNYDY LMYADIDMDH PEVINELRNW GVWYTNTLNL DGFRIDAVKH 240 IKYSYTRDWL THVRNTTGKP MFAVAEFWKN DLAAIENYLN KTSWNHSVFD VPLHYNLYNA 300 SNSGGYFDMR NILNGSVVQK HPIHAVTFVD NHDSQPGEAL ESFVQSWFKP LAYALILTRE 360 QGYPSVFYGD YYGIPTHGVP SMKSKIDPLL QARQTYAYGT QHDYFDHHDI IGWTREGDSS 420 HPNSGLATIM SDGPGGNKWM YVGKHKAGQV WRDITGNRSG TVTINADGWG NFTVNGGAVS 480 VWVKQ 485
3-16	**Sequences**	
3-16-1	Sequence Number [ID]	16
3-16-2	Molecule Type	AA
3-16-3	Length	480
3-16-4	Features	**source 1..480**
	Location/Qualifiers	mol_type=protein organism=Bacillus sp
	NonEnglishQualifier Value	
3-16-5	Residues	DGLNGTMMQY YEWHLENDGQ HWNRLHDDAA ALSDAGITAI WIPPAYKGNS QADVGYGAYD 60 LYDLGEFNQK GTVRTKYGTK AQLERAIGSL KSNDINVYGD VVMNHKMGAD FTEAVQAVQV 120 NPTNRWQDIS GAYTIDAWTG FDFSGRNNAY SDFKWRWFHF NGVDWDQRYQ ENHIFRFANT 180 NWNWRVDEEN GNYDYLLGSN IDFSHPEVQD ELKDWGSWFT DELDLDGYRL DAIKHIPFWY 240 TSDWVRHQRN EADQDLFVVG EYWKDDVGAL EFYLDEMNWE MSLFDVPLNY NFYRASQQGG 300 SYDMRNILRG SLVEAHPMHA VTFVDNHDTQ PGESLESWVA DWFKPLAYAT ILTREGGYPN 360 VFYGDYYGIP NDNISAKKDM IDELLDARQN YAYGTQHDYF DHWDVVGWTR EGSSSRPNSG 420 LATIMSNGPG GSKWMYVGRQ NAGQTWTDLT GNNGASVTIN GDGWGEFFTN GGSVSVYVNQ 480
3-17	**Sequences**	
3-17-1	Sequence Number [ID]	17
3-17-2	Molecule Type	AA
3-17-3	Length	483
3-17-4	Features	**source 1..483**
	Location/Qualifiers	mol_type=protein organism=Bacillus subtilis
	NonEnglishQualifier Value	
3-17-5	Residues	HHNGTNGTLM QYFEWYLPND GNHWNRLRSD ASNLKDKGIS AVWIPPAWKG ASQNDVGYGA 60 YDLYDLGEFN QKGTIRTKYG TRNQLQAAVN ALKSNGIQVY GDVVMNHKGG ADATEMVKAV 120 EVNPNNRNQE VSGEYTIEAW TKFDFPGRAN THSNFKWRWY HFDGVDWDQS RKLNNRIYKF 180 RTKAWDWEVD TEFGNYDYLL YADIDMDHPE VVNELRNWGV WYTNTLGLDG FRIDAVKHIK 240 YSFTRDWINH VRSAIGKNMF AVAEFWKNDL GAIENYLNKT NWNHSVFDVP LHFNLYYASK 300 SGGNYDMRQI FNGTVVQKHP THAVTFVDNH DSQPEESLES FVREWFKPLA YALTLTREQG 360 YPSVFYGDYY GIPTHGVPAM KSKIDPILEA RQKYAYGRQN DYLDHHNIIG WTREGNTAHP 420 NSGLATIMSD GAGGNKWMFV GRNKAGQVWT DITGNKAGTV TINADGWGNF SVNGGSVSIW 480 VNK 483

2026202266 24 Mar 2026

3-18	**Sequences**	
3-18-1	Sequence Number [ID]	18
3-18-2	Molecule Type	DNA
3-18-3	Length	1458
3-18-4	Features	**source 1..1458**
	Location/Qualifiers	mol_type=unassigned DNA
		organism=Bacillus sp
	NonEnglishQualifier Value	
3-18-5	Residues	catcacgatg ggacgaacgg aacgattatg cagtattttg aatggaacgt tccgaatgat 60 ggacaacatt ggaaccgctt acacaacaac gctcaaaatt taaaaaatgc cggaattaca 120 gcaatctgga ttccacctgc gtggaaagga acgagccaaa atgatgtagg ctacggtgcg 180 tatgaccttt atgaccttgg tgaatttaac caaaaaggaa cggtccgtac gaaatatgga 240 acaaaagcag aattagaacg agcgattcgt tcgttaaagg cgaacgggat tcaagtgtat 300 ggcgatgttg ttatgaacca taaaggcgga gctgatttca ccgagcgtgt tcaagcggtt 360 gaagtgaacc cgcaaaaccg aaaccaagaa gtgtctggca cttatcaaat cgaagcatgg 420 acagggttca attttcctgg acgtggcaat caacattctt cgtttaaatg gcgctggtat 480 catttcgatg ggacggattg ggaccagtct cgccaactcg caaatcgtat ttataagttt 540 agaggagacg gaaaagcatg ggactgggaa gttgacactg aaaatgggaa ctatgattac 600 ttaatgtatg cagacgttga catggatcat ccagaagtga ttaacgaact aaaccgttgg 660 ggcgtctggt acgcgaatac ccttaattta gacggcttcc gactggatgc agtgaaacat 720 attaaattta gcttcatgcg tgattggtta gggcatgttc gcgggcaaac gggcaagaat 780 ctttttgccg ttgcagagta ttggaagaat gacctagggg ctttagaaaa ttatttaagc 840 aaaacaaatt ggacgatgag cgcctttgat gttccgcttc attacaacct ttatcaagcg 900 tcaaatagta gcggaaatta cgacatgaga aacttgttaa atggaacact cgttcaacgt 960 catccgagcc atgcggttac gtttgtcgat aaccacgaca cacagcctgg agaagccctc 1020 gaatcgttcg ttcaaggctg gtttaaacca ctagcttatg caacgattct tacgagagag 1080 caaggctacc cacaagtgtt ttacggcgat tattatggca tcccaagtga cggtgttcca 1140 agctaccgtc aacagatcga cccactttta aaagctcgtc aacaatatgc ttatggtaga 1200 cagcacgatt actttgatca ttgggatgta attggctgga cacgtgaagg aaacgcatct 1260 cacccgaact caggacttgc aaccattatg tctgatggtc caggtggatc aaaatggatg 1320 tatgttggcc gtcagaaagc tggcgaagtg tggcatgaca tgactggaaa ccgcagtggc 1380 actgtgacaa ttaatcaaga cggctgggga cacttttttg tcaacggcgg ctctgtctcc 1440 gtatgggtga aacgataa 1458
3-19	**Sequences**	
3-19-1	Sequence Number [ID]	19
3-19-2	Molecule Type	AA
3-19-3	Length	269
3-19-4	Features	**source 1..269**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus sp
	NonEnglishQualifier Value	
3-19-5	Residues	AQSVPWGIRR VQAPTAHNRG LTGSGVKVAV LDTGISTHPD LNIRGGASFV PGEPSTQDEN 60 GHGTHAAGTI AALDNSIGVL GVAPSAELYA VKVLGAGGSG SVSSIAQGLE WAGNNGMHVA 120 NLSLGSPSPS ATLEQAVNSA TSRGVLVVAA SGNSGAGSIS YPARYANAMA VGATDQNNNR 180 ASFSQYGAGL DIVAPGVNVQ STYPGSTYAS LDGTSMATPH VAGAAALVKQ KNPSWSNVRI 240 RNHLKNTATS LGSTNLYGSG LVNAEAATR 269
3-20	**Sequences**	
3-20-1	Sequence Number [ID]	20
3-20-2	Molecule Type	AA
3-20-3	Length	269
3-20-4	Features	**source 1..269**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus sp
	NonEnglishQualifier Value	
3-20-5	Residues	AQSVPWGISR VQAPAAHNRG LTGSGVKVAV LDTGISTHPD LNIRGGASFV PGEPSTQDGN 60 GHGTHVAGTI AALNNSIGVL GVAPNAELYA VKVLGASGSG SVSSIAQGLE WAGNNVMHVA 120 NLSLGLQAPS ATLEQAVNSA TSRGVLVVAA SGNSGAGSIS YPARYANAMA VGATDQNNNR 180 ASFSQYGAGL DIVAPGVNVQ STYPGSTYAS LNGTSMATPH VAGAAALVKQ KNPSWSNVQI 240 RNHLKNTATS LGSTNLYGSG LVNAEAATR 269
3-21	**Sequences**	
3-21-1	Sequence Number [ID]	21
3-21-2	Molecule Type	AA
3-21-3	Length	269
3-21-4	Features	**source 1..269**
	Location/Qualifiers	mol_type=protein
		organism=Bacillus
	NonEnglishQualifier Value	
3-21-5	Residues	AQSVPWGIER VQAPAAHNRG LTGSGVKVAV LDTGISTHPD LRIRGGASFV PGEPSTQDGN 60 GHGTHVAGTI AALDNSIGVL GVAPSAELYA VKVLGASGSG SVSSIAQGLE WAGNNGMHVA 120 NLSLGSPSPS ATLEQAVNSA TSRGVLVVAA SGNSGAGSIS YPARYANAMA VGATDQNNNR 180 ASFSQYGAGL DIVAPGVNIL STWPGSTYAS LNGTSMATPH VAGAAALVKQ KNPSWSNVQI 240 RNHLKNTATS LGDTWEYGSG LVNAEAATR 269