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DESCRIPTION

Technical Field

[0001] The present invention relates to a modified α -glucosidase. Specifically, the present invention relates to a modified α -glucosidase, a method of designing and a method of preparing the modified α -glucosidase, and use of the modified α -glucosidase.

Background Art

[0002] Glycoside hydrolases are enzymes that cleave ester bonds, and many glycoside hydrolases that concurrently have a transglycosylation activity have also been reported. α -Glucosidase, which can be said to be a typical glycoside hydrolase, generally has a hydrolysis activity (hydrolysis reaction) and a transglycosylation activity (condensation reaction) in combination. α -Glucosidase is widely present in nature, from microorganisms to higher animals and higher plants. α -Glucosidase is the most useful enzyme in industries, and is utilized for the decomposition, synthesis and the like of saccharides. For example, the α -Glucosidase of *Aspergillus niger* is used for glucose transfer to lipids and food products having improved emulsification properties (see Patent Document 5).

[0003] Due to advances in technology, it has become possible to vary (improve) the characteristics of enzymes. Various attempts for modification have also been made for α -glucosidase (for example, see Patent Documents 1 to 3).

Prior Art Document

Patent Literature

[0004]

Patent Document 1: Japanese Unexamined Patent Publication No. 2003-88365

Patent Document 2: Japanese Unexamined Patent Publication No. 2005-253302

Patent Document 3: Japanese Unexamined Patent Publication No. 2009-22204

Patent Document 4: Japanese Unexamined Patent Publication No. 2001-046096

Patent Document 5: International Patent Publication No. WO 2010/010463

Summary of the Invention

Problems to be solved by the Invention

[0005] Since either the hydrolysis activity or transglycosylation activity is generally used in the case where α -glucosidase is used in industrial use, it is preferable that the other activity that is not used is low. In the case where α -glucosidase is used for the production of an oligosaccharide, transglycosylation activity of the enzyme could be decreased by increasing the hydrolysis activity. Therefore, the object of the present invention is to provide an α -glucosidase in which the transglycosylation activity predominates, which is suitable for the production of oligosaccharides. Furthermore, another object of the present invention is to provide the use thereof, and the like.

Means for Solving the Problem

[0006] The present inventors attempted to modify the structure of existing α -glucosidase at the molecular level for the purpose of designing a novel enzyme having an improved oligosaccharide production ability. Specifically, they conducted computer simulation and alignment comparison with four kinds of homologues by utilizing a result of an X-ray crystal structure analysis of α -glucosidase derived from human small intestine (Human Maltase-glucoamylase). As a result, three amino acids that constitute the substrate pockets of the enzyme were identified. Subsequently, amino acids that correspond to the amino acids were specified on the amino acid sequence of *Aspergillus niger* α -glucosidase, and modification was introduced into the those amino acids. As a result of an investigation on the characteristics of the obtained modified forms, it was confirmed that the characteristics of the enzyme (specifically the balance between the hydrolysis activity and transglycosylation activity) had significantly changed. Among the modified forms, those not showing a hydrolysis activity against α -1,4 glucosidic linkages and α -1,6 glucosidic linkages, those having a remarkably decreased hydrolysis activity against α -1,6 glucosidic linkages, those having a significantly decreased hydrolysis activity against α -1,3 glucosidic linkages and α -1,6 glucosidic linkages, and the like were observed. It is noteworthy that the wild-type enzymes catalyze formation of α -1,6 glucosidic linkages, mainly, whereas the modified forms (type W343M and type W343M/S496T) catalyze formation of α -1,4 glucosidic linkages, mainly. These facts mean that the above-mentioned amino acid positions that were successfully identified are effective as positions to which mutation is to be added, in the case where structural modification is performed for the purpose of obtaining an α -glucosidase that is suitable for the production of an oligosaccharide, and the like (i.e., an α -glucosidase in which the transglycosylation activity predominates). Furthermore, it can be said that the amino acid positions are especially effective as positions for mutation for acquiring an α -glucosidase having a unique characteristic

that it shows a transglycosylation activity to form α -1,4 glucosidic linkages. On the other hand, modified α -glucosidases that are successfully obtained themselves are of great value in industry.

[0007] The present inventors further advanced their investigation and decided to consider annotated amino acids by a novel procedure. Specifically, first, steric structure models were constructed for *Aspergillus niger* α -glucosidase and *Aspergillus nidulans* α -glucosidase by using another computer simulation software. Subsequently, a docking simulation analysis was performed to thereby predict substrate pockets. Furthermore, based on the results, the amino acids to be an active center were searched, and the positions in each steric structure model were specified. Next, the amino acid sequences were compared between *Aspergillus niger* α -glucosidase and *Aspergillus nidulans* α -glucosidase, and the amino acids that were mismatched among the amino acids of the substrate pockets were specified as amino acids that are suitable for introducing modification. Subsequently, in order to confirm whether or not these amino acids are suitable for introducing mutation (in other words, whether or not these amino acids are beneficial for structural modification), mutation was actually introduced into two amino acids to give modified forms. As a result of the investigation on the characteristics of the obtained modified forms, a modified form showing a transglycosylation activity to form α -1,6 glucosidic linkages and a modified form showing a transglycosylation activity to form α -1,4 glucosidic linkages were observed. This fact supports that the amino acid positions that were successfully identified are effective for structural modification. On the other hand, the modified α -glucosidases that were successfully obtained themselves are of great value in industry.

[0008] On the other hand, as a result of further research, it was confirmed that the modified forms that were successfully obtained are useful for the generation or production of oligosaccharides. It is noteworthy that the modified form showing a transglycosylation activity to form α -1,6 glucosidic linkages was able to form oligosaccharides also from substrates having α -1,4 glucosidic linkages by using the modified form in combination with a wild type α -glucosidase.

[0009] Meanwhile, it is often experienced that it is highly possible that an additive or synergistic effect is generated by combining effective two amino acid substitutions. Therefore, it can be said that the three mutation positions that were successfully identified are effective for changing the characteristics (especially for improving a transglycosylation activity), not only alone but also for the combinations thereof. Actually, the transglycosylation activity was also improved in the case where amino acid substitutions at two positions were combined (Examples mentioned below).

[0010] Furthermore, considering the technical common knowledge that enzymes of the same kind are highly similar in structures (primary structure and steric structure) and that it is highly possible that similar mutation generates a similar effect, it can be said that the mutation technique found by the present inventors can be applied to not only the α -glucosidase derived from *Aspergillus niger* as shown in the following Examples, but also α -glucosidases derived

from other organisms.

[0011] The present invention shown below is based on the above-mentioned accomplishment and observation and relates to the embodiments as characterized in the claims.

[1] A modified α -glucosidase, in which the transglycosylation activity is improved and/or the balance between the hydrolysis activity and the transglycosylation activity is changed in lowering the hydrolysis activity compared to the α -glucosidase to be modified, consisting of an amino acid sequence in which one or two or more of the amino acid(s) selected from the group consisting of the following (1) to (14) has/have been substituted by (an) other amino acid(s) in the amino acid sequence of α -glucosidase:

1. (1) an amino acid corresponding to the amino acid at the position 385 of the amino acid sequence of SEQ ID NO. 1;
2. (2) an amino acid corresponding to the amino acid at the position 491 of the amino acid sequence of SEQ ID NO. 1;
3. (3) an amino acid corresponding to the amino acid at the position 535 of the amino acid sequence of SEQ ID NO. 1;
4. (4) an amino acid corresponding to the amino acid at the position 450 of the amino acid sequence of SEQ ID NO. 1;
5. (5) an amino acid corresponding to the amino acid at the position 534 of the amino acid sequence of SEQ ID NO. 1;
6. (6) an amino acid corresponding to the amino acid at the position 537 of the amino acid sequence of SEQ ID NO. 1;
7. (7) an amino acid corresponding to the amino acid at the position 538 of the amino acid sequence of SEQ ID NO. 1;
8. (8) an amino acid corresponding to the amino acid at the position 554 of the amino acid sequence of SEQ ID NO. 1;
9. (9) an amino acid corresponding to the amino acid at the position 556 of the amino acid sequence of SEQ ID NO. 1;
10. (10) an amino acid corresponding to the amino acid at the position 579 of the amino acid sequence of SEQ ID NO. 2;
11. (11) an amino acid corresponding to the amino acid at the position 585 of the amino acid sequence of SEQ ID NO. 2;
12. (12) an amino acid corresponding to the amino acid at the position 630 of the amino acid sequence of SEQ ID NO. 1;
13. (13) an amino acid corresponding to the amino acid at the position 683 of the amino acid sequence of SEQ ID NO. 1; and
14. (14) an amino acid corresponding to the amino acid at the position 689 of the amino acid sequence of SEQ ID NO. 1,

wherein [2] the α -glucosidase to be modified is Human Maltase-glucoamylase, *Aspergillus niger* α -glucosidase, Human Neutral α -glucosidase C, Mouse Lysosomal α -glucosidase, Yeast GLU2A, *Aspergillus nidulans* α -glucosidase AgdA, *Aspergillus nidulans* α -glucosidase AgdB, *Mucor javanicus* α -glucosidase, *Aspergillus oryzae* α -

glucosidase, *Mortierella alliacea* alpha-glucosidase, *Schizosaccharomyces pombe* alpha-glucosidase, *Debaryomyces occidentalis* alpha-glucosidase, *Hordeum vulgare* subsp. *vulgare* alpha-glucosidase, *Arabidopsis thaliana* alpha-glucosidase, *Spinacia oleracea* alpha-glucosidase, *Beta vulgaris* alpha-glucosidase or *Solanum tuberosum* alpha-glucosidase, and/or

wherein [3] the amino acid sequence of the α -glucosidase to be modified is the amino acid sequence of SEQ ID NO. 2, and

the amino acid of (1) is the amino acid at the position 343 of the amino acid sequence, the amino acid of (2) is the amino acid at the position 452 of the amino acid sequence, the amino acid of (3) is the amino acid at the position 496 of the amino acid sequence, the amino acid of (4) is the amino acid at the position 410 of the amino acid sequence, the amino acid of (5) is the amino acid at the position 495 of the amino acid sequence, the amino acid of (6) is the amino acid at the position 498 of the amino acid sequence, the amino acid of (7) is the amino acid at the position 499 of the amino acid sequence, the amino acid of (8) is the amino acid at the position 531 of the amino acid sequence, the amino acid of (9) is the amino acid at the position 533 of the amino acid sequence, the amino acid of (12) is the amino acid at the position 662 of the amino acid sequence, the amino acid of (13) is the amino acid at the position 715 of the amino acid sequence, and the amino acid of (14) is the amino acid at the position 721 of the amino acid sequence.

[4] The modified α -glucosidase according to [3], wherein the amino acid to be substituted is the amino acid of (1), and the amino acid after the substitution is cysteine, aspartic acid, methionine, histidine, alanine, phenylalanine, glycine, threonine, glutamic acid, valine, glutamine, asparagine or isoleucine.

[5] The modified α -glucosidase according to [3], wherein the amino acid to be substituted is the amino acid of (2), and the amino acid after the substitution is glycine, aspartic acid or glutamic acid.

[6] The modified α -glucosidase according to [3], wherein the amino acid to be substituted is the amino acid of (3), and the amino acid after the substitution is asparagine, glutamine or valine.

[7] The modified α -glucosidase according to [3], wherein the amino acids to be substituted are the amino acid of (1) and the amino acid of (2), and the amino acids after the substitution are aspartic acid for the amino acid of (1) and alanine or glycine for the amino acid of (2).

[8] The modified α -glucosidase according to [3], wherein the amino acids to be substituted are the amino acid of (1) and the amino acid of (3), and the amino acids after the substitution are aspartic acid or methionine for the amino acid of (1) and isoleucine, arginine, cysteine or threonine for the amino acid of (3).

[9] The modified α -glucosidase according to [3], wherein the amino acid to be substituted is the amino acid of (5), and the amino acid after the substitution is glycine, proline or valine.

[10] The modified α -glucosidase according to [3], wherein the amino acid to be substituted is the amino acid of (6), and the amino acid after the substitution is leucine or serine.

[11] The modified α -glucosidase according to [1], which is consisting of any of the amino acid sequences of SEQ ID Nos. 18 to 42 and 77 to 78.

[12] The modified α -glucosidase according to [1], which is consisting of any of the amino acid sequences of SEQ ID Nos. 74 to 76.

[13] A gene coding for the modified α -glucosidase according to any one of [1] to [12].

[14] The gene according to [13], which comprises any of base sequences of SEQ ID Nos. 43 to 67 and 79 to 83.

[15] A recombinant DNA comprising the gene according to [13] or [14].

[16] A microorganism having the recombinant DNA according to [15].

[17] An enzyme agent comprising the modified α -glucosidase according to any one of [1] to [12].

[18] A method for producing an oligosaccharide, comprising reacting the modified α -glucosidase according to any one of [1] to [8], [10] and [11] with an oligosaccharide or polysaccharide of di- or more saccharides having α -1,4 glucosidic linkage.

[19] A method for producing an oligosaccharide, comprising reacting the modified α -glucosidase according to [9] or [12] with an oligosaccharide or polysaccharide of di- or more saccharides having α -1,6 glucosidic linkage .

[20] The method for producing an oligosaccharide according to [18] or [19], comprising using a wild type enzyme in combination.

[21] A method for producing an oligosaccharide, comprising reacting the modified α -glucosidase according to [9] or [12] and a wild type enzyme with an oligosaccharide or polysaccharide of di- or more saccharides having α -1,4 glucosidic linkage(s).

[22] A pharmaceutical composition, a quasi-drug composition, a cosmetic composition, a food composition or a feed composition, comprising the modified α -glucosidase according to any one of [1] to [12] or the enzyme agent according to [17].

[23] A method for preparing a modified α -glucosidase, in which the transglycosylation activity is improved and/or the balance between the hydrolysis activity and the transglycosylation activity is changed in lowering the hydrolysis activity compared to the α -glucosidase to be modified comprising the following steps (i) and (ii):

1. (i) a step of identifying one or two or more amino acid(s) selected from the group consisting of the following (1) to (14) in the amino acid sequence of α -glucosidase as an enzyme to be mutated:
 1. (1) an amino acid corresponding to the amino acid at the position 385 of the amino acid sequence of SEQ ID NO. 1;
 2. (2) an amino acid corresponding to the amino acid at the position 491 of the

- amino acid sequence of SEQ ID NO. 1;
3. (3) an amino acid corresponding to the amino acid at the position 535 of the amino acid sequence of SEQ ID NO. 1;
 4. (4) an amino acid corresponding to the amino acid at the position 450 of the amino acid sequence of SEQ ID NO. 1;
 5. (5) an amino acid corresponding to the amino acid at the position 534 of the amino acid sequence of SEQ ID NO. 1;
 6. (6) an amino acid corresponding to the amino acid at the position 537 of the amino acid sequence of SEQ ID NO. 1;
 7. (7) an amino acid corresponding to the amino acid at the position 538 of the amino acid sequence of SEQ ID NO. 1;
 8. (8) an amino acid corresponding to the amino acid at the position 554 of the amino acid sequence of SEQ ID NO. 1;
 9. (9) an amino acid corresponding to the amino acid at the position 556 of the amino acid sequence of SEQ ID NO. 1;
 10. (10) an amino acid corresponding to the amino acid at the position 579 of the amino acid sequence of SEQ ID NO. 2;
 11. (11) an amino acid corresponding to the amino acid at the position 585 of the amino acid sequence of SEQ ID NO. 2;
 12. (12) an amino acid corresponding to the amino acid at the position 630 of the amino acid sequence of SEQ ID NO. 1;
 13. (13) an amino acid corresponding to the amino acid at the position 683 of the amino acid sequence of SEQ ID NO. 1; and
 14. (14) an amino acid corresponding to the amino acid at the position 689 of the amino acid sequence of SEQ ID NO. 1.
2. (ii) a step of constructing an amino acid sequence in which the amino acid sequence(s) identified in the step (i) has/have been substituted by other amino acid, based on the amino acid sequence of the enzyme to be mutated.

[24] The designing method according to [23], wherein the α -glucosidase is Human Maltase-glucoamylase, *Aspergillus niger* alpha-glucosidase, Human Neutral alpha-glucosidase C, Mouse Lysosomal alpha-glucosidase, Yeast GLU2A, *Aspergillus nidulans* Alpha-glucosidase AgdA, *Aspergillus nidulans* Alpha-glucosidase AgdB, *Mucor javanicus* alpha-glucosidase, *Aspergillus oryzae* alpha-glucosidase, *Mortierella alliacea* alpha-glucosidase, *Schizosaccharomyces pombe* alpha-glucosidase, *Debaryomyces occidentalis* alpha-glucosidase, *Hordeum vulgare* subsp. *vulgare* alpha-glucosidase, *Arabidopsis thaliana* alpha-glucosidase, *Spinacia oleracea* alpha-glucosidase, *Beta vulgaris* alpha-glucosidase or *Solanum tuberosum* alpha-glucosidase.

[25] The designing method according to [23], wherein the α -glucosidase comprises any of the amino acid sequences of SEQ ID Nos. 1 to 17.

[26] The designing method according to [23], wherein the α -glucosidase is consisting of the amino acid sequence of SEQ ID NO. 2, and the amino acid(s) that is/are substituted in the step (i) is/are one amino acid selected from (1) to (14), two amino acids selected from (1) to (14) or

three amino acids selected from (1) to (14).

[27] A method for preparing a modified α -glucosidase, comprising the following steps (I) to (III):

1. (I) a step of preparing a nucleic acid that codes for any of the amino acid sequences of SEQ ID Nos. 18 to 42 and 74 to 78 or an amino acid sequence constituted by the designing method according to any one of [23] to [26];
2. (II) a step of expressing the nucleic acid, and
3. (III) a step of collecting an expression product.

Brief Description of the Drawings

[0012]

FIG. 1 shows positions of annotated amino acids in human α -glucosidase (A), comparison of alignments (B), and the positions of the amino acids corresponding to the annotated amino acids in an amino acid sequence of *Aspergillus niger* (C).

FIG. 2 shows a scheme of a modified TG (transglucosidase) screening system using yeast.

FIG. 3 compares oligosaccharide synthesis activities by HPLC. The oligosaccharide synthesis activities of a WT (wild type) (A) and modified TGs (W343M (B), V452G (C) and S496V (D)) were compared.

FIG. 4 compares synthesis amounts of the oligosaccharides of tri- or more saccharides.

FIG. 5 compares the synthesis amounts of the oligosaccharides of tri- or more saccharides (upper) and compares the synthesis amounts of the oligosaccharides of tetra- or more saccharides (lower). The amounts of the generated oligosaccharides were compared among the modified TGs having different amino acids after substitution (indicated below the graph).

FIG. 6 compares the synthesis amounts of the oligosaccharides of tri- or more saccharides (left) and compares the synthesis amounts of the oligosaccharides of tetra- or more saccharides (right). The amounts of the generated oligosaccharides were compared among the modified TGs having different amino acids after substitution (indicated below the graph).

FIG. 7 compares substrate specificities relating to hydrolysis activities.

FIG. 8 shows the hydrolysis activities of the modified TGs by substitution of two amino acids.

FIG. 9 shows the oligosaccharide synthesis activities of the modified TGs by substitution of two amino acids. The oligosaccharide synthesis activities of the WT (wild type) (A) and modified TGs (W343M (B), W343M/S496T (C) and W343D/V452G (D)) were compared.

FIG. 10 compares the synthesis amounts of the oligosaccharides of tri- or more saccharides

(left) and the comparison of the synthesis amounts of the oligosaccharides of tetra- or more saccharides (right). The amounts of the generated oligosaccharides were compared among the modified TGs having different amino acids after substitution (indicated below the graph).

FIG. 11 shows the substrate specificities of the modified TGs by substitution of two amino acids.

FIG. 12 compares the oligosaccharides that are formed when maltopentaose is used as a start substrate.

FIG. 13 compares the oligosaccharides that are formed when a mixture of maltose and isomaltose is used as the start substrate.

FIG. 14 are computer-simulated steric structure models of α -glucosidase. Left: *Aspergillus niger* TG, right: *Aspergillus nidulans* TG.

FIG. 15 shows the scheme for considering annotated amino acids based on computer simulation.

FIG. 16 compares the oligosaccharide synthesis activities of the modified TGs (S495X). Maltose was used as the substrate. The synthesis amount of the oligosaccharides of tri- or more saccharides (upper) and the synthesis amount of the oligosaccharides of tetra- or more saccharides (lower) were compared.

FIG. 17 compares the oligosaccharide synthesis activities of the modified TGs (S495X). Isomaltose was used as the substrate. The synthesis amount of the oligosaccharides of tri- or more saccharides (upper) and the synthesis amount of the oligosaccharides of tetra- or more saccharides (lower) were compared.

FIG. 18 shows the hydrolysis activities of the modified TGs (S495X).

FIG. 19 compares the oligosaccharide synthesis activities of the modified TGs. Maltopentaose was used as the substrate. (a) A HPLC chart of the WT (wild type). (b) The HPLC chart of the modified TG (S495V). (c) A ratio of the generated oligosaccharides.

FIG. 20 compares the oligosaccharide synthesis activities of the modified TGs (C498X). Maltose was used as the substrate.

FIG. 21 shows the hydrolysis activities of the modified TGs (C498X).

FIG. 22 compares the oligosaccharide-synthesis ability. (a) The case where TG is not added, (b) the case where TG of the WT (wild type) is added, (c) the case where the modified TG (W343M) was added, and (d) comparison of an area surface areas of the tri- or more saccharides.

FIG. 23 is the HPLC chart of the oligosaccharides formed from porridge (at 90 minutes after the initiation of the reaction).

FIG. 24 compares the oligosaccharide synthesis activities. The synthesis amount of the

oligosaccharides of tri- or more saccharides (upper) and the synthesis amount of the oligosaccharides of tetra- or more saccharides (lower) were compared in the case where the modified TG (S495P) was used alone and the cases where the wild type was used in combination. Maltose was used as the substrate.

FIG. 25 is the HPLC chart of the oligosaccharides formed from maltose (substrate) (at 48 hours after the initiation of the reaction).

FIG. 26 compares the oligosaccharide-synthesis ability. (a) The case where the WT (wild type) TG is added, (b) the case where the modified TG (S495P) is added, (c) the case where the WT (wild type) and the modified TG (S495P) are used in combination, and (d) comparison of the area surface areas of the tri- or more saccharides.

FIG. 27 is the HPLC chart of the oligosaccharides formed from porridge (at 90 minutes after the initiation of the reaction).

Description of Embodiments

[0013] For convenience in explanation, a part of the terms used with respect to the present invention will be defined below.

(Terms)

[0014] α -Glucosidase is also referred to as transglucosidase. In the present specification, the term "a-glucosidase" and the term "transglucosidase" are interchangeably used. The term "modified α -glucosidase" is an enzyme that is obtained by modifying or mutating "a base α -glucosidase" by the means disclosed by the present specification. In the present specification, the term "modified α -glucosidase", the term "modified α -glucosidase", the term "modified enzyme" and the term "modified enzyme" are interchangeably used. The base α -glucosidase is typically a wild type α -glucosidase. However, this does not interfere with the application of α -glucosidase that has already undergone an artificial operation to the present invention as the "base α -glucosidase". The "base α -glucosidase" is also referred to as "a-glucosidase to be mutated" or "enzyme to be mutated" in the present specification. In the present specification, an amino acid on a mutation introduction point is expressed by a combination of a single letter that represents the kind of the amino acid and a number that represents the position of the amino acid. For example, when the tryptophan at the position 343 is a mutation introduction point, the amino acid is expressed as "W343".

(Modified α -glucosidase)

[0015] The first aspect of the present invention relates to a modified α -glucosidase (modified enzyme) as characterized in the claims. The modified enzyme of the present invention has an amino acid sequence in which one or two or more of the amino acid(s) selected from the group consisting of the following (1) to (14) has/have been substituted by (an) other amino acid(s) in the amino acid sequence of an enzyme to be mutated.

1. (1) an amino acid corresponding to the amino acid at the position 385 of the amino acid sequence of SEQ ID NO. 1
2. (2) an amino acid corresponding to the amino acid at the position 491 of the amino acid sequence of SEQ ID NO. 1
3. (3) an amino acid corresponding to the amino acid at the position 535 of the amino acid sequence of SEQ ID NO. 1
4. (4) an amino acid corresponding to the amino acid at the position 450 of the amino acid sequence of SEQ ID NO. 1
5. (5) an amino acid corresponding to the amino acid at the position 534 of the amino acid sequence of SEQ ID NO. 1
6. (6) an amino acid corresponding to the amino acid at the position 537 of the amino acid sequence of SEQ ID NO. 1
7. (7) an amino acid corresponding to the amino acid at the position 538 of the amino acid sequence of SEQ ID NO. 1
8. (8) an amino acid corresponding to the amino acid at the position 554 of the amino acid sequence of SEQ ID NO. 1
9. (9) an amino acid corresponding to the amino acid at the position 556 of the amino acid sequence of SEQ ID NO. 1
10. (10) an amino acid corresponding to the amino acid at the position 579 of the amino acid sequence of SEQ ID NO. 2
11. (11) an amino acid corresponding to the amino acid at the position 585 of the amino acid sequence of SEQ ID NO. 2
12. (12) an amino acid corresponding to the amino acid at the position 630 of the amino acid sequence of SEQ ID NO. 1
13. (13) an amino acid corresponding to the amino acid at the position 683 of the amino acid sequence of SEQ ID NO. 1
14. (14) an amino acid corresponding to the amino acid at the position 689 of the amino acid sequence of SEQ ID NO. 1

[0016] As shown in Examples mentioned below, the amino acid at the position 385, the amino acid at the position 491 and the amino acid at the position 535 mentioned above are amino acids that were expected to be important for the functions of enzymes as a result of making full use of the steric structure analysis and prediction of functions of Human Maltase-glucoamylase (SEQ ID NO. 1), as well as techniques such as alignment comparison with homologues, and the like. Thus, the structure of the enzyme of the present invention is modified by mutating amino acids that correspond to these amino acids to thereby change the characteristics of α -

glucosidase. The "characteristics" herein are a transglycosylation activity and a hydrolysis activity. In the modified enzyme of the present invention, the balance between the transglycosylation activity and hydrolysis activity has shifted to the direction in which the transglycosylation activity predominates, on the basis of the balance before the modification. As a result of the modification, improvement of the transglycosylation activity or lowering of the hydrolysis activity, or both generate(s), and thus the enzyme enables effective transglycosylation.

[0017] On the other hand, the amino acids shown in the above-mentioned (4) to (14) are amino acids that were expected to be effective for structure modification as a result of making use of the comparison of the steric structures and the comparison of the amino acid sequences in *Aspergillus niger* alpha-glucosidase and *Aspergillus nidulans* alpha-glucosidase. Thus, the structure of the enzyme of the present invention is modified by mutating amino acids that correspond to these amino acids to thereby change the characteristics of α -glucosidase.

[0018] Herein, the term "corresponding" when used for an amino acid residue in the present specification means contributing equally to exhibition of functions among proteins (enzymes) being compared. For example, when an amino acid sequence for comparison to the base amino acid sequence (that is, the amino acid sequence set forth in SEQ ID NO: 1 or SEQ ID NO: 2) is aligned while considering partial homology of the primary structure (that is, an amino acid sequence) so that the most appropriate comparison can be achieved (in this event, the alignment may be optimized by introducing gaps if necessary), an amino acid located at a position corresponding to a specific amino acid in the base amino acid sequence can be specified as a "corresponding amino acid". The "corresponding amino acid" can also be specified by comparison between conformations (three-dimensional structures) in place of or in addition to the comparison between primary structures. Utilization of conformational information can give highly credible comparison results. In this case, a technique of performing an alignment with comparing atomic coordinates of conformations of a plurality of enzymes can be adopted. Conformational information of an enzyme to be mutated is available from, for example, the Protein Data Bank (http://www.pdbj.org/index_j.html).

[0019] One example of a method for determination of a protein conformation by the X-ray crystal structure analysis will be shown below.

1. (1) A protein is crystallized. Crystallization is essential to determine a conformation, and in addition, crystallization is industrially useful as a purification method of a protein at high purity and a stable preservation method of a protein at high density. In this case, it is preferable that a protein to which a substrate or its analogous compound as a ligand is bound is used for crystallization.
2. (2) The prepared crystal is irradiated with X-ray to collect diffraction data. There are many cases that a protein crystal is damaged due to X-ray irradiation and the diffraction ability is deteriorated. In such cases, a low-temperature measurement technique of rapidly cooling the crystal to about -173°C and collecting diffraction data in the state has recently prevailed. In addition, ultimately, synchrotron orbit radiation having high

luminance is utilized to collect high resolution data that is used for structural determination.

3. (3) In addition to the diffraction data, phase information is necessary in order to perform the crystal structure analysis. When a crystal structure of an analogous protein to a desired protein is unknown, it is impossible to determine the structure in a molecular substitution method, and a phase problem has to be solved by a heavy-atom isomorphous replacement method. The heavy-atom isomorphous replacement method is a method in which a metallic atom having a high atomic number such as mercury or platinum is introduced into a crystal and contribution of a large X-ray scattering ability of such a metallic atom to X ray diffraction data is utilized to collect phase information. The determined phase is possibly improved by smoothing an electron density of a solvent region in the crystal. Since a water molecule in the solvent region has large fluctuation, the electron density is hardly observed, and thus adjusting the electron density in this region to close to 0 makes it possible to approach the real electron density, which results in improving a phase. When plural molecules are contained in an asymmetrical unit, equation of electron densities of these molecules makes it possible to more significantly improve a phase. A model of a protein is fit to an electron density map calculated using the phase improved as described above. This process is performed on computer graphics using a program such as QUANTA made by MSI Co. (USA). After the process, structure refinement is performed using a program such as X-PLOR made by MSI Co. to complete the structure analysis. When a crystal structure of an analogous protein to a desired protein is known, it can be determined in a molecular substitution method using the atomic coordinate of the known protein. Molecular substitution and structure refinement can be performed using a program such as CNS_SOLVE ver.11.

[0020] The enzyme to be mutated in the present invention is Human Maltase-glucoamylase, *Aspergillus niger* alpha-glucosidase, Human Neutral alpha-glucosidase C, Mouse Lysosomal alpha-glucosidase, Yeast GLU2A, *Aspergillus nidulans* Alpha-glucosidase AgdA, *Aspergillus nidulans* Alpha-glucosidase AgdB, *Mucor javanicus* alpha-glucosidase, *Aspergillus oryzae* alpha-glucosidase, *Mortierella alliacea* alpha-glucosidase, *Schizosaccharomyces pombe* alpha-glucosidase, *Debaryomyces occidentalis* alpha-glucosidase, *Hordeum vulgare* subsp. *vulgare* alpha-glucosidase, *Arabidopsis thaliana* alpha-glucosidase, *Spinacia oleracea* alpha-glucosidase, *Beta vulgaris* alpha-glucosidase and *Solanum tuberosum* alpha-glucosidase. The amino acid sequences of these α -glucosidases, which are registered with public database, are shown below.

Human Maltase-glucoamylase: SEQ ID NO. 1

Aspergillus niger alpha-glucosidase: SEQ ID NO. 2

Human Neutral alpha-glucosidase C: SEQ ID NO. 3

Mouse Lysosomal alpha-glucosidase: SEQ ID NO. 4

Yeast GLU2A: SEQ ID NO. 5

Aspergillus nidulans Alpha-glucosidase AgdA: SEQ ID NO. 6

Aspergillus nidulans Alpha-glucosidase AgdB: SEQ ID NO. 7

Mucor javanicus alpha-glucosidase: SEQ ID NO. 8
Aspergillus oryzae alpha-glucosidase: SEQ ID NO. 9
Mortierella alliacea alpha-glucosidase: SEQ ID NO. 10
Schizosaccharomyces pombe alpha-glucosidase: SEQ ID NO. 11
Debaryomyces occidentalis alpha-glucosidase: SEQ ID NO. 12
Hordeum vulgare subsp. *vulgare* alpha-glucosidase: SEQ ID NO. 13
Arabidopsis thaliana alpha-glucosidase: SEQ ID NO. 14
Spinacia oleracea alpha-glucosidase: SEQ ID NO. 15
Beta vulgaris alpha-glucosidase: SEQ ID NO. 16
Solanum tuberosum alpha-glucosidase: SEQ ID NO. 17

[0021] The amino acid sequence of the α -glucosidase to be mutated is derived from *Aspergillus niger* and has the amino acid sequence of SEQ ID NO. 2 and the amino acid of the above-mentioned (1) is the amino acid at the position 343 of SEQ ID NO. 2, the amino acid of the above-mentioned (2) is the amino acid at the position 452 of SEQ ID NO. 2, the amino acid of the above-mentioned (3) is the amino acid at the position 496 of SEQ ID NO. 2, the amino acid of the above-mentioned (4) is the amino acid at the position 410 of SEQ ID NO. 2, the amino acid of the above-mentioned (5) is the amino acid at the position 495 of SEQ ID NO. 2, the amino acid of the above-mentioned (6) is the amino acid at the position 498 of SEQ ID NO. 2, the amino acid of the above-mentioned (7) is the amino acid at the position 499 of SEQ ID NO. 2, the amino acid of the above-mentioned (8) is the amino acid at the position 531 of SEQ ID NO. 2, the amino acid of the above-mentioned (9) is the amino acid at the position 533 of SEQ ID NO. 2, the amino acid of the above-mentioned (10) is the amino acid at the position 579 of SEQ ID NO. 2, the amino acid of the above-mentioned (11) is the amino acid at the position 585 of SEQ ID NO. 2, the amino acid of the above-mentioned (12) is the amino acid at the position 662 of SEQ ID NO. 2, the amino acid of the above-mentioned (13) is the amino acid at the position 715 of SEQ ID NO. 2, and the amino acid of the above-mentioned (14) is the amino acid at the position 721 of SEQ ID NO. 2.

[0022] A kind of an amino acid after substitution is not particularly limited. Thus, it may be "conservative amino acid substitution" or "non-conservative amino acid substitution". The "conservative amino acid substitution" herein refers to substituting a certain amino acid residue with an amino acid residue having a side chain with the same characteristics. Amino acid residues are classified into some families according to their side chains, such as basic side chains (e.g., lysine, arginine, and histidine), acidic side chains (e.g., asparaginic acid, and glutamic acid), uncharged polar side chains (e.g., glycine, asparagine, glutamine, serine, threonine, tyrosine, and cysteine), nonpolar side chains (e.g., alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, and tryptophan), β -branched side chains (e.g., threonine, valine, and isoleucine), and aromatic side chains (e.g., tyrosine, phenylalanine, tryptophan, and histidine). The conservative amino acid substitution is typically substitution between amino acid residues in the same family.

[0023] When the α -glucosidase derived from *Aspergillus niger* having the amino acid sequence of SEQ ID NO. 2 is an enzyme to be mutated, examples of the amino acids after the

substitution are cysteine, aspartic acid, methionine, histidine, alanine, phenylalanine, glycine, threonine, glutamic acid, valine, glutamine, asparagine or isoleucine for the amino acid of (1); glycine, aspartic acid, glutamic acid or alanine for the amino acid of (2); valine, asparagine, glutamine, isoleucine, arginine, cysteine or threonine for the amino acid of (3); glycine, proline or valine for the amino acid of (5); and leucine or serine for the amino acid of (6).

[0024] Two or more amino acids among the above-mentioned amino acids (1) to (14) may be substituted. As combinations of the amino acids to be substituted, a combination of (1) and (2) and a combination of (1) and (3) can be exemplified. These combinations correspond to the modified enzymes that were obtained in the Examples mentioned below.

[0025] Here, examples of the amino acid sequences of the modified enzymes are shown in SEQ ID Nos. 18 to 42 and 74 to 78. These sequences are the amino acid sequences of the modified enzymes obtained by conducting substitution of one amino acid (on any of the amino acids of (1) to (3), (5) and (6)), substitution of two amino acids (on the amino acids of (1) and (2), the amino acids of (1) and (3), or the amino acids of (2) and (3)) or substitution of three amino acids (on the amino acids of (1), (2) and (3)) on *Aspergillus niger* α -glucosidase. The corresponding relations of the sequence identification numbers and the amino acid substitutions are as follows. In the amino acid sequence of *Aspergillus niger* α -glucosidase (SEQ ID NO. 2), the tryptophan at the position 343 (W343) corresponds to the amino acid of (1), the valine at the position 452 (V452) corresponds to the amino acid of (2), the serine at the position 496 (S496) corresponds to the amino acid of (3), the isoleucine at the position 410 (I410) corresponds to the amino acid of (4), the valine at the position 499 (V499) corresponds to the amino acid of (7), the glutamic acid at the position 531 (E531) corresponds to the amino acid of (8), the phenylalanine at the position 533 (F533) corresponds to the amino acid of (9), the histidine at the position 579 (H579) corresponds to the amino acid of (10), the asparagine at the position 585 (N585) corresponds to the amino acid of (11), the tyrosine at the position 662 (Y662) corresponds to the amino acid of (12), the tyrosine at the position 715 (Y715) corresponds to the amino acid of (13), and the leucine at the position 721 (L721) corresponds to the amino acid of (14). Furthermore, in the amino acid sequence of *Aspergillus nidulans* α -glucosidase AgdB (SEQ ID NO. 7), the tyrosine at the position 296 (Y296) corresponds to the amino acid of (1), the asparagine at the position 456 (N456) corresponds to the amino acid of (3), the methionine at the position 363 (M363) corresponds to the amino acid of (4), the alanine at the position 455 (A455) corresponds to the amino acid of (5), the tyrosine at the position 458 (Y458) corresponds to the amino acid of (6), the asparagine at the position 459 (N459) corresponds to the amino acid of (7), the aspartic acid at the position 488 (D488) corresponds to the amino acid of (8), the leucine at the position 490 (L490) corresponds to the amino acid of (9), the arginine at the position 565 (R565) corresponds to the amino acid of (10), the glutamine at the position 571 (Q571) corresponds to the amino acid of (11), the isoleucine at the position 646 (I646) corresponds to the amino acid of (12), the phenylalanine at the position 700 (F700) corresponds to the amino acid of (13), and the isoleucine at the position 706 (I706) corresponds to the amino acid of (14).

Amino acid sequence: substitution of amino acid

[0026]

1. A. SEQ ID NO. 18: W343C
 2. B. SEQ ID NO. 19: W343D
 3. C. SEQ ID NO. 20: W343M
 4. D. SEQ ID NO. 21: W343H
 5. E. SEQ ID NO. 22: W343A
 6. F. SEQ ID NO. 23: W343F
 7. G. SEQ ID NO. 24: W343G
 8. H. SEQ ID NO. 25: W343T
 9. I. SEQ ID NO. 26: W343E
 10. J. SEQ ID NO. 27: W343V
 11. K. SEQ ID NO. 28: W343Q
 12. L. SEQ ID NO. 29: W343N
 13. M. SEQ ID NO. 30: W343I
 14. N. SEQ ID NO. 31: V452G
 15. O. SEQ ID NO. 32: V452D
 16. P. SEQ ID NO. 33: V452E
 17. Q. SEQ ID NO. 34: S496V
 18. R. SEQ ID NO. 35: S496N
 19. S. SEQ ID NO. 36: S496Q
 20. T. SEQ ID NO. 37: W343D and V452A
 21. U. SEQ ID NO. 38: W343D and V452G
 22. V. SEQ ID NO. 39: W343D and S496I
 23. W. SEQ ID NO. 40: W343D and S496R
 24. X. SEQ ID NO. 41: W343M and S496C
 25. Y. SEQ ID NO. 42: W343M and S496T
1. a. SEQ ID NO. 74: S495G
 2. b. SEQ ID NO. 75: S495P
 3. c. SEQ ID NO. 76: S495V
 4. d. SEQ ID NO. 77: C498L
 5. e. SEQ ID NO. 78: C498S

[0027] In light of the experimental results shown in the following Examples (confirmation of the effect of amino acid substitution), the modified α -glucosidases of A to C, O and Q to S are highly useful in that they are specifically excellent in transglycosylation activity. Furthermore, V and W are highly useful in that they have a quite low hydrolysis activity. On the other hand, U, X and Y are highly useful in that they have a quite low decomposition activity against α -1,6 glucosidic linkages. Y is highly useful also in that it is excellent in transglycosylation activity. Furthermore, a to c are characterized in that they show a transglycosylation activity to form α -1,6 glucosidic linkages. d and e are excellent in transglycosylation activity to form α -1,4

glucosidic linkages.

[0028] Generally, when a part of an amino acid sequence of a certain protein is modified, the modified protein may have the equal function to that of the protein before the modification. That is to say, the modification of the amino acid sequence may not have a substantial effect on the function of the protein, so that the function of the protein may be maintained before and after the modification. When this technical common sense is considered, an enzyme that has a recognizable slight difference in the amino acid sequence (provided that the difference occurs in sites other than the sites in which the above substitutions have been made) and has No substantially recognizable difference in the function can be regarded as an enzyme that is substantially the same as the above modified enzyme in comparison with the modified enzyme comprising the amino acid sequence in which one or more amino acids selected from the group consisting of the above (1) to (14) have been substituted with another amino acid. The term "slight difference in the amino acid sequence" as used herein typically means that the amino acid sequence is mutated (changed) by the deletion or substitution of one to several amino acids (the upper limit: e.g. 3, 5, 7, or 10 amino acids) constituting the amino acid sequence, or by the addition, insertion, or combination thereof, of one to several amino acids (the upper limit: e.g. 3, 5, 7, or 10 amino acids). The identity (%) of between the amino acid sequence in the "substantially the same enzyme" and the amino acid sequence of the above modified enzyme as a standard is preferably 90% or more, more preferably 95% or more, yet more preferably 98% or more, and most preferably 99% or more. In addition, the difference in the amino acid sequence may occur in a plurality of positions. The "slight difference in the amino acid sequences" is preferably generated by a conservative amino acid substitution.

(Nucleic acid coding for modified α glucosidase, etc.)

[0029] The second aspect of the present invention provides a nucleic acid relating to the modified enzyme of the invention. That is, the present invention relates to a gene coding for the modified enzyme, and the application provides a nucleic acid that can be used as a probe for identifying a nucleic acid coding for the modified enzyme, and a nucleic acid that can be used as a primer for amplifying or mutating a nucleic acid coding for the modified enzyme.

[0030] The gene coding for a modified enzyme is typically used in preparation of the modified enzyme. According to a genetic engineering procedure using the gene coding for a modified enzyme, a modified enzyme in a more homogeneous state can be obtained. Further, the method can be a preferable method also in the case of preparing a large amount of a modified enzyme. Note that uses of the gene coding for a modified enzyme are not limited to preparation of a modified enzyme. For example, the nucleic acid can also be used as a tool for an experiment intended for clarification of action mechanisms of a modified enzyme or a tool for designing or preparing a further mutant of an enzyme.

[0031] The "gene coding for a modified enzyme" herein refers to a nucleic acid capable of obtaining the modified enzyme when it is expressed, and includes, as a matter of course of a

nucleic acid having a nucleotide sequence corresponding to the amino acid sequence of the modified enzyme, also a nucleic acid obtained by adding a sequence that does not code for an amino acid sequence to such a nucleic acid. Degeneracy of a codon is also considered.

[0032] Examples of sequences (nucleotide sequences) of genes coding for the modified enzyme are shown in SEQ ID Nos.: 43 to 67 and 79 to 83. These sequences are genes coding for the modified enzyme obtained by specific amino acids substitution to *Aspergillus niger* α glucosidase. The relationship between a SEQ ID NO and an amino acid substitution is as follows.

nucleotide sequence : amino acid substitution

1. A. SEQ ID NO 43 : W343C
 2. B. SEQ ID NO 44 : W343D
 3. C. SEQ ID NO 45 : W343M
 4. D. SEQ ID NO 46 : W343H
 5. E. SEQ ID NO 47 : W343A
 6. F. SEQ ID NO 48 : W343F
 7. G. SEQ ID NO 49 : W343G
 8. H. SEQ ID NO 50 : W343T
 9. I. SEQ ID NO 51 : W343E
 10. J. SEQ ID NO 52 : W343V
 11. K. SEQ ID NO 53 : W343Q
 12. L. SEQ ID NO 54 : W343N
 13. M. SEQ ID NO 55 : W343I
 14. N. SEQ ID NO 56 : V452G
 15. O. SEQ ID NO 57 : V452D
 16. P. SEQ ID NO 58 : V452E
 17. Q. SEQ ID NO 59 : S496V
 18. R. SEQ ID NO 60 : S496N
 19. S. SEQ ID NO 61 : S496Q
 20. T. SEQ ID NO 62 : W343D and V452A
 21. U. SEQ ID NO 63 : W343D and V452G
 22. V. SEQ ID NO 64 : W343D and S496I
 23. W. SEQ ID NO 65 : W343D and S496R
 24. X. SEQ ID NO 66 : W343M and S496C
 25. Y. SEQ ID NO 67 : W343M and S496T
1. a. SEQ ID NO 79 : S495G
 2. b. SEQ ID NO 80 : S495P
 3. c. SEQ ID NO 81 : S495V
 4. d. SEQ ID NO 82 : C498L
 5. e. SEQ ID NO 83 : C498S

[0033] The nucleic acid of the present invention can be prepared in an isolated state by use of

a standard genetic engineering technique, molecular biological technique, biochemical technique, and the like in reference to the present specification or the sequence information disclosed in the appended sequence listing.

[0034] Another embodiment of the present invention provides a nucleic acid different in a nucleotide sequence in a part (hereinafter also referred to as a "homologous nucleic acid", and a nucleotide sequence defining a homologous nucleic acid is also referred to as a "homologous nucleotide sequence") as compared to the nucleotide sequence of the gene coding for the modified enzyme of the invention, although functions of a protein coded by the nucleic acid are equal. An example of the homologous nucleic acid includes a DNA composed of a nucleotide sequence containing substitution, deletion, insertion, addition or inversion of 1 to several nucleotides on the basis of the nucleotide sequence of the nucleic acid coding for the modified enzyme of the present invention and coding for a protein having enzyme activity characteristic to the modified enzyme (i.e. glycosyltransferase activity). Substitution or deletion of bases may occur in a plurality of sites. The "plurality" herein depends on positions or kinds of amino acid residues in a conformation of a protein coded by the nucleic acid but means, for example, 2 to 40 bases, preferably 2 to 20 bases, and more preferably 2 to 10 bases.

[0035] Such a homologous nucleic acid as described above can be obtained by, for example, a restriction enzyme treatment, a treatment with exonuclease, DNA ligase, etc., and introduction of mutation by a site-directed mutagenesis method (Molecular Cloning, Third Edition, Chapter 13, Cold Spring Harbor Laboratory Press, New York), and a random mutagenesis method (Molecular Cloning, Third Edition, Chapter 13, Cold Spring Harbor Laboratory Press, New York). The homologous nucleic acid can be obtained also in other methods such as exposure to ultraviolet radiation.

[0036] The present application also discloses a nucleic acid having the complementary nucleotide sequence to the nucleotide sequence of the gene coding for the modified enzyme of the invention. Furthermore, a nucleic acid having a nucleotide sequence with an identity of at least about 60%, 70%, 80%, 90%, 95%, 99%, or 99.9% to the nucleotide sequence of the gene coding for the modified enzyme of the invention or the complementary nucleotide sequence is described.

[0037] The present application further discloses a nucleic acid having a nucleotide sequence hybridizing to the complementary nucleotide sequence to the nucleotide sequence of the gene coding for the modified enzyme of the invention or its homologous nucleotide sequence under stringent conditions. The "stringent conditions" herein refer to conditions wherein a so-called specific hybrid is formed and a nonspecific hybrid is not formed. Such stringent conditions are known by a person skilled in the art and can be set in reference to, for example, Molecular Cloning (Third Edition, Cold Spring Harbor Laboratory Press, New York) and Current protocols in molecular biology (edited by Frederick M. Ausubel et al., 1987). Examples of the stringent conditions include conditions of using a hybridization liquid (50% formamide, 10 × SSC (0.15 M NaCl, 15 mM sodium citrate, pH 7.0), a 5 × Denhardt solution, 1% SDS, 10% dextran sulfate, 10 µg/ml of modified salmon sperm DNA, and a 50 mM phosphate buffer (pH7.5)) and

incubating at about 42°C to about 50°C, thereafter washing with 0.1 × SSC and 0.1% SDS at about 65°C to about 70°C. Examples of more preferable stringent conditions include conditions of using 50% formamide, 5 × SSC (0.15 M NaCl, 15 mM sodium citrate, pH 7.0), a 1 × Denhardt solution, 1% SDS, 10% dextran sulfate, 10 µg/ml of modified salmon sperm DNA, and a 50 mM phosphate buffer (pH 7.5) as a hybridization liquid.

[0038] Furthermore, a nucleic acid (nucleic acid fragment) having a part of the nucleotide sequence of the gene coding for the modified enzyme of the invention or the complementary nucleotide sequence is described. Such a nucleic acid fragment can be used in detection, identification, and/or amplification of a nucleic acid having the nucleotide sequence of the gene coding for the modified enzyme of the present invention. For example, the nucleic acid fragment is designed so as to at least contain a part being hybridized to a sequential nucleotide moiety (for example, about 10 to about 100 nucleotides length, preferably about 20 to about 100 bases length, more preferably about 30 to about 100 bases length) in the nucleotide sequence of the gene coding for the modified enzyme of the invention. When used as a probe, the nucleic acid fragment can be labeled. Examples such as fluorescent substances, enzymes, and radioactive isotopes can be used for the labeling.

[0039] Another aspect of the present invention relates to a recombinant DNA containing the gene of the present invention (the gene coding for a modified enzyme). The recombinant DNA of the invention is provided in, for example, a form of a vector. The term "vector" in the present specification refers to a nucleic acid molecule that can transfer a nucleic acid inserted in the vector to a target such as a cell.

[0040] A suitable vector is selected according to its intended use (cloning, expression of a protein) and in consideration of a kind of a host cell. Examples include a M13 phage or an altered form thereof, a λ phage or an altered form thereof, and pBR322 or an altered form thereof (e.g., pB325, pAT153, pUC8), etc. as a vector having *Escherichia coli* as a host, pYepSec1, pMFa, and pYES2 as a vector having a yeast as a host, pAc, pVL, etc. as a vector having an insect cell as a host, and pCDM8, pMT2PC, etc. as a vector having a mammal cell as a host.

[0041] The vector is preferably an expression vector. The "expression vector" refers to a vector capable of introducing a nucleic acid inserted in the expression vector into a target cell (host cell) and expressing it in the cell. The expression vector generally contains a promoter sequence necessary for expression of a nucleic acid inserted, an enhancer sequence for promoting expression, and the like. An expression vector containing a selective marker can also be used. When such an expression vector is used, presence or absence (and its degree) of introduction of the expression vector can be confirmed using a selective marker.

[0042] Insertion of the nucleic acid of the present invention into the vector, insertion of a selective marker gene (if necessary), insertion of a promoter (if necessary), and the like can be performed by using a standard recombinant DNA technique (for example, a known method of using a restriction enzyme and a DNA ligase, which can be referred in Molecular Cloning, Third

Edition, 1.84, Cold Spring Harbor Laboratory Press, New York).

[0043] For the host cell, microorganisms such as *Escherichia coli* and budding yeasts (*Saccharomyces cerevisiae*) are preferably used from the viewpoint of easiness of handling, and host cells capable of duplicating a recombinant DNA and expressing a gene of a modified enzyme can be used. Examples of *Escherichia coli* include *Escherichia coli* BL21(DE3)pLysS in the case of using a T7 promoter, and *Escherichia coli* JM109 in other cases. Examples of budding yeasts include budding yeast SHY2, AH22, or INVSc1 (Invitrogen Ltd.).

[0044] Another aspect of the present invention relates to a microorganism having the recombinant DNA of the invention (that is, a transformant). The microorganism of the invention can be obtained by transfection or transformation using the vector of the invention described above. The transfection or transformation can be performed in, for example, the calcium chloride method (J. Mol. Biol., 53, 159 (1970)), the Hanahan method (J. Mol. Biol., 166, 557 (1983)), the SEM method (Gene, 96, 23 (1990)), a method by Chung, et al. (Proc. Natl. Acad. Sci. U.S.A. 86, 2172 (1989)), the calcium phosphate coprecipitation method, the electroporation method (Potter, H. et al., Proc. Natl. Acad. Sci. U.S.A. 81, 7161-7165 (1984)), and the lipofectin method (Felgner, P.L. et al., Proc. Natl. Acad. Sci. U.S.A. 84, 7413-7417 (1984)). Note that the microorganism of the present invention can be used in producing the modified enzyme of the present invention (see the section of the preparation method of modified α glucosidase described later).

(Enzyme agent containing modified α -glucosidase)

[0045] The modified enzyme of the present invention is provided, for example, in the form of an enzyme agent. The enzyme agent may contain an excipient, a buffer agent, a suspending agent, a stabilizer, a preservative, an antiseptic, saline and the like besides the active ingredient (the modified enzyme of the present invention). As the excipient, starch, dextrin, maltose, trehalose, lactose, D-glucose, sorbitol, D-mannitol, white soft sugar, glycerol and the like can be used. As the buffer agent, phosphates, citrates, acetates and the like can be used. As the stabilizer, propylene glycol, ascorbic acid and the like can be used. As the preservative, phenol, benzalkonium chloride, benzyl alcohol, chlorobutanol, methylparaben and the like can be used. As the antiseptic, ethanol, benzalkonium chloride, paraoxybenzoic acid, chlorobutanol and the like can be used.

(Use of modified α -glucosidase)

[0046] A further aspect of the present invention relates to use of the modified enzyme. As one of the use, a method for producing an oligosaccharide is provided. In the first embodiment of the method for producing an oligosaccharide of the present invention, in order to utilize the feature of the modified enzyme of the present invention of high specificity against α -1,4

glucosidic linkages, an oligosaccharide or polysaccharide of di- or more saccharides having α -1,4 glucosidic linkage(s) is used as a substrate, and the modified enzyme of the present invention is reacted with the substrate. In this embodiment, enzymes having high specificity against α -1,4 glucosidic linkages such as modified enzymes W343M, W343M/S496T, C498L and C498S shown in the following Examples, and the like are used. Examples of the substrate are maltose, maltotriose, panose, pullulan, maltotetraose, maltopentaose, maltohexaose, maltoheptaose, maltooctaose, dextrin, starches (potato starch, sweet potato starch, corn starch, wheat starch, tapioca starch and the like), and the like. A mixture of two or more oligosaccharides or polysaccharides may be the substrate. According to the production method of the present invention, an oligosaccharide having low-branched chains can be produced in a specific and efficient manner. The reaction conditions may follow those generally adopted in the generation of an oligosaccharide using α -glucosidase.

[0047] In the second embodiment of the method for producing an oligosaccharide of the present invention, modified enzymes that show a transglycosylation activity to form α -1,6 glucosidic linkages (for example, S495G, S495P and S495V shown in the following Examples) are used. Examples of the substrate in this case are isomaltose, isomaltotriose, panose, isopanose, starches (potato starch, sweet potato starch, corn starch, wheat starch, tapioca starch and the like). According to this embodiment, typically, an oligosaccharide having much branched chains can be produced in a specific and efficient manner.

[0048] In order to increase the generation amount of the intended oligosaccharide (an oligosaccharide having low-branched chains in the case of the first embodiment, or typically an oligosaccharide having much branched chains in the case of the second embodiment), a wild type enzyme may be used in addition to the modified enzyme. The wild type enzyme is not specifically limited as long as it is suitable for the generation of the intended oligosaccharide. For example, a wild type enzyme that corresponds to the modified enzyme to be used (i.e., an enzyme that has undergone modification for obtaining the modified enzyme) can be adopted. In contrast to this example, a modified enzyme and wild type enzyme whose origins are different can be used in combination. As an example, an enzyme obtained by modifying *Aspergillus niger* α -glucosidase (modified enzyme) and *Aspergillus nidulans* wild type α -glucosidase AgdB are used in combination.

[0049] Here, as shown in the following Examples, it has become clear that an oligosaccharide can be formed from a substrate having α -1,4 glucosidic linkages when a modified enzyme that shows a transglycosylation activity to form α -1,6 glucosidic linkages and a wild type enzyme in combination. Therefore, in a further embodiment of the present invention, a modified enzyme that shows a transglycosylation activity to form α -1,6 glucosidic linkages (for example, S495G, S495P and S495V shown in the following Examples) is reacted in combination with a wild type enzyme to give an oligosaccharide.

[0050] Due to the transglycosylation activity of the modified enzyme of the present invention, an effect of preventing aging of starches, an effect of improving flavors of foods, an effect of regulating the intestines and the like can be expected. Therefore, examples of the use of the

modified enzyme of the present invention may include prevention of the aging of starches in foods, improvement of the flavors of foods and regulation of the function of the intestines. Assuming application to these uses, the present invention provides compositions containing the modified enzyme (a pharmaceutical composition, a quasi-drug composition, a cosmetic composition, a food composition or a feed composition) as a further aspect.

[0051] The pharmaceutical composition or quasi-drug composition of the present invention can be formulated according to a conventional method. In the case of the formulation, other components that are acceptable in formulation (for example, a carrier, an excipient, a disintegrating agent, a buffer agent, an emulsifying agent, a suspending agent, a soothing agent, a stabilizer, a preservative, an antiseptic, saline and the like) can be incorporated. As the excipient, lactose, starch, sorbitol, D-mannitol, white soft sugar and the like can be used. As the disintegrating agent, starch, carboxymethyl cellulose, calcium carbonate and the like can be used. As the buffer agent, phosphates, citrates, acetates and the like can be used. As the emulsifier, gum arabic, sodium alginate, tragacanth and the like can be used. As the suspending agent, glycerin monostearate, aluminum monostearate, methyl cellulose, carboxymethyl cellulose, hydroxymethyl cellulose, sodium lauryl sulfate and the like can be used. As the soothing agent, benzyl alcohol, chlorobutanol, sorbitol and the like can be used. As the stabilizer, propylene glycol, ascorbic acid and the like can be used. As the preservative, phenol, benzalkonium chloride, benzyl alcohol, chlorobutanol, methylparaben and the like can be used. As the antiseptic, benzalkonium chloride, paraoxybenzoic acid, chlorobutanol and the like can be used.

[0052] The dosage form in the case of the formulation is also not specifically limited, and the pharmaceutical composition or quasi-drug composition of the present invention can be provided, for example, as a tablet, a powder, a fine granule, a granular agent, a capsule agent, a syrup agent, an injection agent, an external preparation and a suppository, and the like.

[0053] The pharmaceutical composition of the present invention contains an active ingredient (modified enzyme) in an amount necessary to obtain the expected therapeutic effect or prophylactic effect (i.e., a therapeutically effective amount). Similarly, the quasi-drug composition of the present invention contains an active ingredient in an amount necessary to obtain the expected improvement effect, prophylactic effect and the like. Although the amount of the active ingredient contained in the pharmaceutical composition or quasi-drug composition of the present invention generally differs depending on the dosage form or form, the amount of the active ingredient is set within the range of, for example, about 0.1% by weight to about 95% by weight so that a desired dose can be achieved.

[0054] The pharmaceutical composition or quasi-drug composition of the present invention is designed to be applied to a subject in an oral or parenteral manner (intravenous, intraarterial, subdermal, intramuscular, or interperitoneal injection, transdermal, pernasal, transmucosal, application, or the like) depending on the dosage form and form thereof. The "subject" as used herein is not specifically limited, and includes humans and mammals other than humans. (Pet animals, farm animals, and experimental animals are included. Specific examples are mice,

rats, guinea pigs, hamsters, monkeys, cows, pigs, goats, sheep, dogs, cats, chickens, quails and the like.) In a preferable embodiment, the subject to be applied is a human.

[0055] The doses and use amounts of the pharmaceutical composition and quasi-drug composition of the present invention are preset so that expected effects would be obtained. In the setting of an effective dose, the symptom, age, sex, body weight and the like of a subject to be applied are considered. Any person skilled in the art can set a suitable dose with consideration for these matters. As an administration schedule, for example, once to several times a day, once every second day, or once every third day can be adopted. In the preparation of the administration schedule, the symptom of the subject, the duration of the effect of the active ingredient, and the like can be considered.

[0056] The cosmetic composition of the present invention can be obtained by incorporating the modified enzyme, and components and substrates that are generally used in cosmetics (for example, various fats and oils, mineral oils, vaseline, squalane, lanolin, beeswax, modified alcohols, dextrin palmitate, glycerin, fatty acid esters of glycerin, ethylene glycol, paraben, camphor, menthol, various vitamins, zinc oxide, titanium oxide, benzoic acid, edetic acid, chamomile oil, carrageenan, chitin powder, chitosan, perfume materials, coloring materials and the like). As the forms of the cosmetic composition, an emulsion liquid for face or body, a skin lotion, a cream, a lotion, an essence, an oil, a pack, a sheet, a cleanser and the like can be exemplified. The addition amount of the modified enzyme in the cosmetic composition is not specifically limited. For example, the modified enzyme can be added so as to be 0.01% by weight to 10% by weight.

[0057] On the other hand, examples of the "food composition" in the present invention may include general foods (cooked rice, bread, cereal, vegetables, edible meat, various processed foods, sweets, milk, soft drink, alcohol beverages and the like), nutritional supplements (supplements, nutrition-supplement drinks and the like) and food additives. In the cases of the nutritional supplement or food additive, it can be provided in the form of a powder, a granule, a tablet, a paste, a liquid or the like.

[0058] Examples of the "feed composition" of the present invention are pet foods (feeds for dogs, cats, birds, fishes, reptiles, amphibians, rodents and the like) and feedstuffs (feeds for farm animals, poultries, cultured fishes and the like).

(Method for designing modified α -glucosidase)

[0059] A further aspect of the present invention relates to a method of designing the modified enzyme as characterized in the claims. In the designing method of the present invention, the following steps (i) and (ii) are carried out.

[0060] Step (i): one or two or more amino acid(s) selected from the group consisting of the following (1) to (14) is/are identified in the amino acid sequence of α -glucosidase as an

enzyme to be mutated:

1. (1) an amino acid corresponding to the amino acid at the position 385 of the amino acid sequence of SEQ ID NO. 1
2. (2) an amino acid corresponding to the amino acid at the position 491 of the amino acid sequence of SEQ ID NO. 1
3. (3) an amino acid corresponding to the amino acid at the position 535 of the amino acid sequence of SEQ ID NO. 1
4. (4) an amino acid corresponding to the amino acid at the position 450 of the amino acid sequence of SEQ ID NO. 1
5. (5) an amino acid corresponding to the amino acid at the position 534 of the amino acid sequence of SEQ ID NO. 1
6. (6) an amino acid corresponding to the amino acid at the position 537 of the amino acid sequence of SEQ ID NO. 1
7. (7) an amino acid corresponding to the amino acid at the position 538 of the amino acid sequence of SEQ ID NO. 1
8. (8) an amino acid corresponding to the amino acid at the position 554 of the amino acid sequence of SEQ ID NO. 1
9. (9) an amino acid corresponding to the amino acid at the position 556 of the amino acid sequence of SEQ ID NO. 1
10. (10) an amino acid corresponding to the amino acid at the position 579 of the amino acid sequence of SEQ ID NO. 2
11. (11) an amino acid corresponding to the amino acid at the position 585 of the amino acid sequence of SEQ ID NO. 2
12. (12) an amino acid corresponding to the amino acid at the position 630 of the amino acid sequence of SEQ ID NO. 1
13. (13) an amino acid corresponding to the amino acid at the position 683 of the amino acid sequence of SEQ ID NO. 1
14. (14) an amino acid corresponding to the amino acid at the position 689 of the amino acid sequence of SEQ ID NO. 1

[0061] The amino acids to be substituted (1) to (14) are amino acids that have been identified as amino acids that are important for the characteristics of enzymes. Therefore, it can be highly expected that change in the characteristics of α -glucosidase is generated if these amino acids are substituted. The characteristics for which change is especially expected are a transglycosylation activity and a hydrolysis activity. Thus, the designing method of the present invention is used for designing an enzyme in which the balance of these two activities has been changed via decreasing or eliminating a hydrolysis activity and increasing a transglycosylation activity.

[0062] The enzyme to be mutated in the designing method of the invention is α -glucosidase. The enzyme to be mutated is typically a wild type enzyme (an enzyme found in nature). However, this does not interfere use of an enzyme that has already undergone any mutation or

modification as an enzyme to be mutated. Examples of the enzyme to be mutated are Human Maltase-glucoamylase, *Aspergillus niger* alpha-glucosidase, Human Neutral alpha-glucosidase C, Mouse Lysosomal alpha-glucosidase, Yeast GLU2A, *Aspergillus nidulans* Alpha-glucosidase AgdA, *Aspergillus nidulans* Alpha-glucosidase AgdB, *Mucor javanicus* alpha-glucosidase, *Aspergillus oryzae* alpha-glucosidase, *Mortierella alliacea* alpha-glucosidase, *Schizosaccharomyces pombe* alpha-glucosidase, *Debaryomyces occidentalis* alpha-glucosidase, *Hordeum vulgare* subsp. *vulgare* alpha-glucosidase, *Arabidopsis thaliana* alpha-glucosidase, *Spinacia oleracea* alpha-glucosidase, *Beta vulgaris* alpha-glucosidase and *Solanum tuberosum* alpha-glucosidase. As mentioned above, the amino acid sequences of these α -glucosidases are registered with public database (SEQ ID Nos. 1 to 17). In a preferable embodiment, an enzyme consisting of any of these amino acid sequences is an enzyme to be mutated.

[0063] In the present invention, the following step (ii) is conducted after the step (i).

[0064] Step (ii): an amino acid sequence in which the amino acid sequence(s) identified in the step (i) has/have been substituted by other amino acid is constructed based on the amino acid sequence of the enzyme to be mutated.

[0065] The kind(s) of the amino acid(s) after the substitution is/are not specifically limited. Therefore, either conservative amino acid substitution or non-conservative amino acid substitution is acceptable.

Examples

(Preparation method of modified α glucosidase)

[0066] A further aspect of the present invention relates to a preparation method of a modified enzyme. In one embodiment of the preparation method of a modified enzyme of the present invention, the modified enzyme that the present inventors succeeded in obtaining is prepared in a genetic engineering technique. In the case of this embodiment, a nucleic acid coding for any one of the amino acid sequences of SEQ ID Nos.: 18 to 42 and 74 to 78, is prepared (step (I)). Herein, "a nucleic acid coding for a specific amino acid sequence" is a nucleic acid capable of obtaining a polypeptide having the amino acid sequence in the case of being expressed, and as a matter of course of a nucleic acid having a nucleotide sequence corresponding to the amino acid sequence, may be a nucleic acid added with an extra sequence (may be a sequence coding for an amino acid sequence or a sequence not coding for an amino acid sequence). Degeneracy of a codon is also considered. "A nucleic acid coding for any one of the amino acid sequences of SEQ ID Nos.: 18 to 42 and 74 to 78" can be prepared into a state of being isolated by using a standard genetic engineering technique, molecular biological technique, biochemical technique, and the like in reference to sequence information disclosed

in the present specification or the appended sequence listing. Herein, all of the amino acid sequences of SEQ ID Nos.: 18 to 42 and 74 to 78 are obtained by mutation to the amino acid sequence of the *Aspergillus niger*-derived α glucosidase. Therefore, a nucleic acid (gene) coding for any one of the amino acid sequences of SEQ ID Nos.: 7 to 10 can be obtained also by adding necessary mutation to the gene coding for the *Aspergillus niger*-derived α glucosidase (SEQ ID NO: 73). A large number of methods for site-directed mutagenesis have been known in the present technical field (for example, see Molecular Cloning, Third Edition, Cold Spring Harbor Laboratory Press, New York), and among those methods, a suitable method can be selected to be used. A method of saturation mutagenesis can be adopted as the method of site-directed mutagenesis. The method of saturation mutagenesis is a "semi-rational, semi-random" technique of assuming a position which relates to a desired function based on a conformation of a protein and introducing amino acid saturation (J. Mol. Biol. 331,585-592 (2003)). For example, use of a kit such as KOD-Plus-Mutagenesis Kit (TOYOBO CO., LTD.), Quick change (Stratagene Corporation) and Overlap extension PCR (Nucleic Acid Res. 16, 7351-7367 (1988)) makes it possible to introduce position specific amino acid saturation. A Taq polymerase and the like can be used for a DNA polymerase used in PCR. Provided that a DNA polymerase having high precision such as KOD-PLUS-(TOYOBO CO., LTD.) or Pfu turbo (Stratagene Corporation) is preferably used.

[0067] In another embodiment of the present invention, a modified enzyme is prepared based on an amino acid sequence that is designed by the designing method of the present invention. In the case of this embodiment, a nucleic acid coding for an amino acid sequence constructed by the designing method of the present invention is prepared in the step (i). For example, based on the amino acid sequence constructed by the designing method of the present invention, necessary mutation (that is, substitution of an amino acid in a specific position in a protein that is an expressed product) is added to a gene coding for a modified enzyme and a nucleic acid (gene) coding for the modified enzyme is obtained.

[0068] Following the step (I), the prepared nucleic acid is expressed (step (II)). For example, firstly, an expression vector inserted with the above described nucleic acid is prepared and a host cell is transformed using this constructed vector. The "expression vector" refers to a vector that can introduce a nucleic acid inserted therein into a desired cell (host cell) and is capable of being expressed in the cell. The expression vector generally contains a promoter sequence that is necessary for expression of an inserted nucleic acid, an enhancer sequence that promotes expression, and the like. An expression vector containing a selection marker can also be used. When such an expression vector is used, presence or absence (and its degree) of the expression vector can be confirmed by using a selection marker.

[0069] Then, a transformant is cultured under the condition of producing a modified enzyme that is an expressed product. Culture of the transformant may follow a general method. An assimilable carbon compound may be used as a carbon source used for a medium, and examples such as glucose, sucrose, lactose, maltose, molasses, and pyruvic acid are used. An available nitrogen compound may be used as a nitrogen source, and examples such as peptone, meat extract, yeast extract, casein hydrolysate, and soybean bran alkali extract are

used. Other than those substances, phosphate, carbonate, sulfate, salts of magnesium, calcium, potassium, iron, manganese and zinc, specific amino acids, specific vitamins, and the like are used according to necessity.

[0070] On the other hand, a culture temperature can be set within the range from 30 to 40°C (preferably at around 37°C). A culture time can be set by considering growing characteristics of a transformant to be cultured and production characteristics of a mutant-type enzyme. A pH of a medium is set within the range wherein a transformant grows and an enzyme is produced. The pH of a medium is preferably set at about 6.0 to 9.0 (preferably at around pH 7.0).

[0071] Subsequently, the expressed product (modified enzyme) is recovered (step (III)). A culture liquid containing fungus bodies after culture may be used as an enzyme solution directly or after undergoing condensation, removal of impurities, or the like, but the expressed product is generally once recovered from the culture liquid or fungus bodies. When the expressed product is a secretion type protein, it can be recovered from the culture liquid, and in other cases, the expressed product can be recovered from cells. In the case of recovering from the culture liquid, for example, an undissolved substance is removed by filtration and centrifugation on a culture supernatant, and then, a purified product of a modified enzyme can be obtained by separation and purification in combination of vacuum concentration, membrane concentration, salting out using ammonium sulfate or sodium sulfate, fractional precipitation by methanol, ethanol, or acetone, dialysis, heating treatment, isoelectric treatment, various kinds of chromatography such as gel filtration, adsorption chromatography, ion exchange chromatography, and affinity chromatography (for example, gel filtration with Sephadex gel (GE Healthcare Life Sciences), etc., DEAE sepharose CL-6B (GE Healthcare Life Sciences), octyl sepharose CL-6B (GE Healthcare Life Sciences), CM sepharose CL-6B (GE Healthcare Life Sciences)). On the other hand, in the case of recovering the expressed product from cells, a culture liquid is subjected to filtration, centrifugation, or the like, to thus obtain the cells, then the cells are crushed by a mechanical method such as a pressure treatment and an ultrasonic treatment, or an enzymatic method with a lysozyme or the like, thereafter carrying out separation and purification in the same manner as described above, and a purified product of a modified enzyme can be thus obtained.

[0072] The purified enzyme obtained as described above can be provided after being powdered, for example, by freeze dry, vacuum dry, or spray dry. In this time, the purified enzyme may be previously dissolved in a phosphoric acid buffer solution, a triethanol amine buffer solution, a tris-hydrochloric acid buffer solution, or a GOOD buffer solution. Preferably, a phosphoric acid buffer solution and a triethanol amine buffer solution can be used. Note that, for the GOOD buffer solution herein, PIPES, MES or MOPS is exemplified.

[0073] Generally, genetic expression and recovery of the expressed product (modified enzyme) are carried out using an appropriate host-vector system as described above, but a cell-free synthesis system may also be employed. Herein, the "cell-free synthesis system (cell-free transcription system, cell-free transcription/translation system)" refers to in vitro synthesis of mRNA or a protein from a nucleic acid (DNA or mRNA) being a template, which codes for

the mRNA or the protein, using a ribosome, a transcription/translation factor derived from living cells (alternately, obtained in a genetic engineering technique) or the like, not using living cells. In the cell-free synthesis system, a cell extraction obtained from a cell disruptor that is purified according to necessity is generally used. The cell extraction generally includes ribosome necessary for protein synthesis and various factors such as an initiation factor, and various enzymes such as tRNA. When a protein is synthesized, this cell extraction is added with other substances necessary for protein synthesis, such as various amino acids, energy sources (e.g., ATP and GTP), and creatine phosphate. As a matter of course, ribosome and various factors and/or various enzymes, and the like, which are separately prepared, may be supplemented if necessary in the protein synthesis.

[0074] Development of a transcription/translation system reconstructing various molecules (factors) necessary for protein synthesis has also been reported (Shimizu, Y. et al.: Nature Biotech., 19, 751-755, 2001). In this synthesis system, a gene of 31 kinds of factors composed of 3 kinds of initiation factors constituting a protein synthesis system of bacteria, 3 kinds of elongation factors, 4 kinds of factors associated with termination, 20 kinds of aminoacyl tRNA synthesis enzymes that make each amino acid combine with tRNA, and a methionyl tRNA formyl transfer enzyme is amplified from an *Escherichia coli* genome, and a protein synthesis system is reconstructed in vitro using them. Such a reconstructed synthesis system may be used in the present invention.

[0075] The term "cell-free transcription/translation system" is interchangeably used with a cell-free protein synthesis system, an in vitro translation system or an in vitro transcription/translation system. In the in vitro translation system, RNA is used as a template to synthesize a protein. Any of RNA, mRNA, an in vitro transcribed product, or the like is used as the template RNA. On the other hand, in the in vitro transcription/translation system, DNA is used as a template. The template DNA should include in a ribosome bonding region, and preferably contains a suitable terminator sequence. In addition, in the in vitro transcription/translation system, a condition of adding factors necessary for each reaction is established so that a transcription reaction and a translation reaction proceed sequentially.

A. Acquirement of modified α -glucosidase 1

[0076] Using α -glucosidase (also referred to as transglucosidase. Hereinafter referred to as "TG".) as a model, a technique for directing a hydrolysis reaction and a dehydration condensation reaction in one direction (One direction technology) was studied by using protein engineering. TG is an enzyme used for the production of oligosaccharides and has an activity to hydrolyze glucosidic linkages and also has a transglycosylation activity, and thus forms oligosaccharides from maltose. The study proceeded in an effort to develop a TG that conducts transglycosylation more efficiently.

(1) Study of annotated amino acids using computer program

[0077] Computer study was carried out aiming at designing a novel enzyme having improved oligosaccharide-producing ability by the structure modification of TG at the molecular level. Using α -glucosidase derived from human small intestine (SEQ ID NO. 1), for which an X-ray crystal structure analysis was reported, annotated amino acids were determined by computer simulation based on the steric structure of TG and functional expectation based on evolutionary findings. Specifically, amino acids that are expected to be annotated amino acids in human α -glucosidase were calculated by using HotSpot Wizard program (Non-patent Document: Pavelka et al., Nucleic Acids Res. 37 W376-83. (2009)), and the three amino acids (the amino acid at the position 385: Y385, the amino acid at the position 491: V491, the amino acid at the position 535: N535) were selected. Since all of the amino acids are present on the regions that contact with a substrate, it can be expected that the amino acids are involved in the activity of the enzymes (FIG. 1,A). Subsequently, five kinds of α -glucosidase homologues were selected, and the sequences in the vicinity of the above-mentioned annotated amino acids were subjected to alignment comparison by using CLUSTALW. Since the homology of the sequences in the vicinity was high and highly conserved in all of Y385, V491 and N535, it was able to be expected that the regions are regions that are important for the functions of the enzyme. The amino acids corresponding to these annotated amino acids were identified by a *Aspergillus niger* TG (*Asp. Niger*) (FIG. 1,C). The amino acid corresponding to Y385 is W343, the amino acid corresponding to V491 is V452, and the amino acid corresponding to N535 is S496. A primer for introducing mutation into these amino acids was designed, and mutation was introduced by an inverse PCR method using a random primer. Transformation into *Escherichia coli* was conducted, and a sequence analysis was conducted after miniprep to confirm introduction of mutation.

(2) Development of screening system

[0078] The plasmid prepared was transformed into yeast INVsc1 strain and cultured. The culture supernatant was collected by centrifugation, and the secreted enzyme was used as modified TG. The broth was concentrated and desalted by ultrafiltration using a spin column. Consequently, an enzyme sample concentrated to approximately 10 to 50-fold was obtained.

[0079] Using maltose, which is an enzyme substrate, the hydrolysis activity was measured. The substrate was adjusted so as to have a final concentration of 1%, and the glucose formed by hydrolysis was reacted with an aminoantipyrine-phenol color developing liquid containing glucose oxidase (GO) and peroxidase (PO) to give a color and quantified by measuring OD500. A calibration curve (standard) was prepared by a glucose standard preparation, and the amount of the generated glucose was calculated from the absorbance.

[0080] In order to examine the oligosaccharide synthesis activities, the generated oligosaccharide was analyzed by HPLC. Using a 50% maltose aqueous solution as a substrate, the generated oligosaccharide was determined. The conditions for HPLC were as follows.

Column: TSKGEL Amido-80 (Tosoh Corporation)

Solvent: MeCN/H₂O = 2/1

Detection: RI

[0081] The area surface areas of HPLC were represented as a graph to thereby estimate the respective saccharide numbers of the generated oligosaccharides. The scheme of the above-mentioned screening method is shown in FIG. 2.

(3) Evaluation of modified TG by substitution of one amino acid

[0082] Random mutation was introduced by a PCR method into the position corresponding to the above-mentioned mutation introduction point (Y385, V491, N535), i.e., W343, V452 or S496, in *Aspergillus niger* α -glucosidase (SEQ ID NO. 2) (substitution of one amino acid). After the introduction of mutation, sequencing was conducted to thereby identify the introduced point mutation. The obtained three modified TGs (W343M, V452G and S496V) were analyzed. In addition, a preliminary experiment was conducted to confirm that a protein derived from the plasmid was expressed in the culture supernatant, and that the enzyme had a hydrolysis activity.

[0083] First, the oligosaccharide synthesis activities were measured by using a high-concentration maltose solution as a substrate. A typical HPLC pattern as the result thereof is shown in FIG. 3. In a sample in which a wild type (WT) TG was expressed, the peak of the substrate maltose decreased, and the peaks of glucose, isomaltose, panose and isomaltotriose were seen (FIG. 3,A). Furthermore, a bipartite peak was seen in the area of the tetrasaccharide (FIG. 3,A).

[0084] On the other hand, as compared to the WT, in the modified TGs, the peak of the substrate maltose decreased, and peaks of glucose, maltotriose and panose were seen (FIG. 3, B to D). Furthermore, gathered peaks were seen in the area of the tetrasaccharide (FIG. 3, B to D). In the oligosaccharides formed by the modified TGs, unlike the WT, the generation amount of the isomalto-based oligosaccharide significantly decreased.

[0085] Subsequently, the oligosaccharide synthesis activities of the modified TGs were compared to that of the WT by quantifying the area surface areas of HPLC. The graph in FIG. 4 shows the total of the area surface areas of tri- or more saccharides. Oligosaccharides of tri- or more saccharides were formed also in the WT, but the area surface areas of the formed oligosaccharides were larger than those of the WT in all of the modified TGs (increased by approximately 20%).

[0086] For the purpose of investigating the relationship between the kinds of the amino acids after substitution and the transglycosylation activity, various modified TGs were prepared with respect to the amino acid W343 corresponding to the mutation introduction point (385Y), and the oligosaccharide synthesizing abilities were compared. As a result, in the cases where the

amino acid after the substitution was cysteine (W343C), aspartic acid (W343D), methionine (W343M), histidine (W343H), alanine (W343A), phenylalanine (W343F), glycine (W343G), threonine (W343T), glutamic acid (W343E), valine (W343V), glutamine (W343Q), asparagine (W343N) or isoleucine (W343I), the amount of the oligosaccharides of tri- or more saccharides formed by the modified TG increased more than that in the WT (FIG. 5, upper). Similar comparison was made for the oligosaccharides of tetra- or more saccharides, and consequently found that the modified TG had more excellent synthesis ability than that of the WT in the cases where the amino acid after the substitution was methionine (W343M), aspartic acid (W343D), cysteine (W343C), phenylalanine (W343F), glutamine (W343Q), histidine (W343H), threonine (W343T), glutamic acid (W343E), glycine (W343G), asparagine (W343N), valine (W343V) or alanine (W343A) (FIG. 5, lower). It can be evaluated that the modified TGs that were in the upper level for either of the synthesized amount of the oligosaccharides of tri- or more saccharides and the synthesized amount of the oligosaccharides of tetra- or more saccharides, i.e., W343C, W343D and W343M, are especially excellent in oligosaccharide synthesis ability. Furthermore, it is suggested that W343M, W343D, W343C, W343F, W343Q and W343H, in which the synthesized amount of the oligosaccharides of tetra- or more saccharides is significantly higher than that in the WT, are advantageous for the synthesis of oligosaccharides having longer chains.

[0087] The transglycosylation activities of the modified TGs were compared to that of the WT by quantifying the area surface areas of HPLC. Various modified TGs were prepared with respect to the amino acid V452, and the oligosaccharide synthesis abilities were compared. As a result, in the cases where the amino acid after the substitution was glycine, aspartic acid or glutamic acid, the amount of the oligosaccharides of tri- or more saccharides increased more than that in the WT (FIG. 6). Furthermore, the oligosaccharides of tetra- or more saccharides were similarly compared, and consequently found that the modified TG in which the amino acid after the substitution was aspartic acid (V452D) was superior to the WT in synthesis ability (FIG. 6). Similarly, various modified TGs were prepared with respect to the amino acid S496, and the oligosaccharide synthesis abilities were compared. As a result, in the cases where the amino acid after the substitution was valine, asparagine or glutamine, the modified TGs were superior to the WT in synthesis ability in both cases of the oligosaccharides of tri- or more saccharides and the oligosaccharides of tetra- or more saccharides (FIG. 6).

[0088] As mentioned above, it was found that the generation amount of the isomalto-based oligosaccharide was greatly decreased in the modified TGs. Therefore, it was thought that the reactivity against glucosidic linkages should change, and thus the hydrolysis activities against various glucosidic linkages were investigated. As enzyme substrates, aqueous solutions of maltose (α -1,4) and isomaltose (α -1,6), which are disaccharides, were prepared. The WT showed substrate affinity for both α -1,4 glucosidic linkages and α -1,6 glucosidic linkages (FIG. 7). In contrast, in the modified TGs, the hydrolysis activity against α -1,4 glucosidic linkages was approximately the same as that of the wild type, whereas the hydrolysis activity against α -1,6 glucosidic linkages decreased to one-fifth or less (FIG. 7).

(4) Evaluation of modified TG by substitution of two amino acids

[0089] Modified TGs in which mutation had been introduced into two amino acids were prepared by introducing further mutation (either of the two amino acids present on the surface of the tunnel structure (V452 and S496)) in the modified TG in which the tryptophan at the position 343 had been substituted. The hydrolysis activities of the obtained modified TGs were measured. As shown in FIG. 8, the activity was not able to be detected at all for W343D/S496I (the W at the position 343 was substituted by D and the S at the position 496 was substituted by I) and W343D/S496R (the W at the position 343 was substituted by D and the S at the position 496 was substituted by R). On the other hand, the hydrolysis activity of isomaltose greatly decreased (approximately 1/20) in the three kinds of modified TGs: W343D/V452G (the W at the position 343 was substituted by D and the V at the position 452 was substituted by G), W343M/S496C (the W at the position 343 was substituted by M and the S at the position 496 was substituted by C) and W343M/S496T (the W at the position 343 was substituted by M and the S at the position 496 was substituted by T).

[0090] Subsequently, the oligosaccharide synthesis activities were measured. In the samples in which the wild type TG was expressed, the peaks of panose and isomaltotriose were seen with respect to trisaccharides (FIG. 9,A). On the other hand, in W343M, the peaks of maltotriose and panose were seen with respect to the trisaccharides as in the previous results (FIG. 9,B). In W343M/S496T and W343D/V452G, which are TGs in which two amino acids have been substituted, only one peak was seen with respect to a trisaccharide, and the peak was anticipated to be of maltotriose (FIG. 9, the arrows in C and D). Furthermore, the peak seen in HPLC was only one also in the region of four saccharides, and this resulted in an analysis pattern greatly different from the analysis pattern of the wild type (FIG. 9, C and D). This peak for the tetrasaccharide is a peak that is seen in only TGs in which two amino acids have been substituted, and shows that the generated oligosaccharide is different from the wild type.

[0091] The transglycosylation activities of the modified TGs were compared to that of the WT by quantifying the area surface areas of HPLC. In all of the TGs in which two amino acids had been substituted, the area surface areas of the generated oligosaccharides were larger than that in the WT, and the synthesis amount of the oligosaccharide of tri- or more saccharides increased by 20 to 50% (FIG. 10). Furthermore, in W343M/S496T, the synthesis amount of the oligosaccharides of tetra- or more saccharides was significantly larger than that of the WT, and increased by about 70% (FIG. 10).

[0092] On the other hand, the hydrolysis activities against glucosidic linkages of the modified TGs were studied. In W343M/S496T, the hydrolysis activities against maltose and maltotriose were each 50%, and the hydrolysis activity against isomaltose was 10% or less (FIG. 11). The hydrolysis activity against kojibiose was approximately 40%, and the hydrolysis activity against nigerose decreased to approximately 10% (FIG. 11). It is suggested that the hydrolysis activity decreased in the modified TGs in which two amino acids had been substituted, and that the hydrolysis activities against specifically α -1,6 glucosidic linkages and α -1,3 glucosidic linkages

greatly decreased.

(5) Analysis of oligosaccharides formed by modified TGs

[0093] According to the previous reports, when the number of saccharides in an initial substrate used for the synthesis of an oligosaccharide is increased, the ratio of the α -1,6 glucosidic linkages in the oligosaccharide formed by a TG increases. Therefore, oligosaccharide synthesis reactions were conducted by using maltopentaose, which is a pentasaccharide, as a substrate, and the formed oligosaccharides were compared between the wild type and modified TGs. First, as a standard, glucose (G=1), maltose (G=2), maltotriose (G=3) and maltopentaose (G=5) were measured, and the positions of the peaks were confirmed (FIG. 12). In the wild type TG, decomposition and production widely occurred from glucose to the areas of hepta- or more saccharides (FIG. 12). However, the ratio of penta- or less saccharides was large, and thus it was suggested that hydrolysis proceeded more than oligosaccharide synthesis did. On the other hand, in the modified TGs (W343M and W343M/S496T), saccharides that had been hydrolyzed to monosaccharide and disaccharide were decreased, and hexa- or more saccharides had been formed more (FIG. 12). In the areas indicated by the arrows in FIG. 12, the difference is specifically great between the WT and modified TGs.

[0094] Next, oligosaccharide synthesis was conducted in a mixed solution of maltose and isomaltose as a start substrate. Although the ratio of the generated oligosaccharides was not greatly changed, a difference appeared in the kinds of the generated trisaccharides. In the wild type, isomaltotriose, which has two α -1,6 glucosidic linkages, was formed much (FIG. 13). On the other hand, in the modified TGs (W343M and W343M/S496T), panose, which has an α -1,4 glucosidic linkage and an α -1,6 glucosidic linkag was formed most (FIG. 13, arrow). Furthermore, the isomaltose as a start substrate was decomposed little in the cases of modified TGs.

[0095] It was suggested by the above-mentioned results that the modified TGs specifically have a transglycosylation activity to form α -1,4 glucosidic linkages, in contrast to that the wild type TG mainly have a transglycosylation activity to form α -1,6 glucosidic linkages.

[0096] The amino acid sequences of the various modified TGs prepared in the investigation at this time are shown below.

SEQ ID NO. 18: W343C

SEQ ID NO. 19: W343D

SEQ ID NO. 20: W343M

SEQ ID NO. 21: W343H

SEQ ID NO. 22: W343A

SEQ ID NO. 23: W343F

SEQ ID NO. 24: W343G

SEQ ID NO. 25: W343T

SEQ ID NO. 26: W343E

SEQ ID NO. 27: W343V

SEQ ID NO. 28: W343Q

SEQ ID NO. 29: W343N

SEQ ID NO. 30: W343I

SEQ ID NO. 31: V452G

SEQ ID NO. 32: V452D

SEQ ID NO. 33: V452E

SEQ ID NO. 34: S496V

SEQ ID NO. 35: S496N

SEQ ID NO. 36: S496Q

SEQ ID NO. 37: W343D/V452A

SEQ ID NO. 38: W343D/V452G

SEQ ID NO. 39: W343D/S496I

SEQ ID NO. 40: W343D/S496R

SEQ ID NO. 41: W343M/S496C

SEQ ID NO. 42: W343M/S496T

B. Acquisition of modified α -glucosidase 2

(1) Study of annotated amino acids using computer software MOE

[0097] For the purpose of identifying annotated amino acids by a novel means, the annotated amino acids of TGs were studied by using computer software MOE (Chemical Computing Group). At this time, the annotated amino acids were selected by comparing the sequences of *Aspergillus niger* and *Aspergillus nidulans*.

[0098] The amino acid sequences of the *Aspergillus niger* TG and *Aspergillus nidulans* TG (α -glucosidase B) were obtained from known data bank and read into MOE, and protein modeling was built on a computer. Based on the respective amino acid sequences, sequences having high homology were searched on the database of MOE. As a result, the same sequence was hit in both cases, and human TG was selected. Subsequently, using the steric structures as templates, the respective proteins are modeled. The force field was "AMBER99", five intermediate models were prepared and one model structure was finally prepared.

[0099] Subsequently, a docking simulation analysis was performed to thereby expect the substrate pockets. The force field was set to "MMFF99x", and the pockets were searched by Site Finder of MOE. As a result, a plurality of candidate regions having possibility of becoming pockets in view of the steric structures were predicted. Therefore, amino acids that become the active center of TG reported in previous articles and the like were searched, and the position of each amino acid on a model was determined. Furthermore, the region containing a plurality of amino acids, which is an active center, was determined as a substrate pocket calculated by the simulation.

[0100] The steric structures that were successfully modeled are shown in FIG. 14. When the structures of *Aspergillus niger* TG and *Aspergillus nidulans* TG were compared, a significant difference was observed between the respective steric structures even though they were modeled based on the same steric structure of human TG. When the simulated substrate pockets were compared, the substrate pocket of *Aspergillus nidulans* was smaller than that of *Aspergillus niger*. The substrate pocket was composed of 30 amino acids in *Aspergillus niger*, whereas the substrate pocket was composed of 22 amino acids in *Aspergillus nidulans* (FIG. 14).

[0101] Subsequently, the amino acid sequence of *Aspergillus niger* TG and the amino acid sequence of *Aspergillus nidulans* TG were aligned by CLASTAL-W. When the whole amino acid sequences were compared, the homology of these proteins was low, and the ratio at which the amino acids were identical was calculated as 35%. However, in the case where only the sequences of the substrate pockets were compared, the sequences had high homology, and 19 of 30 amino acids were identical in the substrate pocket of *Aspergillus niger* and 19 of 22 amino acids were identical in *Aspergillus nidulans* (FIG. 15). This result suggests that the amino acids relating to the activity are highly conserved as compared to the entire sequence. On the other hand, we predicted the amino acids that were not identical have low evolutionary conservation property, and thus it was expected that mutation can be introduced. Therefore, these amino acids were used as candidate annotated amino acids for introducing mutation (FIG. 15). Furthermore, since W343 and S496 in which mutation had been already introduced were selected, it was thought that there is a correlation with simulation by Hot spots wizard

using human TG that has been used in the past.

[0102] Primers were designed so as to actually introduce mutation into *Aspergillus niger* TG, and mutation was introduced by an inverse PCR method using a random primer. Transformation into *Escherichia coli* was conducted, and a sequence analysis was conducted after miniprep to confirm introduction of mutation. Furthermore, transformation into yeast was conducted, and a recombinant modified TG was expressed and analyzed. The analysis results for two amino acids: S495 and C498 among the actual preparation are shown.

(2) Evaluation of S495-modified TG

[0103] In *Aspergillus niger* TG, random mutation was introduced into the 495th serine (S495) by a PCR method (substitution of one amino acid). Sequence was conducted to identify the introduced point mutation, and the modified TG was analyzed.

[0104] These modified TGs were compared by measuring the oligosaccharide synthesis activities by using HPLC. A 50% maltose aqueous solution, an isomaltose aqueous solution, and an aqueous solution of maltopentaose, which is an oligosaccharide of a pentasaccharide, were used as substrates. The aqueous solutions were incubated at a reaction temperature of 50°C for a predetermined time (48 hours for maltose and maltopentaose, and 96 hours for isomaltose).

[0105] The oligosaccharide synthesis activities of the modified TGs were compared by quantifying the area surface areas of HPLC. In the case where the substrate was maltose, the total of the area surface areas of the tri- or more saccharides and tetra- or more saccharides was larger than that of the WT in S495G but was conversely decreased in S495P and S495T (FIG. 16).

[0106] In the case where the substrate was isomaltose, the total of the area surface areas of the tri- or more saccharides was larger than that of the WT in S495G, S495P and S495V (FIG. 17). Furthermore, the total of the area surface areas of the tetra- or more saccharides was larger than that of the WT in S495G and S495P, and thus it was suggested that the oligosaccharide synthesis ability was improved (FIG. 17). When the peaks in the HPLC are observed, isomaltotriose increased in the trisaccharides, and thus it can be presumed that the modified TGs have a transglycosylation activity to form α -1,6 glucosidic linkages as in the WT. It was found from the above-mentioned results that the three kinds: S495G, S495P and S495V increase oligosaccharides with α -1,6 glucosidic linkages by 50% or more.

[0107] Therefore, it was thought that the reactivity against glucosidic linkages should differ in the modified TGs, and thus the hydrolysis activities against various glucosidic linkages were studied (FIG. 18). Using a maltose aqueous solution and an isomaltose aqueous solution as substrates, the amounts of the generated glucose were quantified to thereby evaluate the hydrolysis activities. It is shown that the WT has substrate affinity for both α -1,4 glucosidic

linkages and α -1,6 glucosidic linkages against glucosidic linkages. On the other hand, the hydrolysis activity of maltose decreased more than in the WT whereas the hydrolysis activity of isomaltose relatively increased in S495A, S495G, S495P, S495T and S495V. As mentioned above, the modified TG in which S495 had been substituted had increased transglycosylation activity to form α -1,6 glucosidic linkages.

[0108] Finally, oligosaccharide synthesis reactions were conducted by using maltopentaose, which is a pentasaccharide, as an initial substrate, and the generated oligosaccharides were compared between the wild type TG and modified TGs (FIG. 19). In the wild type TG, decomposition and generation occurred widely in the areas from glucose to hexa- or more saccharides. When a graph was drawn, the amount of monosaccharide was the largest, and hydrolysis proceeded during the reaction. Increase in the oligosaccharides was observed in all of the modified TGs. Specifically, in the modified TGs of S495P-type and S495V-type, the hydrolyzed saccharides were small, whereas hexa- or more saccharides were formed much (FIG. 19c).

[0109] As mentioned above, three kind of modified TGs having transglycosylation activity to form α -1,6 glucosidic linkages were successfully obtained. Furthermore, it was found that the oligosaccharides formed by the modified TGs are polymerized by a bonding manner including α 1,6 glucosidic linkages to thereby increase the formation amounts of the oligosaccharides.

(3) Evaluation of C498-modified TG

[0110] In *Aspergillus niger* TG, random mutation was introduced into the 498th cysteine (C498) by a PCR method (substitution of one amino acid). Sequence was conducted to identify the introduced point mutation, and the modified TG was analyzed.

[0111] These modified TGs were compared by measuring the oligosaccharide synthesis activities by using HPLC. Using a 60% maltose aqueous solution as a substrate, incubation was conducted at a reaction temperature of 50°C for 48 hours.

[0112] The oligosaccharide synthesis activities of the modified TGs were compared by quantifying the area surface areas of HPLC (FIG. 20). When the totals of the area surface areas of tri- or more saccharides were compared, the area surface areas were larger in C498L and C498S than that of the WT. Furthermore, increase in the total of the area surface areas of tetra- or more saccharides was similarly observed in C498L and C498S as compared to the WT.

[0113] It was thought based on the results that the reactivity against glucosidic linkages could be changed in the modified TGs, and thus the hydrolysis activities were measured. Using a maltose aqueous solution and an isomaltose aqueous solution as substrates, the amounts of the generated glucose were quantified. As shown in FIG. 21, it was found that the hydrolysis activity of maltose was higher in C498L and C498S as compared to the WT. Furthermore, it is

also understood that a significant change was observed in the ratio of the maltose hydrolysis activity and isomaltose hydrolysis activity and thus the specificity against α -1,4 glucosidic linkages was improved in these modified TGs.

[0114] As mentioned above, it was shown that the synthesis of oligosaccharides is increased in C498 by introducing mutation. Furthermore, two kinds of modified TGs (these show transglycosylation activity to form α -1,4 glucosidic linkages) in which the ability of synthesizing oligosaccharides had been enhanced were successfully obtained.

[0115] The amino acid sequences of the various modified TGs prepared in the investigation at this time are shown below.

SEQ ID NO. 74: S495G

SEQ ID NO. 75: S495P

SEQ ID NO. 76: S495V

SEQ ID NO. 77: C498L

SEQ ID NO. 78: C498S

C. Application of modified TGs to field of foods

[0116] In order to evaluate the possibility of application of modified TGs to the field of health foods, an experiment using an artificial digestion model system was conducted. In this model system, how TGs act on oligosaccharides that are formed by decomposing porridge by amylase derived from saliva is evaluated. Amylase and TG were reacted with commercially available porridge at an acidic region being close to the pH of gastric juice (30 minutes to 2 hours, warmed at 37°C), sampling was then conducted, and the enzymatic reaction was stopped. Furthermore, the generated oligosaccharides were analyzed by HPLC. The amount of the added amylase was 1.45 U/ml, which corresponds to the amount of the amylase in saliva. Furthermore, in light of the result of the preliminary research, the amount of TG was set to 20 μ g/mL. The specific of the experimental protocol is shown below.

(Protocol)

[0117]

1. (i) Porridge (Ajinomoto Co., Inc.) is crushed in a blender, and 1M NaOAc buffer (pH 5.0) is added in an amount of 1/20.
2. (ii) 340 μ l of an enzyme solution is prepared (protein concentration: 20 μ g/mL).

3. (iii) 0.65 g of the porridge of (i), 1.45 U of amylase and 340 μ l of the enzyme solution are put into a glass test tube.
4. (iv) Incubation is conducted in a hot water bath at 37°C, and 200 μ l is sampled into a micro test tube every 30 minutes.
5. (v) Boiling is conducted for 5 minutes to thereby stop the enzymatic reaction.
6. (vi) Centrifugation is conducted at 12,000 rpm, and the supernatant is transferred to a new tube.
7. (vii) 120 μ l is sorted out and diluted to three-fold with MilliQ (registered trademark) water.
8. (viii) An HPLC analysis is conducted under the following conditions.

(Column conditions)

[0118] Column; TSKGELAmido-80

Solvent; MeCN/H₂O = 2/1

Detector; RI

Flow rate; 1 ml/min

[0119] The result of the analysis of the obtained oligosaccharides by HPLC is shown in FIG. 22. By adding amylase, 40 to 50% of the whole saccharides becomes maltose (FIG. 22 (a)). Furthermore, maltotriose, which is a trisaccharide, and maltotetraose, which is a tetrasaccharide, are formed. Glucose generates little, and decomposition does not proceed from disaccharides. In the case where a wild type (WT) TG was added, the generation amount of glucose increased over time, generation of isomaltose was observed from 60 minutes after the initiation of the reaction, and the oligosaccharides of tri- or more saccharides decreased over the passage of time (FIG. 22 (b) and (d)). In the case where W343M, which is a modified TG having a transglycosylation activity to form α -1,4 glucosidic linkages is added, maltose is decomposed as in the case of the wild type TG and a transglycosylation reaction proceeds. At 30 minutes after the initiation of the reaction, the generated oligosaccharides are not significantly different from those in the wild type TG, and the peaks of maltotriose, maltose and glucose are observed (FIG. 22 (c)). On the other hand, W343M transfers maltose to oligosaccharides of tri- or more saccharides while suppressing the generation of glucose (FIG. 22 (c)). In contrast to the wild type TG, in the case where W343M is added, the decrease in the tri- or more oligosaccharides is small, and the amount of the finally generated oligosaccharides is dramatically large (FIG. 22 (d)). When the actual HPLC pattern (at 90 minutes after the initiation of the reaction) was seen, in the case where W343M was added, the peak of isomaltose was not observed, and the peaks of the oligosaccharides having larger sizes were seen (FIG. 23).

[0120] As mentioned above, when W343M, which is a modified TG, was used, the generation amount of isomaltose decreased as compared to the case where the wild type TG was used, whereas the generation amounts of the oligosaccharides with α -1,4 glucosidic linkages having

long chain lengths such as maltotriose increased. When compared at 90 minutes after the initiation of the reaction, the generation amount of glucose in the modified TG decreased by 19.2%, and the generation amount of the oligosaccharides of tri- or more saccharides increased by 42.7%, as compared to that in the wild type TG. Therefore, the usefulness of the modified TG, i.e., the modified TG is suitable for the generation of oligosaccharides even in an artificial digestion model system, was demonstrated.

D. Combination use of wild type (WT) TG and modified TG

(1) Synthesis of oligosaccharides using maltose as substrate

[0121] When a reaction for synthesizing oligosaccharides was attempted by using a modified TG having a transglycosylation activity to form α -1,6 glucosidic linkages and using maltose, which is a disaccharide with an α 1,4 glucosidic linkage, as a substrate, the synthesis of oligosaccharides did not proceed. The reason therefor was considered that the modified TG having a transglycosylation activity to form α -1,6 glucosidic linkages has low reactivity against α -1,4 glucosidic linkages, and thus the reaction for synthesizing oligosaccharides does not sufficiently proceed even when maltose is used as a substrate. Therefore, it was thought that a reaction for synthesizing oligosaccharides could proceed even when maltose is used as a substrate, if an enzyme that supplies isomaltose is used in combination, and thus the synthesis of oligosaccharides was conducted by using a wild type TG having an enzyme activity to convert maltose to isomaltose and a modified TG (S495P) in combination. The generated oligosaccharides were analyzed by HPLC. In addition, a 50% maltose aqueous solution was used as a substrate, and the reaction was conducted at 50°C for 48 hours.

[0122] The synthesis of oligosaccharides was conducted for the case of S495P alone and the cases where wild type and S495P were mixed (mixing ratio 2:1, 1:1 or 1:2), and the generated oligosaccharides were analyzed by HPLC. In the case of S495P alone, panose, which is a trisaccharide, is formed, whereas the generation of oligosaccharides of tetra- or more saccharides is very low. Namely, the reactions of the tetra- or more saccharides do not proceed (S495P in FIG. 24, and S495P in FIG. 25). On the other hand, in the case where the wild type and S495P were used in combination, both of the amount of the tri- or more oligosaccharides and the amount of the tetra- or more oligosaccharides increased in either mixing ratio (WT/S495P=2/1, WT/S495P=1/1 and WT/S495P=1/2 in FIG. 24). Of particular note is that most of the generated oligosaccharides was panose in the case of S495P alone, whereas in the case where the wild type and S495P were used in combination, generation of panose and isomaltotriose was observed (FIG. 25, the peaks indicated by the arrows), and the generation of oligosaccharides of tetra- or more saccharides was further observed. As mentioned above, combination use of the wild type and the modified TG having a transglycosylation activity to form α -1,6 glucosidic linkages was effective, and it was possible to generate oligosaccharides also from a saccharide with an α -1,4 glucosidic linkage on which a

reaction does not proceed by single use of the modified TG having an α -1,6 transglycosylation activity.

(2) Application of modified TG to field of foods

[0123] For a modified TG having a transglycosylation activity to form α -1,6 glucosidic linkages, an experiment using an artificial digestion model system was conducted. The protocol is the same as in the case of the above-mentioned C.

[0124] In the case where only amylase is added to porridge, 40 to 50% of the generated saccharides is maltose. Furthermore, maltotriose, which is a trisaccharide, and maltotetraose, which is a tetrasaccharide, are formed. Since all of these are saccharides with α -1,4 glucosidic linkages, it was thought that the reaction does not proceed by single use of a modified α -glucosidase having a transglycosylation activity to form α -1,4 glucosidic linkages. Therefore, similarly to (1) of D, synthesis of oligosaccharides was attempted by using a wild type TG and a modified TG (S495P) in combination.

[0125] First, in the case where amylase and the wild type were added to porridge, the reaction proceeded from after 30 minutes, and the generation amount of glucose gradually increased (FIG. 26 (a)). Furthermore, isomaltose was formed from 60 minutes after the initiation of the reaction, and the tri- or more oligosaccharides gradually decreased. On the other hand, in the case where amylase and S495P were added to porridge, only generation of saccharides by amylase occurred, and even at 120 minutes after the initiation of the reaction, most of the saccharides remained as maltose, maltotriose and maltotetraose (FIG. 26 (b)). In contrast, in the case where three kinds of enzymes: amylase, a wild type and S495P were used in combination (the mixing ratio of the wild type and S495P was 1 : 2), the decomposition of maltose occurred and a transglycosylation reaction proceeded. After 60 minutes after the initiation of the reaction, oligosaccharides of tri- or more saccharides increased as compared to that in the wild type alone (FIG. 26 (d)). In the case where three kinds of enzymes were used in combination, decrease in the maltose and increase in the ratio of the oligosaccharides of tri- or more saccharides were observed (FIG. 26 (c)), and thus it is thought that the synthesis of the oligosaccharides proceeded. When the actual HPLC pattern is seen, in the case where the three kinds of enzymes were used in combination, the peaks of the maltose and maltotriose generated by amylase decreased, whereas the peaks of panose and oligosaccharides of tetra- or more saccharides were observed (the arrows at the lower right of FIG. 27). Furthermore, it was found that the oligosaccharides of tri- or more saccharides decreased little as compared to the case where only the wild type was used in combination with amylase (FIG. 27, lower left), and thus it can be said that combination use of three kinds of enzymes (amylase, wild type and S495P) is effective for the generation of oligosaccharides.

[0126] Accordingly, it was shown that combination use of a wild type and a modified TG having a transglycosylation activity to form α -1,4 glucosidic linkages is extremely effective for generating oligosaccharides.

Industrial Applicability

[0127] The modified α -glucosidase of the present invention has a high transglycosylation activity. By utilizing this property, utilization in the production (synthesis) of oligosaccharides is expected. Furthermore, the designing method of the present invention is useful as a means for enhancing the transglycosylation activities of wild type enzymes and the like, and thus can be used for the modification of various α -glucosidases.

SEQUENCE LISTING**[0128]**

<110> AMANO ENZYME INC. ISHIHARA, Satoru

<120> MODIFIED ALPHA-GLUCOSIDASE AND USE THEREOF

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<150> JP P2011-057386

<151> 2011-03-16

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 545 550 555 560
 Gly Tyr Leu Phe Cys Lys Thr Leu Cys Met Asp Ala Val Gln His Trp
 565 570 575
 Gly Lys Gln Tyr Asp Ile His Asn Leu Tyr Gly Tyr Ser Met Ala Val
 580 585 590
 Ala Thr Ala Glu Ala Ala Lys Thr Val Phe Pro Asn Lys Arg Ser Phe
 595 600 605
 Ile Leu Thr Arg Ser Thr Phe Ala Gly Ser Gly Lys Phe Ala Ala His
 610 615 620
 Trp Leu Gly Asp Asn Thr Ala Thr Trp Asp Asp Leu Arg Trp Ser Ile
 625 630 635 640
 Pro Gly Val Leu Glu Phe Asn Leu Phe Gly Ile Pro Met Val Gly Pro
 645 650 655
 Asp Ile Cys Gly Phe Ala Leu Asp Thr Pro Glu Glu Leu Cys Arg Arg
 660 665 670
 Trp Met Gln Leu Gly Ala Phe Tyr Pro Phe Ser Arg Asn His Asn Gly
 675 680 685
 Gln Gly Tyr Lys Asp Gln Asp Pro Ala Ser Phe Gly Ala Asp Ser Leu
 690 695 700

690	695	700
Leu Leu Asn Ser Ser Arg His Tyr Leu Asn Ile Arg Tyr Thr Leu Leu		
705	710	715 720
Pro Tyr Leu Tyr Thr Leu Phe Phe Arg Ala His Ser Arg Gly Asp Thr		
	725	730 735
Val Ala Arg Pro Leu Leu His Glu Phe Tyr Glu Asp Asn Ser Thr Trp		
	740	745 750
Asp Val His Gln Gln Phe Leu Trp Gly Pro Gly Leu Leu Ile Thr Pro		
	755	760 765
Val Leu Asp Glu Gly Ala Glu Lys Val Met Ala Tyr Val Pro Asp Ala		
	770	775 780
Val Trp Tyr Asp Tyr Glu Thr Gly Ser Gln Val Arg Trp Arg Lys Gln		
	785	790 795 800
Lys Val Glu Met Glu Leu Pro Gly Asp Lys Ile Gly Leu His Leu Arg		
	805	810 815
Gly Gly Tyr Ile Phe Pro Thr Gln Gln Pro Asn Thr Thr Thr Leu Ala		
	820	825 830
Ser Arg Lys Asn Pro Leu Gly Leu Ile Ile Ala Leu Asp Glu Asn Lys		
	835	840 845
Glu Ala Lys Gly Glu Leu Phe Trp Asp Asn Gly Glu Thr Lys Asp Thr		
	850	855 860
Val Ala Asn Lys Val Tyr Leu Leu Cys Glu Phe Ser Val Thr Gln Asn		
	865	870 875 880
Arg Leu Glu Val Asn Ile Ser Gln Ser Thr Tyr Lys Asp Pro Asn Asn		
	885	890 895
Leu Ala Phe Asn Glu Ile Lys Ile Leu Gly Thr Glu Glu Pro Ser Asn		
	900	905 910
Val Thr Val Lys His Asn Gly Val Pro Ser Gln Thr Ser Pro Thr Val		
915	920	925
Thr Tyr Asp Ser Asn Leu Lys Val Ala Ile Ile Thr Asp Ile Asp Leu		
	930	935 940
Leu Leu Gly Glu Ala Tyr Thr Val Glu Trp Ser Ile Lys Ile Arg Asp		
	945	950 955 960
Glu Glu Lys Ile Asp Cys Tyr Pro Asp Glu Asn Gly Ala Ser Ala Glu		
	965	970 975
Asn Cys Thr Ala Arg Gly Cys Ile Trp Glu Ala Ser Asn Ser Ser Gly		
	980	985 990

Val Pro Phe Cys Tyr Phe Val Asn Asp Leu Tyr Ser Val Ser Asp Val
 995 1000 1005

Gln Tyr Asn Ser His Gly Ala Thr Ala Asp Ile Ser Leu Lys Ser
 1010 1015 1020

Ser Val Tyr Ala Asn Ala Phe Pro Ser Thr Pro Val Asn Pro Leu
 1025 1030 1035

Arg Leu Asp Val Thr Tyr His Lys Asn Glu Met Leu Gln Phe Lys
 1040 1045 1050

Ile Tyr Asp Pro Asn Lys Asn Arg Tyr Glu Val Pro Val Pro Leu
 1055 1060 1065

Asn Ile Pro Ser Met Pro Ser Ser Thr Pro Glu Gly Gln Leu Tyr
 1070 1075 1080

Asp Val Leu Ile Lys Lys Asn Pro Phe Gly Ile Glu Ile Arg Arg
 1085 1090 1095

Lys Ser Thr Gly Thr Ile Ile Trp Asp Ser Gln Leu Leu Gly Phe
 1100 1105 1110

Thr Phe Ser Asp Met Phe Ile Arg Ile Ser Thr Arg Leu Pro Ser
 1115 1120 1125

Lys Tyr Leu Tyr Gly Phe Gly Glu Thr Glu His Arg Ser Tyr Arg
 1130 1135 1140

Arg Asp Leu Glu Trp His Thr Trp Gly Met Phe Ser Arg Asp Gln
 1145 1150 1155

Pro Pro Gly Tyr Lys Lys Asn Ser Tyr Gly Val His Pro Tyr Tyr
 1160 1165 1170

Met Gly Leu Glu Glu Asp Gly Ser Ala His Gly Val Leu Leu Leu
 1175 1180 1185

Asn Ser Asn Ala Met Asp Val Thr Phe Gln Pro Leu Pro Ala Leu
 1190 1195 1200

Thr Tyr Arg Thr Thr Gly Gly Val Leu Asp Phe Tyr Val Phe Leu
 1205 1210 1215

Gly Pro Thr Pro Glu Leu Val Thr Gln Gln Tyr Thr Glu Leu Ile
 1220 1225 1230

Gly Arg Pro Val Met Val Pro Tyr Trp Ser Leu Gly Phe Gln Leu
 1235 1240 1245

Cys Arg Tyr Gly Tyr Gln Asn Asp Ser Glu Ile Ala Ser Leu Tyr
 1250 1255 1260

Asp Glu Met Val Ala Ala Gln Ile Pro Tyr Asp Val Gln Tyr Ser
 1265 1270 1275

Asp Ile 1280	Asp Tyr Met Glu Arg 1285	Gln Leu Asp Phe Thr 1290	Leu Ser Pro
Lys Phe 1295	Ala Gly Phe Pro Ala 1300	Leu Ile Asn Arg Met 1305	Lys Ala Asp
Gly Met 1310	Arg Val Ile Leu Ile 1315	Leu Asp Pro Ala Ile 1320	Ser Gly Asn
Glu Thr 1325	Gln Pro Tyr Pro Ala 1330	Phe Thr Arg Gly Val 1335	Glu Asp Asp
Val Phe 1340	Ile Lys Tyr Pro Asn 1345	Asp Gly Asp Ile Val 1350	Trp Gly Lys
Val Trp 1355	Pro Asp Phe Pro Asp 1360	Val Val Val Asn Gly 1365	Ser Leu Asp
Trp Asp 1370	Ser Gln Val Glu Leu 1375	Tyr Arg Ala Tyr Val 1380	Ala Phe Pro
Asp Phe 1385	Phe Arg Asn Ser Thr 1390	Ala Lys Trp Trp Lys 1395	Arg Glu Ile
Glu Glu 1400	Leu Tyr Asn Asn Pro 1405	Gln Asn Pro Glu Arg 1410	Ser Leu Lys
Phe Asp 1415	Gly Met Trp Ile Asp 1420	Met Asn Glu Pro Ser 1425	Ser Phe Val
Asn Gly 1430	Ala Val Ser Pro Gly 1435	Cys Arg Asp Ala Ser 1440	Leu Asn His
Pro Pro 1445	Tyr Met Pro His Leu 1450	Glu Ser Arg Asp Arg 1455	Gly Leu Ser
Ser Lys 1460	Thr Leu Cys Met Glu 1465	Ser Gln Gln Ile Leu 1470	Pro Asp Gly
Ser Leu 1475	Val Gln His Tyr Asn 1480	Val His Asn Leu Tyr 1485	Gly Trp Ser
Gln Thr 1490	Arg Pro Thr Tyr Glu 1495	Ala Val Gln Glu Val 1500	Thr Gly Gln
Arg Gly 1505	Val Val Ile Thr Arg 1510	Ser Thr Phe Pro Ser 1515	Ser Gly Arg
Trp Ala 1520	Gly His Trp Leu Gly 1525	Asp Asn Thr Ala Ala 1530	Trp Asp Gln
Leu Lys 1535	Lys Ser Ile Ile Gly 1540	Met Met Glu Phe Ser 1545	Leu Phe Gly
Ile Ser 1550	Tyr Thr Gly Ala Asp 1555	Ile Cys Gly Phe Phe 1560	Gln Asp Ala

Glu Tyr	Glu Met Cys Val	Arg	Trp Met Gln Leu Gly	Ala Phe Tyr
1565		1570		1575
Pro Phe	Ser Arg Asn His	Asn	Thr Ile Gly Thr Arg	Arg Gln Asp
1580		1585		1590
Pro Val	Ser Trp Asp Val	Ala	Phe Val Asn Ile Ser	Arg Thr Val
1595		1600		1605
Leu Gln	Thr Arg Tyr Thr	Leu	Leu Pro Tyr Leu Tyr	Thr Leu Met
1610		1615		1620
His Lys	Ala His Thr Glu Gly	Val Thr Val Val	Arg	Pro Leu Leu
1625		1630		1635
His Glu	Phe Val Ser Asp Gln	Val Thr Trp Asp	Ile	Asp Ser Gln
1640		1645		1650
Phe Leu	Leu Gly Pro Ala Phe	Leu Val Ser Pro	Val	Leu Glu Arg
1655		1660		1665
Asn Ala	Arg Asn Val Thr Ala	Tyr Phe Pro Arg	Ala	Arg Trp Tyr
1670		1675		1680
Asp Tyr	Tyr Thr Gly Val Asp	Ile Asn Ala Arg	Gly	Glu Trp Lys
1685		1690		1695
Thr Leu	Pro Ala Pro Leu Asp	His Ile Asn Leu	His	Val Arg Gly
1700		1705		1710
Gly Tyr	Ile Leu Pro Trp Gln	Glu Pro Ala Leu	Asn	Thr His Leu
1715		1720		1725
Ser Arg	Gln Lys Phe Met Gly	Phe Lys Ile Ala	Leu	Asp Asp Glu
1730		1735		1740
Gly Thr	Ala Gly Gly Trp Leu	Phe Trp Asp Asp	Gly	Gln Ser Ile
1745		1750		1755
Asp Thr	Tyr Gly Lys Gly Leu	Tyr Tyr Leu Ala	Ser	Phe Ser Ala
1760		1765		1770
Ser Gln	Asn Thr Met Gln Ser	His Ile Ile Phe	Asn	Asn Tyr Ile
1775		1780		1785
Thr Gly	Thr Asn Pro Leu Lys	Leu Gly Tyr Ile	Glu	Ile Trp Gly
1790		1795		1800
Val Gly	Ser Val Pro Val Thr	Ser Val Ser Ile	Ser	Val Ser Gly
1805		1810		1815
Met Val	Ile Thr Pro Ser Phe	Asn Asn Asp Pro	Thr	Thr Gln Val
1820		1825		1830
Leu Ser	Ile Asp Val Thr Asp	Arg Asn Ile Ser	Leu	His Asn Phe

1835

1840

1845

Thr Ser Leu Thr Trp Ile Ser Thr Leu
1850 1855

<210> 2

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 2

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe

225		230		235		240									
Tyr	Leu	Asp	Thr	Arg	Tyr	Tyr	Lys	Gly	Asp	Arg	Gln	Asn	Gly	Ser	Tyr
				245					250					255	
Ile	Pro	Val	Lys	Ser	Ser	Glu	Ala	Asp	Ala	Ser	Gln	Asp	Tyr	Ile	Ser
			260					265					270		
Leu	Ser	His	Gly	Val	Phe	Leu	Arg	Asn	Ser	His	Gly	Leu	Glu	Ile	Leu
		275					280					285			
Leu	Arg	Ser	Gln	Lys	Leu	Ile	Trp	Arg	Thr	Leu	Gly	Gly	Gly	Ile	Asp
	290					295					300				
Leu	Thr	Phe	Tyr	Ser	Gly	Pro	Ala	Pro	Ala	Asp	Val	Thr	Arg	Gln	Tyr
305					310					315					320
Leu	Thr	Ser	Thr	Val	Gly	Leu	Pro	Ala	Met	Gln	Gln	Tyr	Asn	Thr	Leu
				325					330					335	
Gly	Phe	His	Gln	Cys	Arg	Trp	Gly	Tyr	Asn	Asn	Trp	Ser	Asp	Leu	Ala
			340					345					350		
Asp	Val	Val	Ala	Asn	Phe	Glu	Lys	Phe	Glu	Ile	Pro	Leu	Glu	Tyr	Ile
		355					360					365			
Trp	Thr	Asp	Ile	Asp	Tyr	Met	His	Gly	Tyr	Arg	Asn	Phe	Asp	Asn	Asp
	370					375					380				
Gln	His	Arg	Phe	Ser	Tyr	Ser	Glu	Gly	Asp	Glu	Phe	Leu	Ser	Lys	Leu
385					390					395					400
His	Glu	Ser	Gly	Arg	Tyr	Tyr	Val	Pro	Ile	Val	Asp	Ala	Ala	Leu	Tyr
				405					410					415	
Ile	Pro	Asn	Pro	Glu	Asn	Ala	Ser	Asp	Ala	Tyr	Ala	Thr	Tyr	Asp	Arg
			420					425					430		
Gly	Ala	Ala	Asp	Asp	Val	Phe	Leu	Lys	Asn	Pro	Asp	Gly	Ser	Leu	Tyr
		435					440					445			
Ile	Gly	Ala	Val	Trp	Pro	Gly	Tyr	Thr	Val	Phe	Pro	Asp	Trp	His	His
	450					455					460				
Pro	Lys	Ala	Val	Asp	Phe	Trp	Ala	Asn	Glu	Leu	Val	Ile	Trp	Ser	Lys
465					470				475						480
Lys	Val	Ala	Phe	Asp	Gly	Val	Trp	Tyr	Asp	Met	Ser	Glu	Val	Ser	Ser
				485				490					495		
Phe	Cys	Val	Gly	Ser	Cys	Gly	Thr	Gly	Asn	Leu	Thr	Leu	Asn	Pro	Ala
			500					505					510		
His	Pro	Ser	Phe	Leu	Leu	Pro	Gly	Glu	Pro	Gly	Asp	Ile	Ile	Tyr	Asp
		515					520					525			

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Glu Val Asn Thr Thr Ile Ser Ala Asp Leu Glu His Ile Asp Val Thr

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 3

<211> 914

<212> PRT

<213> Homo sapiens

<400> 3

Met Glu Ala Ala Val Lys Glu Glu Ile Ser Leu Glu Asp Glu Ala Val
1 5 10 15

Asp Lys Asn Ile Phe Arg Asp Cys Asn Lys Ile Ala Phe Tyr Arg Arg
20 25 30

Gln Lys Gln Trp Leu Ser Lys Lys Ser Thr Tyr Gln Ala Leu Leu Asp
35 40 45

Ser Val Thr Thr Asp Glu Asp Ser Thr Arg Phe Gln Ile Ile Asn Glu
50 55 60

Ala Ser Lys Val Pro Leu Leu Ala Glu Ile Tyr Gly Ile Glu Gly Asn
65 70 75 80

Ile Phe Arg Leu Lys Ile Asn Glu Glu Thr Pro Leu Lys Pro Arg Phe
85 90 95

Glu Val Pro Asp Val Leu Thr Ser Lys Pro Ser Thr Val Arg Leu Ile
100 105 110

Ser Cys Ser Gly Asp Thr Gly Ser Leu Ile Leu Ala Asp Gly Lys Gly
 115 120 125

Asp Leu Lys Cys His Ile Thr Ala Asn Pro Phe Lys Val Asp Leu Val
 130 135 140

Ser Glu Glu Glu Val Val Ile Ser Ile Asn Ser Leu Gly Gln Leu Tyr
 145 150 155 160

Phe Glu His Leu Gln Ile Leu His Lys Gln Arg Ala Ala Lys Glu Asn
 165 170 175

Glu Glu Glu Thr Ser Val Asp Thr Ser Gln Glu Asn Gln Glu Asp Leu
 180 185 190

Gly Leu Trp Glu Glu Lys Phe Gly Lys Phe Val Asp Ile Lys Ala Asn
 195 200 205

Gly Pro Ser Ser Ile Gly Leu Asp Phe Ser Leu His Gly Phe Glu His
 210 215 220

Leu Tyr Gly Ile Pro Gln His Ala Glu Ser His Gln Leu Lys Asn Thr
 225 230 235 240

Gly Asp Gly Asp Ala Tyr Arg Leu Tyr Asn Leu Asp Val Tyr Gly Tyr
 245 250 255

Gln Ile Tyr Asp Lys Met Gly Ile Tyr Gly Ser Val Pro Tyr Leu Leu
 260 265 270

Ala His Lys Leu Gly Arg Thr Ile Gly Ile Phe Trp Leu Asn Ala Ser
 275 280 285

Glu Thr Leu Val Glu Ile Asn Thr Glu Pro Ala Val Glu Tyr Thr Leu
 290 295 300

Thr Gln Met Gly Pro Val Ala Ala Lys Gln Lys Val Arg Ser Arg Thr
 305 310 315 320

His Val His Trp Met Ser Glu Ser Gly Ile Ile Asp Val Phe Leu Leu
 325 330 335

Thr Gly Pro Thr Pro Ser Asp Val Phe Lys Gln Tyr Ser His Leu Thr
 340 345 350

Gly Thr Gln Ala Met Pro Pro Leu Phe Ser Leu Gly Tyr His Gln Cys
 355 360 365

Arg Trp Asn Tyr Glu Asp Glu Gln Asp Val Lys Ala Val Asp Ala Gly
 370 375 380

Phe Asp Glu His Asp Ile Pro Tyr Asp Ala Met Trp Leu Asp Ile Glu
 385 390 395 400

His Thr Glu Gly Lys Arg Tyr Phe Thr Trp Asp Lys Asn Arg Phe Pro
 405 410 415

Asn Pro Lys Arg Met Gln Glu Leu Leu Arg Ser Lys Lys Arg Lys Leu
 420 425 430

Val Val Ile Ser Asp Pro His Ile Lys Ile Asp Pro Asp Tyr Ser Val
 435 440 445

Tyr Val Lys Ala Lys Asp Gln Gly Phe Phe Val Lys Asn Gln Glu Gly
 450 455 460

Glu Asp Phe Glu Gly Val Cys Trp Pro Gly Leu Ser Ser Tyr Leu Asp
 465 470 475 480

Phe Thr Asn Pro Lys Val Arg Glu Trp Tyr Ser Ser Leu Phe Ala Phe
 485 490 495

Pro Val Tyr Gln Gly Ser Thr Asp Ile Leu Phe Leu Trp Asn Asp Met
 500 505 510

Asn Glu Pro Ser Val Phe Arg Gly Pro Glu Gln Thr Met Gln Lys Asn
 515 520 525

Ala Ile His His Gly Asn Trp Glu His Arg Glu Leu His Asn Ile Tyr
 530 535 540

Gly Phe Tyr His Gln Met Ala Thr Ala Glu Gly Leu Ile Lys Arg Ser
 545 550 555 560

Lys Gly Lys Glu Arg Pro Phe Val Leu Thr Arg Ser Phe Phe Ala Gly
 565 570 575

Ser Gln Lys Tyr Gly Ala Val Trp Thr Gly Asp Asn Thr Ala Glu Trp
 580 585 590

Ser Asn Leu Lys Ile Ser Ile Pro Met Leu Leu Thr Leu Ser Ile Thr
 595 600 605

Gly Ile Ser Phe Cys Gly Ala Asp Ile Gly Gly Phe Ile Gly Asn Pro
 610 615 620

Glu Thr Glu Leu Leu Val Arg Trp Tyr Gln Ala Gly Ala Tyr Gln Pro
 625 630 635 640

Phe Phe Arg Gly His Ala Thr Met Asn Thr Lys Arg Arg Glu Pro Trp
 645 650 655

Leu Phe Gly Glu Glu His Thr Arg Leu Ile Arg Glu Ala Ile Arg Glu
 660 665 670

Arg Tyr Gly Leu Leu Pro Tyr Trp Tyr Ser Leu Phe Tyr His Ala His
 675 680 685

Val Ala Ser Gln Pro Val Met Arg Pro Leu Trp Val Glu Phe Pro Asp
 690 695 700

Glu Leu Lys Thr Phe Asp Met Glu Asp Glu Tyr Met Leu Gly Ser Ala
705 710 715 720

Leu Leu Val His Pro Val Thr Glu Pro Lys Ala Thr Thr Val Asp Val
725 730 735

Phe Leu Pro Gly Ser Asn Glu Val Trp Tyr Asp Tyr Lys Thr Phe Ala
740 745 750

His Trp Glu Gly Gly Cys Thr Val Lys Ile Pro Val Ala Leu Asp Thr
755 760 765

Ile Pro Val Phe Gln Arg Gly Gly Ser Val Ile Pro Ile Lys Thr Thr
770 775 780

Val Gly Lys Ser Thr Gly Trp Met Thr Glu Ser Ser Tyr Gly Leu Arg
785 790 795 800

Val Ala Leu Ser Thr Lys Gly Ser Ser Val Gly Glu Leu Tyr Leu Asp
805 810 815

Asp Gly His Ser Phe Gln Tyr Leu His Gln Lys Gln Phe Leu His Arg
820 825 830

Lys Phe Ser Phe Cys Ser Ser Val Leu Ile Asn Ser Phe Ala Asp Gln
835 840 845

Arg Gly His Tyr Pro Ser Lys Cys Val Val Glu Lys Ile Leu Val Leu
850 855 860

Gly Phe Arg Lys Glu Pro Ser Ser Val Thr Thr His Ser Ser Asp Gly
865 870 875 880

Lys Asp Gln Pro Val Ala Phe Thr Tyr Cys Ala Lys Thr Ser Ile Leu
885 890 895

Ser Leu Glu Lys Leu Ser Leu Asn Ile Ala Thr Asp Trp Glu Val Arg
900 905 910

Ile Ile

<210> 4

<211> 953

<212> PRT

<213> Mus musculus

<400> 4

Met Asn Ile Arg Lys Pro Leu Cys Ser Asn Ser Val Val Gly Ala Cys
1 5 10 15

Thr Leu Val Ser Leu Thr Thr Ala Val Ile Leu Gly His Leu Met Leu
20 25 30

Arg Glu Leu Met Leu Leu Pro Gln Asp Leu His Glu Ser Ser Ser Gly
35 40 45

Leu Trp Lys Thr Tyr Arg Pro His His Gln Glu Ser Tyr Glu Pro Ala
 50 55 60

Pro Leu His Ile Gln Glu His Ala Glu Gln Leu Arg Ala Val Pro Thr
 65 70 75 80

Gln Cys Asp Val Thr Pro Asn Ser Arg Phe Asp Cys Ala Pro Asp Lys
 85 90 95

Gly Ile Thr Gln Glu Gln Cys Glu Ala Arg Gly Cys Cys Trp Val Pro
 100 105 110

Ala Gly Gln Val Leu Asn Gly Pro Val Met Gly Gln Pro Trp Cys Phe
 115 120 125

Phe Pro Pro Ser Tyr Pro Ser Tyr Arg Leu Glu Asn Leu Ser Ser Thr
 130 135 140

Glu Ser Gly Tyr Thr Ala Thr Leu Thr Arg Thr Ser Pro Thr Phe Phe
 145 150 155 160

Pro Lys Asp Val Leu Thr Leu Gln Leu Glu Val Leu Met Glu Thr Asp
 165 170 175

Ser Arg Leu His Phe Met Ile Lys Asp Pro Thr Ser Lys Arg Tyr Glu
 180 185 190

Val Pro Leu Glu Thr Pro Arg Val Leu Ser Gln Ala Pro Ser Pro Leu
 195 200 205

Tyr Ser Val Glu Phe Ser Glu Glu Pro Phe Gly Val Ile Val Arg Arg
 210 215 220

Lys Leu Gly Gly Arg Val Leu Leu Asn Thr Thr Val Ala Pro Leu Phe
 225 230 235 240

Phe Ala Asp Gln Phe Leu Gln Leu Ser Thr Ser Leu Pro Ser Gln His
 245 250 255

Ile Ala Gly Leu Gly Glu His Leu Ser Pro Leu Met Leu Ser Thr Glu
 260 265 270

Trp Thr Arg Ile Thr Leu Trp Asn Arg Asp Val Ala Pro Ser Gln Gly
 275 280 285

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

Gly Leu Ala His Gly Val Phe Leu Leu Asn Ser Asn Ala Met Asp Val
 305 310 315 320

Val Leu Gln Pro Ser Pro Ala Leu Thr Trp Arg Ser Thr Gly Gly Ile
 325 330 335

Leu Asp Val Tyr Val Phe Leu Gly Pro Glu Pro Lys Ser Val Val Gln
 340 345 350

Gln Tyr Leu Asp Val Val Gly Tyr Pro Phe Met Pro Pro Tyr Trp Gly
 355 360 365
 Leu Gly Phe His Leu Cys Arg Trp Gly Tyr Ser Ser Thr Ala Ile Val
 370 375 380
 Arg Gln Val Val Glu Asn Met Thr Arg Thr His Phe Pro Leu Asp Val
 385 390 395 400
 Gln Trp Asn Asp Leu Asp Tyr Met Asp Ala Arg Arg Asp Phe Thr Phe
 405 410 415
 Asn Gln Asp Gly Phe Ala Asp Phe Pro Asp Met Val His Glu Leu His
 420 425 430
 Gln Gly Gly Arg Arg Tyr Met Met Ile Val Asp Pro Ala Ile Ser Ser
 435 440 445
 Ser Gly Pro Ala Gly Ser Tyr Arg Pro Tyr Asp Glu Gly Leu Arg Arg
 450 455 460
 Gly Val Phe Ile Thr Asn Glu Thr Gly Gln Pro Leu Ile Gly Lys Val
 465 470 475 480
 Trp Pro Gly Ser Thr Ala Phe Pro Asp Phe Thr Asn Pro Glu Thr Leu
 485 490 495
 Asp Trp Trp Gln Asp Met Val Ser Glu Phe His Ala Gln Val Pro Phe
 500 505 510
 Asp Gly Met Trp Ile Asp Met Asn Glu Pro Ser Asn Phe Ile Arg Gly
 515 520 525
 Ser Gln Gln Gly Cys Pro Asp Asn Glu Leu Glu Asn Pro Pro Tyr Val
 530 535 540
 Pro Gly Val Val Gly Gly Ala Leu Gln Ala Ala Thr Ile Cys Ala Ser
 545 550 555 560
 Ser His Gln Phe Leu Ser Thr His Tyr Asn Leu His Asn Leu Tyr Gly
 565 570 575
 Leu Thr Glu Ala Ile Ala Ser Ser Arg Ala Leu Val Lys Thr Arg Gly
 580 585 590
 Thr Arg Pro Phe Val Ile Ser Arg Ser Thr Phe Ala Gly His Gly Arg
 595 600 605
 Tyr Ala Gly His Trp Thr Gly Asp Val Trp Ser Ser Trp Glu His Leu
 610 615 620
 Ala Tyr Ser Val Pro Glu Ile Leu Gln Phe Asn Leu Leu Gly Val Pro
 625 630 635 640
 Leu Val Gly Ala Asp Ile Cys Gly Phe Gln Gly Asn Thr Thr Glu Glu
 645 650 655

Leu Cys Val Arg Trp Thr Gln Leu Gly Ala Phe Tyr Pro Phe Met Arg
 660 665 670

Asn His Asn Asp Leu Asn Ser Leu Pro Gln Glu Pro Tyr Arg Phe Ser
 675 680 685

Glu Thr Ala Gln Gln Ala Met Arg Lys Ala Phe Thr Leu Arg Tyr Ala
 690 695 700

Leu Leu Pro Tyr Leu Tyr Thr Leu Phe His Gly Ala His Val Lys Gly
 705 710 715 720

Asp Thr Val Ala Arg Pro Leu Phe Leu Glu Phe Pro Glu Asp Pro Ser
 725 730 735

Thr Trp Ser Val Asp Arg Gln Leu Leu Trp Gly Pro Ala Leu Leu Ile
 740 745 750

Thr Pro Val Leu Glu Pro Gly Lys Thr Asp Val Thr Gly Tyr Phe Pro
 755 760 765

Lys Gly Met Trp Tyr Asn Leu Gln Met Val Pro Val Glu Thr Leu Gly
 770 775 780

Ser Leu Pro Ser Ser Ser Pro Ala Ser Ser Phe Arg Ser Ile Val His
 785 790 795 800

Ser Lys Gly Gln Trp Leu Thr Leu Glu Ala Pro Leu Asp Thr Ile Asn
 805 810 815

Val His Leu Arg Ala Gly Tyr Ile Ile Pro Leu Gln Gly Pro Ser Leu
 820 825 830

Thr Thr Thr Glu Ser Arg Lys Gln Pro Met Ala Leu Ala Val Ala Leu
 835 840 845

Thr Glu Ser Gly Glu Ala Ser Gly Glu Leu Phe Trp Asp Asp Gly Glu
 850 855 860

Ser Leu Gly Val Leu Glu Arg Gly Ala Tyr Thr Leu Val Thr Phe Ser
 865 870 875 880

Ala Lys Asn Asn Thr Ile Val Asn Lys Leu Val His Val Thr Lys Glu
 885 890 895

Gly Gly Glu Leu Gln Leu Arg Glu Val Thr Ile Leu Gly Val Thr Thr
 900 905 910

Ala Pro Thr Gln Val Leu Ser Asn Gly Ile Ser Val Ser Asn Phe Thr
 915 920 925

Tyr Ser Pro Asp Asp Lys Ser Leu Ser Ile Pro Val Ser Leu Leu Met
 930 935 940

Gly Glu Arg Phe Gln Ile Asp Trp Ser
945 950

<210> 5

<211> 954

<212> PRT

<213> Yeast GLU2A

<400> 5

Met Val Leu Leu Lys Trp Leu Val Cys Gln Leu Val Phe Phe Thr Ala
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Phe Ser His Ala Phe Thr Asp Tyr Leu Leu Lys Lys Cys Ala Gln Ser
20 25 30

Gly Phe Cys His Arg Asn Arg Val Tyr Ala Glu Asn Ile Ala Lys Ser
35 40 45

His His Cys Tyr Tyr Lys Val Asp Ala Glu Ser Ile Ala His Asp Pro
50 55 60

Leu Glu Asn Val Leu His Ala Thr Ile Ile Lys Thr Ile Pro Arg Leu
65 70 75 80

Glu Gly Asp Asp Ile Ala Val Gln Phe Pro Phe Ser Leu Ser Phe Leu
85 90 95

Gln Asp His Ser Val Arg Phe Thr Ile Asn Glu Lys Glu Arg Met Pro
100 105 110

Thr Asn Ser Ser Gly Leu Leu Ile Ser Ser Gln Arg Phe Asn Glu Thr
115 120 125

Trp Lys Tyr Ala Phe Asp Lys Lys Phe Gln Glu Glu Ala Asn Arg Thr
130 135 140

Ser Ile Pro Gln Phe His Phe Leu Lys Gln Lys Gln Thr Val Asn Ser
145 150 155 160

Phe Trp Ser Lys Ile Ser Ser Phe Leu Ser Leu Ser Asn Ser Thr Ala
165 170 175

Asp Thr Phe His Leu Arg Asn Gly Asp Val Ser Val Glu Ile Phe Ala
180 185 190

Glu Pro Phe Gln Leu Lys Val Tyr Trp Gln Asn Ala Leu Lys Leu Ile
195 200 205

Val Asn Glu Gln Asn Phe Leu Asn Ile Glu His His Arg Thr Lys Gln
210 215 220

Glu Asn Phe Ala His Val Leu Pro Glu Glu Thr Thr Phe Asn Met Phe
225 230 235 240

Lys Asp Asn Phe Leu Tyr Ser Lys His Asp Ser Met Pro Leu Gly Pro
 245 250 255

Glu Ser Val Ala Leu Asp Phe Ser Phe Met Gly Ser Thr Asn Val Tyr
 260 265 270

Gly Ile Pro Glu His Ala Thr Ser Leu Arg Leu Met Asp Thr Ser Gly
 275 280 285

Gly Lys Glu Pro Tyr Arg Leu Phe Asn Val Asp Val Phe Glu Tyr Asn
 290 295 300

Ile Gly Thr Ser Gln Pro Met Tyr Gly Ser Ile Pro Phe Met Phe Ser
 305 310 315 320

Ser Ser Ser Thr Ser Ile Phe Trp Val Asn Ala Ala Asp Thr Trp Val
 325 330 335

Asp Ile Lys Tyr Asp Thr Ser Lys Asn Lys Thr Met Thr His Trp Ile
 340 345 350

Ser Glu Asn Gly Val Ile Asp Val Val Met Ser Leu Gly Pro Asp Ile
 355 360 365

Pro Thr Ile Ile Asp Lys Phe Thr Asp Leu Thr Gly Arg Pro Phe Leu
 370 375 380

Pro Pro Ile Ser Ser Ile Gly Tyr His Gln Cys Arg Trp Asn Tyr Asn
 385 390 395 400

Asp Glu Met Asp Val Leu Thr Val Asp Ser Gln Met Asp Ala His Met
 405 410 415

Ile Pro Tyr Asp Phe Ile Trp Leu Asp Leu Glu Tyr Thr Asn Asp Lys
 420 425 430

Lys Tyr Phe Thr Trp Lys Gln His Ser Phe Pro Asn Pro Lys Arg Leu
 435 440 445

Leu Ser Lys Leu Lys Lys Leu Gly Arg Asn Leu Val Val Leu Ile Asp
 450 455 460

Pro His Leu Lys Lys Asp Tyr Glu Ile Ser Asp Arg Val Ile Asn Glu
 465 470 475 480

Asn Val Ala Val Lys Asp His Asn Gly Asn Asp Tyr Val Gly His Cys
 485 490 495

Trp Pro Gly Asn Ser Ile Trp Ile Asp Thr Ile Ser Lys Tyr Gly Gln
 500 505 510

Lys Ile Trp Lys Ser Phe Phe Glu Arg Phe Met Asp Leu Pro Ala Asp
 515 520 525

Leu Thr Asn Leu Phe Ile Trp Asn Asp Met Asn Glu Pro Ser Ile Phe
 530 535 540

Asp Gly Pro Glu Thr Thr Ala Pro Lys Asp Leu Ile His Asp Asn Tyr
 545 550 555 560

Ile Glu Glu Arg Ser Val His Asn Ile Tyr Gly Leu Ser Val His Glu
 565 570 575

Ala Thr Tyr Asp Ala Ile Lys Ser Ile Tyr Ser Pro Ser Asp Lys Arg
 580 585 590

Pro Phe Leu Leu Thr Arg Ala Phe Phe Ala Gly Ser Gln Arg Thr Ala
 595 600 605

Ala Thr Trp Thr Gly Asp Asn Val Ala Asn Trp Asp Tyr Leu Lys Ile
 610 615 620

Ser Ile Pro Met Val Leu Ser Asn Asn Ile Ala Gly Met Pro Phe Ile
 625 630 635 640

Gly Ala Asp Ile Ala Gly Phe Ala Glu Asp Pro Thr Pro Glu Leu Ile
 645 650 655

Ala Arg Trp Tyr Gln Ala Gly Leu Trp Tyr Pro Phe Phe Arg Ala His
 660 665 670

Ala His Ile Asp Thr Lys Arg Arg Glu Pro Tyr Leu Phe Asn Glu Pro
 675 680 685

Leu Lys Ser Ile Val Arg Asp Ile Ile Gln Leu Arg Tyr Phe Leu Leu
 690 695 700

Pro Thr Leu Tyr Thr Met Phe His Lys Ser Ser Val Thr Gly Phe Pro
 705 710 715 720

Ile Met Asn Pro Met Phe Ile Glu His Pro Glu Phe Ala Glu Leu Tyr
 725 730 735

His Ile Asp Asn Gln Phe Tyr Trp Ser Asn Ser Gly Leu Leu Val Lys
 740 745 750

Pro Val Thr Glu Pro Gly Gln Ser Glu Thr Glu Met Val Phe Pro Pro
 755 760 765

Gly Ile Phe Tyr Glu Phe Ala Ser Leu His Ser Phe Ile Asn Asn Gly
 770 775 780

Thr Asp Leu Ile Glu Lys Asn Ile Ser Ala Pro Leu Asp Lys Ile Pro
 785 790 795 800

Leu Phe Ile Glu Gly Gly His Ile Ile Thr Met Lys Asp Lys Tyr Arg
 805 810 815

Arg Ser Ser Met Leu Met Lys Asn Asp Pro Tyr Val Ile Val Ile Ala
 820 825 830

Pro Asp Thr Glu Gly Arg Ala Val Gly Asp Leu Tyr Val Asp Asp Gly
 835 840 845

Glu Thr Phe Gly Tyr Gln Arg Gly Glu Tyr Val Glu Thr Gln Phe Ile
850 855 860

Phe Glu Asn Asn Thr Leu Lys Asn Val Arg Ser His Ile Pro Glu Asn
865 870 875 880

Leu Thr Gly Ile His His Asn Thr Leu Arg Asn Thr Asn Ile Glu Lys
885 890 895

Ile Ile Ile Ala Lys Asn Asn Leu Gln His Asn Ile Thr Leu Lys Asp
900 905 910

Ser Ile Lys Val Lys Lys Asn Gly Glu Glu Ser Ser Leu Pro Thr Arg
915 920 925

Ser Ser Tyr Glu Asn Asp Asn Lys Ile Thr Ile Leu Asn Leu Ser Leu
930 935 940

Asp Ile Thr Glu Asp Trp Glu Val Ile Phe
945 950

<210> 6

<211> 992

<212> PRT

<213> Aspergillus nidulans

<400> 6

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

Val Thr Ala Thr Ala Thr Val Ala Gly Gln Gln Ala Gln Phe Thr Leu
35 40 45

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

Pro Glu Ala Val Asn Ala Gln Ser Val Cys Pro Gly Tyr Lys Ala Ser
65 70 75 80

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

Gly Glu Pro Cys Asn Val Tyr Gly Thr Asp Val Glu Ser Leu Thr Leu
100 105 110

Glu Met Gln Tyr Gln Asp Thr Asp Arg Leu Asn Ile Gln Ile Thr Pro
115 120 125

Thr Tyr Val Asp Ala Ser Asn Ala Ser Trp Tyr Ile Leu Pro Glu Glu
130 135 140

Phe Val Pro Arg Pro Lys Pro Ala Ala Gly Ala Ser Glu Ser His Ser
145 150 155 160

Asp Phe Ala Val Thr Trp Ser Asn Glu Pro Thr Phe Asn Phe Gln Val
165 170 175

Thr Arg Lys Ser Thr Gly Glu Val Leu Phe Asp Thr Ala Gly Ser Val
180 185 190

Leu Val Phe Glu Asn Gln Phe Ile Glu Phe Val Thr Ser Leu Pro Glu
195 200 205

Glu Tyr Asn Leu Tyr Gly Leu Gly Glu Arg Ile Asn Gln Leu Arg Leu
210 215 220

Leu Arg Asn Ala Thr Leu Thr Ser Tyr Ala Ala Asp Ile Gly Asn Pro
225 230 235 240

Ile Asp Ala Asn Ile Tyr Gly Gln His Ala Phe Tyr Val Asp Thr Arg
245 250 255

Tyr Phe Ser Val Asp Glu Ala Gly Lys His Thr Tyr Val Lys Ser Ser
260 265 270

Glu Ala Asp Pro Ser Ala Thr Tyr Thr Ser Tyr Ser His Gly Val Phe
275 280 285

Leu Arg Asn Ser His Gly His Glu Val Val Leu Asn Pro Gln Gly Leu
290 295 300

Thr Trp Arg Thr Ile Gly Gly Ser Ile Asp Leu Thr Leu Tyr Ser Gly
305 310 315 320

Pro Thr Val Ala Glu Val Thr Lys Gln Tyr Gln Arg Ser Thr Val Gly
325 330 335

Leu Pro Ala Met Gln Lys Tyr Asp Thr Leu Gly Phe His Gln Cys Arg
340 345 350

Trp Gly Tyr Asn Asn Trp Ser Val Phe Ala Asp Val Leu Ala Asn Phe
355 360 365

Glu Lys Phe Glu Ile Pro Leu Glu Tyr Leu Trp Ala Asp Ile Asp Tyr
370 375 380

Met His Gly Tyr Arg Asn Phe Glu Asn Asp Glu Tyr Arg Phe Pro Tyr
385 390 395 400

Asn Glu Thr Lys Val Phe Leu Asp Lys Leu His Ala Gly Gly Arg His
405 410 415

Phe Val Pro Ile Val Asp Ala Ala Leu Tyr Ile Pro Asn Pro Gln Asn
420 425 430

Ala Ser Asp Ser Tyr Glu Thr Tyr Thr Arg Gly Ala Ala Arg Asp Val
435 440 445

Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr Ile Gly Ala Val Trp Pro
450 455 460

Gly Tyr Thr Val Phe Pro Asp Trp His His Pro Asp Ala Ala Asp Phe
465 470 475 480

Trp Ala Asn Glu Leu Val Thr Trp Tyr Glu Lys Val Lys Phe Asp Gly
485 490 495

Val Trp Tyr Asp Met Ser Glu Val Ser Ser Phe Cys Val Gly Ser Cys
500 505 510

Gly Ser Arg Asn Arg Thr Leu Asn Pro Val His Pro Pro Phe Arg Leu
515 520 525

Pro Gly Glu Pro Gly Asn Val Asp Tyr Glu Tyr Pro Glu Gly Phe Glu
530 535 540

Leu Ser Asn Ala Thr Glu Ala Ala Ser Ala Ser Ala Ala Ser Ser Ser
545 550 555 560

Gln Ala Ala Thr Thr Ala Thr Glu Thr Thr Thr Ser Thr Ser Ser Tyr
565 570 575

Leu Arg Thr Ser Pro Thr Pro Gly Val Arg Asn Val Asn Tyr Pro Pro
580 585 590

Tyr Val Ile Asn His Val Gln Thr Gly His Asp Leu Ala Val His Ala
595 600 605

Val Ser Pro Asn Ala Thr His Val Asp Gly Tyr His Glu Tyr Asp Val
610 615 620

His Ser Leu Tyr Gly His Met Gly Ile Gln Ala Thr Tyr Arg Gly Leu
625 630 635 640

Thr Gln Ile Ala Pro Arg Lys Arg Pro Phe Ile Ile Gly Arg Ser Thr
645 650 655

Phe Ala Gly Ser Gly Lys Trp Ala Gly His Trp Gly Gly Asp Asn Tyr
660 665 670

Ser Arg Trp Ser Ser Met Tyr Phe Ser Ile Ser Gln Ala Leu Gln Phe
675 680 685

Ser Leu Tyr Gly Ile Pro Met Phe Gly Val Asp Thr Cys Gly Phe Ser
690 695 700

Gly Asn Thr Ala Glu Glu Leu Cys Asn Arg Trp Met Gln Leu Ser Ala
705 710 715 720

Phe Phe Pro Phe Tyr Arg Asn His Asn Val Leu Gly Thr Ile Pro Gln
725 730 735

Glu Pro Tyr Gln Trp Ala Ser Val Ile Asp Ala Thr Lys Lys Ala Met
740 745 750

Arg Ile Arg Tyr Ala Leu Leu Pro Tyr Phe Tyr Thr Leu Met His Asp
 755 760 765
 Ala His Thr Thr Gly Ser Thr Val Leu Arg Ala Leu Ala Trp Glu Phe
 770 775 780
 Pro Asp Asp Pro Ser Leu Ala Ala Ile Asp Asn Gln Phe Leu Val Gly
 785 790 795 800
 Pro Ser Ile Leu Val Thr Pro Val Leu Glu Pro Gln Val Ser Thr Val
 805 810 815
 Lys Gly Val Phe Pro Gly Val Gly Gln Gly Glu Val Trp Tyr Asp Trp
 820 825 830
 Tyr Thr Gln Thr Ala Val Asp Ala Gln Pro Gly Val Asn Thr Thr Ile
 835 840 845
 Asp Ala Pro Leu Gly His Ile Pro Val Tyr Val Arg Gly Gly Ser Ile
 850 855 860
 Leu Pro Met Gln Glu Pro Ala Leu Thr Thr Arg Asp Ala Arg Lys Thr
 865 870 875 880
 Pro Trp Ala Leu Leu Val Ala Leu Gly Lys Asp Gly Thr Ala Ser Gly
 885 890 895
 His Leu Tyr Leu Asp Asp Gly Glu Ser Ile His Pro Lys Val Ser Leu
 900 905 910
 Asn Val Lys Phe Arg Ala Thr Gln Thr Ala Leu Thr Val Ser Ser Glu
 915 920 925
 Gly Glu Trp Lys Glu Ala Asn Pro Leu Ala Asn Val Thr Ile Leu Gly
 930 935 940
 Val Leu Glu Asn Pro Val Ser Val Thr Ser Asn Gly Gln Gln Val Pro
 945 950 955 960
 Ala Glu Tyr Asp Ala Gln Ser Arg Ile Leu Val Ile Thr Gly Leu Asn
 965 970 975
 Gln Phe Thr Asn Asn Gly Ala Trp Gly Gln Asp Trp Thr Leu Arg Trp
 980 985 990
 <210> 7
 <211> 955
 <212> PRT
 <213> Aspergillus nidulans
 <400> 7
 Met Arg Phe Gln Gln Leu Leu Pro Trp Ala Ala Ala Leu Thr Gly Cys
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 Val Val Ala Gln Ser Gln Ala Gly Val Asp Pro Leu Asp Arg Pro Gly
 20 25 30

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Asn	Asp	Leu	Tyr	Val	Lys	Asp	Leu	Ser	Asn	Cys	Thr	Gly	Tyr	Lys	Val
	35					40					45				
Thr	Lys	His	Trp	Lys	Thr	Arg	Ser	Gly	Phe	Tyr	Ala	Asp	Leu	Ala	Leu
	50					55					60				
Ala	Gly	Pro	Ala	Cys	Asn	Val	Tyr	Gly	Ile	Asp	Leu	Pro	Lys	Leu	Lys
	65					70					75				80
Leu	Glu	Val	Glu	Tyr	Gln	Thr	Asp	Glu	Arg	Leu	His	Val	Lys	Ile	Leu
			85						90					95	
Asp	Thr	Asn	Asn	Thr	Val	Tyr	Gln	Val	Pro	Asp	Ser	Val	Phe	Pro	Arg
			100						105					110	
Pro	Gly	Phe	Gly	Gln	Trp	Cys	Ser	Pro	Lys	Asn	Ser	Lys	Leu	Lys	Phe
		115						120					125		
Asp	Phe	Lys	Pro	Asp	Pro	Phe	Ser	Phe	Thr	Val	Ser	Arg	Thr	Asp	Thr
	130					135						140			
Gly	Glu	Val	Leu	Phe	Asp	Thr	Thr	Gly	Thr	Lys	Leu	Val	Phe	Glu	Asn
	145					150					155				160
Gln	Tyr	Leu	Tyr	Leu	Lys	Thr	His	Leu	Pro	Gln	Asn	Pro	His	Leu	Tyr
				165					170					175	
Gly	Leu	Gly	Glu	His	Ser	Asp	Ser	Phe	Met	Leu	Asn	Thr	Thr	Asn	Tyr
			180						185					190	
Thr	Arg	Thr	Ile	Tyr	Thr	Arg	Asp	Ala	Tyr	Gly	Thr	Pro	Gln	Gly	Gln
		195					200						205		
Asn	Leu	Tyr	Gly	Ala	His	Pro	Ile	Tyr	Phe	Asp	His	Arg	Gln	Asp	Gly
	210						215					220			
Thr	His	Gly	Val	Phe	Leu	Leu	Asn	Ser	Asn	Gly	Met	Asp	Ile	Tyr	Ile
	225					230					235				240
Asp	Asn	Glu	Gly	Gly	Gln	Phe	Leu	Glu	Tyr	Asn	Ile	Ile	Gly	Gly	Val
				245					250					255	
Phe	Asp	Phe	Tyr	Phe	Ile	Ala	Gly	Pro	Ser	Pro	Gln	Asp	Val	Ala	Arg
			260					265						270	
Gln	Tyr	Ala	Glu	Ile	Val	Gln	Pro	Pro	Leu	Met	Val	Pro	Tyr	Trp	Gly
		275					280						285		
Leu	Gly	Phe	His	Gln	Cys	Arg	Tyr	Gly	Tyr	Gln	Asp	Val	Tyr	Glu	Val
	290					295					300				
Ala	Ala	Val	Thr	Ala	Asn	Tyr	Ser	Val	His	Asp	Ile	Pro	Leu	Glu	Thr
	305					310					315				320
Ile	Trp	Thr	Asp	Ile	Asp	Tyr	Met	Asp	Arg	Arg	Arg	Ile	Phe	Thr	Leu
				325					330					335	

Asp Pro Glu Arg Phe Pro Pro Glu Leu Val Lys Asp Leu Val Asp Thr
340 345 350

Leu His Ala Arg Asp Gln His Tyr Ile Val Met Val Asp Pro Ala Val
355 360 365

Tyr Tyr Ser Glu Pro Asn Pro Ala Leu Asp Ala Gly Leu Lys Tyr Asp
370 375 380

Ala Phe Met Lys Glu Leu Asn Gly Thr His Tyr Gln Gly Val Val Trp
385 390 395 400

Ala Gly Pro Ser Tyr Phe Pro Asp Trp Phe His Pro Asn Ala Gln Glu
405 410 415

Tyr Trp Thr Glu Gln Phe Leu Asn Phe Phe Asp Gly Val Asn Gly Pro
420 425 430

Asp Ile Asp Ala Leu Trp Ile Asp Met Asn Glu Pro Ala Asn Phe Tyr
435 440 445

Asn Arg Pro Tyr Pro Gly Asn Asn Thr Thr Pro Glu Glu Phe Ala Glu
450 455 460

Ala Asn Asp Asn Pro Pro Glu Pro Pro Ala Val Arg Asp Gly Pro Asp
465 470 475 480

Ala Pro Ile Pro Gly Phe Pro Asp Ser Leu Gln Pro Asn Phe Ala Ser
485 490 495

Gly Gln Thr Asn Glu Lys Arg Ala Val Val Thr Val Glu Arg Arg Ala
500 505 510

Arg Ser Gln Ser His Arg Gln Leu Gly Ala Gly Arg Trp Arg Ser Ala
515 520 525

Val Arg His Trp Pro Arg Asp Pro Lys Ala Gly Trp Gln His Gly Arg
530 535 540

Lys Ser Gly Ser Gly Cys Gly Pro His Glu Cys Arg Gly Leu Pro Asn
545 550 555 560

Arg Glu Leu Ile Arg Pro Pro Tyr Met Ile Gln Asn Gly Ala Gly Pro
565 570 575

Thr Leu Ala Asp Asn Thr Ala Asp Thr Asp Ile Val Gln Ser Gly Gly
580 585 590

Tyr Val Gln Tyr Asp Thr His Ser Leu Tyr Gly Ala Met Met Ser Thr
595 600 605

His Ser His Asn Ala Met Arg Ala Arg Arg Pro Asp Asp Arg Ala Leu
610 615 620

Val Ile Thr Arg Ser Thr Phe Ala Gly Ser Gly Lys Asp Val Ser His
 625 630 635 640

Trp Leu Gly Asp Asn Ile Ser Asp Trp Leu Ser Tyr Arg Leu Ser Ile
 645 650 655

Ser Gln Ile Leu Gln Phe Ala Ser Leu Tyr Gln Ile Pro Val Val Gly
 660 665 670

Pro Asp Val Cys Gly Phe Gly Gly Asn Val Thr Glu Thr Leu Cys Ala
 675 680 685

Arg Trp Ala Thr Leu Gly Ser Phe Tyr Thr Phe Phe Arg Asn His Ala
 690 695 700

Glu Ile Phe Ala Asn Pro Gln Glu Phe Tyr Arg Trp Pro Ile Val Ala
 705 710 715 720

Glu Ala Ala Arg Asn Gly Ile Ala Ile Arg Tyr Gln Leu Leu Asp Tyr
 725 730 735

Ile Tyr Thr Ala Ile Tyr Lys Gln Thr Gln Thr Gly Thr Pro Ser Leu
 740 745 750

Asn Pro Leu Phe Phe Asn Tyr Pro Phe Asp Gln Asn Thr Tyr Gly Ile
 755 760 765

Asp Leu Gln Phe Phe Tyr Gly Pro Gly Ile Leu Val Ser Pro Val Thr
 770 775 780

Glu Glu Asn Ser Thr Ser Val Ser Tyr Tyr Leu Pro Asp Asp Ile Phe
 785 790 795 800

Tyr Glu Trp Gly Thr Gly Lys Pro Val Arg Gly His Gly Glu Tyr Val
 805 810 815

Ser Ala Glu Val Asp Val Thr His Ile Thr Val His Tyr Lys Gly Gly
 820 825 830

Leu Val Tyr Pro Gln Arg Ile Glu Ser Ala Asn Thr Thr Thr Ala Leu
 835 840 845

Arg Gln Lys Gly Phe Asn Ile Val Ile Ala Pro Gly Leu Asp Gly Ser
 850 855 860

Ala His Gly Glu Leu Tyr Leu Asp Asp Gly Leu Ser Gln Val Gln Asp
 865 870 875 880

Lys Val Ser Glu Ile Asp Phe Ser Tyr Val Asp Gly Val Phe Glu Met
 885 890 895

Lys Gly Ser Phe Glu Tyr Asp Pro Gly Val Gly Ile Glu Arg Ile Thr
 900 905 910

Ile Leu Gly Val Gly Ala Lys Pro Glu Val Ala Ala Glu Asp Ala Glu
 915 920 925

Val Glu Tyr Asp Glu Glu Asn Gln Lys Leu Val Leu His Val Asp Val
 930 935 940

Pro Leu Thr Arg Lys Ser Ser Ile Lys Ile Ala
 945 950 955

<210> 8

<211> 864

<212> PRT

<213> Mucor javanicus

<400> 8

Met Ala Lys Val Ser Phe Ile Phe Val Ala Ile Ala Leu Ile Thr Gly
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Asn Val Leu Cys Gln Thr Asp Ala Thr Tyr Ala Val Ser Ser Ser Ala
 20 25 30

Pro Gly Tyr Lys Ile Asp Gly His Val Arg Lys Thr Glu Ala Gly Leu
 35 40 45

His Ile Pro Leu Thr Leu Asn Ser Arg Gly Asn Lys Lys Thr Gly Ile
 50 55 60

Asp Thr Phe Gly Lys Thr Ile Lys Asp Ile Thr Val Asp Val Glu Tyr
 65 70 75 80

Glu Thr Glu Glu Arg Leu His Val Lys Ile Ser Asp Lys Ala Lys Lys
 85 90 95

Gln Tyr Leu Val Pro Asp Ser Pro Leu Gly Phe Glu Arg Pro Gln Ile
 100 105 110

Lys His Tyr Val Ser Pro Lys His Ser Asn Leu Asp Phe Gln Tyr Thr
 115 120 125

Ala Lys Pro Phe Ser Phe Lys Val Val Arg Lys Asp Asp Lys Thr Thr
 130 135 140

Ile Phe Asp Thr Thr Asn Met Pro Leu Val Phe Glu Asp Gln Tyr Leu
 145 150 155 160

Glu Leu Ser Thr Lys Val Pro Glu Asp Ala Asn Ile Tyr Gly Ile Gly
 165 170 175

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

Ala Arg Asp Asn Pro Asp Asp Phe Tyr Arg Asn Ile Tyr Gly Ala His
 195 200 205

Pro Tyr Tyr Gln Glu Val Arg Asp Gly Lys Ala His Gly Ala Leu Leu
 210 215 220

Met Asn Ala His Glv Met Asp Val Ile Thr Thr Glu Glv Arg Ile Thr

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225          230          235          240
Tyr Lys Val Ile Gly Gly Ile Leu Asp Phe Tyr Phe Phe Ala Pro Lys
                245                250                255
Ser Gly Lys Pro Asn Asp Leu Ser Ile Ala Tyr Thr Asp Leu Ile Gly
                260                265                270
Lys Pro Met Met Pro Ser His Trp Met Leu Gly Trp His His Cys Arg
                275                280                285
Tyr Gly Tyr Pro Asn Ile Asp Lys Val Glu Thr Val Lys Arg Lys Tyr
                290                295                300
Lys Glu Ala Asn Ile Pro Leu Gln Thr Val Trp Val Asp Ile Asp Tyr
305                310                315                320
Met Glu Glu Thr Lys Asp Phe Thr Phe Asp Lys Val Asn Phe Pro Gln
                325                330                335
Asp Arg Met Ile Gly Leu Gly Glu Gln Leu His Lys Asp Gly Gln Asn
                340                345                350
Tyr Val Val Met Val Asp Pro Ala Ile Ser Ala Asn Thr Thr Tyr Glu
                355                360                365
Pro Tyr Val Arg Gly Thr Glu Met Asp Val Trp Ile Lys Asn Ala Asp
                370                375                380
Gly Ser Asp Phe Ile Gly Ser Val Trp Pro Gly Phe Thr Thr Phe Pro
385                390                395                400
Asp Trp Trp His Pro Asn Ala Thr Lys Tyr Trp Asn Lys Glu Ile Ile
                405                410                415
Asp Phe Val Asp Met Leu Gly Val Asp Gly Leu Trp Ile Asp Met Asn
                420                425                430
Glu Pro Ala Ser Phe Cys Leu Gly Ser Cys Gly Ser Gly Lys Val Asp
                435                440                445
Ala Gly Asn Gln Pro Tyr Arg Trp Thr Tyr Thr Glu Glu Glu Gln Ala
                450                455                460
Ala Asn His Thr Arg Trp Glu Lys Glu Leu Lys Ala Met Gly Asn Pro
465                470                475                480
Pro Gly Glu Glu Arg Asn Leu Leu Tyr Pro Lys Tyr Ala Ile Asn Asn
                485                490                495
Gly Ala Gly Asn Leu Ser Glu Phe Thr Val Ala Thr Thr Ala Leu His
                500                505                510
Tyr Gly Asn Ile Pro His Tyr Asp Ile His Asn Leu Tyr Gly His Ala
                515                520                525
Glu Ser His Ile Thr Arg Gln Ala Leu Ile Lys His Lys Asn Lys Ile

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530	535	540
Arg Pro Phe Val Leu Thr Arg Ser Ser Phe Pro Gly Ser Gly Lys Ser		
545	550	555 560
Val Gly His Trp Thr Gly Asp Asn His Ser Phe Trp Pro Tyr Leu Lys		
	565	570 575
Asn Ser Ile Ala Asn Ile Leu Asn Phe Gln Met Phe Gly Val Ser Tyr		
	580	585 590
Ser Gly Ala Asp Val Cys Gly Phe Asn Ser Asp Thr Thr Glu Glu Leu		
	595	600 605
Cys Thr Arg Trp Met Glu Ile Gly Ala Phe Tyr Pro Phe Ala Arg Asn		
610	615	620
His Asn Asn Asn Ala Ala Lys Asp Gln Glu Pro Tyr Leu Trp Glu Ser		
625	630	635 640
Thr Ala Glu Ala Ser Arg Ile Ala Ile Asn Thr Arg Tyr Glu Met Leu		
	645	650 655
Pro Tyr Phe Tyr Thr Leu Phe Glu Glu Ser Asn Arg Leu Gly Leu Gly		
	660	665 670
Val Trp Arg Pro Leu Ile Phe Glu Tyr Pro Ala Tyr Glu Glu Leu Val		
	675	680 685
Ser Asn Asp Val Gln Thr Leu Val Gly Ser Asp Ile Leu Leu Ser Pro		
690	695	700
Val Leu Asp Glu Gly Lys Thr Ser Val Lys Ala Gln Phe Pro Gly Gly		
705	710	715 720
Gln Trp Tyr Asp Trp Tyr Thr His Glu Leu Thr Val Asp Asn Lys Ser		
	725	730 735
Asn Lys Lys Val Lys Thr Val Thr Leu Asp Ala Pro Leu Thr His Ile		
	740	745 750
Pro Ile His Ile Arg Gly Gly Ala Ile Ile Pro Thr Lys Thr Pro Lys		
	755	760 765
Tyr Thr Val Gly Glu Thr Phe Ala Thr Pro Tyr Asn Leu Val Ile Ala		
770	775	780
Leu Asp Lys Lys Gly Gln Ala Ser Gly Arg Leu Tyr Ile Asp Asp Gly		
785	790	795 800
Glu Ser Leu Glu Val Lys Ser Ser Ser Gly Tyr His Phe His Leu Gln		
	805	810 815
Glu Trp Ser Pro Gln Gly Phe Trp Gln Val Trp Leu Gln Glu Gly Arg		
820	825	830

Lys Asp Trp Leu His His His Tyr Trp Gln Ala Arg Gln Gln Val Ala
 835 840 845

Lys Gly Ser Arg Trp Gln Glu Asp Tyr Gln Ile Asp Pro Trp Gln Glu
 850 855 860

<210> 9

<211> 985

<212> PRT

<213> Aspergillus oryzae

<400> 9

Met Ala Gly Leu Lys Ser Phe Leu Ala Ser Ser Trp Leu Leu Pro Val
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Ala Cys Gly Ala Ser Gln Ser Ile Val Pro Ser Thr Ser Ala Thr Ala
 20 25 30

Ala Tyr Ser Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Asn
 35 40 45

Leu Val Ala Asn Ile Asp Asp Pro Gln Ala Val Asn Ala Gln Ser Val
 50 55 60

Cys Pro Gly Tyr Lys Ala Ser Asp Val Lys His Ser Ser Gln Gly Phe
 65 70 75 80

Thr Ala Ser Leu Glu Leu Ala Gly Asp Pro Cys Asn Val Tyr Gly Thr
 85 90 95

Asp Val Asp Ser Leu Thr Leu Thr Val Glu Tyr Gln Ala Lys Asp Arg
 100 105 110

Leu Asn Ile Gln Ile Val Pro Thr Tyr Phe Asp Ala Ser Asn Ala Ser
 115 120 125

Trp Tyr Ile Leu Ser Glu Glu Leu Val Pro Arg Pro Lys Ala Ser Gln
 130 135 140

Asn Ala Ser Val Pro Gln Ser Asp Phe Val Val Ser Trp Ser Asn Glu
 145 150 155 160

Pro Ser Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Val Leu
 165 170 175

Phe Asn Thr Lys Gly Ser Thr Leu Val Tyr Glu Asn Gln Phe Ile Glu
 180 185 190

Phe Val Thr Leu Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu
 195 200 205

Arg Met Asn Gln Leu Arg Leu Leu Glu Asn Ala Asn Leu Thr Leu Tyr
 210 215 220

Ala Ala Asp Ile Ala Asp Pro Ile Asp Asp Asn Ile Tyr Gly His His
 225 230 235 240

Ala Phe Tyr Leu Asp Thr Arg Tyr Tyr Lys Val Gly Gly Gln Asn Lys
 245 250 255

Ser His Thr Ile Val Lys Ser Ser Glu Ala Glu Pro Ser Gln Glu Tyr
 260 265 270

Val Ser Tyr Ser His Gly Val Phe Leu Arg Asn Ala His Gly Gln Glu
 275 280 285

Ile Leu Leu Arg Asp Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Ser
 290 295 300

Val Asp Leu Thr Phe Tyr Ser Gly Pro Thr Gln Ala Glu Val Thr Lys
 305 310 315 320

Gln Tyr Gln Leu Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn
 325 330 335

Thr Leu Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Glu
 340 345 350

Phe Glu Asp Val Leu Ala Asn Phe Glu Arg Phe Glu Ile Pro Leu Glu
 355 360 365

Tyr Leu Trp Ala Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp
 370 375 380

Asn Asp Gln His Arg Phe Ser Tyr Glu Glu Gly Glu Lys Phe Leu Asn
 385 390 395 400

Lys Leu His Ala Gly Gly Arg Arg Trp Val Pro Ile Val Asp Gly Ala
 405 410 415

Leu Tyr Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Glu Thr Tyr
 420 425 430

Asp Arg Gly Ala Lys Asp Asp Val Phe Ile Lys Asn Pro Asp Gly Ser
 435 440 445

Leu Tyr Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Tyr Pro Asp Trp
 450 455 460

His His Pro Lys Ala Ser Asp Phe Trp Ala Asn Glu Leu Val Thr Trp
 465 470 475 480

Trp Asn Lys Leu His Tyr Asp Gly Val Trp Tyr Asp Met Ala Glu Val
 485 490 495

Ser Ser Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Ser Met Asn
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Pro Ala His Pro Pro Phe Ala Leu Pro Gly Glu Pro Gly Asn Val Val
 515 520 525

Tyr Asp Tyr Pro Glu Gly Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala
 530 535 540

Ser Ala Ser Ala Gly Ala Ala Ser Gln Ser Ala Ala Ala Ser Ser Thr
 545 550 555 560

Thr Thr Ser Ala Pro Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg
 565 570 575

Asn Val Asp His Pro Pro Tyr Val Ile Asn His Val Gln Pro Gly His
 580 585 590

Asp Leu Ser Val His Ala Ile Ser Pro Asn Ser Thr His Ser Asp Gly
 595 600 605

Val Gln Glu Tyr Asp Val His Ser Leu Tyr Gly His Gln Gly Ile Asn
 610 615 620

Ala Thr Tyr His Gly Leu Leu Lys Val Trp Glu Asn Lys Arg Pro Phe
 625 630 635 640

Ile Ile Ala Arg Ser Thr Phe Ser Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Phe Ser Lys Trp Gly Ser Met Phe Phe Ser Ile
 660 665 670

Ser Gln Ala Leu Gln Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Val
 675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Thr Asp Glu Glu Leu Cys Asn Arg
 690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Val
 705 710 715 720

Leu Ser Ala Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Asp
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Ala Thr Lys Ala Ala Met Asn Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
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Tyr Thr Leu Phe His Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765

Ala Leu Ala Trp Glu Phe Pro Asn Asp Pro Ser Leu Ala Ala Val Gly
 770 775 780

Thr Gln Phe Leu Val Gly Pro Ser Val Met Val Ile Pro Val Leu Glu
 785 790 795 800

Pro Gln Val Asp Thr Val Gln Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815

Glu Val Trp Tyr Asp Trp Tyr Ser Gln Thr Ala Val Asp Ala Lys Pro
 820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Phe
835 840 845

Val Arg Gly Gly Ser Ile Leu Pro Met Gln Glu Val Ala Leu Thr Thr
850 855 860

Arg Asp Ala Arg Lys Thr Pro Trp Ser Leu Leu Ala Ser Leu Ser Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Val
885 890 895

Tyr Pro Glu Asp Thr Leu Ser Val Asp Phe Leu Ala Ser Arg Ser Thr
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Leu Arg Ala Ser Ala Arg Gly Thr Trp Lys Glu Ala Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Thr Glu Lys Pro Ser Ser Val Thr Leu
930 935 940

Asn Gly Glu Thr Leu Ser Ser Asp Ser Val Lys Tyr Asn Ala Thr Ser
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His Val Leu His Val Gly Gly Leu Gln Lys His Thr Ala Asp Gly Ala
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Trp Ala Lys Asp Trp Val Leu Lys Trp
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<213> Mortierella alliacea

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Met Thr Lys Arg Thr Thr Ala Pro Arg Ala Pro Leu Val Leu Leu Ala
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Ser Asn Ser Ser Gln Ile Ala Pro Leu Ala Val Asp Asp Met Cys Ser
35 40 45

Asn Val Gln Thr Arg Lys Asp Cys Gly Tyr Leu Gly Val Asp Lys Asp
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Gly Cys Asp Gln Arg Gln Cys Cys Trp Ala Glu Ser Lys Asp Pro Ile
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Pro Trp Cys Phe Gln Lys Glu Asn Lys Glu Tyr Ala Cys Ser Thr Asp
85 90 95

Met Ala Ala Arg Arg Asp Arg Glv Phe Leu Glv Ile Thr Asp Gln Gln

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Ala Pro Tyr Cys Phe Ile Gln Gln His Ala Cys Gln Gly Tyr Gln Val
130      135      140
Lys Ala Ala Gln Gly Thr Ala Asn Gly Val Asn Leu Asp Leu Glu Leu
145      150      155      160
Leu Gly Gly Cys Ala Arg Phe Gly Lys Asp Ile Ala Arg Leu Thr Val
165      170      175
Asn Val Asp Phe Glu Thr Glu Ser Arg Ile Arg Val Lys Ile Thr Asp
180      185      190
Lys Asp Lys Gln Arg Tyr Glu Val Pro Lys Glu Ala Leu Pro Ser Thr
195      200      205
Glu Ser Thr Ile Arg Arg Gly Glu Lys Arg Gly Tyr Glu Phe Lys Tyr
210      215      220
Ala Lys Asn Pro Phe Thr Phe Ser Ile Lys Arg Ile Ser Asp Gly Glu
225      230      235      240
Val Leu Phe Asp Ser Ala Val Ala Gly Met Asp Ser Leu Val Phe Glu
245      250      255
Asp Glu Tyr Leu Glu Ile Ser Ser Val Val Pro Ala Asp Ala Asn Ile
260      265      270
Tyr Gly Leu Gly Glu Val Val Ser Ser Phe Arg Arg Asp Pro Gly Asn
275      280      285
Thr Arg Arg Thr Met Trp Ala Arg Asp Ala Pro Thr Pro Val Asp Gln
290      295      300
Asn Leu Tyr Gly Ser His Pro Phe His Leu Glu Met Arg Lys Gly Ala
305      310      315      320
Ala His Gly Val Phe Leu Arg Asn Ser Asn Gly Met Asp Val Ile Leu
325      330      335
Thr Pro Lys Lys Val Thr Tyr Lys Thr Ile Gly Gly Ile Leu Asp Phe
340      345      350
Thr Val Phe Val Gly Pro Lys Pro Glu Glu Val Ile Asn Gln Tyr Thr
355      360      365
Glu Val Ile Gly Arg Pro His Met Pro Pro Ala Trp Ala Leu Gly Trp
370      375      380
His Gln Ser Arg Tyr Gly Tyr Lys Thr Ile Asp Ala Val Glu Ala Thr
385      390      395      400

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Val Gln Arg Tyr Lys Lys Glu Gly Leu Pro Leu Asp Gly Met Trp Ile
 405 410 415
 Asp Ile Asp Tyr Met Asp Arg Phe Arg Asp Phe Thr Tyr Asp Glu Ala
 420 425 430
 Arg Phe Pro Gln Ser Arg Met Lys Ala Leu Ala Ala Asn Leu Ala Ser
 435 440 445
 Ser Asn Gln Ser Met Val Leu Ile Ile Asp Pro Gly Ile Pro Ile Ala
 450 455 460
 Pro Gly Tyr Glu Pro Tyr Asp Ser Gly Met Arg Asp Gly Val Phe Ile
 465 470 475 480
 Lys Thr Leu Gln Gly Gln Pro Ile Glu Gly Arg Val Trp Pro Gly Gln
 485 490 495
 Thr Tyr Phe Pro Asp Phe Met Asn Thr Lys Glu Thr Trp Ala Tyr Trp
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 Glu Arg Gln Leu Lys Lys Thr Arg Asp Asp Ile Gly Ala Asn Val Tyr
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 Pro Trp Ile Asp Met Asn Glu Pro Ser Asn Phe Cys Asn Gly Pro Cys
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 Thr Lys Asp Gly Ala Ser Ala Ser Ala Leu Asp Asp Ala Ser Glu Lys
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 Gln Lys Phe Ala Lys Arg Asp Val Ala Ala Ser Ala Ser Thr Ser Ile
 565 570 575
 Lys Tyr Ser Ile Asn Asn Ala Gly Arg Gln Ala Pro Leu Asp Glu Lys
 580 585 590
 Thr Leu Ala Thr Asn Ala Val Ser Lys Asn Gly Met Leu Leu Thr Asp
 595 600 605
 Thr His Asn Leu Tyr Gly His Met Glu Ser Ala Ala Thr His Asp Ala
 610 615 620
 Leu Leu Asn Ile Asp Pro Asn Thr Arg Pro Phe Ile Leu Thr Arg Ser
 625 630 635 640
 Ser Phe Pro Gly Thr Gly Ala Tyr Ala Ala His Trp Thr Gly Asp Asn
 645 650 655
 Trp Ser Gln Trp Glu His Leu Lys Tyr Ser Ile Ser Gly Val Leu Ser
 660 665 670
 Phe Gly Leu Phe Gly Met Pro Phe Thr Gly Ser Asp Ile Cys Gly Phe
 675 680 685
 Asn Gly Asn Ala Gln Glu Glu Leu Cys Leu Arg Trp His Gln Leu Gly
 690 695 700

690					695					700						
Ala	Leu	Tyr	Pro	Phe	Ala	Arg	Asn	His	Asn	Asp	Ile	Lys	Gly	Ser	Asp	720
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Gln	Glu	Pro	Tyr	Val	Trp	Pro	Asn	Thr	Val	Leu	Pro	Ala	Ala	Lys	Lys	
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Ala	Leu	Glu	Ile	Arg	Tyr	Ser	Leu	Met	Pro	Tyr	Phe	Tyr	Ser	Leu	Phe	
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Glu	Gln	Ala	His	Lys	Thr	Gly	Lys	Pro	Val	Trp	Gln	Pro	Leu	Phe	Phe	
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Gln	Tyr	Pro	Gln	Asp	Ala	Gln	Ala	Leu	Lys	Ile	Asp	Ser	Gln	Phe	Leu	
		770					775					780				
Leu	Gly	Asp	Gly	Ile	Leu	Val	Ser	Pro	Ser	Leu	Thr	Ala	Gly	Glu	Val	
785						790					795				800	
Gln	Val	Lys	Ala	Tyr	Phe	Pro	Gly	Asn	Gly	Arg	Trp	Phe	Asp	Leu	Trp	
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Thr	His	Glu	Val	Val	Met	Glu	Ala	Gly	Ala	Ser	Asn	Arg	Tyr	Ala	Ser	
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Leu	Lys	Ala	Asn	Ala	Gln	Ser	Asp	Ser	Ile	Pro	Met	Ser	Leu	Ala	Gly	
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Arg	Ala	Asn	Pro	Val	Ser	Leu	Val	Ile	Ala	Leu	Asp	Gly	Ser	Gly	Ala	
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Ala	Lys	Gly	Glu	Met	Phe	Val	Asp	Asp	Gly	Lys	Ser	Val	Lys	Thr	Asp	
				885					890					895		
Asn	Gln	Ala	His	Ile	Thr	Phe	Ala	Met	Thr	Ala	Gly	Gln	Lys	Leu	Val	
		900						905					910			
Ser	Asn	Val	Thr	Ser	Ala	Val	Gln	Ala	Gln	Gln	Leu	Lys	Ala	Gly	Leu	
		915					920					925				
Gly	Gly	Lys	His	Gly	Asp	Arg	Ile	Glu	Lys	Ile	Val	Val	Met	Gly	Leu	
	930					935					940					
Asn	Phe	Gly	Lys	Ala	Ala	Ser	Ala	Glu	Pro	Lys	Asn	Val	Lys	Val	Ser	
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Lys	Arg	Gly	Asp	Lys	Val	Arg	Asp	Ile	Val	His	Val	Ser	Lys	Gly	His	
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Val	Thr	Val	Ser	Thr	Thr	Ala	Ala	Ala	Ala	Ala	Ala	Lys	Val	Ser	Lys	
			980				985						990			
Phe	Ser	Ser	Leu	Asn	Ile	Asn	Gly	Val	Glu	Met	Ala	Phe	Gly	Ala	Ser	
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995 1000 1005
 Asn Leu Asp Arg Ser Lys Gly Gln Asp Pro Ala Ser Gly Leu Ala
 1010 1015 1020
 Trp Glu Val Asn Gln Glu Lys Gly Ser Leu Thr Leu Thr Gly Leu
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 Gln Met Asn Leu Phe Glu Ser Trp Phe Ile Asn Trp Lys Met Glu
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 Ser Ala Ile Ser Ile Ala Val Gly Asn Val Tyr Gln Thr Leu Asn Val
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 Ile Gly Asp Arg Asn Val Thr Ile Pro Thr Asn Gly Ile Pro Gln Arg
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 Leu Ser Val Tyr Asp Pro Tyr Arg Gly Val Asn Cys Gln Gly Tyr Gln
 50 55 60
 Ala Val Asn Ile Ser Glu Ser Gln Asn Gly Val Thr Ala Tyr Leu Ala
 65 70 75 80
 Leu Leu Gly Glu Pro Cys Tyr Ala Tyr Gly Thr Asp Tyr Pro Leu Leu
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 Phe Leu Asn Val Thr Tyr Glu Glu Ala Asp Arg Val His Ile Ser Ile
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 Lys Asp Ala Asn Asn Thr Gln Phe Gln Phe Thr Ser Arg Lys Asp Leu
 115 120 125
 Trp Asp Ala Pro Leu Tyr Ser Pro Ser Tyr Asn Asn Thr Asn Leu Leu
 130 135 140
 Tyr Asn Phe Ser Tyr Asn Ala Asn Pro Phe Glu Phe Trp Val Thr Arg
 145 150 155 160
 Lys Ser Asp Gly Glu Val Leu Phe Asp Thr Arg Gly Gln Lys Leu Val
 165 170 175
 Phe Glu Asp Gln Tyr Ile Glu Leu Thr Thr Asn Met Val Glu Asn Tyr
 180 185 190
 Asn Leu Tyr Gly Leu Ala Glu Thr Ile His Gly Leu Arg Leu Gly Asn
 195 200 205

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

Gln Asn Met Tyr Gly Ser His Pro Tyr Tyr Leu Glu Gln Arg Tyr Lys
 225 230 235 240

Ala Asp Gly Ile Asn Ser Thr Leu Asn Glu Thr Thr Tyr Thr Ser Ser
 245 250 255

Ser His Gly Val Leu Met Leu Thr Ala Asn Gly Met Asp Val Leu Leu
 260 265 270

Arg Gln Asp Tyr Leu Gln Tyr Arg Met Ile Gly Gly Val Ile Asp Leu
 275 280 285

Phe Val Tyr Ser Gly Ser Thr Glu Ser Pro Lys Glu Thr Val Lys Gln
 290 295 300

Phe Val Gln Ser Ile Gly Lys Pro Ala Met His Gln Tyr Trp Thr Leu
 305 310 315 320

Gly Tyr His Ser Cys Arg Trp Gly Tyr Thr Asn Ile Thr Glu Ile Met
 325 330 335

Asp Val Arg Gln Asn Tyr Ile Asp Ala Asp Ile Pro Val Glu Thr Phe
 340 345 350

Trp Ser Asp Ile Asp Tyr Met Glu Lys Tyr Arg Asp Phe Thr Val Asp
 355 360 365

Pro Val Ser Tyr Ser Lys Ser Asp Met Gln Thr Phe Phe Ser Asp Leu
 370 375 380

Val Ser Asn His Gln His Tyr Val Pro Ile Ile Asp Ala Ala Ile Tyr
 385 390 395 400

Ala Ala Asn Pro Tyr Asn His Thr Asp Asp Ser Tyr Tyr Pro Tyr Tyr
 405 410 415

Ala Gly Val Glu Lys Asp Ile Phe Leu Lys Asn Pro Asn Gly Ser Ile
 420 425 430

Tyr Ile Gly Ala Val Trp Pro Gly Phe Thr Ala Phe Pro Asp Phe Thr
 435 440 445

Asn Pro Asp Val Val Asp Tyr Trp Lys Asp Cys Leu Ile Asn Leu Thr
 450 455 460

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

Asp Met Asn Glu Pro Ser Ser Phe Cys Val Gly Ser Cys Gly Ser Ala
 485 490 495

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

Ser Ala Tyr Ser Ala Ser Leu Ser Asn Tyr Tyr Ala Thr Ala Thr Ser
530 535 540

Ser Val Phe Gln Ile Val Ser Pro Thr Ala Thr Pro Leu Gly Leu Lys
545 550 555 560

Pro Asp Tyr Asn Ile Asn Trp Pro Pro Tyr Ala Ile Asn Asn Glu Gln
565 570 575

Gly Asn His Asp Ile Ala Asn His Ile Val Ser Pro Asn Ala Thr Thr
580 585 590

His Asp Gly Thr Gln Arg Tyr Asp Ile Phe Asn Met Tyr Gly Tyr Gly
595 600 605

Glu Thr Lys Val Ser Tyr Ala Ala Leu Thr Gln Ile Ser Pro Asn Glu
610 615 620

Arg Pro Phe Ile Leu Ser Arg Ser Thr Phe Leu Gly Ser Gly Val Tyr
625 630 635 640

Gly Ala His Trp Leu Gly Asp Asn His Ser Leu Trp Ser Asn Met Phe
645 650 655

Phe Ser Ile Ser Gly Met Ile Val Phe Asn Met Met Gly Ile Pro Met
660 665 670

Val Gly Ala Asp Val Cys Gly Phe Leu Gly Asp Ser Asp Glu Glu Leu
675 680 685

Cys Ser Arg Trp Met Ala Met Gly Ala Phe Ser Pro Phe Tyr Arg Asn
690 695 700

His Asn Asn Ile Tyr Gln Ile Ser Gln Glu Pro Tyr Thr Trp Ser Ser
705 710 715 720

Val Ala Glu Ala Ser Arg Arg Ala Met Tyr Ile Arg Tyr Ser Leu Leu
725 730 735

Pro Tyr Trp Tyr Thr Ile Met Ala Lys Ala Ser Gln Asp Gly Thr Pro
740 745 750

Ala Leu Arg Ala Leu Phe Val Glu Phe Pro Asn Asp Pro Thr Leu Ala
755 760 765

Asp Val Asp Arg Gln Phe Met Val Gly Asp Ser Leu Leu Val Thr Pro
770 775 780

Val Leu Glu Pro Asn Val Glu Tyr Val Gln Gly Val Phe Pro Gly Asp
785 790 795 800

Asn Ser Thr Val Trp Tyr Asp Trp Tyr Asn His Thr Glu Ile Val Arg

805 - - - - 810 815 -

Gln Tyr Asn Glu Asn Val Thr Leu Tyr Ala Pro Leu Glu His Ile Asn
820 825 830

Val Ala Ile Arg Gly Gly Ser Val Leu Pro Met Gln Gln Pro Ser Leu
835 840 845

Thr Thr Tyr Glu Ser Arg Gln Asn Pro Phe Asn Leu Leu Val Ala Leu
850 855 860

Asp Arg Asp Gly Ser Ala Thr Gly Glu Leu Tyr Leu Asp Asp Gly Val
865 870 875 880

Ser Ile Glu Leu Asn Ala Thr Leu Ser Val Ser Phe Thr Phe Ser Asp
885 890 895

Gly Val Leu Ser Ala Val Pro Thr Gly Ser Tyr Glu Val Ser Gln Pro
900 905 910

Leu Ala Asn Val Thr Ile Leu Gly Leu Thr Glu Ser Pro Ser Ser Ile
915 920 925

Thr Leu Asn Gly Gln Asn Val Ser Ser Phe Gln Tyr Ser Asn Asp Thr
930 935 940

Glu Glu Leu Leu Ile Thr Gly Leu Gln Asn Ile Thr Ser Ser Gly Ala
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Phe Ala Asn Ser Trp Asn Leu Thr Leu
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<212> PRT

<213> Debaryomyces occidentalis

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Ser Ala Ser Ser Ser Ser Glu Ser Ser Gln Ala Thr Ile Pro Asn Asp
35 40 45

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

Val Asp Ala Asn Ala Ala Lys Gly Tyr Asp Leu Val Asn Val Thr
65 70 75 80

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

Asn Ile Tyr Gly Tyr Asp Phe Asp Tyr Leu Asn Leu Thr Val Glu Tyr
 100 105 110

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

Asp Val Phe Val Leu Pro Glu His Leu Val Val Lys Pro Leu Val Glu
 130 135 140

Gly Asp Ala Gln Ser Tyr Asn Phe Asp Asn Ser Asp Leu Val Phe Glu
 145 150 155 160

Tyr Ser Asn Thr Asp Phe Ser Phe Glu Val Ile Arg Ser Ser Thr Lys
 165 170 175

Glu Val Leu Phe Ser Thr Lys Gly Asn Pro Leu Val Phe Ser Asn Gln
 180 185 190

Phe Ile Gln Phe Asn Ser Ser Leu Pro Lys Asn His Val Ile Thr Gly
 195 200 205

Leu Gly Glu Ser Ile His Gly Leu Val Asn Glu Pro Gly Ser Val Lys
 210 215 220

Thr Leu Phe Ala Asn Asp Val Gly Asp Pro Ile Asp Gly Asn Ile Tyr
 225 230 235 240

Gly Val His Pro Val Tyr Leu Asp Gln Arg Tyr Asp Thr Glu Thr Thr
 245 250 255

His Ala Val Tyr Trp Arg Thr Ser Ala Ile Gln Glu Val Leu Ile Gly
 260 265 270

Glu Glu Ser Ile Thr Trp Arg Ala Leu Ser Gly Val Ile Asp Leu Tyr
 275 280 285

Phe Phe Ser Gly Pro Thr Pro Lys Asp Ala Ile Gln Gln Tyr Val Lys
 290 295 300

Glu Ile Gly Leu Pro Ala Phe Gln Pro Tyr Trp Ser Leu Gly Tyr His
 305 310 315 320

Gln Cys Arg Trp Gly Tyr Asp Thr Ile Glu Lys Leu Ser Glu Val Val
 325 330 335

Glu Asn Phe Lys Lys Phe Asn Ile Pro Leu Glu Thr Ile Trp Ser Asp
 340 345 350

Ile Asp Tyr Met Asp Ser Tyr Lys Asp Phe Thr Tyr Asp Pro His Arg
 355 360 365

Phe Pro Leu Asp Glu Tyr Arg Lys Phe Leu Asp Glu Leu His Lys Asn
 370 375 380

Asn Gln His Tyr Val Pro Ile Leu Asp Ala Ala Ile Tyr Val Pro Asn
 385 390 395 400

Pro Asn Asn Ala Thr Asp Asn Glu Tyr Gln Pro Phe His Tyr Gly Asn
 405 410 415
 Glu Thr Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr Ile Gly
 420 425 430
 Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Phe Leu Ala Glu Asn
 435 440 445
 Ile Gln Glu Tyr Trp Asn Lys Val Ile Lys Asp Trp Tyr Glu Leu Thr
 450 455 460
 Pro Phe Asp Gly Ile Trp Ala Asp Met Asn Glu Val Ser Ser Phe Cys
 465 470 475 480
 Val Gly Ser Cys Gly Thr Gly Lys Tyr Phe Glu Asn Pro Ala Tyr Pro
 485 490 495
 Pro Phe Thr Val Gly Ser Lys Ala Thr Ser Tyr Pro Val Gly Phe Asp
 500 505 510
 Val Ser Asn Ala Ser Glu Trp Lys Ser Ile Gln Ser Ser Ile Ser Ala
 515 520 525
 Thr Ala Lys Thr Ser Ser Thr Ser Ser Val Ser Ser Ser Ser Thr
 530 535 540
 Ile Asp Ser Met Asn Thr Leu Ala Pro Gly Lys Gly Asn Ile Asn Tyr
 545 550 555 560
 Pro Pro Tyr Ala Ile Tyr Asn Met Gln Gly Asp Ser Asp Leu Ala Thr
 565 570 575
 His Ala Val Ser Pro Asn Ala Thr His Ala Asp Gly Thr Val Glu Tyr
 580 585 590
 Asp Ile His Asn Leu Tyr Gly Tyr Leu Gln Glu Asn Ala Thr Tyr His
 595 600 605
 Ala Leu Leu Glu Val Phe Pro Asn Lys Arg Pro Phe Met Ile Ser Arg
 610 615 620
 Ser Thr Phe Pro Gly Ala Gly Lys Trp Thr Gly His Trp Gly Gly Asp
 625 630 635 640
 Asn Thr Ala Asp Trp Ala Tyr Ala Tyr Phe Ser Ile Pro Gln Ala Phe
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 Ser Met Gly Ile Ala Gly Leu Pro Phe Phe Gly Ala Asp Val Cys Gly
 660 665 670
 Phe Asn Gly Asn Ser Asp Ser Glu Leu Cys Ser Arg Trp Met Gln Leu
 675 680 685
 Gly Ser Phe Phe Pro Phe Tyr Arg Asn His Asn Tyr Leu Gly Ala Ile
 690 695 700

Asp Gln Glu Pro Tyr Val Trp Glu Ser Val Ala Glu Ala Thr Arg Thr
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 Ser Met Ala Ile Arg Tyr Leu Leu Leu Pro Tyr Tyr Tyr Thr Leu Leu
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 His Glu Ser His Thr Thr Gly Leu Pro Ile Leu Arg Ala Phe Ser Trp
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 Gln Phe Pro Asn Asp Arg Ser Leu Ser Gly Val Asp Asn Gln Phe Phe
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 Val Gly Asp Gly Leu Val Val Thr Pro Val Leu Glu Pro Gly Val Asp
 770 775 780
 Lys Val Lys Gly Val Phe Pro Gly Ala Gly Lys Glu Glu Val Tyr Tyr
 785 790 795 800
 Asp Trp Tyr Thr Gln Arg Glu Val His Phe Lys Asp Gly Lys Asn Glu
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 Thr Leu Asp Ala Pro Leu Gly His Ile Pro Leu His Ile Arg Gly Gly
 820 825 830
 Asn Val Leu Pro Thr Gln Glu Pro Gly Tyr Thr Val Ser Glu Ser Arg
 835 840 845
 Gln Asn Pro Phe Gly Leu Ile Val Ala Leu Asp Asn Asp Gly Lys Ala
 850 855 860
 Gln Gly Ser Leu Tyr Leu Asp Asp Gly Glu Ser Leu Val Val Asp Ser
 865 870 875 880
 Ser Leu Leu Val Ser Phe Ser Val Ser Asp Asn Thr Leu Ser Ala Ser
 885 890 895
 Pro Ser Gly Asp Tyr Lys Ala Asp Gln Pro Leu Ala Asn Val Thr Ile
 900 905 910
 Leu Gly Val Gly His Lys Pro Lys Ser Val Lys Phe Glu Asn Ala Asn
 915 920 925
 Val Asp Phe Thr Tyr Lys Lys Ser Thr Val Phe Val Thr Gly Leu Asp
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 Lys Tyr Thr Lys Asp Gly Ala Phe Ser Lys Asp Phe Thr Ile Thr Trp
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<212> PRT

<213> Hordeum vulgare

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Ala Pro Arg Leu Cys Ser Ser Lys Glu Glu Gly Pro Leu Ala Ala Gly
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Gly Tyr Arg Val Ser Arg Val Ala Val Asp Asp Gly Gly Arg Arg Leu
35 40 45

Arg Ala Glu Ala Ala Ala Thr Gly Gly Ala Ser Ser Thr Gly Asp
50 55 60

Val Gln Arg Leu Ala Val Tyr Ala Ser Leu Glu Thr Asp Ser Arg Leu
65 70 75 80

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

Asp Ile Ile Pro Arg Pro Ala Pro Ala Asp Val Leu His Asp Ala Pro
100 105 110

Pro Ala Ser Ser Ala Pro Leu Gln Gly Ser Arg Val Leu Ser Ala Ala

115 120 125

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

Val Ser Arg Arg Ser Thr Gly Asp Ile Leu Phe Asp Thr Ala Pro Gly
145 150 155 160

Leu Val Phe Arg Asp Lys Tyr Leu Glu Val Thr Ser Ala Leu Pro Ala
165 170 175

Gly Arg Ala Ser Leu Tyr Gly Leu Gly Glu His Thr Lys Ser Ser Phe
180 185 190

Arg Leu Arg His Asn Asp Ser Phe Thr Leu Trp Asn Ala Asp Ile Gly
195 200 205

Ala Ser Tyr Val Asp Val Asn Leu Tyr Gly Ser His Pro Phe Tyr Met
210 215 220

Asp Val Arg Pro Pro Gly Thr Ala His Gly Val Leu Leu Leu Ser Ser
225 230 235 240

Asn Gly Met Asp Val Leu Tyr Gly Gly Ser Tyr Val Thr Tyr Lys Val
245 250 255

Ile Gly Gly Val Leu Asp Phe Tyr Phe Phe Ala Gly Pro Asn Pro Leu
260 265 270

Ala Val Val Asp Gln Tyr Thr Gln Leu Ile Gly Arg Pro Ala Pro Met
275 280 285

Pro Tyr Trp Ser Phe Gly Phe His Gln Cys Arg Tyr Gly Tyr Leu Asn
290 295 300

Val Ser Asp Leu Glu Arg Val Val Ala Gly Tyr Ala Lys Ala Arg Ile
305 310 315 320

Pro Leu Glu Val Met Trp Thr Asp Ile Asp Tyr Met Asp Gly Phe Lys
325 330 335

Asp Phe Thr Leu Asp Arg Val Asn Phe Thr Ala Ala Glu Leu Arg Pro
340 345 350

Phe Val Asp Arg Leu His Arg Asn Ala Gln Lys Tyr Val Leu Ile Leu
355 360 365

Asp Pro Gly Ile Arg Ile Asp Ala Thr Tyr Gly Thr Phe Val Arg Gly
370 375 380

Met Gln Gln Asp Ile Phe Leu Lys Arg Asn Gly Thr Asn Phe Val Gly
385 390 395 400

Asn Val Trp Pro Gly Asp Val Tyr Phe Pro Asp Phe Met His Pro Arg
405 410 415

Ala Ala Glu Phe Trp Ala Arg Glu Ile Ser Leu Phe Arg Arg Thr Ile
420 425 430

Pro Val Asp Gly Leu Trp Ile Asp Met Asn Glu Ile Ser Asn Phe Tyr
435 440 445

Asn Pro Glu Pro Met Asn Ala Leu Asp Asp Pro Pro Tyr Arg Ile Asn
450 455 460

Asn Asp Gly Thr Gly Arg Pro Ile Asn Asn Lys Thr Val Pro Ala Ser
465 470 475 480

Ala Val His Tyr Gly Gly Val Thr Glu Tyr Asp Ala His Asn Leu Phe
485 490 495

Gly Leu Leu Glu Ala Arg Ala Thr His Arg Ala Leu Leu Arg Asp Thr
500 505 510

Gly Arg Arg Pro Phe Val Leu Ser Arg Ser Thr Phe Val Gly Ser Gly
515 520 525

Arg Tyr Thr Ala His Trp Thr Gly Asp Asn Ala Ala Thr Trp Gly Asp
530 535 540

Leu Arg Tyr Ser Ile Asn Thr Met Leu Ser Phe Gly Leu Phe Gly Met
545 550 555 560

Pro Met Ile Gly Ala Asp Ile Cys Gly Phe Asn Gly Asn Thr Thr Glu
565 570 575

Glu Leu Cys Gly Arg Trp Ile Gln Leu Gly Ala Phe Tyr Pro Phe Ser
580 585 590

Asp Asp His Ser Ala Ile Phe Thr Val Asp Arg Glu Leu Thr Leu Thr

Arg Asp His Ser Ala Ile Phe Thr Val Arg Arg Glu Leu Tyr Leu Asp
595 600 605

Pro Ser Val Ala Ala Ser Ala Arg Lys Ala Leu Gly Leu Arg Tyr Gln
610 615 620

Leu Leu Pro Tyr Phe Tyr Thr Leu Met Tyr Glu Ala His Met Thr Gly
625 630 635 640

Ala Pro Ile Ala Arg Pro Leu Phe Phe Ser Tyr Pro His Asp Val Ala
645 650 655

Thr Tyr Gly Val Asp Arg Gln Phe Leu Leu Gly Arg Gly Val Leu Val
660 665 670

Ser Pro Val Leu Glu Pro Gly Ala Thr Thr Val Asp Ala Tyr Phe Pro
675 680 685

Ala Gly Arg Trp Tyr Ser Leu Tyr Asp Tyr Ser Leu Ala Val Ala Thr
690 695 700

Arg Thr Gly Lys His Val Thr Leu Pro Ala Pro Ala Asp Thr Val Asn
705 710 715 720

Val His Val Ala Gly Gly Thr Ile Leu Pro Leu Gln Gln Ser Ala Leu
725 730 735

Thr Thr Ser Arg Ala Arg Arg Thr Ala Phe His Leu Leu Val Ala Leu
740 745 750

Ala Glu Asp Gly Thr Ala Ser Gly Asp Leu Phe Leu Asp Asp Gly Glu
755 760 765

Ser Pro Glu Met Gly Gly Arg Ser Asp Trp Ser Met Val Arg Phe Ser
770 775 780

Cys Glu Met Gly Ser Asp Gly Ala Ile Lys Val Lys Ser Glu Val Val
785 790 795 800

His Asn Ser Tyr Ala Gln Ser Arg Thr Leu Val Ile Ser Lys Val Val
805 810 815

Leu Met Gly His Arg Ser Pro Ala Ala Pro Lys Lys Leu Thr Val His
820 825 830

Val Asn Ser Ala Glu Val Glu Ala Ser Ser Ser Ala Gly Thr Arg Tyr
835 840 845

Gln Asn Ala Gly Gly Leu Gly Gly Val Ala His Ile Gly Gly Leu Ser
850 855 860

Leu Val Val Gly Glu Glu Phe Glu Leu Lys Val Ala Met Ser Tyr
865 870 875

<210> 14

<211> 902

<212> PRT

<213> Arabidopsis thaliana

<400> 14

Met Ser Ser Leu His Trp Phe Pro Asn Ile Phe Ile Val Val Val Val
1 5 10 15

Phe Phe Ser Leu Arg Ser Ser Gln Val Val Leu Glu Glu Glu Glu Ser
20 25 30

Thr Val Val Gly Tyr Gly Tyr Val Val Arg Ser Val Gly Val Asp Ser
35 40 45

Asn Arg Gln Val Leu Thr Ala Lys Leu Asp Leu Ile Lys Pro Ser Ser
50 55 60

Val Tyr Ala Pro Asp Ile Lys Ser Leu Asn Leu His Val Ser Leu Glu
65 70 75 80

Thr Ser Glu Arg Leu Arg Ile Arg Ile Thr Asp Ser Ser Gln Gln Arg
85 90 95

Trp Glu Ile Pro Glu Thr Val Ile Pro Arg Ala Gly Asn His Ser Pro
100 105 110

Arg Arg Phe Ser Thr Glu Glu Asp Gly Gly Asn Ser Pro Glu Asn Asn
115 120 125

Phe Leu Ala Asp Pro Ser Ser Asp Leu Val Phe Thr Leu His Asn Thr
130 135 140

Thr Pro Phe Gly Phe Ser Val Ser Arg Arg Ser Ser Gly Asp Ile Leu
145 150 155 160

Phe Asp Thr Ser Pro Asp Ser Ser Asp Ser Asn Thr Tyr Phe Ile Phe
165 170 175

Lys Asp Gln Phe Leu Gln Leu Ser Ser Ala Leu Pro Glu Asn Arg Ser
180 185 190

Asn Leu Tyr Gly Ile Gly Glu His Thr Lys Arg Ser Phe Arg Leu Ile
195 200 205

Pro Gly Glu Thr Met Thr Leu Trp Asn Ala Asp Ile Gly Ser Glu Asn
210 215 220

Pro Asp Val Asn Leu Tyr Gly Ser His Pro Phe Tyr Met Asp Val Arg
225 230 235 240

Gly Ser Lys Gly Asn Glu Glu Ala Gly Thr Thr His Gly Val Leu Leu
245 250 255

Leu Asn Ser Asn Gly Met Asp Val Lys Tyr Glu Gly His Arg Ile Thr
260 265 270

Tyr Asn Val Ile Gly Gly Val Ile Asp Leu Tyr Val Phe Ala Gly Pro
275 280 285

Ser Pro Glu Met Val Met Asn Gln Tyr Thr Glu Leu Ile Gly Arg Pro
290 295 300

Ala Pro Met Pro Tyr Trp Ser Phe Gly Phe His Gln Cys Arg Tyr Gly
305 310 315 320

Tyr Lys Asn Val Ser Asp Leu Glu Tyr Val Val Asp Gly Tyr Ala Lys
325 330 335

Ala Gly Ile Pro Leu Glu Val Met Trp Thr Asp Ile Asp Tyr Met Asp
340 345 350

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

Met Gln Ser Phe Val Asp Thr Leu His Lys Asn Gly Gln Lys Tyr Val
370 375 380

Leu Ile Leu Asp Pro Gly Ile Gly Val Asp Ser Ser Tyr Gly Thr Tyr
385 390 395 400

Asn Arg Gly Met Glu Ala Asp Val Phe Ile Lys Arg Asn Gly Glu Pro
405 410 415

Tyr Leu Gly Glu Val Trp Pro Gly Lys Val Tyr Phe Pro Asp Phe Leu
420 425 430

Asn Pro Ala Ala Ala Thr Phe Trp Ser Asn Glu Ile Lys Met Phe Gln
435 440 445

Glu Ile Leu Pro Leu Asp Gly Leu Trp Ile Asp Met Asn Glu Leu Ser
450 455 460

Asn Phe Ile Thr Ser Pro Leu Ser Ser Gly Ser Ser Leu Asp Asp Pro
465 470 475 480

Pro Tyr Lys Ile Asn Asn Ser Gly Asp Lys Arg Pro Ile Asn Asn Lys
485 490 495

Thr Val Pro Ala Thr Ser Ile His Phe Gly Asn Ile Ser Glu Tyr Asp
500 505 510

Ala His Asn Leu Tyr Gly Leu Leu Glu Ala Lys Ala Thr His Gln Ala
515 520 525

Val Val Asp Ile Thr Gly Lys Arg Pro Phe Ile Leu Ser Arg Ser Thr
530 535 540

Phe Val Ser Ser Gly Lys Tyr Thr Ala His Trp Thr Gly Asp Asn Ala
545 550 555 560

Ala Lys Trp Glu Asp Leu Ala Tyr Ser Ile Pro Gly Ile Leu Asn Phe
565 570 575

Gly Leu Phe Gly Ile Pro Met Val Gly Ala Asp Ile Cys Gly Phe Ser
 580 585 590
 His Asp Thr Thr Glu Glu Leu Cys Arg Arg Trp Ile Gln Leu Gly Ala
 595 600 605
 Phe Tyr Pro Phe Ala Arg Asp His Ser Ser Leu Gly Thr Ala Arg Gln
 610 615 620
 Glu Leu Tyr Leu Trp Asp Ser Val Ala Ser Ser Ala Arg Lys Val Leu
 625 630 635 640
 Gly Leu Arg Met Arg Leu Leu Pro His Leu Tyr Thr Leu Met Tyr Glu
 645 650 655
 Ala His Val Ser Gly Asn Pro Ile Ala Arg Pro Leu Phe Phe Ser Phe
 660 665 670
 Pro Gln Asp Thr Lys Thr Tyr Glu Ile Asp Ser Gln Phe Leu Ile Gly
 675 680 685
 Lys Ser Ile Met Val Ser Pro Ala Leu Lys Gln Gly Ala Val Ala Val
 690 695 700
 Asp Ala Tyr Phe Pro Ala Gly Asn Trp Phe Asp Leu Phe Asn Tyr Ser
 705 710 715 720
 Phe Ala Val Gly Gly Asp Ser Gly Lys His Val Arg Leu Asp Thr Pro
 725 730 735
 Ala Asp His Val Asn Val His Val Arg Glu Gly Ser Ile Val Ala Met
 740 745 750
 Gln Gly Glu Ala Leu Thr Thr Arg Asp Ala Arg Lys Thr Pro Tyr Gln
 755 760 765
 Leu Leu Val Val Ala Ser Arg Leu Glu Asn Ile Ser Gly Glu Leu Phe
 770 775 780
 Leu Asp Asp Gly Glu Asn Leu Arg Met Gly Ala Gly Gly Gly Asn Arg
 785 790 795 800
 Asp Trp Thr Leu Val Lys Phe Arg Cys Tyr Val Thr Gly Lys Ser Val
 805 810 815
 Val Leu Arg Ser Glu Val Val Asn Pro Glu Tyr Ala Ser Lys Met Lys
 820 825 830
 Trp Ser Ile Gly Lys Val Thr Phe Val Gly Phe Glu Asn Val Glu Asn
 835 840 845
 Val Lys Thr Tyr Glu Val Arg Thr Ser Glu Arg Leu Arg Ser Pro Arg
 850 855 860
 Ile Ser Leu Ile Lys Thr Val Ser Asp Asn Asp Asp Pro Arg Phe Leu
 865 870 875 880

Ser Val Glu Val Ser Lys Leu Ser Leu Leu Val Gly Lys Lys Phe Glu
 885 890 895

Met Arg Leu Arg Leu Thr
 900

<210> 15

<211> 903

<212> PRT

<213> Spinacia oleracea

<400> 15

Met Lys Lys Lys Ile Pro Ser Leu Ala Leu Gly Ile Leu Leu Val Phe
 1 5 10 15

Leu Leu Gln Tyr Leu Val Ala Gly Ile Ser Thr Ser Glu Asn Asp Pro
 20 25 30

Glu Gly Val Ile Gly Tyr Gly Tyr Lys Val Lys Ser Val Lys Val Asp
 35 40 45

Ser Gly Thr Arg Arg Ser Leu Thr Ala Leu Pro Gln Leu Val Lys Asn
 50 55 60

Ser Ser Val Tyr Gly Pro Asp Ile Gln Leu Leu Ser Ile Thr Ala Ser
 65 70 75 80

Leu Glu Ser Asn Asp Arg Leu Arg Val Arg Ile Thr Asp Ala Lys His
 85 90 95

Arg Arg Trp Glu Ile Pro Asp Asn Ile Leu His Arg His Gln Pro Pro
 100 105 110

Pro Pro Pro Pro His Ser Leu Ser Ser Leu Tyr Arg Thr Leu Leu Ser
 115 120 125

Ser Pro Thr Thr Asn Arg Arg Lys Ile Leu Leu Ser His Pro Asn Ser
 130 135 140

Asp Leu Thr Phe Ser Leu Ile Asn Thr Thr Pro Phe Gly Phe Thr Ile
 145 150 155 160

Ser Arg Lys Ser Thr His Asp Val Leu Phe Asp Ala Thr Pro Asp Pro
 165 170 175

Thr Asn Pro Asn Thr Phe Leu Ile Phe Ile Asp Gln Tyr Leu His Leu
 180 185 190

Thr Ser Ser Leu Pro Gly Thr Arg Ala His Ile Tyr Gly Leu Gly Glu
 195 200 205

His Ser Lys Pro Thr Phe Gln Leu Ala His Asn Gln Thr Leu Thr Met
 210 215 220

Arg Ala Ala Asp Ile Pro Ser Ser Asn Pro Asp Val Asn Leu Tyr Gly

225		230		235		240
Ser His Pro Phe Tyr Met Asp Val Arg Ser Ser Pro Val Ala Gly Ser						
	245			250		255
Thr His Gly Val Leu Leu Leu Asn Ser Asn Gly Met Asp Val Glu Tyr						
	260			265		270
Thr Gly Asn Arg Ile Thr Tyr Lys Val Ile Gly Gly Ile Ile Asp Leu						
	275			280		285
Tyr Phe Phe Ala Gly Pro Ser Pro Gly Gln Val Val Glu Gln Phe Thr						
	290			295		300
Arg Val Ile Gly Arg Pro Ala Pro Met Pro Tyr Trp Ala Phe Gly Phe						
	305			310		315
Gln Gln Cys Arg Tyr Gly Tyr His Asp Val Tyr Glu Leu Gln Ser Val						
	325			330		335
Val Ala Gly Tyr Ala Lys Ala Lys Ile Pro Leu Glu Val Met Trp Thr						
	340			345		350
Asp Ile Asp Tyr Met Asp Ala Tyr Lys Asp Phe Thr Leu Asp Pro Val						
	355			360		365
Asn Phe Pro Leu Asp Lys Met Lys Lys Phe Val Asn Asn Leu His Lys						
	370			375		380
Asn Gly Gln Lys Tyr Val Val Ile Leu Asp Pro Gly Ile Ser Thr Asn						
	385			390		395
Lys Thr Tyr Glu Thr Tyr Ile Arg Gly Met Lys His Asp Val Phe Leu						
	405			410		415
Lys Arg Asn Gly Lys Pro Tyr Leu Gly Ser Val Trp Pro Gly Pro Val						
	420			425		430
Tyr Phe Pro Asp Phe Leu Lys Pro Ser Ala Leu Thr Phe Trp Thr Asp						
	435			440		445
Glu Ile Lys Arg Phe Leu Asn Leu Leu Pro Val Asp Gly Leu Trp Ile						
	450			455		460
Asp Met Asn Glu Ile Ser Asn Phe Ile Ser Ser Pro Pro Ile Pro Gly						
	465			470		475
Ser Thr Leu Asp Asn Pro Pro Tyr Lys Ile Asn Asn Ser Gly Val Met						
	485			490		495
Leu Pro Ile Ile Asn Lys Thr Ile Pro Pro Thr Ala Met His Tyr Gly						
	500			505		510
Asp Ile Pro Glu Tyr Asn Val His Asn Leu Phe Gly Tyr Leu Glu Ala						
	515			520		525
Arg Val Thr Arg Ala Ala Leu Ile Lys Leu Thr Glu Lys Arg Pro Phe						
	530			535		540

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545 Val Leu Ser Arg Ser Thr Phe Ser Gly Ser Gly Lys Tyr Thr Ala His
550 555 560

565 Trp Thr Gly Asp Asn Ala Ala Thr Trp Asn Asp Leu Val Tyr Ser Ile
570 575

580 Pro Ser Met Leu Asp Phe Gly Leu Phe Gly Ile Pro Met Val Gly Ala
585 590

595 Asp Ile Cys Gly Phe Leu Gly Asn Thr Thr Glu Glu Leu Cys Arg Arg
600 605

610 Trp Ile Gln Leu Gly Ala Phe Tyr Pro Phe Ser Arg Asp His Ser Ser
615 620

625 Leu Gly Thr Thr Tyr Gln Glu Leu Tyr Arg Trp Glu Ser Val Ala Ala
630 635 640

645 Ser Ala Arg Lys Val Leu Gly Leu Arg Tyr Thr Leu Leu Pro Tyr Phe
650 655

660 Tyr Thr Leu Met Tyr Glu Ala Gln Leu Asn Gly Ile Pro Ile Ala Arg
665 670

675 Pro Leu Phe Phe Ser Phe Pro Asp Asp Ile Lys Thr Tyr Gly Ile Ser
680 685

690 Ser Gln Phe Leu Leu Gly Lys Gly Val Met Val Ser Pro Val Leu Lys
695 700

705 Pro Gly Val Val Ser Val Thr Ala Tyr Phe Pro Arg Gly Asn Trp Phe
710 715 720

725 Asp Leu Phe Asp Tyr Thr Arg Ser Val Thr Ala Ser Thr Gly Arg Tyr
730 735

740 Val Thr Leu Ser Ala Pro Pro Asp His Ile Asn Val His Ile Gln Glu
745 750

755 Gly Asn Ile Leu Ala Met Gln Gly Lys Ala Met Thr Thr Gln Ala Ala
760 765

770 Arg Lys Thr Pro Phe His Leu Leu Val Val Met Ser Asp Cys Gly Ala
775 780

785 Ser Phe Gly Glu Leu Phe Leu Asp Asp Gly Val Glu Val Thr Met Gly
790 795 800

805 Val Asn Arg Gly Lys Trp Thr Phe Val Lys Phe Ile Ala Ala Ser Ala
810 815

820 Lys Gln Thr Cys Ile Ile Thr Ser Asp Val Val Ser Gly Glu Phe Ala
825 830

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Val Ser Gln Lys Trp Val Ile Asp Lys Val Thr Ile Leu Gly Leu Arg
835 840 845

Lys Gly Thr Lys Ile Asn Gly Tyr Thr Val Arg Thr Gly Ala Val Thr
850 855 860

Arg Lys Gly Asp Lys Ser Lys Leu Lys Ser Thr Pro Asp Arg Lys Gly
865 870 875 880

Glu Phe Ile Val Ala Glu Ile Ser Gly Leu Asn Leu Leu Leu Gly Arg
885 890 895

Glu Phe Lys Leu Val Leu His
900

<210> 16

<211> 913

<212> PRT

<213> Beta vulgaris

<400> 16

Met Glu Arg Ser Lys Leu Pro Arg Tyr Ile Cys Pro Thr Leu Ala Val
1 5 10 15

Val Leu Pro Leu Val Leu Cys Met Val Val Glu Gly Ala Thr Thr Ser
20 25 30

Lys Asn Asp Asn Gln Gly Glu Ala Ile Gly Tyr Gly Tyr Gln Val Lys
35 40 45

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

Gln Leu Ile Arg Asn Ser Pro Val Tyr Gly Pro Asp Ile His Phe Leu
65 70 75 80

Ser Phe Thr Ala Ser Phe Glu Glu Asp Asp Thr Leu Arg Ile Arg Phe
85 90 95

Thr Asp Ala Asn Asn Arg Arg Trp Glu Ile Pro Asn Glu Val Leu Pro
100 105 110

Arg Pro Pro Pro Pro Pro Ser Pro Pro Pro Leu Ser Ser Leu Gln His
115 120 125

Leu Pro Lys Pro Ile Pro Gln Asn Gln Pro Thr Thr Thr Val Leu Ser
130 135 140

His Pro His Ser Asp Leu Ala Phe Thr Leu Phe His Thr Thr Pro Phe
145 150 155 160

Gly Phe Thr Ile Tyr Arg Lys Ser Thr His Asp Val Leu Phe Asp Ala
165 170 175

Thr Pro Ile Pro Ser Asn Pro Thr Thr Phe Leu Ile Tyr Lys Asp Gln
 180 185 190
 Tyr Leu Gln Leu Ser Ser Ser Leu Pro Ala Gln Gln Ala His Leu Tyr
 195 200 205
 Gly Leu Gly Glu His Thr Lys Pro Thr Phe Gln Leu Ala His Asn Gln
 210 215 220
 Ile Leu Thr Leu Trp Asn Ala Asp Ile Ala Ser Phe Asn Arg Asp Leu
 225 230 235 240
 Asn Leu Tyr Gly Ser His Pro Phe Tyr Met Asp Val Arg Ser Ser Pro
 245 250 255
 Met Val Gly Ser Thr His Gly Val Phe Leu Leu Asn Ser Asn Gly Met
 260 265 270
 Asp Val Glu Tyr Thr Gly Asp Arg Ile Thr Tyr Lys Val Ile Gly Gly
 275 280 285
 Ile Ile Asp Leu Tyr Ile Phe Ala Gly Arg Thr Pro Glu Met Val Leu
 290 295 300
 Asp Gln Tyr Thr Lys Leu Ile Gly Arg Pro Ala Pro Met Pro Tyr Trp
 305 310 315 320
 Ala Phe Gly Phe His Gln Cys Arg Trp Gly Tyr Arg Asp Val Asn Glu
 325 330 335
 Ile Glu Thr Val Val Asp Lys Tyr Ala Glu Ala Arg Ile Pro Leu Glu
 340 345 350
 Val Met Trp Thr Asp Ile Asp Tyr Met Asp Ala Phe Lys Asp Phe Thr
 355 360 365
 Leu Asp Pro Val His Phe Pro Leu Asp Lys Met Gln Gln Phe Val Thr
 370 375 380
 Lys Leu His Arg Asn Gly Gln Arg Tyr Val Pro Ile Leu Asp Pro Gly
 385 390 395 400
 Ile Asn Thr Asn Lys Ser Tyr Gly Thr Phe Ile Arg Gly Met Gln Ser
 405 410 415
 Asn Val Phe Ile Lys Arg Asn Gly Asn Pro Tyr Leu Gly Ser Val Trp
 420 425 430
 Pro Gly Pro Val Tyr Tyr Pro Asp Phe Leu Asp Pro Ala Ala Arg Ser
 435 440 445
 Phe Trp Val Asp Glu Ile Lys Arg Phe Arg Asp Ile Leu Pro Ile Asp
 450 455 460
 Gly Ile Trp Ile Asp Met Asn Glu Ala Ser Asn Phe Ile Thr Ser Ala
 465 470 475 480

Pro Thr Pro Gly Ser Thr Leu Asp Asn Pro Pro Tyr Lys Ile Asn Asn
 485 490 495

Ser Gly Gly Arg Val Pro Ile Asn Ser Lys Thr Ile Pro Ala Thr Ala
 500 505 510

Met His Tyr Gly Asn Val Thr Glu Tyr Asn Ala His Asn Leu Tyr Gly
 515 520 525

Phe Leu Glu Ser Gln Ala Thr Arg Glu Ala Leu Val Arg Pro Ala Thr
 530 535 540

Arg Gly Pro Phe Leu Leu Ser Arg Ser Thr Phe Ala Gly Ser Gly Lys
 545 550 555 560

Tyr Thr Ala His Trp Thr Gly Asp Asn Ala Ala Arg Trp Asp Asp Leu
 565 570 575

Gln Tyr Ser Ile Pro Thr Met Leu Asn Phe Gly Leu Phe Gly Met Pro
 580 585 590

Met Ile Gly Ala Asp Ile Cys Gly Phe Ala Glu Ser Thr Thr Glu Glu
 595 600 605

Leu Cys Cys Arg Trp Ile Gln Leu Gly Ala Phe Tyr Pro Phe Ser Arg
 610 615 620

Asp His Ser Ala Arg Asp Thr Thr His Gln Glu Leu Tyr Leu Trp Glu
 625 630 635 640

Ser Val Ala Ala Ser Ala Arg Thr Val Leu Gly Leu Arg Tyr Glu Leu
 645 650 655

Leu Pro Tyr Tyr Tyr Thr Leu Met Tyr Asp Ala Asn Leu Arg Gly Ser
 660 665 670

Pro Ile Ala Arg Pro Leu Ser Phe Thr Phe Pro Asp Asp Val Ala Thr
 675 680 685

Tyr Gly Ile Ser Ser Gln Phe Leu Ile Gly Arg Gly Ile Met Val Ser
 690 695 700

Pro Val Leu Gln Pro Gly Ser Ser Ile Val Asn Ala Tyr Ser Pro Arg
 705 710 715 720

Gly Asn Trp Val Ser Leu Ser Asn Tyr Thr Ser Ser Val Ser Val Ser
 725 730 735

Ala Gly Thr Tyr Val Ser Leu Ser Ala Pro Pro Asp His Ile Asn Val
 740 745 750

His Ile His Glu Gly Asn Ile Val Ala Met Gln Gly Glu Ala Met Thr
 755 760 765

Thr Gln Ala Ala Arg Ser Thr Pro Phe His Leu Leu Val Val Met Ser
 770 775 780

Asp His Val Ala Ser Thr Gly Glu Leu Phe Leu Asp Asn Gly Ile Glu
785 790 795 800

Met Asp Ile Gly Gly Pro Gly Gly Lys Trp Thr Leu Val Arg Phe Phe
805 810 815

Ala Glu Ser Gly Ile Asn Asn Leu Thr Ile Ser Ser Glu Val Val Asn
820 825 830

Arg Gly Tyr Ala Met Ser Gln Arg Trp Val Met Asp Lys Ile Thr Ile
835 840 845

Leu Gly Leu Lys Arg Arg Val Lys Ile Lys Glu Tyr Thr Val Gln Lys
850 855 860

Asp Ala Gly Ala Ile Lys Val Lys Gly Leu Gly Arg Arg Thr Ser Ser
865 870 875 880

His Asn Gln Gly Gly Phe Phe Val Ser Val Ile Ser Asp Leu Arg Gln
885 890 895

Leu Val Gly Gln Ala Phe Lys Leu Glu Leu Glu Phe Glu Gly Ala Thr
900 905 910

Arg

<210> 17

<211> 919

<212> PRT

<213> Solanum tuberosum

<400> 17

Met Arg Ala Pro Leu Leu Leu Tyr Pro Leu Leu Leu Leu Leu Phe
1 5 10 15

Val Thr Ser Ala Tyr Ser Trp Lys Lys Glu Glu Phe Arg Asn Cys Asp
20 25 30

Gln Thr Pro Phe Cys Lys Arg Ala Arg Ser Arg Lys Pro Gly Ser Cys
35 40 45

Asn Leu Arg Val Ala Asp Val Ser Ile Ser Asp Gly Asp Leu Ile Ala
50 55 60

Lys Leu Val Pro Lys Glu Glu Asn Pro Glu Ser Glu Gln Pro Asn Lys
65 70 75 80

Pro Leu Val Leu Thr Leu Ser Val Tyr Gln Asp Gly Val Met Arg Val
85 90 95

Lys Ile Asp Glu Asp Gln Asn Leu Asn Pro Pro Lys Lys Arg Phe Glu
100 105 110

Val Pro Glu Val Ile Glu Glu Asp Phe Leu Asn Thr Lys Leu Trp Leu
115 120 125

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Thr Arg Val Lys Glu Glu Gln Ile Asp Gly Val Ser Ser Phe Ser Ser
130                      135                      140

Val Phe Tyr Leu Ser Asp Gly Tyr Glu Gly Val Leu Arg His Asp Pro
145                      150                      155                      160

Phe Glu Val Phe Ala Arg Glu Ser Gly Ser Gly Lys Arg Val Leu Ser
165                      170                      175

Ile Asn Ser Asn Gly Leu Phe Asp Phe Glu Gln Leu Arg Glu Lys Lys
180                      185                      190

Glu Gly Asp Asp Trp Glu Glu Lys Phe Arg Ser His Thr Asp Thr Arg
195                      200                      205

Pro Tyr Gly Pro Gln Ser Ile Ser Phe Asp Val Ser Phe Tyr Gly Ala
210                      215                      220

Asp Phe Val Tyr Gly Ile Pro Glu His Ala Thr Ser Phe Ala Leu Lys
225                      230                      235                      240

Pro Thr Lys Gly Pro Asn Val Glu Glu Tyr Ser Glu Pro Tyr Arg Leu
245                      250                      255

Phe Asn Leu Asp Val Phe Glu Tyr Leu His Glu Ser Pro Phe Gly Leu
260                      265                      270

Tyr Gly Ser Ile Pro Phe Met Ile Ser His Gly Lys Ala Arg Gly Ser
275                      280                      285

Ser Gly Phe Phe Trp Leu Asn Ala Ala Glu Met Gln Ile Asp Val Leu
290                      295                      300

Gly Ser Gly Trp Asn Ser Asp Glu Ser Ser Lys Ile Met Leu Pro Ser
305                      310                      315                      320

Asp Lys His Arg Ile Asp Thr Leu Trp Met Ser Glu Ser Gly Val Val
325                      330                      335

Asp Thr Phe Phe Phe Ile Gly Pro Gly Pro Lys Asp Val Val Arg Gln
340                      345                      350

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

Ala Tyr His Gln Cys Arg Trp Asn Tyr Arg Asp Glu Glu Asp Val Tyr
370                      375                      380

Asn Val Asp Ser Lys Phe Asp Glu His Asp Ile Pro Tyr Asp Val Leu
385                      390                      395                      400

Trp Leu Asp Ile Glu His Thr Asp Gly Lys Lys Tyr Phe Thr Trp Asp
405                      410                      415

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Arg Val Leu Phe Pro Asn Pro Glu Glu Met Gln Lys Lys Leu Ala Ala
 420 425 430

Lys Gly Arg His Met Val Thr Ile Val Asp Pro His Ile Lys Arg Asp
 435 440 445

Glu Ser Tyr His Ile Pro Lys Glu Ala Leu Glu Lys Gly Tyr Tyr Val
 450 455 460

Lys Asp Ala Thr Gly Lys Asp Tyr Asp Gly Trp Cys Trp Pro Gly Ser
 465 470 475 480

Ser Ser Tyr Thr Asp Leu Leu Asn Pro Glu Ile Lys Ser Trp Trp Ser
 485 490 495

Asp Lys Phe Ser Leu Asp Ser Tyr Val Gly Ser Thr Lys Tyr Leu Tyr
 500 505 510

Ile Trp Asn Asp Met Asn Glu Pro Ser Val Phe Asn Gly Pro Glu Val
 515 520 525

Thr Met Pro Arg Asp Ala Leu His His Gly Gly Val Glu His Arg Glu
 530 535 540

Leu His Asn Ser Tyr Gly Tyr Tyr Phe His Met Gly Thr Ser Asp Gly
 545 550 555 560

Leu Leu Lys Arg Gly Asp Gly Lys Asp Arg Pro Phe Val Leu Ala Arg
 565 570 575

Ala Phe Phe Ala Gly Ser Gln Arg Tyr Gly Ala Ile Trp Thr Gly Asp
 580 585 590

Asn Thr Ala Glu Trp Glu His Leu Arg Val Ser Val Pro Met Val Leu
 595 600 605

Thr Leu Ser Ile Ser Gly Ile Val Phe Ser Gly Ala Asp Val Gly Gly
 610 615 620

Phe Phe Gly Asn Pro Asp Thr Glu Leu Leu Val Arg Trp Tyr Gln Val
 625 630 635 640

Gly Ala Tyr Tyr Pro Phe Phe Arg Gly His Ala His His Asp Thr Lys
 645 650 655

Arg Arg Glu Pro Trp Leu Phe Gly Glu Arg Asn Thr Gln Leu Met Arg
 660 665 670

Glu Ala Ile His Val Arg Tyr Met Tyr Leu Pro Tyr Phe Tyr Thr Leu
 675 680 685

Phe Arg Glu Ala Asn Ser Ser Gly Thr Pro Val Ala Arg Pro Leu Trp
 690 695 700

Met Glu Phe Pro Gly Asp Glu Lys Ser Phe Ser Asn Asp Glu Ala Phe
 705 710 715 720

Met Val Gly Asn Gly Leu Leu Val Gln Gly Val Tyr Thr Glu Lys Pro
725 730 735

Lys His Val Ser Val Tyr Leu Pro Gly Glu Glu Ser Trp Tyr Asp Leu
740 745 750

Arg Ser Ala Ser Ala Tyr Asn Gly Gly His Thr His Lys Tyr Glu Val
755 760 765

Ser Glu Asp Ser Ile Pro Ser Phe Gln Arg Ala Gly Thr Ile Ile Pro
770 775 780

Arg Lys Asp Arg Leu Arg Arg Ser Ser Thr Gln Met Glu Asn Asp Pro
785 790 795 800

Tyr Thr Leu Val Ile Ala Leu Asn Ser Ser Lys Ala Ala Glu Gly Glu
805 810 815

Leu Tyr Ile Asp Asp Gly Lys Ser Tyr Glu Phe Lys Gln Gly Ala Phe
820 825 830

Ile Leu Lys Trp Glu Ala Tyr Ile Phe Gln Met Gln Pro Arg Leu Gln
835 840 845

Leu Ala Val Thr His Phe Pro Ser Glu Cys Thr Val Glu Arg Ile Ile
850 855 860

Leu Leu Gly Leu Ser Pro Gly Ala Lys Thr Ala Leu Ile Glu Pro Gly
865 870 875 880

Asn Lys Lys Val Glu Ile Glu Leu Gly Pro Leu Phe Ile Gln Gly Asn
885 890 895

Arg Gly Ser Val Pro Thr Ile Arg Lys Pro Asn Val Arg Ile Thr Asp
900 905 910

Asp Trp Ser Ile Gln Ile Leu
915

<210> 18

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 18

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Cys Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile

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      355              360              365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370              375              380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385              390              395              400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
      405              410              415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
      420              425              430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
      435              440              445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
      450              455              460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465              470              475              480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
      485              490              495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
      500              505              510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
      515              520              525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
      530              535              540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545              550              555              560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
      565              570              575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
      580              585              590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
      595              600              605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
      610              615              620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625              630              635              640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
      645              650              655

Trp Glu Glu Asn Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile

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Asp Gly Gly Asp Asn Tyr Ser Lys Asp Asp Ser Asn Tyr Tyr Ser Asn
660                               665                               670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
675                               680                               685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
690                               695                               700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                               710                               715                               720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
725                               730                               735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
740                               745                               750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
755                               760                               765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
770                               775                               780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785                               790                               795                               800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
805                               810                               815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
820                               825                               830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835                               840                               845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850                               855                               860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865                               870                               875                               880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885                               890                               895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900                               905                               910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915                               920                               925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930                               935                               940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945                               950                               955                               960

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Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 19

<211> 985

<212> PRT

<213> *Aspergillus niger*

<400> 19

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240
 Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255
 Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270
 Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285
 Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300
 Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320
 Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335
 Gly Phe His Gln Cys Arg Asp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350
 Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400
 His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Gly Ala Ala Ser Ala

Tyr Glu Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Glu Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Thr

Gly Val Asn Ile Ile Ser Ala Phe Leu Gly His Ile Phe Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser

945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 20

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 20

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Tyr Thr Tyr Ser Val Gly Thr Glu Ser Ser Ser Ser Ser Ser

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110
 Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125
 Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140
 Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160
 Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
 165 170 175
 Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190
 Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205
 Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220
 Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240
 Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255
 Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270
 Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285
 Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300
 Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320
 Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335
 Gly Phe His Gln Cys Arg Met Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350
 Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu

385	390	395	400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr	405	410	415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg	420	425	430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr	435	440	445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His	450	455	460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys	465	470	475
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser	485	490	495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala	500	505	510
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp	515	520	525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala	530	535	540
Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser	545	550	555
Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn	565	570	575
Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp	580	585	590
Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val	595	600	605
Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala	610	615	620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe	625	630	635
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His	645	650	655
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile	660	665	670
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala	675	680	685
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg	690	695	700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860
 Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
 865 870 875 880
 Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
 885 890 895
 Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
 900 905 910
 Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925
 Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940
 Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960
 Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
 965 970 975
 Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985

<210> 21

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 21

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg His Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 22

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 22

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Ala Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 23

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 23

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

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305                310                315                320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
                325                330                335

Gly Phe His Gln Cys Arg Phe Gly Tyr Asn Asn Trp Ser Asp Leu Ala
                340                345                350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
                355                360                365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
                370                375                380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
                385                390                395                400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
                405                410                415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
                420                425                430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
                435                440                445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
                450                455                460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
                465                470                475                480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
                485                490                495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
                500                505                510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
                515                520                525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
                530                535                540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
                545                550                555                560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
                565                570                575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
                580                585                590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
                595                600                605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
                610                615                620

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Thr	Tyr	Gln	Gly	Leu	Leu	Glu	Val	Trp	Ser	His	Lys	Arg	Arg	Pro	Phe	625	630	635	640
Ile	Ile	Gly	Arg	Ser	Thr	Phe	Ala	Gly	Ser	Gly	Lys	Trp	Ala	Gly	His	645	650	655	
Trp	Gly	Gly	Asp	Asn	Tyr	Ser	Lys	Trp	Trp	Ser	Met	Tyr	Tyr	Ser	Ile	660	665	670	
Ser	Gln	Ala	Leu	Ser	Phe	Ser	Leu	Phe	Gly	Ile	Pro	Met	Phe	Gly	Ala	675	680	685	
Asp	Thr	Cys	Gly	Phe	Asn	Gly	Asn	Ser	Asp	Glu	Glu	Leu	Cys	Asn	Arg	690	695	700	
Trp	Met	Gln	Leu	Ser	Ala	Phe	Phe	Pro	Phe	Tyr	Arg	Asn	His	Asn	Glu	705	710	715	720
Leu	Ser	Thr	Ile	Pro	Gln	Glu	Pro	Tyr	Arg	Trp	Ala	Ser	Val	Ile	Glu	725	730	735	
Ala	Thr	Lys	Ser	Ala	Met	Arg	Ile	Arg	Tyr	Ala	Ile	Leu	Pro	Tyr	Phe	740	745	750	
Tyr	Thr	Leu	Phe	Asp	Leu	Ala	His	Thr	Thr	Gly	Ser	Thr	Val	Met	Arg	755	760	765	
Ala	Leu	Ser	Trp	Glu	Phe	Pro	Asn	Asp	Pro	Thr	Leu	Ala	Ala	Val	Glu	770	775	780	
Thr	Gln	Phe	Met	Val	Gly	Pro	Ala	Ile	Met	Val	Val	Pro	Val	Leu	Glu	785	790	795	800
Pro	Leu	Val	Asn	Thr	Val	Lys	Gly	Val	Phe	Pro	Gly	Val	Gly	His	Gly	805	810	815	
Glu	Val	Trp	Tyr	Asp	Trp	Tyr	Thr	Gln	Ala	Ala	Val	Asp	Ala	Lys	Pro	820	825	830	
Gly	Val	Asn	Thr	Thr	Ile	Ser	Ala	Pro	Leu	Gly	His	Ile	Pro	Val	Tyr	835	840	845	
Val	Arg	Gly	Gly	Asn	Ile	Leu	Pro	Met	Gln	Glu	Pro	Ala	Leu	Thr	Thr	850	855	860	
Arg	Glu	Ala	Arg	Gln	Thr	Pro	Trp	Ala	Leu	Leu	Ala	Ala	Leu	Gly	Ser	865	870	875	880
Asn	Gly	Thr	Ala	Ser	Gly	Gln	Leu	Tyr	Leu	Asp	Asp	Gly	Glu	Ser	Ile	885	890	895	
Tyr	Pro	Asn	Ala	Thr	Leu	His	Val	Asp	Phe	Thr	Ala	Ser	Arg	Ser	Ser	900	905	910	

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
 965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985

<210> 24

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 24

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala

130

135

140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Gly Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 25

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 25

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

-- -- --
 Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
 65 70 75 80

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Thr Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile

355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400
 His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
 865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
 885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
 900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
 965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985

<210> 26

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 26

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Glv Thr Pro Ile Asp Gln Asn Leu Trp Glv Gln His Pro Phe

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225          230          235          240
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
          245          250          255
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
          260          265          270
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
          275          280          285
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
          290          295          300
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
          305          310          315          320
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
          325          330          335
Gly Phe His Gln Cys Arg Glu Gly Tyr Asn Asn Trp Ser Asp Leu Ala
          340          345          350
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
          355          360          365
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
          370          375          380
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
          385          390          395          400
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
          405          410          415
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
          420          425          430
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
          435          440          445
Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
          450          455          460
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
          465          470          475          480
Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
          485          490          495
Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
          500          505          510
His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
          515          520          525
Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala

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Tyr Phe Glu Asn Phe Asn Leu Thr Asn Ala Thr Glu Asn Ala Ser Asn
 530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 27

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 27

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
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Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Val Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400

His Gln Ser Gln Asp Thr Thr Val Pro Ile Val Asp Ala Ala Leu Thr

His Glu Ser Gly Arg Tyr Tyr Val Phe Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu

Alp Met Gln Leu Ser Ala Phe Phe Phe Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860
 Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
 865 870 875 880
 Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
 885 890 895
 Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
 900 905 910
 Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925
 Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940
 Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960
 Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
 965 970 975
 Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 28

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

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser

260 265 270
 Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285
 Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300
 Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320
 Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335
 Gly Phe His Gln Cys Arg Gln Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350
 Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400
 His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn

565										570					575				
Val	Glu	His	Pro	Pro	Tyr	Val	Ile	Asn	His	Asp	Gln	Glu	Gly	His	Asp				
			580					585					590						
Leu	Ser	Val	His	Ala	Val	Ser	Pro	Asn	Ala	Thr	His	Val	Asp	Gly	Val				
		595					600					605							
Glu	Glu	Tyr	Asp	Val	His	Gly	Leu	Tyr	Gly	His	Gln	Gly	Leu	Asn	Ala				
	610					615					620								
Thr	Tyr	Gln	Gly	Leu	Leu	Glu	Val	Trp	Ser	His	Lys	Arg	Arg	Pro	Phe				
625					630					635					640				
Ile	Ile	Gly	Arg	Ser	Thr	Phe	Ala	Gly	Ser	Gly	Lys	Trp	Ala	Gly	His				
				645					650					655					
Trp	Gly	Gly	Asp	Asn	Tyr	Ser	Lys	Trp	Trp	Ser	Met	Tyr	Tyr	Ser	Ile				
			660					665					670						
Ser	Gln	Ala	Leu	Ser	Phe	Ser	Leu	Phe	Gly	Ile	Pro	Met	Phe	Gly	Ala				
		675					680					685							
Asp	Thr	Cys	Gly	Phe	Asn	Gly	Asn	Ser	Asp	Glu	Glu	Leu	Cys	Asn	Arg				
	690					695					700								
Trp	Met	Gln	Leu	Ser	Ala	Phe	Phe	Pro	Phe	Tyr	Arg	Asn	His	Asn	Glu				
705					710					715					720				
Leu	Ser	Thr	Ile	Pro	Gln	Glu	Pro	Tyr	Arg	Trp	Ala	Ser	Val	Ile	Glu				
				725					730					735					
Ala	Thr	Lys	Ser	Ala	Met	Arg	Ile	Arg	Tyr	Ala	Ile	Leu	Pro	Tyr	Phe				
			740					745					750						
Tyr	Thr	Leu	Phe	Asp	Leu	Ala	His	Thr	Thr	Gly	Ser	Thr	Val	Met	Arg				
	755						760					765							
Ala	Leu	Ser	Trp	Glu	Phe	Pro	Asn	Asp	Pro	Thr	Leu	Ala	Ala	Val	Glu				
	770					775					780								
Thr	Gln	Phe	Met	Val	Gly	Pro	Ala	Ile	Met	Val	Val	Pro	Val	Leu	Glu				
785					790					795					800				
Pro	Leu	Val	Asn	Thr	Val	Lys	Gly	Val	Phe	Pro	Gly	Val	Gly	His	Gly				
				805					810					815					
Glu	Val	Trp	Tyr	Asp	Trp	Tyr	Thr	Gln	Ala	Ala	Val	Asp	Ala	Lys	Pro				
			820					825					830						
Gly	Val	Asn	Thr	Thr	Ile	Ser	Ala	Pro	Leu	Gly	His	Ile	Pro	Val	Tyr				
		835					840					845							
Val	Arg	Gly	Gly	Asn	Ile	Leu	Pro	Met	Gln	Glu	Pro	Ala	Leu	Thr	Thr				
	850					855						860							
Arg	Glu	Ala	Arg	Gln	Thr	Pro	Trp	Ala	Leu	Leu	Ala	Ala	Leu	Gly	Ser				
865					870					875					880				

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 29

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 29

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

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
325 330 335

Gly Phe His Gln Cys Arg Asn Gly Tyr Asn Asn Trp Ser Asp Leu Ala
340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
420 425 430

Glu Ala Ala Asn Asn Val Phe Leu Lys Asn Pro Asn Gly Ser Leu Tyr

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Phe Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Asp Ile Asp Thr Ala Ile Leu Asp Thr Phe

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860
 Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
 865 870 875 880
 Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
 885 890 895
 Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
 900 905 910
 Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925
 Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940
 Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960
 Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
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 Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985
 <210> 30
 <211> 985
 <212> PRT
 <213> Aspergillus niger
 <400> 30
 Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
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Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
325 330 335

Gly Phe His Gln Cys Arg Ile Gly Tyr Asn Asn Trp Ser Asp Leu Ala
340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
485 490 495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
500 505 510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
565 570 575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
580 585 590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
595 600 605

Glu Glu Tyr Asp Val His Glu Leu Tyr Glu His Gln Glu Leu Asp Ala

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860
 Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
 865 870 875 880
 Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
 885 890 895
 Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
 900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
 965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985

<210> 31

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 31

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val

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      180              185              190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195              200              205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210              215              220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225              230              235              240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245              250              255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260              265              270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
275              280              285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
290              295              300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305              310              315              320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
325              330              335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
340              345              350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
355              360              365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
370              375              380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385              390              395              400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
405              410              415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
420              425              430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
435              440              445

Ile Gly Ala Gly Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
450              455              460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465              470              475              480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser

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485										490					495				
Phe	Cys	Val	Gly	Ser	Cys	Gly	Thr	Gly	Asn	Leu	Thr	Leu	Asn	Pro	Ala				
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His	Pro	Ser	Phe	Leu	Leu	Pro	Gly	Glu	Pro	Gly	Asp	Ile	Ile	Tyr	Asp				
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Tyr	Pro	Glu	Ala	Phe	Asn	Ile	Thr	Asn	Ala	Thr	Glu	Ala	Ala	Ser	Ala				
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Ser	Ala	Gly	Ala	Ser	Ser	Gln	Ala	Ala	Ala	Thr	Ala	Thr	Thr	Thr	Ser				
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Thr	Ser	Val	Ser	Tyr	Leu	Arg	Thr	Thr	Pro	Thr	Pro	Gly	Val	Arg	Asn				
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Val	Glu	His	Pro	Pro	Tyr	Val	Ile	Asn	His	Asp	Gln	Glu	Gly	His	Asp				
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Leu	Ser	Val	His	Ala	Val	Ser	Pro	Asn	Ala	Thr	His	Val	Asp	Gly	Val				
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Glu	Glu	Tyr	Asp	Val	His	Gly	Leu	Tyr	Gly	His	Gln	Gly	Leu	Asn	Ala				
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Thr	Tyr	Gln	Gly	Leu	Leu	Glu	Val	Trp	Ser	His	Lys	Arg	Arg	Pro	Phe				
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Ile	Ile	Gly	Arg	Ser	Thr	Phe	Ala	Gly	Ser	Gly	Lys	Trp	Ala	Gly	His				
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Trp	Gly	Gly	Asp	Asn	Tyr	Ser	Lys	Trp	Trp	Ser	Met	Tyr	Tyr	Ser	Ile				
			660					665					670						
Ser	Gln	Ala	Leu	Ser	Phe	Ser	Leu	Phe	Gly	Ile	Pro	Met	Phe	Gly	Ala				
		675					680					685							
Asp	Thr	Cys	Gly	Phe	Asn	Gly	Asn	Ser	Asp	Glu	Glu	Leu	Cys	Asn	Arg				
	690					695					700								
Trp	Met	Gln	Leu	Ser	Ala	Phe	Phe	Pro	Phe	Tyr	Arg	Asn	His	Asn	Glu				
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Leu	Ser	Thr	Ile	Pro	Gln	Glu	Pro	Tyr	Arg	Trp	Ala	Ser	Val	Ile	Glu				
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Ala	Thr	Lys	Ser	Ala	Met	Arg	Ile	Arg	Tyr	Ala	Ile	Leu	Pro	Tyr	Phe				
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Tyr	Thr	Leu	Phe	Asp	Leu	Ala	His	Thr	Thr	Gly	Ser	Thr	Val	Met	Arg				
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Ala	Leu	Ser	Trp	Glu	Phe	Pro	Asn	Asp	Pro	Thr	Leu	Ala	Ala	Val	Glu				
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Thr	Gln	Phe	Met	Val	Gly	Pro	Ala	Ile	Met	Val	Val	Pro	Val	Leu	Glu				

785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860
 Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
 865 870 875 880
 Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
 885 890 895
 Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
 900 905 910
 Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925
 Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940
 Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960
 Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
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 Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
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 Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30
 Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400
 His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Asp Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
 865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
 885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
 900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960

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

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asn Asn Glu Phe Asn Ile Asn Gln Asn Leu Thr Glu Gln His Asn Phe

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
325 330 335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
435 440 445

Ile Gly Ala Glu Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
485 490 495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
500 505 510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 34

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<213> Aspergillus niger

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Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
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Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Val
 485 490 495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
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His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
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690	695	700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu		
705	710	715 720
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu		
	725	730 735
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe		
	740	745 750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg		
	755	760 765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu		
	770	775 780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu		
	785	790 795 800
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly		
	805	810 815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro		
	820	825 830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr		
	835	840 845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr		
	850	855 860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser		
	865	870 875 880
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile		
	885	890 895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser		
	900	905 910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala		
	915	920 925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu		
	930	935 940
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser		
	945	950 955 960
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala		
	965	970 975
Trp Ala Glu Asn Trp Val Leu Glu Trp		
	980	985

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<213> Aspergillus niger

<400> 35

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

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285
 Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300
 Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320
 Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335
 Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350
 Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400
 His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Asn
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 36

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 36

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala

130 135 140
 Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160
 Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
 165 170 175
 Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190
 Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205
 Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220
 Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240
 Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255
 Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270
 Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285
 Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300
 Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320
 Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335
 Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350
 Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400
 His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Glv Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Glv Ser Leu Trp

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435                               440                               445
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Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
450                               455                               460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465                               470                               475                               480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Gln
485                               490                               495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
500                               505                               510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
515                               520                               525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
530                               535                               540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545                               550                               555                               560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
565                               570                               575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
580                               585                               590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
595                               600                               605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
610                               615                               620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625                               630                               635                               640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
645                               650                               655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
660                               665                               670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
675                               680                               685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
690                               695                               700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705                               710                               715                               720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
725                               730                               735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe

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740	745	750
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg		
755	760	765
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu		
770	775	780
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu		
785	790	795
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly		
805	810	815
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro		
820	825	830
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr		
835	840	845
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr		
850	855	860
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser		
865	870	875
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile		
885	890	895
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser		
900	905	910
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala		
915	920	925
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu		
930	935	940
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser		
945	950	955
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala		
965	970	975
Trp Ala Glu Asn Trp Val Leu Glu Trp		
980	985	

<210> 37

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 37

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30
 Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45
 Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60
 Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
 65 70 75 80
 Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95
 Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110
 Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125
 Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140
 Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160
 Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
 165 170 175
 Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190
 Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205
 Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220
 Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240
 Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255
 Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270
 Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285
 Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Asp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445

Ile Gly Ala Ala Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860
 Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
 865 870 875 880
 Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
 885 890 895
 Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
 900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
 965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985

<210> 38

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 38

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val

180	185	190
Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile		
195	200	205
Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser		
210	215	220
Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe		
225	230	235
Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr		
	245	250
Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser		
	260	265
Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu		
	275	280
Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp		
	290	295
Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr		
305	310	315
Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu		
	325	330
Gly Phe His Gln Cys Arg Asp Gly Tyr Asn Asn Trp Ser Asp Leu Ala		
	340	345
Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile		
	355	360
Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp		
	370	375
Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu		
385	390	395
His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr		
	405	410
Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg		
	420	425
Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr		
	435	440
Ile Gly Ala Gly Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His		
	450	455
Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys		
465	470	475
		480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 39

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 39

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro

50 55 60
 Gly Tyr Lys Ala Ser Lys Val Gln His Asn Ser Arg Gly Phe Thr Ala
 65 70 75 80
 Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95
 Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110
 Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125
 Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140
 Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160
 Phe Asn Phe Lys Val Ile Arg Lys Ala Thr Gly Asp Ala Leu Phe Ser
 165 170 175
 Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190
 Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205
 Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220
 Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240
 Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255
 Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270
 Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285
 Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300
 Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320
 Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335
 Gly Phe His Gln Cys Arg Asp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400
 His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ile
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705 710 715 720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
725 730 735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser

945 950 955 960
 Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
 965 970 975

 Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985

 <210> 40
 <211> 985
 <212> PRT
 <213> Aspergillus niger

 <400> 40
 Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1 5 10 15

 Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30

 Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

 Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

 Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

 Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

 Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

 Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

 Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

 Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

 Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

 Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240
 Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255
 Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270
 Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285
 Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300
 Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320
 Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335
 Gly Phe His Gln Cys Arg Asp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350
 Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365
 Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380
 Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400
 His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415
 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
 Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Arg
 485 490 495
 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735

Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser

945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 41

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 41

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
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Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
325 330 335

Gly Phe His Gln Cys Arg Met Gly Tyr Asn Asn Trp Ser Asp Leu Ala
340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
370 375 380

Glu His Ser Glu Ser Thr Ser Glu Glu Tyr Gln Phe Thr Glu Ser Tyr

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Cys
485 490 495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
500 505 510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
565 570 575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
580 585 590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
595 600 605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
610 615 620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625 630 635 640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
645 650 655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
660 665 670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
675 680 685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg

690	695	700
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu 705 710 715 720		
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu 725 730 735		
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe 740 745 750		
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg 755 760 765		
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu 770 775 780		
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu 785 790 795 800		
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly 805 810 815		
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro 820 825 830		
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr 835 840 845		
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr 850 855 860		
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser 865 870 875 880		
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile 885 890 895		
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser 900 905 910		
Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala 915 920 925		
Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu 930 935 940		
Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser 945 950 955 960		
Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala 965 970 975		
Trp Ala Glu Asn Trp Val Leu Glu Trp 980 985		

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 42

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
325 330 335

Gly Phe His Gln Cys Arg Met Gly Tyr Asn Asn Trp Ser Asp Leu Ala
340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Thr
485 490 495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
500 505 510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 43

<211> 2958

<212> DNA

<213> *Aspergillus niger*

<400> 43

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gcagatgtcg gtgcgcagct gattgccaac atcgatgac ctcaggctgc cgacgcgcag	180
tgggtttgtc cgggtctaca ggcttcaaaa gtgcagcaca attcacgtgg attcactgcc	240
agtcttcagc tcgcgggcag gccatgtaac gtatacggca cagatgttga gtccttgaca	300
ctgtctgtgg agtaccagga ttccgatcga ctgaatattc agattctccc cactcatgtt	360
gactccacaa acgcttcttg gtactttctt tcggaaaacc tggccccag acccaaggct	420
tccctcaatg catctgtatc ccagagcgac ctttttgtgt catgggtcaa tgagccgtcg	480
ttcaatttca aggtgatccg aaaggctaca ggcgacgcgc ttttcagtac agaaggcact	540
gtgctcgtat atgagaatca gtcatcgaa tttgtgaccg cgctccctga agaataaac	600
ttgtatggcc ttggggagca tatcacgcaa ttccgcctcc agagaaatgc taatctgacc	660
atatatcctt cggatgatgg aacacctatt gacaaaaacc tctacggcca acatcccttc	720
tatctggata caagatatta caaaggagat aggcagaatg ggtcttatat tcccgtaaaa	780
agcagcgagg ctgatgcctc gcaagattat atctccctct ctcatggcgt gtttctgagg	840
aactctcatg gacttgagat actcctccgg tctcaaaaat tgatctggcg gaccctaggt	900
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cttaccagca ctgtgggatt accggccatg cagcaataca acactcttgg attccaccaa	1020

tgtcgttggtg gctacaacaa ctgggtcggat ctggcggacg ttgttgcgaa ctttgagaag	1080
tttgagatcc cgttgaata tatctggacc gatattgact acatgcacgg atatcgcaac	1140
tttgacaacg atcaacatcg cttttcctac agtgagggcg atgaatttct cagcaagcta	1200
catgagagtg gacgctacta tgtaccatt gttgatgagg cgctctacat tctaataccc	1260
gaaaatgcct ctgatgcata cgctacgtat gacagaggag ctgcggacga cgtcttcctc	1320
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gattggcatc atcccaaggc agttgacttc tgggctaacg agcttggtat ctggtcgaag	1440
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acttcggtat catatctgcg gacaacgccc acgcctgggtg tccgcaatgt tgagcaccca	1740
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attattggcc gctcaacctt cgctggctct ggcaaaggc caggccactg gggcggcgac	1980
aactattcca aatggtggtc catgtactac tccatctcgc aagccctctc cttctcactt	2040
ttcggcatte cgatgtttgg tgcggacacc tgtgggttta acggaactc cgatgaggag	2100
ctctgcaacc gatggatgca actgtccgca ttcttcccat tctaccgaaa ccacaatgag	2160
ctctccacaa tcccacagga gccttatcgg tgggcttctg ttattgaagc aaccaagtcc	2220
gccatgagaa ttcggtacgc catcctacct tacttttata cgttggttga cctggcccac	2280
accacgggct cactgtaat gcgcgcactt tcctgggaat tccctaata cccaacattg	2340
gctgcgggtg agactcaatt catggttggg ccggccatca tgggtgtccc ggtattggag	2400
cctctggtca atacggtcaa ggcgtattc ccaggagttg gacatggcga agtgtgttac	2460
gattgttaca cccaggtgc agttgatgcg aagcccgggg tcaacacgac catttcggca	2520
ccattgggcc acatcccagt ttatgtacga ggtggaaca tcttgccgat gcaagagccg	2580
gcattgacca ctctgaagc ccggcaaacc ccgtgggctt tgctagctgc actaggaagc	2640
aatggaaccg cgtcggggca gctctatctc gatgatggag agagcatcta cccaatgcc	2700
accctccatg tggacttcac ggcacgcggg tcaagcctgc gctcgtcggc tcaaggaaga	2760
tggaaagaga ggaacccgct tgctaattgt acggtgctcg gagtgaacaa ggagccctct	2820
gcggtgaccc tgaatggaca ggccgtattt cccgggtctg tcacgtacaa ttctacgtcc	2880
caggttctct ttgttggggg gctgcaaaac ttgacgaagg gcggcgcatg ggcgaaaaac	2940
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<210> 44

<211> 2958

<212> DNA

<213> *Aspergillus niger*

<400> 44

atggtgaagt tgacgcatct ccttgccaga gcatggcttg tccctctggc ttatggagcg	60
agccagtcac tcttatccac cactgcccct tcgcagccgc agtttaccat tcttgcttcc	120
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<212> DNA

<213> *Aspergillus niger*

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<213> Aspergillus niger

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<213> *Aspergillus niger*

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<213> *Aspergillus niger*

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<212> DNA

<213> *Aspergillus niger*

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<213> *Aspergillus niger*

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<213> *Aspergillus niger*

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<210> 66

<211> 2958

<212> DNA

<213> *Aspergillus niger*

<400> 66

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<210> 67

<211> 2958

<212> DNA

<213> *Aspergillus niger*

<400> 67

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<211> 45

<212> PRT

<213> Homo sapiens

<400> 68

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Asp Met Asn Glu Val Ser Asn Phe Val Asp Gly Ser Val
 35 40 45

<210> 69

<211> 45

<212> PRT

<213> Aspergillus niger

<400> 69

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Asp Met Ser Glu Val Ser Ser Phe Cys Val Gly Ser Cys
35 40 45

<210> 70

<211> 45

<212> PRT

<213> Homo sapiens

<400> 70

Gly Tyr His Gln Cys Arg Trp Asn Tyr Glu Asp Glu Gln Gln Asp Phe
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Glu Gly Val Cys Trp Pro Gly Leu Ser Ser Tyr Leu Asp Leu Trp Asn
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Asp Met Asn Glu Pro Ser Val Phe Arg Gly Pro Glu Asp
35 40 45

<210> 71

<211> 45

<212> PRT

<213> Mus musculus

<400> 71

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

<210> 72

<211> 45

<212> PRT

<213> Yeast GLU2A

<400> 72

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Asp Met Asn Glu Pro Ser Ile Phe Asp Gly Pro Glu Thr
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<210> 73

<211> 2958

<212> DNA

<213> *Aspergillus niger*

<400> 73

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<210> 74

<211> 985

<212> PRT

<213> *Aspergillus niger*

<400> 74

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Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20           25           30

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Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35           40           45

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Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50           55           60

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

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Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85           90           95

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

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
325 330 335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
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 Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430
 Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445
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 450 455 460
 Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480
 Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Gly Ser
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 Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
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 545 550 555 560
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 565 570 575
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 595 600 605
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 675 680 685
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 690 695 700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
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 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
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 835 840 845
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<210> 75

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 75

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20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe

225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

260 265 270 275 280 285 290 295 300 305 310 315 320 325 330 335 340 345 350 355 360 365 370 375 380 385 390 395 400

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Pro Ser
 485 490 495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780
 Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
 785 790 795 800
 Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
 805 810 815
 Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
 820 825 830
 Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
 835 840 845
 Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
 850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 76

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 76

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
325 330 335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
435 440 445

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Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
450          455          460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
465          470          475          480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Val Ser
          485          490          495

Phe Cys Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
          500          505          510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
515          520          525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
530          535          540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
545          550          555          560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
          565          570          575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
          580          585          590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
          595          600          605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
610          615          620

Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
625          630          635          640

Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
          645          650          655

Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
          660          665          670

Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
          675          680          685

Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
690          695          700

Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
705          710          715          720

Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
          725          730          735

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Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
740 745 750

Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
755 760 765

Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 77

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 77

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
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Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
305 310 315 320

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305              310              315              320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
              325              330              335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
              340              345              350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
              355              360              365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
              370              375              380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
              385              390              395              400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
              405              410              415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
              420              425              430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
              435              440              445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
              450              455              460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
              465              470              475              480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
              485              490              495

Phe Leu Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
              500              505              510

His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
              515              520              525

Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
              530              535              540

Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
              545              550              555              560

Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
              565              570              575

Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
              580              585              590

Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
              595              600              605

Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala

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610	615	620
Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe 625 630 635 640		
Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His 645 650 655		
Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile 660 665 670		
Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala 675 680 685		
Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg 690 695 700		
Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu 705 710 715 720		
Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu 725 730 735		
Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe 740 745 750		
Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg 755 760 765		
Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu 770 775 780		
Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu 785 790 795 800		
Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly 805 810 815		
Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro 820 825 830		
Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr 835 840 845		
Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr 850 855 860		
Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser 865 870 875 880		
Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile 885 890 895		
Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser 900 905 910		

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
 915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
 930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser
 945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
 965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
 980 985

<210> 78

<211> 985

<212> PRT

<213> Aspergillus niger

<400> 78

Met Val Lys Leu Thr His Leu Leu Ala Arg Ala Trp Leu Val Pro Leu
 1 5 10 15

Ala Tyr Gly Ala Ser Gln Ser Leu Leu Ser Thr Thr Ala Pro Ser Gln
 20 25 30

Pro Gln Phe Thr Ile Pro Ala Ser Ala Asp Val Gly Ala Gln Leu Ile
 35 40 45

Ala Asn Ile Asp Asp Pro Gln Ala Ala Asp Ala Gln Ser Val Cys Pro
 50 55 60

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

Ser Leu Gln Leu Ala Gly Arg Pro Cys Asn Val Tyr Gly Thr Asp Val
 85 90 95

Glu Ser Leu Thr Leu Ser Val Glu Tyr Gln Asp Ser Asp Arg Leu Asn
 100 105 110

Ile Gln Ile Leu Pro Thr His Val Asp Ser Thr Asn Ala Ser Trp Tyr
 115 120 125

Phe Leu Ser Glu Asn Leu Val Pro Arg Pro Lys Ala Ser Leu Asn Ala
 130 135 140

Ser Val Ser Gln Ser Asp Leu Phe Val Ser Trp Ser Asn Glu Pro Ser
 145 150 155 160

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

Thr Glu Gly Thr Val Leu Val Tyr Glu Asn Gln Phe Ile Glu Phe Val
 180 185 190

Thr Ala Leu Pro Glu Glu Tyr Asn Leu Tyr Gly Leu Gly Glu His Ile
 195 200 205

Thr Gln Phe Arg Leu Gln Arg Asn Ala Asn Leu Thr Ile Tyr Pro Ser
 210 215 220

Asp Asp Gly Thr Pro Ile Asp Gln Asn Leu Tyr Gly Gln His Pro Phe
 225 230 235 240

Tyr Leu Asp Thr Arg Tyr Tyr Lys Gly Asp Arg Gln Asn Gly Ser Tyr
 245 250 255

Ile Pro Val Lys Ser Ser Glu Ala Asp Ala Ser Gln Asp Tyr Ile Ser
 260 265 270

Leu Ser His Gly Val Phe Leu Arg Asn Ser His Gly Leu Glu Ile Leu
 275 280 285

Leu Arg Ser Gln Lys Leu Ile Trp Arg Thr Leu Gly Gly Gly Ile Asp
 290 295 300

Leu Thr Phe Tyr Ser Gly Pro Ala Pro Ala Asp Val Thr Arg Gln Tyr
 305 310 315 320

Leu Thr Ser Thr Val Gly Leu Pro Ala Met Gln Gln Tyr Asn Thr Leu
 325 330 335

Gly Phe His Gln Cys Arg Trp Gly Tyr Asn Asn Trp Ser Asp Leu Ala
 340 345 350

Asp Val Val Ala Asn Phe Glu Lys Phe Glu Ile Pro Leu Glu Tyr Ile
 355 360 365

Trp Thr Asp Ile Asp Tyr Met His Gly Tyr Arg Asn Phe Asp Asn Asp
 370 375 380

Gln His Arg Phe Ser Tyr Ser Glu Gly Asp Glu Phe Leu Ser Lys Leu
 385 390 395 400

His Glu Ser Gly Arg Tyr Tyr Val Pro Ile Val Asp Ala Ala Leu Tyr
 405 410 415

Ile Pro Asn Pro Glu Asn Ala Ser Asp Ala Tyr Ala Thr Tyr Asp Arg
 420 425 430

Gly Ala Ala Asp Asp Val Phe Leu Lys Asn Pro Asp Gly Ser Leu Tyr
 435 440 445

Ile Gly Ala Val Trp Pro Gly Tyr Thr Val Phe Pro Asp Trp His His
 450 455 460

Pro Lys Ala Val Asp Phe Trp Ala Asn Glu Leu Val Ile Trp Ser Lys
 465 470 475 480

Lys Val Ala Phe Asp Gly Val Trp Tyr Asp Met Ser Glu Val Ser Ser
 485 490 495
 Phe Ser Val Gly Ser Cys Gly Thr Gly Asn Leu Thr Leu Asn Pro Ala
 500 505 510
 His Pro Ser Phe Leu Leu Pro Gly Glu Pro Gly Asp Ile Ile Tyr Asp
 515 520 525
 Tyr Pro Glu Ala Phe Asn Ile Thr Asn Ala Thr Glu Ala Ala Ser Ala
 530 535 540
 Ser Ala Gly Ala Ser Ser Gln Ala Ala Ala Thr Ala Thr Thr Thr Ser
 545 550 555 560
 Thr Ser Val Ser Tyr Leu Arg Thr Thr Pro Thr Pro Gly Val Arg Asn
 565 570 575
 Val Glu His Pro Pro Tyr Val Ile Asn His Asp Gln Glu Gly His Asp
 580 585 590
 Leu Ser Val His Ala Val Ser Pro Asn Ala Thr His Val Asp Gly Val
 595 600 605
 Glu Glu Tyr Asp Val His Gly Leu Tyr Gly His Gln Gly Leu Asn Ala
 610 615 620
 Thr Tyr Gln Gly Leu Leu Glu Val Trp Ser His Lys Arg Arg Pro Phe
 625 630 635 640
 Ile Ile Gly Arg Ser Thr Phe Ala Gly Ser Gly Lys Trp Ala Gly His
 645 650 655
 Trp Gly Gly Asp Asn Tyr Ser Lys Trp Trp Ser Met Tyr Tyr Ser Ile
 660 665 670
 Ser Gln Ala Leu Ser Phe Ser Leu Phe Gly Ile Pro Met Phe Gly Ala
 675 680 685
 Asp Thr Cys Gly Phe Asn Gly Asn Ser Asp Glu Glu Leu Cys Asn Arg
 690 695 700
 -
 Trp Met Gln Leu Ser Ala Phe Phe Pro Phe Tyr Arg Asn His Asn Glu
 705 710 715 720
 Leu Ser Thr Ile Pro Gln Glu Pro Tyr Arg Trp Ala Ser Val Ile Glu
 725 730 735
 Ala Thr Lys Ser Ala Met Arg Ile Arg Tyr Ala Ile Leu Pro Tyr Phe
 740 745 750
 Tyr Thr Leu Phe Asp Leu Ala His Thr Thr Gly Ser Thr Val Met Arg
 755 760 765
 Ala Leu Ser Trp Glu Phe Pro Asn Asp Pro Thr Leu Ala Ala Val Glu
 770 775 780

Thr Gln Phe Met Val Gly Pro Ala Ile Met Val Val Pro Val Leu Glu
785 790 795 800

Pro Leu Val Asn Thr Val Lys Gly Val Phe Pro Gly Val Gly His Gly
805 810 815

Glu Val Trp Tyr Asp Trp Tyr Thr Gln Ala Ala Val Asp Ala Lys Pro
820 825 830

Gly Val Asn Thr Thr Ile Ser Ala Pro Leu Gly His Ile Pro Val Tyr
835 840 845

Val Arg Gly Gly Asn Ile Leu Pro Met Gln Glu Pro Ala Leu Thr Thr
850 855 860

Arg Glu Ala Arg Gln Thr Pro Trp Ala Leu Leu Ala Ala Leu Gly Ser
865 870 875 880

Asn Gly Thr Ala Ser Gly Gln Leu Tyr Leu Asp Asp Gly Glu Ser Ile
885 890 895

Tyr Pro Asn Ala Thr Leu His Val Asp Phe Thr Ala Ser Arg Ser Ser
900 905 910

Leu Arg Ser Ser Ala Gln Gly Arg Trp Lys Glu Arg Asn Pro Leu Ala
915 920 925

Asn Val Thr Val Leu Gly Val Asn Lys Glu Pro Ser Ala Val Thr Leu
930 935 940

Asn Gly Gln Ala Val Phe Pro Gly Ser Val Thr Tyr Asn Ser Thr Ser

945 950 955 960

Gln Val Leu Phe Val Gly Gly Leu Gln Asn Leu Thr Lys Gly Gly Ala
965 970 975

Trp Ala Glu Asn Trp Val Leu Glu Trp
980 985

<210> 79

<211> 2958

<212> DNA

<213> Aspergillus niger

<400> 79

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agtcttcagc tcgcgggcag gccatgtaac gtatacggca cagatgttga gtccttgaca	300
ctgtctgtgg agtaccagga ttccgatcga ctgaatatc agattctccc cactcatgtt	360
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tatctggata	caagatatta	caaaggagat	aggcagaatg	ggtcttatat	tcccgtcaaa	780
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ggaggaatcg	atctcacctt	ctactcaggc	cccgcctccg	ccgatgttac	caggcaatat	960
cttaccagca	ctgtgggatt	accggccatg	cagcaataca	acactcttgg	attccaccaa	1020
tgctgttggg	gctacaacaa	ctggtcggat	ctggcggacg	ttgttgcgaa	ctttgagaag	1080
tttgagatcc	cgttgaata	tatctggacc	gatattgact	acatgcacgg	atatcgcaac	1140
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<213> *Aspergillus niger*

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<213> *Aspergillus niger*

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gattggtaca ccaggetgc agttgatgcg aagcccgggg tcaacacgac catttcggca	2520
ccattgggcc acatcccagt ttatgtacga ggtggaaca tcttgccgat gcaagagccg	2580
gcattgacca ctcgtgaagc ccggcaaacc ccgtgggctt tgctagctgc actaggaagc	2640
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```

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tgggtattgg aatggtag                                     2958

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REFERENCES CITED IN THE DESCRIPTION

This list of references cited by the applicant is for the reader's convenience only. It does not form part of the European patent document. Even though great care has been taken in compiling the references, errors or omissions cannot be excluded and the EPO disclaims all liability in this regard.

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Patentkrav

- 1.** Modificeret α -glucosidase, i hvilken transglykosyleringsaktiviteten er forbedret og/eller balancen mellem hydrolyseaktiviteten og transglykosyleringsaktiviteten er ændret ved sænkning af hydrolyseaktiviteten sammenlignet med α -glucosidasen
- 5 som skal modificeres, bestående af en aminosyresekvens i hvilken en eller to eller flere af aminosyrerne valgt fra gruppen bestående af de følgende (1) til (14) er blevet substitueret af en anden/andre aminosyrer i aminosyresekvensen af α -glucosidasen:
- 10 (1) en aminosyre svarende til aminosyren i position 385 af aminosyresekvensen af SEQ ID NO. 1;
- (2) en aminosyre svarende til aminosyren i position 491 af aminosyresekvensen af SEQ ID NO. 1;
- (3) en aminosyre svarende til aminosyren i position 535 af aminosyresekvensen af SEQ ID NO. 1;
- 15 (4) en aminosyre svarende til aminosyren i position 450 af aminosyresekvensen af SEQ ID NO. 1;
- (5) en aminosyre svarende til aminosyren i position 534 af aminosyresekvensen af SEQ ID NO. 1;
- (6) en aminosyre svarende til aminosyren i position 537 af aminosyresekvensen af SEQ ID NO. 1;
- 20 (7) en aminosyre svarende til aminosyren i position 538 af aminosyresekvensen af SEQ ID NO. 1;
- (8) en aminosyre svarende til aminosyren i position 554 af aminosyresekvensen af SEQ ID NO. 1;
- 25 (9) en aminosyre svarende til aminosyren i position 556 af aminosyresekvensen af SEQ ID NO. 1;
- (10) en aminosyre svarende til aminosyren i position 579 af aminosyresekvensen af SEQ ID NO. 2;
- (11) en aminosyre svarende til aminosyren i position 585 af aminosyresekvensen af SEQ ID NO. 2;
- 30

(12) en aminosyre svarende til aminosyren i position 630 af aminosyresekvensen af SEQ ID NO. 1;

(13) en aminosyre svarende til aminosyren i position 683 af aminosyresekvensen af SEQ ID NO. 1; og

5 (14) en aminosyre svarende til aminosyren i position 689 af aminosyresekvensen af SEQ ID NO. 1,

10 (a) hvor α -glucosidasen, som skal modificeres, er human maltase-glucoamylase, *Aspergillus niger alpha*-glucosidase, human neutral alpha-glucosidase C, muse-lysosomal alpha-glucosidase, gær GLU2A, *Aspergillus nidulans alpha*-glucosidase AgdA, *Aspergillus nidulans Alpha*-glucosidase AgdB, *Mucor javanicus alpha*-glucosidase, *Aspergillus oryzae alpha*-glucosidase, *Mortierella alliacea alpha*-glucosidase, *Schizosaccharomyces pombe alpha*-glucosidase, *Debaryomyces occidentalis alpha*-glucosidase, *Hordeum*
15 *vulgare subsp. vulgare alpha*-glucosidase, *Arabidopsis thaliana alpha*-glucosidase, *Spinacia oleracea alpha*-glucosidase, *Beta vulgaris alpha*-glucosidase eller *Solanum tuberosum alpha*-glucosidase, og/eller

20 (b) hvor aminosyresekvensen af α -glucosidasen, som skal modificeres, er aminosyresekvensen af SEQ ID NO. 2 og aminosyren af (1) er aminosyren i position 343 af aminosyresekvensen, aminosyren af (2) er aminosyren i position 452 af aminosyresekvensen, aminosyren af (3) er aminosyren i position 496 af aminosyresekvensen, aminosyren af (4) er aminosyren i
25 position 410 af aminosyresekvensen, aminosyren af (5) er aminosyren i position 495 af aminosyresekvensen, aminosyren af (6) er aminosyren i position 498 af aminosyresekvensen, aminosyren af (7) er aminosyren i position 499 af aminosyresekvensen, aminosyren af (8) er aminosyren i position
30 531 af aminosyresekvensen, aminosyren af (9) er aminosyren i position 533 af aminosyresekvensen, aminosyren af (12) er aminosyren i position 662 af aminosyresekvensen, aminosyren af (13) er aminosyren i position 715 af aminosyresekvensen, og

aminosyren af (14) er aminosyren i position 721 af aminosyresekvensen.

2. Den modificerede α -glucosidase ifølge krav 1(b), hvor aminosyren, som skal
5 substitueres, er

(1) aminosyren af (1), og aminosyren er blevet substitueret af cystein, asparaginsyre, methionin, histidin, alanin, phenylalanin, glycin, threonin, glutaminsyre, valin, glutamin, asparagin eller isoleucin;

10 (2) aminosyren af (2), og aminosyren er blevet substitueret af glycin, asparaginsyre eller glutaminsyre;

(3) aminosyren af (3), og aminosyren er blevet substitueret af valin, asparagin eller glutamin;

15 (4) aminosyren af (1) og aminosyren af (2), og aminosyrerne er blevet substitueret af asparaginsyre for aminosyren af (1) og alanin eller glycin for aminosyren af (2);

(5) aminosyren af (1) og aminosyren af (3), og aminosyrerne er blevet substitueret af asparaginsyre eller methionin for aminosyren af (1) og isoleucin, arginin, cystein eller threonin for aminosyren af (3);

20 (6) aminosyren af (5), og aminosyren er blevet substitueret af glycin, proline eller valin; eller

(7) aminosyren af (6), og aminosyren er blevet substitueret af leucin eller serin.

3. Den modificerede α -glucosidase ifølge krav 1,

25 (1) hvilken består af en hvilken som helst af aminosyresekvenserne af SEQ ID Nos. 18 til 42 og 77 til 78; eller

(2) hvilken består af en hvilken som helst af aminosyresekvenserne af SEQ ID Nos. 74 til 76.

4. Gen, som koder for den modificerede α -glucosidase ifølge et hvilket som helst af kravene 1 til 3.

5. Genet ifølge krav 4, hvilket omfatter en hvilken som helst af basesekvenserne af SEQ ID Nos. 43 til 67 og 79 til 83.

6. Rekombinant DNA omfattende genet ifølge krav 4 eller 5.

7. Mikroorganisme med det rekombinante DNA ifølge krav 6.

10

8. Enzymmiddel omfattende den modificerede α -glucosidase ifølge et hvilket som helst af kravene 1 til 3.

9. Fremgangsmåde til fremstilling af et oligosaccharid, omfattende at reagere

15 (i) den modificerede α -glucosidase ifølge et hvilket som helst af kravene 1, 2 (1) til 2 (5), 2 (7) eller 3 (1) med et oligosaccharid eller polysaccharid af di- eller flere saccharider med α -1,4 glucosidbinding, eventuelt omfattende anvendelse af et vild type-enzym i kombination;

20 (ii) den modificerede α -glucosidase ifølge krav 2 (6) eller 3 (2) med et oligosaccharid eller polysaccharid af di- eller flere saccharider med α -1,6 glucosidbinding, eventuelt omfattende anvendelse af et vild type-enzym i kombination; eller

25 (iii) den modificerede α -glucosidase ifølge krav 2 (6) eller 3 (2) og et vild type-enzym med et oligosaccharid eller polysaccharid af di- eller flere saccharider med α -1,4 glucosidbinding(er).

10. Farmaceutisk sammensætning, en kvasi-lægemiddelssammensætning, en kosmetisk sammensætning, en fødevarersammensætning eller en fodersammensætning, omfattende den modificerede α -glucosidase ifølge et
30 hvilket som helst af kravene 1 til 3 eller enzymmidlet ifølge krav 8.

11. Fremgangsmåde til fremstilling af en modificeret α -glucosidase i hvilken transglykosyleringsaktiviteten er forbedret og/eller balancen mellem hydrolyseaktiviteten og transglykosyleringsaktiviteten ændres ved sænkning af hydrolyseaktiviteten sammenlignet med α -glucosidase som skal modificeres,

5 omfattende de følgende trin (i) og (ii):

(i) et trin til at identificere en eller to eller flere aminosyrer valgt fra gruppen bestående af de følgende (1) til (14) i aminosyresekvensen af α -glucosidase som et enzym der skal muteres:

10 (1) en aminosyre svarende til aminosyren i position 385 af aminosyresekvensen af SEQ ID NO. 1;

(2) en aminosyre svarende til aminosyren i position 491 af aminosyresekvensen af SEQ ID NO. 1;

(3) en aminosyre svarende til aminosyren i position 535 af aminosyresekvensen af SEQ ID NO. 1;

15 (4) en aminosyre svarende til aminosyren i position 450 af aminosyresekvensen af SEQ ID NO. 1;

(5) en aminosyre svarende til aminosyren i position 534 af aminosyresekvensen af SEQ ID NO. 1;

20 (6) en aminosyre svarende til aminosyren i position 537 af aminosyresekvensen af SEQ ID NO. 1;

(7) en aminosyre svarende til aminosyren i position 538 af aminosyresekvensen af SEQ ID NO. 1;

(8) en aminosyre svarende til aminosyren i position 554 af aminosyresekvensen af SEQ ID NO. 1;

25 (9) en aminosyre svarende til aminosyren i position 556 af aminosyresekvensen af SEQ ID NO. 1;

(10) en aminosyre svarende til aminosyren i position 579 af aminosyresekvensen af SEQ ID NO. 2;

30 (11) en aminosyre svarende til aminosyren i position 585 af aminosyresekvensen af SEQ ID NO. 2;

(12) en aminosyre svarende til aminosyren i position 630 af aminosyresekvensen af SEQ ID NO. 1;

(13) en aminosyre svarende til aminosyren i position 683 af aminosyresekvensen af SEQ ID NO. 1; og

5 (14) en aminosyre svarende til aminosyren i position 689 af aminosyresekvensen af SEQ ID NO. 1;

(ii) et trin til at danne en aminosyresekvens i hvilken aminosyrerne identificeret i trin (i) er blevet substitueret med en anden/andre aminosyrer, baseret på aminosyresekvensen af enzymet der skal muteres.

10

12. Fremgangsmåden ifølge krav 11, hvor α -glucosidasen

(1) er *human maltase-glucoamylase*, *Aspergillus niger alpha-glucosidase*, *human neutral alpha-glucosidase C*, *muse-lysosomal alpha-glucosidase*, *gær GLU2A*, *Aspergillus nidulans Alpha-glucosidase AgdA*, *Aspergillus*
 15 *nidulans Alpha-glucosidase AgdB*, *Mucor javanicus alpha-glucosidase*, *Aspergillus oryzae alpha-glucosidase*, *Mortierella alliacea alpha-glucosidase*, *Schizosaccharomyces pombe alpha-glucosidase*, *Debaryomyces occidentalis alpha-glucosidase*, *Hordeum vulgare subsp. vulgare alpha-glucosidase*, *Arabidopsis thaliana alpha-glucosidase*, *Spinacia oleracea alpha-*
 20 *glucosidase*, *Beta vulgaris alpha-glucosidase* eller *Solanum tuberosum alpha-glucosidase*;

(2) omfatter en hvilken som helst af aminosyresekvenserne af SEQ ID Nos. 1 til 17; eller

25 (3) består af aminosyresekvensen af SEQ ID NO. 2, og aminosyrer der er substitueret i trin (i) er én aminosyre valgt fra (1) til (14), to aminosyrer valgt fra (1) til (14) eller tre aminosyrer valgt fra (1) til (14).

13. Fremgangsmåde til fremstilling af en modificeret α -glucosidase, omfattende de følgende trin (I) til (III):

30 (I) et trin til at fremstille en nukleinsyre der koder for en hvilken som helst af aminosyresekvenserne af SEQ ID Nos. 18 til 42 og 74 til 78 eller en

7

aminosyresekvens sammensat ved fremgangsmåden ifølge et hvilket som helst af kravene 11 eller 12;

(II) et trin til at udtrykke nukleinsyren, og

(III) et trin til at opsamle et ekspressionsprodukt.

5

DRAWINGS

Fig. 1

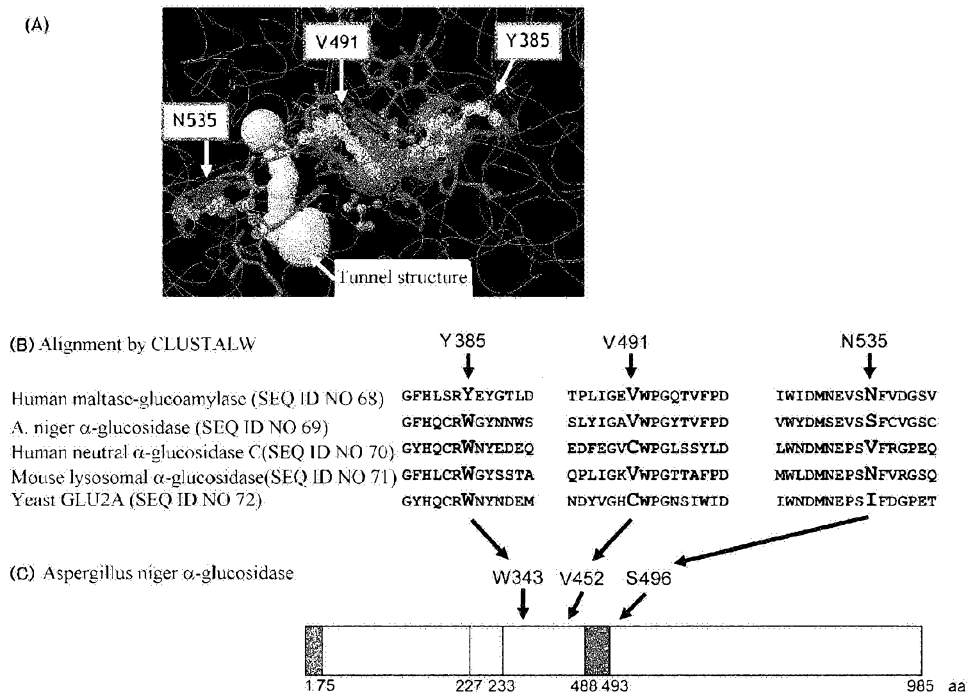


Fig. 2

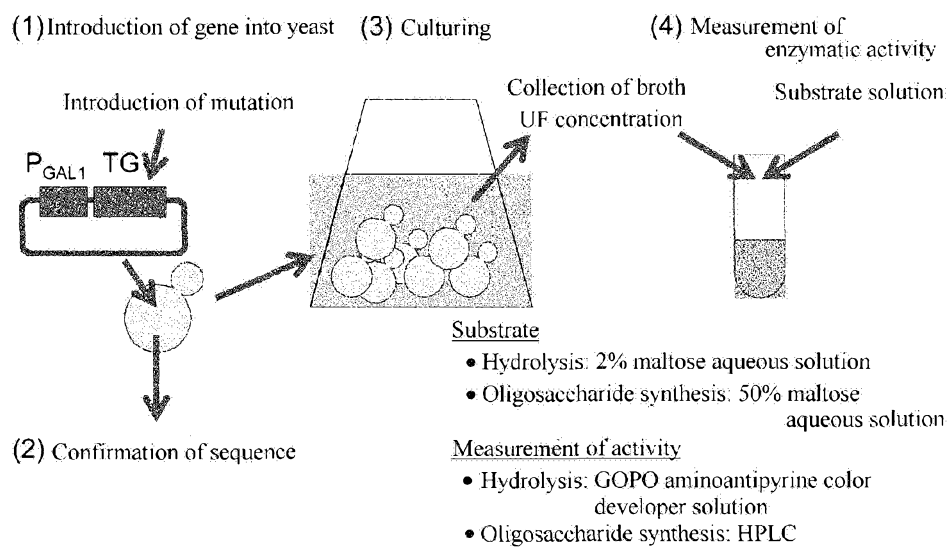
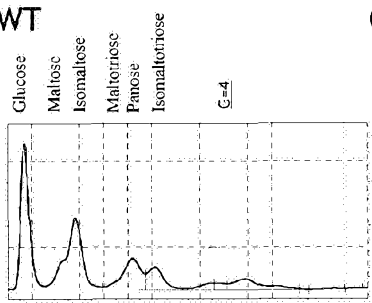
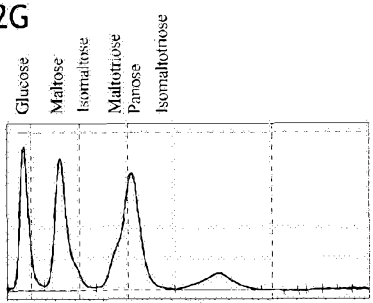


Fig. 3

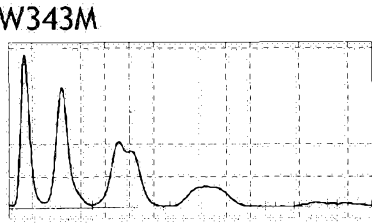
(A) WT



(C) V452G



(B) W343M



(D) S496V

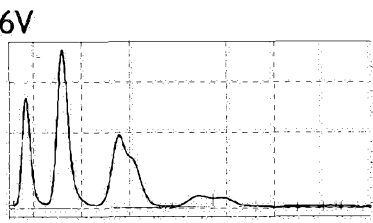


Fig. 4

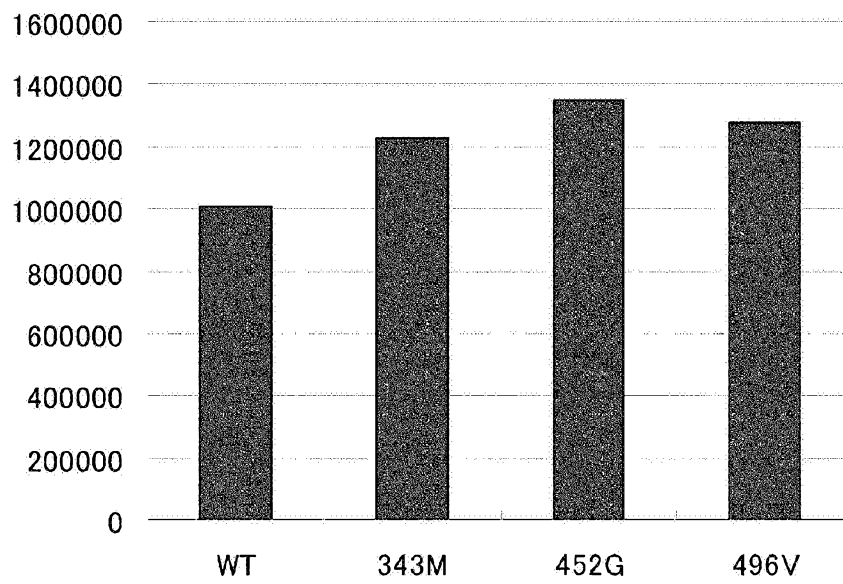


Fig. 5

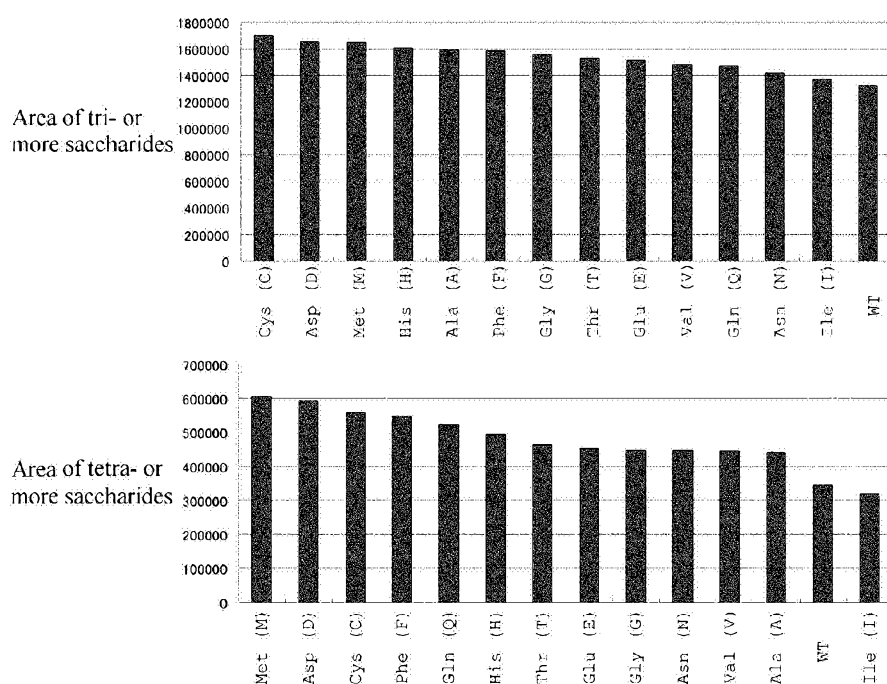


Fig. 6

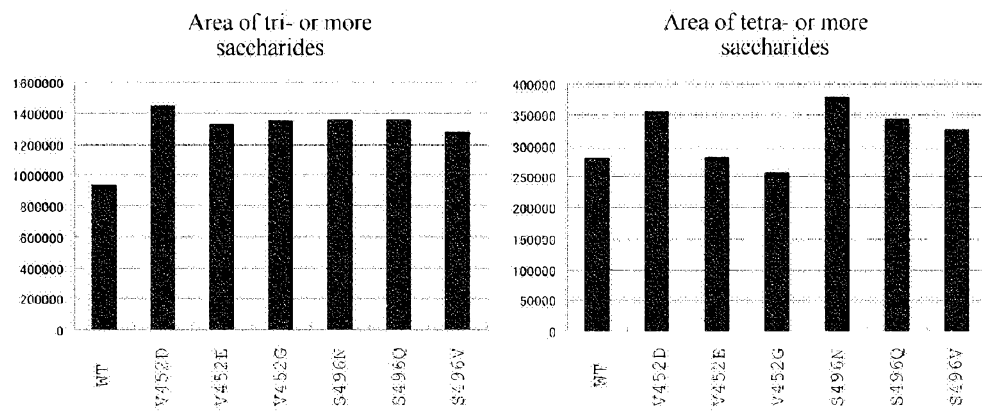


Fig. 7

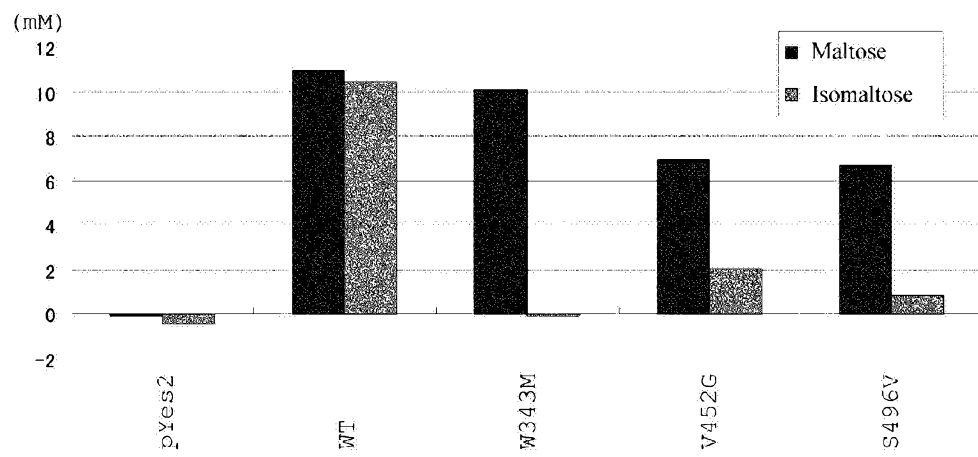


Fig. 8

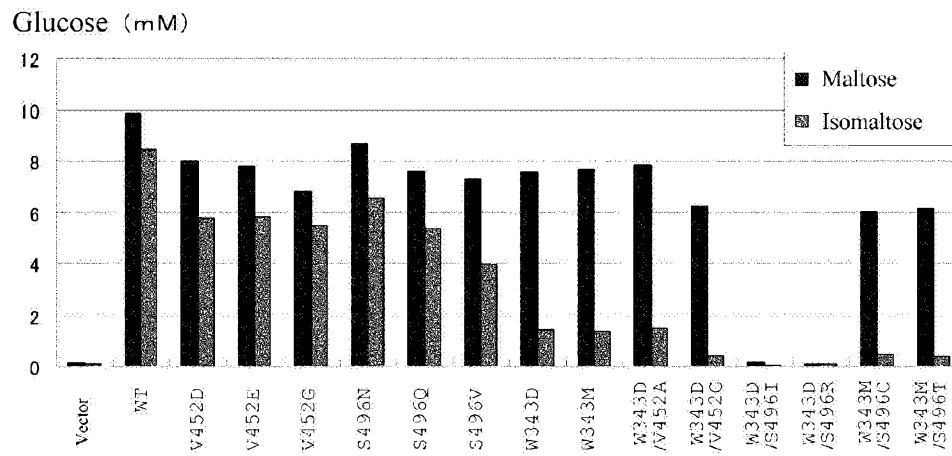


Fig. 9

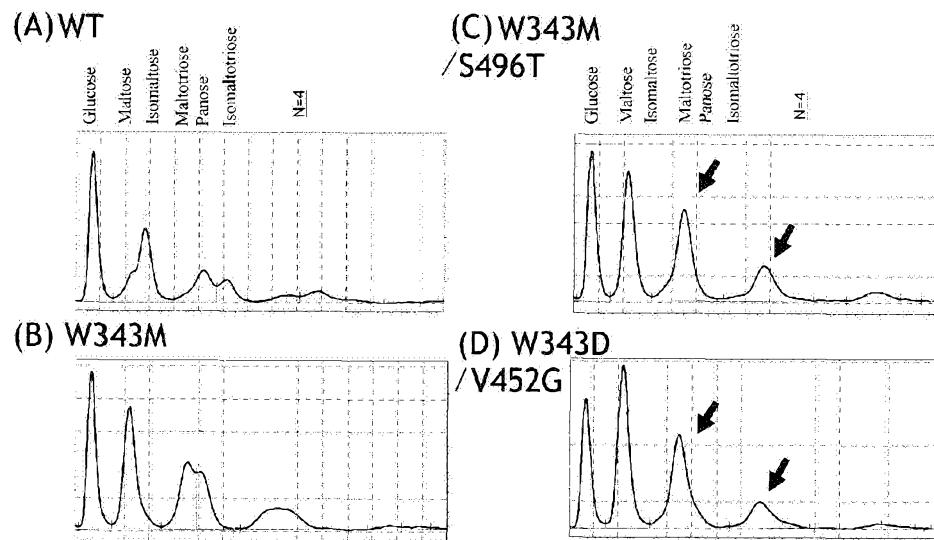


Fig. 10

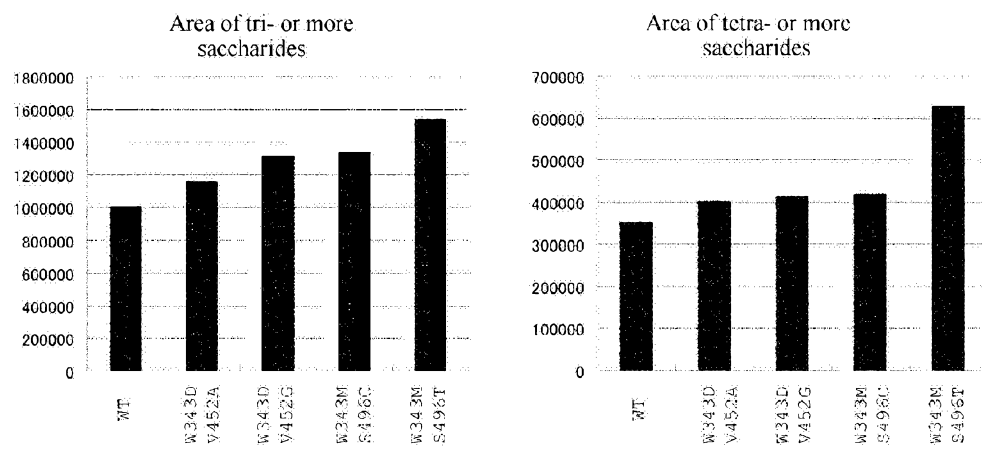


Fig. 11

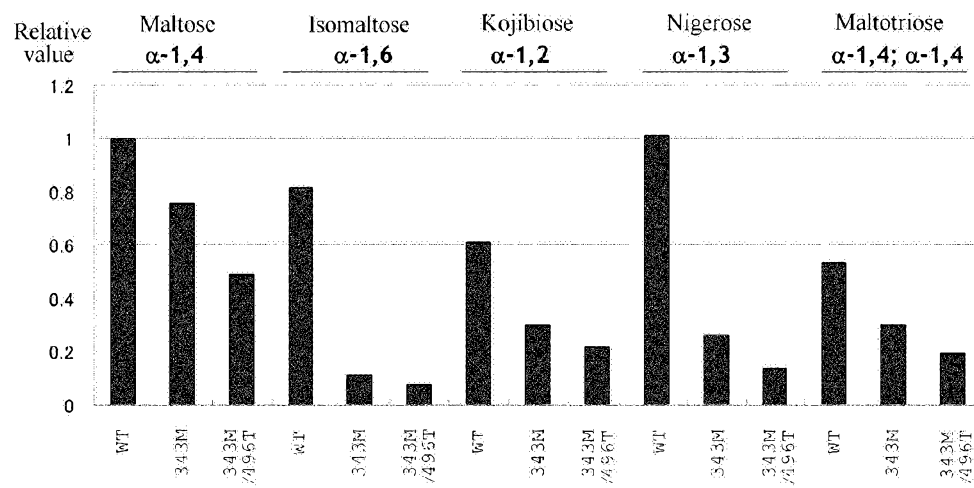


Fig. 12

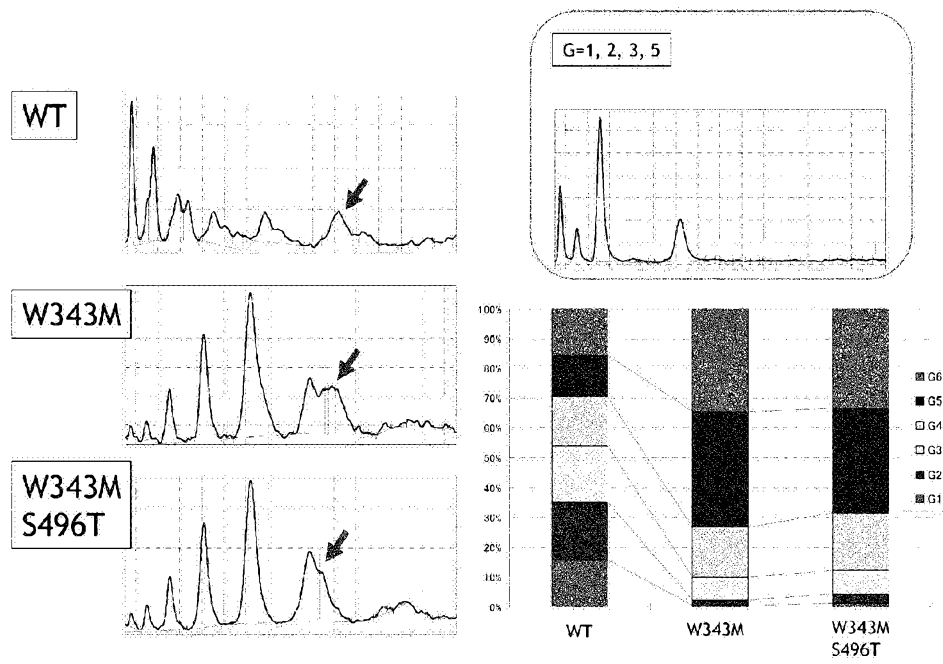


Fig. 13

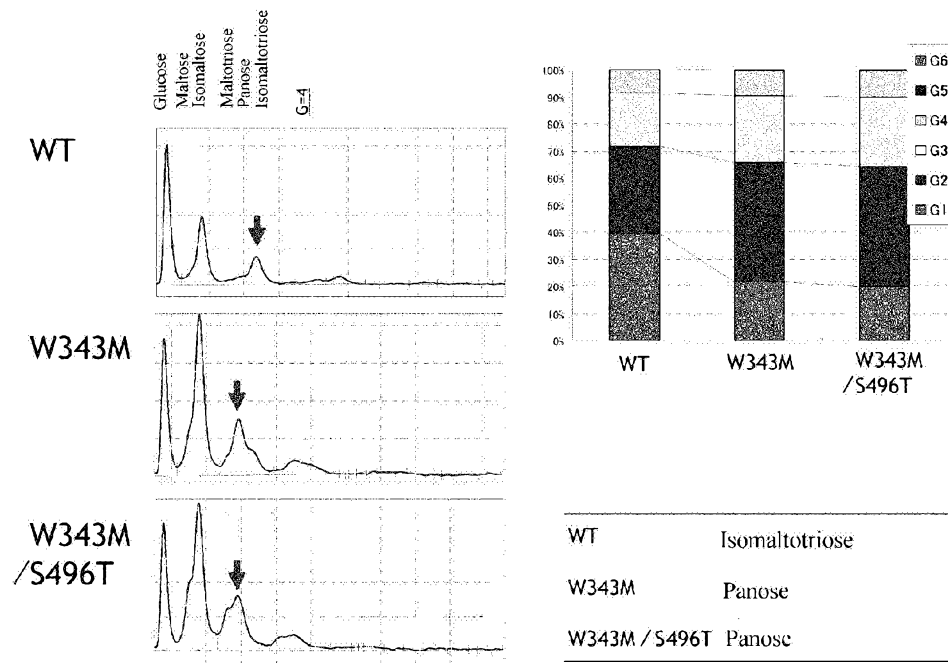


Fig. 14

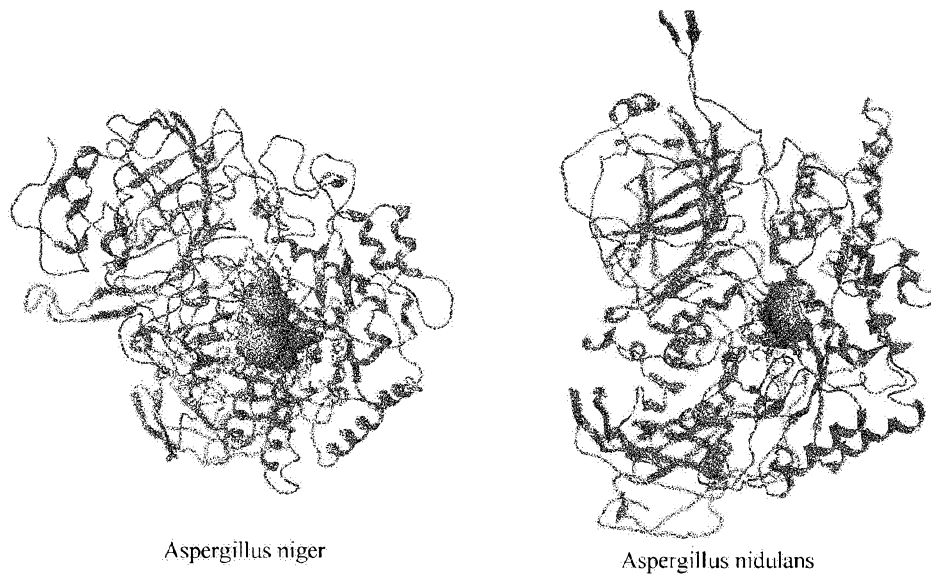


Fig. 15

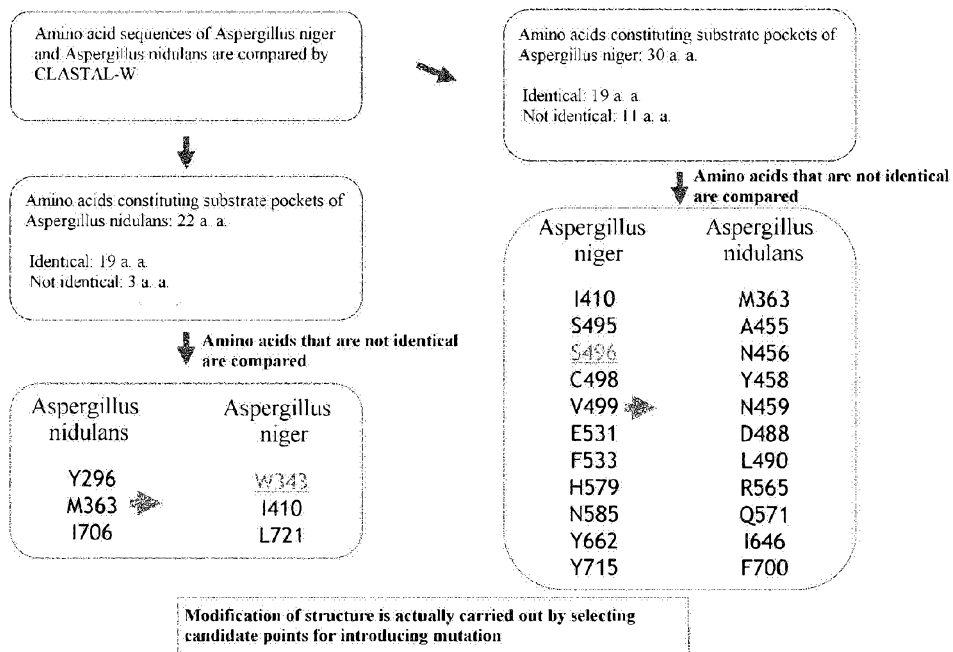


Fig. 16

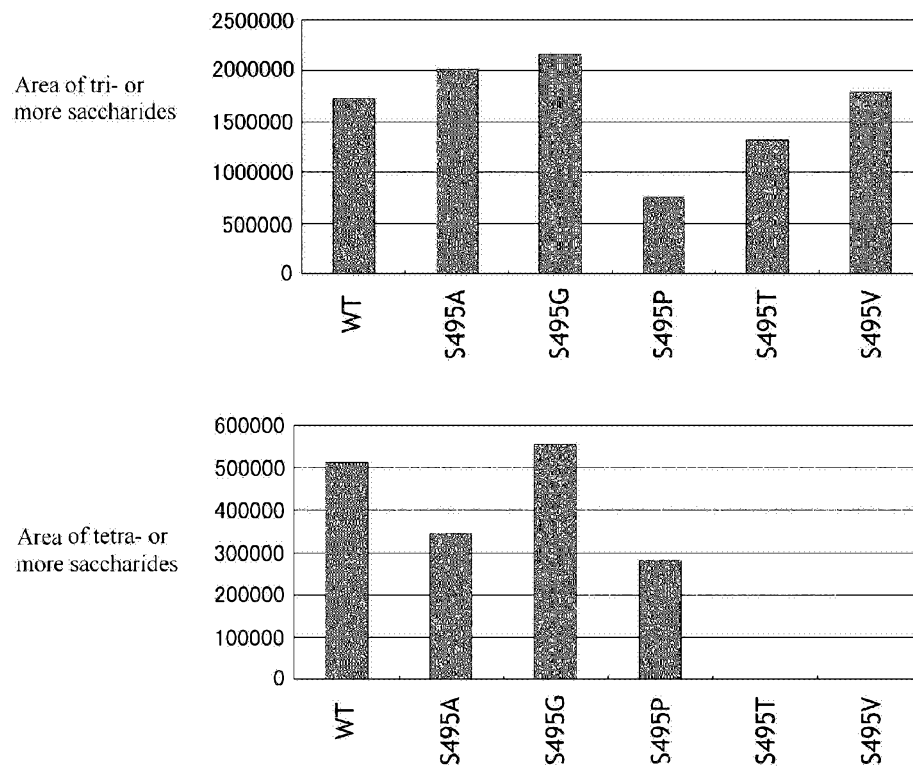


Fig. 17

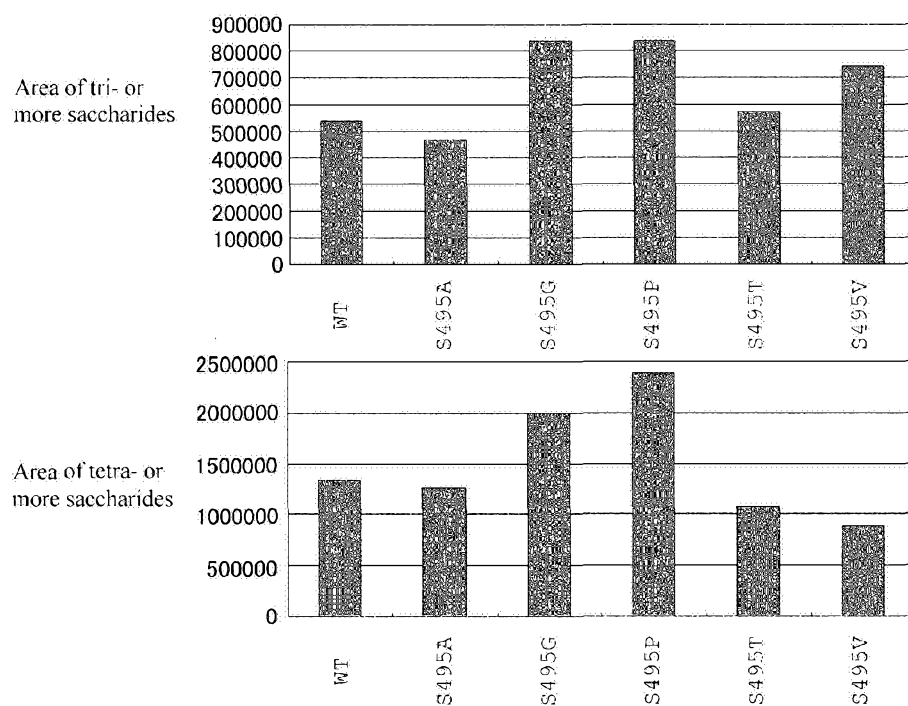


Fig. 18

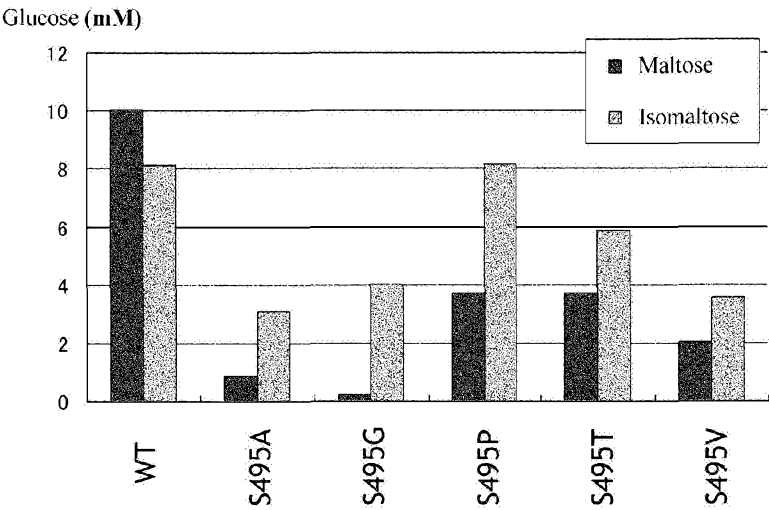


Fig. 19

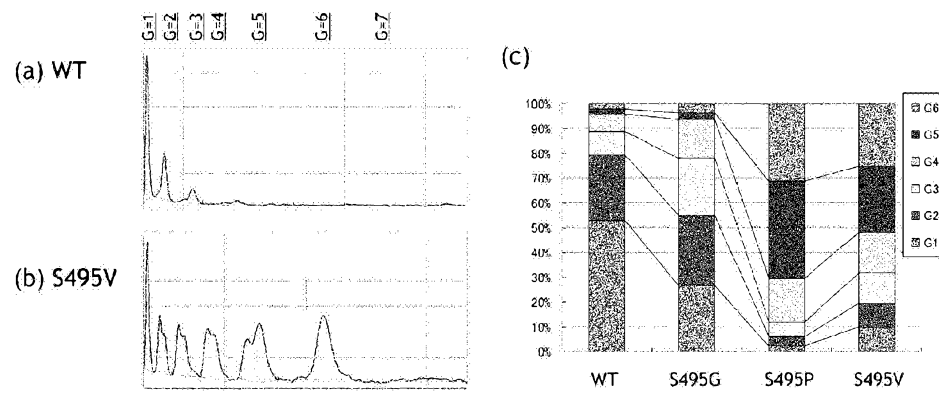


Fig. 20

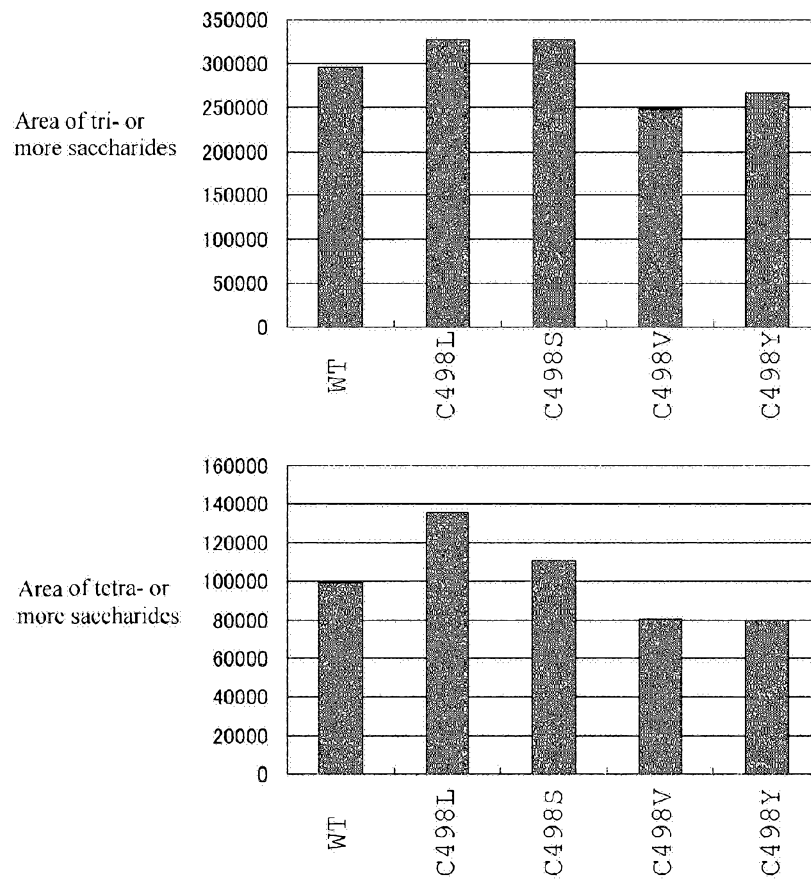


Fig. 21

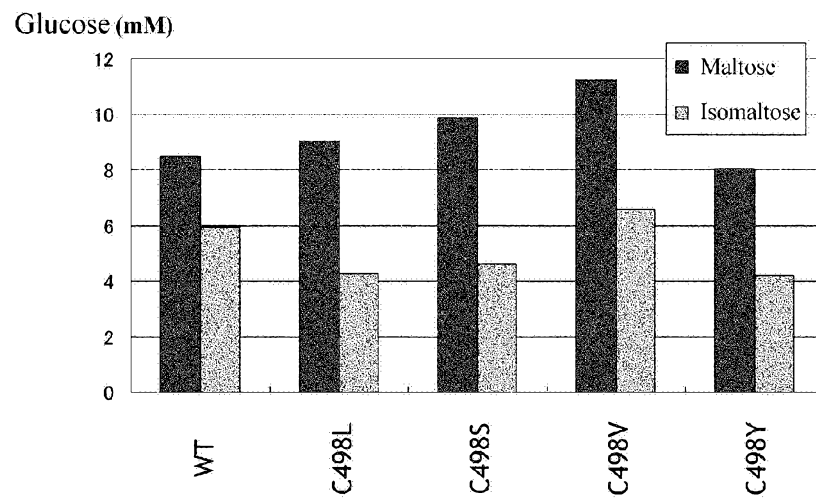


Fig. 22

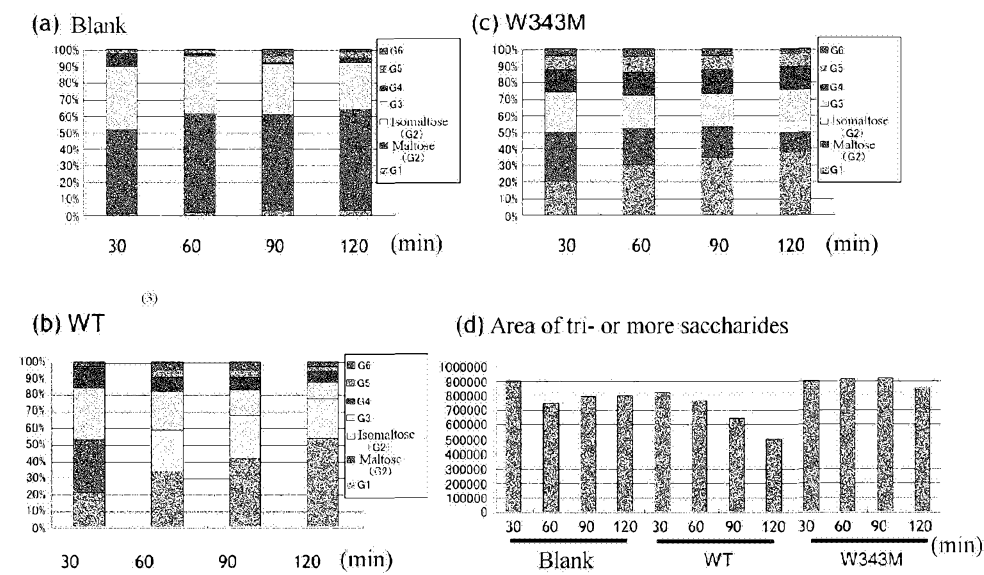


Fig. 23

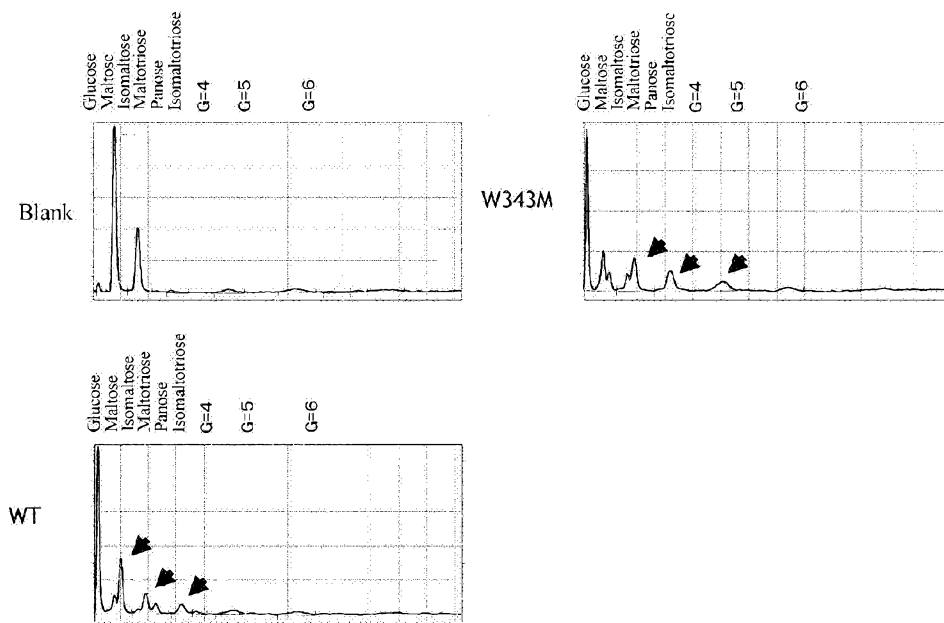


Fig. 24

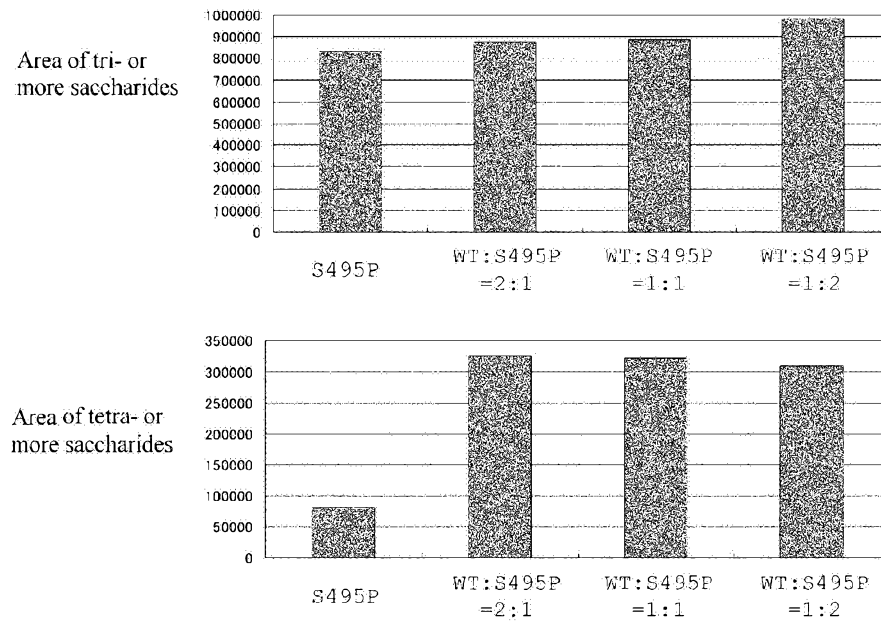


Fig. 25

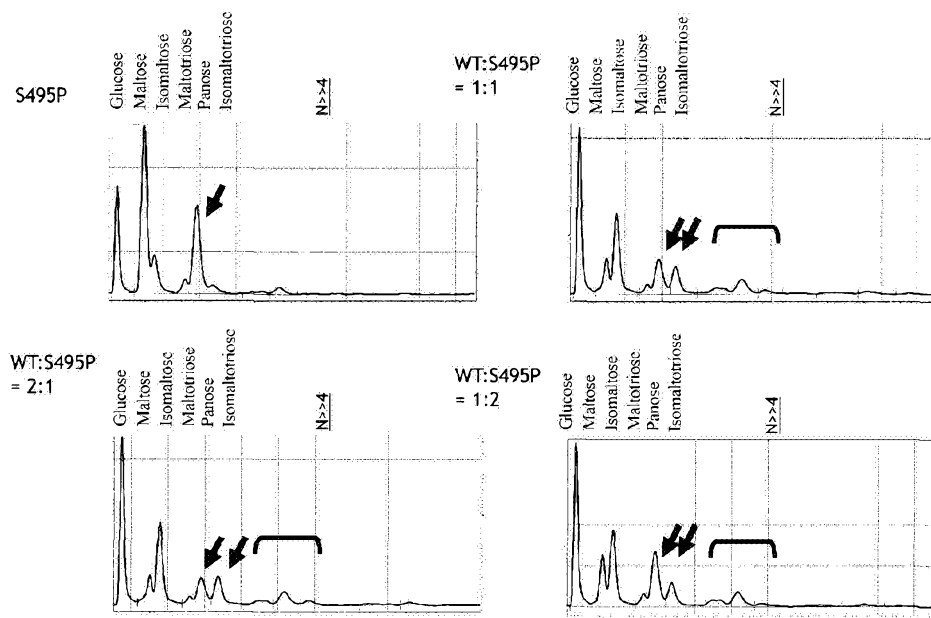


Fig. 26

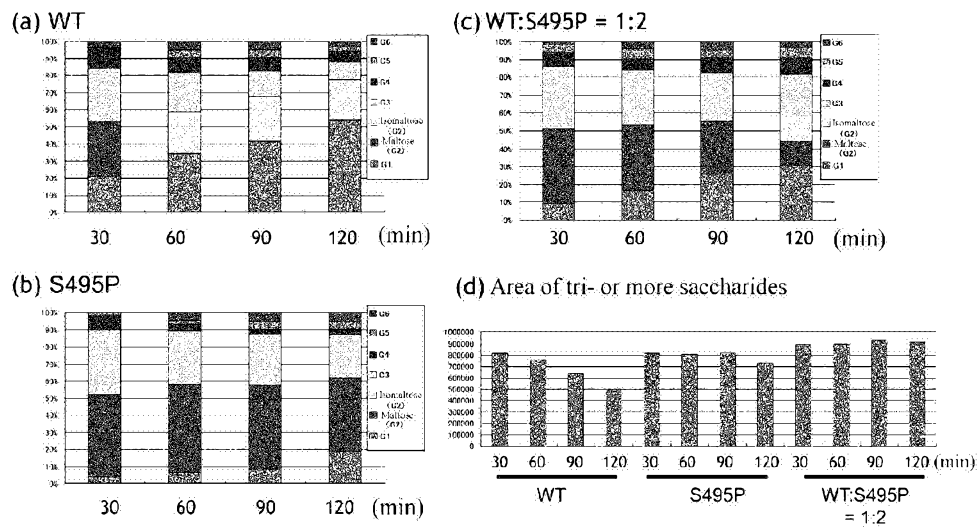


Fig. 27

