(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) **World Intellectual Property Organization**
International Bureau

(43) **International Publication Date**
16 April 2020 (16.04.2020)

(10) **International Publication Number**
WO 2020/076697 A1

(51) **International Patent Classification:**
C12P 7/06 (2006.01)

(21) **International Application Number:**
PCT/US2019/054996

(22) **International Filing Date:**
07 October 2019 (07.10.2019)

(25) **Filing Language:** English

(26) **Publication Language:** English

(30) **Priority Data:**
62/742,805 08 October 2018 (08.10.2018) US

(71) **Applicant: NOVOZYMES A/S** [DK/DK]; Krogshoejvej 36, DK-2880 Bagsvaerd (DK).

(72) **Inventor; and**
(71) **Applicant** *(for BW only)*: **TASSONE, Monica** [US/US]; 1445 Drew Avenue, Davis, California 95618 (US).

(72) **Inventors: HUFFMAN, James Ron**; 77 Perry Chapel Church Road, P.O. Box 576, Franklinton, North Carolina 27525 (US). **SOONG, Chee-Leong**; 77 Perry Chapel Church Road, P.O. Box 576, Franklinton, North Carolina 27525 (US). **YI, Jung**; 1445 Drew Avenue, Davis, California 95618 (US). **OUYANG, Hanlin**; 77 Perry Chapel Church Road, Franklinton, NC 27525 (US).

(74) **Agent: FECHTER, Eric J.** et al.; Novozymes North America, Inc., 77 Perry Chapel Church Road, P.O. Box 576, Franklinton, North Carolina 27525 (US).

(81) **Designated States** *(unless otherwise indicated, for every kind of national protection available)*: AE, AG, AL, AM, AO, AT, AU, AZ, BA, BB, BG, BH, BN, BR, BW, BY, BZ, CA, CH, CL, CN, CO, CR, CU, CZ, DE, DJ, DK, DM, DO, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, GT, HN, HR, HU, ID, IL, IN, IR, IS, JO, JP, KE, KG, KH, KN, KP, KR, KW, KZ, LA, LC, LK, LR, LS, LU, LY, MA, MD, ME, MG, MK, MN, MW, MX, MY, MZ, NA, NG, NI, NO, NZ, OM, PA, PE, PG, PH, PL, PT, QA, RO, RS, RU, RW, SA, SC, SD, SE, SG, SK, SL, SM, ST, SV, SY, TH, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, ZA, ZM, ZW.

(84) **Designated States** *(unless otherwise indicated, for every kind of regional protection available)*: ARIPO (BW, GH, GM, KE, LR, LS, MW, MZ, NA, RW, SD, SL, ST, SZ, TZ, UG, ZM, ZW), Eurasian (AM, AZ, BY, KG, KZ, RU, TJ, TM), European (AL, AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HR, HU, IE, IS, IT, LT, LU, LV, MC, MK, MT, NL, NO, PL, PT, RO, RS, SE, SI, SK, SM,

(54) Title: ENZYME-EXPRESSING YEAST FOR ETHANOL PRODUCTION

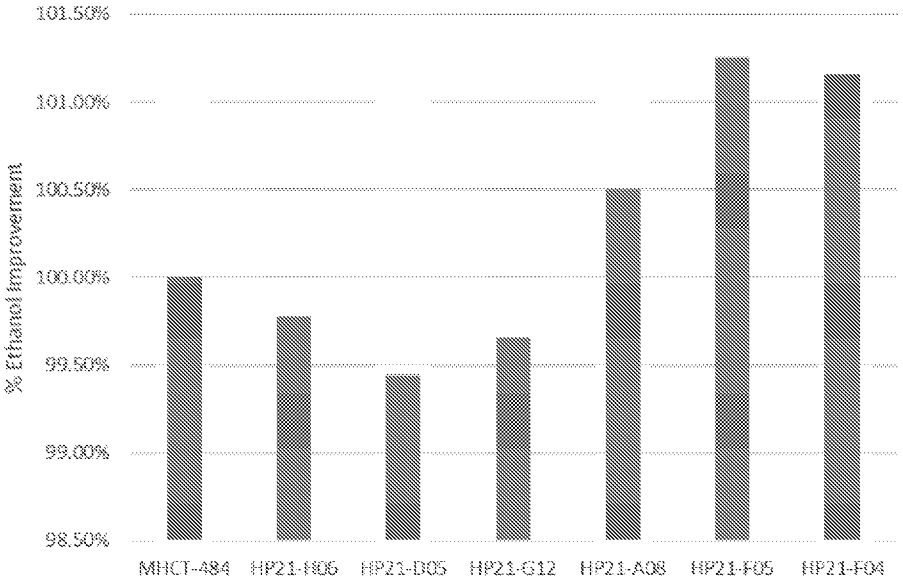

FIG. 1

(57) **Abstract:** Described herein are recombinant fermenting organisms having a heterologous polynucleotide encoding a phospholipase. Also described are processes for producing a fermentation product, such as ethanol, from starch or cellulosic-containing material with the recombinant fermenting organisms.

WO 2020/076697 A1

[Continued on next page]

TR), OAPI (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, KM, ML, MR, NE, SN, TD, TG).

Published:

- *with international search report (Art. 21(3))*
- *before the expiration of the time limit for amending the claims and to be republished in the event of receipt of amendments (Rule 48.2(h))*
- *with sequence listing part of description (Rule 5.2(a))*

ENZYME-EXPRESSING YEAST FOR ETHANOL PRODUCTION

Referenct to a Sequence Listing

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

Background

Production of ethanol from starch and cellulosic containing materials is well-known in the art.

The most commonly industrially used commercial process for starch-containing material, often referred to as a “conventional process”, includes liquefying gelatinized starch at high temperature (about 85°C) using typically a bacterial alpha-amylase, followed by simultaneous saccharification and fermentation (SSF) carried out anaerobically in the presence of typically a glucoamylase and a *Saccharomyces cerevisae* yeast.

Yeasts which are used for production of ethanol for use as fuel, such as in the corn ethanol industry, require several characteristics to ensure cost effective production of the ethanol. These characteristics include ethanol tolerance, low by-product yield, rapid fermentation, and the ability to limit the amount of residual sugars remaining in the ferment. Such characteristics have a marked effect on the viability of the industrial process.

Yeast of the genus *Saccharomyces* exhibits many of the characteristics required for production of ethanol. In particular, strains of *Saccharomyces cerevisiae* are widely used for the production of ethanol in the fuel ethanol industry. Strains of *Saccharomyces cerevisiae* that are widely used in the fuel ethanol industry have the ability to produce high yields of ethanol under fermentation conditions found in, for example, the fermentation of corn mash. An example of such a strain is the yeast used in commercially available ethanol yeast product called ETHANOL RED®.

Saccharomyces cerevisae yeast have been genetically engineered to express alpha-amylase and/or glucoamylase to improve yield and decrease the amount of exogenously added enzymes necessary during SSF (e.g., WO2018/098381, WO2017/087330, WO2017/037614, WO2011/128712, WO2011/153516, US2018/0155744). Yeast have also been engineered to express trehalase in an attempt to increase fermentation yield by breaking down residual trehalose (e.g., WO2017/077504).

WO2008/135547 concerns reducing foam in processes for production of a fermentation product by contacting the fermentation media comprising a fermenting organism with a lipolytic enzyme selected from the group consisting of phospholipase, lyso-phospholipase and lipase, and a metal salt.

WO2014/147219 concerns a phospholipase A from *Talaromyces leycettanus*.

WO2015/140275 discloses a phospholipase C from *Bacillus thuringiensis*.

Despite significant improvement of ethanol production processes over the past decade there is still a desire and need for providing improved processes of ethanol fermentation from starch and cellulosic containing material in an economically and commercially relevant scale.

For example, foam generation during ethanol fermentation is a major problem, especially in ethanol production processes where starch-containing material is liquefied with an alpha-amylase and a protease before saccharification and fermentation. Additionally, the use of nitrogen supplements (e.g., urea) is an added expense during fermentation. Therefore, there is a desire to, *inter alia*, reduce foam and/or reduce supplemental nitrogen requirements in ethanol fermentation.

Summary

Described herein are, *inter alia*, methods for producing a fermentation product, such as ethanol, from starch or cellulosic-containing material, and yeast suitable for use in such processes. The Applicant has surprisingly found that yeasts expressing a phospholipase provide beneficial properties during fermentation, such as reduced foaming, improved oil extraction yield, and improved ethanol yield.

A first aspect relates to methods of producing a fermentation product from a starch-containing or cellulosic-containing material comprising: (a) saccharifying the starch-containing or cellulosic-containing material; and (b) fermenting the saccharified material of step (a) with a fermenting organism; wherein the fermenting organism comprises a heterologous polynucleotide encoding a phospholipase. In some embodiments, the phospholipase is a Phospholipase A or a Phospholipase C.

In some embodiments of the methods, fermentation and saccharification are performed simultaneously in a simultaneous saccharification and fermentation (SSF). In other embodiments, fermentation and saccharification are performed sequentially (SHF).

In some embodiments of the methods, the method comprises recovering the fermentation product from the from the fermentation (e.g., by distillation).

In some embodiments of the methods, the fermentation product is ethanol.

In some embodiments of the methods, fermentation is performed under reduced nitrogen conditions (e.g., less than 1000 ppm urea or ammonium hydroxide, such as less than 750 ppm, less than 500 ppm, less than 400 ppm, less than 300 ppm, less than 250 ppm, less than 200 ppm, less than 150 ppm, less than 100 ppm, less than 75 ppm, less than 50 ppm, less than 25 ppm, or less than 10 ppm).

In some embodiments of the methods, the method results in higher yield of fermentation product (e.g., ethanol) and/or reduced foam accumulation when compared to the same process using an identical cell without the heterologous polynucleotide encoding the phospholipase under the same conditions (e.g., at about or after 54 hours fermentation, such as the conditions described in Examples 3 or 4). In some embodiments, the method results in at least 0.25% (e.g., 0.5%, 0.75%, 1.0%, 1.25%, 1.5%, 1.75%, 2%, 3% or 5%) higher yield of fermentation product.

In some embodiments of the methods, the phospholipase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342. In some embodiments of the methods, the phospholipase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242. In some embodiments of the methods, the heterologous polynucleotide encodes a phospholipase having a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342 (e.g., anoy one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242). In some embodiments of the methods, the heterologous polynucleotide encodes a phospholipase having a mature polypeptide sequence comprising or consisting of the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342 (e.g., any one of SEQ ID NOs: SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242).

In some embodiments of the methods, saccharification of step occurs on a starch-containing material, and wherein the starch-containing material is either gelatinized or ungelatinized starch.

In some embodiments of the methods, the method comprises liquefying the starch-containing material by contacting the material with an alpha-amylase prior to saccharification.

In some embodiments of the methods, liquefying the starch-containing material and/or saccharifying the starch-containing material is conducted in presence of exogenously added protease.

In some embodiments of the methods, the fermenting organism comprises a heterologous polynucleotide encoding a glucoamylase, such as a glucoamylase having a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of a *Pycnoporus* glycoamylase (e.g., a *Pycnoporus sanguineus* glucoamylase of SEQ ID NO: 229), a *Gloeophyllum* glucoamylase (e.g. a *Gloeophyllum sepiarium* of SEQ ID NO: 8), or a glucoamylase of any one of SEQ ID NOs: 102-113 (e.g., a *Saccharomycopsis fibuligera* glucoamylase of SEQ ID NO: 103 or 104, or a *Trichoderma reesei* glucoamylase of SEQ ID NO: 230).

In some embodiments of the methods, the fermenting organism comprises a heterologous polynucleotide encoding an alpha-amylase, such as an alpha-amylase having a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 76-101, 121-174 and 231. In some embodiments of the methods, the heterologous polynucleotide encodes an alpha-amylase having a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of SEQ ID NOs: 76-101, 121-174 and 231. In some embodiments of the methods, the heterologous polynucleotide encodes an alpha-amylase having a mature polypeptide sequence comprising or consisting of the amino acid sequence of any one of SEQ ID NOs: SEQ ID NOs: 76-101, 121-174 and 231.

In some embodiments of the methods, the fermenting organism comprises a heterologous polynucleotide encoding a trehalase, such as a trehalase having a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 175-226. In some embodiments of the methods, the heterologous polynucleotide encodes a trehalase having a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of SEQ ID NOs: 175-226. In some embodiments of the methods, the heterologous polynucleotide encodes a trehalase having a mature polypeptide sequence comprising or consisting of the amino acid sequence of any one of SEQ ID NOs: SEQ ID NOs: 175-226.

In some embodiments of the methods, the fermenting organism comprises a heterologous polynucleotide encoding a protease, such as a protease having a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100%

sequence identity to the amino acid sequence of any one of SEQ ID NOs: 9-73 (e.g., any one of SEQ ID NOs: 9, 14, 16, 21, 22, 33, 41, 45, 61, 62, 66, 67, and 69; such as any one of SEQ NOs: 9, 14, 16, and 69).

In some embodiments of the methods, saccharification of step occurs on a cellulosic-containing material, and wherein the cellulosic-containing material is pretreated (e.g. a dilute acid pretreatment).

In some embodiments of the methods, saccharification occurs on a cellulosic-containing material, and wherein the enzyme composition comprises one or more enzymes selected from a cellulase (e.g., endoglucanase, a cellobiohydrolase, or a beta-glucosidase), an AA9 polypeptide, a hemicellulase (e.g., a xylanase, an acetylxylan esterase, a feruloyl esterase, an arabinofuranosidase, a xylosidase, or a glucuronidase), a CIP, an esterase, an expansin, a ligninolytic enzyme, an oxidoreductase, a pectinase, a protease, and a swollenin.

In some embodiments of the methods, the fermenting organism is a *Saccharomyces, Rhodotorula, Schizosaccharomyces, Kluyveromyces, Pichia, Hansenula, Rhodosporidium*, *Candida, Yarrowia*, *Lipomyces, Cryptococcus,* or *Dekkera sp.* cell. In some embodiments, the fermenting organism is a *Saccharomyces cerevisiae* cell.

Another aspect relates to a recombinant yeast cell comprising a heterologous polynucleotide encoding a phospholipase. In some embodiments, the phospholipase is a Phospholipase A or a Phospholipase C.

In some embodiments of the yeast cell, the cell is capable of higher yield of fermentation product and/or reduced foam accumulation when compared to fermentation using the same process and an identical cell without the heterologous polynucleotide encoding the phospholipase under the same conditions (e.g., at about or after 54 hours fermentation, such as the conditions described in Examples 3 or 4). In some embodiments, the cell is capable of at least 0.25% (e.g., 0.5%, 0.75%, 1.0%, 1.25%, 1.5%, 1.75%, 2%, 3% or 5%) higher yield of fermentation product.

In some embodiments, the recombinant yeast cell is a *Saccharomyces, Rhodotorula, Schizosaccharomyces, Kluyveromyces, Pichia, Hansenula, Rhodosporidium*, *Candida, Yarrowia*, *Lipomyces, Cryptococcus,* or *Dekkera sp.* cell. In some embodiments, the recombinant yeast cell is a *Saccharomyces cerevisiae* cell.

In some embodiments of the yeast cell, the fermenting organism comprises a heterologous polynucleotide encoding a glucoamylase, such as a glucoamylase having a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of a *Pycnoporus* glycoamylase (e.g., a *Pycnoporus sanguineus* glucoamylase of SEQ ID NO: 229), a *Gloeophyllum* glucoamylase (e.g. a *Gloeophyllum sepiarium* of SEQ ID NO: 8), or a glucoamylase of any one of SEQ ID NOs: 102-113 (e.g., a *Saccharomycopsis fibuligera* glucoamylase of SEQ ID NO: 103 or 104, or a *Trichoderma reesei* glucoamylase of SEQ ID NO: 230).

In some embodiments of the yeast cell, the fermenting organism comprises a heterologous polynucleotide encoding an alpha-amylase, wherein the alpha-amylase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 76-101, 121-174 and 231. In some embodiments of the methods, the heterologous polynucleotide encodes an alpha-amylase having a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of SEQ ID NOs: 76-101, 121-174 and 231. In some embodiments of the methods, the heterologous polynucleotide encodes an alpha-amylase having a mature polypeptide sequence comprising or consisting of the amino acid sequence of any one of SEQ ID NOs: SEQ ID NOs: 76-101, 121-174 and 231.

In some embodiments of the yeast cell, the fermenting organism comprises a heterologous polynucleotide encoding a trehalase, wherein the trehalase has mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 175-226. In some embodiments of the methods, the heterologous polynucleotide encodes a trehalase having a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of SEQ ID NOs: 175-226. In some embodiments of the methods, the heterologous polynucleotide encodes a trehalase having a mature polypeptide sequence comprising or consisting of the amino acid sequence of any one of SEQ ID NOs: SEQ ID NOs: 175-226.

In some embodiments of the yeast cell, the fermenting organism comprises a heterologous polynucleotide encoding a protease, such as a protease having a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 9-73 (e.g., any one of SEQ ID NOs: 9, 14, 16, 21, 22, 33, 41, 45, 61, 62, 66, 67, and 69; such as any one of SEQ NOs: 9, 14, 16, and 69).

Brief Description of the Figures

Figure 1 shows % ethanol improvement for phoshoplipase-expressing yeast strains and control strain MHCT-484 described in Example 3.

Figure 2 shows normalized mean ethanol improvement after 54 hours of fermentation of AMP mash at 0 and 150 ppm urea as described in Example 4.

Figure 3 shows normalized mean ethanol improvement after 54 hours of fermentation of the non-AMP mash at 0 and 300 ppm urea as described in Example 4.

Figure 4 shows improved defoaming capability during fermentation of a phospholipase-expressing yeast strain HP21-F04 (right) compared to control strain yMHCT48 (left) as described in Example 9.

Definitions

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

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

Alpha-amylase: The term “alpha amylase” means an 1,4-alpha-D-glucan glucanohydrolase, EC. 3.2.1.1, which catalyze hydrolysis of starch and other linear and branched 1,4-glucosidic oligo- and polysaccharides. For purposes of the present invention, alpha amylase activity can be determined using an alpha amylase assay described in the examples section below.

Auxiliary Activity 9: The term “Auxiliary Activity 9” or “AA9” means a polypeptide classified as a lytic polysaccharide monooxygenase (Quinlan *et al.*, 2011, *Proc. Natl. Acad. Sci. USA* 208: 15079-15084; Phillips *et al.*, 2011, *ACS Chem. Biol.* 6: 1399-1406; Lin *et al.*, 2012, *Structure* 20: 1051-1061). AA9 polypeptides were formerly classified into the glycoside hydrolase Family 61 (GH61) according to Henrissat, 1991, *Biochem. J.* 280: 309-316, and Henrissat and Bairoch, 1996, *Biochem. J.* 316: 695-696.

AA9 polypeptides enhance the hydrolysis of a cellulosic-containing material by an enzyme having cellulolytic activity. Cellulolytic enhancing activity can be determined by measuring the increase in reducing sugars or the increase of the total of cellobiose and glucose from the hydrolysis of a cellulosic-containing material by cellulolytic enzyme under the following conditions:

1-50 mg of total protein/g of cellulose in pretreated corn stover (PCS), wherein total protein is comprised of 50-99.5% w/w cellulolytic enzyme protein and 0.5-50% w/w protein of an AA9 polypeptide for 1-7 days at a suitable temperature, such as 40C-80°C, *e.g.*, 50°C, 55°C, 60°C, 65°C, or 70°C, and a suitable pH, such as 4-9, *e.g.*, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, or 8.5, compared to a control hydrolysis with equal total protein loading without cellulolytic enhancing activity (1-50 mg of cellulolytic protein/g of cellulose in PCS).

AA9 polypeptide enhancing activity can be determined using a mixture of CELLUCLAST® 1.5L (Novozymes A/S, Bagsværd, Denmark) and beta-glucosidase as the source of the cellulolytic activity, wherein the beta-glucosidase is present at a weight of at least 2-5% protein of the cellulase protein loading. In one embodiment, the beta-glucosidase is an *Aspergillus oryzae* beta-glucosidase (*e.g.*, recombinantly produced in *Aspergillus oryzae* according to WO 02/095014). In another embodiment, the beta-glucosidase is an *Aspergillus fumigatus* beta-glucosidase (*e.g.*, recombinantly produced in *Aspergillus oryzae* as described in WO 02/095014).

AA9 polypeptide enhancing activity can also be determined by incubating an AA9 polypeptide with 0.5% phosphoric acid swollen cellulose (PASC), 100 mM sodium acetate pH 5, 1 mM $MnSO_4$, 0.1% gallic acid, 0.025 mg/mL of *Aspergillus fumigatus* beta-glucosidase, and 0.01% TRITON® X-100 (4-(1,1,3,3-tetramethylbutyl)phenyl-polyethylene glycol) for 24-96 hours at 40°C followed by determination of the glucose released from the PASC.

AA9 polypeptide enhancing activity can also be determined according to WO 2013/028928 for high temperature compositions.

AA9 polypeptides enhance the hydrolysis of a cellulosic-containing material catalyzed by enzyme having cellulolytic activity by reducing the amount of cellulolytic enzyme required to reach the same degree of hydrolysis preferably at least 1.01-fold, *e.g.*, at least 1.05-fold, at least 1.10-fold, at least 1.25-fold, at least 1.5-fold, at least 2-fold, at least 3-fold, at least 4-fold, at least 5-fold, at least 10-fold, or at least 20-fold.

Beta-glucosidase: The term “beta-glucosidase” means a beta-D-glucoside glucohydrolase (E.C. 3.2.1.21) that catalyzes the hydrolysis of terminal non-reducing beta-D-glucose residues with the release of beta-D-glucose. Beta-glucosidase activity can be determined using *p*-nitrophenyl-beta-D-glucopyranoside as substrate according to the procedure of Venturi *et al.*, 2002, *J. Basic Microbiol.* 42: 55-66. One unit of beta-glucosidase is defined as 1.0 µmole of *p*-nitrophenolate anion produced per minute at 25°C, pH 4.8 from 1 mM *p*-nitrophenyl-beta-D-glucopyranoside as substrate in 50 mM sodium citrate containing 0.01% TWEEN® 20.

Beta-xylosidase: The term “beta-xylosidase” means a beta-D-xyloside xylohydrolase (E.C. 3.2.1.37) that catalyzes the exo-hydrolysis of short beta (1→4)-xylooligosaccharides to remove successive D-xylose residues from non-reducing termini. Beta-xylosidase activity can be determined using 1 mM *p*-nitrophenyl-beta-D-xyloside as substrate in 100 mM sodium citrate containing 0.01% TWEEN® 20 at pH 5, 40°C. One unit of beta-xylosidase is defined as 1.0 µmole of *p*-nitrophenolate anion produced per minute at 40°C, pH 5 from 1 mM *p*-nitrophenyl-beta-D-xyloside in 100 mM sodium citrate containing 0.01% TWEEN® 20.

Catalase: The term “catalase” means a hydrogen-peroxide:hydrogen-peroxide oxidoreductase (EC 1.11.1.6) that catalyzes the conversion of 2 H_2O_2 to O_2 + 2 H_2O. For purposes of the present invention, catalase activity is determined according to U.S. Patent No. 5,646,025. One unit of catalase activity equals the amount of enzyme that catalyzes the oxidation of 1 µmole of hydrogen peroxide under the assay conditions.

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

Cellobiohydrolase: The term “cellobiohydrolase” means a 1,4-beta-D-glucan cellobiohydrolase (E.C. 3.2.1.91 and E.C. 3.2.1.176) that catalyzes the hydrolysis of 1,4-beta-D-glucosidic linkages in cellulose, cellooligosaccharides, or any beta-1,4-linked glucose containing polymer, releasing cellobiose from the reducing end (cellobiohydrolase I) or non-reducing end (cellobiohydrolase II) of the chain (Teeri, 1997, *Trends in Biotechnology* 15: 160-167; Teeri *et al.*, 1998, *Biochem. Soc. Trans.* 26: 173-178). Cellobiohydrolase activity can be determined according to the procedures described by Lever *et al.*, 1972, *Anal. Biochem.* 47: 273-279; van Tilbeurgh *et al.*, 1982, *FEBS Letters* 149: 152-156; van Tilbeurgh and Claeyssens, 1985, *FEBS Letters* 187: 283-288; and Tomme *et al.*, 1988, *Eur. J. Biochem.* 170: 575-581.

Cellulolytic enzyme or cellulase: The term “cellulolytic enzyme” or “cellulase” means one or more (*e.g.*, several) enzymes that hydrolyze a cellulosic-containing material. Such enzymes include endoglucanase(s), cellobiohydrolase(s), beta-glucosidase(s), or combinations thereof. The two basic approaches for measuring cellulolytic enzyme activity include: (1) measuring the total cellulolytic enzyme activity, and (2) measuring the individual cellulolytic enzyme activities (endoglucanases, cellobiohydrolases, and beta-glucosidases) as reviewed in Zhang *et al.*, 2006, *Biotechnology Advances* 24: 452-481. Total cellulolytic enzyme activity can be measured using insoluble substrates, including Whatman №1 filter paper, microcrystalline cellulose, bacterial cellulose, algal cellulose, cotton, pretreated lignocellulose, etc. The most common total cellulolytic activity assay is the filter paper assay using Whatman №1 filter paper as the substrate. The assay was established by the International Union of Pure and Applied Chemistry (IUPAC) (Ghose, 1987, *Pure Appl. Chem.* 59: 257-68).

Cellulolytic enzyme activity can be determined by measuring the increase in production/release of sugars during hydrolysis of a cellulosic-containing material by cellulolytic enzyme(s) under the following conditions: 1-50 mg of cellulolytic enzyme protein/g of cellulose in pretreated corn stover (PCS) (or other pretreated cellulosic-containing material) for 3-7 days at a suitable temperature such as 40°C-80°C, *e.g.*, 50°C, 55°C, 60°C, 65°C, or 70°C, and a suitable pH such as 4-9, *e.g.*, 5.0, 5.5, 6.0, 6.5, or 7.0, compared to a control hydrolysis without addition of cellulolytic enzyme protein. Typical conditions are 1 mL reactions, washed or unwashed PCS, 5% insoluble solids (dry weight), 50 mM sodium acetate pH 5, 1 mM $MnSO_4$, 50°C, 55°C, or 60°C, 72 hours, sugar analysis by AMINEX® HPX-87H column chromatography (Bio-Rad Laboratories, Inc., Hercules, CA, USA).

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

Control sequence: The term “control sequence” means a nucleic acid sequence necessary for polypeptide expression. Control sequences may be native or foreign to the polynucleotide encoding the polypeptide, and native or foreign to each other. Such control sequences include, but are not limited to, a leader sequence, polyadenylation sequence, propeptide sequence, promoter sequence, signal peptide sequence, and transcription terminator sequence. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the polynucleotide encoding a polypeptide.

Disruption: The term “disruption” means that a coding region and/or control sequence of a referenced gene is partially or entirely modified (such as by deletion, insertion, and/or substitution of one or more nucleotides) resulting in the absence (inactivation) or decrease in expression, and/or the absence or decrease of enzyme activity of the encoded polypeptide. The effects of disruption can be measured using techniques known in the art such as detecting the absence or decrease of enzyme activity using from cell-free extract measurements referenced herein; or by the absence or decrease of corresponding mRNA (e.g., at least 25% decrease, at least 50% decrease, at least 60% decrease, at least 70% decrease, at least 80% decrease, or at least 90% decrease); the absence or decrease in the amount of corresponding polypeptide having enzyme activity (e.g., at least 25% decrease, at least 50% decrease, at least 60% decrease, at least 70% decrease, at least 80% decrease, or at least 90% decrease); or the absence or decrease of the specific activity of the corresponding polypeptide having enzyme activity (e.g., at least 25% decrease, at least 50% decrease, at least 60% decrease, at least 70% decrease, at least 80% decrease, or at least 90% decrease). Disruptions of a particular gene of interest can be generated by methods known in the art, e.g., by directed homologous recombination (see *Methods in Yeast Genetics* (1997 edition), Adams, Gottschling, Kaiser, and Stems, Cold Spring Harbor Press (1998)).

Endogenous gene: The term “endogenous gene” means a gene that is native to the referenced host cell. “Endogenous gene expression” means expression of an endogenous gene.

Endoglucanase: The term “endoglucanase” means a 4-(1,3;1,4)-beta-D-glucan 4-glucanohydrolase (E.C. 3.2.1.4) that catalyzes endohydrolysis of 1,4-beta-D-glycosidic linkages in cellulose, cellulose derivatives (such as carboxymethyl cellulose and hydroxyethyl cellulose), lichenin, beta-1,4 bonds in mixed beta-1,3-1,4 glucans such as cereal beta-D-glucans or xyloglucans, and other plant material containing cellulosic components. Endoglucanase activity can be determined by measuring reduction in substrate viscosity or increase in reducing ends determined by a reducing sugar assay (Zhang *et al.*, 2006, *Biotechnology Advances* 24: 452-481). Endoglucanase activity can also be determined using carboxymethyl cellulose (CMC) as substrate according to the procedure of Ghose, 1987, *Pure and Appl. Chem.* 59: 257-268, at pH 5, 40°C.

Expression: The term “expression” includes any step involved in the production of the polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion. Expression can be measured—for example, to detect increased expression—by techniques known in the art, such as measuring levels of mRNA and/or translated polypeptide.

Expression vector: The term “expression vector” means a linear or circular DNA molecule that comprises a polynucleotide encoding a polypeptide and is operably linked to control sequences that provide for its expression.

Fermentable medium: The term “fermentable medium” or “fermentation medium” refers to a medium comprising one or more (e.g., two, several) sugars, such as glucose, fructose, sucrose, cellobiose, xylose, xylulose, arabinose, mannose, galactose, and/or soluble oligosaccharides, wherein the medium is capable, in part, of being converted (fermented) by a host cell into a desired product, such as ethanol. In some instances, the fermentation medium is derived from a natural source, such as sugar cane, starch, or cellulose, and may be the result of pretreating the source by enzymatic hydrolysis (saccharification). The term fermentation medium is understood herein to refer to a medium before the fermenting organism is added, such as, a medium resulting from a saccharification process, as well as a medium used in a simultaneous saccharification and fermentation process (SSF).

Glucoamylase: The term "glucoamylase" (1,4-alpha-D-glucan glucohydrolase, EC 3.2.1.3) is defined as an enzyme that catalyzes the release of D-glucose from the non-reducing ends of starch or related oligo- and polysaccharide molecules. For purposes of the present invention, glucoamylase activity may be determined according to the procedures known in the art, such as those described in the Examples of US Provisional Patent Application No. 62/703,103, filed July 25, 2018.

Hemicellulolytic enzyme or hemicellulase: The term "hemicellulolytic enzyme" or "hemicellulase" means one or more (*e.g.*, several) enzymes that hydrolyze a hemicellulosic material. See, for example, Shallom and Shoham, 2003, *Current Opinion In Microbiology* 6(3): 219-228). Hemicellulases are key components in the degradation of plant biomass. Examples of hemicellulases include, but are not limited to, an acetylmannan esterase, an acetylxylan esterase, an arabinanase, an arabinofuranosidase, a coumaric acid esterase, a feruloyl esterase, a galactosidase, a glucuronidase, a glucuronoyl esterase, a mannanase, a mannosidase, a xylanase, and a xylosidase. The substrates for these enzymes, hemicelluloses, are a heterogeneous group of branched and linear polysaccharides that are bound via hydrogen bonds to the cellulose microfibrils in the plant cell wall, crosslinking them into a robust network. Hemicelluloses are also covalently attached to lignin, forming together with cellulose a highly complex structure. The variable structure and organization of hemicelluloses require the concerted action of many enzymes for its complete degradation. The catalytic modules of hemicellulases are either glycoside hydrolases (GHs) that hydrolyze glycosidic bonds, or carbohydrate esterases (CEs), which hydrolyze ester linkages of acetate or ferulic acid side groups. These catalytic modules, based on homology of their primary sequence, can be assigned into GH and CE families. Some families, with an overall similar fold, can be further grouped into clans, marked alphabetically (*e.g.*, GH-A). A most informative and updated classification of these and other carbohydrate active enzymes is available in the Carbohydrate-Active Enzymes (CAZy) database. Hemicellulolytic enzyme activities can be measured according to Ghose and Bisaria, 1987, *Pure & Appl. Chem.* 59: 1739-1752, at a suitable temperature such as 40°C-80°C, *e.g.*, 50°C, 55°C, 60°C, 65°C, or 70°C, and a suitable pH such as 4-9, *e.g.*, 5.0, 5.5, 6.0, 6.5, or 7.0.

Heterologous polynucleotide: The term "heterologous polynucleotide" is defined herein as a polynucleotide that is not native to the host cell; a native polynucleotide in which structural modifications have been made to the coding region; a native polynucleotide whose expression is quantitatively altered as a result of a manipulation of the DNA by recombinant DNA techniques, e.g., a different (foreign) promoter; or a native polynucleotide in a host cell having one or more extra copies of the polynucleotide to quantitatively alter expression. A "heterologous gene" is a gene comprising a heterologous polynucleotide.

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

Host cell: The term "host cell" means any cell type that is susceptible to transformation, transfection, transduction, and the like with a nucleic acid construct or expression vector comprising a polynucleotide described herein (e.g., a polynucleotide encoding an alpha-amylase and/or trehalase). The term "host cell" encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication. The term "recombinant cell" is defined herein as a non-naturally occurring host cell comprising one or more (e.g., two, several) heterologous polynucleotides.

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

Mature polypeptide: The term "mature polypeptide" is defined herein as a polypeptide having biological activity that is in its final form following translation and any post-translational modifications, such as N-terminal processing, C-terminal truncation, glycosylation, phosphorylation, etc. The mature polypeptide sequence lacks a signal sequence, which may be determined using techniques known in the art (*See*, e.g., Zhang and Henzel, 2004, *Protein Science* 13: 2819-2824).

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

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

Nucleic acid construct: The term "nucleic acid construct" means a polynucleotide comprises one or more (e.g., two, several) control sequences. The polynucleotide may be single-stranded or double-stranded, and may be isolated from a naturally occurring gene, modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature, or synthetic.

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

Phospholipase: The term “phospholipase” means an enzyme that catalyzes the conversion of phospholipids into fatty acids and other lipophilic substances, such as phospholipase A (EC numbers 3.1.1.4, 3.1.1.5 and 3.1.1.32) or phospholipase C (EC numbers 3.1.4.3 and 3.1.4.11). For purposes of the present invention, phospholipase activity may be determined using activity assays known in the art, or according to the procedures described in the Examples herein (Example 2).

Pretreated corn stover: The term “Pretreated Corn Stover” or “PCS” means a cellulosic-containing material derived from corn stover by treatment with heat and dilute sulfuric acid, alkaline pretreatment, neutral pretreatment, or any pretreatment known in the art.

Protease: The term “protease” is defined herein as an enzyme that hydrolyses peptide bonds. It includes any enzyme belonging to the EC 3.4 enzyme group (including each of the thirteen subclasses thereof). The EC number refers to Enzyme Nomenclature 1992 from NC-IUBMB, Academic Press, San Diego, California, including supplements 1-5 published in *Eur. J. Biochem.* 223: 1-5 (1994); *Eur. J. Biochem.* 232: 1-6 (1995); *Eur. J. Biochem.* 237: 1-5 (1996); *Eur. J. Biochem.* 250: 1-6 (1997); and *Eur. J. Biochem.* 264: 610-650 (1999); respectively. The term "subtilases" refer to a sub-group of serine protease according to Siezen et al., 1991, *Protein Engng.* 4: 719-737 and Siezen et al., 1997, *Protein Science* 6: 501-523. Serine proteases or serine peptidases is a subgroup of proteases characterised by having a serine in the active site, which forms a covalent adduct with the substrate. Further the subtilases (and the serine proteases) are characterised by having two active site amino acid residues apart from the serine, namely a histidine and an aspartic acid residue. The subtilases may be divided into 6 sub-divisions, i.e. the Subtilisin family, the Thermitase family, the Proteinase K family, the Lantibiotic peptidase family, the Kexin family and the Pyrolysin family. The term “protease activity” means a proteolytic activity (EC 3.4). Protease activity may be determined using methods described in the art (e.g., US 2015/0125925) or using commercially available assay kits (e.g., Sigma-Aldrich).

Pullulanase: The term "pullulanase" means a starch debranching enzyme having pullulan 6-glucano-hydrolase activity (EC 3.2.1.41) that catalyzes the hydrolysis the α-1,6-glycosidic bonds in pullulan, releasing maltotriose with reducing carbohydrate ends. For purposes of the present invention, pullulanase activity can be determined according to a PHADEBAS assay or the sweet potato starch assay described in WO2016/087237.

Sequence Identity: The relatedness between two amino acid sequences or between two nucleotide sequences is described by the parameter "sequence identity".

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

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

For purposes described herein, the degree of sequence identity between two deoxyribonucleotide sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, **1970**, *supra*) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et al., 2000, *supra*), preferably version 3.0.0 or later. The optional parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EDNAFULL (EMBOSS version of NCBI NUC4.4) substitution matrix. The output of Needle labeled "longest identity" (obtained using the –nobrief option) is used as the percent identity and is calculated as follows:

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

Signal peptide: The term "signal peptide" is defined herein as a peptide linked (fused) in frame to the amino terminus of a polypeptide having biological activity and directs the polypeptide into the cell's secretory pathway. Signal sequences may be determined using techniques known in the art (*See*, e.g., Zhang and Henzel, 2004, *Protein Science* 13: 2819-2824). The polypeptides described herein may comprise any suitable signal peptide known in the art, or any signal peptide described herein (e.g., the *S. cerevisiae* MFα1 signal peptide of SEQ ID NO: 7, the *S. cerevisiae* EXG1 signal peptide of SEQ ID NO: 227, or the *S. cerevisiae* AG2 signal peptide of SEQ ID NO: 234, or a signal peptide having at least 80%, 85%, 90%, 95%, 96%, 97%, 98% or 99% sequence identity thereof).

Trehalase: The term "trehalase" means an enzyme which degrades trehalose into its unit monosaccharides (i.e., glucose). Trehalases are classified in EC 3.2.1.28 (alpha,alpha-trehalase) and EC. 3.2.1.93 (alpha,alpha-phosphotrehalase). The EC classes are based on recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUBMB). Description of EC classes can be found on the internet, e.g., on "http://www.expasy.org/enzyme/". Trehalases are enzymes that catalyze the following reactions:

EC 3.2.1.28: Alpha,alpha-trehalose + $H_2O \Leftrightarrow$ 2 D-glucose;

EC 3.2.1. 93: Alpha,alpha-trehalose 6-phosphate + $H_2O \Leftrightarrow$ D-glucose + D-glucose 6-phosphate.

For purposes of the present invention, trehalase activity may be determined according to the trehalase activity assay described herein in the experimental section.

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

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

Xylanase: The term "xylanase" means a 1,4-beta-D-xylan-xylohydrolase (E.C. 3.2.1.8) that catalyzes the endohydrolysis of 1,4-beta-D-xylosidic linkages in xylans. Xylanase activity can be determined with 0.2% AZCL-arabinoxylan as substrate in 0.01% TRITON® X-100 and 200 mM sodium phosphate pH 6 at 37°C. One unit of xylanase activity is defined as 1.0 µmole of azurine produced per minute at 37°C, pH 6 from 0.2% AZCL-arabinoxylan as substrate in 200 mM sodium phosphate pH 6.

Xylose Isomerase: The term "Xylose Isomerase" or "XI" means an enzyme which can catalyze D-xylose into D-xylulose in vivo, and convert D-glucose into D-fructose in vitro. Xylose isomerase is also known as "glucose isomerase" and is classified as E.C. 5.3.1.5. As the structure of the enzyme is very stable, the xylose isomerase is a good model for studying the relationships between protein structure and functions (Karimaki et al., Protein Eng Des Sel, 12004, 17 (12):861-869). Xylose Isomerase activity may be determined using techniques known in the art (e.g., a coupled enzyme assay using D-sorbitol dehygrogenase, as described by Verhoeven et. al., 2017, *Sci Rep* 7, 46155).

Reference to "about" a value or parameter herein includes embodiments that are directed to that value or parameter *per se*. For example, description referring to "about X" includes the embodiment "X". When used in combination with measured values, "about" includes a range that encompasses at least the uncertainty associated with the method of measuring the particular value, and can include a range of plus or minus two standard deviations around the stated value.

Likewise, reference to a gene or polypeptide that is "derived from" another gene or polypeptide X, includes the gene or polypeptide X.

As used herein and in the appended claims, the singular forms "a," "or," and "the" include plural referents unless the context clearly dictates otherwise.

It is understood that the embodiments described herein include "consisting" and/or "consisting essentially of" embodiments. As used herein, except where the context requires otherwise due to express language or necessary implication, the word "comprise" or variations such as "comprises" or "comprising" is used in an inclusive sense, i.e. to specify the presence of the stated features but not to preclude the presence or addition of further features in various embodiments.

DETAILED DESCRIPTION

Described herein, *inter alia*, are methods for producing a fermentation product, such as ethanol, from starch or cellulosic containing material.

During industrial scale fermentation, yeast encounter various physiological challenges including variable concentrations of sugars, high concentrations of yeast metabolites such as ethanol, glycerol, organic acids, osmotic stress, as well as potential competition from contaminating microbes such as wild yeasts and bacteria. As a consequence, many yeasts are not suitable for use in industrial fermentation. The most widely used commercially available industrial strain of *Saccharomyces* (i.e. for industrial scale fermentation) is the *Saccharomyces cerevisiae* strain used, for example, in the product ETHANOL RED®. This strain is well suited to industrial ethanol production; however, it remains unclear how modifications to the yeast will impact performance. In particular, the functional expression of heterologous enzymes by an industrially-relevant *Saccharomyces cerevisiae* yeast is uncertain (See, for example US

9,206,444 where the applicant was unable to functionally express numerous enzymes/enzyme classes).

The Applicant has surprisingly found that yeast expressing a phosholipase provide beneficial properties that may be useful for ethanol fermentation, such as reduced need for supplemental nitrogen.

In one aspect is a method of producing a fermentation product from a starch-containing or cellulosic-containing material comprising:

(a) saccharifying the starch-containing or cellulosic-containing material; and

(b) fermenting the saccharified material of step (a) with a fermenting organism;

wherein the fermenting organism comprises a heterologous polynucleotide encoding a phospholipase.

Steps of saccharifying and fermenting are carried out either sequentially or simultaneously (SSF). In one embodiment, steps of saccharifying and fermenting are carried out simultaneously (SSF). In another embodiment, steps of saccharifying and fermenting are carried out sequentially.

Fermenting organism

The fermenting organism described herein may be derived from any host cell known to the skilled artisan capable of producing a fermentation product, such as ethanol. As used herein, a "derivative" of strain is derived from a referenced strain, such as through mutagenesis, recombinant DNA technology, mating, cell fusion, or cytoduction between yeast strains. Those skilled in the art will understand that the genetic alterations, including metabolic modifications exemplified herein, may be described with reference to a suitable host organism and their corresponding metabolic reactions or a suitable source organism for desired genetic material such as genes for a desired metabolic pathway. However, given the complete genome sequencing of a wide variety of organisms and the high level of skill in the area of genomics, those skilled in the art can apply the teachings and guidance provided herein to other organisms. For example, the metabolic alterations exemplified herein can readily be applied to other species by incorporating the same or analogous encoding nucleic acid from species other than the referenced species.

The host cells for preparing the recombinant cells described herein can be from any suitable host, such as a yeast strain, including, but not limited to, a *Saccharomyces*, *Rhodotorula*, *Schizosaccharomyces*, *Kluyveromyces*, *Pichia*, *Hansenula*, *Rhodosporidium*, *Candida*, *Yarrowia*, *Lipomyces*, *Cryptococcus*, or *Dekkera sp.* cell. In particular, *Saccharomyces* host cells are contemplated, such as *Saccharomyces cerevisiae*, *bayanus* or *carlsbergensis* cells. Preferably, the yeast cell is a *Saccharomyces cerevisiae* cell. Suitable cells can, for example, be derived from commercially available strains and polyploid or aneuploid industrial strains, including but not limited to those from Superstart™, THERMOSACC®, C5 FUEL™, XyloFerm®, etc. (Lallemand); RED STAR and ETHANOL RED® (Fermentis/Lesaffre); FALI (AB Mauri); Baker's Best Yeast, Baker's Compressed Yeast, etc. (Fleishmann's Yeast); BIOFERM AFT, XP, CF, and XR (North American Bioproducts Corp.); Turbo Yeast (Gert Strand AB); and FERMIOL® (DSM Specialties). Other useful yeast strains are available from biological depositories such as the American Type Culture Collection (ATCC) or the Deutsche Sammlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), such as, e.g., BY4741 (e.g., ATCC 201388); Y108-1 (ATCC PTA.10567) and NRRL YB-1952 (ARS Culture Collection). Still other *S. cerevisiae* strains suitable as host cells DBY746, [Alpha][Eta]22, S150-2B, GPY55-15Ba, CEN.PK, USM21, TMB3500, TMB3400, VTT-A-63015, VTT-A-85068, VTT-c-79093 and their derivatives as well as Saccharomyces sp. 1400, 424A (LNH-ST), 259A (LNH-ST) and derivatives thereof. In one embodiment, the recombinant cell is a derivative of a strain *Saccharomyces cerevisiae* CIBTS1260 (deposited under Accession No. NRRL Y-50973 at the Agricultural Research Service Culture Collection (NRRL), Illinois 61604 U.S.A.).

The fermenting organism may be *Saccharomyces* strain, e.g., *Saccharomyces cerevisiae* strain produced using the method described and concerned in US patent no. 8,257,959-BB.

The strain may also be a derivative of *Saccharomyces cerevisiae* strain NMI V14/004037 (*See*, WO2015/143324 and WO2015/143317 each incorporated herein by reference), strain nos. V15/004035, V15/004036, and V15/004037 (*See*, WO 2016/153924 incorporated herein by reference), strain nos. V15/001459, V15/001460, V15/001461 (*See*, WO2016/138437 incorporated herein by reference), strain no. NRRL Y67342 (*See*, WO2017/063159 incorporated herein by reference), or any strain described in WO2017/087330 (incorporated herein by reference).

The fermenting organisms according to the invention have been generated in order to, e.g., improve fermentation yield and to improve process economy by cutting enzyme costs since part or all of the necessary enzymes needed to improve method performance are be produced by the fermenting organism.

The fermenting organisms described herein may utilize expression vectors comprising the coding sequence of one or more (e.g., two, several) heterologous genes linked to one or more control sequences that direct expression in a suitable cell under conditions compatible with the control sequence(s). Such expression vectors may be used in any of the cells and methods described herein. The polynucleotides described herein may be manipulated in a variety of ways to provide for expression of a desired polypeptide. Manipulation of the polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides utilizing recombinant DNA methods are well known in the art.

A construct or vector (or multiple constructs or vectors) comprising the one or more (e.g., two, several) heterologous genes may be introduced into a cell so that the construct or vector is maintained as a chromosomal integrant or as a self-replicating extra-chromosomal vector as described earlier.

The various nucleotide and control sequences may be joined together to produce a recombinant expression vector that may include one or more (e.g., two, several) convenient restriction sites to allow for insertion or substitution of the polynucleotide at such sites. Alternatively, the polynucleotide(s) may be expressed by inserting the polynucleotide(s) or a nucleic acid construct comprising the sequence into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

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

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

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

Each heterologous polynucleotide described herein may be operably linked to a promoter that is foreign to the polynucleotide. For example, in one embodiment, the heterologous polynucleotide encoding the hexose transporter is operably linked to a promoter foreign to the polynucleotide. The promoters may be identical to or share a high degree of sequence identity (e.g., at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%) with a selected native promoter.

Examples of suitable promoters for directing the transcription of the nucleic acid constructs in a yeast cells, include, but are not limited to, the promoters obtained from the genes for enolase, (e.g., *S. cerevisiae* enolase or *I. orientalis* enolase (ENO1)), galactokinase (e.g., *S. cerevisiae* galactokinase or *I. orientalis* galactokinase (GAL1)), alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (e.g., *S. cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase or *I. orientalis* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH1, ADH2/GAP)), triose phosphate isomerase (e.g., *S. cerevisiae* triose phosphate isomerase or *I. orientalis* triose phosphate isomerase (TPI)), metallothionein (e.g., *S. cerevisiae* metallothionein or *I. orientalis* metallothionein (CUP1)), 3-phosphoglycerate kinase (e.g., *S. cerevisiae* 3-phosphoglycerate kinase or *I. orientalis* 3-phosphoglycerate kinase (PGK)), PDC1, xylose reductase (XR), xylitol dehydrogenase (XDH), L-(+)-lactate-cytochrome c oxidoreductase (CYB2), translation elongation factor-1 (TEF1), translation elongation factor-2 (TEF2), glyceraldehyde-3-phosphate dehydrogenase (GAPDH), and orotidine 5'-phosphate decarboxylase (URA3) genes. Other suitable promoters may be obtained from *S. cerevisiae* TDH3, HXT7, PGK1, RPL18B and CCW12 genes. Additional useful promoters for yeast host cells are described by Romanos *et al.*, 1992, *Yeast* 8: 423-488.

The control sequence may also be a suitable transcription terminator sequence, which is recognized by a host cell to terminate transcription. The terminator sequence is operably linked to the 3’-terminus of the polynucleotide encoding the polypeptide. Any terminator that is functional in the yeast cell of choice may be used. The terminator may be identical to or share a high degree of sequence identity (e.g., at least about 80%, at least about 85%, at least about 90%, at least about 95%, at least about 96%, at least about 97%, at least about 98%, or at least about 99%) with the selected native terminator.

Suitable terminators for yeast host cells may be obtained from the genes for enolase (e.g., *S. cerevisiae* or *I. orientalis* enolase cytochrome C (e.g., *S. cerevisiae* or *I. orientalis* cytochrome (CYC1)), glyceraldehyde-3-phosphate dehydrogenase (e.g., *S. cerevisiae* or *I. orientalis* glyceraldehyde-3-phosphate dehydrogenase (gpd)), PDC1, XR, XDH, transaldolase (TAL), transketolase (TKL), ribose 5-phosphate ketol-isomerase (RKI), CYB2, and the galactose family of genes (especially the GAL10 terminator). Other suitable terminators may be obtained from *S. cerevisiae* ENO2 or TEF1 genes. Additional useful terminators for yeast host cells are described by Romanos *et al.*, 1992, *supra*.

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

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

The control sequence may also be a suitable leader sequence, when transcribed is a nontranslated region of an mRNA that is important for translation by the host cell. The leader sequence is operably linked to the 5'-terminus of the polynucleotide encoding the polypeptide. Any leader sequence that is functional in the yeast cell of choice may be used.

Suitable leaders for yeast host cells are obtained from the genes for enolase (e.g., *S. cerevisiae* or *I. orientalis* enolase (ENO-1)), 3-phosphoglycerate kinase (e.g., *S. cerevisiae* or *I. orientalis* 3-phosphoglycerate kinase), alpha-factor (e.g., *S. cerevisiae* or *I. orientalis* alpha-factor), and alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (e.g., *S. cerevisiae* or *I. orientalis* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP)).

The control sequence may also be a polyadenylation sequence; a sequence operably linked to the 3'-terminus of the polynucleotide and, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence that is functional in the host cell of choice may be used. Useful polyadenylation sequences for yeast cells are described by Guo and Sherman, 1995, *Mol. Cellular Biol.* 15: 5983-5990.

It may also be desirable to add regulatory sequences that allow the regulation of the expression of the polypeptide relative to the growth of the host cell. Examples of regulatory systems are those that cause the expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory systems in prokaryotic systems include the *lac*, *tac*, and *trp* operator systems. In yeast, the ADH2 system or GAL1 system may be used.

The vectors may contain one or more (e.g., two, several) selectable markers that permit easy selection of transformed, transfected, transduced, or the like cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like. Suitable markers for yeast host cells include, but are not limited to, ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3.

The vectors may contain one or more (e.g., two, several) elements that permit integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

For integration into the host cell genome, the vector may rely on the polynucleotide’s sequence encoding the polypeptide or any other element of the vector for integration into the genome by homologous or non-homologous recombination. Alternatively, the vector may contain additional polynucleotides for directing integration by homologous recombination into the genome of the host cell at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should contain a sufficient number of nucleic acids, such as 100 to 10,000 base pairs, 400 to 10,000 base pairs, and 800 to 10,000 base pairs, which have a high degree of sequence identity to the corresponding target sequence to enhance the probability of homologous recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding polynucleotides. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination. Potential integration loci include those described in the art (e.g., See US2012/0135481).

For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the yeast cell. The origin of replication may be any plasmid replicator mediating autonomous replication that functions in a cell. The term “origin of replication” or “plasmid replicator” means a polynucleotide that enables a plasmid or vector to replicate *in vivo*. Examples of origins of replication for use in a yeast host cell are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6.

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

The procedures used to ligate the elements described above to construct the recombinant expression vectors described herein are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York).

Additional procedures and techniques known in the art for the preparation of recombinant cells for ethanol fermentation, are described in, e.g., WO 2016/045569, the content of which is hereby incorporated by reference.

The fermenting organism may be in the form of a composition comprising a fermenting organism (e.g., a yeast strain described herein) and a naturally occurring and/or a nonenaturally occurring component.

The fermenting organism described herein may be in any viable form, including crumbled, dry, including active dry and instant, compressed, cream (liquid) form etc. In one embodiment, the fermenting organism (e.g., a *Saccharomyces cerevisiae* yeast strain) is dry yeast, such as active dry yeast or instant yeast. In one embodiment, the fermenting organism (e.g., a *Saccharomyces cerevisiae* yeast strain) is crumbled yeast. In one embodiment, the fermenting organism (e.g., a *Saccharomyces cerevisiae* yeast strain) is compressed yeast. In one embodiment, the fermenting organism (e.g., a *Saccharomyces cerevisiae* yeast strain) is cream yeast.

In one embodiment is a composition comprising a fermenting organism described herein (e.g., a *Saccharomyces cerevisiae* yeast strain), and one or more of the component selected from the group consisting of: surfactants, emulsifiers, gums, swelling agent, and antioxidants and other processing aids.

The compositions described herein may comprise a fermenting organism described herein (e.g., a *Saccharomyces cerevisiae* yeast strain) and any suitable surfactants. In one embodiment, the surfactant(s) is/are an anionic surfactant, cationic surfactant, and/or nonionic surfactant.

The compositions described herein may comprise a fermenting organism described herein (e.g., a *Saccharomyces cerevisiae* yeast strain) and any suitable emulsifier. In one embodiment, the emulsifier is a fatty-acid ester of sorbitan. In one embodiment, the emulsifier is selected from the group of sorbitan monostearate (SMS), citric acid esters of monodiglycerides, polyglycerolester, fatty acid esters of propylene glycol.

In one embodiment, the composition comprises a fermenting organism described herein (e.g., a *Saccharomyces cerevisiae* yeast strain), and Olindronal SMS, Olindronal SK, or Olindronal SPL including composition concerned in European Patent No. 1,724,336 (hereby incorporated by reference). These products are commercially available from Bussetti, Austria, for active dry yeast.

The compositions described herein may comprise a fermenting organism described herein (e.g., a *Saccharomyces cerevisiae* yeast strain) and any suitable gum. In one embodiment, the gum is selected from the group of carob, guar, tragacanth, arabic, xanthan and acacia gum, in particular for cream, compressed and dry yeast.

The compositions described herein may comprise a fermenting organism described herein (e.g., a *Saccharomyces cerevisiae* yeast strain) and any suitable swelling agent. In one embodiment, the swelling agent is methyl cellulose or carboxymethyl cellulose.

The compositions described herein may comprise a fermenting organism described herein (e.g., a *Saccharomyces cerevisiae* yeast strain) and any suitable anti-oxidant. In one embodiment, the antioxidant is butylated hydroxyanisol (BHA) and/or butylated hydroxytoluene (BHT), or ascorbic acid (vitamin C), particular for active dry yeast.

Gene Disruptions

The fermenting organisms described herein may also comprise one or more (e.g., two, several) gene disruptions, e.g., to divert sugar metabolism from undesired products to ethanol. In some aspects, the recombinant host cells produce a greater amount of ethanol compared to the cell without the one or more disruptions when cultivated under identical conditions. In some aspects, one or more of the disrupted endogenous genes is inactivated.

In certain embodiments, the fermenting organism provided herein comprises a disruption of one or more endogenous genes encoding enzymes involved in producing alternate fermentative products such as glycerol or other byproducts such as acetate or diols. For example, the cells provided herein may comprise a disruption of one or more of glycerol 3-phosphate dehydrogenase (GPD, catalyzes reaction of dihydroxyacetone phosphate to glycerol 3-phosphate), glycerol 3-phosphatase (GPP, catalyzes conversion of glycerol-3 phosphate to glycerol), glycerol kinase (catalyzes conversion of glycerol 3-phosphate to glycerol), dihydroxyacetone kinase (catalyzes conversion of dihydroxyacetone phosphate to dihydroxyacetone), glycerol dehydrogenase (catalyzes conversion of dihydroxyacetone to glycerol), and aldehyde dehydrogenase (ALD, e.g., converts acetaldehyde to acetate).

Modeling analysis can be used to design gene disruptions that additionally optimize utilization of the pathway. One exemplary computational method for identifying and designing metabolic alterations favoring biosynthesis of a desired product is the OptKnock computational framework, Burgard *et al.*, 2003, *Biotechnol. Bioeng.* 84: 647-657.

The fermenting organisms comprising a gene disruption may be constructed using methods well known in the art, including those methods described herein. A portion of the gene can be disrupted such as the coding region or a control sequence required for expression of the coding region. Such a control sequence of the gene may be a promoter sequence or a functional part thereof, *i.e.*, a part that is sufficient for affecting expression of the gene. For example, a promoter sequence may be inactivated resulting in no expression or a weaker promoter may be substituted for the native promoter sequence to reduce expression of the coding sequence. Other control sequences for possible modification include, but are not limited to, a leader, propeptide sequence, signal sequence, transcription terminator, and transcriptional activator.

The fermenting organisms comprising a gene disruption may be constructed by gene deletion techniques to eliminate or reduce expression of the gene. Gene deletion techniques enable the partial or complete removal of the gene thereby eliminating their expression. In such methods, deletion of the gene is accomplished by homologous recombination using a plasmid that has been constructed to contiguously contain the 5' and 3' regions flanking the gene.

The fermenting organisms comprising a gene disruption may also be constructed by introducing, substituting, and/or removing one or more (e.g., two, several) nucleotides in the gene or a control sequence thereof required for the transcription or translation thereof. For example, nucleotides may be inserted or removed for the introduction of a stop codon, the removal of the start codon, or a frame-shift of the open reading frame. Such a modification may be accomplished by site-directed mutagenesis or PCR generated mutagenesis in accordance with methods known in the art. See, for example, Botstein and Shortle, 1985, *Science* 229: 4719; Lo *et al.*, 1985, *Proc. Natl. Acad. Sci. U.S.A.* 81: 2285; Higuchi *et al.*, 1988, *Nucleic Acids Res* 16: 7351; Shimada, 1996, *Meth. Mol. Biol.* 57: 157; Ho *et al.*, 1989, *Gene* 77: 61; Horton *et al.*, 1989, *Gene* 77: 61; and Sarkar and Sommer, 1990, *BioTechniques* 8: 404.

The fermenting organisms comprising a gene disruption may also be constructed by inserting into the gene a disruptive nucleic acid construct comprising a nucleic acid fragment homologous to the gene that will create a duplication of the region of homology and incorporate construct DNA between the duplicated regions. Such a gene disruption can eliminate gene expression if the inserted construct separates the promoter of the gene from the coding region or interrupts the coding sequence such that a non-functional gene product results. A disrupting construct may be simply a selectable marker gene accompanied by 5' and 3' regions homologous to the gene. The selectable marker enables identification of transformants containing the disrupted gene.

The fermenting organisms comprising a gene disruption may also be constructed by the process of gene conversion (see, for example, Iglesias and Trautner, 1983, *Molecular General Genetics* 189: 73-76). For example, in the gene conversion method, a nucleotide sequence corresponding to the gene is mutagenized *in vitro* to produce a defective nucleotide sequence, which is then transformed into the recombinant strain to produce a defective gene. By homologous recombination, the defective nucleotide sequence replaces the endogenous gene. It may be desirable that the defective nucleotide sequence also comprises a marker for selection of transformants containing the defective gene.

The fermenting organisms comprising a gene disruption may be further constructed by random or specific mutagenesis using methods well known in the art, including, but not limited to, chemical mutagenesis (see, for example, Hopwood, *The Isolation of Mutants* in *Methods in Microbiology* (J.R. Norris and D.W. Ribbons, eds.) pp. 363-433, Academic Press, New York, 1970). Modification of the gene may be performed by subjecting the parent strain to mutagenesis and screening for mutant strains in which expression of the gene has been reduced or inactivated. The mutagenesis, which may be specific or random, may be performed, for example, by use of a suitable physical or chemical mutagenizing agent, use of a suitable oligonucleotide, or subjecting the DNA sequence to PCR generated mutagenesis. Furthermore, the mutagenesis may be performed by use of any combination of these mutagenizing methods.

Examples of a physical or chemical mutagenizing agent suitable for the present purpose include ultraviolet (UV) irradiation, hydroxylamine, N-methyl-N'-nitro-N-nitrosoguanidine (MNNG), N-methyl-N’-nitrosogaunidine (NTG) O-methyl hydroxylamine, nitrous acid, ethyl methane sulphonate (EMS), sodium bisulphite, formic acid, and nucleotide analogues. When such agents are used, the mutagenesis is typically performed by incubating the parent strain to be mutagenized in the presence of the mutagenizing agent of choice under suitable conditions, and selecting for mutants exhibiting reduced or no expression of the gene.

A nucleotide sequence homologous or complementary to a gene described herein may be used from other microbial sources to disrupt the corresponding gene in a recombinant strain of choice.

In one aspect, the modification of a gene in the recombinant cell is unmarked with a selectable marker. Removal of the selectable marker gene may be accomplished by culturing the mutants on a counter-selection medium. Where the selectable marker gene contains repeats flanking its 5' and 3' ends, the repeats will facilitate the looping out of the selectable marker gene by homologous recombination when the mutant strain is submitted to counter-selection. The selectable marker gene may also be removed by homologous recombination by introducing into the mutant strain a nucleic acid fragment comprising 5' and 3' regions of the defective gene, but lacking the selectable marker gene, followed by selecting on the counter-selection medium. By homologous recombination, the defective gene containing the selectable marker gene is replaced with the nucleic acid fragment lacking the selectable marker gene. Other methods known in the art may also be used.

Methods using a Starch-Containing Material

In some aspects, the methods described herein produce a fermentation product from a starch-containing material. Starch-containing material is well-known in the art, contining two typs of homopolysaccharides (amylose and amylopectin) and is linked by alpha-(1-4)-D-glycosidic bonds. Any suitable starch-containing starting material may be used. The starting material is generally selected based on the desired fermentation product, such as ethanol. Examples of starch-containing starting materials include cereal, tubers or grains. Specifically, the starch-containing material may be corn, wheat, barley, rye, milo, sago, cassava, tapioca, sorghum, oat, rice, peas, beans, or sweet potatoes, or mixtures thereof. Contemplated are also waxy and non-waxy types of corn and barley.

In one embodiment, the starch-containing starting material is corn. In one embodiment, the starch-containing starting material is wheat. In one embodiment, the starch-containing starting material is barley. In one embodiment, the starch-containing starting material is rye. In one embodiment, the starch-containing starting material is milo. In one embodiment, the starch-containing starting material is sago. In one embodiment, the starch-containing starting material is cassava. In one embodiment, the starch-containing starting material is tapioca. In one embodiment, the starch-containing starting material is sorghum. In one embodiment, the starch-containing starting material is rice. In one embodiment, the starch-containing starting material is peas. In one embodiment, the starch-containing starting material is beans. In one embodiment, the starch-containing starting material is sweet potatoes. In one embodiment, the starch-containing starting material is oats.

The methods using a starch-containing material may include a conventional process (e.g., including a liquefaction step described in more detail below) or a raw starch hydrolysis process. In some embodiments using a starch-containing material, saccarification of the starch-containing material is at a temperature above the initial gelatinization temperature. In some embodiments using a starch-containing material, saccarification of the starch-containing material is at a temperature below the initial gelatinization temperature.

Liquefaction

In aspects using a starch-containing material, the methods may further comprise a liquefaction step carried out by subjecting the starch-containing material at a temperature above the initial gelatinization temperature to an alpha-amylase and optionally a protease and/or a glucoamylase. Other enzymes such as a pullulanase and phytase may also be present and/or added in liquefaction. In some embodiments, the liquefaction step is carried out prior to steps a) and b) of the described methods.

Liquefaction step may be carried out for 0.5-5 hours, such as 1-3 hours, such as typically about 2 hours.

The term “initial gelatinization temperature” means the lowest temperature at which gelatinization of the starch-containing material commences. In general, starch heated in water begins to gelatinize between about 50°C and 75°C; the exact temperature of gelatinization depends on the specific starch and can readily be determined by the skilled artisan. Thus, the initial gelatinization temperature may vary according to the plant species, to the particular variety of the plant species as well as with the growth conditions. The initial gelatinization temperature of a given starch-containing material may be determined as the temperature at which birefringence is lost in 5% of the starch granules using the method described by Gorinstein and Lii, 1992, *Starch/Stärke* 44(12): 461-466.

Liquefaction is typically carried out at a temperature in the range from 70-100ºC. In one embodiment, the temperature in liquefaction is between 75-95°C, such as between 75-90°C, between 80-90°C, or between 82-88°C, such as about 85ºC.

A jet-cooking step may be carried out prior to liquefaction in step, for example, at a temperature between 110-145°C, 120-140ºC, 125-135°C, or about 130ºC for about 1-15 minutes, for about 3-10 minutes, or about 5 minutes.

The pH during liquefaction may be between 4 and 7, such as pH 4.5-6.5, pH 5.0-6.5, pH 5.0-6.0, pH 5.2-6.2, or about 5.2, about 5.4, about 5.6, or about 5.8.

In one embodiment, the process further comprises, prior to liquefaction, the steps of:

i) reducing the particle size of the starch-containing material, preferably by dry milling;

ii) forming a slurry comprising the starch-containing material and water.

The starch-containing starting material, such as whole grains, may be reduced in particle size, e.g., by milling, in order to open up the structure, to increase surface area, and allowing for further processing. Generally, there are two types of processes: wet and dry milling. In dry milling whole kernels are milled and used. Wet milling gives a good separation of germ and meal (starch granules and protein). Wet milling is often applied at locations where the starch hydrolysate is used in production of, e.g., syrups. Both dry milling and wet milling are well known in the art of starch processing. In one embodiment the starch-containing material is subjected to dry milling. In one embodiment, the particle size is reduced to between 0.05 to 3.0 mm, e.g., 0.1-0.5 mm, or so that at least 30%, at least 50%, at least 70%, or at least 90% of the starch-containing material fit through a sieve with a 0.05 to 3.0 mm screen, e.g., 0.1-0.5 mm screen. In another embodiment, at least 50%, e.g., at least 70%, at least 80%, or at least 90% of the starch-containing material fit through a sieve with # 6 screen.

The aqueous slurry may contain from 10-55 w/w-% dry solids (DS), e.g., 25-45 w/w-% dry solids (DS), or 30-40 w/w-% dry solids (DS) of starch-containing material.

The alpha-amylase, optionally a protease, and optionally a glucoamylase may initially be added to the aqueous slurry to initiate liquefaction (thinning). In one embodiment, only a portion of the enzymes (e.g., about 1/3) is added to the aqueous slurry, while the rest of the enzymes (e.g., about 2/3) are added during liquefaction step.

A non-exhaustive list of alpha-amylases used in liquefaction can be found below in the "Alpha-Amylases" section. Examples of suitable proteases used in liquefaction include any protease described *supra* in the "Proteases" section. Examples of suitable glucoamylases used in liquefaction include any glucoamylase found in the "Glucoamylases" section.

Saccharification and Fermentation of Starch-containing material

In aspects using a starch-containing material, a glucoamylase may be present and/or added in saccharification step a) and/or fermentation step b) or simultaneous saccharification and fermentation (SSF). The glucoamylase of the saccharification step a) and/or fermentation step b) or simultaneous saccharification and fermentation (SSF) is typically different from the glucoamylase optionally added to any liquefaction step described *supra*. In one embodiment, the glucoamylase is present and/or added together with a fungal alpha-amylase.

In some aspects, the fermenting organism comprises a heterologous polynucleotide encoding a glucoamylase, for example, as described in WO2017/087330, the content of which is hereby incorporated by reference.

Examples of glucoamylases can be found in the "Glucoamylases" section below.

When doing sequential saccharification and fermentation, saccharification step a) may be carried out under conditions well-known in the art. For instance, saccharification step a) may last up to from about 24 to about 72 hours. In one embodiment, pre-saccharification is done. Pre-saccharification is typically done for 40-90 minutes at a temperature between 30-65ºC, typically about 60ºC. Pre-saccharification is, in one embodiment, followed by saccharification during fermentation in simultaneous saccharification and fermentation (SSF). Saccharification is typically carried out at temperatures from 20-75ºC, preferably from 40-70ºC, typically about 60ºC, and typically at a pH between 4 and 5, such as about pH 4.5.

Fermentation is carried out in a fermentation medium, as known in the art and, e.g., as described herein. The fermentation medium includes the fermentation substrate, that is, the carbohydrate source that is metabolized by the fermenting organism. With the processes described herein, the fermentation medium may comprise nutrients and growth stimulator(s) for the fermenting organism(s). Nutrient and growth stimulators are widely used in the art of fermentation and include nitrogen sources, such as ammonia; urea, vitamins and minerals, or combinations thereof.

Generally, fermenting organisms such as yeast, including *Saccharomyces cerevisiae* yeast, require an adequate source of nitrogen for propagation and fermentation. Many sources of supplemental nitrogen, if necessary, can be used and such sources of nitrogen are well known in the art. The nitrogen source may be organic, such as urea, DDGs, wet cake or corn mash, or inorganic, such as ammonia or ammonium hydroxide. In one embodiment, the nitrogen source is urea.

Fermentation can be carried out under low nitrogen conditions, e.g., when using a protease-expressing yeast. In some embodiments, the fermentation step is conducted with less than 1000 ppm supplemental nitrogen (e.g., urea or ammonium hydroxide), such as less than 750 ppm, less than 500 ppm, less than 400 ppm, less than 300 ppm, less than 250 ppm, less than 200 ppm, less than 150 ppm, less than 100 ppm, less than 75 ppm, less than 50 ppm, less than 25 ppm, or less than 10 ppm, supplemental nitrogen. In some embodiments, the fermentation step is conducted with no supplemental nitrogen.

Simultaneous saccharification and fermentation (“SSF”) is widely used in industrial scale fermentation product production processes, especially ethanol production processes. When doing SSF the saccharification step a) and the fermentation step b) are carried out simultaneously. There is no holding stage for the saccharification, meaning that a fermenting organism, such as yeast, and enzyme(s), may be added together. However, it is also contemplated to add the fermenting organism and enzyme(s) separately. SSF is typically carried out at a temperature from 25°C to 40°C, such as from 28°C to 35°C, such as from 30°C to 34°C, or about 32°C. In one embodiment, fermentation is ongoing for 6 to 120 hours, in particular 24 to 96 hours. In one embodiment, the pH is between 4-5.

In one embodiment, a cellulolytic enzyme composition is present and/or added in saccharification, fermentation or simultaneous saccharification and fermentation (SSF). Examples of such cellulolytic enzyme compositions can be found in the “Cellulolytic Enzymes and Compositions” section below. The cellulolytic enzyme composition may be present and/or added together with a glucoamylase, such as one disclosed in the “Glucoamylases” section below.

Phospholipases

The expressed phospholipase may be any phospholipase that is suitable for the host cells and/or the methods described herein, such as a naturally occurring phospholipase (e.g., a native phospholipase from another species or an endogenous phospholipase expressed from a modified expression vector) or a variant thereof that retains phospholipase activity.

In some embodiments, the fermenting organism comprises a heterologous polynucleotide encoding a phospholipase, for example, as described in WO2018/075430, the content of which is hereby incorporated by reference. In some embodiments, the phospholipase is classified as a phospholipase A. In other embodiemts, the phospholipase is classified as a phospholipase C. Any phospholipase described or referenced herein is contemplated for expression in the fermenting organism.

In some embodiments, the fermenting organism comprising a heterologous polynucleotide encoding a phosphorlipase has an increased level of phosphorlipase activity compared to the host cells without the heterologous polynucleotide encoding the phosphorlipase, when cultivated under the same conditions. In some embodiments, the fermenting organism has an increased level of phospholipase activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the fermenting organism without the heterologous polynucleotide encoding the phospholipase, when cultivated under the same conditions.

Exemplary phospholipases that can be used with the host cells and/or the methods described herein include bacterial, yeast, or filamentous fungal phospholipases, e.g., derived from any of the microorganisms described or referenced herein.

Additional phospholipases that may be expressed with the fermenting organisms and used with the methods described herein are described in the examples, and include, but are not limited to phospholipases shown in Table 1 (or derivatives thereof).

Table 1.

Donor Organism (catalytic domain)	**SEQ ID NO: (mature polypeptide)**
Thermomyces lanuginosus	235
Talaromyces leycettanus	236
Penicillium emersonii	237
Bacillus thuringiensis	238
Pseudomonas sp.	239
Kionochaeta sp.	240
Mariannaea pinicola	241

Fictibacillus macauensis	242
Aspergillus wentii	252
Penicillium cylindrosporum	253
Penicillium meridianum	254
Penicillium bialowiezense	255
Penicillium sclerotiorum	256
Rasamsonia byssochlamydoides	257
Rasamsonia eburnea	258
Penicillium brefeldianum	259
Penicillium adametzii	260
Rasamsonia brevistipitata	261
Penicillium scabrosum	262
Penicillium manginii	263
Penicillium emersonii	264
Rasamsonia argillacea	265
Penicillium parviverrucosum	266
Penicillium flavescens	267
Penicillium hispanicum	268
Penicillium simplicissimum	269
Penicillium vasconiae	270
Talaromyces columbinus	271
Talaromyces variabilis	272
Talaromyces rugulosus	273
Hamigera terricola	274
Penicillium piscarium	275
Talaromyces bacillisporus	276
Galactomyces candidus	277
Penicillium megasporum	278
Penicillium jensenii	279
Aspergillus stramenius	280
Bacillus pseudomycoides	281
Bacillus mycoides	282
Bacillus thuringiensis	283
Listeria innocua	284
Aspergillus egyptiacus	285
Aspergillus tamarii	286
Aspergillus niger	287
Bacillus luciferensis	288
Bacillus mycoides	289
Bacillus mycoides	290
Bacillus sp.	291

Bacillus drentensis	292
Aspergillus turcosus	293
Talaromyces subinflatus	294
Aspergillus tubingensis	295
Bacillus acidiceler	296
Lysinibacillus xylanilyticus	297
Bacillus toyonensis	298
Bacillus wiedmannii	299
Listeria seeligeri	300
Penicillium swiecickii	301
Talaromyces boninensis	302
Hamigera striata	303
Bacillus sp.	304
Bacillus thuringiensis	305
Bacillus mycoides	306
Fictibacillus macauensis	307
Listeria seeligeri	308
Penicillium donkii	309
Hamigera paravellanea	310
Talaromyces lecycettanus	311
Paenibacillus sp.	312
Bacillus toyonensis	313
Bacillus thuringiensis	314
Bacillus thuringiensis	315
Talaromyces rugulosus	316
Penicillium sp.	317
Hamigera avellanea	318
Penicillium spikei	319
Paenibacillus alginolyticus	320
Bacillus mycoides	321
Bacillus bingmayongensis	322
Bacillus mycoides	323
Brevibacillus sp.	324
Penicillium vasconiae	325
Talaromyces diversus	326
Aspergillus wentii	327
Bacillus acidiceler	328
Bacillus luti	329
Bacillus pseudomycoides	330
Bacillus mycoides	331
Penicillium cinnamopurpureum	332

Talaromyces verruculosus	333
Talaromyces cellulolyticus	334
Penicillium megasporum	335
Bacillus toyonensis	336
Bacillus sp.	337
Bacillus manliponensis	338
Penicillium simplicissimum	339
Penicillium arenicola	340
Aspergillus aculeatus	341
Bacillus acidiceler	342

Additional phospholipases contemplated for use with the present invention can be found in WO2018/075430 (the content of which is incorporated herein).

Additional polynucleotides encoding suitable phospholipases may be obtained from microorganisms of any genus, including those readily available within the UniProtKB database (www.uniprot.org).

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

In one embodiment, the phospholipase is derived from *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus lautus*, *Bacillus lentus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, or *Bacillus thuringiensis*.

In another embodiment, the phospholipase is derived from *Streptococcus equisimilis*, *Streptococcus pyogenes*, *Streptococcus uberis*, or *Streptococcus equi* subsp. *Zooepidemicus*.

In another embodiment, the phospholipase is derived from *Streptomyces achromogenes*, *Streptomyces avermitilis*, *Streptomyces coelicolor*, *Streptomyces griseus*, or *Streptomyces lividans*.

The phospholipase may be a fungal phospholipase. For example, the phospholipase may be derived from a yeast such as a *Candida*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, *Yarrowia* or *Issatchenkia*; or derived from a filamentous fungus such as an *Acremonium*, *Agaricus*, *Alternaria*, *Aspergillus*, *Aureobasidium*, *Botryospaeria*, *Ceriporiopsis*, *Chaetomidium*, *Chrysosporium*, *Claviceps*, *Cochliobolus*, *Coprinopsis*, *Coptotermes*, *Corynascus*, *Cryphonectria*, *Cryptococcus*, *Diplodia*, *Exidia*, *Filibasidium*, *Fusarium*, *Gibberella*, *Holomastigotoides*, *Humicola*, *Irpex*, *Lentinula*, *Leptospaeria*, *Magnaporthe*, *Melanocarpus*, *Meripilus*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Piromyces*, *Poitrasia*, *Pseudoplectania*, *Pseudotrichonympha*, *Rhizomucor*, *Schizophyllum*, *Scytalidium*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, *Trichoderma*, *Trichophaea*, *Verticillium*, *Volvariella*, or *Xylaria*.

In another embodiment, the phospholipase is derived from *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis*, or *Saccharomyces oviformis*.

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

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

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

The phospholipase coding sequences described or referenced herein, or a subsequence thereof, as well as the phospholipases described or referenced herein, or a fragment thereof, may be used to design nucleic acid probes to identify and clone DNA encoding a phospholipase from strains of different genera or species according to methods well known in the art. In particular, such probes can be used for hybridization with the genomic DNA or cDNA of a cell of interest, following standard Southern blotting procedures, in order to identify and isolate the corresponding gene therein. Such probes can be considerably shorter than the entire sequence, but should be at least 15, e.g., at least 25, at least 35, or at least 70 nucleotides in length. Preferably, the nucleic acid probe is at least 100 nucleotides in length, e.g., at least 200 nucleotides, at least 300 nucleotides, at least 400 nucleotides, at least 500 nucleotides, at least 600 nucleotides, at least 700 nucleotides, at least 800 nucleotides, or at least 900 nucleotides in length. Both DNA and RNA probes can be used. The probes are typically labeled for detecting the corresponding gene (for example, with ^{32}P, ^{3}H, ^{35}S, biotin, or avidin).

A genomic DNA or cDNA library prepared from such other strains may be screened for DNA that hybridizes with the probes described above and encodes a parent. Genomic or other DNA from such other strains may be separated by agarose or polyacrylamide gel electrophoresis, or other separation techniques. DNA from the libraries or the separated DNA may be transferred to and immobilized on nitrocellulose or other suitable carrier material. In order to identify a clone or DNA that hybridizes with a coding sequence, or a subsequence thereof, the carrier material is used in a Southern blot.

In one embodiment, the nucleic acid probe is a polynucleotide, or subsequence thereof, that encodes the phospholipase of any one of SEQ ID NOs: 235-242 and 252-342 (such as the coding sequence of SEQ ID NOs: 244-251 and 343-433, respectively), or a fragment thereof.

In one embodiment, the nucleic acid probe is a polynucleotide, or subsequence thereof, that encodes the phospholipase of any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242 (such as the coding sequence of SEQ ID NO: 244, 245, 246, 247, 248, 249, 250 or 251, respectively), or a fragment thereof.

For purposes of the probes described above, hybridization indicates that the polynucleotide hybridizes to a labeled nucleic acid probe, or the full-length complementary strand thereof, or a subsequence of the foregoing; under very low to very high stringency conditions. Molecules to which the nucleic acid probe hybridizes under these conditions can be detected using, for example, X-ray film. Stringency and washing conditions are defined as described *supra*.

In one embodiment, the phospholipase is encoded by a polynucleotide that hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence for any one of the phospholipases described or referenced herein (e.g., the coding sequence that encodes any one of SEQ ID NOs: 235-242 and 252-342; such as the corresponding coding sequence of SEQ ID NO: 244-251 or 343-433, respectively, or the coding sequence that encodes any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242; such as the corresponding coding sequence of SEQ ID NO: 244, 245, 246, 247, 248, 249, 250 or 251, respectively). (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York).

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

Once a polynucleotide encoding a phospholipase has been detected with a suitable probe as described herein, the sequence may be isolated or cloned by utilizing techniques that are known to those of ordinary skill in the art (see, e.g., Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). Techniques used to isolate or clone polynucleotides encoding alpha-amylases include isolation from genomic DNA, preparation from cDNA, or a combination thereof. The cloning of the polynucleotides from such genomic DNA can be effected, e.g., by using the well-known polymerase chain reaction (PCR) or antibody screening of expression libraries to detect cloned DNA fragments with shares structural features. See, e.g., Innis et al., 1990, *PCR: A Guide to Methods and Application*, Academic Press, New York. Other nucleic acid amplification procedures such as ligase chain reaction (LCR), ligated activated transcription (LAT) and nucleotide sequence-based amplification (NASBA) may be used.

In one embodiment, the phospholipase has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any one of the phospholipases described or referenced herein (e.g., any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242). In another embodiment, the phospholipase has a mature polypeptide sequence that is a fragment of the any one of the phospholipases described or referenced herein (e.g., any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242). In one embodiment, the number of amino acid residues in the fragment is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of amino acid residues in referenced full length phospholipase (e.g., any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242). In other embodiments, the phospholipase may comprise the catalytic domain of any phospholipase described or referenced herein (e.g., the catalytic domain of any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242).

The phospholipase may be a variant of any one of the phospholipases described *supra* (e.g., any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242). In one embodiment, the phospholipase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to any one of the phospholipases described *supra* (e.g., any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242).

In one embodiment, the phospholipase has a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of the phospholipases described *supra* (e.g., any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242). In one embodiment, the phospholipase has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) of amino acid sequence of any one of the phospholipases described *supra* (e.g., any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242). In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

The amino acid changes are generally of a minor nature, that is conservative amino acid substitutions or insertions that do not significantly affect the folding and/or activity of the protein; small deletions, typically of one to about 30 amino acids; small amino-terminal or carboxyl-terminal extensions, such as an amino-terminal methionine residue; a small linker peptide of up to about 20-25 residues; or a small extension that facilitates purification by changing net charge or another function, such as a poly-histidine tract, an antigenic epitope or a binding domain.

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

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

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

Additional guidance on the structure-activity relationship of the polypeptides herein can be determined using multiple sequence alignment (MSA) techniques well-known in the art. Based on the teachings herein, the skilled artisan could make similar alignments with any number of phospholipases described herein or known in the art. Such alignments aid the skilled artisan to determine potentially relevant domains (e.g., binding domains or catalytic domains), as well as which amino acid residues are conserved and not conserved among the different alpha-amylase sequences. It is appreciated in the art that changing an amino acid that is conserved at a particular position between disclosed polypeptides will more likely result in a change in biological activity (Bowie *et al.*, 1990, *Science* 247: 1306-1310: “Residues that are directly involved in protein functions such as binding or catalysis will certainly be among the most conserved”). In contrast, substituting an amino acid that is not highly conserved among the polypeptides will not likely or significantly alter the biological activity.

Even further guidance on the structure-activity relationship for the skilled artisan can be found in published x-ray crystallography studies known in the art.

Single or multiple amino acid substitutions, deletions, and/or insertions can be made and tested using known methods of mutagenesis, recombination, and/or shuffling, followed by a relevant screening procedure, such as those disclosed by Reidhaar-Olson and Sauer, 1988, *Science* 241: 53-57; Bowie and Sauer, 1989, *Proc. Natl. Acad. Sci. USA* 86: 2152-2156; WO 95/17413; or WO 95/22625. Other methods that can be used include error-prone PCR, phage display (e.g., Lowman *et al.*, 1991, *Biochemistry* 30: 10832-10837; U.S. Patent No. 5,223,409; WO 92/06204), and region-directed mutagenesis (Derbyshire *et al.*, 1986, *Gene* 46: 145; Ner *et al.*, 1988, *DNA* 7: 127).

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

In some embodiments, the phospholipase has at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of the phospholipase activity of any phospholipase described or referenced herein (e.g., any one of SEQ ID NOs: 235-242 and 252-342, such as any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242) under the same conditions.

In one embodiment, the phospholipase coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any phospholipase described or referenced herein (e.g., a coding sequence for the phospholipase of any one of SEQ ID NOs: 235-242 and 252-342; such as the corresponding coding sequence of SEQ ID NO: 244-251 or 343-433, respectively; or the phospholipase of any one of SEQ ID NO: 235, 236, 237, 238, 239, 240, 241 or 242; such as the corresponding coding sequence of SEQ ID NO: 244, 245, 246, 247, 248, 249, 250 or 251, respectively). In one embodiment, the phospholipase coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any phospholipase described or referenced herein (e.g., a coding sequence for the phospholipase of any one of SEQ

ID NOs: 235-242 and 252-342; such as the corresponding coding sequence of SEQ ID NO: 244-251 or 343-433, respectively; or the phospholipase of any one of SEQ ID NO: 235, 236, 237, 238, 239, 240, 241 or 242; such as the corresponding coding sequence of SEQ ID NO: 244, 245, 246, 247, 248, 249, 250 or 251, respectively).

In one embodiment, the phospholipase comprises the coding sequence of any phospholipase described or referenced herein (e.g., a coding sequence for the phospholipase of any one of SEQ ID NOs: 235-242 and 252-342; such as the corresponding coding sequence of SEQ ID NO: 244-251 or 343-433, respectively; or the phospholipase of any one of SEQ ID NO: 235, 236, 237, 238, 239, 240, 241 or 242; such as the corresponding coding sequence of SEQ ID NO: 244, 245, 246, 247, 248, 249, 250 or 251, respectively). In one embodiment, the phospholipase comprises a coding sequence that is a subsequence of the coding sequence from any phospholipase described or referenced herein, wherein the subsequence encodes a polypeptide having phospholipase activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The referenced coding sequence of any related aspect or embodiment described herein can be the native coding sequence or a degenerate sequence, such as a codon-optimized coding sequence designed for use in a particular host cell (e.g., optimized for expression in *Saccharomyces cerevisiae*).

The phospholipase may be a fused polypeptide or cleavable fusion polypeptide in which another polypeptide is fused at the N-terminus or the C-terminus of the alpha-amylase. A fused polypeptide may be produced by fusing a polynucleotide encoding another polypeptide to a polynucleotide encoding the phospholipase. Techniques for producing fusion polypeptides are known in the art, and include ligating the coding sequences encoding the polypeptides so that they are in frame and that expression of the fused polypeptide is under control of the same promoter(s) and terminator. Fusion proteins may also be constructed using intein technology in which fusions are created post-translationally (Cooper *et al.*, 1993, *EMBO J.* 12: 2575-2583; Dawson *et al.*, 1994, *Science* 266: 776-779).

Alpha-Amylases

The expressed and/or exogenous alpha-amylase may be any alpha-amylase that is suitable for the host cells and/or the methods described herein, such as a naturally occurring alpha-amylase (e.g., a native alpha-amylase from another species or an endogenous alpha-amylase expressed from a modified expression vector) or a variant thereof that retains alpha-amylase activity. Any alpha-amylase contemplated for expression by a fermenting organism described below is also contemplated for aspects of the invention involving exogenous addition of an alpha-amylase.

In some embodiments, the fermenting organism comprises a heterologous polynucleotide encoding an alpha-amylase, for example, as described in WO2017/087330, the content of which is hereby incorporated by reference. Any alpha-amylase described or referenced herein is contemplated for expression in the fermenting organism.

In some embodiments, the fermenting organism comprising a heterologous polynucleotide encoding an alpha-amylase has an increased level of alpha-amylase activity compared to the host cells without the heterologous polynucleotide encoding the alpha-amylase, when cultivated under the same conditions. In some embodiments, the fermenting organism has an increased level of alpha-amylase activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the fermenting organism without the heterologous polynucleotide encoding the alpha-amylase, when cultivated under the same conditions.

Exemplary alpha-amylases that can be used with the host cells and/or the methods described herein include bacterial, yeast, or filamentous fungal alpha-amylases, e.g., derived from any of the microorganisms described or referenced herein.

The term “bacterial alpha-amylase” means any bacterial alpha-amylase classified under EC 3.2.1.1. A bacterial alpha-amylase used herein may, e.g., be derived from a strain of the genus *Bacillus*, which is sometimes also referred to as the genus *Geobacillus*. In one embodiment, the *Bacillus* alpha-amylase is derived from a strain of *Bacillus amyloliquefaciens*, *Bacillus licheniformis*, *Bacillus stearothermophilus*, or *Bacillus subtilis*, but may also be derived from other *Bacillus* sp.

Specific examples of bacterial alpha-amylases include the *Bacillus stearothermophilus* alpha-amylase (BSG) of SEQ ID NO: 3 in WO 99/19467, the *Bacillus amyloliquefaciens* alpha-amylase (BAN) of SEQ ID NO: 5 in WO 99/19467, and the *Bacillus licheniformis* alpha-amylase (BLA) of SEQ ID NO: 4 in WO 99/19467 (all sequences are hereby incorporated by reference). In one embodiment, the alpha-amylase may be an enzyme having a mature polypeptide sequence with a degree of identity of at least 60%, e.g., at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99% to any of the sequences shown in SEQ ID NOs: 3, 4 or 5, in WO 99/19467.

In one embodiment, the alpha-amylase is derived from *Bacillus stearothermophilus.* The *Bacillus stearothermophilus* alpha-amylase may be a mature wild-type or a mature variant thereof.

The mature *Bacillus stearothermophilus* alpha-amylases may naturally be truncated during recombinant production. For instance, the *Bacillus stearothermophilus* alpha-amylase may be a truncated at the C-terminal, so that it is from 480-495 amino acids long, such as about 491 amino acids long, e.g., so that it lacks a functional starch binding domain (compared to SEQ ID NO: 3 in WO 99/19467).

The *Bacillus* alpha-amylase may also be a variant and/or hybrid. Examples of such a variant can be found in any of WO 96/23873, WO 96/23874, WO 97/41213, WO 99/19467, WO 00/60059, and WO 02/10355 (each hereby incorporated by reference). Specific alpha-amylase variants are disclosed in U.S. Patent Nos. 6,093,562, 6,187,576, 6,297,038, and 7,713,723 (hereby incorporated by reference) and include *Bacillus stearothermophilus* alpha-amylase (often referred to as BSG alpha-amylase) variants having a deletion of one or two amino acids at positions R179, G180, I181 and/or G182, preferably a double deletion disclosed in WO 96/23873 – see, e.g., page 20, lines 1-10 (hereby incorporated by reference), such as corresponding to deletion of positions I181 and G182 compared to the amino acid sequence of *Bacillus stearothermophilus* alpha-amylase set forth in SEQ ID NO: 3 disclosed in WO 99/19467 or the deletion of amino acids R179 and G180 using SEQ ID NO: 3 in WO 99/19467 for numbering (which reference is hereby incorporated by reference). In some embodimenst, the *Bacillus* alpha-amylases, such as *Bacillus stearothermophilus* alpha-amylases, have a double deletion corresponding to a deletion of positions 181 and 182 and further optionally comprise a N193F substitution (also denoted I181* + G182* + N193F) compared to the wild-type BSG alpha-amylase amino acid sequence set forth in SEQ ID NO: 3 disclosed in WO 99/19467. The bacterial alpha-amylase may also have a substitution in a position corresponding to S239 in the *Bacillus licheniformis* alpha-amylase shown in SEQ ID NO: 4 in WO 99/19467, or a S242 and/or E188P variant of the *Bacillus stearothermophilus* alpha-amylase of SEQ ID NO: 3 in WO 99/19467.

In one embodiment, the variant is a S242A, E or Q variant, e.g., a S242Q variant, of the *Bacillus stearothermophilus* alpha-amylase.

In one embodiment, the variant is a position E188 variant, e.g., E188P variant of the *Bacillus stearothermophilus* alpha-amylase.

The bacterial alpha-amylase may, in one embodiment, be a truncated *Bacillus* alpha-amylase. In one embodiment, the truncation is so that, e.g., the *Bacillus stearothermophilus* alpha-amylase shown in SEQ ID NO: 3 in WO 99/19467, is about 491 amino acids long, such as from 480 to 495 amino acids long, or so it lacks a functional starch bind domain.

The bacterial alpha-amylase may also be a hybrid bacterial alpha-amylase, e.g., an alpha-amylase comprising 445 C-terminal amino acid residues of the *Bacillus licheniformis* alpha-amylase (shown in SEQ ID NO: 4 of WO 99/19467) and the 37 N-terminal amino acid residues of the alpha-amylase derived from *Bacillus amyloliquefaciens* (shown in SEQ ID NO: 5 of WO 99/19467). In one embodiment, this hybrid has one or more, especially all, of the following substitutions: G48A+T49I+G107A+H156Y+A181T+N190F+I201F+A209V+Q264S (using the *Bacillus licheniformis* numbering in SEQ ID NO: 4 of WO 99/19467). In some embodiments, the variants have one or more of the following mutations (or corresponding mutations in other *Bacillus* alpha-amylases): H154Y, A181T, N190F, A209V and Q264S and/or the deletion of two residues between positions 176 and 179, e.g., deletion of E178 and G179 (using SEQ ID NO: 5 of WO 99/19467 for position numbering).

In one embodiment, the bacterial alpha-amylase is the mature part of the chimeric alpha-amylase disclosed in Richardson et al. (2002), The Journal of Biological Chemistry, Vol. 277, No 29, Issue 19 July, pp. 267501-26507, referred to as BD5088 or a variant thereof. This alpha-amylase is the same as the one shown in SEQ ID NO: 2 in WO 2007/134207. The mature enzyme sequence starts after the initial “Met” amino acid in position 1.

The alpha-amylase may be a thermostable alpha-amylase, such as a thermostable bacterial alpha-amylase, e.g., from *Bacillus stearothermophilus*. In one embodiment, the alpha-amylase used in a process described herein has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$ of at least 10 determined as described in Example 1 of WO2018/098381.

In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, of at least 15. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, of as at least 20. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, of as at least 25. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, of as at least 30. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, of as at least 40.

In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, of at least 50. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, of at least 60. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, between 10-70. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, between 15-70. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, between 20-70. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, between 25-70. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, between 30-70. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, between 40-70. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, between 50-70. In one embodiment, the thermostable alpha-amylase has a T½ (min) at pH 4.5, 85°C, 0.12 mM $CaCl_2$, between 60-70.

In one embodiment, the alpha-amylase is a bacterial alpha-amylase, e.g., derived from the genus *Bacillus*, such as a strain of *Bacillus stearothermophilus,* e.g., the *Bacillus stearothermophilus* as disclosed in WO 99/019467 as SEQ ID NO: 3 with one or two amino acids deleted at positions R179, G180, I181 and/or G182, in particular with R179 and G180 deleted, or with I181 and G182 deleted, with mutations in below list of mutations.

In some embodiment, the *Bacillus stearothermophilus* alpha-amylases have double deletion I181 + G182, and optional substitution N193F, further comprising one of the following substitutions or combinations of substitutions:

V59A+Q89R+G112D+E129V+K177L+R179E+K220P+N224L+Q254S;
V59A+Q89R+E129V+K177L+R179E+H208Y+K220P+N224L+Q254S;
V59A+Q89R+E129V+K177L+R179E+K220P+N224L+Q254S+D269E+D281N;
V59A+Q89R+E129V+K177L+R179E+K220P+N224L+Q254S+I270L;
V59A+Q89R+E129V+K177L+R179E+K220P+N224L+Q254S+H274K;
V59A+Q89R+E129V+K177L+R179E+K220P+N224L+Q254S+Y276F;
V59A+E129V+R157Y+K177L+R179E+K220P+N224L+S242Q+Q254S;
V59A+E129V+K177L+R179E+H208Y+K220P+N224L+S242Q+Q254S;
V59A+E129V+K177L+R179E+K220P+N224L+S242Q+Q254S;
V59A+E129V+K177L+R179E+K220P+N224L+S242Q+Q254S+H274K;
V59A+E129V+K177L+R179E+K220P+N224L+S242Q+Q254S+Y276F;
V59A+E129V+K177L+R179E+K220P+N224L+S242Q+Q254S+D281N;
V59A+E129V+K177L+R179E+K220P+N224L+S242Q+Q254S+M284T;
V59A+E129V+K177L+R179E+K220P+N224L+S242Q+Q254S+G416V;
V59A+E129V+K177L+R179E+K220P+N224L+Q254S;
V59A+E129V+K177L+R179E+K220P+N224L+Q254S+M284T;
A91L+M96I+E129V+K177L+R179E+K220P+N224L+S242Q+Q254S;
E129V+K177L+R179E;
E129V+K177L+R179E+K220P+N224L+S242Q+Q254S;
E129V+K177L+R179E+K220P+N224L+S242Q+Q254S+Y276F+L427M;
E129V+K177L+R179E+K220P+N224L+S242Q+Q254S+M284T;
E129V+K177L+R179E+K220P+N224L+S242Q+Q254S+N376*+I377*;

E129V+K177L+R179E+K220P+N224L+Q254S;
E129V+K177L+R179E+K220P+N224L+Q254S+M284T;
E129V+K177L+R179E+S242Q;
E129V+K177L+R179V+K220P+N224L+S242Q+Q254S;
K220P+N224L+S242Q+Q254S;
M284V;
V59A+Q89R+ E129V+ K177L+ R179E+ Q254S+ M284V; and
V59A+E129V+K177L+R179E+Q254S+ M284V;

In one embodiment, the alpha-amylase is selected from the group of *Bacillus stearothermophilus* alpha-amylase variants with double deletion I181*+G182*, and optionally substitution N193F, and further one of the following substitutions or combinations of substitutions:

E129V+K177L+R179E;
V59A+Q89R+E129V+K177L+R179E+H208Y+K220P+N224L+Q254S;
V59A+Q89R+ E129V+ K177L+ R179E+ Q254S+ M284V;
V59A+E129V+K177L+R179E+Q254S+ M284V; and
E129V+K177L+R179E+K220P+N224L+S242Q+Q254S (using SEQ ID NO: 1 herein for numbering).

It should be understood that when referring to *Bacillus stearothermophilus* alpha-amylase and variants thereof they are normally produced in truncated form. In particular, the truncation may be so that the *Bacillus stearothermophilus* alpha-amylase shown in SEQ ID NO: 3 in WO 99/19467, or variants thereof, are truncated in the C-terminal and are typically from 480-495 amino acids long, such as about 491 amino acids long, e.g., so that it lacks a functional starch binding domain.

In one embodiment, the alpha-amylase variant may be an enzyme having a mature polypeptide sequence with a degree of identity of at least 60%, e.g., at least 70%, at least 80%, at least 90%, at least 95%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98% or at least 99%, but less than 100% to the sequence shown in SEQ ID NO: 3 in WO 99/19467.

In one embodiment, the bacterial alpha-amylase, e.g., *Bacillus* alpha-amylase, such as especially *Bacillus stearothermophilus* alpha-amylase, or variant thereof, is dosed to liquefaction in a concentration between 0.01-10 KNU-A/g DS, e.g., between 0.02 and 5 KNU-A/g DS, such as 0.03 and 3 KNU-A, preferably 0.04 and 2 KNU-A/g DS, such as especially 0.01 and 2 KNU-A/g DS. In one embodiment, the bacterial alpha-amylase, e.g., *Bacillus* alpha-amylase, such as especially *Bacillus stearothermophilus* alpha-amylases, or variant thereof, is dosed to liquefaction in a concentration of between 0.0001-1 mg EP (Enzyme Protein)/g DS, e.g., 0.0005-0.5 mg EP/g DS, such as 0.001-0.1 mg EP/g DS.

In one embodiment, the bacterial alpha-amylase is derived from the *Bacillus subtilis* alpha-amylase of SEQ ID NO: 76, the *Bacillus subtilis* alpha-amylase of SEQ ID NO: 82, the *Bacillus subtilis* alpha-amylase of SEQ ID NO: 83, the *Bacillus subtilis* alpha-amylase of SEQ ID NO: 84, or the *Bacillus licheniformis* alpha-amylase of SEQ ID NO: 85, the *Clostridium phytofermentans* alpha-amylase of SEQ ID NO: 89, the *Clostridium phytofermentans* alpha-amylase of SEQ ID NO: 90, the *Clostridium phytofermentans* alpha-amylase of SEQ ID NO: 91, the *Clostridium phytofermentans* alpha-amylase of SEQ ID NO: 92, the *Clostridium phytofermentans* alpha-amylase of SEQ ID NO: 93, the *Clostridium phytofermentans* alpha-amylase of SEQ ID NO: 94, the *Clostridium thermocellum* alpha-amylase of SEQ ID NO: 95, the *Thermobifida fusca* alpha-amylase of SEQ ID NO: 96, the *Thermobifida fusca* alpha-amylase of SEQ ID NO: 97, the *Anaerocellum thermophilum* of SEQ ID NO: 98, the *Anaerocellum thermophilum* of SEQ ID NO: 99, the *Anaerocellum thermophilum* of SEQ ID NO: 100, the *Streptomyces avermitilis* of SEQ ID NO: 101, or the *Streptomyces avermitilis* of SEQ ID NO: 88.

In one embodiment, the alpha-amylase is derived from *Bacillus amyloliquefaciens*, such as the *Bacillus amyloliquefaciens* alpha-amylase of SEQ ID NO: 231 (e.g., as described in WO2018/002360, or variants thereof as described in WO2017/037614).

In one embodiment, the alpha-amylase is derived from a yeast alpha-amylase, such as the *Saccharomycopsis fibuligera* alpha-amylase of SEQ ID NO: 77, the *Debaryomyces occidentalis* alpha-amylase of SEQ ID NO: 78, the *Debaryomyces occidentalis* alpha-amylase of SEQ ID NO: 79, the *Lipomyces kononenkoae* alpha-amylase of SEQ ID NO: 80, the *Lipomyces kononenkoae* alpha-amylase of SEQ ID NO: 81.

In one embodiment, the alpha-amylase is derived from a filamentous fungal alpha-amylase, such as the *Aspergillus niger* alpha-amylase of SEQ ID NO: 86, or the *Aspergillus niger* alpha-amylase of SEQ ID NO: 87.

Additional alpha-amylases that may be expressed with the fermenting organisms and used with the methods described herein are described in the examples, and include, but are not limited to alpha-amylases shown in Table 2 (or derivatives thereof).

Table 2.

Donor Organism (catalytic domain)	**SEQ ID NO: (mature polypeptide)**
Rhizomucor pusillus	121
Bacillus licheniformis	122

Aspergillus niger	123
Aspergillus tamarii	124
Acidomyces richmondensis	125
Aspergillus bombycis	126
Alternaria sp	127
Rhizopus microsporus	128
Syncephalastrum racemosum	129
Rhizomucor pusillus	130
Dichotomocladium hesseltinei	131
Lichtheimia ramosa	132
Penicillium aethiopicum	133
Subulispora sp	134
Trichoderma paraviridescens	135
Byssoascus striatosporus	136
Aspergillus brasiliensis	137
Penicillium subspinulosum	138
Penicillium antarcticum	139
Penicillium coprophilum	140
Penicillium olsonii	141
Penicillium vasconiae	142
Penicillium sp	143
Heterocephalum aurantiacum	144
Neosartorya massa	145
Penicillium janthinellum	146
Aspergillus brasiliensis	147
Aspergillus westerdijkiae	148
Hamigera avellanea	149
Hamigera avellanea	150
Meripilus giganteus	151
Cerrena unicolor	152
Physalacria cryptomeriae	153
Lenzites betulinus	154
Trametes ljubarskyi	155
Bacillus subtilis	156
Bacillus subtilis subsp. subtilis	157
Schwanniomyces occidentalis	158
Rhizomucor pusillus	159
Aspergillus niger	160
Bacillus stearothermophilus	161
Bacillus halmapalus	162
Aspergillus oryzae	163

Bacillus amyloliquefaciens	164
Rhizomucor pusillus	165
Kionochaeta ivoriensis	166
Aspergillus niger	167
Aspergillus oryzae	168
Penicillium canescens	169
Acidomyces acidothermus	170
Kinochaeta ivoriensis	171
Aspergillus terreus	172
Thamnidium elegans	173
Meripilus giganteus	174

Additional alpha-amylases contemplated for use with the present invention can be found in WO2011/153516 (the content of which is incorporated herein).

Additional polynucleotides encoding suitable alpha-amylases may be obtained from microorganisms of any genus, including those readily available within the UniProtKB database (www.uniprot.org).

The alpha-amylase coding sequences can also be used to design nucleic acid probes to identify and clone DNA encoding trehalases from strains of different genera or species, as described *supra*.

The polynucleotides encoding alpha-amylases may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc,) as described *supra*.

Techniques used to isolate or clone polynucleotides encoding alpha-amylases are described *supra*.

In one embodiment, the alpha-amylase has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any one of the alpha-amylases described or referenced herein (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231). In another embodiment, the alpha-amylase has a mature polypeptide sequence that is a fragment of the any one of the alpha-amylases described or referenced herein (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231). In one embodiment, the number of amino acid residues in the fragment is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of amino acid residues in referenced full length alpha-amylase (e.g. any one of SEQ ID NOs: 76-101, 121-174 and 231). In other embodiments, the alpha-amylase may comprise the catalytic domain of any alpha-amylase described or referenced herein (e.g., the catalytic domain of any one of SEQ ID NOs: 76-101, 121-174 and 231).

The alpha-amylase may be a variant of any one of the alpha-amylases described *supra* (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231). In one embodiment, the alpha-amylase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to any one of the alpha-amylases described *supra* (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231).

In one embodiment, the alpha-amylase has a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of the alpha-amylases described *supra* (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231). In one embodiment, the alpha-amylase has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) of amino acid sequence of any one of the alpha-amylases described *supra* (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231). In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

In some embodiments, the alpha-amylase has at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of the alpha-amylase activity of any alpha-amylase described or referenced herein (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231) under the same conditions.

In one embodiment, the alpha-amylase coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any alpha-amylase described or referenced herein (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231). In one embodiment, the alpha-amylase coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any alpha-amylase described or referenced herein (e.g., any one of SEQ ID NOs: 76-101, 121-174 and 231).

In one embodiment, the alpha-amylase comprises the coding sequence of any alpha-amylase described or referenced herein (any one of SEQ ID NOs: 76-101, 121-174 and 231). In one embodiment, the alpha-amylase comprises a coding sequence that is a subsequence of the coding sequence from any alpha-amylase described or referenced herein, wherein the subsequence encodes a polypeptide having alpha-amylase activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The referenced coding sequence of any related aspect or embodiment described herein can be the native coding sequence or a degenerate sequence, such as a codon-optimized coding sequence designed for use in a particular host cell (e.g., optimized for expression in *Saccharomyces cerevisiae*).

The alpha-amylase can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

Trehalases

The expressed and/or exogenous trehalase can be any trehalase that is suitable for the fermenting organisms and/or their methods of use described herein, such as a naturally occurring trehalase or a variant thereof that retains trehalase activity. Any trehalase contemplated for expression by a fermenting organism described below is also contemplated for aspects of the invention involving exogenous addition of a trehalase (e.g., added before, during or after liquefaction and/or saccharification).

In some embodiments, the fermenting organism comprising a heterologous polynucleotide encoding a trehalase has an increased level of trehalase activity compared to the host cells without the heterologous polynucleotide encoding the trehalase, when cultivated under the same conditions. In some embodiments, the fermenting organism has an increased level of trehalase activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the fermenting organism without the heterologous polynucleotide encoding the trehalase, when cultivated under the same conditions.

Trehalases that may be expressed with the fermenting organisms and used with the methods described herein include, but are not limited to, trehalases shown in Table 3 (or derivatives thereof).

Table 3.

Donor Organism (catalytic domain)	**SEQ ID NO: (mature polypeptide)**
Chaetomium megalocarpum	175
Lecanicillium psalliotae	176

Doratomyces sp	177
Mucor moelleri	178
Phialophora cyclaminis	179
Thielavia arenaria	180
Thielavia antarctica	181
Chaetomium sp	182
Chaetomium nigricolor	183
Chaetomium jodhpurense	184
Chaetomium piluliferum	185
Myceliophthora hinnulea	186
Chloridium virescens	187
Gelasinospora cratophora	188
Acidobacteriaceae bacterium	189
Acidobacterium capsulatum	190
Acidovorax wautersii	191
Xanthomonas arborícola	192
Kosakonia sacchari	193
Enterobacter sp	194
Saitozyma flava	195
Phaeotremella skinneri	196
Trichoderma asperellum	197
Corynascus sepedonium	198
Myceliophthora thermophila	199
Trichoderma reesei	200
Chaetomium virescens	201
Rhodothermus marinus	202
Myceliophthora sepedonium	203
Moelleriella libera	204
Acremonium dichromosporum	205
Fusarium sambucinum	206
Phoma sp	207
Lentinus similis	208
Diaporthe nobilis	209
Solicoccozyma terricola	210
Dioszegia cryoxerica	211
Talaromyces funiculosus	212
Hamigera avellanea	213
Talaromyces ruber	214
Trichoderma lixii	215
Aspergillus cervinus	216
Rasamsonia brevistipitata	217

Acremonium curvulum	218
Talaromyces piceae	219
Penicillium sp	220
Talaromyces aurantiacus	221
Talaromyces pinophilus	222
Talaromyces leycettanus	223
Talaromyces variabilis	224
Aspergillus niger	225
Trichoderma reesei	226

Additional polynucleotides encoding suitable trehalases may be derived from microorganisms of any suitable genus, including those readily available within the UniProtKB database (www.uniprot.org).

The trehalase coding sequences can also be used to design nucleic acid probes to identify and clone DNA encoding trehalases from strains of different genera or species, as described *supra*.

The polynucleotides encoding trehalases may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc,) as described *supra*.

Techniques used to isolate or clone polynucleotides encoding trehalases are described *supra*.

In one embodiment, the trehalase has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any one of the trehalases described or referenced herein (e.g., any one of SEQ ID NOs: 175-226). In another embodiment, the trehalase has a mature polypeptide sequence that is a fragment of the any one of the trehalases described or referenced herein (e.g., any one of SEQ ID NOs: 175-226). In one embodiment, the number of amino acid residues in the fragment is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of amino acid residues in referenced full length trehalase (e.g. any one of SEQ ID NOs: 175-226). In other embodiments, the trehalase may comprise the catalytic domain of any trehalase described or referenced herein (e.g., the catalytic domain of any one of SEQ ID NOs: 175-226).

The trehalase may be a variant of any one of the trehalases described *supra* (e.g., any one of SEQ ID NOs: 175-226). In one embodiment, the trehalase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to any one of the trehalases described *supra* (e.g., any one of SEQ ID NOs: 175-226).

In one embodiment, the trehalase has a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of the trehalases described *supra* (e.g., any one of SEQ ID NOs: 175-226). In one embodiment, the trehalase has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) of amino acid sequence of any one of the trehalases described *supra* (e.g., any one of SEQ ID NOs: 175-226). In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

In some embodiments, the trehalase has at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of the trehalase activity of any trehalase described or referenced herein (e.g., any one of SEQ ID NOs: 175-226) under the same conditions.

In one embodiment, the trehalase coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any trehalase described or referenced herein (e.g., any one of SEQ ID NOs: 175-226). In one embodiment, the trehalase coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any trehalase described or referenced herein (e.g., any one of SEQ ID NOs: 175-226).

In one embodiment, the trehalase comprises the coding sequence of any trehalase described or referenced herein (any one of SEQ ID NOs: 175-226). In one embodiment, the trehalase comprises a coding sequence that is a subsequence of the coding sequence from any trehalase described or referenced herein, wherein the subsequence encodes a polypeptide having trehalase activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The referenced coding sequence of any related aspect or embodiment described herein can be the native coding sequence or a degenerate sequence, such as a codon-optimized coding sequence designed for use in a particular host cell (e.g., optimized for expression in *Saccharomyces cerevisiae*).

The trehalase can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

Glucoamylases

The expressed and/or exogenous glucoamylase can be any glucoamylase that is suitable for the fermenting organisms and/or their methods of use described herein, such as a naturally occurring glucoamylase or a variant thereof that retains glucoamylase activity. Any glucoamylase contemplated for expression by a fermenting organism described below is also contemplated for aspects of the invention involving exogenous addition of a glucoamylase (e.g., added before, during or after liquefaction and/or saccharification).

In some embodiments, the fermenting organism comprises a heterologous polynucleotide encoding a glucoamylase, for example, as described in WO2017/087330, the content of which is hereby incorporated by reference. Any glucoamylase described or referenced herein is contemplated for expression in the fermenting organism.

In some embodiments, the fermenting organism comprising a heterologous polynucleotide encoding an glucoamylase has an increased level of glucoamylase activity compared to the host cells without the heterologous polynucleotide encoding the glucoamylase, when cultivated under the same conditions. In some embodiments, the fermenting organism has an increased level of glucoamylase activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the fermenting organism without the heterologous polynucleotide encoding the glucoamylase, when cultivated under the same conditions.

Exemplary glucoamylases that can be used with the host cells and/or the methods described herein include bacterial, yeast, or filamentous fungal glucoamylases, e.g., obtained from any of the microorganisms described or referenced herein, as described *supra* under the sections related to alpha-amylases.

The glucoamylase may be derived from any suitable source, e.g., derived from a microorganism or a plant. Preferred glucoamylases are of fungal or bacterial origin, selected from the group consisting of *Aspergillus* glucoamylases, in particular *Aspergillus niger* G1 or G2 glucoamylase (Boel et al. (1984), EMBO J. 3 (5), p. 1097-1102), or variants thereof, such as those disclosed in WO 92/00381, WO 00/04136 and WO 01/04273 (from Novozymes, Denmark); the *A. awamori* glucoamylase disclosed in WO 84/02921, *Aspergillus oryzae* glucoamylase (Agric. Biol. Chem. (1991), 55 (4), p. 941-949), or variants or fragments thereof. Other *Aspergillus* glucoamylase variants include variants with enhanced thermal stability: G137A and G139A (Chen et al. (1996), Prot. Eng. 9, 499-505); D257E and D293E/Q (Chen et al. (1995), Prot. Eng. 8, 575-582); N182 (Chen et al. (1994), Biochem. J. 301, 275-281); disulphide bonds, A246C (Fierobe et al. (1996), Biochemistry, 35, 8698-8704; and introduction of Pro residues in position A435 and S436 (Li et al. (1997), Protein Eng. 10, 1199-1204.

Other glucoamylases include *Athelia rolfsii* (previously denoted *Corticium rolfsii*) glucoamylase (see US patent no. 4,727,026 and (Nagasaka et al. (1998) "Purification and properties of the raw-starch-degrading glucoamylases from *Corticium rolfsii*, Appl Microbiol Biotechnol 50:323-330), *Talaromyces* glucoamylases, in particular derived from *Talaromyces emersonii* (WO 99/28448), *Talaromyces leycettanus* (US patent no. Re. 32,153), *Talaromyces duponti, Talaromyces thermophilus* (US patent no. 4,587,215). In one embodiment, the glucoamylase used during saccharification and/or fermentation is the *Talaromyces emersonii* glucoamylase disclosed in WO 99/28448.

Bacterial glucoamylases contemplated include glucoamylases from the genus *Clostridium*, in particular *C. thermoamylolyticum* (EP 135,138), and *C. thermohydrosulfuricum* (WO 86/01831).

Contemplated fungal glucoamylases include *Trametes cingulate*, *Pachykytospora papyracea*; and *Leucopaxillus giganteus* all disclosed in WO 2006/069289; or *Peniophora rufomarginata* disclosed in WO2007/124285; or a mixture thereof. Also hybrid glucoamylase are contemplated. Examples include the hybrid glucoamylases disclosed in WO 2005/045018.

In one embodiment, the glucoamylase is derived from a strain of the genus *Pycnoporus*, in particular a strain of *Pycnoporus* as described in WO 2011/066576 (SEQ ID NO: 2, 4 or 6 therein), including the *Pycnoporus sanguineus* glucoamylase, or from a strain of the genus *Gloeophyllum*, such as a strain of *Gloeophyllum sepiarium* or *Gloeophyllum trabeum*, in particular a strain of *Gloeophyllum* as described in WO 2011/068803 (SEQ ID NO: 2, 4, 6, 8, 10, 12, 14 or 16 therein). In one embodiment, the glucoamylase is SEQ ID NO: 2 in WO 2011/068803 (i.e. *Gloeophyllum sepiarium* glucoamylase). In one embodiment, the glucoamylase is the *Gloeophyllum sepiarium* glucoamylase of SEQ ID NO: 8. In one embodiment, the glucoamylase is the *Pycnoporus sanguineus* glucoamylase of SEQ ID NO: 229.

In one embodiment, the glucoamylase is a *Gloeophyllum trabeum* glucoamylase (disclosed as SEQ ID NO: 3 in WO2014/177546). In another embodiment, the glucoamylase is derived from a strain of the genus *Nigrofomes,* in particular a strain of *Nigrofomes sp.* disclosed in WO 2012/064351 (disclosed as SEQ ID NO: 2 therein).

Also contemplated are glucoamylases with a mature polypeptide sequence which exhibit a high identity to any of the above mentioned glucoamylases, i.e., at least 60%, such as at least

70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or even 100% identity to any one of the mature polypeptide sequences mentioned above.

Glucoamylases may be added to the saccharification and/or fermentation in an amount of 0.0001-20 AGU/g DS, such as 0.001-10 AGU/g DS, 0.01-5 AGU/g DS, or 0.1-2 AGU/g DS.

Glucoamylases may be added to the saccharification and/or fermentation in an amount of 1-1,000 µg EP/g DS, such as 10-500 µg/gDS, or 25-250 µg/g DS.

Glucoamylases may be added to liquefaction in an amount of 0.1-100 µg EP/g DS, such as 0.5-50 µg EP/g DS, 1-25 µg EP/g DS, or 2-12 µg EP/g DS.

In one embodiment, the glucoamylase is added as a blend further comprising an alpha-amylase (e.g., any alpha-amylase described herein). In one embodiment, the alpha-amylase is a fungal alpha-amylase, especially an acid fungal alpha-amylase. The alpha-amylase is typically a side activity.

In one embodiment, the glucoamylase is a blend comprising *Talaromyces emersonii* glucoamylase disclosed in WO 99/28448 as SEQ ID NO: 34 and *Trametes cingulata* glucoamylase disclosed as SEQ ID NO: 2 in WO 06/069289.

In one embodiment, the glucoamylase is a blend comprising *Talaromyces emersonii* glucoamylase disclosed in WO 99/28448, *Trametes cingulata* glucoamylase disclosed as SEQ ID NO: 2 in WO 06/69289, and an alpha-amylase.

In one embodiment, the glucoamylase is a blend comprising *Talaromyces emersonii* glucoamylase disclosed in WO99/28448, *Trametes cingulata* glucoamylase disclosed in WO 06/69289, and *Rhizomucor pusillus* alpha-amylase with *Aspergillus niger* glucoamylase linker and SBD disclosed as V039 in Table 5 in WO 2006/069290.

In one embodiment, the glucoamylase is a blend comprising *Gloeophyllum sepiarium* glucoamylase shown as SEQ ID NO: 2 in WO 2011/068803 and an alpha-amylase, in particular *Rhizomucor pusillus* alpha-amylase with an *Aspergillus niger* glucoamylase linker and starch-binding domain (SBD), disclosed SEQ ID NO: 3 in WO 2013/006756, in particular with the following substitutions: G128D+D143N.

In one embodiment, the alpha-amylase may be derived from a strain of the genus *Rhizomucor*, preferably a strain the *Rhizomucor pusillus*, such as the one shown in SEQ ID NO: 3 in WO2013/006756, or the genus *Meripilus*, preferably a strain of *Meripilus giganteus*. In one embodiment, the alpha-amylase is derived from a *Rhizomucor pusillus* with an *Aspergillus niger* glucoamylase linker and starch-binding domain (SBD), disclosed as V039 in Table 5 in WO 2006/069290.

In one embodiment, the *Rhizomucor pusillus* alpha-amylase or the *Rhizomucor pusillus* alpha-amylase with an *Aspergillus niger* glucoamylase linker and starch-binding domain (SBD) has at least one of the following substitutions or combinations of substitutions: D165M; Y141W; Y141R; K136F; K192R; P224A; P224R; S123H+Y141W; G20S + Y141W; A76G + Y141W; G128D + Y141W; G128D + D143N; P219C + Y141W; N142D + D143N; Y141W + K192R; Y141W + D143N; Y141W + N383R; Y141W + P219C + A265C; Y141W + N142D + D143N; Y141W + K192R V410A; G128D + Y141W + D143N; Y141W + D143N + P219C; Y141W + D143N + K192R; G128D + D143N + K192R; Y141W + D143N + K192R + P219C; and G128D + Y141W + D143N + K192R; or G128D + Y141W + D143N + K192R + P219C (using SEQ ID NO: 3 in WO 2013/006756 for numbering).

In one embodiment, the glucoamylase blend comprises *Gloeophyllum sepiarium glucoamylase* (e.g., SEQ ID NO: 2 in WO 2011/068803) and *Rhizomucor pusillus* alpha-amylase.

In one embodiment, the glucoamylase blend comprises *Gloeophyllum sepiarium* glucoamylase shown as SEQ ID NO: 2 in WO 2011/068803 and *Rhizomucor pusillus* with an *Aspergillus niger* glucoamylase linker and starch-binding domain (SBD), disclosed SEQ ID NO: 3 in WO 2013/006756 with the following substitutions: G128D+D143N.

Commercially available compositions comprising glucoamylase include AMG 200L; AMG 300 L; SAN™ SUPER, SAN™ EXTRA L, SPIRIZYME® PLUS, SPIRIZYME® FUEL, SPIRIZYME® B4U, SPIRIZYME® ULTRA, SPIRIZYME® EXCEL, SPIRIZYME ACHIEVE®, and AMG® E (from Novozymes A/S); OPTIDEX™ 300, GC480, GC417 (from DuPont-Danisco); AMIGASE™ and AMIGASE™ PLUS (from DSM); G-ZYME™ G900, G-ZYME™ and G990 ZR (from DuPont-Danisco).

In one embodiment, the glucoamylase is derived from the *Debaryomyces occidentalis* glucoamylase of SEQ ID NO: 102. In one embodiment, the glucoamylase is derived from the *Saccharomycopsis fibuligera* glucoamylase of SEQ ID NO: 103. In one embodiment, the glucoamylase is derived from the *Saccharomycopsis fibuligera* glucoamylase of SEQ ID NO: 104. In one embodiment, the glucoamylase is derived from the *Saccharomyces cerevisiae* glucoamylase of SEQ ID NO: 105. In one embodiment, the glucoamylase is derived from the *Aspergillus niger* glucoamylase of SEQ ID NO: 106. In one embodiment, the glucoamylase is derived from the *Aspergillus oryzae* glucoamylase of SEQ ID NO: 107. In one embodiment, the glucoamylase is derived from the *Rhizopus oryzae* glucoamylase of SEQ ID NO: 108. In one embodiment, the glucoamylase is derived from the *Clostridium thermocellum* glucoamylase of SEQ ID NO: 109. In one embodiment, the glucoamylase is derived from the *Clostridium thermocellum* glucoamylase of SEQ ID NO: 110. In one embodiment, the glucoamylase is derived from the *Arxula adeninivorans* glucoamylase of SEQ ID NO: 111. In one embodiment, the glucoamylase is derived from the *Hormoconis resinae* glucoamylase of SEQ ID NO: 112. In one embodiment, the glucoamylase is derived from the *Aureobasidium pullulans* glucoamylase of SEQ ID NO: 113.

In one embodiment, the glucoamylase is a *Trichoderma reesei* glucoamylase, such as the*Trichoderma reesei* glucoamylase of SEQ ID NO: 230.

In one embodiment, the glucoamylase has a Relative Activity heat stability at 85ºC of at least 20%, at least 30%, or at least 35% determined as described in Example 4 of WO2018/098381 (heat stability).

In one embodiment, the glucoamylase has a relative activity pH optimum at pH 5.0 of at least 90%, e.g., at least 95%, at least 97%, or 100% determined as described in Example 4 of WO2018/098381 (pH optimum).

In one embodiment, the glucoamylase has a pH stability at pH 5.0 of at least 80%, at least 85%, at least 90% determined as described in Example 4 of WO2018/098381 (pH stability).

In one embodiment, the glucoamylase used in liquefaction, such as a *Penicillium oxalicum* glucoamylase variant, has a thermostability determined as DSC Td at pH 4.0 as described in Example 15 of WO2018/098381 of at least 70ºC, preferably at least 75ºC, such as at least 80ºC, such as at least 81ºC, such as at least 82ºC, such as at least 83ºC, such as at least 84ºC, such as at least 85ºC, such as at least 86ºC, such as at least 87%, such as at least 88ºC, such as at least 89ºC, such as at least 90ºC. In one embodiment, the glucoamylase, such as a *Penicillium oxalicum* glucoamylase variant, has a thermostability determined as DSC Td at pH 4.0 as described in Example 15 of WO2018/098381 in the range between 70ºC and 95ºC, such as between 80ºC and 90ºC.

In one embodiment, the glucoamylase, such as a *Penicillium oxalicum* glucoamylase variant, used in liquefaction has a thermostability determined as DSC Td at pH 4.8 as described in Example 15 of WO2018/098381 of at least 70ºC, preferably at least 75ºC, such as at least 80ºC, such as at least 81ºC, such as at least 82ºC, such as at least 83ºC, such as at least 84ºC, such as at least 85ºC, such as at least 86ºC, such as at least 87%, such as at least 88ºC, such as at least 89ºC, such as at least 90ºC, such as at least 91ºC. In one embodiment, the glucoamylase, such as a *Penicillium oxalicum* glucoamylase variant, has a thermostability determined as DSC Td at pH 4.8 as described in Example 15 of WO2018/098381 in the range between 70ºC and 95ºC, such as between 80ºC and 90ºC.

In one embodiment, the glucoamylase, such as a *Penicillium oxalicum* glucoamylase variant, used in liquefaction has a residual activity determined as described in Example 16 of

WO2018/098381, of at least 100% such as at least 105%, such as at least 110%, such as at least 115%, such as at least 120%, such as at least 125%. In one embodiment, the glucoamylase, such as a *Penicillium oxalicum* glucoamylase variant, has a thermostability determined as residual activity as described in Example 16 of WO2018/098381, in the range between 100% and 130%.

In one embodiment, the glucoamylase, e.g., of fungal origin such as a filamentous fungi, from a strain of the genus *Penicillium*, e.g., a strain of *Penicillium oxalicum*, in particular the *Penicillium oxalicum* glucoamylase disclosed as SEQ ID NO: 2 in WO 2011/127802 (which is hereby incorporated by reference).

In one embodiment, the glucoamylase has a mature polypeptide sequence of at least 80%, e.g., at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99% or 100% identity to the mature polypeptide shown in SEQ ID NO: 2 in WO 2011/127802.

In one embodiment, the glucoamylase is a variant of the *Penicillium oxalicum* glucoamylase disclosed as SEQ ID NO: 2 in WO 2011/127802, having a K79V substitution. The K79V glucoamylase variant has reduced sensitivity to protease degradation relative to the parent as disclosed in WO 2013/036526 (which is hereby incorporated by reference).

In one embodiment, the glucoamylase is derived from *Penicillium oxalicum*.

In one embodiment, the glucoamylase is a variant of the *Penicillium oxalicum* glucoamylase disclosed as SEQ ID NO: 2 in WO 2011/127802. In one embodiment, the *Penicillium oxalicum* glucoamylase is the one disclosed as SEQ ID NO: 2 in WO 2011/127802 having Val (V) in position 79.

Contemplated *Penicillium oxalicum* glucoamylase variants are disclosed in WO 2013/053801 which is hereby incorporated by reference.

In one embodiment, these variants have reduced sensitivity to protease degradation.

In one embodiment, these variant have improved thermostability compared to the parent.

In one embodiment, the glucoamylase has a K79V substitution (using SEQ ID NO: 2 of WO 2011/127802 for numbering), corresponding to the PE001 variant, and further comprises one of the following alterations or combinations of alterations

T65A; Q327F; E501V; Y504T; Y504*; T65A + Q327F; T65A + E501V; T65A + Y504T; T65A + Y504*; Q327F + E501V; Q327F + Y504T; Q327F + Y504*; E501V + Y504T; E501V + Y504*; T65A + Q327F + E501V; T65A + Q327F + Y504T; T65A + E501V + Y504T; Q327F + E501V + Y504T; T65A + Q327F + Y504*; T65A + E501V + Y504*; Q327F + E501V + Y504*; T65A + Q327F + E501V + Y504T; T65A + Q327F + E501V + Y504*; E501V + Y504T; T65A + K161S; T65A + Q405T; T65A + Q327W; T65A + Q327F; T65A + Q327Y; P11F + T65A + Q327F;

R1K + D3W + K5Q + G7V + N8S + T10K + P11S + T65A + Q327F; P2N + P4S + P11F + T65A + Q327F; P11F + D26C + K33C + T65A + Q327F; P2N + P4S + P11F + T65A + Q327W + E501V + Y504T; R1E + D3N + P4G + G6R + G7A + N8A + T10D+ P11D + T65A + Q327F; P11F + T65A + Q327W; P2N + P4S + P11F + T65A + Q327F + E501V + Y504T; P11F + T65A + Q327W + E501V + Y504T; T65A + Q327F + E501V + Y504T; T65A + S105P + Q327W; T65A + S105P + Q327F; T65A + Q327W + S364P; T65A + Q327F + S364P; T65A + S103N + Q327F; P2N + P4S + P11F + K34Y + T65A + Q327F; P2N + P4S + P11F + T65A + Q327F + D445N + V447S; P2N + P4S + P11F + T65A + I172V + Q327F; P2N + P4S + P11F + T65A + Q327F + N502*; P2N + P4S + P11F + T65A + Q327F + N502T + P563S + K571E; P2N + P4S + P11F + R31S + K33V + T65A + Q327F + N564D + K571S; P2N + P4S + P11F + T65A + Q327F + S377T; P2N + P4S + P11F + T65A + V325T+ Q327W; P2N + P4S + P11F + T65A + Q327F + D445N + V447S + E501V + Y504T; P2N + P4S + P11F + T65A + I172V + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + S377T + E501V + Y504T; P2N + P4S + P11F + D26N + K34Y + T65A + Q327F; P2N + P4S + P11F + T65A + Q327F + I375A + E501V + Y504T; P2N + P4S + P11F + T65A + K218A + K221D + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + S103N + Q327F + E501V + Y504T; P2N + P4S + T10D + T65A + Q327F + E501V + Y504T; P2N + P4S + F12Y + T65A + Q327F + E501V + Y504T; K5A + P11F + T65A + Q327F + E501V + Y504T; P2N + P4S + T10E + E18N + T65A + Q327F + E501V + Y504T; P2N + T10E + E18N + T65A + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + E501V + Y504T + T568N; P2N + P4S + P11F + T65A + Q327F + E501V + Y504T + K524T + G526A; P2N + P4S + P11F + K34Y + T65A + Q327F + D445N + V447S + E501V + Y504T; P2N + P4S + P11F + R31S + K33V + T65A + Q327F + D445N + V447S + E501V + Y504T; P2N + P4S + P11F + D26N + K34Y + T65A + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + F80* + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + K112S + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + E501V + Y504T + T516P + K524T + G526A; P2N + P4S + P11F + T65A + Q327F + E501V + N502T + Y504*; P2N + P4S + P11F + T65A + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + S103N + Q327F + E501V + Y504T; K5A + P11F + T65A + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + E501V + Y504T + T516P + K524T + G526A; P2N + P4S + P11F + T65A + V79A + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + V79G + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + V79I + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + V79L + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + V79S + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + L72V + Q327F + E501V + Y504T; S255N + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + E74N + V79K + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + G220N + Q327F + E501V + Y504T; P2N + P4S + P11F +

T65A + Y245N + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + Q253N + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + D279N + Q327F + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + S359N + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + D370N + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + V460S + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + V460T + P468T + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + T463N + E501V + Y504T; P2N + P4S + P11F + T65A + Q327F + S465N + E501V + Y504T; and P2N + P4S + P11F + T65A + Q327F + T477N + E501V + Y504T.

In one embodiment, the *Penicillium oxalicum* glucoamylase variant has a K79V substitution (using SEQ ID NO: 2 of WO 2011/127802 for numbering), corresponding to the PE001 variant, and further comprises one of the following substitutions or combinations of substitutions:

P11F + T65A + Q327F;
P2N + P4S + P11F + T65A + Q327F;
P11F + D26C + K33C + T65A + Q327F;
P2N + P4S + P11F + T65A + Q327W + E501V + Y504T;
P2N + P4S + P11F + T65A + Q327F + E501V + Y504T; and
P11F + T65A + Q327W + E501V + Y504T.

Additional glucoamylases contemplated for use with the present invention can be found in WO2011/153516 (the content of which is incorporated herein).

Additional polynucleotides encoding suitable glucoamylases may be obtained from microorganisms of any genus, including those readily available within the UniProtKB database (www.uniprot.org).

The glucoamylase coding sequences can also be used to design nucleic acid probes to identify and clone DNA encoding glucoamylases from strains of different genera or species, as described *supra.*

The polynucleotides encoding glucoamylases may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc,) as described *supra.*

Techniques used to isolate or clone polynucleotides encoding glucoamylases are described *supra.*

In one embodiment, the glucoamylase has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any one of the glucoamylases described or referenced herein (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230). In another embodiment, the glucoamylase has a mature polypeptide sequence that is a fragment of the any one of the glucoamylases described or referenced herein (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230). In one embodiment, the number of amino acid residues in the fragment is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of amino acid residues in referenced full length glucoamylase (e.g. any one of SEQ ID NOs: 8, 102-113, 229 and 230). In other embodiments, the glucoamylase may comprise the catalytic domain of any glucoamylase described or referenced herein (e.g., the catalytic domain of any one of SEQ ID NOs: 8, 102-113, 229 and 230).

The glucoamylase may be a variant of any one of the glucoamylases described *supra* (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230). In one embodiment, the glucoamylase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to any one of the glucoamylases described *supra* (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230).

In one embodiment, the glucoamylase has a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of the glucoamylases described *supra* (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230). In one embodiment, the glucoamylase has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) of amino acid sequence of any one of the glucoamylases described *supra* (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230). In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

In some embodiments, the glucoamylase has at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of the glucoamylase activity of any glucoamylase described or referenced herein (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230) under the same conditions.

In one embodiment, the glucoamylase coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any glucoamylase described or referenced herein (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230). In one embodiment, the glucoamylase coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any glucoamylase described or referenced herein (e.g., any one of SEQ ID NOs: 8, 102-113, 229 and 230).

In one embodiment, the glucoamylase comprises the coding sequence of any glucoamylase described or referenced herein (any one of SEQ ID NOs: 8, 102-113, 229 and 230). In one embodiment, the glucoamylase comprises a coding sequence that is a subsequence of the coding sequence from any glucoamylase described or referenced herein, wherein the subsequence encodes a polypeptide having glucoamylase activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The referenced coding sequence of any related aspect or embodiment described herein can be the native coding sequence or a degenerate sequence, such as a codon-optimized coding sequence designed for use in a particular host cell (e.g., optimized for expression in *Saccharomyces cerevisiae*).

The glucoamylase can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

Proteases

The expressed and/or exogenous protease can be any protease that is suitable for the fermenting organisms and/or their methods of use described herein, such as a naturally occurring protease or a variant thereof that retains protease activity. Any protease contemplated for expression by a fermenting organism described below is also contemplated for aspects of the invention involving exogenous addition of a protease.

Proteases are classified on the basis of their catalytic mechanism into the following groups: Serine proteases (S), Cysteine proteases (C), Aspartic proteases (A), Metallo proteases (M), and Unknown, or as yet unclassified, proteases (U), see Handbook of Proteolytic Enzymes, A.J.Barrett, N.D.Rawlings, J.F.Woessner (eds), Academic Press (1998), in particular the general introduction part.

Protease activity can be measured using any suitable assay, in which a substrate is employed, that includes peptide bonds relevant for the specificity of the protease in question. Assay-pH and assay-temperature are likewise to be adapted to the protease in question. Examples of assay-pH-values are pH 6, 7, 8, 9, 10, or 11. Examples of assay-temperatures are 30, 35, 37, 40, 45, 50, 55, 60, 65, 70 or 80°C.

In some aspects, the fermenting organism comprising a heterologous polynucleotide encoding a protease has an increased level of protease activity compared to the fermenting organism without the heterologous polynucleotide encoding the protease, when cultivated under the same conditions. In some aspects, the fermenting organism has an increased level of protease activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the fermenting organism without the heterologous polynucleotide encoding the protease, when cultivated under the same conditions.

Exemplary proteases that may be expressed with the fermenting organisms and used with the methods described herein include, but are not limited to, proteases shown in Table 4 (or derivatives thereof).

Table 4.

Donor Organism (catalytic domain)	**SEQ ID NO: (mature polypeptide)**	**Family**
Aspergillus niger	9	A1
Trichoderma reesei	10	
Thermoascus aurantiacus	11	M35
Dichomitus squalens	12	S53
Nocardiopsis prasina	13	S1
Penicillium simplicissimum	14	S10
Aspergillus niger	15	
Meriphilus giganteus	16	S53
Lecanicillium sp. WMM742	17	S53
Talaromyces proteolyticus	18	S53
Penicillium ranomafanaense	19	A1A
Aspergillus oryzae	20	S53
Talaromyces liani	21	S10
Thermoascus thermophilus	22	S53
Pyrococcus furiosus	23	
Trichoderma reesei	24	
Rhizomucor miehei	25	
Lenzites betulinus	26	S53
Neolentinus lepideus	27	S53
Thermococcus sp.	28	S8
Thermococcus sp.	29	S8
Thermomyces lanuginosus	30	S53
Thermococcus thioreducens	31	S53

Polyporus arcularius	32	S53
Ganoderma lucidum	33	S53
Ganoderma lucidum	34	S53
Ganoderma lucidum	35	S53
Trametes sp. AH28-2	36	S53
Cinereomyces lindbladii	37	S53
Trametes versicolor O82DDP	38	S53
Paecilomyces hepiali	39	S53
Isaria tenuipes	40	S53
Aspergillus tamarii	41	S53
Aspergillus brasiliensis	42	S53
Aspergillus iizukae	43	S53
Penicillium sp-72364	44	S10
Aspergillus denticulatus	45	S10
Hamigera sp. t184-6	46	S10
Penicillium janthinellum	47	S10
Penicillium vasconiae	48	S10
Hamigera paravellanea	49	S10
Talaromyces variabilis	50	S10
Penicillium arenicola	51	S10
Nocardiopsis kunsanensis	52	S1
Streptomyces parvulus	53	S1
Saccharopolyspora endophytica	54	S1
luteus cellwall enrichments K	55	S1
Saccharothrix australiensis	56	S1
Nocardiopsis baichengensis	57	S1
Streptomyces sp. SM15	58	S1
Actinoalloteichus spitiensis	59	S1
Byssochlamys verrucosa	60	M35
Hamigera terricola	61	M35
Aspergillus tamarii	62	M35
Aspergillus niveus	63	M35
Penicillium sclerotiorum	64	A1
Penicillium bilaiae	65	A1
Penicillium antarcticum	66	A1
Penicillium sumatrense	67	A1
Trichoderma lixii	68	A1
Trichoderma brevicompactum	69	A1
Penicillium cinnamopurpureum	70	A1

Bacillus licheniformis	71	S8
Bacillus subtilis	72	S8
Trametes cf versicol	73	S53

Additional polynucleotides encoding suitable proteases may be derived from microorganisms of any suitable genus, including those readily available within the UniProtKB database (www.uniprot.org).

In one embodiment, the protease is derived from *Aspergillus*, such as the *Aspergillus niger* protease of SEQ ID NO: 9, the *Aspergillus tamarii* protease of SEQ ID NO: 41, or the *Aspergillus denticulatus* protease of SEQ ID NO: 45. In one embodiment, the protease is derived from *Dichomitus*, such as the *Dichomitus squalens* protease of SEQ ID NO: 12. In one embodiment, the protease is derived from *Penicillium*, such as the *Penicillium simplicissimum* protease of SEQ ID NO: 14, the *Penicillium antarcticum* protease of SEQ ID NO: 66, or the *Penicillium sumatrense* protease of SEQ ID NO: 67. In one aspect, the protease is derived from *Meriphilus*, such as the *Meriphilus giganteus* protease of SEQ ID NO: 16. In one aspect, the protease is derived from *Talaromyces*, such as the *Talaromyces liani* protease of SEQ ID NO: 21. In one aspect, the protease is derived from *Thermoascus*, such as the *Thermoascus thermophilus* protease of SEQ ID NO: 22. In one aspect, the protease is derived from *Ganoderma*, such as the *Ganoderma lucidum* protease of SEQ ID NO: 33. In one aspect, the protease is derived from *Hamigera*, such as the *Hamigera terricola* protease of SEQ ID NO: 61. In one aspect, the protease is derived from *Trichoderma*, such as the *Trichoderma brevicompactum* protease of SEQ ID NO: 69.

The protease coding sequences can also be used to design nucleic acid probes to identify and clone DNA encoding proteases from strains of different genera or species, as described *supra*.

The polynucleotides encoding proteases may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc,) as described *supra*.

Techniques used to isolate or clone polynucleotides encoding proteases are described *supra*.

In one embodiment, the protease has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any one of SEQ ID NOs: 9-73 (e.g., any one of SEQ ID NOs: 9, 14, 16, 21, 22, 33, 41, 45, 61, 62, 66, 67, and 69; such as any one of SEQ NOs: 9, 14, 16, and 69). In another embodiment, the protease has a mature polypeptide sequence that is a fragment of the protease of any one of SEQ ID NOs: 9-73 (e.g., wherein the fragment has protease activity). In one embodiment, the number of amino acid residues in the fragment is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of amino acid residues in referenced full length protease (e.g. any one of SEQ ID NOs: 9-73). In other embodiments, the protease may comprise the catalytic domain of any protease described or referenced herein (e.g., the catalytic domain of any one of SEQ ID NOs: 9-73).

The protease may be a variant of any one of the proteases described *supra* (e.g., any one of SEQ ID NOs: 9-73. In one embodiment, the protease has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to any one of the proteases described *supra* (e.g., any one of SEQ ID NOs: 9-73).

In one embodiment, the protease has a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of the proteases described *supra* (e.g., any one of SEQ ID NOs: 9-73). In one embodiment, the protease has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) of amino acid sequence of any one of the proteases described *supra* (e.g., any one of SEQ ID NOs: 9-73). In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

In one embodiment, the protease coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any protease described or referenced herein (e.g., any one of SEQ ID NOs: 9-73). In one embodiment, the protease coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any protease described or referenced herein (e.g., any one of SEQ ID NOs: 9-73).

In one embodiment, the protease comprises the coding sequence of any protease described or referenced herein (any one of SEQ ID NOs: 9-73). In one embodiment, the protease comprises a coding sequence that is a subsequence of the coding sequence from any protease described or referenced herein, wherein the subsequence encodes a polypeptide having protease activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The referenced coding sequence of any related aspect or embodiment described herein can be the native coding sequence or a degenerate sequence, such as a codon-optimized coding sequence designed for use in a particular host cell (e.g., optimized for expression in *Saccharomyces cerevisiae*).

The protease can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

In one embodiment, the protease used according to a process described herein is a Serine proteases. In one particular embodiment, the protease is a serine protease belonging to the family 53, e.g., an endo-protease, such as S53 protease from *Meripilus giganteus, Dichomitus squalens Trametes versicolor*, *Polyporus arcularius, Lenzites betulinus, Ganoderma lucidum, Neolentinus lepideus,* or *Bacillus* sp. 19138, in a process for producing ethanol from a starch-containing material, the ethanol yield was improved, when the S53 protease was present/or added during saccharification and/or fermentation of either gelatinized or un-gelatinized starch. In one embodiment, the proteases is selected from: (a) proteases belonging to the EC 3.4.21 enzyme group; and/or (b) proteases belonging to the EC 3.4.14 enzyme group; and/or (c) Serine proteases of the peptidase family S53 that comprises two different types of peptidases: tripeptidyl aminopeptidases (exo-type) and endo-peptidases; as described in 1993, *Biochem. J.* 290:205-218 and in MEROPS protease database, release, 9.4 (31 January 2011) (www.merops.ac.uk). The database is described in Rawlings, N.D., Barrett, A.J. and Bateman, A., 2010, “MEROPS: the peptidase database”, *Nucl. Acids Res.* 38: D227-D233.

For determining whether a given protease is a Serine protease, and a family S53 protease, reference is made to the above Handbook and the principles indicated therein. Such determination can be carried out for all types of proteases, be it naturally occurring or wild-type proteases; or genetically engineered or synthetic proteases.

Peptidase family S53 contains acid-acting endopeptidases and tripeptidyl-peptidases. The residues of the catalytic triad are Glu, Asp, Ser, and there is an additional acidic residue, Asp, in the oxyanion hole. The order of the residues is Glu, Asp, Asp, Ser. The Ser residue is the nucleophile equivalent to Ser in the Asp, His, Ser triad of subtilisin, and the Glu of the triad is a substitute for the general base, His, in subtilisin.

The peptidases of the S53 family tend to be most active at acidic pH (unlike the homologous subtilisins), and this can be attributed to the functional importance of carboxylic residues, notably Asp in the oxyanion hole. The amino acid sequences are not closely similar to those in family S8 (i.e. serine endopeptidase subtilisins and homologues), and this, taken together with the quite different active site residues and the resulting lower pH for maximal activity, provides for a substantial difference to that family. Protein folding of the peptidase unit for members of this family resembles that of subtilisin, having the clan type SB.

In one embodiment, the protease used according to a process described herein is a Cysteine proteases.

In one embodiment, the protease used according to a process described herein is a Aspartic proteases. Aspartic acid proteases are described in, for example, Hand-book of Proteolytic En-zymes, Edited by A.J. Barrett, N.D. Rawlings and J.F. Woessner, Aca-demic Press, San Diego, 1998, Chapter 270). Suitable examples of aspartic acid protease include, e.g., those disclosed in R.M. Berka et al. Gene, 96, 313 (1990)); (R.M. Berka et al. Gene, 125, 195-198 (1993)); and Gomi et al. Biosci. Biotech. Biochem. 57, 1095-1100 (1993), which are hereby incorporated by reference.

The protease also may be a metalloprotease, which is defined as a protease selected from the group consisting of:

(a) proteases belonging to EC 3.4.24 (metalloendopeptidases); preferably EC 3.4.24.39 (acid metallo proteinases);

(b) metalloproteases belonging to the M group of the above Handbook;

(c) metalloproteases not yet assigned to clans (designation: Clan MX), or belonging to either one of clans MA, MB, MC, MD, ME, MF, MG, MH (as defined at pp. 989-991 of the above Handbook);

(d) other families of metalloproteases (as defined at pp. 1448-1452 of the above Handbook);

(e) metalloproteases with a HEXXH motif;

(f) metalloproteases with an HEFTH motif;

(g) metalloproteases belonging to either one of families M3, M26, M27, M32, M34, M35, M36, M41, M43, or M47 (as defined at pp. 1448-1452 of the above Handbook);

(h) metalloproteases belonging to the M28E family; and

(i) metalloproteases belonging to family M35 (as defined at pp. 1492-1495 of the above Handbook).

In other particular embodiments, metalloproteases are hydrolases in which the nucleophilic attack on a peptide bond is mediated by a water molecule, which is activated by a divalent metal cation. Examples of divalent cations are zinc, cobalt or manganese. The metal ion may be held in place by amino acid ligands. The number of ligands may be five, four, three, two, one or zero. In a particular embodiment the number is two or three, preferably three.

There are no limitations on the origin of the metalloprotease used in a process of the invention. In an embodiment the metalloprotease is classified as EC 3.4.24, preferably EC 3.4.24.39. In one embodiment, the metalloprotease is an acid-stable metalloprotease, *e.g.*, a fungal acid-stable metalloprotease, such as a metalloprotease derived from a strain of the genus *Thermoascus*, preferably a strain of *Thermoascus aurantiacus*, especially *Thermoascus aurantiacus* CGMCC No. 0670 (classified as EC 3.4.24.39). In another embodiment, the metalloprotease is derived from a strain of the genus *Aspergillus*, preferably a strain of *Aspergillus oryzae*.

In one embodiment the metalloprotease has a degree of sequence identity to amino acids -178 to 177, -159 to 177, or preferably amino acids 1 to 177 (the mature polypeptide) of SEQ ID NO: 1 of WO 2010/008841 (a *Thermoascus aurantiacus* metalloprotease) of at least 80%, at least 82%, at least 85%, at least 90%, at least 95%, or at least 97%; and which have metalloprotease activity. In particular embodiments, the metalloprotease consists of an amino acid sequence with a degree of identity to SEQ ID NO: 1 as mentioned above.

The *Thermoascus aurantiacus* metalloprotease is a preferred example of a metalloprotease suitable for use in a process of the invention. Another metalloprotease is derived from *Aspergillus oryzae* and comprises the sequence of SEQ ID NO: 11 disclosed in WO 2003/048353, or amino acids -23-353; -23-374; -23-397; 1-353; 1-374; 1-397; 177-353; 177-374; or 177-397 thereof, and SEQ ID NO: 10 disclosed in WO 2003/048353.

Another metalloprotease suitable for use in a process of the invention is the *Aspergillus oryzae* metalloprotease comprising SEQ ID NO: 5 of WO 2010/008841, or a metalloprotease is an isolated polypeptide which has a degree of identity to SEQ ID NO: 5 of at least about 80%, at least 82%, at least 85%, at least 90%, at least 95%, or at least 97%; and which have metalloprotease activity. In particular embodiments, the metalloprotease consists of the amino acid sequence of SEQ ID NO: 5 of WO 2010/008841.

In a particular embodiment, a metalloprotease has an amino acid sequence that differs by forty, thirty-five, thirty, twenty-five, twenty, or by fifteen amino acids from amino acids -178 to 177, -159 to 177, or +1 to 177 of the amino acid sequences of the *Thermoascus aurantiacus* or *Aspergillus oryzae* metalloprotease.

In another embodiment, a metalloprotease has an amino acid sequence that differs by ten, or by nine, or by eight, or by seven, or by six, or by five amino acids from amino acids -178 to 177, -159 to 177, or +1 to 177 of the amino acid sequences of these metalloproteases, *e.g.*, by four, by three, by two, or by one amino acid.

In particular embodiments, the metalloprotease a) comprises or b) consists of

i) the amino acid sequence of amino acids -178 to 177, -159 to 177, or +1 to 177 of SEQ ID NO:1 of WO 2010/008841;

ii) the amino acid sequence of amino acids -23-353, -23-374, -23-397, 1-353, 1-374, 1-397, 177-353, 177-374, or 177-397 of SEQ ID NO: 3 of WO 2010/008841;

iii) the amino acid sequence of SEQ ID NO: 5 of WO 2010/008841; or

allelic variants, or fragments, of the sequences of i), ii), and iii) that have protease activity.

A fragment of amino acids -178 to 177, -159 to 177, or +1 to 177 of SEQ ID NO: 1 of WO 2010/008841 or of amino acids -23-353, -23-374, -23-397, 1-353, 1-374, 1-397, 177-353, 177-374, or 177-397 of SEQ ID NO: 3 of WO 2010/008841; is a polypeptide having one or more amino acids deleted from the amino and/or carboxyl terminus of these amino acid sequences. In one embodiment a fragment contains at least 75 amino acid residues, or at least 100 amino acid residues, or at least 125 amino acid residues, or at least 150 amino acid residues, or at least 160 amino acid residues, or at least 165 amino acid residues, or at least 170 amino acid residues, or at least 175 amino acid residues.

To determine whether a given protease is a metallo protease or not, reference is made to the above “Handbook of Proteolytic Enzymes” and the principles indicated therein. Such determination can be carried out for all types of proteases, be it naturally occurring or wild-type proteases; or genetically engineered or synthetic proteases.

The protease may be a variant of, e.g., a wild-type protease, having thermostability properties defined herein. In one embodiment, the thermostable protease is a variant of a metallo protease. In one embodiment, the thermostable protease used in a process described herein is of fungal origin, such as a fungal metallo protease, such as a fungal metallo protease derived from a strain of the genus *Thermoascus*, preferably a strain of *Thermoascus aurantiacus*, especially *Thermoascus aurantiacus* CGMCC No. 0670 (classified as EC 3.4.24.39).

In one embodiment, the thermostable protease is a variant of the mature part of the metallo protease shown in SEQ ID NO: 2 disclosed in WO 2003/048353 or the mature part of SEQ ID NO: 1 in WO 2010/008841 further with one of the following substitutions or combinations of substitutions:

S5*+D79L+S87P+A112P+D142L;

D79L+S87P+A112P+T124V+D142L;

S5*+N26R+D79L+S87P+A112P+D142L;

N26R+T46R+D79L+S87P+A112P+D142L;

T46R+D79L+S87P+T116V+D142L;

D79L+P81R+S87P+A112P+D142L;
A27K+D79L+S87P+A112P+T124V+D142L;
D79L+Y82F+S87P+A112P+T124V+D142L;
D79L+Y82F+S87P+A112P+T124V+D142L;
D79L+S87P+A112P+T124V+A126V+D142L;
D79L+S87P+A112P+D142L;
D79L+Y82F+S87P+A112P+D142L;
S38T+D79L+S87P+A112P+A126V+D142L;
D79L+Y82F+S87P+A112P+A126V+D142L;
A27K+D79L+S87P+A112P+A126V+D142L;
D79L+S87P+N98C+A112P+G135C+D142L;
D79L+S87P+A112P+D142L+T141C+M161C;
S36P+D79L+S87P+A112P+D142L;
A37P+D79L+S87P+A112P+D142L;
S49P+D79L+S87P+A112P+D142L;
S50P+D79L+S87P+A112P+D142L;
D79L+S87P+D104P+A112P+D142L;
D79L+Y82F+S87G+A112P+D142L;
S70V+D79L+Y82F+S87G+Y97W+A112P+D142L;
D79L+Y82F+S87G+Y97W+D104P+A112P+D142L;
S70V+D79L+Y82F+S87G+A112P+D142L;
D79L+Y82F+S87G+D104P+A112P+D142L;
D79L+Y82F+S87G+A112P+A126V+D142L;
Y82F+S87G+S70V+D79L+D104P+A112P+D142L;
Y82F+S87G+D79L+D104P+A112P+A126V+D142L;
A27K+D79L+Y82F+S87G+D104P+A112P+A126V+D142L;
A27K+Y82F+S87G+D104P+A112P+A126V+D142L;
A27K+D79L+Y82F+ D104P+A112P+A126V+D142L;
A27K+Y82F+D104P+A112P+A126V+D142L;
A27K+D79L+S87P+A112P+D142L; and
D79L+S87P+D142L.

In one embodiment, the thermostable protease is a variant of the metallo protease disclosed as the mature part of SEQ ID NO: 2 disclosed in WO 2003/048353 or the mature part of SEQ ID NO: 1 in WO 2010/008841 with one of the following substitutions or combinations of substitutions:

D79L+S87P+A112P+D142L;
D79L+S87P+D142L; and
A27K+ D79L+Y82F+S87G+D104P+A112P+A126V+D142L.

In one embodiment, the protease variant has at least 75% identity preferably at least 80%, more preferably at least 85%, more preferably at least 90%, more preferably at least 91%, more preferably at least 92%, even more preferably at least 93%, most preferably at least 94%, and even most preferably at least 95%, such as even at least 96%, at least 97%, at least 98%, at least 99%, but less than 100% identity to the mature part of the polypeptide of SEQ ID NO: 2 disclosed in WO 2003/048353 or the mature part of SEQ ID NO: 1 in WO 2010/008841.

The thermostable protease may also be derived from any bacterium as long as the protease has the thermostability properties.

In one embodiment, the thermostable protease is derived from a strain of the bacterium *Pyrococcus*, such as a strain of *Pyrococcus furiosus* (pfu protease).

In one embodiment, the protease is one shown as SEQ ID NO: 1 in US patent No. 6,358,726-B1 (Takara Shuzo Company).

In one embodiment, the thermostable protease is a protease having a mature polypeptide sequence of at least 80% identity, such as at least 85%, such as at least 90%, such as at least 95%, such as at least 96%, such as at least 97%, such as at least 98%, such as at least 99% identity to SEQ ID NO: 1 in US patent no. 6,358,726-B1. The *Pyroccus furiosus* protease can be purchased from Takara Bio, Japan.

The *Pyrococcus furiosus* protease may be a thermostable protease as described in SEQ ID NO: 13 of WO2018/098381. This protease (PfuS) was found to have a thermostability of 110% (80°C/70°C) and 103% (90°C/70°C) at pH 4.5 determined.

In one embodiment a thermostable protease used in a process described herein has a thermostability value of more than 20% determined as Relative Activity at 80ºC/70ºC determined as described in Example 2 of WO2018/098381.

In one embodiment, the protease has a thermostability of more than 30%, more than 40%, more than 50%, more than 60%, more than 70%, more than 80%, more than 90%, more than 100%, such as more than 105%, such as more than 110%, such as more than 115%, such as more than 120% determined as Relative Activity at 80ºC/70ºC.

In one embodiment, protease has a thermostability of between 20 and 50%, such as between 20 and 40%, such as 20 and 30% determined as Relative Activity at 80ºC/70ºC. In one embodiment, the protease has a thermostability between 50 and 115%, such as between 50 and 70%, such as between 50 and 60%, such as between 100 and 120%, such as between 105 and 115% determined as Relative Activity at 80ºC/70ºC.

In one embodiment, the protease has a thermostability value of more than 10% determined as Relative Activity at 85ºC/70ºC determined as described in Example 2 of WO2018/098381.

In one embodiment, the protease has a thermostability of more than 10%, such as more than 12%, more than 14%, more than 16%, more than 18%, more than 20%, more than 30%, more than 40%, more that 50%, more than 60%, more than 70%, more than 80%, more than 90%, more than 100%, more than 110% determined as Relative Activity at 85ºC/70ºC.

In one embodiment, the protease has a thermostability of between 10% and 50%, such as between 10% and 30%, such as between 10% and 25% determined as Relative Activity at 85ºC/70ºC.

In one embodiment, the protease has more than 20%, more than 30%, more than 40%, more than 50%, more than 60%, more than 70%, more than 80%, more than 90% determined as Remaining Activity at 80ºC; and/or the protease has more than 20%, more than 30%, more than 40%, more than 50%, more than 60%, more than 70%, more than 80%, more than 90% determined as Remaining Activity at 84ºC.

Determination of “Relative Activity” and “Remaining Activity” is done as described in Example 2 of WO2018/098381.

In one embodiment, the protease may have a themostability for above 90, such as above 100 at 85ºC as determined using the Zein-BCA assay as disclosed in Example 3 of WO2018/098381.

In one embodiment, the protease has a themostability above 60%, such as above 90%, such as above 100%, such as above 110% at 85ºC as determined using the Zein-BCA assay of WO2018/098381.

In one embodiment, protease has a themostability between 60-120, such as between 70-120%, such as between 80-120%, such as between 90-120%, such as between 100-120%, such as 110-120% at 85ºC as determined using the Zein-BCA assay of WO2018/098381.

In one embodiment, the thermostable protease has at least 20%, such as at least 30%, such as at least 40%, such as at least 50%, such as at least 60%, such as at least 70%, such as at least 80%, such as at least 90%, such as at least 95%, such as at least 100% of the activity of the JTP196 protease variant or Protease Pfu determined by the AZCL-casein assay of WO2018/098381, and described herein.

In one embodiment, the thermostable protease has at least 20%, such as at least 30%, such as at least 40%, such as at least 50%, such as at least 60%, such as at least 70%, such as at least 80%, such as at least 90%, such as at least 95%, such as at least 100% of the protease activity of the Protease 196 variant or Protease Pfu determined by the AZCL-casein assay of WO2018/098381, and described herein.

Pullulanases

In some embodiments, a pullulanase is present and/or added in liquefaction step and/or saccharification step, or simultaneous saccharification and fermentation (SSF).

Pullulanases (E.C. 3.2.1.41, pullulan 6-glucano-hydrolase), are debranching enzymes characterized by their ability to hydrolyze the alpha-1,6-glycosidic bonds in, for example, amylopectin and pullulan.

In some embodiments, the fermenting organism comprises a heterologous polynucleotide encoding a pullulanase. Any pullulanase described or referenced herein is contemplated for expression in the fermenting organism.

The pullulanase may be any pullulanase that is suitable for the host cells and/or the methods described herein, such as a naturally occurring pullulanase or a variant thereof that retains pullulanase activity.

In some embodiments, the fermenting organism comprising a heterologous polynucleotide encoding a pullulanase has an increased level of pullulanase activity compared to the host cells without the heterologous polynucleotide encoding the pullulanase, when cultivated under the same conditions. In some embodiments, the fermenting organism has an increased level of pullulanase activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the fermenting organism without the heterologous polynucleotide encoding the pullulanase, when cultivated under the same conditions.

Exemplary pullulanasees that can be used with the host cells and/or the methods described herein include bacterial, yeast, or filamentous fungal pullulanases, e.g., obtained from any of the microorganisms described or referenced herein, as described *supra* under the sections related to alpha-amylases.

Contemplated pullulanases include the pullulanases from *Bacillus amyloderamificans* disclosed in U.S. Patent No. 4,560,651 (hereby incorporated by reference), the pullulanase disclosed as SEQ ID NO: 2 in WO 01/151620 (hereby incorporated by reference), the *Bacillus deramificans* disclosed as SEQ ID NO: 4 in WO 01/151620 (hereby incorporated by reference), and the pullulanase from *Bacillus acidopullulyticus* disclosed as SEQ ID NO: 6 in WO 01/151620 (hereby incorporated by reference) and also described in FEMS Mic. Let. (1994) 115, 97-106.

Additional pullulanases contemplated include the pullulanases from *Pyrococcus woesei*, specifically from *Pyrococcus woesei* DSM No. 3773 disclosed in WO92/02614.

In one embodiment, the pullulanase is a family GH57 pullulanase. In one embodiment, the pullulanase includes an X47 domain as disclosed in US 61/289,040 published as WO 2011/087836 (which are hereby incorporated by reference). More specifically the pullulanase may be derived from a strain of the genus *Thermococcus*, including *Thermococcus litoralis* and *Thermococcus hydrothermalis*, such as the *Thermococcus hydrothermalis* pullulanase truncated at site X4 right after the X47 domain (i.e., amino acids 1-782). The pullulanase may also be a hybrid of the *Thermococcus litoralis* and *Thermococcus hydrothermalis* pullulanases or a *T. hydrothermalis/T. litoralis* hybrid enzyme with truncation site X4 disclosed in US 61/289,040 published as WO 2011/087836 (which is hereby incorporated by reference).

In another embodiment, the pullulanase is one comprising an X46 domain disclosed in WO 2011/076123 (Novozymes).

The pullulanase may be added in an effective amount which include the preferred amount of about 0.0001-10 mg enzyme protein per gram DS, preferably 0.0001-0.10 mg enzyme protein per gram DS, more preferably 0.0001-0.010 mg enzyme protein per gram DS. Pullulanase activity may be determined as NPUN. An Assay for determination of NPUN is described in WO2018/098381.

Suitable commercially available pullulanase products include PROMOZYME D, PROMOZYME™ D2 (Novozymes A/S, Denmark), OPTIMAX L-300 (DuPont-Danisco, USA), and AMANO 8 (Amano, Japan).

In one embodiment, the pullulanase is derived from the *Bacillus subtilis* pullulanase of SEQ ID NO: 114. In one embodiment, the pullulanase is derived from the *Bacillus licheniformis* pullulanase of SEQ ID NO: 115. In one embodiment, the pullulanase is derived from the *Oryza sativa* pullulanase of SEQ ID NO: 116. In one embodiment, the pullulanase is derived from the *Triticum aestivum* pullulanase of SEQ ID NO: 117. In one embodiment, the pullulanase is derived from the *Clostridium phytofermentans* pullulanase of SEQ ID NO: 118. In one embodiment, the pullulanase is derived from the *Streptomyces avermitilis* pullulanase of SEQ ID NO: 119. In one embodiment, the pullulanase is derived from the *Klebsiella pneumoniae* pullulanase of SEQ ID NO: 120.

Additional pullulanases contemplated for use with the present invention can be found in WO2011/153516 (the content of which is incorporated herein).

Additional polynucleotides encoding suitable pullulanases may be obtained from microorganisms of any genus, including those readily available within the UniProtKB database (www.uniprot.org).

The pullulanase coding sequences can also be used to design nucleic acid probes to identify and clone DNA encoding pullulanases from strains of different genera or species, as described *supra*.

The polynucleotides encoding pullulanases may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc,) as described *supra*.

Techniques used to isolate or clone polynucleotides encoding pullulanases are described *supra*.

In one embodiment, the pullulanase has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any one of the pullulanases described or referenced herein (e.g., any one of SEQ ID NOs: 114-120). In another embodiment, the pullulanase has a mature polypeptide sequence that is a fragment of the any one of the pullulanases described or referenced herein (e.g., any one of SEQ ID NOs: 114-120). In one embodiment, the number of amino acid residues in the fragment is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of amino acid residues in referenced full length pullulanase. In other embodiments, the pullulanase may comprise the catalytic domain of any pullulanase described or referenced herein (e.g., any one of SEQ ID NOs: 114-120).

The pullulanase may be a variant of any one of the pullulanases described *supra* (e.g., any one of SEQ ID NOs: 114-120). In one embodiment, the pullulanase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to any one of the pullulanases described *supra* (e.g., any one of SEQ ID NOs: 114-120).

In one embodiment, the pullulanase has a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of the pullulanases described *supra* (e.g., any one of SEQ ID NOs: 114-120). In one embodiment, the pullulanase has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) of amino acid sequence of any one of the pullulanases described *supra* (e.g., any one of SEQ ID NOs: 114-120). In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

In some embodiments, the pullulanase has at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of the pullulanase activity of any pullulanase described or referenced herein under the same conditions (e.g., any one of SEQ ID NOs: 114-120).

In one embodiment, the pullulanase coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any pullulanase described or referenced herein (e.g., any one of SEQ ID NOs: 114-120). In one embodiment, the pullulanase coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any pullulanase described or referenced herein (e.g., any one of SEQ ID NOs: 114-120).

In one embodiment, the pullulanase comprises the coding sequence of any pullulanase described or referenced herein (e.g., any one of SEQ ID NOs: 114-120). In one embodiment, the pullulanase comprises a coding sequence that is a subsequence of the coding sequence from any pullulanase described or referenced herein, wherein the subsequence encodes a polypeptide having pullulanase activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The referenced coding sequence of any related aspect or embodiment described herein can be the native coding sequence or a degenerate sequence, such as a codon-optimized coding sequence designed for use in a particular host cell (e.g., optimized for expression in *Saccharomyces cerevisiae*).

The pullulanase can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

Methods using a Cellulosic-Containing Material

In some aspects, the methods described herein produce a fermentation product from a cellulosic-containing material. The predominant polysaccharide in the primary cell wall of biomass is cellulose, the second most abundant is hemicellulose, and the third is pectin. The secondary cell wall, produced after the cell has stopped growing, also contains polysaccharides and is strengthened by polymeric lignin covalently cross-linked to hemicellulose. Cellulose is a homopolymer of anhydrocellobiose and thus a linear beta-(1-4)-D-glucan, while hemicelluloses include a variety of compounds, such as xylans, xyloglucans, arabinoxylans, and mannans in complex branched structures with a spectrum of substituents. Although generally polymorphous, cellulose is found in plant tissue primarily as an insoluble crystalline matrix of parallel glucan chains. Hemicelluloses usually hydrogen bond to cellulose, as well as to other hemicelluloses, which help stabilize the cell wall matrix.

Cellulose is generally found, for example, in the stems, leaves, hulls, husks, and cobs of plants or leaves, branches, and wood of trees. The cellulosic-containing material can be, but is not limited to, agricultural residue, herbaceous material (including energy crops), municipal solid waste, pulp and paper mill residue, waste paper, and wood (including forestry residue) (see, for example, Wiselogel *et al.*, 1995, in Handbook on Bioethanol (Charles E. Wyman, editor), pp. 105-118, Taylor & Francis, Washington D.C.; Wyman, 1994, *Bioresource Technology* 50: 3-16; Lynd, 1990, *Applied Biochemistry and Biotechnology* 24/25: 695-719; Mosier *et al.*, 1999, Recent Progress in Bioconversion of Lignocellulosics, in *Advances in Biochemical Engineering/Biotechnology*, T. Scheper, managing editor, Volume 65, pp. 23-40, Springer-Verlag, New York). It is understood herein that the cellulose may be in the form of lignocellulose, a plant cell wall material containing lignin, cellulose, and hemicellulose in a mixed matrix. In one embodiment, the cellulosic-containing material is any biomass material. In another embodiment, the cellulosic-containing material is lignocellulose, which comprises cellulose, hemicelluloses, and lignin.

In one embodiment, the cellulosic-containing material is agricultural residue, herbaceous material (including energy crops), municipal solid waste, pulp and paper mill residue, waste paper, or wood (including forestry residue).

In another embodiment, the cellulosic-containing material is arundo, bagasse, bamboo, corn cob, corn fiber, corn stover, miscanthus, rice straw, switchgrass, or wheat straw.

In another embodiment, the cellulosic-containing material is aspen, eucalyptus, fir, pine, poplar, spruce, or willow.

In another embodiment, the cellulosic-containing material is algal cellulose, bacterial cellulose, cotton linter, filter paper, microcrystalline cellulose (*e.g.*, AVICEL®), or phosphoric-acid treated cellulose.

In another embodiment, the cellulosic-containing material is an aquatic biomass. As used herein the term “aquatic biomass” means biomass produced in an aquatic environment by a photosynthesis process. The aquatic biomass can be algae, emergent plants, floating-leaf plants, or submerged plants.

The cellulosic-containing material may be used as is or may be subjected to pretreatment, using conventional methods known in the art, as described herein. In a preferred embodiment, the cellulosic-containing material is pretreated.

The methods of using cellulosic-containing material can be accomplished using methods conventional in the art. Moreover, the methods of can be implemented using any conventional biomass processing apparatus configured to carry out the processes.

Cellulosic Pretreatment

In one embodiment the cellulosic-containing material is pretreated before saccharification.

In practicing the processes described herein, any pretreatment process known in the art can be used to disrupt plant cell wall components of the cellulosic-containing material (Chandra *et al.*, 2007, *Adv. Biochem. Engin./Biotechnol.* 108: 67-93; Galbe and Zacchi, 2007, *Adv. Biochem. Engin./Biotechnol.* 108: 41-65; Hendriks and Zeeman, 2009, *Bioresource Technology* 100: 10-18; Mosier *et al.*, 2005, *Bioresource Technology* 96: 673-686; Taherzadeh and Karimi, 2008, *Int. J. Mol. Sci.* 9: 1621-1651; Yang and Wyman, 2008, *Biofuels Bioproducts and Biorefining-Biofpr.* 2: 26-40).

The cellulosic-containing material can also be subjected to particle size reduction, sieving, pre-soaking, wetting, washing, and/or conditioning prior to pretreatment using methods known in the art.

Conventional pretreatments include, but are not limited to, steam pretreatment (with or without explosion), dilute acid pretreatment, hot water pretreatment, alkaline pretreatment, lime pretreatment, wet oxidation, wet explosion, ammonia fiber explosion, organosolv pretreatment, and biological pretreatment. Additional pretreatments include ammonia percolation, ultrasound, electroporation, microwave, supercritical CO_2, supercritical H_2O, ozone, ionic liquid, and gamma irradiation pretreatments.

In a one embodiment, the cellulosic-containing material is pretreated before saccharification (i.e., hydrolysis) and/or fermentation. Pretreatment is preferably performed prior to the hydrolysis. Alternatively, the pretreatment can be carried out simultaneously with enzyme hydrolysis to release fermentable sugars, such as glucose, xylose, and/or cellobiose. In most cases the pretreatment step itself results in some conversion of biomass to fermentable sugars (even in absence of enzymes).

In one embodiment, the cellulosic-containing material is pretreated with steam. In steam pretreatment, the cellulosic-containing material is heated to disrupt the plant cell wall components, including lignin, hemicellulose, and cellulose to make the cellulose and other fractions, *e.g.*, hemicellulose, accessible to enzymes. The cellulosic-containing material is passed to or through a reaction vessel where steam is injected to increase the temperature to the required temperature and pressure and is retained therein for the desired reaction time. Steam pretreatment is preferably performed at 140-250°C, *e.g.*, 160-200°C or 170-190°C, where the optimal temperature range depends on optional addition of a chemical catalyst. Residence time for the steam pretreatment is preferably 1-60 minutes, *e.g.*, 1-30 minutes, 1-20 minutes, 3-12 minutes, or 4-10 minutes, where the optimal residence time depends on the temperature and optional addition of a chemical catalyst. Steam pretreatment allows for relatively high solids loadings, so that the cellulosic-containing material is generally only moist during the pretreatment. The steam pretreatment is often combined with an explosive discharge of the material after the pretreatment, which is known as steam explosion, that is, rapid flashing to atmospheric pressure and turbulent flow of the material to increase the accessible surface area by fragmentation (Duff and Murray, 1996, *Bioresource Technology* 855: 1-33; Galbe and Zacchi, 2002, *Appl. Microbiol. Biotechnol.* 59: 618-628; U.S. Patent Application No. 2002/0164730). During steam pretreatment, hemicellulose acetyl groups are cleaved and the resulting acid autocatalyzes partial hydrolysis of the hemicellulose to monosaccharides and oligosaccharides. Lignin is removed to only a limited extent.

In one embodiment, the cellulosic-containing material is subjected to a chemical pretreatment. The term “chemical treatment” refers to any chemical pretreatment that promotes the separation and/or release of cellulose, hemicellulose, and/or lignin. Such a pretreatment can convert crystalline cellulose to amorphous cellulose. Examples of suitable chemical pretreatment processes include, for example, dilute acid pretreatment, lime pretreatment, wet oxidation, ammonia fiber/freeze expansion (AFEX), ammonia percolation (APR), ionic liquid, and organosolv pretreatments.

A chemical catalyst such as H_2SO_4 or SO_2 (typically 0.3 to 5% w/w) is sometimes added prior to steam pretreatment, which decreases the time and temperature, increases the recovery, and improves enzymatic hydrolysis (Ballesteros *et al.*, 2006, *Appl. Biochem. Biotechnol.* 129-132: 496-508; Varga *et al.*, 2004, *Appl. Biochem. Biotechnol.* 113-116: 509-523; Sassner *et al.*, 2006, *Enzyme Microb. Technol.* 39: 756-762). In dilute acid pretreatment, the cellulosic-containing material is mixed with dilute acid, typically H_2SO_4, and water to form a slurry, heated by steam to the desired temperature, and after a residence time flashed to atmospheric pressure. The dilute acid pretreatment can be performed with a number of reactor designs, *e.g.*, plug-flow reactors, counter-current reactors, or continuous counter-current shrinking bed reactors (Duff and Murray, 1996, *Bioresource Technology* 855: 1-33; Schell *et al.*, 2004, *Bioresource Technology* 91: 179-188; Lee *et al.*, 1999, *Adv. Biochem. Eng. Biotechnol.* 65: 93-115). In a specific embodiment the dilute acid pretreatment of cellulosic-containing material is carried out using 4% w/w sulfuric acid at 180ºC for 5 minutes.

Several methods of pretreatment under alkaline conditions can also be used. These alkaline pretreatments include, but are not limited to, sodium hydroxide, lime, wet oxidation, ammonia percolation (APR), and ammonia fiber/freeze expansion (AFEX) pretreatment. Lime pretreatment is performed with calcium oxide or calcium hydroxide at temperatures of 85-150°C and residence times from 1 hour to several days (Wyman *et al.*, 2005, *Bioresource Technology* 96: 1959-1966; Mosier *et al.*, 2005, *Bioresource Technology* 96: 673-686). WO 2006/110891, WO 2006/110899, WO 2006/110900, and WO 2006/110901 disclose pretreatment methods using ammonia.

Wet oxidation is a thermal pretreatment performed typically at 180-200°C for 5-15 minutes with addition of an oxidative agent such as hydrogen peroxide or over-pressure of oxygen (Schmidt and Thomsen, 1998, *Bioresource Technology* 64: 139-151; Palonen *et al.*, 2004, *Appl. Biochem. Biotechnol.* 117: 1-17; Varga *et al.*, 2004, *Biotechnol. Bioeng.* 88: 567-574; Martin *et al.*, 2006, *J. Chem. Technol. Biotechnol.* 81: 1669-1677). The pretreatment is performed preferably at 1-40% dry matter, *e.g.*, 2-30% dry matter or 5-20% dry matter, and often the initial pH is increased by the addition of alkali such as sodium carbonate.

A modification of the wet oxidation pretreatment method, known as wet explosion (combination of wet oxidation and steam explosion) can handle dry matter up to 30%. In wet explosion, the oxidizing agent is introduced during pretreatment after a certain residence time. The pretreatment is then ended by flashing to atmospheric pressure (WO 2006/032282).

Ammonia fiber expansion (AFEX) involves treating the cellulosic-containing material with liquid or gaseous ammonia at moderate temperatures such as 90-150°C and high pressure such as 17-20 bar for 5-10 minutes, where the dry matter content can be as high as 60% (Gollapalli *et al.*, 2002, *Appl. Biochem. Biotechnol.* 98: 23-35; Chundawat *et al.*, 2007, *Biotechnol. Bioeng.* 96: 219-231; Alizadeh *et al.*, 2005, *Appl. Biochem. Biotechnol.* 121: 1133-1141; Teymouri *et al.*, 2005, *Bioresource Technology* 96: 2014-2018). During AFEX pretreatment cellulose and hemicelluloses remain relatively intact. Lignin-carbohydrate complexes are cleaved.

Organosolv pretreatment delignifies the cellulosic-containing material by extraction using aqueous ethanol (40-60% ethanol) at 160-200°C for 30-60 minutes (Pan *et al.*, 2005, *Biotechnol.*

Bioeng. 90: 473-481; Pan *et al.*, 2006, *Biotechnol. Bioeng.* 94: 851-861; Kurabi *et al.*, 2005, *Appl. Biochem. Biotechnol.* 121: 219-230). Sulphuric acid is usually added as a catalyst. In organosolv pretreatment, the majority of hemicellulose and lignin is removed.

Other examples of suitable pretreatment methods are described by Schell *et al.*, 2003, *Appl. Biochem. Biotechnol.* 105-108: 69-85, and Mosier *et al.*, 2005, *Bioresource Technology* 96: 673-686, and U.S. Published Application 2002/0164730.

In one embodiment, the chemical pretreatment is carried out as a dilute acid treatment, and more preferably as a continuous dilute acid treatment. The acid is typically sulfuric acid, but other acids can also be used, such as acetic acid, citric acid, nitric acid, phosphoric acid, tartaric acid, succinic acid, hydrogen chloride, or mixtures thereof. Mild acid treatment is conducted in the pH range of preferably 1-5, *e.g.*, 1-4 or 1-2.5. In one aspect, the acid concentration is in the range from preferably 0.01 to 10 wt. % acid, *e.g.*, 0.05 to 5 wt. % acid or 0.1 to 2 wt. % acid. The acid is contacted with the cellulosic-containing material and held at a temperature in the range of preferably 140-200°C, *e.g.*, 165-190°C, for periods ranging from 1 to 60 minutes.

In another embodiment, pretreatment takes place in an aqueous slurry. In preferred aspects, the cellulosic-containing material is present during pretreatment in amounts preferably between 10-80 wt. %, *e.g.*, 20-70 wt. % or 30-60 wt. %, such as around 40 wt. %. The pretreated cellulosic-containing material can be unwashed or washed using any method known in the art, *e.g.*, washed with water.

In one embodiment, the cellulosic-containing material is subjected to mechanical or physical pretreatment. The term “mechanical pretreatment” or “physical pretreatment” refers to any pretreatment that promotes size reduction of particles. For example, such pretreatment can involve various types of grinding or milling (*e.g.*, dry milling, wet milling, or vibratory ball milling).

The cellulosic-containing material can be pretreated both physically (mechanically) and chemically. Mechanical or physical pretreatment can be coupled with steaming/steam explosion, hydrothermolysis, dilute or mild acid treatment, high temperature, high pressure treatment, irradiation (*e.g.*, microwave irradiation), or combinations thereof. In one aspect, high pressure means pressure in the range of preferably about 100 to about 400 psi, *e.g.*, about 150 to about 250 psi. In another aspect, high temperature means temperature in the range of about 100 to about 300°C, *e.g.*, about 140 to about 200°C. In a preferred aspect, mechanical or physical pretreatment is performed in a batch-process using a steam gun hydrolyzer system that uses high pressure and high temperature as defined above, *e.g.*, a Sunds Hydrolyzer available from Sunds Defibrator AB, Sweden. The physical and chemical pretreatments can be carried out sequentially or simultaneously, as desired.

Accordingly, in one embodiment, the cellulosic-containing material is subjected to physical (mechanical) or chemical pretreatment, or any combination thereof, to promote the separation and/or release of cellulose, hemicellulose, and/or lignin.

In one embodiment, the cellulosic-containing material is subjected to a biological pretreatment. The term "biological pretreatment" refers to any biological pretreatment that promotes the separation and/or release of cellulose, hemicellulose, and/or lignin from the cellulosic-containing material. Biological pretreatment techniques can involve applying lignin-solubilizing microorganisms and/or enzymes (see, for example, Hsu, T.-A., 1996, Pretreatment of biomass, in *Handbook on Bioethanol: Production and Utilization*, Wyman, C. E., ed., Taylor & Francis, Washington, DC, 179-212; Ghosh and Singh, 1993, *Adv. Appl. Microbiol.* 39: 295-333; McMillan, J. D., 1994, Pretreating lignocellulosic biomass: a review, in *Enzymatic Conversion of Biomass for Fuels Production*, Himmel, M. E., Baker, J. O., and Overend, R. P., eds., ACS Symposium Series 566, American Chemical Society, Washington, DC, chapter 15; Gong, C. S., Cao, N. J., Du, J., and Tsao, G. T., 1999, Ethanol production from renewable resources, in *Advances in Biochemical Engineering/Biotechnology*, Scheper, T., ed., Springer-Verlag Berlin Heidelberg, Germany, 65: 207-241; Olsson and Hahn-Hagerdal, 1996, *Enz. Microb. Tech.* 18: 312-331; and Vallander and Eriksson, 1990, *Adv. Biochem. Eng./Biotechnol.* 42: 63-95).

Saccharification and Fermentation of Cellulosic-containing material

Saccharification (i.e., hydrolysis) and fermentation, separate or simultaneous, include, but are not limited to, separate hydrolysis and fermentation (SHF); simultaneous saccharification and fermentation (SSF); simultaneous saccharification and co-fermentation (SSCF); hybrid hydrolysis and fermentation (HHF); separate hydrolysis and co-fermentation (SHCF); hybrid hydrolysis and co-fermentation (HHCF).

SHF uses separate process steps to first enzymatically hydrolyze the cellulosic-containing material to fermentable sugars, *e.g.*, glucose, cellobiose, and pentose monomers, and then ferment the fermentable sugars to ethanol. In SSF, the enzymatic hydrolysis of the cellulosic-containing material and the fermentation of sugars to ethanol are combined in one step (Philippidis, G. P., 1996, Cellulose bioconversion technology, in *Handbook on Bioethanol: Production and Utilization*, Wyman, C. E., ed., Taylor & Francis, Washington, DC, 179-212). SSCF involves the co-fermentation of multiple sugars (Sheehan and Himmel, 1999, *Biotechnol. Prog.* 15: 817-827). HHF involves a separate hydrolysis step, and in addition a simultaneous saccharification and hydrolysis step, which can be carried out in the same reactor. The steps in an HHF process can be carried out at different temperatures, *i.e.*, high temperature enzymatic saccharification followed by SSF at a lower temperature that the fermentation organismcan tolerate. It is understood herein that any method known in the art comprising pretreatment, enzymatic hydrolysis (saccharification), fermentation, or a combination thereof, can be used in the practicing the processes described herein.

A conventional apparatus can include a fed-batch stirred reactor, a batch stirred reactor, a continuous flow stirred reactor with ultrafiltration, and/or a continuous plug-flow column reactor (de Castilhos Corazza *et al.*, 2003, *Acta Scientiarum. Technology* 25: 33-38; Gusakov and Sinitsyn, 1985, *Enz. Microb. Technol.* 7: 346-352), an attrition reactor (Ryu and Lee, 1983, *Biotechnol. Bioeng.* 25: 53-65). Additional reactor types include fluidized bed, upflow blanket, immobilized, and extruder type reactors for hydrolysis and/or fermentation.

In the saccharification step (i.e., hydrolysis step), the cellulosic and/or starch-containing material, *e.g.*, pretreated, is hydrolyzed to break down cellulose, hemicellulose, and/or starch to fermentable sugars, such as glucose, cellobiose, xylose, xylulose, arabinose, mannose, galactose, and/or soluble oligosaccharides. The hydrolysis is performed enzymatically e.g., by a cellulolytic enzyme composition. The enzymes of the compositions can be added simultaneously or sequentially.

Enzymatic hydrolysis may be carried out in a suitable aqueous environment under conditions that can be readily determined by one skilled in the art. In one aspect, hydrolysis is performed under conditions suitable for the activity of the enzymes(s), *i.e.*, optimal for the enzyme(s). The hydrolysis can be carried out as a fed batch or continuous process where the cellulosic and/or starch-containing material is fed gradually to, for example, an enzyme containing hydrolysis solution.

The saccharification is generally performed in stirred-tank reactors or fermentors under controlled pH, temperature, and mixing conditions. Suitable process time, temperature and pH conditions can readily be determined by one skilled in the art. For example, the saccharification can last up to 200 hours, but is typically performed for preferably about 12 to about 120 hours, *e.g.*, about 16 to about 72 hours or about 24 to about 48 hours. The temperature is in the range of preferably about 25°C to about 70°C, *e.g.*, about 30°C to about 65°C, about 40°C to about 60°C, or about 50°C to about 55°C. The pH is in the range of preferably about 3 to about 8, *e.g.*, about 3.5 to about 7, about 4 to about 6, or about 4.5 to about 5.5. The dry solids content is in the range of preferably about 5 to about 50 wt. %, *e.g.*, about 10 to about 40 wt. % or about 20 to about 30 wt. %.

Saccharification in may be carried out using a cellulolytic enzyme composition. Such enzyme compositions are described below in the “Cellulolytic Enzyme Composition’-section below. The cellulolytic enzyme compositions can comprise any protein useful in degrading the cellulosic-containing material. In one aspect, the cellulolytic enzyme composition comprises or further comprises one or more (*e.g.*, several) proteins selected from the group consisting of a cellulase, an AA9 (GH61) polypeptide, a hemicellulase, an esterase, an expansin, a ligninolytic enzyme, an oxidoreductase, a pectinase, a protease, and a swollenin.

In another embodiment, the cellulase is preferably one or more (*e.g.*, several) enzymes selected from the group consisting of an endoglucanase, a cellobiohydrolase, and a beta-glucosidase.

In another embodiment, the hemicellulase is preferably one or more (*e.g.*, several) enzymes selected from the group consisting of an acetylmannan esterase, an acetylxylan esterase, an arabinanase, an arabinofuranosidase, a coumaric acid esterase, a feruloyl esterase, a galactosidase, a glucuronidase, a glucuronoyl esterase, a mannanase, a mannosidase, a xylanase, and a xylosidase. In another embodiment, the oxidoreductase is one or more (*e.g.*, several) enzymes selected from the group consisting of a catalase, a laccase, and a peroxidase. The enzymes or enzyme compositions used in a processes of the present invention may be in any form suitable for use, such as, for example, a fermentation broth formulation or a cell composition, a cell lysate with or without cellular debris, a semi-purified or purified enzyme preparation, or a host cell as a source of the enzymes. The enzyme composition may be a dry powder or granulate, a non-dusting granulate, a liquid, a stabilized liquid, or a stabilized protected enzyme. Liquid enzyme preparations may, for instance, be stabilized by adding stabilizers such as a sugar, a sugar alcohol or another polyol, and/or lactic acid or another organic acid according to established processes.

In one embodiment, an effective amount of cellulolytic or hemicellulolytic enzyme composition to the cellulosic-containing material is about 0.5 to about 50 mg, *e.g.*, about 0.5 to about 40 mg, about 0.5 to about 25 mg, about 0.75 to about 20 mg, about 0.75 to about 15 mg, about 0.5 to about 10 mg, or about 2.5 to about 10 mg per g of the cellulosic-containing material.

In one embodiment, such a compound is added at a molar ratio of the compound to glucosyl units of cellulose of about 10^{-6} to about 10, *e.g.*, about 10^{-6} to about 7.5, about 10^{-6} to about 5, about 10^{-6} to about 2.5, about 10^{-6} to about 1, about 10^{-5} to about 1, about 10^{-5} to about 10^{-1}, about 10^{-4} to about 10^{-1}, about 10^{-3} to about 10^{-1}, or about 10^{-3} to about 10^{-2}. In another aspect, an effective amount of such a compound is about 0.1 μM to about 1 M, *e.g.*, about 0.5 μM to about 0.75 M, about 0.75 μM to about 0.5 M, about 1 μM to about 0.25 M, about 1 μM to about 0.1 M, about 5 μM to about 50 mM, about 10 μM to about 25 mM, about 50 μM to about 25 mM, about 10 μM to about 10 mM, about 5 μM to about 5 mM, or about 0.1 mM to about 1 mM.

The term “liquor” means the solution phase, either aqueous, organic, or a combination thereof, arising from treatment of a lignocellulose and/or hemicellulose material in a slurry, or monosaccharides thereof, *e.g.*, xylose, arabinose, mannose, etc., under conditions as described in WO 2012/021401, and the soluble contents thereof. A liquor for cellulolytic enhancement of an AA9 polypeptide (GH61 polypeptide) can be produced by treating a lignocellulose or hemicellulose material (or feedstock) by applying heat and/or pressure, optionally in the presence of a catalyst, *e.g.*, acid, optionally in the presence of an organic solvent, and optionally in combination with physical disruption of the material, and then separating the solution from the residual solids. Such conditions determine the degree of cellulolytic enhancement obtainable through the combination of liquor and an AA9 polypeptide during hydrolysis of a cellulosic substrate by a cellulolytic enzyme preparation. The liquor can be separated from the treated material using a method standard in the art, such as filtration, sedimentation, or centrifugation.

In one embodiment, an effective amount of the liquor to cellulose is about 10^{-6} to about 10 g per g of cellulose, *e.g.*, about 10^{-6} to about 7.5 g, about 10^{-6} to about 5 g, about 10^{-6} to about 2.5 g, about 10^{-6} to about 1 g, about 10^{-5} to about 1 g, about 10^{-5} to about 10^{-1} g, about 10^{-4} to about 10^{-1} g, about 10^{-3} to about 10^{-1} g, or about 10^{-3} to about 10^{-2} g per g of cellulose.

In the fermentation step, sugars, released from the cellulosic-containing material, e.g., as a result of the pretreatment and enzymatic hydrolysis steps, are fermented to ethanol, by a fermenting organism, such as yeast described herein. Hydrolysis (saccharification) and fermentation can be separate or simultaneous.

Any suitable hydrolyzed cellulosic-containing material can be used in the fermentation step in practicing the processes described herein. Such feedstocks include, but are not limited to carbohydrates (e.g., lignocellulose, xylans, cellulose, starch, etc.). The material is generally selected based on economics, *i.e.*, costs per equivalent sugar potential, and recalcitrance to enzymatic conversion.

Production of ethanol by a fermenting organism using cellulosic-containing material results from the metabolism of sugars (monosaccharides). The sugar composition of the hydrolyzed cellulosic-containing material and the ability of the fermenting organism to utilize the different sugars has a direct impact in process yields. Prior to Applicant’s disclosure herein, strains known in the art utilize glucose efficiently but do not (or very limitedly) metabolize pentoses like xylose, a monosaccharide commonly found in hydrolyzed material.

Compositions of the fermentation media and fermentation conditions depend on the fermenting organism and can easily be determined by one skilled in the art. Typically, the fermentation takes place under conditions known to be suitable for generating the fermentation product. In some embodiments, the fermentation process is carried out under aerobic or microaerophilic (i.e., where the concentration of oxygen is less than that in air), or anaerobic conditions. In some embodiments, fermentation is conducted under anaerobic conditions (i.e., no detectable oxygen), or less than about 5, about 2.5, or about 1 mmol/L/h oxygen. In the absence of oxygen, the NADH produced in glycolysis cannot be oxidized by oxidative phosphorylation. Under anaerobic conditions, pyruvate or a derivative thereof may be utilized by the host cell as an electron and hydrogen acceptor in order to generate NAD+.

The fermentation process is typically run at a temperature that is optimal for the recombinant fungal cell. For example, in some embodiments, the fermentation process is performed at a temperature in the range of from about 25°C to about 42°C. Typically the process is carried out a temperature that is less than about 38°C, less than about 35°C, less than about 33°C, or less than about 38°C, but at least about 20°C, 22°C, or 25°C.

A fermentation stimulator can be used in a process described herein to further improve the fermentation, and in particular, the performance of the fermenting organism, such as, rate enhancement and product yield (*e.g.*, ethanol yield). A “fermentation stimulator” refers to stimulators for growth of the fermenting organisms, in particular, yeast. Preferred fermentation stimulators for growth include vitamins and minerals. Examples of vitamins include multivitamins, biotin, pantothenate, nicotinic acid, meso-inositol, thiamine, pyridoxine, para-aminobenzoic acid, folic acid, riboflavin, and Vitamins A, B, C, D, and E. See, for example, Alfenore *et al.*, Improving ethanol production and viability of *Saccharomyces cerevisiae* by a vitamin feeding strategy during fed-batch process, Springer-Verlag (2002), which is hereby incorporated by reference. Examples of minerals include minerals and mineral salts that can supply nutrients comprising P, K, Mg, S, Ca, Fe, Zn, Mn, and Cu.

Cellulolytic Enzymes and Compositions

A cellulolytic enzyme or cellulolytic enzyme composition may be present and/or added during saccharification. A cellulolytic enzyme composition is an enzyme preparation containing one or more (*e.g.*, several) enzymes that hydrolyze cellulosic-containing material. Such enzymes include endoglucanase, cellobiohydrolase, beta-glucosidase, and/or combinations thereof.

In some embodiments, the fermenting organism comprises one or more (e.g., several) heterologous polynucleotides encoding enzymes that hydrolyze cellulosic-containing material (e.g., an endoglucanase, cellobiohydrolase, beta-glucosidase or combinations thereof). Any enzyme described or referenced herein that hydrolyzes cellulosic-containing material is contemplated for expression in the fermenting organism.

The cellulolytic enzyme may be any cellulolytic enzyme that is suitable for the host cells and/or the methods described herein (e.g., an endoglucanase, cellobiohydrolase, beta-glucosidase), such as a naturally occurring cellulolytic enzyme or a variant thereof that retains cellulolytic enzyme activity.

In some embodiments, the fermenting organism comprising a heterologous polynucleotide encoding a cellulolytic enzyme has an increased level of cellulolytic enzyme activity (e.g., increased endoglucanase, cellobiohydrolase, and/or beta-glucosidase) compared to the host cells without the heterologous polynucleotide encoding the cellulolytic enzyme, when cultivated under the same conditions. In some embodiments, the fermenting organism has an increased level of cellulolytic enzyme activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the fermenting organism without the heterologous polynucleotide encoding the cellulolytic enzyme, when cultivated under the same conditions.

Exemplary cellulolytic enzymes that can be used with the host cells and/or the methods described herein include bacterial, yeast, or filamentous fungal cellulolytic enzymes, e.g., obtained from any of the microorganisms described or referenced herein, as described *supra* under the sections related to proteases.

The cellulolytic enzyme may be of any origin. In an embodiment the cellulolytic enzyme is derived from a strain of *Trichoderma*, such as a strain of *Trichoderma reesei*; a strain of *Humicola*, such as a strain of *Humicola insolens*, and/or a strain of *Chrysosporium*, such as a strain of *Chrysosporium lucknowense*. In a preferred embodiment the cellulolytic enzyme is derived from a strain of *Trichoderma reesei*.

The cellulolytic enzyme composition may further comprise one or more of the following polypeptides, such as enzymes: AA9 polypeptide (GH61 polypeptide) having cellulolytic enhancing activity, beta-glucosidase, xylanase, beta-xylosidase, CBH I, CBH II, or a mixture of two, three, four, five or six thereof.

The further polypeptide(s) (*e.g.*, AA9 polypeptide) and/or enzyme(s) (*e.g.*, beta-glucosidase, xylanase, beta-xylosidase, CBH I and/or CBH II may be foreign to the cellulolytic enzyme composition producing organism (*e.g.*, *Trichoderma reesei*).

In an embodiment the cellulolytic enzyme composition comprises an AA9 polypeptide having cellulolytic enhancing activity and a beta-glucosidase.

In another embodiment the cellulolytic enzyme composition comprises an AA9 polypeptide having cellulolytic enhancing activity, a beta-glucosidase, and a CBH I.

In another embodiment the cellulolytic enzyme composition comprises an AA9 polypeptide having cellulolytic enhancing activity, a beta-glucosidase, a CBH I and a CBH II.
Other enzymes, such as endoglucanases, may also be comprised in the cellulolytic enzyme composition.

As mentioned above the cellulolytic enzyme composition may comprise a number of difference polypeptides, including enzymes.

In one embodiment, the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Thermoascus aurantiacus* AA9 (GH61A) polypeptide having cellulolytic enhancing activity (e.g., WO 2005/074656), and *Aspergillus oryzae* beta-glucosidase fusion protein (e.g., one disclosed in WO 2008/057637, in particular shown as SEQ ID NOs: 59 and 60).

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Thermoascus aurantiacus* AA9 (GH61A) polypeptide having cellulolytic enhancing activity (e.g., SEQ ID NO: 2 in WO 2005/074656), and *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499).

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Penicillium emersonii* AA9 (GH61A) polypeptide having cellulolytic enhancing activity, in particular the one disclosed in WO 2011/041397, and *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499).

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Penicillium emersonii* AA9 (GH61A) polypeptide having cellulolytic enhancing activity, in particular the one disclosed in WO 2011/041397, and *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499) or a variant disclosed in WO 2012/044915 (hereby incorporated by reference), in particular one comprising one or more such as all of the following substitutions: F100D, S283G, N456E, F512Y.

In an embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic composition, further comprising an AA9 (GH61A) polypeptide having cellulolytic enhancing activity, in particular the one derived from a strain of *Penicillium emersonii* (e.g., SEQ ID NO: 2 in WO 2011/041397), *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 in WO 2005/047499) variant with one or more, in particular all of the following substitutions: F100D, S283G, N456E, F512Y and disclosed in WO 2012/044915; *Aspergillus fumigatus* Cel7A CBH1, e.g., the one disclosed as SEQ ID NO: 6 in WO2011/057140 and *Aspergillus fumigatus* CBH II, e.g., the one disclosed as SEQ ID NO: 18 in WO 2011/057140.

In a preferred embodiment the cellulolytic enzyme composition is a *Trichoderma reesei,* cellulolytic enzyme composition, further comprising a hemicellulase or hemicellulolytic enzyme composition, such as an *Aspergillus fumigatus* xylanase and *Aspergillus fumigatus* beta-xylosidase.

In an embodiment the cellulolytic enzyme composition also comprises a xylanase (*e.g.*, derived from a strain of the genus *Aspergillus*, in particular *Aspergillus aculeatus* or *Aspergillus fumigatus;* or a strain of the genus *Talaromyces*, in particular *Talaromyces leycettanus*) and/or a beta-xylosidase (*e.g.*, derived from *Aspergillus*, in particular *Aspergillus fumigatus*, or a strain of *Talaromyces*, in particular *Talaromyces emersonii*).

In an embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Thermoascus aurantiacus* AA9 (GH61A) polypeptide having cellulolytic enhancing activity (e.g., WO 2005/074656), *Aspergillus oryzae* beta-glucosidase fusion protein (e.g., one disclosed in WO 2008/057637, in particular as SEQ ID NOs: 59 and 60), and *Aspergillus aculeatus* xylanase (e.g., Xyl II in WO 94/21785).

In another embodiment the cellulolytic enzyme composition comprises a *Trichoderma reesei* cellulolytic preparation, further comprising *Thermoascus aurantiacus* GH61A polypeptide having cellulolytic enhancing activity (e.g., SEQ ID NO: 2 in WO 2005/074656), *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499) and *Aspergillus aculeatus* xylanase (Xyl II disclosed in WO 94/21785).

In another embodiment the cellulolytic enzyme composition comprises a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Thermoascus aurantiacus* AA9 (GH61A) polypeptide having cellulolytic enhancing activity (e.g., SEQ ID NO: 2 in WO 2005/074656), *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499) and *Aspergillus aculeatus* xylanase (e.g., Xyl II disclosed in WO 94/21785).

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Penicillium emersonii* AA9 (GH61A) polypeptide having cellulolytic enhancing activity, in particular the one disclosed in WO 2011/041397, *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499) and *Aspergillus fumigatus* xylanase (e.g., Xyl III in WO 2006/078256).

In another embodiment the cellulolytic enzyme composition comprises a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Penicillium emersonii* AA9 (GH61A) polypeptide having cellulolytic enhancing activity, in particular the one disclosed in WO

2011/041397, *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499), *Aspergillus fumigatus* xylanase (e.g., Xyl III in WO 2006/078256), and CBH I from *Aspergillus fumigatus*, in particular Cel7A CBH1 disclosed as SEQ ID NO: 2 in WO2011/057140.

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Penicillium emersonii* AA9 (GH61A) polypeptide having cellulolytic enhancing activity, in particular the one disclosed in WO 2011/041397, *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499), *Aspergillus fumigatus* xylanase (e.g., Xyl III in WO 2006/078256), CBH I from *Aspergillus fumigatus*, in particular Cel7A CBH1 disclosed as SEQ ID NO: 2 in WO 2011/057140, and CBH II derived from *Aspergillus fumigatus* in particular the one disclosed as SEQ ID NO: 4 in WO 2013/028928.

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition, further comprising *Penicillium emersonii* AA9 (GH61A) polypeptide having cellulolytic enhancing activity, in particular the one disclosed in WO 2011/041397, *Aspergillus fumigatus* beta-glucosidase (e.g., SEQ ID NO: 2 of WO 2005/047499) or variant thereof with one or more, in particular all, of the following substitutions: F100D, S283G, N456E, F512Y; *Aspergillus fumigatus* xylanase (e.g., Xyl III in WO 2006/078256), CBH I from *Aspergillus fumigatus*, in particular Cel7A CBH I disclosed as SEQ ID NO: 2 in WO 2011/057140, and CBH II derived from *Aspergillus fumigatus*, in particular the one disclosed in WO 2013/028928.

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition comprising the CBH I (GENSEQP Accession No. AZY49536 (WO2012/103293); a CBH II (GENSEQP Accession No. AZY49446 (WO2012/103288); a beta-glucosidase variant (GENSEQP Accession No. AZU67153 (WO 2012/44915)), in particular with one or more, in particular all, of the following substitutions: F100D, S283G, N456E, F512Y; and AA9 (GH61 polypeptide) (GENSEQP Accession No. BAL61510 (WO 2013/028912)).

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition comprising a CBH I (GENSEQP Accession No. AZY49536 (WO2012/103293)); a CBH II (GENSEQP Accession No. AZY49446 (WO2012/103288); a GH10 xylanase (GENSEQP Accession No. BAK46118 (WO 2013/019827)); and a beta-xylosidase (GENSEQP Accession No. AZI04896 (WO 2011/057140)).

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition comprising a CBH I (GENSEQP Accession No. AZY49536

(WO2012/103293)); a CBH II (GENSEQP Accession No. AZY49446 (WO2012/103288)); and an AA9 (GH61 polypeptide; GENSEQP Accession No. BAL61510 (WO 2013/028912)).

In another embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition comprising a CBH I (GENSEQP Accession No. AZY49536 (WO2012/103293)); a CBH II (GENSEQP Accession No. AZY49446 (WO2012/103288)), an AA9 (GH61 polypeptide; GENSEQP Accession No. BAL61510 (WO 2013/028912)), and a catalase (GENSEQP Accession No. BAC11005 (WO 2012/130120)).

In an embodiment the cellulolytic enzyme composition is a *Trichoderma reesei* cellulolytic enzyme composition comprising a CBH I (GENSEQP Accession No. AZY49446 (WO2012/103288); a CBH II (GENSEQP Accession No. AZY49446 (WO2012/103288)), a beta-glucosidase variant (GENSEQP Accession No. AZU67153 (WO 2012/44915)), with one or more, in particular all, of the following substitutions: F100D, S283G, N456E, F512Y; an AA9 (GH61 polypeptide; GENSEQP Accession No. BAL61510 (WO 2013/028912)), a GH10 xylanase (GENSEQP Accession No. BAK46118 (WO 2013/019827)), and a beta-xylosidase (GENSEQP Accession No. AZI04896 (WO 2011/057140)).

In an embodiment the cellulolytic composition is a *Trichoderma reesei* cellulolytic enzyme preparation comprising an EG I (Swissprot Accession No. P07981), EG II (EMBL Accession No. M19373), CBH I (*supra*); CBH II (*supra*); beta-glucosidase variant (*supra*) with the following substitutions: F100D, S283G, N456E, F512Y; an AA9 (GH61 polypeptide; *supra*), GH10 xylanase (*supra*); and beta-xylosidase (*supra*).

All cellulolytic enzyme compositions disclosed in WO 2013/028928 are also contemplated and hereby incorporated by reference.

The cellulolytic enzyme composition comprises or may further comprise one or more (several) proteins selected from the group consisting of a cellulase, a AA9 (i.e., GH61) polypeptide having cellulolytic enhancing activity, a hemicellulase, an expansin, an esterase, a laccase, a ligninolytic enzyme, a pectinase, a peroxidase, a protease, and a swollenin.

In one embodiment the cellulolytic enzyme composition is a commercial cellulolytic enzyme composition. Examples of commercial cellulolytic enzyme compositions suitable for use in a process of the invention include: CELLIC® CTec (Novozymes A/S), CELLIC® CTec2 (Novozymes A/S), CELLIC® CTec3 (Novozymes A/S), CELLUCLAST™ (Novozymes A/S), SPEZYME™ CP (Genencor Int.), ACCELLERASE™ 1000, ACCELLERASE 1500, ACCELLERASE™ TRIO (DuPont), FILTRASE® NL (DSM); METHAPLUS® S/L 100 (DSM), ROHAMENT™ 7069 W (Röhm GmbH), or ALTERNAFUEL® CMAX3™ (Dyadic International, Inc.). The cellulolytic enzyme composition may be added in an amount effective from about 0.001

to about 5.0 wt. % of solids, *e.g.*, about 0.025 to about 4.0 wt. % of solids or about 0.005 to about 2.0 wt. % of solids.

Additional enzymes, and compositions thereof can be found in WO2011/153516 and WO2016/045569 (the contents of which are incorporated herein).

Additional polynucleotides encoding suitable cellulolytic enzymes may be obtained from microorganisms of any genus, including those readily available within the UniProtKB database (www.uniprot.org).

The cellulolytic enzyme coding sequences can also be used to design nucleic acid probes to identify and clone DNA encoding cellulolytic enzymes from strains of different genera or species, as described *supra*.

The polynucleotides encoding cellulolytic enzymes may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc,) as described *supra*.

Techniques used to isolate or clone polynucleotides encoding cellulolytic enzymes are described *supra*.

In one embodiment, the cellulolytic enzyme has a mature polypeptide sequence of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any cellulolytic enzyme described or referenced herein (e.g., any endoglucanase, cellobiohydrolase, or beta-glucosidase). In one aspect, the cellulolytic enzyme ha a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from any cellulolytic enzyme described or referenced herein. In one embodiment, the cellulolytic enzyme has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any cellulolytic enzyme described or referenced herein, allelic variant, or a fragment thereof having cellulolytic enzyme activity. In one embodiment, the cellulolytic enzyme has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) amino acids. In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

In some embodiments, the cellulolytic enzyme has at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of the cellulolytic enzyme activity of any cellulolytic enzyme described or referenced herein (e.g., any endoglucanase, cellobiohydrolase, or beta-glucosidase) under the same conditions.

In one embodiment, the cellulolytic enzyme coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any cellulolytic enzyme described or referenced herein (e.g., any endoglucanase, cellobiohydrolase, or beta-glucosidase). In one embodiment, the cellulolytic enzyme coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any cellulolytic enzyme described or referenced herein.

In one embodiment, the polynucleotide encoding the cellulolytic enzyme comprises the coding sequence of any cellulolytic enzyme described or referenced herein (e.g., any endoglucanase, cellobiohydrolase, or beta-glucosidase). In one embodiment, the polynucleotide encoding the cellulolytic enzyme comprises a subsequence of the coding sequence from any cellulolytic enzyme described or referenced herein, wherein the subsequence encodes a polypeptide having cellulolytic enzyme activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The cellulolytic enzyme can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

Xylose metabolism

In one aspect, the fermenting organism (e.g., yeast cell) further comprises a heterologous polynucleotide encoding a xylose isomerase (XI). The xylose isomerase may be any xylose isomerase that is suitable for the host cells and the methods described herein, such as a naturally occurring xylose isomerase or a variant thereof that retains xylose isomerase activity. In one embodiment, the xylose isomerase is present in the cytosol of the host cells.

In some embodiments, the fermenting organism comprising a heterologous polynucleotide encoding a xylose isomerase has an increased level of xylose isomerase activity compared to the host cells without the heterologous polynucleotide encoding the xylose isomerase, when cultivated under the same conditions. In some embodiments, the fermenting organisms have an increased level of xylose isomerase activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the host cells without the heterologous polynucleotide encoding the xylose isomerase, when cultivated under the same conditions.

Exemplary xylose isomerases that can be used with the recombinant host cells and methods of use described herein include, but are not limited to, XIs from the fungus *Piromyces sp.* (WO2003/062430) or other sources (Madhavan et al., 2009, *Appl Microbiol Biotechnol.* 82(6), 1067-1078) have been expressed in *S. cerevisiae* host cells. Still other XIs suitable for expression in yeast have been described in US 2012/0184020 (an XI from *Ruminococcus flavefaciens*), WO2011/078262 (several XIs from *Reticulitermes speratus* and *Mastotermes darwiniensis*) and WO2012/009272 (constructs and fungal cells containing an XI from *Abiotrophia defectiva*). US 8,586,336 describes a *S. cerevisiae* host cell expressing an XI obtained by bovine rumen fluid (shown herein as SEQ ID NO: 74).

Additional polynucleotides encoding suitable xylose isomerases may be obtained from microorganisms of any genus, including those readily available within the UniProtKB database (www.uniprot.org). In one embodiment, the xylose isomerases is a bacterial, a yeast, or a filamentous fungal xylose isomerase, e.g., obtained from any of the microorganisms described or referenced herein, as described *supra*.

The xylose isomerase coding sequences can also be used to design nucleic acid probes to identify and clone DNA encoding xylose isomerases from strains of different genera or species, as described *supra*.

The polynucleotides encoding xylose isomerases may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc,) as described *supra*.

Techniques used to isolate or clone polynucleotides encoding xylose isomerases are described *supra*.

In one embodiment, the xylose isomerase has a mature polypeptide sequence of having at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any xylose isomerase described or referenced herein (e.g., the xylose isomerase of SEQ ID NO: 74). In one aspect, the xylose isomerase has a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from any xylose isomerase described or referenced herein (e.g., the xylose isomerase of SEQ ID NO: 74). In one embodiment, the xylose isomerase has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any xylose isomerase described or referenced herein (e.g., the xylose isomerase of SEQ ID NO: 74), allelic variant, or a fragment thereof having xylose isomerase activity. In one embodiment, the xylose isomerase has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) amino acids. In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

In some embodiments, the xylose isomerase has at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of the xylose isomerase activity of any xylose isomerase described or referenced herein (e.g., the xylose isomerase of SEQ ID NO: 74) under the same conditions.

In one embodiment, the xylose isomerase coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any xylose isomerase described or referenced herein (e.g., the xylose isomerase of SEQ ID NO: 74). In one embodiment, the xylose isomerase coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any xylose isomerase described or referenced herein (e.g., the xylose isomerase of SEQ ID NO: 74).

In one embodiment, the heterologous polynucleotide encoding the xylose isomerase comprises the coding sequence of any xylose isomerase described or referenced herein (e.g., the xylose isomerase of SEQ ID NO: 74). In one embodiment, the heterologous polynucleotide encoding the xylose isomerase comprises a subsequence of the coding sequence from any xylose isomerase described or referenced herein, wherein the subsequence encodes a polypeptide having xylose isomerase activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The xylose isomerases can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

In one aspect, the fermenting organism (e.g., yeast cell) further comprises a heterologous polynucleotide encoding a xylulokinase (XK). A xylulokinase, as used herein, provides enzymatic activity for converting D-xylulose to xylulose 5-phosphate. The xylulokinase may be any xylulokinase that is suitable for the host cells and the methods described herein, such as a naturally occurring xylulokinase or a variant thereof that retains xylulokinase activity. In one embodiment, the xylulokinase is present in the cytosol of the host cells.

In some embodiments, the fermenting organisms comprising a heterologous polynucleotide encoding a xylulokinase have an increased level of xylulokinase activity compared to the host cells without the heterologous polynucleotide encoding the xylulokinase, when cultivated under the same conditions. In some embodiments, the host cells have an increased level of xylose isomerase activity of at least 5%, e.g., at least 10%, at least 15%, at least 20%, at least 25%, at least 50%, at least 100%, at least 150%, at least 200%, at least 300%, or at 500% compared to the host cells without the heterologous polynucleotide encoding the xylulokinase, when cultivated under the same conditions.

Exemplary xylulokinases that can be used with the fermenting organisms and methods of use described herein include, but are not limited to, the *Saccharomyces cerevisiae* xylulokinase of SEQ ID NO: 75. Additional polynucleotides encoding suitable xylulokinases may be obtained from microorganisms of any genus, including those readily available within the UniProtKB database (www.uniprot.org). In one embodiment, the xylulokinases is a bacterial, a yeast, or a filamentous fungal xylulokinase, e.g., obtained from any of the microorganisms described or referenced herein, as described *supra*.

The xylulokinase coding sequences can also be used to design nucleic acid probes to identify and clone DNA encoding xylulokinases from strains of different genera or species, as described *supra*.

The polynucleotides encoding xylulokinases may also be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc,) as described *supra*.

Techniques used to isolate or clone polynucleotides encoding xylulokinases are described *supra*.

In one embodiment, the xylulokinase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to any xylulokinase described or referenced herein (e.g., the *Saccharomyces cerevisiae* xylulokinase of SEQ ID NO: 75). In one embodiment, the xylulokinase has a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from any xylulokinase described or referenced herein (e.g., the *Saccharomyces cerevisiae* xylulokinase of SEQ ID NO: 75). In one embodiment, the xylulokinase has a mature polypeptide sequence that comprises or consists of the amino acid sequence of any xylulokinase described or referenced herein (e.g., the *Saccharomyces cerevisiae* xylulokinase of SEQ ID NO: 75), allelic variant, or a fragment thereof having xylulokinase activity. In one embodiment, the xylulokinase has an amino acid substitution, deletion, and/or insertion of one or more (e.g., two, several) amino acids. In some embodiments, the total number of amino acid substitutions, deletions and/or insertions is not more than 10, e.g., not more than 9, 8, 7, 6, 5, 4, 3, 2, or 1.

In some embodiments, the xylulokinase has at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% of the xylulokinase activity of any xylulokinase described or referenced herein (e.g., the *Saccharomyces cerevisiae* xylulokinase of SEQ ID NO: 75) under the same conditions.

In one embodiment, the xylulokinase coding sequence hybridizes under at least low stringency conditions, e.g., medium stringency conditions, medium-high stringency conditions, high stringency conditions, or very high stringency conditions with the full-length complementary strand of the coding sequence from any xylulokinase described or referenced herein (e.g., the *Saccharomyces cerevisiae* xylulokinase of SEQ ID NO: 75). In one embodiment, the xylulokinase coding sequence has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity with the coding sequence from any xylulokinase described or referenced herein (e.g., the *Saccharomyces cerevisiae* xylulokinase of SEQ ID NO: 75).

In one embodiment, the heterologous polynucleotide encoding the xylulokinase comprises the coding sequence of any xylulokinase described or referenced herein (e.g., the *Saccharomyces cerevisiae* xylulokinase of SEQ ID NO: 75). In one embodiment, the heterologous polynucleotide encoding the xylulokinase comprises a subsequence of the coding sequence from any xylulokinase described or referenced herein, wherein the subsequence encodes a polypeptide having xylulokinase activity. In one embodiment, the number of nucleotides residues in the subsequence is at least 75%, e.g., at least 80%, 85%, 90%, or 95% of the number of the referenced coding sequence.

The xylulokinases can also include fused polypeptides or cleavable fusion polypeptides, as described *supra*.

In one aspect, the fermenting organism (e.g., yeast cell) further comprises a heterologous polynucleotide encoding a ribulose 5 phosphate 3-epimerase (RPE1). A ribulose 5 phosphate 3-epimerase, as used herein, provides enzymatic activity for converting L-ribulose 5-phosphate to L-xylulose 5-phosphate (EC 5.1.3.22). The RPE1 may be any RPE1 that is suitable for the host cells and the methods described herein, such as a naturally occurring RPE1 or a variant thereof that retains RPE1 activity. In one embodiment, the RPE1 is present in the cytosol of the host cells. In one embodiment, the recombinant cell comprises a heterologous polynucleotide encoding a ribulose 5 phosphate 3-epimerase (RPE1), wherein the RPE1 is *Saccharomyces cerevisiae* RPE1, or an RPE1 having at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a *Saccharomyces cerevisiae* RPE1.

In one aspect, the fermenting organism (e.g., yeast cell) further comprises a heterologous polynucleotide encoding a ribulose 5 phosphate isomerase (RKI1). A ribulose 5 phosphate isomerase, as used herein, provides enzymatic activity for converting ribose-5-phophate to ribulose 5-phosphate. The RKI1 may be any RKI1 that is suitable for the host cells and the methods described herein, such as a naturally occurring RKI1 or a variant thereof that retains RKI1 activity. In one embodiment, the RKI1 is present in the cytosol of the host cells.

In one embodiment, the fermenting organism comprises a heterologous polynucleotide encoding a ribulose 5 phosphate isomerase (RKI1), wherein the RKI1 is a *Saccharomyces cerevisiae* RKI1, or an RKI1 having a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a *Saccharomyces cerevisiae* RKI1.

In one aspect, the fermenting organism (e.g., yeast cell) further comprises a heterologous polynucleotide encoding a transketolase (TKL1). The TKL1 may be any TKL1 that is suitable for the host cells and the methods described herein, such as a naturally occurring TKL1 or a variant thereof that retains TKL1 activity. In one embodiment, the TKL1 is present in the cytosol of the host cells.

In one embodiment, the fermenting organism comprises a heterologous polynucleotide encoding a transketolase (TKL1), wherein the TKL1 is a *Saccharomyces cerevisiae* TKL1, or a TKL1 having a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a *Saccharomyces cerevisiae* TKL1.

In one aspect, the fermenting organism (e.g., yeast cell) further comprises a heterologous polynucleotide encoding a transaldolase (TAL1). The TAL1 may be any TAL1 that is suitable for the host cells and the methods described herein, such as a naturally occurring TAL1 or a variant thereof that retains TAL1 activity. In one embodiment, the TAL1 is present in the cytosol of the host cells.

In one embodiment, the fermenting organism comprises a heterologous polynucleotide encoding a transketolase (TAL1), wherein the TAL1 is a *Saccharomyces cerevisiae* TAL1, or a TAL1 having a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to a *Saccharomyces cerevisiae* TAL1.

Fermentation products

A fermentation product can be any substance derived from the fermentation. The fermentation product can be, without limitation, an alcohol (*e.g.*, arabinitol, n-butanol, isobutanol, ethanol, glycerol, methanol, ethylene glycol, 1,3-propanediol [propylene glycol], butanediol, glycerin, sorbitol, and xylitol); an alkane (*e.g.*, pentane, hexane, heptane, octane, nonane, decane, undecane, and dodecane), a cycloalkane (*e.g.*, cyclopentane, cyclohexane, cycloheptane, and cyclooctane), an alkene (*e.g.*, pentene, hexene, heptene, and octene); an amino acid (*e.g.*, aspartic acid, glutamic acid, glycine, lysine, serine, and threonine); a gas (*e.g.*, methane, hydrogen (H_2), carbon dioxide (CO_2), and carbon monoxide (CO)); isoprene; a ketone (*e.g.*, acetone); an organic acid (*e.g.*, acetic acid, acetonic acid, adipic acid, ascorbic acid, citric acid, 2,5-diketo-D-gluconic acid, formic acid, fumaric acid, glucaric acid, gluconic acid, glucuronic acid, glutaric acid, 3-hydroxypropionic acid, itaconic acid, lactic acid, malic acid, malonic acid, oxalic acid, oxaloacetic acid, propionic acid, succinic acid, and xylonic acid); and polyketide.

In one aspect, the fermentation product is an alcohol. The term “alcohol” encompasses a substance that contains one or more hydroxyl moieties. The alcohol can be, but is not limited to, n-butanol, isobutanol, ethanol, methanol, arabinitol, butanediol, ethylene glycol, glycerin, glycerol, 1,3-propanediol, sorbitol, xylitol. See, for example, Gong *et al.*, 1999, Ethanol production from renewable resources, in *Advances in Biochemical Engineering/Biotechnology*, Scheper, T., ed., Springer-Verlag Berlin Heidelberg, Germany, 65: 207-241; Silveira and Jonas, 2002, *Appl. Microbiol. Biotechnol.* 59: 400-408; Nigam and Singh, 1995, *Process Biochemistry* 30(2): 117-124; Ezeji *et al.*, 2003, *World Journal of Microbiology and Biotechnology* 19(6): 595-603. In one embodiment, the fermentation product is ethanol.

In another aspect, the fermentation product is an alkane. The alkane may be an unbranched or a branched alkane. The alkane can be, but is not limited to, pentane, hexane, heptane, octane, nonane, decane, undecane, or dodecane.

In another aspect, the fermentation product is a cycloalkane. The cycloalkane can be, but is not limited to, cyclopentane, cyclohexane, cycloheptane, or cyclooctane.

In another aspect, the fermentation product is an alkene. The alkene may be an unbranched or a branched alkene. The alkene can be, but is not limited to, pentene, hexene, heptene, or octene.

In another aspect, the fermentation product is an amino acid. The organic acid can be, but is not limited to, aspartic acid, glutamic acid, glycine, lysine, serine, or threonine. See, for example, Richard and Margaritis, 2004, *Biotechnology and Bioengineering* 87(4): 501-515.

In another aspect, the fermentation product is a gas. The gas can be, but is not limited to, methane, H_2, CO_2, or CO. See, for example, Kataoka *et al.*, 1997, *Water Science and Technology* 36(6-7): 41-47; and Gunaseelan, 1997, *Biomass and Bioenergy* 13(1-2): 83-114.

In another aspect, the fermentation product is isoprene.

In another aspect, the fermentation product is a ketone. The term “ketone” encompasses a substance that contains one or more ketone moieties. The ketone can be, but is not limited to, acetone.

In another aspect, the fermentation product is an organic acid. The organic acid can be, but is not limited to, acetic acid, acetonic acid, adipic acid, ascorbic acid, citric acid, 2,5-diketo-D-gluconic acid, formic acid, fumaric acid, glucaric acid, gluconic acid, glucuronic acid, glutaric acid, 3-hydroxypropionic acid, itaconic acid, lactic acid, malic acid, malonic acid, oxalic acid, propionic acid, succinic acid, or xylonic acid. See, for example, Chen and Lee, 1997, *Appl. Biochem. Biotechnol.* 63-65: 435-448.

In another aspect, the fermentation product is polyketide.

In some aspects, the fermenting organism (or processes thereof), provide higher yield of fermentation product (e.g., ethanol) when compared to the same process using an identical cell without the heterologous polynucleotide encoding the phospholipase under the same conditions (e.g., at about or after 54 hours fermentation, such as the conditions described in Example 3 or 4). In some embodiments, the process results in at least 0.25%, such as 0.5%, 0.75%, 1.0%, 1.25%, 1.5%, 1.75%, 2%, 3% or 5% higher yield of the fermentation product (e.g., ethanol).

Recovery

The fermentation product, e.g., ethanol, can optionally be recovered from the fermentation medium using any method known in the art including, but not limited to, chromatography, electrophoretic procedures, differential solubility, distillation, or extraction. For example, alcohol is separated from the fermented cellulosic material and purified by conventional methods of distillation. Ethanol with a purity of up to about 96 vol. % can be obtained, which can be used as, for example, fuel ethanol, drinking ethanol, *i.e.*, potable neutral spirits, or industrial ethanol.

In some aspects of the methods, the fermentation product after being recovered is substantially pure. With respect to the methods herein, "substantially pure" intends a recovered preparation that contains no more than 15% impurity, wherein impurity intends compounds other than the fermentation product (e.g., ethanol). In one variation, a substantially pure preparation is provided wherein the preparation contains no more than 25% impurity, or no more than 20% impurity, or no more than 10% impurity, or no more than 5% impurity, or no more than 3% impurity, or no more than 1% impurity, or no more than 0.5% impurity.

Suitable assays to test for the production of ethanol and contaminants, and sugar consumption can be performed using methods known in the art. For example, ethanol product, as well as other organic compounds, can be analyzed by methods such as HPLC (High Performance Liquid Chromatography), GC-MS (Gas Chromatography Mass Spectroscopy) and LC-MS (Liquid Chromatography-Mass Spectroscopy) or other suitable analytical methods using routine procedures well known in the art. The release of ethanol in the fermentation broth can also be tested with the culture supernatant. Byproducts and residual sugar in the fermentation medium (e.g., glucose or xylose) can be quantified by HPLC using, for example, a refractive index detector for glucose and alcohols, and a UV detector for organic acids (Lin et al., *Biotechnol. Bioeng.* 90:775 -779 (2005)), or using other suitable assay and detection methods well known in the art.

The invention may further be described in the following numbered paragraphs:

Paragraph [1]. A method of producing a fermentation product from a starch-containing or cellulosic-containing material comprising:

(a) saccharifying the starch-containing or cellulosic-containing material; and

(b) fermenting the saccharified material of step (a) with a fermenting organism;

wherein the fermenting organism comprises a heterologous polynucleotide encoding a phospholipase.

Paragraph [2]. The method of paragraph [1], wherein the phospholipase is a Phospholipase A or a Phospholipase C.

Paragraph [3]. The method of paragraph [1] or [2], wherein the phospholipase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342 (e.g., any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242).

Paragraph [4]. The method of any one of paragraphs [1]-[3], wherein the heterologous polynucleotide encodes a phospholipase having a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342 (e.g., any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242).

Paragraph [5]. The method of any one of paragraphs [1]-[4], wherein the heterologous polynucleotide encodes a phospholipase having a mature polypeptide sequence comprising or consisting of the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342 (e.g., any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242).

Paragraph [6]. The method of any one of paragraphs [1]-[5], wherein saccharification of step (a) occurs on a starch-containing material, and wherein the starch-containing material is either gelatinized or ungelatinized starch.

Paragraph [7]. The method of paragraph [6], comprising liquefying the starch-containing material by contacting the material with an alpha-amylase prior to saccharification.

Paragraph [8]. The method of paragraph [7], wherein liquefying the starch-containing material and/or saccharifying the starch-containing material is conducted in presence of exogenously added protease.

Paragraph [9]. The method of any one of paragraphs [1]-[8], wherein fermentation is performed under reduced nitrogen conditions (e.g., less than 1000 ppm urea or ammonium hydroxide, such as less than 750 ppm, less than 500 ppm, less than 400 ppm, less than 300 ppm, less than 250 ppm, less than 200 ppm, less than 150 ppm, less than 100 ppm, less than 75 ppm, less than 50 ppm, less than 25 ppm, or less than 10 ppm).

Paragraph [10]. The method of any one of paragraphs [1]-[9], wherein fermentation and saccharification are performed simultaneously in a simultaneous saccharification and fermentation (SSF).

Paragraph [11]. The method of any one of paragraphs [1]-[9], wherein fermentation and saccharification are performed sequentially (SHF).

Paragraph [12]. The method of any one of paragraphs paragraph [1]-[11], comprising recovering the fermentation product from the fermentation.

Paragraph [13]. The method of paragraph [12], wherein recovering the fermentation product from the from the fermentation comprises distillation.

Paragraph [14]. The method of any one of paragraphs [1]-[13], wherein the fermentation product is ethanol.

Paragraph [15]. The method of any one of paragraphs [1]-[14], wherein the fermenting organism comprises a heterologous polynucleotide encoding a glucoamylase.

Paragraph [16]. The method of paragraph [15], wherein the glucoamylase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of a *Pycnoporus* glycoamylase (e.g., a *Pycnoporus sanguineus* glucoamylase of SEQ ID NO: 229), a *Gloeophyllum* glucoamylase (e.g. a *Gloeophyllum sepiarium* of SEQ ID NO: 8), or a glucoamylase of any one of SEQ ID NOs: 102-113 (e.g., a *Saccharomycopsis fibuligera* glucoamylase of SEQ ID NO: 103 or 104, or a *Trichoderma reesei* glucoamylase of SEQ ID NO: 230).

Paragraph [17]. The method of any one of paragraphs [1]-[16], wherein the fermenting organism comprises a heterologous polynucleotide encoding an alpha-amylase.

Paragraph [18]. The method of paragraph [17], wherein the alpha-amylase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 76-101, 121-174 and 231.

Paragraph [19]. The method of any one of paragraphs [1]-[18], wherein the fermenting organism comprises a heterologous polynucleotide encoding a protease.

Paragraph [20]. The method of paragraph [19], wherein the protease has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 9-73 (e.g., any one of SEQ ID NOs: 9, 14, 16, 21, 22, 33, 41, 45, 61, 62, 66, 67, and 69; such as any one of SEQ NOs: 9, 14, 16, and 69).

Paragraph [21]. The method of any one of paragraphs [1]-[20], wherein the fermenting organism comprises a heterologous polynucleotide encoding a trehalase.

Paragraph [22]. The method of paragraph [21], wherein the trehalase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 175-226.

Paragraph [23]. The method of any one of paragraphs [1]-[22], wherein saccharification of step occurs on a cellulosic-containing material, and wherein the cellulosic-containing material is pretreated.

Paragraph [24]. The method of paragraph [23], wherein the pretreatment is a dilute acid pretreatment.

Paragraph [25]. The method of any one of paragraphs [1]-[24], wherein saccharification occurs on a cellulosic-containing material, and wherein the enzyme composition comprises one or more enzymes selected from a cellulase, an AA9 polypeptide, a hemicellulase, a CIP, an esterase, an expansin, a ligninolytic enzyme, an oxidoreductase, a pectinase, a protease, and a swollenin.

Paragraph [26]. The method of paragraph [25], wherein the cellulase is one or more enzymes selected from an endoglucanase, a cellobiohydrolase, and a beta-glucosidase.

Paragraph [27]. The method of paragraph [25] or [26], wherein the hemicellulase is one or more enzymes selected a xylanase, an acetylxylan esterase, a feruloyl esterase, an arabinofuranosidase, a xylosidase, and a glucuronidase.

Paragraph [28]. The method of any one of paragraphs [1]-[27], wherein the fermenting organism is a *Saccharomyces, Rhodotorula, Schizosaccharomyces, Kluyveromyces, Pichia, Hansenula, Rhodosporidium*, *Candida, Yarrowia*, *Lipomyces, Cryptococcus,* or *Dekkera sp.* cell.

Paragraph [29]. The method of any one of paragraphs [1]-[28], wherein the fermenting organism is a *Saccharomyces cerevisiae* cell.

Paragraph [30]. The method of any one of paragraphs [1]-[29], wherein the method results in higher yield of fermentation product and/or reduced foam accumulation when compared to the same process using an identical cell without the heterologous polynucleotide encoding the phospholipase under the same conditions (e.g., at about or after 54 hours fermentation, such as the conditions described in Examples 3 or 4).

Paragraph [31]. The method of paragraph [30], wherein the method results in at least 0.25% (e.g., 0.5%, 0.75%, 1.0%, 1.25%, 1.5%, 1.75%, 2%, 3% or 5%) higher yield of fermentation product.

Paragraph [32]. A recombinant yeast cell comprising a heterologous polynucleotide encoding a phospholipase.

Paragraph [33]. The recombinant yeast cell of paragraph [32], wherein the phospholipase is a Phospholipase A or a Phospholipase C.

Paragraph [34]. The recombinant yeast cell of paragraph [32] or [33], wherein the phospholipase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342 (e.g., any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242).

Paragraph [35]. The recombinant yeast cell of any one of paragraphs [32]-[34], wherein the heterologous polynucleotide encodes a phospholipase having a mature polypeptide sequence that differs by no more than ten amino acids, e.g., by no more than five amino acids, by no more than four amino acids, by no more than three amino acids, by no more than two amino acids, or by one amino acid from the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342 (e.g., any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242).

Paragraph [36]. The recombinant yeast cell of any one of paragraphs [32]-[35], wherein the heterologous polynucleotide encodes a phospholipase having a mature polypeptide sequence comprising or consisting of the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342 (e.g., any one of SEQ ID NOs: 235, 236, 237, 238, 239, 240, 241 and 242.

Paragraph [37]. The recombinant yeast cell of any one of paragraphs [32]-[36], wherein the fermenting organism comprises a heterologous polynucleotide encoding a glucoamylase.

Paragraph [38]. The recombinant yeast cell of paragraph [37], wherein the glucoamylase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of a *Pycnoporus* glycoamylase (e.g., a *Pycnoporus sanguineus* glucoamylase of SEQ ID NO: 229), a *Gloeophyllum* glucoamylase (e.g. a *Gloeophyllum sepiarium* of SEQ ID NO: 8), or a glucoamylase of any one of SEQ ID NOs: 102-113 (e.g., a *Saccharomycopsis fibuligera* glucoamylase of SEQ ID NO: 103 or 104, or a *Trichoderma reesei* glucoamylase of SEQ ID NO: 230).

Paragraph [39]. The recombinant yeast cell of any one of paragraphs [32]-[38], wherein the fermenting organism comprises a heterologous polynucleotide encoding an alpha-amylase.

Paragraph [40]. The recombinant yeast cell of paragraph [39], wherein the alpha-amylase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 76-101, 121-174 and 231.

Paragraph [41]. The recombinant yeast cell of any one of paragraphs [32]-[40], wherein the fermenting organism comprises a heterologous polynucleotide encoding a protease.

Paragraph [42]. The recombinant yeast cell of paragraph [41], wherein the protease has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 9-73 (e.g., any one of SEQ ID NOs: 9, 14, 16, 21, 22, 33, 41, 45, 61, 62, 66, 67, and 69; such as any one of SEQ NOs: 9, 14, 16, and 69).

Paragraph [43]. The recombinant yeast cell of any one of paragraphs [32]-[42], wherein the fermenting organism comprises a heterologous polynucleotide encoding a trehalase.

Paragraph [44]. The recombinant yeast cell of paragraph [43], wherein the trehalase has a mature polypeptide sequence of at least 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity to the amino acid sequence of any one of SEQ ID NOs: 175-226.

Paragraph [45]. The recombinant yeast of any one of paragraphs [32]-[44], wherein the cell is a *Saccharomyces, Rhodotorula, Schizosaccharomyces, Kluyveromyces, Pichia, Hansenula, Rhodosporidium*, *Candida, Yarrowia*, *Lipomyces, Cryptococcus,* or *Dekkera sp.* cell.

Paragraph [46]. The recombinant yeast of paragraph [45], wherein the cell is a *Saccharomyces cerevisiae* cell.

Paragraph [47]. The recombinant cell of any one of paragraphs [32]-[46], wherein the cell is capable of higher yield of fermentation product and/or reduced foam accumulation when compared to fermentation using the same process and an identical cell without the heterologous polynucleotide encoding the phospholipase under the same conditions (e.g., at about or after 54 hours fermentation, such as the conditions described in Examples 3 or 4).

Paragraph [48]. The recombinant cell of paragraph [47], wherein the cell is capable of at least 0.25% (e.g., 0.5%, 0.75%, 1.0%, 1.25%, 1.5%, 1.75%, 2%, 3% or 5%) higher yield of fermentation product.

The invention described and claimed herein is not to be limited in scope by the specific aspects herein disclosed, since these aspects are intended as illustrations of several aspects of the invention. Any equivalent aspects are intended to be within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. In the case of conflict, the present disclosure including definitions will control. All references are specifically incorporated by reference for that which is described.

The following examples are offered to illustrate certain aspects of the present invention, but not in any way intended to limit the scope of the invention as claimed.

Examples

Materials and Methods

Chemicals used as buffers and substrates were commercial products of at least reagent grade.

ETHANOL RED® ("ER"): *Saccharomyces cerevisiae* yeast available from Fermentis/Lesaffre, USA.

YPD + clonNAT plates were composed of 10 g of yeast extract, 20 g of peptone, 20 g bacto agar, and deionized water to 960 ml, followed by autoclave treatment. 40 mL sterile 50% glucose and 1 mL clonNAT stock solution was added, followed by mixing and pouring.

clonNAT stock solution was composed of 2 g nourseothricin sulfate and deionized water to 20 ml.

Example 1: Construction of yeast strains expressing a heterologous phospholipase

This example describes the construction of yeast cells containing a heterologous phospholipase under control of a *S. cerevisiae* TDH3, TEF2, PGK1, ADH1 or RPL18B promoter. Three pieces of DNA containing the promoter, gene and terminator were designed to allow for homologous recombination between the three DNA fragments and into the X-3 locus of the yeast MHCT-484 (WO2018/222990). The resulting strain has one promoter-containing fragment (left fragment), one gene-containing fragment (middle fragment) and one PRM9 terminator fragment (right fragment) integrated into the *S. cerevisiae* genome at the X-3 locus.

Construction of the promoter containing fragments (left fragments)

Synthetic linear uncloned DNA containing 60 bp homology to the X-3 site, *S. cerevisiae* promoter TDH3, TEF2, PGK1, ADH1 or RPL18B (SEQ ID NOs: 1, 2, 4, 5, and 6, respectively) and coding sequence for the *S. cerevisiae* MF1α signal peptide (SEQ ID NO: 7) were synthesized by Thermo Fisher Scientific (Waltham, MA). To generate additional linear DNA for transformation into yeast, each of the five linear DNAs containing the left cassette above was PCR amplified.

Construction of the terminator containing fragment (right fragment)

Synthetic linear uncloned DNA containing the *S. cerevisiae* PRM9 terminator (SEQ ID NO: 243) and 300bp homology to the X-3 site was synthetized by Thermo Fisher Scientific.

Construction of the gene containing fragment (middle fragment)

Synthetic linear uncloned DNA containing coding sequence for the *S. cerevisiae* MF1α signal peptide, coding sequence for the mature polypeptide and 50bp PRM9 terminator was synthetized by Thermo Fisher Scientific.

Integration of the left, middle and right-hand fragments to generate yeast strains with a heterologous phospholipase

The yeast MHCT-484 (WO2018/222990) was transformed with the left, middle and right integration fragments described above. In each transformation pool a fixed left fragment and right fragment were used as well as a fixed middle fragment containing the phospholipase gene with 100 ng of each fragment. To aid homologous recombination of the left, middle and right fragments at the genomic X-3 sites a plasmid containing Cas9 and guide RNA specific to X-3 (pMcTs442) was also used in the transformation. These four components were transformed into the *S. cerevisiae* strain MHCT-484 following a yeast electroporation protocol. Transformants were selected on YPD+cloNAT to select for transformants that contain the CRISPR/Cas9 plasmid pMcTs442. Transformants were picked using a Q-pix Colony Picking System (Molecular Devices; San Jose, CA) to inoculate one well of 96-well plate containing YPD+cloNAT media. The plates were grown for 2 days then glycerol was added to 20% final concentration and the plates were stored at -80°C until needed. Integration of specific phospholipase construct was verified by PCR with locus specific primers and subsequent sequencing. The strains generated in this example are shown in Table 5.

Table 5.

Strain Name	Promoter	SEQ ID NO: (mature polypeptide)	Donor Organism (catalytic domain)
HP21-B03	pADH1v1	236	*Talaromyces leycettanus*
HP21-C03	pADH1v1	236	*Talaromyces leycettanus*
HP21-D04	pTEF2	236	*Talaromyces leycettanus*
HP21-D05	pTDH3	236	*Talaromyces leycettanus*
HP21-E01	pPGK1	236	*Talaromyces leycettanus*
HP21-F01	pPGK1	236	*Talaromyces leycettanus*
HP21-G06	pRPL18B	236	*Talaromyces leycettanus*
HP21-A02	pADH1v1	237	*Penicillium emersonii*
HP21-F04	pTDH3	237	*Penicillium emersonii*
HP21-F05	pRPL18B	237	*Penicillium emersonii*
HP21-A04	pTEF2	240	*Kionochaeta sp.*
HP21-B01	pPGK1	240	*Kionochaeta sp.*
HP21-C05	pTDH3	240	*Kionochaeta sp.*
HP21-G02	pADH1v1	240	*Kionochaeta sp.*
HP21-B05	pTDH3	241	*Mariannaea pinicola*
HP21-B06	pRPL18B	241	*Mariannaea pinicola*
HP21-C06	pRPL18B	241	*Mariannaea pinicola*
HP21-F02	pADH1v1	241	*Mariannaea pinicola*
HP21-H03	pTEF2	241	*Mariannaea pinicola*
HP21-G04	pTDH3	239	*Pseudomonas sp.* 62186
HP21-G05	pRPL18B	239	*Pseudomonas sp.* 62186

HP21-H05	pRPL18B	239	*Pseudomonas sp.* 62186
HP21-A03	pADH1v1	238	*Bacillus thuringiensis*
HP21-B04	pTEF2	238	*Bacillus thuringiensis*
HP21-C01	pPGK1	238	*Bacillus thuringiensis*
HP21-C04	pTEF2	238	*Bacillus thuringiensis*
HP21-D01	pPGK1	238	*Bacillus thuringiensis*
HP21-D06	pRPL18B	238	*Bacillus thuringiensis*
HP21-E06	pRPL18B	238	*Bacillus thuringiensis*
HP21-F06	pRPL18B	238	*Bacillus thuringiensis*
HP21-H02	pADH1v1	238	*Bacillus thuringiensis*
HP21-D03	pADH1v1	235	*Thermomyces lanuginosus*
HP21-E04	pTEF2	235	*Thermomyces lanuginosus*
HP21-E05	pTDH3	235	*Thermomyces lanuginosus*
HP21-G01	pPGK1	235	*Thermomyces lanuginosus*
HP21-H06	pRPL18B	235	*Thermomyces lanuginosus*
HP21-A01	pPGK1	242	*Fictibacillus macauensis*
HP21-A05	pTDH3	242	*Fictibacillus macauensis*
HP21-A06	pRPL18B	242	*Fictibacillus macauensis*
HP21-F03	pTEF2	242	*Fictibacillus macauensis*
HP21-G03	pTEF2	242	*Fictibacillus macauensis*
HP21-H04	pTDH3	242	*Fictibacillus macauensis*

Example 2: Activity assay and small-scale fermentation of yeast strains expressing phospholipase

Preparation of yeast cells for activity assays

Yeast strains were cultivated for 24 hours in standard YPD media containing 2 % glucose. After the cultivation, samples were centrifuged, and the supernatants assayed for enzyme activity as described below.

PLA (Phospholipase A) activity assay

PLA activity was detected by using the EnzChek® PLA1 Kit from Invitrogen (Carlsbad, CA). The EnzChek® Direct Phospholipase A Assay Kit measures phosphatidylcholine-specific phospholipase C (PC-PLC) activity. PLA1 hydrolyzes the ester linkage of phospholipids and fatty acids. The EnzChek® Phospholipase A1 substrate (PED-A1) is a dye-labeled glycerophosphoethanolamines with BODIPY® FL dye-labeled acyl chain. PLA assay measures the release of the dye at a fluorescence emission at 515nm. Reaction conditions are described in Table 6.

Initial Preparation of Solutions for PLA1 Activity Assay:

1. Reaction Buffer: 100mM MOPS + 0.5mM Zn pH 7
2. PLA substrate:
    a. 40ul DMSO (Comp E) to one vial PLA sub (Comp A)

   - b. Protected from light
   - c. Sufficient volume for 100 rxns
3. 500U/mL stock of positive control PLA (Comp D)
   - a. Dissolved Comp D vial in 100uL of reaction buffer
4. 10mM DOPC (Comp B)
   - a. Dissolved Comp B vial in 100ul of ETOH
5. 10mM DOPG (Comp C)
   - a. Dissolved Comp C vial in 100ul of ETOH

Final Preparation of Solutions and Samples for PLA1 Activity Assay:

1. 10U/mL positive control made by diluting 500U/mL stock positive control in reaction buffer
   - a. Example: added 20ul of 500U/mL positive control to 980mL of Reaction buffer
2. Serial dilutions of positive control to obtain 8-point standard curve with initial concentration beginning at 10U/ml
   - a. Final positive control concentration two-fold lower (5U/ml) when substrate added
3. When necessary, samples diluted in reaction buffer
4. Lipid Mix: 30ul 10mM DOPC, 30ul 10mM DOPG, 30ul 1mM PLA substrate
5. PLA substrate
   - a. 50ul lipid mixed slowly to 5mL reaction buffer in a smaller beaker containing a stir bar.
   - b. Stirred for ~2-5 minutes

Assay Protocol for PLA1 Activity Assay:

1. 50ul of 8-point standard curve to columns 10,11,12
   - a. last row left blank for buffer
2. Added 50ul of samples to remaining wells
3. Added 50ul of PLA-lipid substrate to wells containing samples and controls. Mixed well without introducing bubbles.
4. Read a T0 at 505EX/515EM (450EX/515EM is ok as well)
5. Covered plate and incubate protected from light
6. Read after 5 hours of incubation

Table 6. PLA1 Activity Assay Condition

Amount of yeast supernatant	50 µl
Amount of PLA-lipid substrate	50 µl
Substrate	PLA1 substrate from Kit
Buffer	100mM MOPS + 0.5mM Zn
pH	7.0 ± 0.05
Incubation temperature	22 °C (room Temperature)
Reaction time	5 hrs
Wavelength	505EX/515EM

PLC (Phospholipase C) Activity Assay

PLC activity was detected by using EnzChek® PLC Kit from Invitrogen. The EnzChek® Phospholipase A Assay Kit measures phosphatidylcholine-specific phospholipase C (PC-PLC) activity by measuring the amount of starch degraded through enzymatic hydrolysis of starch. The assay uses a proprietary substrate (glycero-phosphoethanolamine with a dye-labeled sn-2 acyl chain) to detect PLC activity. Substrate cleavage by PLC releases the dye-labeled diacylglycerol, which produces a fluorescence signal that can be measure at 516nm emission. Reaction conditions are described in Table 7.

Initial Preparation of Solutions for PLC Activity Assay:

1. Reaction Buffer: 100mM NaAc + 0.5mM Zn pH 5
2. 200X stock of PLC substrate
    a. 100ul DMSO (Comp B) added to one vial PLC sub
    b. Protected from light
    c. Sufficient volume for 125 rxns
3. 40U/mL stock of positive control PC-PLC (Comp E)
    a. Dissolved Comp E vial in 200uL of reaction buffer

Final Secondary Preparation of Solutions and Samples for PLC Activity Assay

1. 1U/mL positive control made by diluting 40U/mL stock positive control 40-fold
    a. Example: added 25ul of 40U/mL positive control to 0.975mL of Reaction buffer
2. Serial dilutions of positive control to obtain 8-point standard curve with initial concentration beginning at 0.125U/ml
    a. Final positive control concentration two-fold lower (0.0625U/ml) when substrate is added
3. When necessary, samples diluted in reaction buffer

4. PLC substrate: Added 40ul of lecithin (Comp D) and 100ul of PLC Substrate 200X stock solution (prepared in earlier step) to 9.86mL of reaction buffer.

Assay Protocol for PLC Activity Assay:

1. 75ul of 8-point standard curve to columns 10,11,12
    a. last row left blank for buffer
2. Added 75ul of samples to remaining wells
3. Added 75ul of PLC substrate to wells containing samples and controls. Mixed well without introducing bubbles.
4. Read a T0 at 509EX/516EM (490EX/520EM is ok as well)
5. Covered plate and incubate protected from light
6. Read after 5 hours

Table 7. PLC Activity Assay Condition

Amount of yeast supernatant	75 µl
Amount of PLA-lipid substrate	75 µl
Substrate	PLC substrate from Kit
Buffer	100mM NaAc + 0.5mM Zn
pH	5.0 ± 0.05
Incubation temperature	22 °C (room Temperature)
Reaction time	5 hrs
Wavelength	509EX/516EM

Preparation of yeast culture for microtiter plate fermentations

Simultaneous saccharification and fermentation (SSF) was performed via mini-scale fermentations using industrial corn mash (Avantec® Amp; Novozymes A/S). Yeast strains were cultivated overnight in YPD media with 6 % glucose for 24 hours at 30 °C and 300 rpm. The corn mash was supplemented with 250 ppm of urea and dosed with 0.45 AGU/g-DS of an exogenous glucoamylase enzyme product (Spirizyme® Excel; Novozymes A/S). Approximately 0.6 mL of corn mash was dispensed per well to 96 well microtiter plates, followed by the addition of approximately 10^8 yeast cells/g of corn mash from the overnight culture. Plates were incubated at 32°C without shaking. Fermentation was stopped by the addition of 100 µL of 8 % H_2SO_4, followed by centrifugation at 3000 rpm for 10 min. The supernatant was analyzed for ethanol using HPLC. Fermentation reaction conditions are summarized in Table 8. SSF and activity assay results of yeast strains expressing a phospholipase are in Table 9.

Table 8. Microtiter plate fermentation reaction conditions

Substrate	Avantec® Amp corn mash

Yeast pitch	10^8 cells/g corn mash
Supplementary urea	250 ppm
Exogenous glucoamylase product dose	0.15 AGU/g-DS
pH	5.0 ± 0.05
Incubation temperature	32°C
Reaction time	48 hours

Table 9. Phospholipase yeast strains enzyme activity measurements and ethanol titers from SSF

Strain ID	**Promoter**	**SEQ ID NO: (mature polypeptide)**	**PLC activity units**	**PLA1 activity units**	**Mean Ethanol (g/L)**
MHCT-484	none	none	99	0	107.31
HP21-D04	TEF2	236	776	23	110.67
HP21-G06	RPL18B	236	793	0	110.6105
HP21-B03	ADH1v1	236	863	43	110.2833
HP21-D05	TDH3	236	688	29	110.0453
HP21-C03	ADH1v1	236	878	47	108.885
HP21-E01	PGK1	236	710	11	108.2008
HP21-F01	PGK1	236	680	0	106.1183
HP21-F04	TDH3	237	207	0	110.67
HP21-F05	RPL18B	237	174	0	109.1528
HP21-A02	ADH1v1	237	273	0	109.0933
HP21-B01	PGK1	240	452	0	94.0695
HP21-A04	TEF2	240	451	0	83.27025
HP21-G02	ADH1v1	240	410	0	82.19925
HP21-C05	TDH3	240	426	0	81.36625
HP21-C06	RPL18B	241	236	0	112.455
HP21-B06	RPL18B	241	201	0	107.8735
HP21-B05	TDH3	241	356	0	100.436
HP21-H03	TEF2	241	275	0	99.3055
HP21-F02	ADH1v1	241	364	0	97.58
HP21-G04	TDH3	239	85	0	107.1893
HP21-G05	RPL18B	239	251	0	84.7875
HP21-H05	RPL18B	239	220	0	84.609
HP21-E06	RPL18B	238	156	0	109.599
HP21-B04	TEF2	238	152	0	108.6768
HP21-D01	PGK1	238	99	0	108.0223
HP21-C01	PGK1	238	116	0	107.5463
HP21-F06	RPL18B	238	142	0	105.077
HP21-A03	ADH1v1	238	99	0	104.5118
HP21-H02	ADH1v1	238	93	0	102.102
HP21-C04	TEF2	238	146	0	101.9235
HP21-D06	RPL18B	238	141	0	82.25875
HP21-E05	TDH3	235	846	31	110.5808
HP21-H06	RPL18B	235	685	56	109.0635
HP21-E04	TEF2	235	500	139	100.5253
HP21-G01	PGK1	235	428	123	96.06275
HP21-D03	ADH1v1	235	462	142	88.08975
HP21-F03	TEF2	242	115	0	108.171

HP21-A05	TDH3	242	126	0	108.0818
HP21-A06	RPL18B	242	135	0	106.2373
HP21-G03	TEF2	242	113	0	105.791
HP21-H04	TDH3	242	102	0	104.6903
HP21-A01	PGK1	242	91	0	104.4523

Example 3: Fermentation of yeast strains expressing phospholipase

The purpose of this experiment was to determine if expressing phospholipase in yeast would enhance ethanol yields at the end of fermentation. Yeast strains (HP21-H06, HP21-D05, HP21-G12, HP21-A08, HP21-F05 and HP21-F04) were propagated overnight, and then used to dose a fermentation of industrially liquified mash. The fermented mash was sampled at the end of fermentation and the supernatant was filtered and analyzed by HPLC to determine the final ethanol titers and residual sugars.

Yeast Propagation

Yeast strains were received as glycerol stocks and were kept frozen at -80°C until used. The yeast strains were propagated according to the following procedure:

1. Cryo-vials of yeast were removed from the -80°C freezer.
2. For each sample, 2 x 50 mL sterile Erlenmeyer flasks were obtained and labeled.
3. The flasks were placed into a sterile hood along with 6% YPD media, pipettes and tips, and cryovials.
4. Using sterile technique, ~50 mL of 6% YPD media was poured into each bottle.
5. 150 uL of the appropriate yeast sample was added to each flask using a sterile 200 uL pipette and sterile tips.
6. The flasks were capped after each addition to maintain a sterile solution.
7. The flasks were placed into a 32°C shaking incubator and mixed at ~150 rpm overnight.

Cell Counting

The propagation slurries described above were then tested to determine the number of yeast cells present for dosing, according to the following procedure:

1. The propagated yeast samples were removed from the incubator.
2. The 50 mL samples were poured into 50 mL flip top falcon tubes.
3. The samples were centrifuged 3,500 rpm for 7 min.
4. The supernatant was discarded into the old 50 mL flasks to be autoclaved.
5. 10 mL of deionized water was added to each tube.
6. The tubes were vortex mixed to suspend the pellet.
7. The replicate samples were combined into a single 50 mL falcon tube.

8. The samples were centrifuged 3,500 rpm for 7 min.
9. The supernatant was discarded into the original 50 mL flasks to be autoclaved.
10. 10 mL of deionized water was added to each remaining tube.
11. The tubes were vortex mixed to suspend the pellet.
    a. This slurry was saved and will be used to dose into the fermentations.
12. The yeast slurries were diluted 100X into 15 mL falcon tubes by adding 100 uL to 9.9 mL of deionized water.
13. The samples subjected to cell count using a NucleoCounter® YC-100 (Chemometec A/S) as follows:
    a. 50 uL of the 100X slurry dilution was added to 450 uL of Lysis buffer.
    b. The samples were vortexed and allowed to sit ~5 min for the cell lysis to occur.
    c. A nucleo-casette was used to sample the lysed solution, then placed into the NucleoCounter® YC-100.
    d. The NucleoCounter® YC-100 analyzed the slurry and produced a cell count number.
    e. The resulting number is multiplied by 1000 to get the final cell counts for use in the spreadsheet.
14. The yeasts used in this experiment, and the yeast counts that were obtained according to the procedure above are displayed in the Table 10 below.

Table 10.

Strain ID	**YCL-1**	**YCL-2**	**Average total cells**
MHCT-484	1.26E+09	1.28E+09	1.27E+09
HP21-H06	1.23E+09	1.16E+09	1.19E+09
HP21-D05	1.38E+09	1.43E+09	1.40E+09
HP21-G12	1.14E+09	1.12E+09	1.13E+09
HP21-A08	1.38E+09	1.29E+09	1.33E+09
HP21-F05	1.28E+09	1.28E+09	1.28E+09
HP21-F04	1.41E+09	1.24E+09	1.33E+09

15. The calculation below was used to determine the number of mL of yeast slurry to add to each tube.

$$\frac{10{,}000{,}000\text{ cells}}{\text{mL mash}} \times \frac{1\text{mL mash}}{1.15\text{g mash}} \times \text{g mash} \times \frac{\text{mL}}{X\text{ cells}} \times \frac{1000\ \mu\text{L}}{\text{mL}} = \mu\text{L yeast to add}$$

Fermentation

Fermentations of industrially liquified mash were conducted according to the following procedure:

1. Industrially liquefied mash was acquired and stored frozen for future analysis. The mash used in this experiment was from a plant using Avantec® Amp and running a hydro-heater or jet cooker during liquefaction stage.
2. Two liters of the mash was thawed for approximately 2 hours prior to starting this study.
3. The mash was adjusted to 500 ppm urea and 3 ppm penicillin using stock solutions of 200 g/L urea and 1 g/L penicillin.
4. The mash was adjusted to pH 5 using 40% v/v H_2SO_4 and the dry solids content were measured on a Mettler-Toledo moisture balance.
5. 50.0 +/-0.05 g of prepared mash was weighed into 250 mL media bottles.
6. The bottles were capped and stored in a refrigerator overnight.
7. The bottles were dosed with enzymes and yeast in the morning using a repeater pipette.
8. The conditions tested include Achieve® glucoamylase (0.42 AGU/gDS), trehalase (2 μg/gDS), and yeast dosed to approximately 7,000,000 cells per fermenation.
9. The bottles were capped with hole drilled caps. The holes were covered with labeling tape. A 0.24-gauge syringe needle was used to pierce a uniform vent hole to allow for CO_2 gas to escape during fermentation.
10. The bottles were placed into a 32°C air shaker set to 150 rpm to begin fermentation.
11. Fermentation was run for 54 hours.

Sampling of Fermentations

1. After 52 hours of fermentation, 5 g of fermented mash were pipetted into a 15 mL conical falcon tube with 5 mL pipette equipped with a cut tip.
2. 50 uL of 40% H_2SO_4 were added to each of the tubes to stop fermentation and enzymatic hydrolysis.
3. The tubes were briefly mixed with a vortex mixer and centrifuged at 3,500 rpm for 7 minutes.
4. The supernatant was poured into a syringe equipped with a 0.45 um filter and the plunger of the syringe was used to push the sample through the filter into prenumbered HPLC vials.

5. The HPLC vials were capped and the samples were submitted to HPLC for analysis of the ethanol and sugars produced during fermentation. The HPLC setup was as shown in Table 11.

Table 11.

HPLC system	• Agilent's 1100/1200 series with Chem station software • Degasser • Quaternary Pump • Auto-Sampler • Column Compartment /w Heater • Refractive Index Detector (RI)
Column	• Bio-Rad HPX- 87H Ion Exclusion Column 300mm x 7.8mm parts# 125-0140 • Bio-Rad guard cartridge cation H parts# 125-0129, Holder parts# 125-0131
Method	• 0.005M H_2SO_4 mobile phase • Flow rate of 0.6 ml/min • Column temperature - 65°C • RI detector temperature - 55°C

The method quantifies analytes using calibration standards for dextrins (DP4+), maltotriose, maltose, glucose, fructose, acetic acid, lactic acid, glycerol and ethanol. A 4-point calibration including the origin was used.

Ethanol improvement for tested strains is shown in Figure 1. Strains HP21-F05 and HP21-F04 show approximately 1.1% improvement in ethanol over control strain MHCT-484, while strain HP21-A08 showed approximately 0.5% improvement in ethanol titer of the control.

Example 4: Fermentation of yeast strains expressing phospholipase at varying urea levels

The purpose of this experiment was to examine the effect of nitrogen loading (urea level) on ethanol yields of phospholipase-expressing yeasts. Yeast strains (HP21-H08, HP21-F04 and HP21-F05) were propagated overnight, and then used to dose a fermentation of industrially liquified mash. The fermented mash was sampled at the end of fermentation and the supernatant was filtered and run on HPLC to determine the final ethanol titers and residual sugars.

Yeast Propagation

Yeast strains were propagated as described above in Example 3.

Cell Counting

The propagation slurries described above were then tested to determine the number of yeast cells present for dosing according to the procedure described above in Example 3. The yeasts used in this experiment, and the corresponding yeast counts are displayed in the Table 12.

Table 12.

Strain ID	YCL-1	YCL-2	Average total cells
MHCT-484	1.48E+09	1.44E+09	1.46E+09
HP21-A08	1.24E+09	1.24E+09	1.24E+09
HP21-F05	1.50E+09	1.48E+09	1.49E+09
HP21-F04	1.37E+09	1.40E+09	1.38E+09

Fermentation

Fermentations of industrially liquified mash were conducted according to the following procedure:

1. Industrially liquefied mash was acquired and stored frozen for future analysis. The two mashes used in this experiment were from a plant using Avantec® Amp (Novozymes A/S) and a plant running another product Liquozyme® Pro (Novozymes A/S). Both mashes were from plants running a hydro-heater or jet cooker during liquefaction stage.
2. Two liters of each mash was thawed for approximately 2 hours prior to starting this study.
3. The mash was dosed with 3 ppm penicillin using a stock solution 1 g/L penicillin. Urea was added to the fermentation during enzyme dosing using stock solutions of 100 and 20 g/L.
4. The mash was adjusted to pH 5 using 40% v/v H_2SO_4 and the dry solids content were measured on a Mettler-Toledo moisture balance.
5. ~5 g of the prepared mash was added to preweighed 15 mL tubes
6. The tubes were reweighed and the weight of mash was used in calculating enzymes, yeast and urea dosing.
7. The tubes were capped and stored in a refrigerator overnight.
8. The tubes were dosed with enzymes, yeast and urea in the morning using a Biomek FX liquid handling robot.
9. The conditions tested in this experiment are displayed in Table 13 below. Yeast dose in this experiment was 7,000,000 cells per ferm.
10. The tubes were capped with holes to allow released CO_2 from fermentation.
11. Tubes were placed into a 32°C incubator to begin fermentation.
12. Tubes were mixed with a vortex mixer twice a day for 52 hours.

Table 13.

Treatment	#	Yeast#	Glucoamylase	Dose	Units	Trehalase	Dose	Units	PLC	Dose	Units	Urea	Dose	Units
MHCT-484 - Control	**1**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	0	ppm
MHCT-484 - 5 ug PLC	**2**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	5	µg/g DS	Urea	0	ppm
MHCT-484 - 20 ug PLC	**3**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	20	µg/g DS	Urea	0	ppm
HP21-A08	**4**	2	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	0	ppm
HP21-F05	**5**	3	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	0	ppm
HP21-F04	**6**	4	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	0	ppm
MHCT-484 - Control	**7**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	150	ppm
MHCT-484 - 5 ug PLC	**8**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	5	µg/g DS	Urea	150	ppm
MHCT-484 - 20 ug PLC	**9**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	20	µg/g DS	Urea	150	ppm
HP21-A08	**10**	2	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	150	ppm
HP21-F05	**11**	3	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	150	ppm
HP21-F04	**12**	4	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	150	ppm
MHCT-484 - Control	**13**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	500	ppm
MHCT-484 - 5 ug PLC	**14**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	5	µg/g DS	Urea	500	ppm
MHCT-484 - 20 ug PLC	**15**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	20	µg/g DS	Urea	500	ppm
HP21-A08	**16**	2	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	500	ppm
HP21-F05	**17**	3	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	500	ppm
HP21-F04	**18**	4	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	500	ppm
MHCT-484 - Control	**19**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	0	ppm
MHCT-484 - 5 ug PLC	**20**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	5	µg/g DS	Urea	0	ppm
MHCT-484 - 20 ug PLC	**21**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	20	µg/g DS	Urea	0	ppm
HP21-A08	**22**	2	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	0	ppm
HP21-F05	**23**	3	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	0	ppm
HP21-F04	**24**	4	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	0	ppm
MHCT-484 - Control	**25**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	300	ppm
MHCT-484 - 5 ug PLC	**26**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	5	µg/g DS	Urea	300	ppm
MHCT-484 - 20 ug PLC	**27**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	20	µg/g DS	Urea	300	ppm
HP21-A08	**28**	2	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	300	ppm
HP21-F05	**29**	3	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	300	ppm
HP21-F04	**30**	4	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	300	ppm
MHCT-484 - Control	**31**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	1000	ppm
MHCT-484 - 5 ug PLC	**32**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	5	µg/g DS	Urea	1000	ppm
MHCT-484 - 20 ug PLC	**33**	1	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	20	µg/g DS	Urea	1000	ppm
HP21-A08	**34**	2	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	1000	ppm
HP21-F05	**35**	3	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	1000	ppm
HP21-F04	**36**	4	Achieve	0.42	AGU/gDS	Trehelase	1	ug/gDS	P.emersonii	0	µg/g DS	Urea	1000	ppm

Sampling of Fermentations

1. After 52 hours of fermentation, 50 uL of 40% H_2SO_4 were added to each of the tubes to stop fermentation and enzymatic hydrolysis.
2. The tubes were briefly mixed with a vortex mixer and centrifuged at 3,500 rpm for 7 minutes.
3. The tubes were placed onto a Biomek liquid handler which was used to pipette 200 uL of supernatant from the tubes into a 96 well 0.22 um filter plate.
4. The filter plate was placed on top of a round bottom 96 well polypropylene plate.
5. The filter and plate were placed into a floor centrifuge with bioseal caps on the buckets and spun at 3,500 rpm for 7 minutes or until liquid had passed through all the wells of the 96 well filter plate.
6. The plates were removed from the centrifuge and the round bottom plate with the filtered sample was heat sealed and submitted to HPLC for analysis of the ethanol and sugars produced during fermentation. The HPLC setup was as shown in Table 14.

Table 14.

HPLC system	• Agilent’s 1100/1200 series with Chem station software • Degasser • Quaternary Pump • Auto-Sampler • Column Compartment /w Heater • Refractive Index Detector (RI)
Column	• Bio-Rad HPX- 87H Ion Exclusion Column 300mm x 7.8mm parts# 125-0140 • Bio-Rad guard cartridge cation H parts# 125-0129, Holder parts# 125-0131
Method	• 0.005M H_2SO_4 mobile phase • Flow rate of 0.6 ml/min • Column temperature - 65°C • RI detector temperature - 55°C

The method quantifies analytes using calibration standards for dextrins (DP4+), maltotriose, maltose, glucose, fructose, acetic acid, lactic acid, glycerol and ethanol. A 4-point calibration including the origin was used. Normalized mean ethanol values after 54 hours of fermentation of AMP mash at 0 and 150 ppm urea are shown in Figure 2.

All tested strains expressing phospholipase showed greater increases in ethanol titer with no urea loading. Normalized mean ethanol values after 54 hours of fermentation of non-AMP mash at 0 and 150 ppm urea are shown in Figure 3. All tested strains expressing phospholipase showed greater increases in ethanol titer with no urea loading.

Example 5: Construction of additional yeast strains expressing a heterologous phospholipase

This example describes the construction of yeast cells containing the remaining heterologous phospholipases of Table 1 under the control of an *S. cerevisiae* PGK1 promoter. Three pieces of DNA containing the promoter, gene and terminator were designed to allow for homologous recombination between the four DNA fragments and into the XII-2 locus of the strain MeJi797 (a derivative of MBG5012 expressing both alpha-amylase and glucoamylase; WO2019/161227). The resulting strain has one promoter-containing fragment (left fragment), one gene-containing fragment (middle fragment) and one PRM9 terminator fragment (right fragment) integrated into the *S. cerevisiae* genome at the XII-2 locus.

Construction of the promoter-containing fragment (left fragment)

Linear DNA containing 500 bp homology to the XII-2 site and the *S. cerevisiae* pPGK1 promoter was PCR amplified from HP27 plasmid DNA with primers 1229945 (5'-TCTTT TCGCG CCCTG GAAAG G-3'; SEQ ID NO: 434) and 1227122 (5'-TGTTT TATAT TTGTT GTAAA AAGTA GATAA TTACT TCCTT GATGA TCTG-3'; SEQ ID NO: 435). Fifty pmoles each of forward and reverse primer was used in a PCR reaction containing 5 ng of plasmid DNA as template, 0.1 mM each dATP, dGTP, dCTP, dTTP, 1X Phusion HF Buffer (Thermo Fisher Scienctific), and 2 units Phusion Hot Start DNA polymerase in a final volume of 50 µL. The PCR was performed in a T100™ Thermal Cycler (Bio-Rad Laboratories, Inc.) programmed for one cycle at 98°C for 30 seconds followed by 32 cycles each at 98°C for 10 seconds, 59°C for 20 seconds, and 72°C for 40 seconds with a final extension at 72°C for 10 minutes. Following thermocycling, the PCR reaction products gel isolated and cleaned up using the NucleoSpin Gel and PCR clean-up kit (Machery-Nagel).

The linear DNA containing 243 bp homology to the *S. cerevisiae* pPGK1 promoter (SEQ ID NO: 4) and the MF1α signal peptide (SEQ ID NO: 7) was PCR amplified from DNA synthesized by GeneArt with primers 1229946 (5'-GTGAC AACAA CAGCC TGTTC TC-3'; SEQ ID NO: 436) and 1222995 (5'-AGCTA ATGCG GAGGA TGCTG C-3'; SEQ ID NO: 437). Fifty pmoles each of forward and reverse primer was used in a PCR reaction containing 5 ng of plasmid DNA as template, 0.1 mM each dATP, dGTP, dCTP, dTTP, 1X Phusion HF Buffer (Thermo Fisher Scientific), and 2 units Phusion Hot Start DNA polymerase in a final volume of 50 µL. The PCR was performed in a T100™ Thermal Cycler (Bio-Rad Laboratories, Inc.) programmed for one cycle at 98°C for 30 seconds followed by 32 cycles each at 98°C for 10 seconds, 59°C for 20 seconds, and 72°C for 20 seconds with a final extension at 72°C for 5 minutes. Following thermocycling, the PCR reaction products gel isolated and cleaned up using the NucleoSpin Gel and PCR clean-up kit (Machery-Nagel).

Construction of the terminator-containg fragment (right fragment)

The DNA containing 250 bp of the PRM9 terminator and 500 bp of the XII-2 3'-end homology was PCR amplified from TH12 plasmid DNA (GeneArt) with primers 1221473 (5'-ACAGA AGACG GGAGA CACTA GC-3'; SEQ ID NO: 438) and 1229949 (5'-GGGGT CGCAA CTTTT CCC-3'; SEQ ID NO: 439). Fifty pmoles each of forward and reverse primer was used in a PCR reaction containing 5 ng of plasmid DNA as template, 0.1 mM each dATP, dGTP, dCTP, dTTP, 1X Phusion HF Buffer (Thermo Fisher Scientific), and 2 units Phusion Hot Start DNA polymerase in a final volume of 50 µL. The PCR was performed in a T100™ Thermal Cycler (Bio-Rad Laboratories, Inc.) programmed for one cycle at 98°C for 30 seconds followed by 32 cycles each at 98°C for 10 seconds, 59°C for 20 seconds, and 72°C for 40 seconds with a final extension at 72°C for 10 minutes. Following thermocycling, the PCR reaction products gel isolated and cleaned up using the NucleoSpin Gel and PCR clean-up kit (Machery-Nagel).

Construction of the phospholipase-containing fragments (middle fragments)

Synthetic linear uncloned DNA containing the MF1α signal peptide, phospholipase gene and 50bp of the PRM9 terminator were obtained from Geneart or Twist Bioscience.

Integration of the left, middle and right-hand fragments to generate yeast strains with a heterologous phosphoplipase

The yeast MeJi797 was transformed with the left, middle and right integration fragments described above. In each transformation pool a fixed left fragment and right fragment with 100ng of each fragment was used. The middle fragment consisted of a signal peptide and phospholipase gene with ~100ng of each fragment (700ng total). To aid homologous recombination of the left, middle and right fragments at the genomic XII-2 sites a plasmid containing MAD7 and guide RNA specific to XII-2 (pMIBa638) was also used in the transformation. These four components were transformed into the into *S. cerevisiae* strain MeJi797 following a yeast electroporation protocol. Transformants were selected on YPD+cloNAT to select for transformants that contain the Mad7 plasmid pMIBa638. Transformants were picked using a Q-pix Colony Picking System (Molecular Devices) to inoculate one well of 96-well plate containing YPD+cloNAT media. The plates were grown for two days then glycerol was added to 20% final concentration and the plates were stored at -80°C until needed. Integration of specific phospholipase construct was verified by PCR with locus specific primers and subsequent sequencing. The strains generated were used in the following examples.

Example 6: Corn mash fermentations of phospholipase-expressing yeast strains

The strains described in Example 5 were tested for ethanol production and residual glucose using a 96-well corn mash fermentation described below. Propagation plates were prepared by inoculating 10 µL of each strain into a 96-well seed plate containing 150uL YP+2% glucose medium per well. Plates were incubated at 30°C and 300 RPM overnight. The following day, 10 µL of the seed culture was transferred to 96-deep well plates containing 500 µL of East Kansas Agri-Energy Liquefact Amp corn mash supplemented with 100 ppm urea and 0.42 AGU/g Spirizyme Excel. Plates were sealed with EnzyScreen plate covers and tightly clamped to limit oxygen transfer. Corn mash plates were incubated statically at 32 °C for 56 hours. After fermentation was completed, the plates were placed at -80C for about 10 minutes before 100 µL of 8% H_2SO_4 was added to each well of the 96-deep well corn mash plates. Plates were sealed and mixed by inversion and centrifuged at 3000 rpm for 10 minutes. Supernatants were removed and diluted to 12x in sterile deionized water prior to HPLC analysis. The average ethanol and residual glucose per integrated heterologous phospholipase gene are shown in Table 15.

Table 15.

Donor Organism (catalytic domain)	**SEQ ID NO: (coding)**	**SEQ ID NO: (mature polypeptide)**	**mean ethanol (g/L)**	**mean glucose (g/L)**
N/A (MeJi797 control strain)	-----	-----	128.84	4.82
Penicillium cinnamopurpureum	423	332	138.52	3.30
Talaromyces rugulosus	407	316	138.39	1.28
Aspergillus turcosus	384	293	136.06	1.42
Aspergillus egyptiacus	376	285	135.98	2.97
Bacillus mycoides	381	290	135.88	5.16
Penicillium swiecickii	392	301	134.40	5.30
Lysinibacillus xylanilyticus	388	297	134.23	1.94
Listeria seeligeri	391	300	133.80	3.99
Penicillium spikei	410	319	133.37	1.68
Talaromyces leycettanus	402	311	133.29	1.02
Bacillus toyonensis	404	313	133.10	2.35
Bacillus mycoides	373	282	132.84	5.32
Bacillus mycoides	397	306	132.72	5.88
Rasamsonia argillacea	356	265	132.72	0.96
Bacillus toyonensis	427	336	132.66	4.17
Rasamsonia byssochlamydoides	348	257	132.53	1.34
Bacillus mycoides	414	323	132.42	3.18

Listeria innocua	375	284	132.36	5.22
Penicillium simplicissimum	430	339	132.26	2.57
Bacillus mycoides	380	289	132.26	2.40
Talaromyces boninensis	393	302	132.05	1.08
Hamigera paravellanea	401	310	131.88	2.04
Penicillium vasconiae	416	325	131.76	1.08
Rasamsonia brevistipitata	352	261	131.76	2.52
Bacillus mycoides	422	331	131.68	4.36
Bacillus pseudomycoides	372	281	131.66	3.57
Bacillus sp.	428	337	131.60	2.88
Bacillus acidiceler	419	328	131.50	4.78
Bacillus manliponensis	429	338	131.36	2.44
Hamigera avellanea	409	318	131.23	1.49
Penicillium flavescens	358	267	131.22	4.68
Bacillus sp.	420	329	130.98	5.96
Talaromyces bacillisporus	367	276	130.86	3.80
Talaromyces cellulolyticus	425	334	130.74	0.84
Rasamsonia eburnea	349	258	130.61	2.07
Bacillus acidiceler	433	342	130.52	5.04
Talaromyces rugulosus	364	273	130.52	1.00
Bacillus thuringiensis	396	305	130.46	3.89
Brevibacillus sp.	415	324	130.44	18.72
Bacillus drentensis	383	292	130.41	6.75
Talaromyces verruculosus	424	333	129.78	3.18
Penicillium piscarium	366	275	129.74	4.37
Penicillium sclerotiorum	347	256	129.72	9.06
Hamigera terricola	365	274	129.68	10.32
Penicillium arenicola	431	340	129.65	1.34
Aspergillus tamarii	377	286	128.86	1.03
Penicillium sp.	408	317	128.04	1.92
Bacillus sp.	382	291	127.84	3.64
Aspergillus tubingensis	386	295	127.66	3.89
Penicillium emersonii	355	264	127.65	3.75
Talaromyces subinflatus	385	294	127.26	6.60
Bacillus thuringiensis	405	314	127.08	3.00
Penicillium vasconiae	361	270	126.96	12.44
Talaromyces columbinus	362	271	126.69	4.05
Bacillus bingmayongensis	413	322	126.67	6.86
Bacillus luciferensis	379	288	126.51	5.46
Hamigera striata	394	303	126.36	2.04
Bacillus thuringiensis	406	315	126.30	9.00

Bacillus toyonensis	389	298	126.30	11.82
Bacillus mycoides	412	321	126.15	13.95
Bacillus acidiceler	387	296	125.85	5.37
Bacillus wiedmannii	390	299	125.67	7.25
Talaromyces variabilis	363	272	125.33	5.78
Bacillus thuringiensis	374	283	125.32	4.08
Penicillium simplicissimum	360	269	125.04	10.32
Aspergillus stramenius	371	280	124.92	3.52
Penicillium brefeldianum	350	259	124.86	17.10
Penicillium bialowiezense	346	255	124.72	3.00
Penicillium scabrosum	353	262	124.56	14.67
Penicillium megasporum	369	278	124.44	2.10
Penicillium donkii	400	309	123.96	0.84
Penicillium jensenii	370	279	123.75	5.58
Galactomyces candidus	368	277	123.36	14.37
Bacillus sp.	395	304	123.18	8.82
Aspergillus niger	378	287	123.00	8.28
Bacillus pseudomycoides	421	330	122.22	4.86
Penicillium hispanicum	359	268	118.14	19.95
Penicillium manginii	354	263	117.96	13.15
Penicillium meridianum	345	254	117.72	14.92
Paenibacillus sp.	403	312	110.07	38.28
Paenibacillus alginolyticus	411	320	106.52	43.96

Example 7: Enhancement of ethanol yield with phospholipase-expressing yeast strains

Commercial Amp corn mash was obtained from Trenton Agri at 35.9% (w/w) of dry solids content and was diluted with tape water to 32.0% (w/w). After dilution, the pH value of the mash was adjusted to 5.1 with 39% (w/v) NaOH solution. Urea and lactrol were added into the pH adjusted Amp mash to final concentration at 150 ppm and 3 ppm, respectively. The prepared corn mash was aliquoted into 250 mL flasks (100 g/flask).

To propagate yeast, 50 mL of 6% YPD and 100 µl of yeast-glycerol stock solution were mixed in a 125-mL flask and then incubated at 32ºC for overnight. After incubation, 45 mL of propagation was transferred to a 50 mL centrifuge tube and centrifuged at 3500 rpm for 10 minutes. The liquid fraction was decanted and deionized water was used to twic wash the cells. The cells were resuspended in 10 mL of deionized water and the total and dead cell accounts were measured using a NucleoCounter® YC-100.

The exogenous α-glucoamylase (Spirizyme Achieve-T™; Novozymes A/S) was added into the flasks containing corn mash per DOE and mixed well. Then the pre-determined amount of yeast suspension was added and mixed well. The fermentation was performed at 32°C for 54 hours. After the fermentation, 5 g of slurry was taken out and the fermentation was stopped by adding 50 µL of 40% H_2SO_4. The liquid was separated from solid by centrifuging whole slurry at 900 g for 10 min. The ethanol concentration was measured using HPLC.

Compared with the control strain MHCT-484, both phospholipase-expressing yeast strains showed significantly increased final ethanol yield (13.30% for control strain MHCT-484, to 13.43% and to 13.42% for strains HP21-F04 and HP21-F05, respectively.

Example 8: Enhancement of oil extraction with phospholipase-expressing yeast strains

Commercial Amp corn mash was obtained from Trenton Agri at 35.9% (w/w) of dry solids content and was diluted water to 32.0% (w/w). After dilution, the pH value of the mash was adjusted to 5.1 with 39% (w/v) NaOH solution. Urea and lactrol were added into the pH adjusted Amp mash to final concentration at 150 ppm and 3 ppm, respectively. The prepared corn mash was aliquoted into 250-mL flasks (100 g/flask).

To propagate yeast, 50 mL of 6% YPD and 100 µL of yeast-glycerol stock solution were mixed in a 125-mL flask and then incubated at 32ºC for overnight. After incubation, 45 mL of propagation was transferred to a 50-mL centrifuge tube and centrifuged at 3500 rpm for 10 minutes. The liquid fraction was decanted, and deionized water was used to twice wash the cells. The cells were resuspended in 10 mL of deionized water and the total and dead cell accounts were measured using a NucleoCounter® YC-100.

Exogenous α-glucoamylase (Spirizyme Achieve-T^{TM}; Novozymes A/S), was added into the flasks containing corn mash per DOE and mixed well. Then the pre-determined amount of yeast suspension was added and mixed well. The fermentation was performed at 32°C for 54 hours. After fermentation, 10 mL of 95% hexane was added to 95 grams of whole slurry. The slurry-hexane mixture was mixed well and then centrifuged at 3000x g for 10 minutes. After centrifuge, the top layer was transferred into a 15-mL tube using positive displacement pipettes. The oil was extracted from the slurry again with the same method. The total weight of transferred liquor was measured. The oil content and density were measured on densiometer. The final extracted oil was calculated as:

Extracted oil (g/flask) = first extracted oil (g/flask) + second extracted oil (g/flask)

Compared with the control strain MHCT-484, both lipase-expressing yeast strains HP21-F04 and HP21-F05 improved the final oil yield (0.518 g/flask and 0.966 g/flask for strains HP21-F04 and HP21-F05, respectively compared to 0.483 g/flask for control strain MHCT-484).

Example 9: Defoaming capabilities with phospholipase-expressing yeast strains

Commercial Amp corn mash was obtained from Trenton Agri at 35.9% (w/w) of dry solids content and was diluted with tape water to 32.0% (w/w). After dilution, the pH value of the mash was adjusted to 5.1 with 39% (w/v) NaOH solution. Urea and lactrol were added into the pH adjusted Amp mash to final concentration at 150 ppm and 3 ppm, respectively. The prepared corn mash was aliquoted into 250-mL flasks (100 g/flask).

To propagate yeast, 50 mL of 6% YPD and 100 µL of yeast-glycerol stock solution were mixed in a 125-mL flask and then incubated at 32ºC for overnight. After incubation, 45 mL of propagation was transferred to a 50-mL centrifuge tube and centrifuged at 3500 rpm for 10 minutes. The liquid fraction was decanted, and deionized water was used to twice wash the cells. The cells were resuspended in 10 mL of deionized water and the total and dead cell accounts were measured using a NucleoCounter® YC-100.

The exogenous α-glucoamylase, Spirizyme Achieve-T^{TM} (Novozyems A/S), was added into the flasks containing corn mash per DOE and mixed well. Then the pre-determined amount of yeast suspension was added and mixed well. Also, the pre-determined exogenous lipase was added and used as control. The fermentation was performed at 32°C for 54 hours.

The defoaming capability of control MHCT-484 and lipase-expressing yeast HP21-F04 was monitored using video camera after 12-hour fermentation. Compared with control yMHCT48, lipase-expressing yeast HP21-F04 showed significant defoaming capability (Figure 4).

CLAIMS

Claim 1. A method of producing a fermentation product from a starch-containing or cellulosic-containing material comprising:

(a) saccharifying the starch-containing or cellulosic-containing material; and

(b) fermenting the saccharified material of step (a) with a fermenting organism;

wherein the fermenting organism comprises a heterologous polynucleotide encoding a phospholipase.

Claim 2. The method of claim 1, wherein the phospholipase is a Phospholipase A or a Phospholipase C.

Claim 3. The method of claim 1 or 2, wherein the phospholipase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342.

Claim 4. The method of any one of claims 1-3, wherein saccharification of step (a) occurs on a starch-containing material, and wherein the starch-containing material is either gelatinized or ungelatinized starch.

Claim 5. The method of claim 4, comprising liquefying the starch-containing material by contacting the material with an alpha-amylase prior to saccharification.

Claim 6. The method of claim 5, wherein liquefying the starch-containing material and/or saccharifying the starch-containing material is conducted in presence of exogenously added protease.

Claim 7. The method of any one of claims 1-6, wherein fermentation is performed under reduced nitrogen conditions (e.g., less than 1000 ppm urea or ammonium hydroxide, such as less than 750 ppm, less than 500 ppm, less than 400 ppm, less than 300 ppm, less than 250 ppm, less than 200 ppm, less than 150 ppm, less than 100 ppm, less than 75 ppm, less than 50 ppm, less than 25 ppm, or less than 10 ppm).

Claim 8. The method of any one of claims 1-7, wherein the fermenting organism comprises a heterologous polynucleotide encoding a glucoamylase.

Claim 9. The method of any one of claims 1-8, wherein the fermenting organism comprises a heterologous polynucleotide encoding an alpha-amylase.

Claim 10. The method of any one of claims 1-9, wherein the fermenting organism comprises a heterologous polynucleotide encoding a protease.

Claim 11. The method of any one of claims 1-10, wherein the fermenting organism is a *Saccharomyces cerevisiae* cell.

Claim 12. The method of any one of claims 1-11, wherein the method results in higher yield of fermentation product and/or reduced foam accumulation when compared to the same process using an identical cell without the heterologous polynucleotide encoding the phospholipase under the same conditions.

Claim 13. The method of any one of claims 1-12, wherein the method results in at least 0.25% (e.g., 0.5%, 0.75%, 1.0%, 1.25%, 1.5%, 1.75%, 2%, 3% or 5%) higher yield of fermentation product.

Claim 14. A recombinant yeast cell comprising a heterologous polynucleotide encoding a phospholipase.

Claim 15. The recombinant yeast cell of claim 14, wherein the phospholipase is a Phospholipase A or a Phospholipase C.

Claim 16. The recombinant yeast cell of claim 14 or 15, wherein the phospholipase has a mature polypeptide sequence with 60%, e.g., at least 65%, 70%, 75%, 80%, 85%, 90%, 95%, 97%, 98%, 99%, or 100% sequence identity, to the amino acid sequence of any one of SEQ ID NOs: 235-242 and 252-342.

Claim 17. The recombinant yeast cell of any one of claims 14-16, wherein the fermenting organism comprises a heterologous polynucleotide encoding a glucoamylase.

Claim 18. The recombinant yeast cell of any one of claims 14-17, wherein the fermenting organism comprises a heterologous polynucleotide encoding an alpha-amylase.

Claim 19. The recombinant yeast cell of any one of claims 14-18, wherein the fermenting organism comprises a heterologous polynucleotide encoding a protease.

Claim 20. The recombinant yeast of any one of claims 14-19, wherein the cell is a *Saccharomyces cerevisiae* cell.

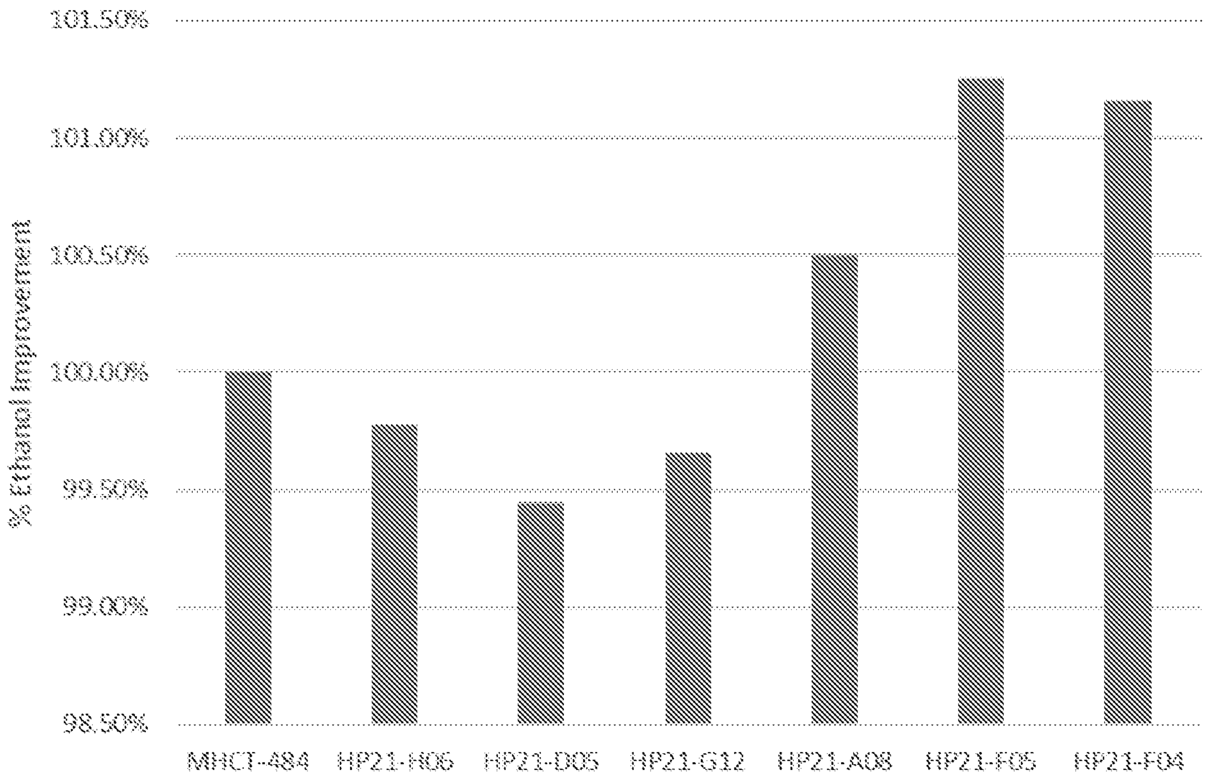
% Ethanol Improvement
101.50%
101.00%
100.50%
100.00%
99.50%
99.00%
98.50%
MHCT-484
HP21-H06
HP21-D05
HP21-G12
HP21-A08
HP21-F05
HP21-F04

FIG. 1

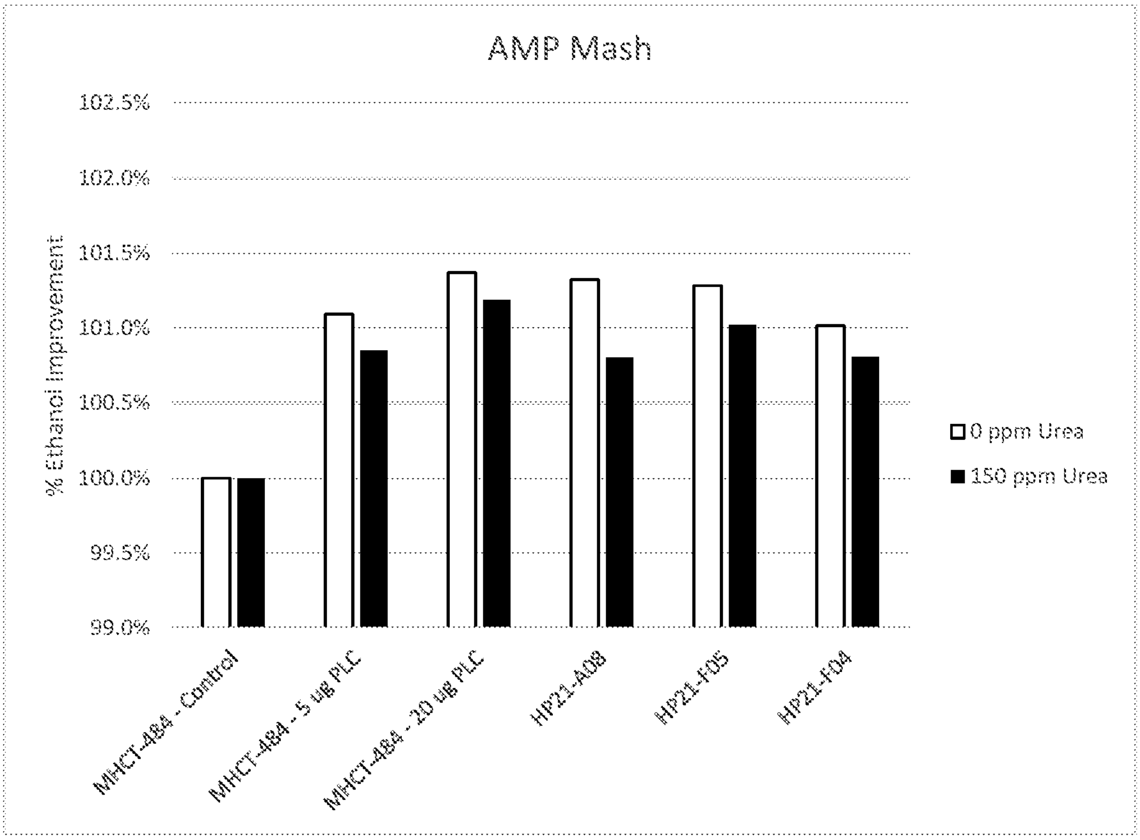
AMP Mash
% Ethanol Improvement
102.5%
102.0%
101.5%
101.0%
100.5%
100.0%
99.5%
99.0%
MHCT-484 - Control
MHCT-484 - 5 ug PLC
MHCT-484 - 10 ug PLC
HP21-A08
HP21-F05
HP21-F04
☐ 0 ppm Urea
■ 150 ppm Urea

FIG. 2

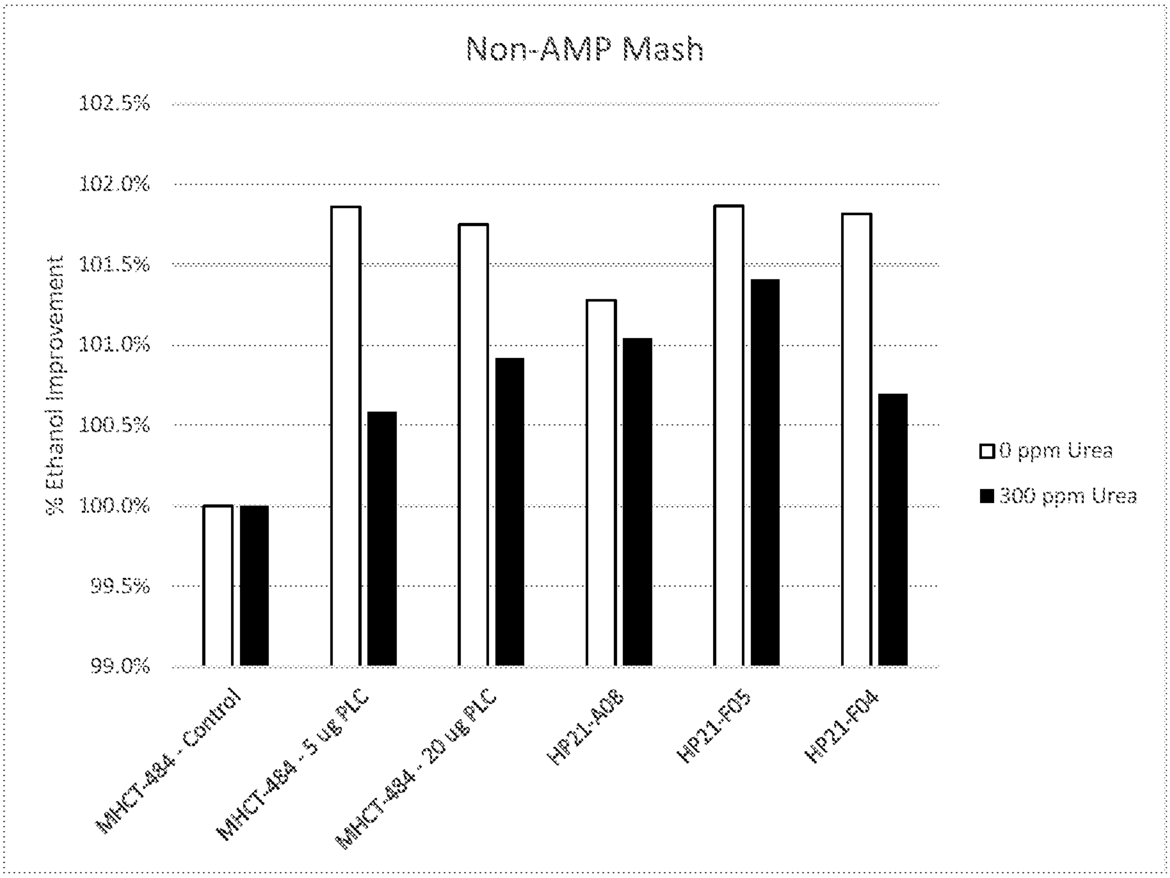
Non-AMP Mash
102.5%
102.0%
101.5%
101.0%
100.5%
100.0%
99.5%
99.0%
% Ethanol Improvement
MHCT-484 - Control
MHCT-484 - 5 ug PLC
MHCT-484 - 20 ug PLC
HP21-A08
HP21-F05
HP21-F04
☐ 0 ppm Urea
■ 300 ppm Urea

FIG. 3

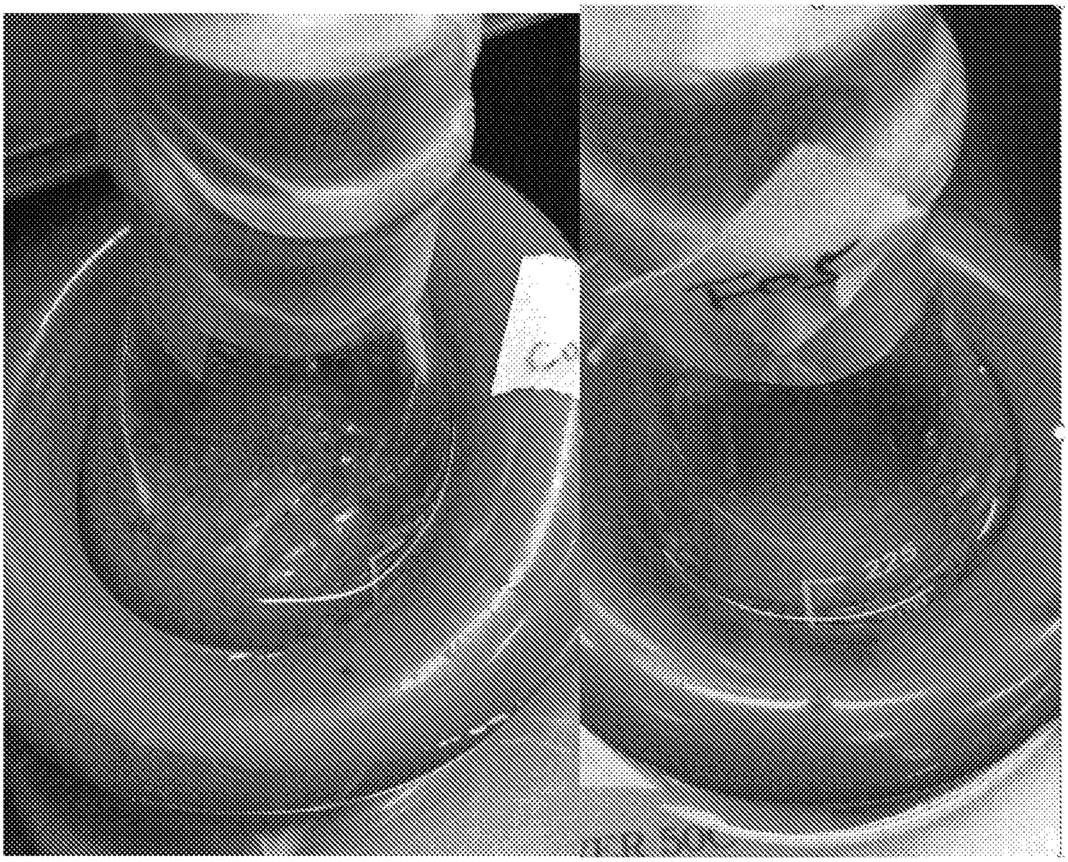

FIG. 4

SEQUENCE LISTING

<110> Novozymes A/S
       Tassone, Monica
       Huffman, James R.
       Soong, Chee-Leong
       Yi, Jung

<120> Enzyme-Expressing Yeast For Ethanol Production

<130> 14781-WO-PCT

<150> US 62/742,805
<151> 2018-10-08

<160> 439

<170> PatentIn version 3.5

<210> 1
<211> 621
<212> DNA
<213> Saccharomyces cerevisiae

<400> 1
cagttcgagt ttatcattat caatactgcc atttcaaaga atacgtaaat aattaatagt 60

agtgattttc ctaactttat ttagtcaaaa aattagcctt ttaattctgc tgtaacccgt 120

acatgcccaa aatagggggc gggttacaca gaatatataa catcgtaggt gtctgggtga 180

acagtttatt cctggcatcc actaaatata atggagcccg ctttttaagc tggcatccag 240

aaaaaaaaag aatcccagca ccaaaatatt gttttcttca ccaaccatca gttcataggt 300

ccattctctt agcgcaacta cagagaacag ggcacaaac aggcaaaaaa cgggcacaac 360

ctcaatggag tgatgcaacc tgcctggagt aaatgatgac acaaggcaat tgacccacgc 420

atgtatctat ctcattttct tacaccttct attaccttct gctctctctg atttggaaaa 480

agctgaaaaa aaaggttgaa accagttccc tgaaattatt cccctacttg actaataagt 540

atataaagac ggtaggtatt gattgtaatt ctgtaaatct atttcttaaa cttcttaaat 600

tctactttta tagttagtct t 621

<210> 2
<211> 644
<212> DNA
<213> Saccharomyces cerevisiae

```
<400>  2
agctacctat attccaccat aatatcaatc atgcggttgc tggtgtattt accaataatg       60

tttaatgtat atatattagg ggccgtatac ttacatatag tagatgtcaa gcgtaggcgc      120

ttcccctgcc ggctgtgacg gcgccataac caaggtatct atagaccgcc aatcagcaaa      180

ctacctccgt acattcatgt tgcacccaca catgtacaca cccagaccgc aacaaattac      240

ccataaggtt gtttgtgacg gcgtcgtaca agagaacgtg ggaacttttt aggctcacca      300

aaaaagaaag gaaaaatacg agttgctgac agaagcctca agaaaaaaaa aattcttctt      360

cgactatgct ggaggcagag atgatcgagc cggtagttaa ctatatatag ctaaattggt      420

tccatcacct tcttttctgg tgtcgctcct tctagtgcta tttctggctt ttcctatttt      480

ttttttttcc atttttcttt ctctctttct aatatataaa ttctcttgca ttttctattt      540

ttctctctat ctattctact tgtttattcc cttcaaggtt ttttttaag gagtacttgt       600

ttttagaata tacggtcaac gaactataat taagctagaa caaa                       644


<210>  3
<211>  457
<212>  DNA
<213>  Saccharomyces cerevisiae

<400>  3
ctccagaaag gcaacgcaaa atttttttc cagggaataa actttctatg acccactact        60

tctcgtagga acaatttcgg gcccctgcgt gttcttctga ggttcatctt ttacatttgc      120

ttctgctgga taattttcag aggcaacaag gaaaaattag atggcaaaaa gtcgtctttc      180

aaggaaaaat ccccaccatc cttcgagatc ccctgtaact tattggcaac tgaaagaatg      240

aaaaggagga aaatacaaaa tatactagaa ctgaaaaaaa aaagtataaa tagagacgat      300

atatgccaat acttcacaat gttcgaatcc attcttcatt tgcagctatt gtaaaataat      360

aaaacatcaa gaacaaacaa gctcaacttg tcttttctaa gaacaaagaa taaacacaaa      420

aacaaaaagt ttttttaatt ttaatcgcta gaacaaa                               457


<210>  4
<211>  700
<212>  DNA
<213>  Saccharomyces cerevisiae
```

```
<400>  4
gtgagtaagg aaagagtgag gaactatcgc atacctgcat ttaaagatgc cgatttgggc       60

gcgaatcctt tattttggct tcaccctcat actattatca gggccagaaa aaggaagtgt      120

ttccctcctt cttgaattga tgttaccctc ataaagcacg tggcctctta tcgagaaaga      180

aattaccgtc gctcgtgatt tgtttgcaaa aagaacaaaa ctgaaaaaac ccagacacgc      240

tcgacttcct gtcatcctat tgattgcagc ttccaatttc gtcacacaac aaggtcctag      300

cgacggctca caggttttgt aacaagcaat cgaaggttct ggaatggcgg gaaagggttt      360

agtaccacat gctatgatgc ccactgtgat ctccagagca aagttcgttc gatcgtactg      420

ttactctctc tctttcaaac agaattgtcc gaatcgtgtg acaacaacag cctgttctca      480

cacactcttt tcttctaacc aagggggtgg tttagtttag tagaacctcg tgaaacttac      540

atttacatat atataaactt gcataaattg gtcaatgcaa gaaatacata tttggtcttt      600

tctaattcgt agtttttcaa gttcttagat gctttctttt tctctttttt acagatcatc      660

aaggaagtaa ttatctactt tttacaacaa atataaaaca                            700


<210>  5
<211>  705
<212>  DNA
<213>  Sacharromyces cerevisiae

<400>  5
atccttttgt tgtttccggg tgtacaatat ggacttcctc ttttctggca accaaaccca       60

tacatcggga ttcctataat accttcgttg gtctccctaa catgtaggtg gcggagggga      120

gatatacaat agaacagata ccagacaaga cataatgggc taaacaagac tacaccaatt      180

acactgcctc attgatggtg gtacataacg aactaatact gtagccctag acttgatagc      240

catcatcata tcgaagtttc actacccttt ttccatttgc catctattga agtaataata      300

ggcgcatgca acttcttttc ttttttttc ttttctctct cccccgttgt tgtctcacca      360

tatccgcaat gacaaaaaaa tgatggaaga cactaaagga aaaaattaac gacaaagaca      420

gcaccaacag atgtcgttgt tccagagctg atgaggggta tctcgaagca cacgaaactt      480

tttccttcct tcattcacgc acactactct ctaatgagca acggtatacg gccttccttc      540

cagttacttg aatttgaaat aaaaaaaagt ttgctgtctt gctatcaagt ataaatagac      600
```

ctgcaattat taatcttttg tttcctcgtc attgttctcg ttccctttct tccttgtttc   660

tttttctgca caatatttca agctatacca agcatacaat caact   705

<210> 6
<211> 700
<212> DNA
<213> Saccharomyces cerevisiae

<400> 6
aagaggatgt ccaatatttt ttttaaggaa taaggatact tcaagactag attcccccct   60

gcattcccat cagaaccgta aaccttggcg ctttccttgg gaagtattca agaagtgcct   120

tgtccggttt ctgtggctca caaaccagcg cgcccgatat ggctttcttt tcacttatga   180

atgtaccagt acgggacaat tagaacgctc ctgtaacaat ctctttgcaa atgtggggtt   240

acattctaac catgtcacac tgctgacgaa attcaaagta aaaaaaaatg ggaccacgtc   300

ttgagaacga tagattttct ttattttaca ttgaacagtc gttgtctcag cgcgctttat   360

gttttcattc atacttcata ttataaaata acaaaagaag aatttcatat tcacgcccaa   420

gaaatcaggc tgctttccaa atgcaattga cacttcatta gccatcacac aaaactcttt   480

cttgctggag cttcttttaa aaaagacctc agtacaccaa acacgttacc cgacctcgtt   540

attttacgac aactatgata aaattctgaa gaaaaaataa aaaaattttc atacttcttg   600

cttttattta aaccattgaa tgatttcttt tgaacaaaac tacctgtttc accaaaggaa   660

atagaaagaa aaaatcaatt agaagaaaac aaaaaacaaa   700

<210> 7
<211> 19
<212> PRT
<213> Saccharomyces cerevisiae

<400> 7

Met Arg Phe Pro Ser Ile Phe Thr Thr Val Leu Phe Ala Ala Ser Ser
1   5   10   15

Ala Leu Ala

```
<210>  8
<211>  556
<212>  PRT
<213>  Gloeophyllum sepiarium

<400>  8

Gln Ser Val Asp Ser Tyr Val Ser Ser Glu Gly Pro Ile Ala Lys Ala
1               5                   10                  15


Gly Val Leu Ala Asn Ile Gly Pro Asn Gly Ser Lys Ala Ser Gly Ala
            20                  25                  30


Ser Ala Gly Val Val Val Ala Ser Pro Ser Thr Ser Asp Pro Asp Tyr
        35                  40                  45


Trp Tyr Thr Trp Thr Arg Asp Ser Ser Leu Val Phe Lys Ser Leu Ile
    50                  55                  60


Asp Gln Tyr Thr Thr Gly Ile Asp Gly Thr Ser Ser Leu Arg Thr Leu
65                  70                  75                  80


Ile Asp Asp Phe Val Thr Ala Glu Ala Asn Leu Gln Gln Val Ser Asn
                85                  90                  95


Pro Ser Gly Thr Leu Thr Thr Gly Gly Leu Gly Glu Pro Lys Phe Asn
            100                 105                 110


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


Gly Pro Ala Leu Arg Ser Thr Ala Leu Ile Thr Tyr Gly Asn Trp Leu
    130                 135                 140


Leu Ser Asn Gly Asn Thr Ser Tyr Val Thr Ser Asn Leu Trp Pro Ile
145                 150                 155                 160


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


Tyr Asp Leu Trp Glu Glu Val Asp Ser Ser Ser Phe Phe Thr Thr Ala
```

```
            180                 185                 190

Val Gln His Arg Ala Leu Arg Glu Gly Ala Ala Phe Ala Thr Ala Ile
        195                 200                 205

Gly Gln Thr Ser Gln Val Ser Ser Tyr Thr Thr Gln Ala Asp Asn Leu
    210                 215                 220

Leu Cys Phe Leu Gln Ser Tyr Trp Asn Pro Ser Gly Gly Tyr Ile Thr
225                 230                 235                 240

Ala Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp Ala Asn Thr Leu Leu
                245                 250                 255

Ala Ser Ile His Thr Tyr Asp Pro Ser Ala Gly Cys Asp Ala Ala Thr
            260                 265                 270

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

Asp Ser Phe Arg Ser Val Tyr Ser Ile Asn Ser Gly Ile Ala Ser Asn
    290                 295                 300

Ala Ala Val Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Gln Gly Gly
305                 310                 315                 320

Asn Pro Trp Tyr Leu Thr Thr Phe Ala Val Ala Glu Gln Leu Tyr Asp
                325                 330                 335

Ala Leu Asn Val Trp Glu Ser Gln Gly Ser Leu Glu Val Thr Ser Thr
            340                 345                 350

Ser Leu Ala Phe Phe Gln Gln Phe Ser Ser Gly Val Thr Ala Gly Thr
        355                 360                 365

Tyr Ser Ser Ser Ser Ser Thr Tyr Ser Thr Leu Thr Ser Ala Ile Lys
    370                 375                 380

Ser Phe Ala Asp Gly Phe Val Ala Val Asn Ala Lys Tyr Thr Pro Ser
```

```
385                 390                 395                 400

Asn Gly Gly Leu Ala Glu Gln Tyr Ser Lys Ser Asp Gly Ser Pro Leu
                405                 410                 415

Ser Ala Val Asp Leu Thr Trp Ser Tyr Ala Ser Ala Leu Thr Ala Phe
            420                 425                 430

Glu Ala Arg Asn Asn Thr Gln Phe Ala Gly Trp Gly Ala Ala Gly Leu
        435                 440                 445

Thr Val Pro Ser Ser Cys Ser Gly Asn Ser Gly Gly Pro Thr Val Ala
    450                 455                 460

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

Leu Thr Gly Ser Val Asp Ala Leu Glu Asn Trp Ser Ala Asp Asn Ala
                485                 490                 495

Leu Leu Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ile Thr Val Asn
            500                 505                 510

Leu Pro Ala Ser Thr Ala Ile Glu Tyr Lys Tyr Ile Arg Lys Asn Asn
        515                 520                 525

Gly Ala Val Thr Trp Glu Ser Asp Pro Asn Asn Ser Ile Thr Thr Pro
    530                 535                 540

Ala Ser Gly Ser Thr Thr Glu Asn Asp Thr Trp Arg
545                 550                 555


<210>  9
<211>  374
<212>  PRT
<213>  Aspergillus niger

<400>  9

Ala Pro Ala Pro Thr Arg Lys Gly Phe Thr Ile Asn Gln Ile Ala Arg
1               5                   10                  15
```

```
Pro Ala Asn Lys Thr Arg Thr Ile Asn Leu Pro Gly Met Tyr Ala Arg
            20                  25                  30

Ser Leu Ala Lys Phe Gly Gly Thr Val Pro Gln Ser Val Lys Glu Ala
        35                  40                  45

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

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

Asp Thr Gly Ser Ala Asp Leu Trp Val Phe Ser Asp Glu Leu Pro Ser
                85                  90                  95

Ser Glu Gln Thr Gly His Asp Leu Tyr Thr Pro Ser Ser Ser Ala Thr
            100                 105                 110

Lys Leu Ser Gly Tyr Thr Trp Asp Ile Ser Tyr Gly Asp Gly Ser Ser
        115                 120                 125

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

Thr Asn Lys Gln Ala Val Glu Ala Ala Ser Lys Ile Ser Ser Glu Phe
145                 150                 155                 160

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

Ile Asn Thr Val Gln Pro Lys Ala Gln Thr Thr Phe Phe Asp Thr Val
            180                 185                 190

Lys Ser Gln Leu Asp Ser Pro Leu Phe Ala Val Gln Leu Lys His Asp
        195                 200                 205

Ala Pro Gly Val Tyr Asp Phe Gly Tyr Ile Asp Asp Ser Lys Tyr Thr
    210                 215                 220
```

```
Gly Ser Ile Thr Tyr Thr Asp Ala Asp Ser Ser Gln Gly Tyr Trp Gly
225                 230                 235                 240


Phe Ser Thr Asp Gly Tyr Ser Ile Gly Asp Gly Ser Ser Ser Ser Ser
                245                 250                 255


Gly Phe Ser Ala Ile Ala Asp Thr Gly Thr Thr Leu Ile Leu Leu Asp
            260                 265                 270


Asp Glu Ile Val Ser Ala Tyr Tyr Glu Gln Val Ser Gly Ala Gln Glu
        275                 280                 285


Ser Glu Glu Ala Gly Gly Tyr Val Phe Ser Cys Ser Thr Asn Pro Pro
    290                 295                 300


Asp Phe Thr Val Val Ile Gly Asp Tyr Lys Ala Val Val Pro Gly Lys
305                 310                 315                 320


Tyr Ile Asn Tyr Ala Pro Ile Ser Thr Gly Ser Ser Thr Cys Phe Gly
                325                 330                 335


Gly Ile Gln Ser Asn Ser Gly Leu Gly Leu Ser Ile Leu Gly Asp Val
            340                 345                 350


Phe Leu Lys Ser Gln Tyr Val Val Phe Asn Ser Glu Gly Pro Lys Leu
        355                 360                 365


Gly Phe Ala Ala Gln Ala
    370


<210>  10
<211>  590
<212>  PRT
<213>  Trichoderma reesei

<400>  10

Ser Val His Leu Leu Glu Ser Leu Glu Lys Leu Pro His Gly Trp Lys
1               5                   10                  15
```

```
Ala Ala Glu Thr Pro Ser Pro Ser Ser Gln Ile Val Leu Gln Val Ala
            20                  25                  30


Leu Thr Gln Gln Asn Ile Asp Gln Leu Glu Ser Arg Leu Ala Ala Val
        35                  40                  45


Ser Thr Pro Thr Ser Ser Thr Tyr Gly Lys Tyr Leu Asp Val Asp Glu
    50                  55                  60


Ile Asn Ser Ile Phe Ala Pro Ser Asp Ala Ser Ser Ser Ala Val Glu
65                  70                  75                  80


Ser Trp Leu Gln Ser His Gly Val Thr Ser Tyr Thr Lys Gln Gly Ser
                85                  90                  95


Ser Ile Trp Phe Gln Thr Asn Ile Ser Thr Ala Asn Ala Met Leu Ser
            100                 105                 110


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


Thr Leu Lys Tyr Ser Ile Pro Glu Ser Leu Ile Gly His Val Asp Leu
    130                 135                 140


Ile Ser Pro Thr Thr Tyr Phe Gly Thr Thr Lys Ala Met Arg Lys Leu
145                 150                 155                 160


Lys Ser Ser Gly Val Ser Pro Ala Ala Asp Ala Leu Ala Ala Arg Gln
                165                 170                 175


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


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


Tyr Thr Pro Ser Val Lys Ser Gly Ser Arg Ile Gly Phe Gly Ser Phe
    210                 215                 220
```

```
Leu Asn Glu Ser Ala Ser Phe Ala Asp Gln Ala Leu Phe Glu Lys His
225                 230                 235                 240

Phe Asn Ile Pro Ser Gln Asn Phe Ser Val Val Leu Ile Asn Gly Gly
                245                 250                 255

Thr Asp Leu Pro Gln Pro Pro Ser Asp Ala Asn Asp Gly Glu Ala Asn
            260                 265                 270

Leu Asp Ala Gln Thr Ile Leu Thr Ile Ala His Pro Leu Pro Ile Thr
        275                 280                 285

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

Pro Ala Gly Thr Pro Asn Glu Asn Glu Pro Tyr Leu Gln Tyr Tyr Glu
305                 310                 315                 320

Phe Leu Leu Ser Lys Ser Asn Ala Glu Ile Pro Gln Val Ile Thr Asn
                325                 330                 335

Ser Tyr Gly Asp Glu Glu Gln Thr Val Pro Arg Ser Tyr Ala Val Arg
            340                 345                 350

Val Cys Asn Leu Ile Gly Leu Leu Gly Leu Arg Gly Ile Ser Val Leu
        355                 360                 365

His Ser Ser Gly Asp Glu Gly Val Gly Ala Ser Cys Val Ala Thr Asn
    370                 375                 380

Ser Thr Thr Pro Gln Phe Asn Pro Ile Phe Pro Ala Thr Cys Pro Tyr
385                 390                 395                 400

Val Thr Ser Val Gly Gly Thr Val Ser Phe Asn Pro Glu Val Ala Trp
                405                 410                 415

Ala Gly Ser Ser Gly Gly Phe Ser Tyr Tyr Phe Ser Arg Pro Trp Tyr
            420                 425                 430
```

```
Gln Gln Glu Ala Val Gly Thr Tyr Leu Glu Lys Tyr Val Ser Ala Glu
        435                 440                 445


Thr Lys Lys Tyr Tyr Gly Pro Tyr Val Asp Phe Ser Gly Arg Gly Phe
    450                 455                 460


Pro Asp Val Ala Ala His Ser Val Ser Pro Asp Tyr Pro Val Phe Gln
465                 470                 475                 480


Gly Gly Glu Leu Thr Pro Ser Gly Gly Thr Ser Ala Ala Ser Pro Val
                485                 490                 495


Val Ala Ala Ile Val Ala Leu Leu Asn Asp Ala Arg Leu Arg Glu Gly
            500                 505                 510


Lys Pro Thr Leu Gly Phe Leu Asn Pro Leu Ile Tyr Leu His Ala Ser
        515                 520                 525


Lys Gly Phe Thr Asp Ile Thr Ser Gly Gln Ser Glu Gly Cys Asn Gly
    530                 535                 540


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


Gly Ala His Trp Asn Ala Thr Lys Gly Trp Asp Pro Thr Thr Gly Phe
                565                 570                 575


Gly Val Pro Asn Leu Lys Lys Leu Leu Ala Leu Val Arg Phe
            580                 585                 590


<210>  11
<211>  511
<212>  PRT
<213>  Thermoascus aurantiacus

<400>  11

Val Pro Val Glu Val Ala Gly Ser Ala Gln Gly Leu Asp Val Thr Leu
1               5                   10                  15
```

```
Ser Gln Val Gly Asn Thr Arg Ile Lys Ala Val Val Lys Asn Thr Gly
            20                  25                  30


Ser Glu Asp Val Thr Phe Val His Leu Asn Phe Phe Lys Asp Ala Ala
        35                  40                  45


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


Gln Gly Ile Lys Gln Arg Leu Ile Thr Glu Gly Leu Ser Asp Asp Ala
65                  70                  75                  80


Leu Thr Thr Leu Ala Pro Gly Ala Thr Ile Glu Asp Glu Phe Asp Ile
                85                  90                  95


Ala Ser Thr Ser Asp Leu Ser Glu Gly Gly Thr Ile Thr Ile Asn Ser
            100                 105                 110


Asn Gly Leu Val Pro Ile Thr Thr Asp Asn Lys Val Thr Gly Tyr Ile
        115                 120                 125


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


Ala Ser Val Thr Gln Ala Val Lys Ile Leu Glu Arg Arg Thr Arg Ile
145                 150                 155                 160


Ser Ser Cys Ser Gly Ser Arg Gln Ser Ala Leu Thr Thr Ala Leu Arg
                165                 170                 175


Asn Ala Ala Ser Leu Ala Asn Lys Ala Ala Asp Ala Ala Gln Ser Gly
            180                 185                 190


Ser Ala Ser Lys Phe Ser Glu Tyr Phe Lys Thr Thr Ser Ser Ser Thr
        195                 200                 205


Arg Gln Thr Val Ala Ala Arg Leu Arg Ala Val Ala Arg Glu Ala Ser
    210                 215                 220
```

```
Ser Ser Ser Ser Gly Ala Thr Thr Tyr Tyr Cys Leu Asp Pro Phe Gly
225                 230                 235                 240

Tyr Cys Ser Gly Asn Val Leu Ala Tyr Thr Leu Pro Ser Tyr Asn Ile
                245                 250                 255

Ile Ala Asn Cys Pro Ile Phe Tyr Thr Tyr Leu Pro Pro Leu Thr Ser
            260                 265                 270

Thr Cys His Ala Gln Asp Gln Ala Thr Thr Val Leu His Glu Phe Thr
        275                 280                 285

His Ala Pro Gly Val Tyr Ser Pro Gly Thr Leu Asp Leu Ala Tyr Gly
    290                 295                 300

Tyr Gln Ala Ala Met Gly Leu Ser Ser Ser Gln Ala Val Met Asn Ala
305                 310                 315                 320

Asp Thr Tyr Ala Leu Tyr Ala Asn Ala Ile Tyr Leu Gly Cys Thr Arg
                325                 330                 335

Ile Ser Ser Cys Ser Gly Ser Arg Gln Ser Ala Leu Thr Thr Ala Leu
            340                 345                 350

Arg Asn Ala Ala Ser Leu Ala Asn Ala Ala Ala Asp Ala Ala Gln Ser
        355                 360                 365

Gly Ser Ala Ser Lys Phe Ser Glu Tyr Phe Lys Thr Thr Ser Ser Ser
    370                 375                 380

Thr Arg Gln Thr Val Ala Ala Arg Leu Arg Ala Val Ala Arg Glu Ala
385                 390                 395                 400

Ser Ser Ser Ser Ser Gly Ala Thr Thr Tyr Tyr Cys Asp Asp Pro Tyr
                405                 410                 415

Gly Tyr Cys Ser Ser Asn Val Leu Ala Tyr Thr Leu Pro Ser Tyr Asn
            420                 425                 430
```

```
Ile Ile Ala Asn Cys Asp Ile Phe Tyr Thr Tyr Leu Pro Ala Leu Thr
        435                 440                 445


Ser Thr Cys His Ala Gln Asp Gln Ala Thr Thr Ala Leu His Glu Phe
    450                 455                 460


Thr His Ala Pro Gly Val Tyr Ser Pro Gly Thr Asp Asp Leu Ala Tyr
465                 470                 475                 480


Gly Tyr Gln Ala Ala Met Gly Leu Ser Ser Ser Gln Ala Val Met Asn
                485                 490                 495


Ala Asp Thr Tyr Ala Leu Tyr Ala Asn Ala Ile Tyr Leu Gly Cys
            500                 505                 510


<210>  12
<211>  550
<212>  PRT
<213>  Dichomitus squalens

<400>  12

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


Pro Asn Gly Phe Ser Leu Val Gly Ser Ala Asp Ser Asn Arg Thr Leu
            20                  25                  30


Lys Leu Arg Leu Ala Leu Ala Glu Ser Asn Phe Ser Glu Leu Glu Arg
        35                  40                  45


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


Leu Ser Lys Ala Glu Val Gln Gln Leu Val Ala Pro Gly Gln Asp Ser
65                  70                  75                  80


Ile Asp Ala Val Asn Ala Trp Leu Lys Glu Asn Asp Ile Thr Ala Lys
                85                  90                  95


Thr Ile Ser Ser Thr Gly Glu Trp Ile Ser Phe Glu Val Pro Val Ser
```

```
            100                 105                 110

Lys Ala Asn Asp Leu Phe Asp Ala Asp Phe Ser Val Phe Lys His Asp
        115                 120                 125

Asp Thr Gly Val Glu Ala Ile Arg Thr Leu Ser Tyr Ser Ile Pro Ala
    130                 135                 140

Glu Leu Gln Gly His Leu Asp Leu Val His Pro Thr Val Thr Phe Pro
145                 150                 155                 160

Asn Pro Tyr Ser His Leu Pro Val Phe Gln Ser Pro Val Lys Lys Thr
                165                 170                 175

Ala Glu Ile Gln Asn Phe Thr Ala Gly Ala Ile Pro Ser Ser Cys Ser
            180                 185                 190

Ser Thr Ile Thr Pro Ala Cys Leu Gln Ala Ile Tyr Asn Ile Pro Thr
        195                 200                 205

Thr Ala Ala Thr Glu Ser Ser Asn Gln Leu Gly Val Thr Gly Phe Ile
    210                 215                 220

Asp Gln Tyr Ala Asn Lys Lys Asp Leu Lys Thr Phe Leu Lys Lys Tyr
225                 230                 235                 240

Arg Thr Asp Ile Ser Ser Ser Thr Thr Phe Thr Leu Gln Thr Leu Asp
                245                 250                 255

Gly Gly Ser Asn Ser Gln Thr Gly Ser Lys Ala Gly Val Glu Ala Asn
            260                 265                 270

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

Phe Ile Ser Val Gly Asp Asp Phe Gln Asp Gly Asp Leu Glu Gly Phe
    290                 295                 300

Leu Asp Val Ile Asn Ala Leu Leu Asp Glu Asp Ala Pro Pro Ser Val
```

```
305                 310                 315                 320

Leu Thr Thr Ser Tyr Gly Gln Asp Glu Ser Thr Ile Ser Arg Ala Leu
                325                 330                 335

Ala Val Lys Leu Cys Asn Ala Tyr Ala Gln Leu Gly Ala Arg Gly Val
            340                 345                 350

Ser Ile Leu Phe Ala Ser Gly Asp Gly Gly Val Ser Gly Ser Gln Ser
        355                 360                 365

Ala Ser Cys Ser Lys Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Tyr
    370                 375                 380

Met Thr Ser Val Gly Ala Thr Gln Gly Val Asn Pro Glu Thr Ala Ala
385                 390                 395                 400

Asp Phe Ser Ser Gly Gly Phe Ser Asn Tyr Trp Gly Val Pro Asp Tyr
                405                 410                 415

Gln Ser Asp Ala Val Ser Thr Tyr Leu Ser Ala Leu Gly Lys Thr Asn
            420                 425                 430

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

Gln Gly Val Ser Phe Glu Val Val Val Asp Gly Ser Val Glu Ala Val
    450                 455                 460

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

Val Asn Asp Lys Leu Val Ala Ala Gly Lys Ser Pro Leu Gly Phe Leu
                485                 490                 495

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

Ser Gly Ser Asn Pro Gly Cys Asn Thr Asn Gly Phe Pro Ala Lys Lys
```

```
        515                 520                 525


Gly Trp Asp Pro Val Thr Gly Leu Gly Thr Pro Asp Phe Lys Lys Leu
    530                 535                 540


Leu Thr Ala Val Gly Leu
545                 550


<210>  13
<211>  353
<212>  PRT
<213>  Nocardiopsis prasina

<400>  13

Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val
1               5                   10                  15


Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu
            20                  25                  30


Ala Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu
        35                  40                  45


Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe Asp
    50                  55                  60


Thr Glu Ser Leu Glu Leu Thr Val Leu Val Thr Asp Ala Ala Ala Val
65                  70                  75                  80


Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu Val Ser Tyr Gly
                85                  90                  95


Ile Asp Gly Leu Asp Glu Ile Val Gln Glu Leu Asn Ala Ala Asp Ala
            100                 105                 110


Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala Gly Asp Thr Val
        115                 120                 125


Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Ser Gly Leu Leu
    130                 135                 140
```

```
Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val Thr Thr Ser Asp
145                 150                 155                 160


Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu Ala Tyr Thr Met
                165                 170                 175


Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn Ala Ala Gly Gln
            180                 185                 190


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


Thr Ile Gly Asn Gly Arg Gly Val Phe Glu Gln Ser Val Phe Pro Gly
    210                 215                 220


Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe Thr Leu Thr Asn
225                 230                 235                 240


Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr Val Ala Gly His
                245                 250                 255


Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser Gly Ser Thr Thr
            260                 265                 270


Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln Ser Val Ser Tyr
        275                 280                 285


Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr Val Cys Ala Glu
    290                 295                 300


Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr Gln Ala Gln Gly
305                 310                 315                 320


Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr Phe
                325                 330                 335


Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly Val Arg Leu Arg
            340                 345                 350
```

```
Thr



<210>  14
<211>  456
<212>  PRT
<213>  Penicillium simplicissimum

<400>  14

Ala Pro Ala Ser Thr Ala Lys Asp Ser Val Ser Ser Val Val Lys Asn
1               5                   10                  15


Gly Val Lys Tyr Thr Val Phe Glu His Ala Ala Thr Gly Ala Lys Met
            20                  25                  30


Glu Phe Val Lys Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn
        35                  40                  45


Gln Tyr Ser Gly Tyr Leu Ser Val Gly Ser Asn Met Asn Met Trp Phe
    50                  55                  60


Trp Phe Phe Glu Ala Arg Asn Asn Pro Gln Gln Ala Pro Leu Ala Ala
65                  70                  75                  80


Trp Phe Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln
                85                  90                  95


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


Asn Glu Tyr Ser Trp Asn Asn Tyr Ala Asn Met Leu Tyr Val Asp Gln
        115                 120                 125


Pro Ile Gly Val Gly Phe Ser Tyr Gly Thr Asp Asp Val Thr Ser Thr
    130                 135                 140


Val Thr Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala
145                 150                 155                 160
```

```
Gln Phe Pro Glu Tyr Glu Ser Arg Asp Phe Ala Ile Phe Thr Glu Ser
                165                 170                 175


Tyr Gly Gly His Tyr Gly Pro Glu Phe Ala Ser Tyr Ile Gln Glu Gln
            180                 185                 190


Asn Ser Ala Ile Lys Thr Gly Ser Ile Ser Gly Glu Asn Ile Asn Leu
        195                 200                 205


Val Ala Leu Gly Val Asn Asn Gly Trp Ile Asp Ser Thr Ile Gln Glu
    210                 215                 220


Lys Ala Tyr Ile Asp Phe Ser Tyr Asn Asn Ser Tyr Gln Gln Leu Ile
225                 230                 235                 240


Asp Asp Ser Gln Arg Thr Ser Leu Leu Ser Ala Tyr Asn Ser Gln Cys
                245                 250                 255


Leu Pro Ala Ile Gln Lys Cys Thr Lys Ser Gly Ser Asn Ser Asp Cys
            260                 265                 270


Gln Asn Ala Asp Ser Val Cys Tyr Asn Lys Ile Glu Gly Pro Ile Ser
        275                 280                 285


Ser Ser Gly Asp Trp Asp Val Tyr Asp Ile Arg Glu Pro Ser Asn Asp
    290                 295                 300


Pro Tyr Pro Pro Ser Thr Tyr Ser Thr Tyr Leu Ser Asn Ala Asp Val
305                 310                 315                 320


Val Lys Ala Ile Gly Ala Gln Ser Ser Tyr Gln Glu Cys Pro Asn Gly
                325                 330                 335


Pro Tyr Asn Lys Phe Ala Ser Thr Gly Asp Asn Pro Arg Ser Phe Leu
            340                 345                 350


Ser Thr Leu Ser Ser Val Val Lys Ser Gly Ile Asn Val Leu Val Trp
        355                 360                 365
```

```
Ala Gly Asp Ala Asp Trp Ile Cys Asn Trp Leu Gly Asn Tyr Glu Val
    370                 375                 380


Ala Asn Ala Val Asp Phe Ser Gly His Thr Glu Phe Ser Ala Lys Asp
385                 390                 395                 400


Leu Ala Pro Tyr Thr Val Asn Gly Thr Glu Lys Gly Met Phe Lys Asn
                405                 410                 415


Val Ala Asn Phe Ser Phe Leu Lys Val Tyr Gly Ala Gly His Glu Val
            420                 425                 430


Pro Tyr Tyr Gln Pro Asp Thr Ala Leu Gln Val Phe Glu Gln Val Leu
        435                 440                 445


Gln Asn Lys Pro Ile Phe Ser Thr
    450                 455


<210>  15
<211>  502
<212>  PRT
<213>  Aspergillus niger

<400>  15

Leu Gln Asn Pro His Arg Arg Ala Val Pro Pro Pro Leu Ser His Arg
1               5                   10                  15


Ser Val Ala Ser Arg Ser Val Pro Val Glu Arg Arg Thr Thr Asp Phe
            20                  25                  30


Glu Tyr Leu Thr Asn Lys Thr Ala Arg Phe Leu Val Asn Gly Thr Ser
        35                  40                  45


Ile Pro Glu Val Asp Phe Asp Val Gly Glu Ser Tyr Ala Gly Leu Leu
    50                  55                  60


Pro Asn Thr Pro Thr Gly Asn Ser Ser Leu Phe Phe Trp Phe Phe Pro
65                  70                  75                  80
```

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


Gly Pro Gly Cys Ser Ser Leu Asp Gly Leu Leu Gln Glu Asn Gly Pro
            100                 105                 110


Phe Leu Trp Gln Pro Gly Thr Tyr Lys Pro Val Pro Asn Pro Tyr Ser
        115                 120                 125


Trp Thr Asn Leu Thr Asn Val Val Tyr Ile Asp Gln Pro Ala Gly Thr
    130                 135                 140


Gly Phe Ser Pro Gly Pro Ser Thr Val Asn Asn Glu Glu Asp Val Ala
145                 150                 155                 160


Ala Gln Phe Asn Ser Trp Phe Lys His Phe Val Asp Thr Phe Asp Leu
                165                 170                 175


His Gly Arg Lys Val Tyr Ile Thr Gly Glu Ser Tyr Ala Gly Met Tyr
            180                 185                 190


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


Phe Asn Leu Lys Gly Ile Gln Ile Asn Asp Pro Ser Ile Asn Ser Asp
    210                 215                 220


Ser Val Met Met Tyr Ser Pro Ala Val Arg His Leu Asn His Tyr Asn
225                 230                 235                 240


Asn Ile Phe Gln Leu Asn Ser Thr Phe Leu Ser Tyr Ile Asn Ala Lys
                245                 250                 255


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


Pro Pro Pro Ser Pro Phe Pro Thr Ala Pro Glu Ile Thr Glu Asp Cys
        275                 280                 285
```

```
Gln Val Trp Asp Glu Val Val Met Ala Ala Tyr Asp Ile Asn Pro Cys
    290                 295                 300


Phe Asn Tyr Tyr His Leu Ile Asp Phe Cys Pro Tyr Leu Trp Asp Val
305                 310                 315                 320


Leu Gly Phe Pro Ser Leu Ala Ser Gly Pro Asn Asn Tyr Phe Asn Arg
                325                 330                 335


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


Cys Ser Glu Thr Val Ile Phe Ala Asn Gly Asp Gly Ser Asp Pro Ser
        355                 360                 365


Ser Trp Gly Pro Leu Pro Ser Val Ile Glu Arg Thr Asn Asn Thr Ile
    370                 375                 380


Ile Gly His Gly Trp Leu Asp Tyr Leu Leu Phe Leu Asn Gly Ser Leu
385                 390                 395                 400


Ala Thr Ile Gln Asn Met Thr Trp Asn Gly Lys Gln Gly Phe Gln Arg
                405                 410                 415


Pro Pro Val Glu Pro Leu Phe Val Pro Tyr His Tyr Gly Leu Ala Glu
            420                 425                 430


Leu Tyr Trp Gly Asp Glu Pro Asp Pro Tyr Asn Leu Asp Ala Gly Ala
        435                 440                 445


Gly Tyr Leu Gly Thr Ala His Thr Glu Arg Gly Leu Thr Phe Ser Ser
    450                 455                 460


Val Tyr Leu Ser Gly His Glu Ile Pro Gln Tyr Val Pro Gly Ala Ala
465                 470                 475                 480


Tyr Arg Gln Leu Glu Phe Leu Leu Gly Arg Ile Ser Ser Leu Ser Ala
                485                 490                 495
```

```
Lys Gly Asn Tyr Thr Ser
            500


<210>  16
<211>  547
<212>  PRT
<213>  Meriphilus giganteus

<400>  16

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


Pro Ala Gly Phe Ser Leu Arg Gly Ala Ala Ser Pro Asp Thr Thr Leu
            20                  25                  30


Lys Leu Arg Ile Ala Leu Val Gln Asn Asn Phe Ala Glu Leu Glu Asp
        35                  40                  45


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


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


Val Lys Ala Val Asn Ala Trp Leu Thr Glu Asn Gly Leu Asp Ala His
                85                  90                  95


Thr Ile Ser Pro Ala Gly Asp Trp Leu Ala Phe Glu Val Pro Val Ser
            100                 105                 110


Lys Ala Asn Glu Leu Phe Asp Ala Asp Phe Ser Val Phe Thr His Asp
        115                 120                 125


Glu Ser Gly Leu Glu Ala Ile Arg Thr Leu Ala Tyr Ser Ile Pro Ala
    130                 135                 140


Glu Leu Gln Gly His Leu Asp Leu Val His Pro Thr Val Thr Phe Pro
145                 150                 155                 160


Asn Pro Asn Ala His Leu Pro Val Val Arg Ser Thr Gln Pro Ile Arg
```

```
                165                 170                 175


Asn Leu Thr Gly Arg Ala Ile Pro Ala Ser Cys Ala Ser Thr Ile Thr
            180                 185                 190


Pro Ala Cys Leu Gln Ala Ile Tyr Gly Ile Pro Thr Thr Lys Ala Thr
        195                 200                 205


Gln Ser Ser Asn Lys Leu Ala Val Ser Gly Phe Ile Asp Gln Phe Ala
    210                 215                 220


Asn Lys Ala Asp Leu Lys Ser Phe Leu Ala Gln Phe Arg Lys Asp Ile
225                 230                 235                 240


Ser Ser Ser Thr Thr Phe Ser Leu Gln Thr Leu Asp Gly Gly Glu Asn
                245                 250                 255


Asp Gln Ser Pro Ser Glu Ala Gly Ile Glu Ala Asn Leu Asp Ile Gln
            260                 265                 270


Tyr Thr Val Gly Leu Ala Thr Gly Val Pro Thr Thr Phe Ile Ser Val
        275                 280                 285


Gly Asp Asp Phe Gln Asp Gly Asn Leu Glu Gly Phe Leu Asp Ile Ile
    290                 295                 300


Asn Phe Leu Leu Gly Glu Ser Asn Pro Pro Gln Val Leu Thr Thr Ser
305                 310                 315                 320


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


Cys Asn Ala Tyr Ala Gln Leu Gly Ala Arg Gly Thr Ser Ile Leu Phe
            340                 345                 350


Ala Ser Gly Asp Gly Gly Val Ser Gly Ser Gln Ser Ala His Cys Ser
        355                 360                 365


Asn Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Phe Met Thr Ser Val
```

```
    370                 375                 380


Gly Ala Thr Gln Gly Val Ser Pro Glu Thr Ala Ala Ala Phe Ser Ser
385                 390                 395                 400


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


Val Ser Gly Tyr Leu Ser Ala Leu Gly Ser Thr Asn Ser Gly Lys Phe
            420                 425                 430


Asn Arg Ser Gly Arg Gly Phe Pro Asp Val Ser Thr Gln Gly Val Asp
        435                 440                 445


Phe Gln Ile Val Ser Gly Gly Gln Thr Ile Gly Val Asp Gly Thr Ser
    450                 455                 460


Cys Ala Ser Pro Thr Phe Ala Ser Val Ile Ser Leu Val Asn Asp Arg
465                 470                 475                 480


Leu Ile Ala Ala Gly Lys Ser Pro Leu Gly Phe Leu Asn Pro Phe Leu
                485                 490                 495


Tyr Ser Ser Ala Gly Lys Ala Ala Leu Asn Asp Val Thr Ser Gly Ser
            500                 505                 510


Asn Pro Gly Cys Ser Thr Asn Gly Phe Pro Ala Lys Ala Gly Trp Asp
        515                 520                 525


Pro Val Thr Gly Leu Gly Thr Pro Asn Phe Ala Lys Leu Leu Thr Ala
    530                 535                 540


Val Gly Leu
545


<210>  17
<211>  541
<212>  PRT
<213>  Lecanicillium sp.
```

```
<400>  17

Ala Pro Ala Pro His Gly Pro Leu Val Lys Phe Gly Glu Ile Thr Lys
1               5                   10                  15


Leu Pro Ser Lys Trp Ile Ala Thr Gly Ala Ala Asp Ser Asp Ala Val
            20                  25                  30


Ile Lys Ala Gln Ile Gly Ile Lys Gln Asn Asn Ile Lys Gly Leu Gln
        35                  40                  45


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


Trp Leu Ser Lys Glu Glu Val Asp Lys Tyr Ser Ala Pro Ala Ala Ala
65                  70                  75                  80


Asp Val Ala Ala Val Lys Ala Trp Leu Ala Ser Ser Gly Ile Thr Asp
                85                  90                  95


Val Thr Met Pro Thr Asn Asp Trp Ile Glu Phe Ser Val Pro Val Ser
            100                 105                 110


Lys Met Glu Ser Leu Leu Gly Ser Lys Tyr Glu Trp Phe Val His Leu
        115                 120                 125


Glu Thr Gly Glu Lys Val Pro Arg Thr Lys Gln Phe Ser Val Pro Gln
    130                 135                 140


Asn Leu His Asp Leu Ile Asp Val Val Thr Pro Thr Thr Val Leu Tyr
145                 150                 155                 160


His Asn Met Gly Pro His Ala His Ala Ser Pro Gln Ala Ala Asp Ala
                165                 170                 175


Ser Gly Leu Thr Ser Pro Ala Ser Ile Lys Ser Ala Tyr Asn Val Asp
            180                 185                 190


Tyr Lys Gly Thr Gly Asn Thr Leu Val Gly Thr Thr Gly Phe Leu Gly
        195                 200                 205
```

```
Val Gly Ala Ser His Gln Asp Tyr Ala Asn Phe Ala Arg Gln Phe Ser
    210                 215                 220

Pro Gly Leu Thr Asp Phe Lys Asp Val Ser Ile Asn Gly Gly Ser Asn
225                 230                 235                 240

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

Gly Ala Leu Ala Ala Pro Asn Pro Ser Glu Tyr Leu Ala His Ala Pro
            260                 265                 270

Glu Gly Ser Asp Gly Ser Ser Phe Asn Asp Ala Met Leu Ala Phe Gly
        275                 280                 285

Asn Tyr Leu Asn Ala Asn Ser Asn Pro Pro Ser Ala Val Ser Thr Ser
    290                 295                 300

Tyr Gly Gly Glu Glu Asp Gly Thr Asp Pro Asn Tyr Met Asp Arg Ile
305                 310                 315                 320

Cys Asn Glu Phe Met Lys Ala Gly Ser Arg Gly Val Ser Ile Phe Phe
                325                 330                 335

Ser Ser Gly Asp Asn Gly Val Gly Gly Asn Gly Glu Ser Ser Cys Tyr
            340                 345                 350

Asn Gly Tyr Tyr Pro Leu Trp Pro Ala Ser Cys Pro Tyr Val Thr Thr
        355                 360                 365

Val Gly Gly Thr Glu Phe Asp Gly Ser Gly Arg Glu Val Val Ala Asn
    370                 375                 380

Phe Glu Gln Tyr Asn Lys Asn Val Lys Ser Pro Gly Gly Gly Phe Ser
385                 390                 395                 400

Asn His Phe Pro Ala Pro Ser Tyr Asn Lys Asn Val Thr Thr Ala Tyr
                405                 410                 415
```

```
Ala Asn Ser Leu Ser Ala Ala Gln Lys Gln Arg Leu Asn Pro Asn Gly
            420                 425                 430


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


Val Asn Gly Gln Ile Ser Gln Val Leu Gly Thr Ser Ala Ser Ser Pro
    450                 455                 460


Ser Met Ala Gly Leu Val Gly Leu Leu Asn Asp Tyr Arg Lys Thr Gln
465                 470                 475                 480


Gly Lys Pro Asn Leu Gly Phe Ile Asn Pro Leu Leu Tyr Ser Asp Lys
                485                 490                 495


Val Lys Pro Ala Leu Arg Asp Val Thr Ser Gly Ala Asn Lys Gly Cys
            500                 505                 510


Asp Ser Ser Gly Leu Pro Ala Lys Thr Gly Trp Asp Ala Ala Ser Gly
        515                 520                 525


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


<210>  18
<211>  633
<212>  PRT
<213>  Talaromyces proteolyticus

<400>  18

Val Pro Ala Pro Ser Lys Arg His Val Val His Glu Arg Arg Asp Ala
1               5                   10                  15


Leu Pro His Ser Trp Ser Glu Pro Arg Arg Val Asp Gly Arg Thr Gln
            20                  25                  30


Leu Pro Val Arg Ile Gly Leu Thr Gln Ser Asn Ile Asp Glu Ser His
        35                  40                  45
```

```
Asp Met Leu Met Asp Ile Ala Ser Pro Ser Ser Pro Asn Tyr Arg Lys
    50                  55                  60


Tyr Met Thr Val His Glu Val Asn Glu Leu Phe Ala Pro Ala Gly Glu
65                  70                  75                  80


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


Glu Arg Val Thr Gln Ser Ala Asn Lys Gln Trp Leu Gln Phe Asp Gly
            100                 105                 110


Asp Ala Ala Glu Val Glu Ser Leu Leu Gly Ala Glu Tyr Tyr Ile Tyr
        115                 120                 125


Thr His Asp Thr Asn Gly Arg Ser His Met Gly Cys Glu Lys Tyr His
    130                 135                 140


Val Pro Glu His Ile Ser His His Ile Asp Tyr Ile Ile Pro Gly Val
145                 150                 155                 160


Lys Ser Leu Glu Val Arg Glu Pro Gln Pro Ala Glu Leu Glu Lys Arg
                165                 170                 175


Thr Phe Gly Phe Arg Lys Pro Gln Pro Pro Leu Phe Lys Ala Leu Pro
            180                 185                 190


Glu Ser Leu Glu Thr Ile Ile Asn Ser Ile Leu Gly Gly Leu Leu Asp
        195                 200                 205


Leu Cys Ser Thr Val Ile Thr Pro Ser Cys Ile Lys Thr Leu Tyr Asn
    210                 215                 220


Ile Thr Glu Gly Thr Thr Ala Thr Lys Gly Asn Glu Leu Gly Ile Phe
225                 230                 235                 240


Glu Asp Leu Gly Asp Tyr Tyr Ser Gln Thr Asp Leu Asp Leu Phe Phe
                245                 250                 255
```

```
Thr Leu Phe Tyr Ser Gln Ile Pro Ala Gly Thr Gly Pro Thr Leu Lys
            260                 265                 270


Gly Ile Asp Gly Ala Gln Ala Pro Thr Gln Thr Leu Thr Gln Ala Gly
        275                 280                 285


Pro Glu Ser Asp Leu Asp Phe Gln Val Ser Tyr Pro Ile Ile Trp Pro
    290                 295                 300


Gln Asn Ser Ile Leu Phe Gln Thr Asp Asp Ala Asn Tyr Glu Ala Asn
305                 310                 315                 320


Tyr Thr Phe Asn Gly Phe Leu Asn Asn Phe Leu Asp Ala Ile Asp Gly
                325                 330                 335


Ser Tyr Cys Thr Tyr Ser Ala Phe Gly Ile Asp Gly Asn Thr Ala Asp
            340                 345                 350


Asp Pro Pro Tyr Pro Asp Pro Ala Ser Asn Gly Tyr Lys Gly Ser Leu
        355                 360                 365


Gln Cys Gly Val Tyr Glu Pro Thr Asn Val Ile Ser Ile Ser Tyr Gly
    370                 375                 380


Gly Asp Glu Ala Gly Leu Ser Val Asn Tyr Gln Lys Arg Gln Cys Asn
385                 390                 395                 400


Glu Tyr Lys Lys Leu Gly Leu Gln Gly Val Ser Val Val Val Ser Ser
                405                 410                 415


Gly Asp Ser Gly Val Ala Gly Ala Asp Gly Cys Leu Gly Gly Gly Lys
            420                 425                 430


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


Gly Ala Thr Tyr Leu Pro Ser Gly Ala Ser Ser Thr Ser Asp Ser Glu
    450                 455                 460
```

```
Val Ala Val Ser Arg Phe Pro Ser Gly Gly Gly Phe Ser Asn Ile Tyr
465                 470                 475                 480


Ser Gln Pro Ser Tyr Gln Ser Asp Ala Val Asn Thr Tyr Leu Thr Gln
                485                 490                 495


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


Gly Ala Asn Gly Gly Ile Tyr Asn Lys Ala Gly Arg Gly Tyr Pro Asp
        515                 520                 525


Val Ala Ala Val Gly Asp Asn Ile Val Ile Phe Asn Ala Gly Ala Pro
    530                 535                 540


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


Leu Thr Arg Ile Asn Glu Val Leu Leu Ala Lys Lys Gly Thr Thr Val
                565                 570                 575


Gly Phe Val Asn Pro Thr Leu Tyr Ala Asn Pro Asp Ala Phe His Asp
            580                 585                 590


Ile Thr Ser Gly Asp Asn Pro Gly Cys Ser Thr Asn Gly Phe Ser Thr
        595                 600                 605


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


Ala Leu Leu Lys Val Phe Leu Gly Glu
625                 630


<210>  19
<211>  371
<212>  PRT
<213>  Penicillium ranomafanaense

<400>  19
```

```
Val Pro Thr Gly Gly Lys Lys Ser Phe Thr Val Asn Gln Val Ala Val
1               5                   10                  15


Ser Ala Thr Lys Thr Gln Asn Phe Ala Asn Asn Tyr Ala Arg Ala Leu
            20                  25                  30


Ala Lys Tyr Gly Ala Lys Val Pro Thr His Val Gln Ala Ala Ala Gln
        35                  40                  45


Gln Ser Gly Ser Ala Thr Thr Thr Pro Glu Ser Asp Asp Glu Glu Tyr
    50                  55                  60


Leu Thr Pro Val Asn Val Gly Gly Thr Thr Leu Asn Leu Asp Phe Asp
65                  70                  75                  80


Thr Gly Ser Ala Asp Leu Trp Val Phe Ser Ser Glu Leu Pro Ala Ser
                85                  90                  95


Glu Gln Thr Gly His Ser Leu Tyr Lys Pro Asn Asn Gly Thr Lys Leu
            100                 105                 110


Ser Gly Tyr Thr Trp Ser Ile Ser Tyr Gly Asp Gly Ser Ser Ala Ser
        115                 120                 125


Gly Asp Val Tyr Arg Asp Thr Val Ser Val Gly Gly Val Lys Ala Thr
    130                 135                 140


Gly Gln Ala Val Glu Ala Ala Ser Thr Ile Ser Gln Gln Phe Thr Gln
145                 150                 155                 160


Asp Gln Asn Asn Asp Gly Leu Leu Gly Leu Ala Phe Ser Ser Ile Asn
                165                 170                 175


Thr Val Lys Pro Lys Ser Gln Thr Thr Phe Phe Asp Thr Val Lys Ser
            180                 185                 190


Thr Leu Ala Ser Pro Leu Phe Ala Val Ser Leu Lys His Asn Ala Pro
        195                 200                 205
```

```
Gly Ser Tyr Asp Phe Gly Phe Ile Asp Lys Ser Lys Tyr Thr Gly Ser
    210                 215                 220


Leu Thr Tyr Thr Asp Val Asp Ser Ser Gln Gly Phe Trp Gly Phe Thr
225                 230                 235                 240


Ala Asp Ser Tyr Lys Ile Gly Ser Thr Thr Gly Ser Ser Ile Lys Gly
                245                 250                 255


Ile Ala Asp Thr Gly Thr Thr Leu Leu Leu Leu Asp Asp Glu Val Val
            260                 265                 270


Ser Ala Tyr Tyr Lys Gln Val Ser Gly Ala Ala Ser Asp Ser Ser Ala
        275                 280                 285


Gly Gly Tyr Thr Phe Asp Cys Ser Ser Thr Leu Pro Asp Phe Thr Val
    290                 295                 300


Ser Ile Ser Gly Tyr Asp Ala Val Val Pro Gly Ser Leu Ile Asn Tyr
305                 310                 315                 320


Thr Pro Val Ser Gln Gly Ser Ser Lys Cys Leu Gly Gly Ile Gln Ser
                325                 330                 335


Asn Ser Gly Leu Gly Phe Ser Ile Phe Gly Asp Ile Phe Leu Lys Ser
            340                 345                 350


Gln Tyr Val Val Phe Asp Ser Asn Gly Pro Arg Leu Gly Phe Ala Ala
        355                 360                 365


Gln Ser Ser
    370


<210>  20
<211>  578
<212>  PRT
<213>  Aspergillus oryzae

<400>  20

Glu Ala Phe Glu Lys Leu Ser Ala Val Pro Lys Gly Trp His Tyr Ser
```

```
1               5                   10                  15

Ser Thr Pro Lys Gly Asn Thr Glu Val Cys Leu Lys Ile Ala Leu Ala
            20                  25                  30

Gln Lys Asp Ala Ala Gly Phe Glu Lys Thr Val Leu Glu Met Ser Asp
        35                  40                  45

Pro Asp His Pro Ser Tyr Gly Gln His Phe Thr Thr His Asp Glu Met
    50                  55                  60

Lys Arg Met Leu Leu Pro Arg Asp Asp Thr Val Asp Ala Val Arg Gln
65                  70                  75                  80

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

Ile Asn Phe Cys Thr Thr Val Asp Thr Ala Asn Lys Leu Leu Asn Ala
            100                 105                 110

Gln Phe Lys Trp Tyr Val Ser Asp Val Lys His Ile Arg Arg Leu Arg
        115                 120                 125

Thr Leu Gln Tyr Asp Val Pro Glu Ser Val Thr Pro His Ile Asn Thr
    130                 135                 140

Ile Gln Pro Thr Thr Arg Phe Gly Lys Ile Ser Pro Lys Lys Ala Val
145                 150                 155                 160

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

Val Val Ala Lys Asn Ile Ser His Cys Asp Ser Ile Ile Thr Pro Thr
            180                 185                 190

Cys Leu Lys Glu Leu Tyr Asn Ile Gly Asp Tyr Gln Ala Asp Ala Asn
        195                 200                 205

Ser Gly Ser Lys Ile Ala Phe Ala Ser Tyr Leu Glu Glu Tyr Ala Arg
```

```
    210                 215                 220

Tyr Ala Asp Leu Glu Asn Phe Glu Asn Tyr Leu Ala Pro Trp Ala Lys
225                 230                 235                 240

Gly Gln Asn Phe Ser Val Thr Thr Phe Asn Gly Gly Leu Asn Asp Gln
                245                 250                 255

Asn Ser Ser Ser Asp Ser Gly Glu Ala Asn Leu Asp Leu Gln Tyr Ile
            260                 265                 270

Leu Gly Val Ser Ala Pro Leu Pro Val Thr Glu Phe Ser Thr Gly Gly
        275                 280                 285

Arg Gly Pro Leu Val Pro Asp Leu Thr Gln Pro Asp Pro Asn Ser Asn
    290                 295                 300

Ser Asn Glu Pro Tyr Leu Glu Phe Phe Gln Asn Val Leu Lys Leu Asp
305                 310                 315                 320

Gln Lys Asp Leu Pro Gln Val Ile Ser Thr Ser Tyr Gly Glu Asn Glu
                325                 330                 335

Gln Glu Ile Pro Glu Lys Tyr Ala Arg Thr Val Cys Asn Leu Ile Ala
            340                 345                 350

Gln Leu Gly Ser Arg Gly Val Ser Val Leu Phe Ser Ser Gly Asp Ser
        355                 360                 365

Gly Val Gly Glu Gly Cys Met Thr Asn Asp Gly Thr Asn Arg Thr His
    370                 375                 380

Phe Pro Pro Gln Phe Pro Ala Ala Cys Pro Trp Val Thr Ser Val Gly
385                 390                 395                 400

Ala Thr Phe Lys Thr Thr Pro Glu Arg Gly Thr Tyr Phe Ser Ser Gly
                405                 410                 415

Gly Phe Ser Asp Tyr Trp Pro Arg Pro Glu Trp Gln Asp Glu Ala Val
```

```
            420                 425                 430

Ser Ser Tyr Leu Glu Thr Ile Gly Asp Thr Phe Lys Gly Leu Tyr Asn
        435                 440                 445

Ser Ser Gly Arg Ala Phe Pro Asp Val Ala Ala Gln Gly Met Asn Phe
    450                 455                 460

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

Ser Ala Pro Ala Phe Ser Ala Val Ile Ala Leu Leu Asn Asp Ala Arg
                485                 490                 495

Leu Arg Ala Gly Lys Pro Thr Leu Gly Phe Leu Asn Pro Trp Leu Tyr
            500                 505                 510

Lys Thr Gly Arg Gln Gly Leu Gln Asp Ile Thr Leu Gly Ala Ser Ile
        515                 520                 525

Gly Cys Thr Gly Arg Ala Arg Phe Gly Gly Ala Pro Asp Gly Gly Pro
    530                 535                 540

Val Val Pro Tyr Ala Ser Trp Asn Ala Thr Gln Gly Trp Asp Pro Val
545                 550                 555                 560

Thr Gly Leu Gly Thr Pro Asp Phe Ala Glu Leu Lys Lys Leu Ala Leu
                565                 570                 575

Gly Asn



<210>  21
<211>  456
<212>  PRT
<213>  Talaromyces liani

<400>  21

Ala Pro Ala Ser Thr Thr Lys Asp Asn Val Ser Ser Val Val Lys Asn
1               5                   10                  15
```

```
Gly Val Thr Tyr Thr Val Phe Glu His Ala Ala Thr Gly Ala Lys Met
            20                  25                  30


Glu Phe Val Lys Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn
        35                  40                  45


Gln Tyr Ser Gly Tyr Leu Ser Val Gly Asn Asn Met Asn Met Trp Phe
    50                  55                  60


Trp Phe Phe Glu Ala Arg Asn Asn Pro Gln Thr Ala Pro Leu Ala Ala
65                  70                  75                  80


Trp Phe Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln
                85                  90                  95


Glu Asn Gly Pro Cys His Phe Val Asn Gly Ala Ser Thr Pro Ser Leu
            100                 105                 110


Asn Glu Tyr Ser Trp Asn Asn Tyr Ala Asn Met Leu Tyr Val Asp Gln
        115                 120                 125


Pro Ile Gly Val Gly Phe Ser Tyr Gly Thr Asp Asp Val Thr Ser Thr
    130                 135                 140


Val Thr Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala
145                 150                 155                 160


Gln Phe Pro Glu Tyr Gln Ser Arg Asp Phe Ala Ile Phe Thr Glu Ser
                165                 170                 175


Tyr Gly Gly His Tyr Gly Pro Glu Phe Ala Ala Tyr Ile Gln Glu Gln
            180                 185                 190


Asn Ser Gly Ile Ala Ala Gly Ser Val Ser Gly Glu Asn Ile Asn Leu
        195                 200                 205


Ile Ala Leu Gly Val Asn Asn Gly Trp Ile Asp Pro Ala Ile Gln Glu
    210                 215                 220
```

```
Lys Ala Tyr Ile Asp Phe Ser Tyr Asn Asn Ser Tyr Gln Gln Leu Ile
225                 230                 235                 240


Asp Asp Ser Gln Arg Thr Asn Leu Leu Ser Asp Tyr Asn Asp Gln Cys
                245                 250                 255


Leu Pro Ala Ile Gln Gln Cys Ala Gln Thr Gly Arg Asn Ser Asp Cys
            260                 265                 270


Gln Asn Ala Asp Asn Val Cys Tyr Asp Thr Ile Glu Gly Pro Ile Ser
        275                 280                 285


Ser Ser Gly Asn Trp Asp Val Tyr Asp Ile Arg Glu Pro Ser Asn Asp
    290                 295                 300


Pro Tyr Pro Pro Ser Thr Tyr Ser Ser Tyr Leu Ser Asn Ser Arg Val
305                 310                 315                 320


Val Lys Ala Ile Gly Ala Gln Thr Ser Tyr Gln Glu Cys Pro Asn Gly
                325                 330                 335


Pro Tyr Asn Lys Phe Ala Ser Thr Gly Asp Asn Pro Arg Ser Phe Leu
            340                 345                 350


Ser Thr Leu Ser Ser Val Val Gln Ser Gly Ile His Val Leu Val Trp
        355                 360                 365


Ala Gly Asp Ala Asp Trp Ile Cys Asn Trp Leu Gly Asn Tyr Arg Val
    370                 375                 380


Ala Asn Ala Val Asp Phe Pro Gly His Ala Glu Phe Ser Ala Lys Ala
385                 390                 395                 400


Leu Ala Pro Tyr Thr Val Asn Gly Thr Glu Lys Gly Met Phe Lys Asn
                405                 410                 415


Val Asp Asn Phe Ser Phe Leu Lys Val Tyr Gly Ala Gly His Glu Val
            420                 425                 430
```

```
Pro Tyr Tyr Gln Pro Ala Thr Ala Leu Gln Val Phe Glu Gln Ile Leu
        435                 440                 445


Gln Asn Lys Ser Ile Thr Ser Thr
    450                 455



<210>  22
<211>  589
<212>  PRT
<213>  Thermoascus thermophilus

<400>  22

Glu Val Phe Glu Arg Leu Arg Ala Val Pro Glu Gly Trp Arg Phe Ser
1               5                   10                  15


Ala Thr Pro Ser Asp Asp Gln Pro Ile Arg Leu Gln Ile Ala Leu Gln
            20                  25                  30


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


Pro Ser Ser Pro Asn Tyr Gly Lys His Phe Gln Ser His Asp Glu Met
    50                  55                  60


Lys Arg Met Leu Leu Pro Ser Asp Asp Ala Val Asp Ala Val Leu Asp
65                  70                  75                  80


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


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


Gln Phe Gln Trp Phe Val Ser Glu Thr Ser Ser His Val Arg Arg Leu
        115                 120                 125


Arg Ala Leu Glu Tyr Ser Ile Pro Glu Ser Val Thr Pro His Ile His
    130                 135                 140
```

```
Met Val Gln Pro Thr Thr Arg Phe Gly Gln Ile Gly Arg His His Thr
145                 150                 155                 160

Thr Ser Arg Glu Lys Pro Ile Val Ser Gly Ala Asp Ile His Ala Ser
                165                 170                 175

Ile Ala Gly Ala Asn Asn Gln Thr Thr Gly Thr Asp Cys Asn Thr Glu
            180                 185                 190

Ile Thr Pro Lys Cys Leu Gln Asp Leu Tyr Lys Phe Gly Gly Tyr Lys
        195                 200                 205

Ala Ser Ala Asn Ser Gly Ser Lys Val Gly Phe Cys Ser Tyr Leu Glu
    210                 215                 220

Glu Tyr Ala Arg Tyr Asp Asp Leu Ala Leu Phe Glu Glu Ala Leu Ala
225                 230                 235                 240

Pro Tyr Ala Ala Gly Gln Asn Phe Ser Val Ile Thr Tyr Asn Gly Gly
                245                 250                 255

Leu Asn Asp Gln His Ser Ser Ser Asp Ser Gly Glu Ala Asn Leu Asp
            260                 265                 270

Leu Gln Tyr Ile Val Gly Val Ser Ala Pro Leu Pro Val Thr Glu Phe
        275                 280                 285

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

Pro Ala Asp Asn Ser Asn Glu Pro Tyr Leu Asp Phe Leu Gln Asn Val
305                 310                 315                 320

Leu Lys Leu Asp Gln Lys Asp Leu Pro Gln Val Ile Ser Thr Ser Tyr
                325                 330                 335

Gly Glu Asn Glu Gln Ser Val Pro Glu Lys Tyr Ala Arg Ser Val Cys
            340                 345                 350
```

```
Asn Leu Phe Met Gln Leu Gly Ser Arg Gly Val Ser Val Ile Phe Ser
        355                 360                 365


Ser Gly Asp Ser Gly Val Gly Ser Ala Cys Leu Thr Asn Asp Gly Lys
    370                 375                 380


Asn Gln Thr Arg Phe Met Pro Gln Phe Pro Ala Ser Cys Pro Trp Val
385                 390                 395                 400


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


Phe Ser Ser Gly Gly Phe Ser Asp Leu Trp Pro Met Pro Asp Tyr Gln
            420                 425                 430


Lys Ser Ala Val Gly Glu Tyr Leu Asp Arg Leu Gly Ser Lys Trp Ala
        435                 440                 445


Gly Leu Tyr Asn Pro Gln Gly Arg Gly Phe Pro Asp Val Ala Ala Gln
    450                 455                 460


Gly Val Asn Phe Asn Val Tyr Asp Lys Gly Ser Leu Lys Arg Phe Asp
465                 470                 475                 480


Gly Thr Ser Cys Ser Ala Pro Thr Phe Ala Gly Val Ile Ala Leu Leu
                485                 490                 495


Asn Asp Ala Arg Leu Arg Ala Arg Gln Pro Pro Met Gly Phe Leu Asn
            500                 505                 510


Pro Trp Leu Tyr Gly Ala Gly Lys Gly Gly Leu Asn Asp Ile Val Asn
        515                 520                 525


Gly Gly Ser Thr Gly Cys Asp Gly Asn Ala Arg Phe Gly Gly Ala Pro
    530                 535                 540


Asn Gly Ser Pro Val Val Pro Phe Ala Ser Trp Asn Ala Thr Gln Gly
545                 550                 555                 560
```

```
Trp Asp Pro Val Ser Gly Leu Gly Thr Pro Asp Phe Ser Arg Leu Leu
                565                 570                 575


Lys Leu Ala Val Pro Ser Arg Val Gly Gly Arg Leu Ala
            580                 585


<210>  23
<211>  413
<212>  PRT
<213>  Pyrococcus furiosus

<400>  23

Ala Glu Leu Glu Gly Leu Asp Glu Ser Ala Ala Gln Val Met Ala Thr
1               5                   10                  15


Tyr Val Trp Asn Leu Gly Tyr Asp Gly Ser Gly Ile Thr Ile Gly Ile
            20                  25                  30


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


Ile Gly Trp Val Asp Phe Val Asn Gly Arg Ser Tyr Pro Tyr Asp Asp
    50                  55                  60


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


Ala Ser Asn Gly Lys Tyr Lys Gly Met Ala Pro Gly Ala Lys Leu Ala
                85                  90                  95


Gly Ile Lys Val Leu Gly Ala Asp Gly Ser Gly Ser Ile Ser Thr Ile
            100                 105                 110


Ile Lys Gly Val Glu Trp Ala Val Asp Asn Lys Asp Lys Tyr Gly Ile
        115                 120                 125


Lys Val Ile Asn Leu Ser Leu Gly Ser Ser Gln Ser Ser Asp Gly Thr
    130                 135                 140
```

```
Asp Ala Leu Ser Gln Ala Val Asn Ala Ala Trp Asp Ala Gly Leu Val
145                 150                 155                 160


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


Ser Pro Ala Ala Ala Ser Lys Val Ile Thr Val Gly Ala Val Asp Lys
            180                 185                 190


Tyr Asp Val Ile Thr Ser Phe Ser Ser Arg Gly Pro Thr Ala Asp Gly
        195                 200                 205


Arg Leu Lys Pro Glu Val Val Ala Pro Gly Asn Trp Ile Ile Ala Ala
    210                 215                 220


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


Ala Ala Pro Gly Thr Ser Met Ala Thr Pro His Val Ala Gly Ile Ala
                245                 250                 255


Ala Leu Leu Leu Gln Ala His Pro Ser Trp Thr Pro Asp Lys Val Lys
            260                 265                 270


Thr Ala Leu Ile Glu Thr Ala Asp Ile Val Lys Pro Asp Glu Ile Ala
        275                 280                 285


Asp Ile Ala Tyr Gly Ala Gly Arg Val Asn Ala Tyr Lys Ala Ile Asn
    290                 295                 300


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


Gly Ser Gln Thr His Gln Phe Val Ile Ser Gly Ala Ser Phe Val Thr
                325                 330                 335


Ala Thr Leu Tyr Trp Asp Asn Ala Asn Ser Asp Leu Asp Leu Tyr Leu
            340                 345                 350
```

```
Tyr Asp Pro Asn Gly Asn Gln Val Asp Tyr Ser Tyr Thr Ala Tyr Tyr
        355                 360                 365


Asp Phe Glu Lys Val Gly Tyr Tyr Asn Pro Thr Asp Gly Thr Trp Thr
    370                 375                 380


Ile Lys Val Val Ser Tyr Ser Gly Ser Ala Asn Tyr Gln Val Asp Val
385                 390                 395                 400


Val Ser Asp Gly Ser Leu Ser Gln Pro Gly Ser Ser Pro
                405                 410


<210>  24
<211>  387
<212>  PRT
<213>  Trichoderma reesei

<400>  24

Leu Pro Thr Glu Gly Gln Lys Thr Ala Ser Val Glu Val Gln Tyr Asn
1               5                   10                  15


Lys Asn Tyr Val Pro His Gly Pro Thr Ala Leu Phe Lys Ala Lys Arg
            20                  25                  30


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


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


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


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


Ser Asp Leu Trp Val Phe Ser Ser Glu Thr Pro Lys Ser Ser Ala Thr
            100                 105                 110


Gly His Ala Ile Tyr Thr Pro Ser Lys Ser Ser Thr Ser Lys Lys Val
```

```
        115                 120                 125


Ser Gly Ala Ser Trp Ser Ile Ser Tyr Gly Asp Gly Ser Ser Ser Ser
    130                 135                 140


Gly Asp Val Tyr Thr Asp Lys Val Thr Ile Gly Gly Phe Ser Val Asn
145                 150                 155                 160


Thr Gln Gly Val Glu Ser Ala Thr Arg Val Ser Thr Glu Phe Val Gln
                165                 170                 175


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


Gln Val Arg Pro His Pro Gln Lys Thr Trp Phe Ser Asn Ala Ala Ser
        195                 200                 205


Ser Leu Ala Glu Pro Leu Phe Thr Ala Asp Leu Arg His Gly Gln Asn
    210                 215                 220


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


Val Ala Tyr Thr Pro Val Asp Asn Ser Gln Gly Phe Trp Glu Phe Thr
                245                 250                 255


Ala Ser Gly Tyr Ser Val Gly Gly Gly Lys Leu Asn Arg Asn Ser Ile
            260                 265                 270


Asp Gly Ile Ala Asp Thr Gly Thr Thr Leu Leu Leu Leu Asp Asp Asn
        275                 280                 285


Val Val Asp Ala Tyr Tyr Ala Asn Val Gln Ser Ala Gln Tyr Asp Asn
    290                 295                 300


Gln Gln Glu Gly Val Val Phe Asp Cys Asp Glu Asp Leu Pro Ser Phe
305                 310                 315                 320


Ser Phe Gly Val Gly Ser Ser Thr Ile Thr Ile Pro Gly Asp Leu Leu
```

```
                325                 330                 335


Asn Leu Thr Pro Leu Glu Glu Gly Ser Ser Thr Cys Phe Gly Gly Leu
            340                 345                 350


Gln Ser Ser Ser Gly Ile Gly Ile Asn Ile Phe Gly Asp Val Ala Leu
        355                 360                 365


Lys Ala Ala Leu Val Val Phe Asp Leu Gly Asn Glu Arg Leu Gly Trp
    370                 375                 380


Ala Gln Lys
385


<210>  25
<211>  408
<212>  PRT
<213>  Rhizomucor miehei

<400>  25

Arg Pro Val Ser Lys Gln Ser Glu Ser Lys Asp Lys Leu Leu Ala Leu
1               5                   10                  15


Pro Leu Thr Ser Val Ser Arg Lys Phe Ser Gln Thr Lys Phe Gly Gln
            20                  25                  30


Gln Gln Leu Ala Glu Lys Leu Ala Gly Leu Lys Pro Phe Ser Glu Ala
        35                  40                  45


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


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


Leu Leu Leu Phe Asp Thr Gly Ser Ser Asp Thr Trp Val Pro His Lys
                85                  90                  95


Gly Cys Thr Lys Ser Glu Gly Cys Val Gly Ser Arg Phe Phe Asp Pro
            100                 105                 110
```

```
Ser Ala Ser Ser Thr Phe Lys Ala Thr Asn Tyr Asn Leu Asn Ile Thr
        115                 120                 125


Tyr Gly Thr Gly Gly Ala Asn Gly Leu Tyr Phe Glu Asp Ser Ile Ala
    130                 135                 140


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


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


Asp Gly Leu Phe Gly Ala Ala Tyr Pro Asp Asn Thr Ala Met Glu Ala
            180                 185                 190


Glu Tyr Gly Ser Thr Tyr Asn Thr Val His Val Asn Leu Tyr Lys Gln
        195                 200                 205


Gly Leu Ile Ser Ser Pro Leu Phe Ser Val Tyr Met Asn Thr Asn Ser
    210                 215                 220


Gly Thr Gly Glu Val Val Phe Gly Gly Val Asn Asn Thr Leu Leu Gly
225                 230                 235                 240


Gly Asp Ile Ala Tyr Thr Asp Val Met Ser Arg Tyr Gly Gly Tyr Tyr
                245                 250                 255


Phe Trp Asp Ala Pro Val Thr Gly Ile Thr Val Asp Gly Ser Ala Ala
            260                 265                 270


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


Phe Phe Ile Met Pro Ser Ser Ala Ala Ser Lys Ile Val Lys Ala Ala
    290                 295                 300


Leu Pro Asp Ala Thr Glu Thr Gln Gln Gly Trp Val Val Pro Cys Ala
305                 310                 315                 320
```

```
Ser Tyr Gln Asn Ser Lys Ser Thr Ile Ser Ile Val Met Gln Lys Ser
                325                 330                 335


Gly Ser Ser Ser Asp Thr Ile Glu Ile Ser Val Pro Val Ser Lys Met
            340                 345                 350


Leu Leu Pro Val Asp Gln Ser Asn Glu Thr Cys Met Phe Ile Ile Leu
        355                 360                 365


Pro Asp Gly Gly Asn Gln Tyr Ile Val Gly Asn Leu Phe Leu Arg Phe
    370                 375                 380


Phe Val Asn Val Tyr Asp Phe Gly Asn Asn Arg Ile Gly Phe Ala Pro
385                 390                 395                 400


Leu Ala Ser Ala Tyr Glu Asn Glu
                405


<210>  26
<211>  548
<212>  PRT
<213>  Lenzites betulinus

<400>  26

Lys Pro Met Gly Arg Asn Leu Lys Val His Glu Ala Arg Glu Glu Ile
1               5                   10                  15


Pro Asp Gly Phe Ser Leu Gln Gly Ser Ala Ala Pro Asp Thr Thr Leu
            20                  25                  30


Lys Leu Arg Ile Ala Leu Val Gln Ser Asn Phe Ala Glu Leu Glu Gln
        35                  40                  45


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


Leu Ser Lys Glu Glu Val Glu Gln Leu Val Ala Pro Ser Ala Asp Ser
65                  70                  75                  80
```

```
Val Asp Ala Val Asn Ala Trp Leu Lys Glu Asn Asp Leu Ser Ala Gln
                85                  90                  95


Thr Ile Ser Pro Ala Gly Asp Trp Leu Ala Phe Glu Val Pro Val Ser
            100                 105                 110


Lys Ala Asn Glu Leu Phe Asp Ala Asp Phe Ser Val Phe Thr His Asp
        115                 120                 125


Gln Thr Gly Leu Glu Ala Ile Arg Thr Met Ser Tyr Ser Ile Pro Ala
    130                 135                 140


Glu Leu Gln Gly His Leu Asp Leu Val His Pro Thr Val Thr Phe Pro
145                 150                 155                 160


Asn Pro Tyr Ser His Leu Pro Val Val Arg Ser Pro Ile Lys Ala Ser
                165                 170                 175


Gln Asn Leu Thr Ser Arg Ala Thr Ile Pro Ala Ser Cys Ala Ser Thr
            180                 185                 190


Ile Thr Pro Ala Cys Leu Gln Asp Ile Tyr Gly Ile Pro Thr Thr Lys
        195                 200                 205


Ala Thr Gln Ser Ser Asn Lys Leu Ala Val Ser Gly Phe Ile Asp Gln
    210                 215                 220


Phe Ala Asn Ser Ala Asp Leu Ala Thr Phe Leu Lys Lys Phe Arg Thr
225                 230                 235                 240


Asp Ile Ser Ser Thr Thr Thr Phe Ala Leu Gln Thr Leu Asp Gly Gly
                245                 250                 255


Ser Asn Ser Gln Ser Gly Ser Gln Ala Gly Val Glu Ala Asn Leu Asp
            260                 265                 270


Ile Gln Tyr Thr Val Gly Leu Ala Ser Gly Val Pro Val Thr Phe Ile
        275                 280                 285
```

```
Ser Val Gly Asp Asn Phe Gln Asp Gly Asp Leu Glu Gly Phe Leu Asp
    290                 295                 300


Ile Ile Asn Phe Leu Leu Ala Glu Ser Ala Pro Pro Gln Val Leu Thr
305                 310                 315                 320


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


Gln Leu Cys Asn Ala Tyr Ala Gln Leu Gly Ala Arg Gly Thr Ser Ile
            340                 345                 350


Leu Phe Ala Ser Gly Asp Gly Gly Val Ser Gly Ser Gln Ser Ser Ser
        355                 360                 365


Cys Ser Lys Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Phe Met Thr
    370                 375                 380


Ser Val Gly Ala Thr Gln Gly Val Asn Pro Glu Thr Ala Ala Asp Phe
385                 390                 395                 400


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


Thr Ala Val Lys Thr Tyr Leu Thr Ala Leu Gly Thr Thr Asn Ser Gly
            420                 425                 430


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


Val Asp Phe Glu Ile Val Val Asp Gly Arg Thr Glu Gly Val Asp Gly
    450                 455                 460


Thr Ser Cys Ala Ser Pro Thr Phe Ala Ala Ile Ile Ser Leu Val Asn
465                 470                 475                 480


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

```
Phe Leu Tyr Ser Thr Gly Ala Ser Ala Phe Thr Asp Ile Thr Ser Gly
            500                 505                 510


Ser Asn Pro Gly Cys Asn Thr Lys Gly Phe Pro Ala Lys Ala Gly Trp
        515                 520                 525


Asp Pro Val Thr Gly Leu Gly Thr Pro Asn Phe Ala Lys Leu Leu Ala
    530                 535                 540


Ala Ala Gly Val
545


<210>  27
<211>  547
<212>  PRT
<213>  Neolentinus lepideus

<400>  27

Gly Pro Ala Pro Arg Asn Leu Val Leu His Glu Ser Arg Asp Gly Val
1               5                   10                  15


Pro Glu Gly Phe Val Lys Ser Ser Thr Ala Ser Pro Asp Thr Thr Leu
            20                  25                  30


Lys Leu Arg Ile Ala Leu Val Gln Gly Asp Met Ala Ser Leu Glu Lys
        35                  40                  45


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


Leu Ser Lys Gln Glu Val Glu Glu Tyr Val Lys Pro Thr Gln Glu Ser
65                  70                  75                  80


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


Thr Ile Ser Pro Ala Gly Asp Trp Leu Gln Phe Ser Val Pro Val Ser
            100                 105                 110
```

```
Lys Ala Asn Glu Met Phe Asp Ala Asp Phe Ser Val Phe Thr His Thr
        115                 120                 125


Glu Ser Gly Gln Gln Ala Ile Arg Thr Leu Ser Tyr Ser Ile Pro Lys
    130                 135                 140


Glu Leu Val Gly His Leu Asp Leu Val His Pro Thr Ile Thr Phe Pro
145                 150                 155                 160


Asn Pro Tyr Ser His Leu Pro Val Val Ser Ser Pro Ala Pro Arg Asn
                165                 170                 175


Leu Thr Ile Asp Ala Ser Val Pro Ser Ser Cys Gly Ser Thr Ile Thr
            180                 185                 190


Pro Thr Cys Leu Gln Asp Leu Tyr Gly Ile Pro Thr Thr Ala Ala Thr
        195                 200                 205


Gln Ser Ser Asn Lys Leu Ala Val Ser Gly Phe Ile Asp Gln Tyr Ala
    210                 215                 220


Asn Lys Ala Asp Leu Lys Ser Phe Leu Thr Thr Tyr Arg Lys Asp Ile
225                 230                 235                 240


Ser Ser Ser Thr Thr Phe Thr Leu Glu Thr Ile Asp Gly Gly Glu Asn
                245                 250                 255


Pro Gln Asp Gly Ser Asp Ala Gly Val Glu Ala Asn Leu Asp Thr Gln
            260                 265                 270


Tyr Thr Val Gly Leu Ala Thr Gly Val Pro Thr Tyr Phe Ile Ser Val
        275                 280                 285


Gly Asp Asp Tyr Gln Asp Gly Asp Leu Glu Gly Phe Leu Asp Ile Val
    290                 295                 300


Asn Tyr Leu Leu Ser Met Asp Gln Pro Gln Gln Val Leu Thr Thr Ser
305                 310                 315                 320
```

```
Tyr Gly Gln Asn Glu Asn Thr Met Ser Arg Ser Leu Ala Asn Asn Leu
                325                 330                 335

Cys Asn Ala Tyr Met Gln Leu Gly Ala Arg Gly Thr Ser Ile Leu Phe
            340                 345                 350

Ala Ser Gly Asp Gly Gly Val Ser Gly Ser Gln Ser Gly Ser Cys Gly
        355                 360                 365

Ser Lys Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Tyr Leu Thr Ser
    370                 375                 380

Val Gly Ala Thr Thr Gly Ile Asn Pro Glu Val Ala Ala Ser Phe Ser
385                 390                 395                 400

Ser Gly Gly Phe Ser Asn Tyr Trp Gly Val Pro Ser Tyr Gln Gln Ser
                405                 410                 415

Val Val Ser Ser Tyr Ile Ser Gly Leu Gly Ser Thr Asn Lys Gly Lys
            420                 425                 430

Tyr Asn Ser Ser Gly Arg Gly Phe Pro Asp Val Ser Ala Gln Gly Glu
        435                 440                 445

Asn Val Glu Ile Val Val Asp Gly Ser Thr Glu Gly Val Asp Gly Thr
    450                 455                 460

Ser Cys Ser Ser Pro Ile Phe Ala Ser Ile Val Ser Leu Leu Asn Asp
465                 470                 475                 480

Glu Leu Ile Ala Ala Gly Lys Ser Pro Leu Gly Phe Leu Asn Pro Phe
                485                 490                 495

Leu Tyr Ser Asp Gly Ala Ser Ala Phe Asn Asp Ile Thr Ser Gly Asp
            500                 505                 510

Asn Pro Gly Cys Asn Thr Asn Gly Phe Ser Ala Lys Ser Gly Trp Asp
        515                 520                 525
```

```
Pro Val Thr Gly Leu Gly Thr Pro Asn Tyr Ala Lys Leu Arg Thr Ala
    530                 535                 540


Val Gly Phe
545


<210>  28
<211>  399
<212>  PRT
<213>  Thermococcus sp.

<400>  28

Val Ser Ala Glu Lys Val Arg Val Ile Ile Thr Ile Asp Lys Asp Phe
1               5                   10                  15


Asn Glu Asn Ser Val Phe Ala Leu Gly Gly Asn Val Val Ala Arg Gly
            20                  25                  30


Lys Val Phe Pro Ile Val Ile Ala Glu Leu Ser Pro Arg Ala Val Glu
        35                  40                  45


Arg Leu Lys Asn Ala Lys Gly Val Val Arg Val Glu Tyr Asp Ala Glu
    50                  55                  60


Val Gln Val Leu Lys Gly Lys Ser Pro Gly Ala Gly Lys Pro Lys Pro
65                  70                  75                  80


Ser Gln Pro Ala Gln Thr Ile Pro Trp Gly Ile Glu Arg Ile Lys Ala
                85                  90                  95


Pro Asp Val Trp Ser Ile Thr Asp Gly Ser Ser Ser Gly Val Ile Glu
            100                 105                 110


Val Ala Ile Leu Asp Thr Gly Ile Asp Tyr Asp His Pro Asp Leu Ala
        115                 120                 125


Ala Asn Leu Ala Trp Gly Val Ser Val Leu Arg Gly Lys Val Ser Thr
    130                 135                 140


Lys Pro Lys Asp Tyr Lys Asp Gln Asn Gly His Gly Thr His Val Ala
```

```
145                 150                 155                 160


Gly Thr Val Ala Ala Leu Asn Asn Asp Ile Gly Val Val Gly Val Ala
                165                 170                 175


Pro Ala Val Glu Ile Tyr Ala Val Arg Val Leu Asp Ala Ser Gly Arg
            180                 185                 190


Gly Ser Tyr Ser Asp Ile Ile Leu Gly Ile Glu Gln Ala Leu Leu Gly
        195                 200                 205


Pro Asp Gly Val Leu Asp Ser Asp Gly Asp Gly Ile Ile Val Gly Asp
    210                 215                 220


Pro Asp Asp Asp Ala Ala Glu Val Ile Ser Met Ser Leu Gly Gly Leu
225                 230                 235                 240


Ser Asp Val Gln Ala Phe His Asp Ala Ile Ile Glu Ala Tyr Asn Tyr
                245                 250                 255


Gly Val Val Ile Val Ala Ala Ser Gly Asn Glu Gly Ala Ser Ser Pro
            260                 265                 270


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


Val Asn Asp Gln Val Pro Trp Trp Ser Asn Arg Gly Val Glu Val Ser
    290                 295                 300


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


Thr Leu Ser Gly Thr Ser Met Ala Thr Pro His Val Ser Gly Val Val
                325                 330                 335


Ala Leu Ile Gln Ala Ala Tyr Tyr Asn Lys Tyr Gly Ser Val Leu Pro
            340                 345                 350


Val Gly Thr Phe Asp Asp Asn Thr Met Ser Thr Val Arg Gly Ile Leu
```

```
        355                 360                 365


His Ile Thr Ala Asp Asp Leu Gly Ser Ser Gly Trp Asp Ala Asp Tyr
    370                 375                 380


Gly Tyr Gly Ile Val Arg Ala Asp Leu Ala Val Gln Ala Val Asn
385                 390                 395


<210>  29
<211>  396
<212>  PRT
<213>  Thermococcus sp.

<400>  29

Glu Lys Val Arg Val Ile Ile Thr Ile Asp Lys Asp Phe Asn Glu Asn
1               5                   10                  15


Ser Val Phe Ala Leu Gly Gly Asn Val Val Ala Arg Gly Lys Val Phe
            20                  25                  30


Pro Ile Val Ile Ala Glu Leu Ser Pro Arg Ala Val Glu Arg Leu Lys
        35                  40                  45


Asn Ala Lys Gly Val Val Arg Val Glu Tyr Asp Ala Glu Val Gln Val
    50                  55                  60


Leu Lys Gly Lys Ser Pro Gly Ala Gly Lys Pro Lys Pro Ser Gln Pro
65                  70                  75                  80


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


Trp Ser Ile Thr Asp Gly Ser Ser Ser Gly Val Ile Glu Val Ala Ile
            100                 105                 110


Leu Asp Thr Gly Ile Asp Tyr Asp His Pro Asp Leu Ala Ala Asn Leu
        115                 120                 125


Ala Trp Gly Val Ser Val Leu Arg Gly Lys Val Ser Thr Lys Pro Lys
    130                 135                 140
```

```
Asp Tyr Lys Asp Gln Asn Gly His Gly Thr His Val Ala Gly Thr Val
145                 150                 155                 160

Ala Ala Leu Asn Asn Asp Ile Gly Val Val Gly Val Ala Pro Ala Val
                165                 170                 175

Glu Ile Tyr Ala Val Arg Val Leu Asp Ala Ser Gly Arg Gly Ser Tyr
            180                 185                 190

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

Val Leu Asp Ser Asp Gly Asp Gly Ile Ile Val Gly Asp Pro Asp Asp
    210                 215                 220

Asp Ala Ala Glu Val Ile Ser Met Ser Leu Gly Gly Leu Ser Asp Val
225                 230                 235                 240

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

Ile Val Ala Ala Ser Gly Asn Glu Gly Ala Ser Ser Pro Ser Tyr Pro
            260                 265                 270

Ala Ala Tyr Pro Glu Val Ile Ala Val Gly Ala Thr Asp Val Asn Asp
        275                 280                 285

Gln Val Pro Trp Trp Ser Asn Arg Gly Val Glu Val Ser Ala Pro Gly
    290                 295                 300

Val Asp Val Leu Ser Thr Tyr Pro Asp Asp Ser Tyr Glu Thr Leu Ser
305                 310                 315                 320

Gly Thr Ser Met Ala Thr Pro His Val Ser Gly Val Val Ala Leu Ile
                325                 330                 335

Gln Ala Ala Tyr Tyr Asn Lys Tyr Gly Ser Val Leu Pro Val Gly Thr
            340                 345                 350
```

```
Phe Asp Asp Asn Thr Met Ser Thr Val Arg Gly Ile Leu His Ile Thr
        355                 360                 365

Ala Asp Asp Leu Gly Ser Ser Gly Trp Asp Ala Asp Tyr Gly Tyr Gly
    370                 375                 380

Ile Val Arg Ala Asp Leu Ala Val Gln Ala Val Asn
385                 390                 395


<210>  30
<211>  572
<212>  PRT
<213>  Thermomyces lanuginosus

<400>  30

Ala Pro Phe Gln Val Val Glu Arg Leu Ser Ala Pro Pro Asp Gly Trp
1               5                   10                  15

Ile Lys Lys Glu Lys Ala Ala Pro Ser Ala Gln Ile Gln Phe Arg Leu
            20                  25                  30

Gly Leu Pro Gln Gln Asn Ser Glu Gln Leu Glu Gln Leu Ala Leu Asn
        35                  40                  45

Ile Ala Thr Pro Gly His Glu Leu Tyr Arg Lys His Leu Lys Arg Asp
    50                  55                  60

Glu Ile Lys Ala Leu Val Arg Pro Leu Ala Ser Val Ser Glu Lys Val
65                  70                  75                  80

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

Asp Gly Ala Trp Ile Lys Phe Thr Val Pro Val Ser Thr Ala Glu Lys
            100                 105                 110

Leu Leu Asn Thr Glu Phe Phe Val Phe His Asn Glu Arg Thr Gly Ala
        115                 120                 125
```

```
Glu Gln Ile Arg Thr Leu Glu Tyr Ser Val Pro Gln Asp Ile His Ser
    130                 135                 140


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


Gln Val Arg Arg Val Val Pro Leu Asp Val Leu Pro Lys Leu Arg Ile
                165                 170                 175


Thr Leu Glu Asp Cys Asn Lys Lys Ile Thr Pro Asp Cys Leu Lys Gln
            180                 185                 190


Leu Tyr Lys Ile Gly Asp Tyr Val Ala Pro Glu Asp Pro Arg Asn Arg
        195                 200                 205


Ile Gly Ile Ser Gly Tyr Leu Glu Gln Phe Ala Arg Tyr Ala Asp Phe
    210                 215                 220


Glu Glu Phe Leu Glu Ser Tyr Ala Pro Asp Arg Thr Asp Ala Asn Phe
225                 230                 235                 240


Thr Val Val Ser Ile Asn Gly Gly Arg Asn Asp Gln Asn Ser Thr Leu
                245                 250                 255


Asp Ser Thr Glu Ala Ser Leu Asp Ile Asp Tyr Ala Val Thr Leu Ser
            260                 265                 270


Tyr Lys Thr Gln Ala Val Tyr Tyr Thr Thr Ala Gly Arg Gly Pro Leu
        275                 280                 285


Val Pro Asp Glu Ser Gln Pro Asp Pro Asn Glu Val Ser Asn Glu Pro
    290                 295                 300


Tyr Met Glu Gln Leu Gln Phe Leu Leu Asp Leu Pro Asp Glu Glu Leu
305                 310                 315                 320


Pro Thr Val Leu Thr Thr Ser Tyr Gly Glu Asn Glu Gln Ser Leu Pro
                325                 330                 335
```

```
Gly Ser Tyr Ala Asp Glu Thr Cys Asn Met Phe Arg Leu Leu Gly Met
            340                 345                 350


Arg Gly Val Ser Val Ile Phe Ser Ser Gly Asp Trp Gly Thr Gly Ile
        355                 360                 365


Val Cys Lys Ala Asn Asp Gly Ser Glu Arg Ile Lys Phe Asp Pro Val
    370                 375                 380


Tyr Pro Ala Ser Cys Pro Tyr Val Thr Ser Val Gly Gly Thr Thr Gly
385                 390                 395                 400


Val Asn Pro Glu Arg Ala Val Glu Phe Ser Ser Gly Gly Phe Ser Asp
                405                 410                 415


Arg Phe Pro Arg Pro Lys Tyr Gln Asp Glu Ala Val Arg Ser Tyr Leu
            420                 425                 430


Thr Lys Leu Gly Asp His Trp Lys Gly Leu Tyr Asn Glu Ser Gly Arg
        435                 440                 445


Ala Phe Pro Asp Val Ala Ala Gln Ala Asp Asn Phe Val Val Arg Asp
    450                 455                 460


Gln Gly Gln Trp Val Ser Val Gly Gly Thr Ser Ala Ser Ala Pro Val
465                 470                 475                 480


Phe Ala Ala Ile Ile Ala Asn Val Asn Ala Glu Leu Leu Lys Ala Gly
                485                 490                 495


Lys Pro Pro Leu Gly Phe Leu Asn Pro Trp Leu Tyr Gly Leu Lys Gly
            500                 505                 510


Arg Gly Phe Thr Asp Val Val His Gly Gly Ser Thr Gly Cys Pro Gly
        515                 520                 525


Thr Val Pro Trp Thr Gly Leu Pro Ala Gly His Val Pro Tyr Ala Ser
    530                 535                 540
```

```
Trp Asn Ala Thr Glu Gly Trp Asp Pro Val Thr Gly Leu Gly Thr Pro
545                 550                 555                 560


Leu Tyr Asp Glu Leu Val Lys Ala Ala Leu Gly Lys
                565                 570


<210>  31
<211>  397
<212>  PRT
<213>  Thermococcus thioreducens

<400>  31

Glu Lys Pro Glu Leu Val Arg Val Ile Val His Val Asp Arg Gly His
1               5                   10                  15


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


Phe Lys Leu Ile Asp Ala Val Val Val Glu Val Pro Ser Thr Ala Val
        35                  40                  45


Gly Arg Leu Lys Lys Leu Pro Gly Val Lys Met Val Glu Phe Asp His
    50                  55                  60


Lys Ala Arg Ile Leu Ala Gly Pro Pro Ser Trp Leu Gly Gly Gly Gln
65                  70                  75                  80


Pro Ser Gln Gln Ile Pro Trp Gly Ile Ser Arg Val Arg Ala Pro Asp
                85                  90                  95


Val Trp Gly Ile Thr Asp Gly Ser Gly Gly Val Ile Glu Val Ala Val
            100                 105                 110


Leu Asp Thr Gly Val Asp Tyr Asp His Pro Asp Leu Ala Gly Asn Ile
        115                 120                 125


Ala Trp Cys Val Ser Thr Leu Arg Gly Arg Val Thr Thr Asn Pro Ala
    130                 135                 140
```

```
Gln Cys Lys Asp Gln Asn Gly His Gly Thr His Val Ile Gly Thr Ile
145                 150                 155                 160


Ala Ala Leu Asn Asn Asp Ile Gly Val Val Gly Val Ala Pro Gly Val
                165                 170                 175


Glu Ile Tyr Ser Ile Arg Val Leu Asp Ala Ser Gly Ser Gly Ser Tyr
            180                 185                 190


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


Ile Leu Asp Lys Asp Gly Asp Gly Ile Ile Val Gly Asp Pro Asp Asp
    210                 215                 220


Asp Ala Ala Glu Val Ile Ser Met Ser Leu Gly Gly Pro Thr Asp Asp
225                 230                 235                 240


Gln Tyr Leu His Asp Met Ile Ile Thr Ala Tyr Asn Tyr Gly Val Val
                245                 250                 255


Ile Val Ala Ala Ser Gly Asn Glu Gly Ala Ser Ser Pro Ser Tyr Pro
            260                 265                 270


Ala Ala Tyr Pro Glu Val Ile Ala Val Gly Ala Ser Asp Val Asn Asp
        275                 280                 285


Gln Ile Ala Ser Trp Ser Asn Arg Gln Pro Glu Val Ser Ala Pro Gly
    290                 295                 300


Val Asp Ile Leu Ser Thr Tyr Pro Asp Asp Thr Tyr Glu Thr Leu Ser
305                 310                 315                 320


Gly Thr Ser Met Ala Thr Pro His Val Ser Gly Val Val Ala Leu Ile
                325                 330                 335


Gln Ala Ala Tyr Tyr Asn Lys Tyr Gly Lys Val Leu Pro Val Gly Thr
            340                 345                 350
```

```
Phe Asp Asp Met Gly Thr Asn Thr Val Arg Gly Ile Leu His Val Thr
        355                 360                 365


Ala Asp Asp Leu Gly Asp Ala Gly Trp Asp Ile Tyr Tyr Gly Tyr Gly
    370                 375                 380


Ile Val Arg Ala Asp Leu Ala Val Gln Ala Ala Ile Gly
385                 390                 395


<210>  32
<211>  549
<212>  PRT
<213>  Polyporus arcularius

<400>  32

Lys Pro Met Ala Arg Ser Met Lys Leu His Glu Ser Arg Glu Gly Ile
1               5                   10                  15


Pro Glu Gly Phe Ser Leu Arg Gly Ala Ala Gln Pro Glu Gln Thr Ile
            20                  25                  30


Lys Leu Arg Leu Ala Leu Val Gln Ser Asn Phe Ala Glu Leu Glu Arg
        35                  40                  45


Lys Leu Met Asp Val Ser Thr Pro Ser Ser Ala Asn Tyr Gly Lys His
    50                  55                  60


Leu Ser Lys Ala Glu Val Gln Gln Leu Val Ala Pro Thr Gln Asp Ser
65                  70                  75                  80


Val Asp Ala Val Lys Ser Trp Leu Lys Glu Asn Asp Ile Ser Ala Lys
                85                  90                  95


Thr Ile Ser Ala Thr Gly Asp Trp Leu Ser Phe Glu Val Pro Val Ser
            100                 105                 110


Lys Ala Asn Glu Leu Phe Asp Ala Asp Phe Ser Ile Tyr Thr His Asp
        115                 120                 125


Glu Thr Gly Thr Glu Ala Val Arg Thr Leu Ser Tyr Ser Ile Pro Ala
```

```
    130                 135                 140


Glu Leu Gln Gly His Leu Asp Leu Val His Pro Thr Val Thr Phe Pro
145                 150                 155                 160


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


Ala Gln Asn Leu Thr Ser Arg Ala Thr Ile Pro Ser Ser Cys Ala Arg
            180                 185                 190


Thr Ile Thr Pro Ala Cys Leu Gln Ala Ile Tyr Asn Ile Pro Ser Thr
        195                 200                 205


Pro Ala Thr Glu Ser Ser Asn Lys Leu Ala Val Thr Gly Phe Ile Glu
    210                 215                 220


Gln Phe Ala Asn Lys Ala Asp Leu Lys Thr Phe Leu Thr Arg Phe Arg
225                 230                 235                 240


Thr Asp Ile Ser Ser Ser Thr Ser Phe Thr Leu Gln Thr Leu Asp Gly
                245                 250                 255


Gly Ser Asn Pro Gln Ser Ser Ser Glu Ala Gly Val Glu Ala Asn Leu
            260                 265                 270


Asp Ile Gln Tyr Thr Val Gly Val Ala Thr Gly Val Pro Thr Val Phe
        275                 280                 285


Ile Ser Val Gly Glu Asp Phe Gln Asp Gly Asp Leu Glu Gly Phe Leu
    290                 295                 300


Asp Val Val Asn Ser Leu Leu Asp Glu Asp Thr Pro Pro Phe Val Met
305                 310                 315                 320


Thr Thr Ser Tyr Gly Gln Asn Glu Asn Thr Ile Ser Arg Asn Leu Ala
                325                 330                 335


Asn Asn Leu Cys Asn Ala Tyr Ala Gln Leu Gly Ala Arg Gly Val Ser
```

```
            340                 345                 350

Ile Leu Phe Ala Ser Gly Asp Gly Gly Val Ala Gly Ser Gln Ser Ala
        355                 360                 365

Ser Cys Ser Lys Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Phe Met
    370                 375                 380

Thr Ser Val Gly Ala Thr Gln Gly Phe Ser Pro Glu Thr Ala Ala Asp
385                 390                 395                 400

Phe Ser Ser Gly Gly Phe Ser Asn Tyr Phe Ala Ile Pro Asp Tyr Gln
                405                 410                 415

Thr Ser Ala Val Ser Gly Tyr Ile Lys Ala Leu Gly Asn Thr Asn Ser
            420                 425                 430

Gly Lys Tyr Asn Ala Thr Gly Arg Gly Phe Pro Asp Ile Ala Thr Gln
        435                 440                 445

Gly Val Asn Phe Glu Val Val Val Gly Gly Gln Ser Gly Thr Val Glu
    450                 455                 460

Gly Thr Ser Cys Ser Ser Pro Thr Leu Ala Ser Ile Ile Ser Leu Leu
465                 470                 475                 480

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

Pro Phe Leu Tyr Ser Thr Gly Thr Ser Ala Leu Asn Asp Ile Thr Ser
            500                 505                 510

Gly Ser Asn Pro Gly Cys Asn Thr Asn Gly Phe Pro Ala Lys Ala Gly
        515                 520                 525

Trp Asp Pro Val Thr Gly Leu Gly Thr Pro Asp Phe Asn Lys Leu Leu
    530                 535                 540

Ser Ala Val Gly Leu
```

```
545


<210>  33
<211>  548
<212>  PRT
<213>  Ganoderma lucidum

<400>  33

Lys Ser Thr Thr Arg Asn Leu Lys Leu His Glu Thr Arg Gln Gly Ala
1               5                   10                  15


Pro Ser Gly Phe Ser His Thr Gly Ser Ala Asp Pro Asn Gln Thr Leu
            20                  25                  30


Lys Leu Arg Leu Ala Leu Val Gln Gly Asn Thr Ala Glu Leu Glu Arg
        35                  40                  45


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


Leu Ser Lys Glu Glu Val Arg Gln Leu Val Ala Pro Ala Gln Gly Ser
65                  70                  75                  80


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


Ser Thr Ser Ala Ala Gly Asp Trp Leu Ser Phe Glu Val Pro Val Ser
            100                 105                 110


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


Asp Thr Gly Val Lys Ala Val Arg Thr Leu Ser Tyr Ser Ile Pro Ala
    130                 135                 140


Glu Leu Gln Gly His Leu Asp Leu Val His Pro Thr Val Thr Phe Pro
145                 150                 155                 160


Asn Pro Asn Gly His Met Pro Val Phe Gln Ala Pro Val Lys Asp Thr
                165                 170                 175
```

```
Asp Ala Val Gln Asn Phe Ser Ala Arg Ala Val Pro Ser Ser Cys Ser
            180                 185                 190


Asn Thr Ile Thr Pro Ala Cys Leu Gln Ala Leu Tyr Asn Ile Pro Ser
        195                 200                 205


Asp Ala Ala Thr Gln Ser Ser Asn Lys Leu Ala Val Thr Gly Phe Ile
    210                 215                 220


Glu Gln Tyr Ala Asn Gln Val Asp Leu Ala Val Phe Leu Lys Gln Tyr
225                 230                 235                 240


Arg Ala Asp Ile Ser Ser Asn Thr Thr Phe Ala Leu Gln Thr Leu Asp
                245                 250                 255


Gly Gly Ser Asn Ser Gln Thr Asn Val Pro Gly Val Glu Ala Asn Leu
            260                 265                 270


Asp Ile Gln Tyr Thr Val Gly Ile Ala Thr Gly Val Pro Thr Val Phe
        275                 280                 285


Ile Ser Val Gly Asp Gln Tyr Gln Asp Gly Asp Leu Glu Gly Phe Leu
    290                 295                 300


Asp Val Ile Asn Phe Leu Leu Asp Glu Asp Thr Pro Pro Tyr Val Val
305                 310                 315                 320


Thr Thr Ser Tyr Gly Gln Asp Glu His Thr Ile Ser Arg Lys Leu Ala
                325                 330                 335


Gln Asn Leu Cys Asn Ala Tyr Ala Gln Leu Gly Ala Arg Gly Val Ser
            340                 345                 350


Ile Leu Phe Ala Ser Gly Asp Gly Gly Val Ala Gly Ser Arg Ser Asn
        355                 360                 365


Ser Cys Ser Lys Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Tyr Met
    370                 375                 380
```

```
Thr Ser Val Gly Ala Thr Gln Gly Val Pro Glu Thr Ala Ala Asp Phe
385                 390                 395                 400


Ser Ser Gly Gly Phe Ser Asn Tyr Phe Gly Thr Pro Asp Tyr Gln Ala
                405                 410                 415


Ser Ala Val Lys Ser Tyr Leu Ser Thr Leu Gly Ser Thr Asn Arg Gly
            420                 425                 430


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


Val Asn Phe Glu Val Ile Val Asp Gly Glu Val Glu Gly Val Ser Gly
    450                 455                 460


Thr Ser Ala Ala Ser Pro Met Phe Ala Ala Ile Val Ala Leu Leu Asn
465                 470                 475                 480


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


Phe Leu Tyr Ser Lys Gly Val Glu Ala Leu Asn Asp Ile Thr Thr Gly
            500                 505                 510


Ser Asn Pro Gly Cys Gly Thr Ile Gly Phe Pro Ala Lys Glu Gly Trp
        515                 520                 525


Asp Pro Val Thr Gly Leu Gly Thr Pro Asp Phe Gln Lys Leu Ala Ser
    530                 535                 540


Ala Ala Gly Leu
545


<210>  34
<211>  548
<212>  PRT
<213>  Ganoderma lucidum

<400>  34
```

```
Lys Thr Ala Thr Arg Asn Leu Lys Leu His Glu Thr Ser Gln Gly Ala
1               5                   10                  15


Pro Ser Gly Phe Ser Leu Thr Gly Ser Ala Asp Pro Asp Gln Thr Leu
            20                  25                  30


Lys Leu Arg Leu Ala Leu Val Gln Gly Asn Val Ala Glu Leu Glu Arg
        35                  40                  45


Arg Leu Tyr Asp Val Ser Thr Pro Ser Ser Pro Asn Tyr Gly Lys His
    50                  55                  60


Leu Ser Lys Ser Glu Val Gln Gln Leu Val Ala Pro Ala Gln Asp Ser
65                  70                  75                  80


Ile Asp Ala Ile Asn Ala Trp Leu Lys Glu Asn Gly Ile Ser Ala Lys
                85                  90                  95


Thr Thr Ser Ala Thr Gly Asp Trp Leu Ser Phe Glu Val Pro Val Ser
            100                 105                 110


Lys Ala Asn Glu Leu Phe Asp Ala Asp Phe Ser Val Tyr Lys His His
        115                 120                 125


Asp Thr Gly Met Glu Val Val Arg Thr Leu Ser Tyr Ser Ile Pro Ala
    130                 135                 140


Glu Leu Gln Ala His Leu Asp Leu Val His Pro Thr Val Thr Phe Pro
145                 150                 155                 160


Asn Pro Lys Gly His Pro Pro Val Phe Gln Ala Pro Ala Met Ile Thr
                165                 170                 175


Asn Asp Val Gln Asn Phe Ser Ala Gly Ala Val Pro Ser Ser Cys Ser
            180                 185                 190


Ser Arg Ile Thr Pro Ala Cys Leu Gln Ala Leu Tyr Asn Ile Pro Ser
        195                 200                 205
```

```
Asp Pro Ala Thr Gln Pro Ser Asn Lys Leu Ala Val Thr Gly Tyr Ile
    210                 215                 220


Glu Gln Tyr Ala Asn Gln Asp Asp Leu Ala Val Phe Leu Lys Glu Tyr
225                 230                 235                 240


Arg Ala Asp Met Ser Ser Asn Thr Thr Phe Thr Leu Gln Thr Leu Asp
                245                 250                 255


Gly Gly Val Asn Ser Gln Thr Asp Glu Ala Gly Ile Glu Ala Asn Leu
            260                 265                 270


Asp Val Gln Tyr Thr Val Gly Ile Ala Thr Gly Val Pro Thr Val Phe
        275                 280                 285


Ile Ser Val Gly Asp Gln Tyr Gln Asp Gly Asn Leu Glu Gly Phe Leu
    290                 295                 300


Asp Val Val Asn Phe Leu Leu Asp Glu Asp Thr Pro Pro Tyr Val Met
305                 310                 315                 320


Thr Thr Ser Tyr Gly Gln Asp Glu His Thr Met Ser Arg Lys Leu Ala
                325                 330                 335


Gln Asn Leu Cys Asn Ala Tyr Ala Gln Leu Gly Ala Arg Gly Val Ser
            340                 345                 350


Ile Leu Phe Ala Ser Gly Asp Gly Gly Val Ala Gly Ser Arg Ser Ser
        355                 360                 365


Ser Cys Ser Lys Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Tyr Met
    370                 375                 380


Thr Ser Val Gly Ala Thr Gln Gly Val Pro Glu Thr Ala Ala Asp Phe
385                 390                 395                 400


Ser Ser Gly Gly Phe Ser Asn Tyr Phe Gly Ile Pro Asp Tyr Gln Ala
                405                 410                 415
```

```
Ser Ala Val Ser Gly Tyr Leu Ser Ala Leu Gly His Thr Asn Lys Gly
            420                 425                 430


Lys Tyr Asn Ala Ser Gly Arg Gly Phe Pro Asp Val Ser Thr Gln Gly
        435                 440                 445


Val Asn Phe Glu Val Met Val Asp Gly Ala Leu Glu Gly Val Ser Gly
    450                 455                 460


Thr Ser Ala Ala Ser Pro Thr Phe Ala Ala Val Val Ala Leu Leu Asn
465                 470                 475                 480


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


Phe Leu Tyr Ser Lys Gly Val Ser Ala Leu Asn Asp Ile Thr Ser Gly
            500                 505                 510


Ser Asn Pro Gly Cys Arg Thr Asn Gly Phe Pro Ala Lys Glu Gly Trp
        515                 520                 525


Asp Pro Val Thr Gly Leu Gly Thr Pro Asp Phe Gln Lys Leu Ala Ser
    530                 535                 540


Ala Ala Gly Leu
545


<210>  35
<211>  541
<212>  PRT
<213>  Ganoderma lucidum

<400>  35

Lys Pro Thr Ala Arg Asn Leu Arg Leu His Glu Thr Arg Gln Gly Ala
1               5                   10                  15


Pro Ser Gly Phe Ser Leu Thr Gly Ser Ala Asp Pro Asn Gln Thr Val
            20                  25                  30
```

```
Arg Leu Arg Leu Ala Leu Val Gln Gly Asn Thr Gly Glu Leu Glu Arg
        35                  40                  45

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

Leu Ser Lys Ala Glu Val Gln Gln Leu Val Ala Pro Ala Gln Gly Ser
65                  70                  75                  80

Ile Asp Ala Val Asn Ala Trp Leu Lys Glu Asn Asp Ile Thr Ala Lys
                85                  90                  95

Thr Ile Ser Ala Thr Gly Asp Trp Leu Ser Phe Glu Val Pro Val Asn
            100                 105                 110

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

Asp Thr Gly Met Glu Ala Val Arg Thr Leu Ser Tyr Ser Ile Pro Ala
    130                 135                 140

Glu Leu Gln Gly His Leu Asp Leu Val His Pro Thr Val Thr Phe Pro
145                 150                 155                 160

Asn Pro Lys Gly Asn Leu Pro Leu Phe Gln Thr Pro Ile Lys Ser Lys
                165                 170                 175

Arg Asp Val Pro Ala Asp Cys Ser Asn Asn Ile Thr Pro Ala Cys Leu
            180                 185                 190

Gln Ala Leu Tyr Asn Ile Pro Ser Asp Ala Ala Thr Gln Ser Ser Asn
        195                 200                 205

Thr Leu Ala Val Thr Gly Tyr Ile Glu Gln Tyr Ala Asn Gln Gln Asp
    210                 215                 220

Leu Thr Ser Phe Leu Gly Gln Phe Arg Pro Asp Ile Ser Ser Asn Thr
225                 230                 235                 240
```

```
Thr Phe Ala Leu Gln Thr Ile Asp Gly Gly Ser Asn Ser Gln Asn Gly
                245                 250                 255


Ser Asp Ala Gly Gly Glu Ala Asn Leu Asp Ile Gln Tyr Thr Val Gly
            260                 265                 270


Leu Ala Thr Gly Val Pro Thr Val Phe Ile Ser Val Gly Glu Gln Tyr
        275                 280                 285


Gln Asp Gly Asp Leu Gly Gly Leu Leu Asp Val Ile Asn Phe Val Leu
    290                 295                 300


Ala Glu Asp Ala Pro Pro Asn Val Ile Thr Thr Ser Tyr Gly Gln Asn
305                 310                 315                 320


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


Ala Gln Leu Gly Ala Arg Gly Val Ser Ile Leu Phe Ala Ser Gly Asp
            340                 345                 350


Gly Gly Val Ala Gly Ser Gln Ser Asp Asn Cys Thr Gln Phe Val Pro
        355                 360                 365


Thr Phe Pro Ser Gly Cys Pro Tyr Met Thr Ser Val Gly Ala Thr Gln
    370                 375                 380


Gly Val Pro Glu Thr Ala Ala Asp Phe Ser Thr Gly Gly Phe Ser Asn
385                 390                 395                 400


Leu Phe Ser Val Pro Asp Tyr Gln Ala Ala Ala Val Gln Ser Tyr Leu
                405                 410                 415


Ser Ala Leu Gly Gly Thr Tyr Gln Gly Leu Phe Asn Ala Ser Gly Arg
            420                 425                 430


Ala Phe Pro Asp Val Ser Thr Gln Gly Val Asn Phe Glu Thr Val Val
        435                 440                 445
```

```
Asp Gly Ser Val Ser Gly Ala Ser Gly Thr Ser Ala Ala Ser Pro Thr
    450                 455                 460


Phe Ala Ala Ile Val Ala Leu Leu Asn Asp Arg Leu Val Ala Ala Gly
465                 470                 475                 480


Lys Ser Pro Leu Gly Phe Leu Asn Pro Phe Leu Tyr Ser Thr Gly Ala
                485                 490                 495


Ser Ala Leu Asn Asp Ile Ala Thr Gly Ser Asn Pro Gly Cys Gly Thr
            500                 505                 510


Asn Gly Phe Ser Ala Gln Lys Gly Trp Asp Pro Val Thr Gly Leu Gly
        515                 520                 525


Thr Pro Asp Phe Gln Lys Leu Ala Ala Ala Ala Gly Leu
    530                 535                 540


<210>  36
<211>  547
<212>  PRT
<213>  Trametes sp.

<400>  36

Thr Pro Thr Gly Arg Asn Leu Lys Leu His Glu Ala Arg Glu Asp Ile
1               5                   10                  15


Pro Thr Gly Tyr Ser Leu Arg Gly Ala Ala Ser Pro Asp Thr Thr Leu
            20                  25                  30


Lys Leu Arg Leu Ala Leu Val Gln Asn Asn Phe Ala Glu Leu Glu Asp
        35                  40                  45


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


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


Val Lys Ala Val Asn Ala Trp Leu Thr Glu Asn Gly Leu Asp Ala His
```

```
                85                  90                  95


Thr Ile Ser Pro Ala Gly Asp Trp Leu Ala Phe Glu Val Pro Val Ser
            100                 105                 110


Lys Ala Asn Glu Leu Phe Asp Ala Asp Phe Ser Val Phe Thr His Asp
        115                 120                 125


Glu Ser Gly Leu Glu Ala Ile Arg Thr Leu Ala Tyr Ser Ile Pro Ala
    130                 135                 140


Glu Leu Gln Gly His Leu Asp Leu Val His Pro Thr Val Thr Phe Pro
145                 150                 155                 160


Asn Pro Asn Ala His Leu Pro Val Val Arg Ser Thr Lys Pro Ile Gln
                165                 170                 175


Asn Leu Thr Gly Arg Ala Ile Pro Ala Ser Cys Ala Ser Thr Ile Thr
            180                 185                 190


Pro Ala Cys Leu Gln Ala Ile Tyr Gly Ile Pro Thr Thr Lys Ala Thr
        195                 200                 205


Gln Ser Ser Asn Lys Leu Ala Val Ser Gly Phe Ile Asp Gln Phe Ala
    210                 215                 220


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


Ser Ser Ser Thr Thr Phe Ala Leu Gln Thr Leu Asp Gly Gly Gln Asn
                245                 250                 255


Asn Gln Ser Pro Ser Gln Ala Gly Ile Glu Ala Asn Leu Asp Ile Gln
            260                 265                 270


Tyr Thr Val Gly Leu Ala Thr Gly Val Pro Val Thr Phe Ile Ser Val
        275                 280                 285


Gly Asp Asn Phe Gln Asp Gly Asp Leu Glu Gly Phe Leu Asp Ile Ile
```

```
    290                 295                 300

Asn Phe Leu Leu Ser Glu Ser Asn Pro Pro Gln Val Leu Thr Thr Ser
305                 310                 315                 320

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

Cys Asn Ala Tyr Ala Gln Leu Gly Ala Arg Gly Thr Ser Ile Leu Phe
            340                 345                 350

Ala Ser Gly Asp Gly Gly Val Ala Gly Ser Gln Ser Ser Ser Cys Arg
        355                 360                 365

Asn Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Phe Met Thr Ser Val
    370                 375                 380

Gly Ala Thr Gln Gly Val Ser Pro Glu Thr Ala Ala Asp Phe Ser Ser
385                 390                 395                 400

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

Val Ser Gly Tyr Leu Ser Ala Leu Gly Asn Thr Asn Ser Gly Lys Phe
            420                 425                 430

Asn Arg Ser Gly Arg Gly Phe Pro Asp Val Ala Thr Gln Gly Val Asn
        435                 440                 445

Phe Gln Ile Val Ser Gly Gly Asp Thr Gly Gly Val Asp Gly Thr Ser
    450                 455                 460

Cys Ala Ser Pro Thr Phe Ala Ser Val Ile Ser Leu Ile Asn Asp Arg
465                 470                 475                 480

Leu Ile Ala Ala Gly Lys Ser Pro Leu Gly Phe Leu Asn Pro Phe Leu
                485                 490                 495

Tyr Ser Ala Ala Gly Lys Ala Ala Leu Asn Asp Val Thr Ser Gly Ser
```

```
            500                 505                 510


Asn Pro Gly Cys Asn Thr Asn Gly Phe Pro Ala Lys Ala Gly Trp Asp
        515                 520                 525


Pro Val Thr Gly Leu Gly Thr Pro Asn Phe Ala Lys Leu Leu Thr Ala
    530                 535                 540


Val Gly Leu
545


<210>  37
<211>  553
<212>  PRT
<213>  Cinereomyces lindbladii

<400>  37

Lys Pro Thr Ala Arg Asn Leu Leu Val His Glu Ser Leu Asp Gly Val
1               5                   10                  15


Pro Thr Gly Phe Gln Leu Val Gly Pro Ala Ser Pro Asp Thr Val Leu
            20                  25                  30


Ser Met Arg Ile Ala Leu Val Gln Ser Asp Pro Ala Gly Leu Glu Ala
        35                  40                  45


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


Leu Ser Lys Ala Glu Val Glu Lys Phe Val Ser Pro Thr Ser Glu Ser
65                  70                  75                  80


Val Gln Ala Val Asn Ala Trp Leu Thr Glu Asn Asp Leu Thr Ala Thr
                85                  90                  95


Gln Leu Ser Pro Ala Gly Asp Trp Leu Gly Phe Glu Val Pro Val Ser
            100                 105                 110


Lys Ala Glu Asp Leu Phe Gly Thr Gln Phe Ser Val Phe Thr His Glu
        115                 120                 125
```

```
Ala Thr Gly Met Gln Thr Val Arg Thr Leu Ser Tyr Ser Ile Pro Ser
    130                 135                 140


Glu Leu Gln Gly His Leu Asp Leu Val Phe Pro Thr Ile Asn Phe Pro
145                 150                 155                 160


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


Glu Val Thr Thr Leu Asn Ala Asn Leu Thr Ser Asp Ala Val Pro Ser
            180                 185                 190


Ser Cys Ala Asp Thr Ile Thr Pro Ala Cys Leu Gln Ala Leu Tyr Gly
        195                 200                 205


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


Gly Phe Ile Asp Gln Phe Ala Asn Gln Ala Asp Leu Lys Thr Phe Leu
225                 230                 235                 240


Gln Asn Phe Arg Thr Asp Ile Ser Ser Ser Thr Thr Phe Ser Leu Glu
                245                 250                 255


Thr Leu Asp Gly Gly Ser Asn Ser Gln Asn Arg Gly Asp Ala Gly Val
            260                 265                 270


Glu Ala Asn Leu Asp Thr Gln Tyr Thr Val Gly Leu Ala Thr Asp Val
        275                 280                 285


Pro Thr Val Phe Ile Ser Val Gly Glu Asp Asn Gln Asp Gly Ser Leu
    290                 295                 300


Gly Gly Phe Leu Asp Ile Ile Asn Phe Leu Leu Asp Gln Asp Ser Pro
305                 310                 315                 320


Pro Gln Val Leu Thr Thr Ser Tyr Gly Gln Asn Glu Asn Thr Val Ser
                325                 330                 335
```

```
Arg Ala Val Ala Asn Asn Leu Cys Asn Ala Tyr Ala Gln Leu Gly Ala
            340                 345                 350


Arg Gly Thr Ser Ile Leu Phe Ala Ser Gly Asp Gly Gly Val Ser Gly
        355                 360                 365


Ser Gln Ser Ala Ser Cys Arg Thr Phe Val Pro Thr Phe Pro Ser Gly
    370                 375                 380


Cys Pro Phe Met Thr Ser Val Gly Ala Thr Thr Gly Ile Asn Pro Glu
385                 390                 395                 400


Thr Ala Ala Thr Phe Ser Ala Gly Gly Phe Ser Asn Tyr Phe Gly Thr
                405                 410                 415


Pro Ser Tyr Gln Ala Ser Ala Val Ser Ser Tyr Leu Ala Ala Leu Gly
            420                 425                 430


Ser Thr Asn Ser Gly Lys Phe Asn Thr Ser Gly Arg Gly Tyr Pro Asp
        435                 440                 445


Val Ser Thr Gln Gly Glu Asn Phe Glu Ile Val Val Ser Gly Glu Glu
    450                 455                 460


Glu Gly Val Asp Gly Thr Ser Cys Ala Ser Pro Thr Phe Ala Ser Ile
465                 470                 475                 480


Ile Ser Leu Val Asn Asp Arg Leu Ile Ala Ala Gly Lys Pro Pro Leu
                485                 490                 495


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


Asp Ile Thr Thr Gly Asp Asn Pro Gly Cys Asn Thr Asn Gly Phe Pro
        515                 520                 525


Ala Lys Ser Gly Trp Asp Pro Val Thr Gly Leu Gly Thr Pro Asn Phe
    530                 535                 540
```

```
Ser Lys Leu Leu Thr Ala Val Gly Leu
545                 550


<210>  38
<211>  559
<212>  PRT
<213>  Trametes versicolor

<400>  38

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


Ala Gly Phe Ser Leu His Gly Ala Ala Ser Pro Asp Thr Val Leu Asn
            20                  25                  30


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


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


Ser Lys Ala Glu Val Glu Gln Tyr Val Ala Pro Arg Gln Gln Ser Ile
65                  70                  75                  80


Thr Ala Val Lys Ala Trp Leu Ala Ala Asn Gly Leu Ser Gly Thr Ser
                85                  90                  95


Ile Ser Pro Ala Gly Asp Trp Ile Ala Ala Lys Val Pro Val Ser Lys
            100                 105                 110


Ala Asn Lys Leu Leu Gly Ala Gln Phe Ser Val Phe Asn Asn Asp Ala
        115                 120                 125


Thr Gly Arg Gln Ile Ile Arg Thr Leu Ala Tyr Ser Ile Pro Ala Glu
    130                 135                 140


Leu Lys Gly His Leu Asp Leu Val His Pro Thr Ile Thr Phe Ala Asp
145                 150                 155                 160
```

```
Ile Lys Pro Leu Val Pro Val Val Ser Ala Arg Arg Glu Ser Arg Val
                165                 170                 175


Leu Val Asp Ser Asp Leu Val Ala Asn Thr Ile Pro Ala Ser Cys Asn
            180                 185                 190


Ala Ala Ile Thr Pro Ala Cys Leu Gln Asp Leu Tyr Gly Ile Pro Ser
        195                 200                 205


Thr Pro Ala Thr Gln Ser Ser Asn Gln Leu Gly Val Ser Gly Phe Ile
    210                 215                 220


Asp Gln Phe Ala Asn Gln Ala Asp Leu Ala Thr Phe Leu Thr Glu Phe
225                 230                 235                 240


Arg Pro Asp Val Ser Asn Ser Thr Thr Phe Thr Leu Gln Thr Leu Asp
                245                 250                 255


Gly Gly Gln Asn Pro Gln Asp Pro Ser Asp Ala Gly Val Glu Ala Asn
            260                 265                 270


Leu Asp Thr Gln Tyr Thr Val Gly Val Ala Thr Asn Val Pro Thr Thr
        275                 280                 285


Phe Phe Ser Val Gly Asp Asp Thr Lys Asp Gly Ile Phe Gly Phe Leu
    290                 295                 300


Asp Leu Ile Ser Phe Leu Leu Ala Ala Ala Ala Pro Pro Gln Val Leu
305                 310                 315                 320


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


Arg Asn Leu Cys Gln Ala Tyr Ala Gln Leu Gly Ala Arg Gly Thr Ser
            340                 345                 350


Ile Leu Phe Ser Ser Gly Asp Gly Gly Val Ser Gly Ser Gln Ala Glu
        355                 360                 365
```

```
Gly Cys Val Asp Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Phe Leu
    370                 375                 380


Thr Ser Val Gly Ala Thr Gln Leu Thr Thr Ala Ser Gly Leu Thr Val
385                 390                 395                 400


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


Thr Pro Pro Tyr Gln Gln Ala Val Val Asp Ala Tyr Ile Lys Lys Thr
            420                 425                 430


Leu Val Asn Gly Thr Val Asn Glu Gly Leu Phe Asn Ala Ser Gly Arg
        435                 440                 445


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


Gly Gly Gly Thr Asp Ile Val Ser Gly Thr Ser Ala Ser Ser Pro Leu
465                 470                 475                 480


Phe Ala Ser Val Ile Ala Leu Ile Asn Asp Arg Arg Leu Ala Ala Gly
                485                 490                 495


Lys Pro Pro Leu Gly Phe Leu Asn Pro Phe Leu Tyr Ser Gln Ala Gly
            500                 505                 510


Ala Ser Ala Leu Asn Asp Val Thr Val Gly Ser Asn Pro Gly Cys Ala
        515                 520                 525


Ser Pro Gly Phe Pro Ala Ala Gln Gly Trp Asp Pro Val Thr Gly Leu
    530                 535                 540


Gly Thr Pro Asn Phe Ala Lys Leu Leu Ala Ala Ala Leu Ala Leu
545                 550                 555


<210>  39
<211>  541
<212>  PRT
```

```
<213>  Paecilomyces hepialid

<400>  39

Ala Pro Ala Pro His Gly Pro Leu Val Lys Phe Gly Glu Ile Arg Lys
1               5                   10                  15


Leu Pro Ser Lys Trp Val Ala Thr Gly Ala Ala Asp Ala Asn Ala Val
            20                  25                  30


Ile Lys Gly Gln Ile Gly Ile Lys Gln Asn Asn Ile Gln Gly Leu Gln
        35                  40                  45


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


Trp Leu Ser Lys Glu Glu Val Asp Lys Tyr Ser Ala Pro Ala Ala Ala
65                  70                  75                  80


Asp Val Ala Ala Val Lys Ala Trp Leu Ala Ser Ser Gly Ile Thr Asp
                85                  90                  95


Val Thr Met Pro Thr Asn Asp Trp Ile Glu Phe Ser Val Pro Val Ser
            100                 105                 110


Lys Met Glu Ser Leu Leu Gly Ser Lys Tyr Glu Trp Phe Val His Leu
        115                 120                 125


Glu Thr Gly Glu Lys Val Pro Arg Thr Lys Glu Phe Ser Val Pro Gln
    130                 135                 140


Asn Leu His Asp Leu Ile Asp Val Val Thr Pro Thr Thr Val Leu Tyr
145                 150                 155                 160


His Asn Ile Asn Pro His Thr His Ser Ser Pro Gln Ala Ala Gly Ala
                165                 170                 175


Ala Gly Leu Thr Ser Pro Ala Ser Ile Lys Ser Ala Tyr Asn Val Asp
            180                 185                 190
```

```
Tyr Lys Gly Thr Gly Asn Thr Leu Val Gly Thr Thr Gly Phe Leu Gly
        195                 200                 205

Val Gly Ala Ser His Thr Asp Tyr Ala Asn Phe Gly Gln Gln Phe Ser
    210                 215                 220

Pro Gly Leu Lys Asp Phe Gln Asp Val Ser Val Asn Gly Gly Ser Asn
225                 230                 235                 240

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

Gly Ala Leu Ala Ala Pro Asn Pro Ser Glu Tyr Leu Ala His Ala Pro
            260                 265                 270

Glu Gly Ser Asp Asn Asn Ser Phe Asn Asp Ala Met Leu Ala Phe Gly
        275                 280                 285

Asn Tyr Leu Asn Ser Ala Arg Asn Pro Pro Ser Ala Val Ser Thr Ser
    290                 295                 300

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

Cys Asn Glu Phe Met Lys Ala Gly Ser Arg Gly Val Ser Ile Phe Phe
                325                 330                 335

Ser Ser Gly Asp Asn Gly Val Gly Gly Asn Gly Glu Ser Ser Cys Gln
            340                 345                 350

Asn Gly Tyr Tyr Pro Leu Trp Pro Ala Thr Cys Pro Tyr Val Thr Thr
        355                 360                 365

Val Gly Gly Thr Glu Phe Asp Asn Ser Gly Arg Glu Val Val Ala Asn
    370                 375                 380

Phe Glu Gln Tyr Asn Lys Asn Ile Lys Ser Pro Gly Gly Gly Tyr Ser
385                 390                 395                 400
```

```
Asn His Phe Ala Ala Pro Ser Tyr Asn Lys Ala Val Thr Thr Ser Tyr
                405                 410                 415


Ala Asn Gly Leu Ala Ala Pro Gln Lys Gln Arg Leu Asn Pro Asn Gly
            420                 425                 430


Arg Gly Tyr Pro Asp Ile Ser Leu Val Ser Val Lys Tyr Gln Val Asn
        435                 440                 445


Val Asn Asn Gln Ile Ser Gln Val Leu Gly Thr Ser Ala Ser Ser Pro
    450                 455                 460


Ser Ile Ala Gly Leu Val Gly Leu Leu Asn Asp Tyr Arg Lys Thr Gln
465                 470                 475                 480


Gly Lys Pro Asn Leu Gly Phe Ile Asn Pro Leu Leu Tyr Ser Asp Lys
                485                 490                 495


Val Lys Pro Ala Leu Arg Asp Val Thr Ser Gly Ser Asn Lys Gly Cys
            500                 505                 510


Asp Ser Val Gly Leu Pro Ala Lys Thr Gly Trp Asp Ala Ala Ser Gly
        515                 520                 525


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


<210>  40
<211>  541
<212>  PRT
<213>  Isaria tenuipes

<400>  40

Ala Pro Ala Pro His Gly Pro Leu Val Lys Phe Gly Glu Leu Lys Lys
1               5                   10                  15


Leu Pro Ser Gln Trp Val Ala Thr Gly Ala Ala Asn Gly Asp Ala Val
            20                  25                  30


Ile Lys Ala Gln Ile Gly Ile Lys Gln Asn Asn Ile Lys Gly Leu Gln
```

```
        35                  40                  45


Asp Lys Leu Ala Glu Ile Ser Asp Pro Asn Ser Pro Ser Tyr Gly Gln
    50                  55                  60


Trp Leu Ser Lys Glu Glu Val Ala Lys Tyr Thr Ala Pro Ala Asp Ala
65                  70                  75                  80


Asp Val Ala Ala Val Lys Ala Trp Leu Ser Ser Ala Gly Ile Thr Glu
                85                  90                  95


Val Thr Met Pro Thr Asn Asp Trp Leu Glu Phe Ser Val Pro Val Ser
            100                 105                 110


Lys Met Glu Ser Leu Leu Gly Ser Lys Tyr Glu Trp Phe Val His Leu
        115                 120                 125


Glu Thr Gly Glu Lys Ala Pro Arg Thr Lys Glu Phe Ser Val Pro Gln
    130                 135                 140


Asn Leu His Gly Ile Ile Asp Val Val Thr Pro Thr Thr Val Leu Tyr
145                 150                 155                 160


His Asn Ile Asn Pro Asn Ser His Gly Asn Glu Leu Ser Ala Ser Ala
                165                 170                 175


Ser Gly Leu Thr Ser Pro Ala Ser Ile Lys Ser Ala Tyr Asn Val Asp
            180                 185                 190


Tyr Lys Gly Thr Gly Asn Thr Leu Val Ala Thr Thr Gly Phe Leu Gly
        195                 200                 205


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


Pro Gly Leu Lys Asp Phe Gln Asp Val Ser Val Asn Gly Gly Ser Asn
225                 230                 235                 240


Ser Gly Asp Gly Ser Ala Leu Glu Gly Asn Leu Asp Thr Gln Tyr Cys
```

```
                245                 250                 255


Gly Ala Leu Ala Ser Pro Asn Pro Ser Gln Tyr Leu Ala Asn Ser Pro
            260                 265                 270


Glu Gly Ser Asp Asn Asn Ser Phe Asn Asp Ala Met Thr Ala Phe Gly
        275                 280                 285


Asn Tyr Leu Asn Ser Ala Ser Asn Pro Pro Ser Ala Val Ser Thr Ser
    290                 295                 300


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


Cys Asn Glu Phe Met Lys Ala Gly Ser Arg Gly Ile Ser Val Phe Phe
                325                 330                 335


Ser Ser Gly Asp Asn Gly Val Gly Gly Asn Gly Glu Pro Ser Cys Gln
            340                 345                 350


Asn Gly Tyr Tyr Pro Leu Trp Pro Ala Thr Cys Pro Tyr Val Thr Thr
        355                 360                 365


Val Gly Gly Thr Glu Phe Asp Asp Ser Gly Arg Glu Val Val Ala Asn
    370                 375                 380


Phe Glu Gln Tyr Asn Lys Asn Val Lys Ser Pro Gly Gly Gly Tyr Ser
385                 390                 395                 400


Asn His Phe Pro Ala Pro Asp Tyr Asn Lys Asn Val Thr Thr Ala Tyr
                405                 410                 415


Ala Asn Ser Leu Ser Ala Ala Gln Gln Gln Arg Leu Asn Pro Asn Gly
            420                 425                 430


Arg Gly Phe Pro Asp Ile Ser Leu Val Ser Val Lys Tyr Gln Val Ser
        435                 440                 445


Leu Asn Gly Gln Thr Lys Gln Val Leu Gly Thr Ser Ala Ser Ser Pro
```

```
    450                 455                 460


Ser Val Ala Gly Leu Val Gly Leu Leu Asn Asp Tyr Arg Lys Thr Gln
465                 470                 475                 480


Gly Lys Ser Asn Leu Gly Phe Leu Asn Pro Leu Leu Tyr Ser Gly Lys
                485                 490                 495


Val Asn Ala Ala Leu Arg Asp Val Thr Ser Gly Ser Asn Lys Gly Cys
            500                 505                 510


Asp Ser Val Gly Leu Pro Ala Lys Ser Gly Trp Asp Ala Ala Ser Gly
        515                 520                 525


Leu Gly Ser Phe Asp Phe Ala Lys Leu Arg Ser Leu Ile
    530                 535                 540


<210>  41
<211>  578
<212>  PRT
<213>  Aspergillus tamarii

<400>  41

Glu Ala Phe Glu Lys Leu Ser Ala Val Pro Lys Gly Trp His Tyr Ser
1               5                   10                  15


Ser Thr Pro Glu Gly Ser Thr Ser Val Cys Leu Lys Ile Ala Leu Ala
            20                  25                  30


Gln Lys Asp Ala Ala Gly Phe Glu Lys Arg Val Tyr Glu Met Ser Asp
        35                  40                  45


Pro Asp His Pro Asn Tyr Gly Gln His Phe Thr Thr His Glu Glu Met
    50                  55                  60


Lys Arg Met Leu Leu Pro Arg Asp Asp Thr Val Asp Ala Val Arg Gln
65                  70                  75                  80


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

```
Ile Asn Phe Cys Thr Thr Val Asp Thr Ala Asn Lys Leu Leu Asn Ala
            100                 105                 110


Gln Phe Lys Trp Tyr Val Ser Asp Val Lys His Ile Arg Arg Leu Arg
        115                 120                 125


Thr Leu Gln Tyr Asp Val Pro Gly Ser Val Ala Ser His Val Asn Thr
    130                 135                 140


Ile Gln Pro Thr Thr Arg Phe Gly Lys Ile Thr Pro Lys Lys Ala Val
145                 150                 155                 160


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


Val Val Ala Lys Asn Ile Ser His Cys Asp Ser Ile Ile Thr Pro Thr
            180                 185                 190


Cys Leu Lys Glu Leu Tyr Asn Ile Gly Asp Tyr Gln Ala Asp Ala Asn
        195                 200                 205


Ser Gly Ser Lys Ile Ala Phe Ala Ser Tyr Leu Glu Glu Tyr Ala Arg
    210                 215                 220


Tyr Ala Asp Leu Glu Asn Phe Glu Asn Tyr Leu Ala Pro Trp Ala Lys
225                 230                 235                 240


Gly Gln Asn Phe Ser Val Ile Thr Tyr Asn Gly Gly Leu Asn Asp Gln
                245                 250                 255


Asn Ser Ser Ser Asp Ser Gly Glu Ala Asn Leu Asp Leu Gln Tyr Ile
            260                 265                 270


Leu Gly Val Ser Ala Pro Leu Pro Val Thr Glu Phe Ser Thr Gly Gly
        275                 280                 285


Arg Gly Pro Leu Val Pro Asp Leu Thr Gln Pro Asp Pro Asn Ala Asn
    290                 295                 300
```

```
Ser Asn Glu Pro Tyr Leu Glu Phe Phe Gln Asn Val Leu Lys Leu Asp
305                 310                 315                 320


Gln Glu Gln Leu Pro Gln Val Ile Ser Thr Ser Tyr Gly Glu Asn Glu
                325                 330                 335


Gln Glu Ile Pro Glu Lys Tyr Ala Arg Thr Val Cys Asn Leu Ile Ala
            340                 345                 350


Gln Leu Gly Ser Arg Gly Val Ser Val Leu Phe Ser Ser Gly Asp Ser
        355                 360                 365


Gly Val Gly Glu Gly Cys Met Thr Asn Asp Gly Thr Asn Arg Thr His
    370                 375                 380


Phe Pro Pro Gln Phe Pro Ala Ala Cys Pro Trp Val Thr Ser Val Gly
385                 390                 395                 400


Ala Thr Tyr Lys Thr Thr Pro Glu Arg Ala Thr Tyr Phe Ser Ser Gly
                405                 410                 415


Gly Phe Ser Asp Tyr Trp Ala Arg Pro Glu Trp Gln Glu Glu Ala Val
            420                 425                 430


Ser Ser Tyr Leu Glu Thr Ile Gly Asp Ala Phe Lys Gly Leu Tyr Asn
        435                 440                 445


Ala Ser Gly Arg Ala Phe Pro Asp Val Ala Ala Gln Gly Met Asn Phe
    450                 455                 460


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


Ser Ala Pro Ala Phe Ser Ala Ile Ile Ala Leu Leu Asn Asp Ala Arg
                485                 490                 495


Leu Arg Ala Gly Lys Pro Thr Leu Gly Phe Leu Asn Pro Trp Leu Tyr
            500                 505                 510
```

```
Lys Thr Gly Arg Gln Gly Leu Gln Asp Ile Thr Leu Gly Ala Ser Thr
        515                 520                 525


Gly Cys Thr Gly Arg Ala Arg Phe Gly Gly Ala Pro Asp Gly Gly Pro
    530                 535                 540


Val Val Pro Phe Ala Ser Trp Asn Ala Thr Gln Gly Trp Asp Pro Val
545                 550                 555                 560


Thr Gly Leu Gly Thr Pro Asp Phe Ala Glu Leu Lys Lys Leu Ala Leu
                565                 570                 575


Ala Asn



<210>  42
<211>  587
<212>  PRT
<213>  Aspergillus brasiliensis

<400>  42

Glu Ile Phe Glu Lys Leu Ser Gly Val Pro Asn Gly Trp Arg Tyr Ala
1               5                   10                  15


Asn Asn Pro Gln Gly Asn Glu Val Ile Arg Leu Gln Ile Ala Leu Gln
            20                  25                  30


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


Pro Gly His Ala Asp Tyr Gly Lys His Phe Arg Thr His Glu Glu Met
    50                  55                  60


Lys Arg Met Leu Leu Pro Ser Asp Thr Ala Val Asp Ser Val Arg Asp
65                  70                  75                  80


Trp Leu Glu Ser Ala Gly Val His Asn Ile Gln Val Asp Ala Asp Trp
                85                  90                  95
```

```
Ile Lys Phe His Thr Thr Val Thr Lys Ala Asn Ala Leu Leu Asp Ala
            100                 105                 110


Asp Phe Lys Trp Tyr Val Ser Glu Ala Arg His Ile Arg Arg Leu Arg
        115                 120                 125


Thr Leu Gln Tyr Ser Ile Pro Asp Ala Leu Val Ser His Ile Asn Met
    130                 135                 140


Ile Gln Pro Thr Thr Arg Phe Gly Gln Ile Gln Pro Asn Arg Ala Thr
145                 150                 155                 160


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


Thr Leu Ala Gln Asn Thr Ser His Cys Asp Ser Ile Ile Thr Pro Ser
            180                 185                 190


Cys Leu Lys Gln Leu Tyr Asn Ile Gly Asp Tyr Gln Ala Asp Pro Lys
        195                 200                 205


Ser Gly Ser Lys Ile Gly Phe Ala Ser Tyr Leu Glu Glu Tyr Ala Arg
    210                 215                 220


Tyr Ala Asp Leu Glu Lys Phe Glu Gln His Leu Ala Pro Asn Ala Ile
225                 230                 235                 240


Gly Gln Asn Phe Thr Val Val Gln Phe Asn Gly Gly Leu Asn Asp Gln
                245                 250                 255


Leu Ser Thr Lys Asp Ser Gly Glu Ala Asn Leu Asp Leu Gln Tyr Ile
            260                 265                 270


Leu Gly Val Ser Ala Pro Leu Pro Val Thr Glu Tyr Ser Thr Gly Gly
        275                 280                 285


Arg Gly Glu Leu Val Pro Asp Leu Ser Ser Pro Asp Pro Asn Asp Asn
    290                 295                 300
```

```
Ser Asn Glu Pro Tyr Leu Asp Phe Leu Gln Asn Ile Leu Lys Leu Asn
305                 310                 315                 320


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


Gln Thr Ile Pro Val Pro Tyr Ala Arg Ala Val Cys Asn Leu Tyr Ala
            340                 345                 350


Gln Leu Gly Ser Arg Gly Val Ser Val Ile Phe Ser Ser Gly Asp Ser
        355                 360                 365


Gly Val Gly Ala Ala Cys Leu Thr Asn Asp Gly Thr Asn Arg Thr His
    370                 375                 380


Phe Pro Pro Gln Phe Pro Ala Ser Cys Pro Trp Val Thr Ser Val Gly
385                 390                 395                 400


Ala Thr Ser Lys Thr Ser Pro Glu Gln Ala Val Ser Phe Ser Ser Gly
                405                 410                 415


Gly Phe Ser Asp Leu Trp Pro Arg Pro Ser Tyr Gln His Ala Ala Val
            420                 425                 430


Gln Thr Tyr Leu Thr Glu His Leu Gly Asn Lys Phe Ser Gly Leu Phe
        435                 440                 445


Asn Ala Ser Gly Arg Ala Phe Pro Asp Val Ser Ala Gln Gly Val Asn
    450                 455                 460


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


Cys Ser Ala Pro Thr Phe Ser Gly Val Ile Ala Leu Leu Asn Asp Ala
                485                 490                 495


Arg Leu Arg Ala Gly Leu Pro Val Met Gly Phe Leu Asn Pro Phe Leu
            500                 505                 510
```

```
Tyr Gly Ala Gly Ser Lys Leu Gly Gly Leu Asn Asp Ile Val Thr Gly
        515                 520                 525


Gly Ser Val Gly Cys Asp Gly Arg Asn Arg Phe Gly Gly Thr Pro Asn
    530                 535                 540


Gly Ser Pro Val Val Pro Phe Ala Ser Trp Asn Ala Thr Thr Gly Trp
545                 550                 555                 560


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


Val Ala Leu Gly Glu Ser Glu Gly Asp Glu Asn
            580                 585


<210>  43
<211>  582
<212>  PRT
<213>  Aspergillus iizukae

<400>  43

Glu Val Phe Asp Thr Leu Ala Ala Val Pro Lys Gly Trp His Tyr Ser
1               5                   10                  15


His Thr Pro Arg Ala Asp Gln Pro Ile Ser Leu Lys Ile Ala Leu Lys
            20                  25                  30


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


Pro Gly His Glu His Tyr Gly Lys His Phe Arg Glu His Asp Glu Met
    50                  55                  60


Lys Arg Met Leu Leu Pro Ser Asp Ala Thr Val Asp Ala Val Lys Asp
65                  70                  75                  80


Trp Leu Leu Ala Ala Asp Val Thr Asp Tyr Glu Val Asp Ala Asp Trp
                85                  90                  95
```

```
Ile Asn Leu His Thr Thr Val Gln Gln Ala Asn Glu Leu Leu Asp Thr
            100                 105                 110


Glu Phe Ala Trp Tyr Val Ser Asp Val Arg Ala Val Arg Arg Leu Arg
        115                 120                 125


Thr Leu Arg Tyr Ser Val Pro Asp Ala Val Ala Pro His Ile Asn Met
    130                 135                 140


Val Gln Pro Thr Thr Arg Phe Gly Gln Ile His Pro Asp Arg Ala Thr
145                 150                 155                 160


Phe Arg Ala Gly Ser Thr His Phe Gly Ala His Ile Leu Ser Ala Met
                165                 170                 175


Ser Ala Val Gly Asp Val Ser Ser Ala Asn Val Thr Cys Asp Asp Val
            180                 185                 190


Ile Thr Pro Leu Cys Leu Lys Glu Leu Tyr Lys Val Asp Gly Tyr Arg
        195                 200                 205


Ala Glu Ala Glu His Gly Ser Lys Ile Ala Phe Ala Ser Tyr Leu Glu
    210                 215                 220


Glu Tyr Ala Arg Tyr Asp Asp Met Val Arg Phe Gln Glu Lys Leu Ala
225                 230                 235                 240


Pro Tyr Ala Lys Gly Glu Asn Phe Ser Val Ile Leu Tyr Asn Gly Gly
                245                 250                 255


Val Asp Asp Gln Gln Ser Thr Ser Asp Ser Gly Glu Ala Asn Leu Asp
            260                 265                 270


Leu Gln Thr Ile Met Gly Leu Ser Ala Pro Leu Pro Ile Thr Glu Tyr
        275                 280                 285


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

```
Pro Asn Asp Asn Ser Asn Glu Pro Tyr Leu Glu Trp Ile Gln Asn Val
305                 310                 315                 320


Leu Lys His Ser Pro Glu Glu Leu Pro Gln Val Ile Ser Thr Ser Tyr
                325                 330                 335


Gly Glu Asp Glu Gln Thr Ile Pro Arg Gly Tyr Ala Glu Ser Val Cys
            340                 345                 350


Asn Leu Leu Ala Gln Leu Gly Ser Arg Gly Val Ser Val Ile Phe Ser
        355                 360                 365


Ser Gly Asp Ser Gly Val Gly Ser Ala Cys Gln Thr Asn Asp Gly Thr
    370                 375                 380


Asn Thr Thr His Phe Pro Pro Gln Phe Pro Ala Ser Cys Pro Trp Val
385                 390                 395                 400


Thr Ser Val Gly Ala Thr Ser Lys Thr His Pro Glu Glu Ala Val Tyr
                405                 410                 415


Phe Ser Ser Gly Gly Phe Ser Asp Leu Trp Ala Arg Pro Ala Trp Gln
            420                 425                 430


Asp Asp Ala Val Ser Thr Tyr Ile Glu Ser Ile Gly Gly Lys Phe Ala
        435                 440                 445


Gly Leu Tyr Asn Ala Ser Gly Arg Ala Phe Pro Asp Val Ser Ala Gln
    450                 455                 460


Gly Gln Asn Tyr Ala Ile Phe Asp Lys Gly Arg Leu Gly Lys Met Asp
465                 470                 475                 480


Gly Thr Ser Cys Ser Ala Pro Ala Phe Ala Gly Ile Val Ser Leu Leu
                485                 490                 495


Asn Asp Ala Arg Leu Arg Ala Asn Arg Pro Val Leu Gly Phe Leu Asn
            500                 505                 510
```

```
Pro Trp Leu Tyr Gly Thr Ala Arg Glu Gly Leu Asn Asp Ile Val His
        515                 520                 525


Gly Gly Ser Lys Gly Cys Asp Gly Arg Asp Arg Phe Gly Gly Lys Pro
    530                 535                 540


Asn Gly Ser Pro Val Val Pro Tyr Ala Ser Trp Asn Ala Thr Pro Gly
545                 550                 555                 560


Trp Asp Pro Val Ser Gly Leu Gly Thr Pro Asn Phe Ala Thr Leu Val
                565                 570                 575


Gln Val Ala Leu His Asp
            580


<210>  44
<211>  456
<212>  PRT
<213>  Penicillium sp.

<400>  44

Ala Pro Ala Ser Thr Ala Lys Asp Ser Val Ser Ser Val Val Lys Asn
1               5                   10                  15


Gly Val Lys Tyr Thr Val Phe Glu His Ala Ala Thr Gly Ala Lys Met
            20                  25                  30


Glu Phe Val Lys Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn
        35                  40                  45


Gln Tyr Ser Gly Tyr Leu Ser Val Gly Ser Asn Met Asn Met Trp Phe
    50                  55                  60


Trp Phe Phe Glu Ala Arg Asn Asn Pro Gln Gln Ala Pro Leu Ala Ala
65                  70                  75                  80


Trp Phe Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln
                85                  90                  95


Glu Asn Gly Pro Cys His Phe Val Asn Gly Asp Ser Thr Pro Ser Leu
```

```
            100                 105                 110

Asn Glu Tyr Ser Trp Asn Asn Tyr Ala Asn Met Leu Tyr Val Asp Gln
        115                 120                 125

Pro Ile Gly Val Gly Phe Ser Tyr Gly Thr Asp Asp Val Thr Ser Thr
    130                 135                 140

Val Thr Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala
145                 150                 155                 160

Gln Phe Pro Glu Tyr Glu Ser Arg Asp Phe Ala Ile Phe Thr Glu Ser
                165                 170                 175

Tyr Gly Gly His Tyr Gly Pro Glu Phe Ala Ser Tyr Ile Gln Asp Gln
            180                 185                 190

Asn Ala Ala Ile Lys Ala Gly Ser Val Ser Gly Glu Asn Ile Asn Leu
        195                 200                 205

Val Ala Leu Gly Val Asn Asn Gly Trp Ile Asp Ser Thr Ile Gln Glu
    210                 215                 220

Lys Ala Tyr Ile Asp Phe Ser Tyr Asn Asn Ser Tyr Lys Gln Leu Ile
225                 230                 235                 240

Asp Asp Ser Gln Arg Thr Ser Leu Leu Ser Ala Tyr Asn Asp Gln Cys
                245                 250                 255

Leu Pro Ala Ile Gln Lys Cys Thr Ser Ser Gly Ser Asn Ser Asp Cys
            260                 265                 270

Lys Asn Ala Asp Ser Val Cys Tyr Asn Gln Ile Glu Gly Pro Ile Ser
        275                 280                 285

Ser Ser Gly Asp Trp Asp Val Tyr Asp Ile Arg Glu Pro Ser Asn Asp
    290                 295                 300

Pro Tyr Pro Pro Ser Thr Tyr Ser Thr Tyr Leu Ser Asn Ala Asp Val
```

```
305                 310                 315                 320


Val Lys Ala Ile Gly Ala Gln Ser Ser Tyr Gln Glu Cys Pro Asn Gly
                325                 330                 335


Pro Tyr Asn Lys Phe Thr Ser Thr Gly Asp Asn Pro Arg Ser Phe Leu
            340                 345                 350


Ser Thr Leu Ser Ser Val Val Lys Ser Gly Ile Asn Val Leu Val Trp
        355                 360                 365


Ala Gly Asp Ala Asp Trp Ile Cys Asn Trp Leu Gly Asn Tyr Glu Val
    370                 375                 380


Ala Asn Ala Val Asp Phe Ser Gly His Thr Asp Phe Ser Ala Lys Asp
385                 390                 395                 400


Leu Ala Pro Tyr Thr Val Asn Gly Thr Glu Lys Gly Leu Phe Lys Asn
                405                 410                 415


Val Asp Asn Phe Ser Phe Leu Arg Val Tyr Gly Ala Gly His Glu Val
            420                 425                 430


Pro Tyr Tyr Gln Pro Asp Thr Ala Leu Gln Val Phe Glu Gln Ile Leu
        435                 440                 445


Gln Lys Lys Pro Ile Phe Ser Thr
    450                 455


<210>  45
<211>  456
<212>  PRT
<213>  Aspergillus denticulatus

<400>  45

Ser Thr Ala Ser Ala Ala Lys Asp Ser Val Ser Ser Ile Val Lys Asn
1               5                   10                  15


Gly Val Lys Tyr Thr Val Phe Glu His Ala Ala Thr Gly Ala Lys Met
            20                  25                  30
```

```
Glu Phe Val Lys Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn
        35                  40                  45


Gln Tyr Ser Gly Tyr Leu Ser Val Gly Asp Asn Met Asn Met Trp Phe
    50                  55                  60


Trp Phe Phe Glu Ala Arg Asn Asn Pro Gln Gln Ala Pro Leu Ala Ala
65                  70                  75                  80


Trp Phe Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln
                85                  90                  95


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


Asn Glu Tyr Ser Trp Asn Asn Tyr Ala Asn Met Leu Tyr Val Asp Gln
        115                 120                 125


Pro Ile Gly Val Gly Phe Ser Tyr Gly Thr Asp Asp Val Thr Ser Thr
    130                 135                 140


Val Thr Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala
145                 150                 155                 160


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


Tyr Gly Gly His Tyr Gly Pro Glu Phe Ala Ser Tyr Ile Gln Gln Gln
            180                 185                 190


Asn Ala Ala Ile Lys Ala Gly Thr Val Ser Gly Glu Asn Ile Asn Leu
        195                 200                 205


Ile Ala Leu Gly Val Asn Asn Gly Trp Ile Asp Ser Ala Ile Gln Glu
    210                 215                 220


Lys Ala Tyr Ile Asp Phe Ser Tyr Asn Asn Thr Tyr Lys Gln Leu Ile
225                 230                 235                 240
```

```
Ser Ser Ser Asp Arg Thr Arg Leu Leu Ser Val Tyr Asn Ser Gln Cys
                245                 250                 255


Leu Pro Ala Ile Gln Lys Cys Thr Ser Thr Gly Thr Thr Ala Ala Cys
            260                 265                 270


Arg Asn Ala Asp Ser Val Cys Tyr Asn Asn Ile Glu Gly Pro Ile Ser
        275                 280                 285


Ser Ser Gly Asp Trp Asp Val Tyr Asp Ile Arg Glu Pro Ala Asn Asp
    290                 295                 300


Pro Tyr Pro Pro Ala Thr Tyr Ser Thr Tyr Leu Ala Asp Pro Asp Val
305                 310                 315                 320


Val Lys Ala Ile Gly Ala Gln Thr Ser Tyr Gln Glu Cys Pro Asn Gly
                325                 330                 335


Pro Tyr Asn Lys Phe Ala Ser Thr Gly Asp Asn Pro Arg Ser Phe Leu
            340                 345                 350


Ser Thr Leu Ser Asn Val Val Lys Ser Gly Ile Asn Val Leu Val Trp
        355                 360                 365


Ala Gly Asp Ala Asp Trp Ile Cys Asn Trp Leu Gly Asn Tyr Glu Val
    370                 375                 380


Ala Asn Ala Val Asp Tyr Pro Gly Gln Ser Glu Phe Glu Ala Lys Asp
385                 390                 395                 400


Leu Ala Pro Tyr Thr Val Asn Gly Ala Glu Lys Gly Met Phe Lys Asn
                405                 410                 415


Val Asp Asn Phe Ser Phe Leu Arg Val Tyr Gly Ala Gly His Glu Val
            420                 425                 430


Pro Tyr Tyr Gln Pro Glu Thr Ala Leu Gln Val Phe Gln Gln Thr Leu
        435                 440                 445
```

```
Gln Lys Lys Pro Ile Phe Ser Thr
    450                 455


<210>  46
<211>  456
<212>  PRT
<213>  Hamigera sp.

<400>  46

Ala Pro Ala Ser Thr Ala Lys Asp Thr Leu Ser Ser Ile Val Lys Asn
1               5                   10                  15


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


Glu Phe Val Lys Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn
        35                  40                  45


Gln Tyr Ser Gly Tyr Leu Ser Val Gly Asp Asn Met Asn Met Trp Phe
    50                  55                  60


Trp Phe Phe Glu Ala Arg Asn Asn Pro Gln Lys Ala Pro Leu Ala Ala
65                  70                  75                  80


Trp Phe Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln
                85                  90                  95


Glu Asn Gly Pro Cys His Phe Val Asn Gly Glu Asn Thr Pro Ser Leu
            100                 105                 110


Asn Glu Tyr Ser Trp Asn Asn Tyr Ala Asn Met Leu Tyr Val Asp Gln
        115                 120                 125


Pro Ile Gly Val Gly Phe Ser Tyr Gly Thr Asp Asp Val Asp Ser Thr
    130                 135                 140


Val Thr Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala
145                 150                 155                 160
```

```
Gln Phe Pro Glu Tyr Glu Ser Arg Asp Phe Ala Ile Phe Thr Glu Ser
                165                 170                 175


Tyr Gly Gly His Tyr Gly Pro Glu Phe Ala His Tyr Ile Gln Gln Gln
            180                 185                 190


Asn Ala Ala Ile Lys Ser Gly Ser Val Lys Gly Glu Asn Ile Asn Leu
        195                 200                 205


Ile Gly Leu Gly Val Asn Asn Gly Trp Ile Asp Ser Ala Ile Gln Glu
    210                 215                 220


Lys Ala Tyr Ile Asp Phe Ser Tyr Asn Asn Ser Tyr Lys Gln Leu Ile
225                 230                 235                 240


Asp Phe Ser Gln Arg Thr Ser Leu Met Arg Ala Tyr Lys Asn Gln Cys
                245                 250                 255


Leu Pro Ala Ile Gln Lys Cys Tyr Gln Thr Gly Thr Asn Ala Asp Cys
            260                 265                 270


Thr Asp Ala Ser Ser Val Cys Tyr Asn Asn Ile Glu Gly Pro Ile Ser
        275                 280                 285


Ser Ser Gly Asp Trp Asp Val Tyr Asp Ile Arg Glu Pro Ser Asn Asp
    290                 295                 300


Pro Tyr Pro Pro Lys Thr Tyr Ser Ser Tyr Leu Ser Asp Pro Lys Val
305                 310                 315                 320


Val Lys Ala Ile Gly Ala Arg Thr Asn Tyr Lys Glu Cys Pro Asn Gly
                325                 330                 335


Pro Tyr Asn Lys Phe Ser Thr Thr Gly Asp Asn Pro Arg Ser Phe Leu
            340                 345                 350


Ser Thr Leu Ser Asp Val Val Lys Ser Gly Ile Asn Val Ile Leu Trp
        355                 360                 365
```

```
Ala Gly Asp Ala Asp Trp Ile Cys Asn Trp Leu Gly Gly Tyr Gly Val
    370                 375                 380


Ala Asn Ala Val Asp Tyr Pro Gly His Ala Gln Phe Arg Ala Lys Ala
385                 390                 395                 400


Leu Ala Pro Tyr Thr Val Asn Gly Thr Glu Lys Gly Gln Phe Lys Thr
                405                 410                 415


Val Asp Asn Phe Gln Phe Leu Lys Val Tyr Gly Ala Gly His Glu Val
            420                 425                 430


Pro Tyr Tyr Gln Pro Glu Thr Ala Leu Gln Val Phe Glu Gln Ile Leu
        435                 440                 445


Gln Lys Lys Pro Ile His Ser Thr
    450                 455


<210>  47
<211>  456
<212>  PRT
<213>  Penicillium janthinellum

<400>  47

Ala Pro Ala Ser Thr Ala Lys Asp Thr Val Ser Ser Val Val Lys Asp
1               5                   10                  15


Gly Val Thr Tyr Thr Val Phe Glu His Ala Ala Thr Gly Ala Lys Met
            20                  25                  30


Glu Phe Val Lys Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn
        35                  40                  45


Gln Tyr Ser Gly Tyr Leu Ser Val Gly Ser Asn Met Asn Met Trp Phe
    50                  55                  60


Trp Phe Phe Glu Ala Arg Asn Asn Pro Gln Gln Ala Pro Leu Ala Ala
65                  70                  75                  80
```

```
Trp Phe Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln
                85                  90                  95


Glu Asn Gly Pro Cys His Phe Val Asn Gly Glu Ser Thr Pro Ser Leu
            100                 105                 110


Asn Glu Asn Ser Trp Asn Asn Tyr Ala Asn Met Ile Tyr Ile Asp Gln
        115                 120                 125


Pro Ile Gly Val Gly Phe Ser Tyr Gly Thr Asp Arg Val Thr Ser Thr
    130                 135                 140


Val Thr Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala
145                 150                 155                 160


Gln Phe Pro Glu Tyr Glu Ser Arg Asp Phe Ala Ile Phe Thr Glu Ser
                165                 170                 175


Tyr Gly Gly His Tyr Gly Pro Glu Phe Ala Ser Tyr Ile Glu Gln Gln
            180                 185                 190


Asn Ala Ala Ile Lys Ala Gly Ser Val Thr Gly Gln Asn Val Asn Ile
        195                 200                 205


Val Ala Leu Gly Val Asn Asn Gly Trp Ile Asp Ala Thr Ile Gln Glu
    210                 215                 220


Lys Ala Tyr Ile Asp Phe Ser Tyr Asn Asn Ser Tyr Gln Gln Ile Ile
225                 230                 235                 240


Asp Ser Ser Thr Arg Asp Ser Leu Leu Asp Ala Tyr Asn Asn Gln Cys
                245                 250                 255


Leu Pro Ala Leu Gln Gln Cys Ala Gln Ser Gly Ser Asn Ser Asp Cys
            260                 265                 270


Thr Asn Ala Asp Ser Val Cys Tyr Gln Asn Ile Glu Gly Pro Ile Ser
        275                 280                 285
```

```
Ser Ser Gly Asp Phe Asp Val Tyr Asp Ile Arg Glu Pro Ser Asn Asp
    290                 295                 300


Pro Tyr Pro Pro Lys Thr Tyr Ser Thr Tyr Leu Ser Asp Pro Thr Val
305                 310                 315                 320


Val Lys Ala Ile Gly Ala Arg Thr Asn Tyr Gln Glu Cys Pro Asn Gly
                325                 330                 335


Pro Tyr Asn Lys Phe Ala Ser Thr Gly Asp Asn Pro Arg Ser Phe Leu
            340                 345                 350


Ser Thr Leu Ser Ser Val Val Gln Ser Gly Ile Asn Val Leu Val Trp
        355                 360                 365


Ala Gly Asp Ala Asp Trp Ile Cys Asn Trp Leu Gly Asn Tyr Ala Val
    370                 375                 380


Ala Asn Ala Val Asp Phe Pro Gly Asn Ala Gln Phe Ser Ala Met Asp
385                 390                 395                 400


Leu Ala Pro Tyr Thr Val Asn Gly Val Glu Lys Gly Gln Phe Lys Thr
                405                 410                 415


Val Asp Asn Phe Ser Phe Leu Lys Val Tyr Gly Ala Gly His Glu Val
            420                 425                 430


Pro Tyr Tyr Gln Pro Asp Thr Ala Leu Gln Val Phe Lys Gln Ile Leu
        435                 440                 445


Gln Lys Lys Pro Ile Ser Ser Thr
    450                 455


<210>  48
<211>  456
<212>  PRT
<213>  Penicillium vasconiae

<400>  48

Ala Pro Ala Ser Thr Ala Lys Asp Ser Val Ser Ser Val Val Lys Asn
```

```
1               5                   10                  15


Gly Val Lys Tyr Thr Val Phe Glu His Ala Ala Thr Gly Ala Lys Met
            20                  25                  30


Glu Phe Val Lys Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn
        35                  40                  45


Gln Tyr Ser Gly Tyr Leu Ser Val Gly Ser Asn Met Asn Met Trp Phe
    50                  55                  60


Trp Phe Phe Glu Ala Arg Asn Asn Pro Gln Gln Ala Pro Leu Ala Ala
65                  70                  75                  80


Trp Phe Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln
                85                  90                  95


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


Asn Glu Tyr Ser Trp Asn Asn Tyr Ala Asn Met Leu Tyr Val Asp Gln
        115                 120                 125


Pro Ile Gly Val Gly Phe Ser Tyr Gly Thr Asp Asp Val Thr Ser Thr
    130                 135                 140


Val Thr Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala
145                 150                 155                 160


Gln Phe Pro Glu Tyr Glu Ser Arg Asp Phe Ala Ile Phe Thr Glu Ser
                165                 170                 175


Tyr Gly Gly His Tyr Gly Pro Glu Phe Ala Ser Tyr Ile Gln Glu Gln
            180                 185                 190


Asn Ala Ala Ile Thr Ala Gly Ser Val Ser Gly Gln Lys Ile Asn Leu
        195                 200                 205


Ile Ala Leu Gly Val Asn Asn Gly Trp Ile Asp Ser Thr Ile Gln Glu
```

```
    210                 215                 220


Lys Ala Tyr Ile Asp Phe Ser Tyr Asn Asn Ser Tyr Gln Gln Leu Ile
225                 230                 235                 240


Asp Asp Ser Gln Arg Thr Ser Leu Leu Ser Ala Tyr Asn Lys Gln Cys
                245                 250                 255


Leu Pro Ala Ile Gln Lys Cys Thr Gln Thr Gly Ser Asn Ser Ala Cys
            260                 265                 270


Gln Asn Ala Ala Asn Val Cys Tyr Asn Asn Ile Glu Gly Pro Ile Ser
        275                 280                 285


Ser Ser Gly Asp Trp Asp Val Tyr Asp Ile Arg Glu Pro Ser Asn Asp
    290                 295                 300


Pro Tyr Pro Pro Ser Thr Tyr Ser Thr Tyr Leu Ala Asn Ser Asp Val
305                 310                 315                 320


Val Lys Ala Ile Gly Ala Gln Ser Ser Tyr Gln Glu Cys Pro Asn Gly
                325                 330                 335


Pro Tyr Asn Lys Phe Ala Ser Thr Gly Asp Asn Pro Arg Ser Phe Leu
            340                 345                 350


Ser Thr Leu Ser Ser Val Val Lys Ser Gly Ile Asn Val Leu Val Trp
        355                 360                 365


Ala Gly Asp Ala Asp Trp Ile Cys Asn Trp Leu Gly Asn Tyr Glu Val
    370                 375                 380


Ala Asn Ala Val Asp Phe Ser Gly His Ala Glu Phe Ser Ala Lys Asp
385                 390                 395                 400


Leu Ala Pro Tyr Thr Val Asn Gly Ala Glu Lys Gly Met Phe Lys Asn
                405                 410                 415


Val Asp Asn Phe Ser Phe Leu Lys Val Tyr Gly Ala Gly His Glu Val
```

```
            420                 425                 430


Pro Tyr Tyr Gln Pro Glu Thr Ala Leu Gln Val Phe Glu Gln Ile Leu
        435                 440                 445


Gln Lys Lys Pro Ile Ser Ser Thr
    450                 455


<210>  49
<211>  454
<212>  PRT
<213>  Hamigera paravellanea

<400>  49

Ala Pro Ser Leu Arg Asp Lys Arg Ser Phe Val Glu Arg Asp Gly Val
1               5                   10                  15


Thr Tyr Thr Val Phe Glu His Ala Ala Thr Gly Ala Lys Met Glu Phe
            20                  25                  30


Val Gln Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn Gln Tyr
        35                  40                  45


Ser Gly Tyr Leu Ser Val Gly Asp Asn Met Asn Met Trp Phe Trp Phe
    50                  55                  60


Phe Glu Ala Arg Asn Asn Pro Thr Ala Ala Pro Leu Ala Ala Trp Phe
65                  70                  75                  80


Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln Glu Asn
                85                  90                  95


Gly Pro Cys His Phe Val Asn Gly Glu Ser Thr Pro Ser Leu Asn Glu
            100                 105                 110


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


Gly Thr Gly Phe Ser Tyr Gly Thr Asp Asp Val Thr Ser Thr Val Thr
    130                 135                 140
```

```
Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala Gln Phe
145                 150                 155                 160


Pro Glu Tyr Glu Ser Arg Asp Phe Gly Ile Phe Thr Glu Ser Tyr Gly
                165                 170                 175


Gly His Tyr Gly Pro Glu Phe Ala Ser Tyr Ile Gln Glu Gln Asn Ala
            180                 185                 190


Ala Ile Lys Ala Gly Ser Val Ser Gly Asp Asn Ile Asn Leu Val Ala
        195                 200                 205


Leu Gly Ile Asn Asn Gly Trp Phe Asp Ala Gly Ile Gln Glu Lys Ala
    210                 215                 220


Tyr Ile Asp Phe Ser Tyr Asn Asn Ser Tyr Arg Gln Ile Ile Ser Ser
225                 230                 235                 240


Ser Gln Arg Ser Ser Tyr Leu Asp Ala Tyr Asn His Asp Cys Leu Pro
                245                 250                 255


Ala Ile Glu Ser Cys Ala Ser Ser Gly Thr Asn Ser Ala Cys Lys Asn
            260                 265                 270


Ala Glu Ser Val Cys Tyr Asn Gly Ile Glu Gly Pro Ile Ser Ser Ala
        275                 280                 285


Ala Asp Phe Asp Val Tyr Asp Val Arg Gln Pro Ser Asn Asp Pro Tyr
    290                 295                 300


Pro Pro Ala Thr Tyr Ser Thr Tyr Leu Gln Ser Ala Ser Val Arg Lys
305                 310                 315                 320


Ala Ile Gly Ala Arg Thr Lys Tyr Gln Glu Cys Pro Asn Gly Pro Tyr
                325                 330                 335


Asn Lys Phe Glu Thr Thr Gly Asp Asn Ser Arg Ser Phe Leu Ser Thr
            340                 345                 350
```

```
Leu Ser Asp Val Val Asn Thr Gly Ile Thr Val Leu Val Trp Ala Gly
        355                 360                 365


Asp Ala Asp Trp Ile Cys Asn Trp Val Gly Gly His Ala Val Ala Asp
    370                 375                 380


Ala Val Thr Phe Ala Arg Gln Lys Thr Phe Gln Ala Lys Pro Leu Glu
385                 390                 395                 400


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


Asn Phe Thr Phe Leu Arg Val Tyr Glu Ala Gly His Glu Val Pro Tyr
            420                 425                 430


Tyr Gln Pro Glu Thr Ala Leu Gln Val Phe Val Gln Thr Met Gln Lys
        435                 440                 445


Lys Ala Ile Phe Ser Thr
    450


<210>  50
<211>  453
<212>  PRT
<213>  Talaromyces variabilis

<400>  50

Ala Ala Val Pro Gln Asp Lys Arg Ser Ile Val Lys Arg Asp Gly Val
1               5                   10                  15


Thr Tyr Asn Val Phe Glu His Ala Ala Thr Gly Ala Lys Met Glu Phe
            20                  25                  30


Val Lys Asn Ser Gly Ile Cys Glu Thr Thr Pro Gly Val Asn Gln Tyr
        35                  40                  45


Ser Gly Tyr Leu Ser Val Gly Asp Asn Met Asn Met Trp Phe Trp Phe
    50                  55                  60
```

```
Phe Glu Ser Arg Asn Asn Ala Ser Gly Ala Pro Leu Ala Ala Trp Phe
65                  70                  75                  80


Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln Glu Asn
                85                  90                  95


Gly Pro Cys His Phe Val Asn Gly Glu Lys Lys Pro Ser Leu Asn Lys
            100                 105                 110


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


Gly Val Gly Phe Ser Tyr Gly Thr Asp Asp Val Thr Ser Thr Glu Ser
    130                 135                 140


Ala Ala Pro Tyr Val Trp Lys Leu Leu Gln Ala Phe Tyr Ala Gln Phe
145                 150                 155                 160


Pro Gln Tyr Glu Ser Arg Asp Phe Gly Ile Phe Thr Glu Ser Tyr Gly
                165                 170                 175


Gly His Tyr Gly Pro Glu Phe Ala His Tyr Leu Gln Gln Gln Asn Glu
            180                 185                 190


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


Leu Gly Ile Asn Asn Gly Trp Phe Asp Thr Gln Leu Gln Glu Gly Ala
    210                 215                 220


Tyr Ile Asp Tyr Ala Tyr Ser Asn Asn Tyr Lys Lys Ile Ile Asp Ser
225                 230                 235                 240


Ser Gln Arg Ser Ser Leu Glu Asp Ser Leu Lys Ser Asp Cys Leu Pro
                245                 250                 255


Ala Val Lys Gln Cys Leu Ser Ser Gly Ser Asp Ser Asp Cys Glu Asn
            260                 265                 270
```

```
Ala Ser Asp Thr Cys Gly Gln Ile Glu Ser Ser Ile Gln Gln Ala Ala
        275                 280                 285


Asp Phe Asp Val Tyr Asp Val Arg Glu Pro Ser Asn Asp Pro Tyr Pro
    290                 295                 300


Pro Ser Thr Tyr Ser Asp Tyr Leu Ala Asp Ser Ser Val Val Lys Ala
305                 310                 315                 320


Ile Gly Ala Lys Ser Thr Tyr Lys Glu Cys Pro Asn Gly Pro Tyr Tyr
                325                 330                 335


Lys Phe Ser Ser Thr Gly Asp Asn Thr Arg Ser Phe Leu Ser Glu Leu
            340                 345                 350


Ser Ser Val Val Gln Ser Gly Ile Gln Val Leu Val Trp Ala Gly Asp
        355                 360                 365


Ala Asp Trp Ile Cys Asn Tyr Met Gly Val Gln Arg Val Ala Asp Ala
    370                 375                 380


Val Glu Phe Asp Gly Ser Ser Gln Phe Ser Asn Ala Thr Leu Lys Pro
385                 390                 395                 400


Tyr Thr Val Asn Gly Thr Lys Lys Gly Glu Tyr Lys Asn Val Asp Asn
                405                 410                 415


Phe Ser Tyr Leu Arg Val Tyr Gly Ala Gly His Glu Val Pro Tyr Tyr
            420                 425                 430


Gln Pro Ala Val Ala Leu Gln Val Phe Lys Gln Thr Met Gln Gln Gln
        435                 440                 445


Ala Ile Lys Ser Thr
    450


<210>  51
<211>  456
<212>  PRT
```

```
<213>  Penicillium arenicola

<400>  51

Ala Pro Ala Thr His Leu Gln Asp Lys Arg Ser Ile Val Glu Arg Asp
1               5                   10                  15


Gly Val Asn Tyr Thr Val Phe Glu His Ala Ala Thr Gly Ala Lys Leu
                20                  25                  30


Glu Phe Val Thr Asn Ser Gly Ile Cys Glu Thr Thr Ser Gly Val Asn
            35                  40                  45


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


Trp Phe Phe Glu Ser Arg Asn Ser Pro Ser Thr Ala Pro Leu Ala Ala
65                  70                  75                  80


Trp Phe Asn Gly Gly Pro Gly Cys Ser Ser Met Ile Gly Leu Phe Gln
                85                  90                  95


Glu Asn Gly Pro Cys Gln Phe Tyr Asp Gly Ala Ser Thr Pro Ser Leu
                100                 105                 110


Asn Pro Tyr Ser Phe Asn Glu Tyr Ala Asn Met Ile Tyr Ile Asp Gln
            115                 120                 125


Pro Ile Gly Val Gly Phe Ser Tyr Gly Thr Asp Asp Val Thr Ser Thr
        130                 135                 140


Val Thr Ala Ala Pro Tyr Val Trp Lys Leu Ile Gln Ala Phe Tyr Ala
145                 150                 155                 160


Ser Phe Pro Ala Tyr Glu Ser Arg Glu Phe Gly Leu Phe Thr Glu Ser
                165                 170                 175


Tyr Gly Gly His Tyr Gly Pro Glu Phe Ala Tyr Tyr Ile Gln Gln Gln
                180                 185                 190
```

```
Asn Ala Ala Ile Ala Ser Gly Thr Val Thr Gly Asp Thr Ile Asp Ile
        195                 200                 205


Val Ala Leu Gly Ile Asn Asn Gly Trp Ile Asp Ser Ala Leu Gln Glu
    210                 215                 220


Lys Ala Tyr Ile Glu Tyr Ser Tyr Asn Asn Ser Tyr Lys Gln Ile Ile
225                 230                 235                 240


Thr Ser Ser Gln Arg Thr Ser Tyr Leu Ser Thr Tyr Thr Asn Asp Cys
                245                 250                 255


Leu Pro Ala Ile Asn Lys Cys Thr Thr Gly Gly Ser Asn Ser Ala Cys
            260                 265                 270


Ser Asn Ala Ala Asp Val Cys Tyr Asn Asp Ile Glu Ser Pro Ile Met
        275                 280                 285


Ser Asp Ala Asp Phe Asp Val Tyr Asp Ile Arg Gln Pro Ser Asn Asp
    290                 295                 300


Ala Tyr Pro Pro Glu Thr Tyr Val Thr Tyr Leu Gln Thr Ser Ser Val
305                 310                 315                 320


Val Lys Ala Ile Gly Ala Ser Ser Thr Tyr Gln Glu Cys Pro Asp Ala
                325                 330                 335


Pro Tyr Asn Lys Phe Ala Thr Thr Gly Asp Asn Asp Arg Ser Phe Leu
            340                 345                 350


Ala Thr Leu Ser Thr Val Val Gln Ser Gly Ile Thr Val Leu Leu Trp
        355                 360                 365


Ala Gly Asp Ala Asp Trp Ile Cys Asn Trp Val Gly Asn Gln Tyr Val
    370                 375                 380


Ala Asp Ala Val Thr Trp Ser Gly Gln Ser Ser Phe Ala Ala Gln Thr
385                 390                 395                 400
```

```
Leu Thr Pro Tyr Thr Val Asn Gly Ser Glu Val Gly Thr Phe Lys Thr
                405                 410                 415


Leu Asp Asn Leu Ser Phe Leu Arg Val Tyr Glu Ala Gly His Glu Val
            420                 425                 430


Pro Tyr Tyr Gln Pro Ala Thr Ala Leu Gln Ala Phe Ile Gln Thr Met
        435                 440                 445


Gln Lys Lys Ala Leu Ser Ser Thr
    450                 455


<210>  52
<211>  354
<212>  PRT
<213>  Nocardiopsis kunsanensis

<400>  52

Ala Pro Ala Pro Gln Asn Pro Thr Glu Pro Ala Glu Ala Thr Thr Met
1               5                   10                  15


Ala Glu Ala Leu Glu Arg Asp Leu Gly Leu Asn Glu Ala Glu Ala Thr
            20                  25                  30


Asp Leu Ile Asp Ala Gln Glu Ser Ala Leu Asp Val Asp Ala Glu Ala
        35                  40                  45


Thr Glu Ala Ala Gly Glu His Tyr Gly Gly Ser Leu Phe Asp Thr Glu
    50                  55                  60


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


Val Glu Ala Ala Gly Ala Glu Ala Ala Val Val Glu His Gly Val Glu
                85                  90                  95


Gly Leu Asp Asp Leu Ile Ser Asp Leu Asp Ser Ala Gly Ala Gln Glu
            100                 105                 110


Gly Val Val Gly Trp Tyr Pro Glu Val Glu Asn Asp Thr Val Val Ile
```

```
        115                 120                 125


Glu Thr Leu Glu Gly Ala Asp Ala Asp Val Asp Ala Leu Leu Ser Ser
    130                 135                 140


Ala Gly Val Asp Pro Ala Asp Val Arg Val Glu Thr Thr Asp Glu Ala
145                 150                 155                 160


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


Gly Ser Ser Arg Cys Ser Val Gly Phe Pro Ala Ser Asp Ser Tyr Gly
            180                 185                 190


Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr Thr Gly Ser Ser
        195                 200                 205


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


Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe Ser Leu Thr
225                 230                 235                 240


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


Ser Thr Gln Ala Pro Ile Gly Ser Gln Val Cys Arg Ser Gly Ser Thr
            260                 265                 270


Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln Thr Val Ser
        275                 280                 285


Tyr Pro Gln Gly Thr Val Arg Asp Leu Thr Arg Thr Ser Val Cys Ala
    290                 295                 300


Glu Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly Ser Gln Ala Gln
305                 310                 315                 320


Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Trp Gly Gly Thr Thr
```

```
                325                 330                 335

Tyr Tyr Gln Glu Val Asn Pro Met Leu Asn Ser Trp Asn Leu Asn Leu
            340                 345                 350

Ser Thr



<210>  53
<211>  425
<212>  PRT
<213>  Streptomyces parvulus

<400>  53

Gly Thr Ala Pro Ser Pro Ala Ala Pro Thr Ala Ala Glu Ser Leu Arg
1               5                   10                  15

Ala Asp Ala Ala Pro Pro Ala Leu Leu Arg Ala Met Glu Arg Asp Leu
            20                  25                  30

Gly Leu Gly Arg Glu Gln Ala Glu Arg Arg Leu Gly Asn Glu Ala Glu
        35                  40                  45

Ala Gly Ala Val Ala Gly Arg Leu Arg Ala Asp Leu Gly Gly Asp Phe
    50                  55                  60

Ala Gly Ala Trp Val Arg Gly Ala Glu Ser Gly Thr Leu Thr Val Ala
65                  70                  75                  80

Thr Thr Asp Ala Ala Asp Val Pro Ala Ile Glu Ala Arg Gly Ala Val
                85                  90                  95

Ala Glu Val Val Arg His Ser Leu Ala Asp Leu Gly Ala Ala Lys Ser
            100                 105                 110

Arg Leu Asp Arg Ala Ala Ala His Arg Asp Thr Ala Glu Ala Pro Val
        115                 120                 125

Arg Tyr Val Asp Val Arg Thr Asn Thr Val Thr Val Gln Ala Val Arg
    130                 135                 140
```

```
Pro Ser Ala Ala Arg Ala Leu Leu Ala Ala Ala Gly Val Asp Ala Gly
145                 150                 155                 160

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

Leu Arg Gly Gly Glu Ala Tyr Tyr Ile Asn Asn Ser Gly Arg Cys Ser
            180                 185                 190

Val Gly Phe Pro Val Thr Lys Gly Thr Gln Gln Gly Phe Ala Thr Ala
        195                 200                 205

Gly His Cys Gly Arg Ala Gly Ala Ser Thr Ser Gly Ala Asn Arg Val
    210                 215                 220

Ala Gln Gly Thr Phe Gln Gly Ser Val Phe Pro Gly Arg Asp Met Ala
225                 230                 235                 240

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

Ala Gly Gly Gln Asn Val Gln Val Ala Gly Ser Thr Gln Ala Pro Val
            260                 265                 270

Gly Ala Ser Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly
        275                 280                 285

Thr Ile Gln Gln His Asp Thr Ser Val Thr Tyr Pro Glu Gly Thr Ile
    290                 295                 300

Thr Gly Val Thr Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly
305                 310                 315                 320

Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val Thr Ser Gly Gly
                325                 330                 335

Ser Gly Asn Cys Gly Ser Gly Gly Thr Thr Phe Phe Gln Pro Ile Asn
            340                 345                 350
```

```
Pro Leu Leu Gln Asn Tyr Gly Leu Thr Leu Lys Thr Thr Gly Gly Gly
        355                 360                 365


Gly Glu Asp Pro Gly Glu Pro Gly Glu Pro Gly Gly Thr Trp Ala Ala
    370                 375                 380


Gly Thr Val Tyr Arg Pro Gly Asp Thr Val Thr Tyr Gly Gly Ala Thr
385                 390                 395                 400


Tyr Arg Cys Leu Gln Gly His Gln Ala Gln Arg Gly Trp Glu Pro Ala
                405                 410                 415


Asn Val Pro Ala Leu Trp Gln Arg Val
            420                 425


<210>  54
<211>  350
<212>  PRT
<213>  Saccharopolyspora endophytica

<400>  54

Leu Thr Ala Thr Ile Ala Asp Pro Ala Gly Pro Pro Val Ser Pro Glu
1               5                   10                  15


Leu Val Thr Ala Met Gln Arg Asp Leu Gly Leu Thr Ala Asp Gln Ala
            20                  25                  30


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


Leu Arg Asp Ala Leu Ala Gly Ser Tyr Gly Gly Ser Tyr Phe Asp Ala
    50                  55                  60


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


Glu Val Arg Ala Ala Gly Ala Glu Pro Arg Gln Val Asp Ala Ser Glu
                85                  90                  95
```

```
Arg Gln Leu Asp Gly Ile Val Glu Ala Leu Asn Gly Arg Gly Ala Gln
            100                 105                 110


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


Val Val Val Thr Thr Gln Pro Gly Thr Ala Glu Gln Ala Thr Gly Phe
    130                 135                 140


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


Pro Ala Gln Pro Glu Thr Tyr Ala Asp Val Val Gly Gly Tyr Ala Tyr
                165                 170                 175


Tyr Thr Ala Ser Gly Ala Arg Cys Ser Met Gly Phe Ala Val Gln Gly
            180                 185                 190


Gly Phe Val Thr Ala Gly His Cys Gly Ala Pro Gly Glu Ser Thr Thr
        195                 200                 205


Gln Pro Thr Gly Tyr Phe Ala Gly Ser Ser Phe Pro Gly Asn Asp Tyr
    210                 215                 220


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


Asn Tyr Ser Ser Gly Tyr Val Arg Val Ser Gly Ser Ala Glu Ala Pro
                245                 250                 255


Leu Gly Ser Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys
            260                 265                 270


Gly Thr Val Leu Ala Lys Asn Gln Ser Val Arg Tyr Gln Glu Gly Thr
        275                 280                 285


Val Ser Gly Leu Thr Arg Thr Asn Val Cys Ala Glu Pro Gly Asp Ser
    290                 295                 300
```

```
Gly Gly Ser Phe Ile Ser Gly Asn Gln Ala Gln Gly Met Thr Ser Gly
305                 310                 315                 320


Gly Trp Gly Asp Cys Arg Thr Gly Gly Glu Thr Tyr Tyr Gln Pro Val
                325                 330                 335


Arg Glu Ala Leu Ser Ala Tyr Gly Leu Thr Leu Leu Thr Gln
            340                 345                 350


<210>  55
<211>  355
<212>  PRT
<213>  Luteus cellwall

<400>  55

Ala Ser Gly Pro Leu Pro Gln Ser Pro Ser Pro Asp Ser Asp Val Ala
1               5                   10                  15


Thr Thr Met Ala Glu Ala Leu Glu Arg Asp Leu Asn Leu Thr Ser Thr
            20                  25                  30


Glu Ala Gln Glu Leu Leu Thr Ala Gln Glu Ala Ala Phe Glu Ala Asp
        35                  40                  45


Glu Ala Ala Ala Gln Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe
    50                  55                  60


Asp Thr Glu Thr Leu Asp Leu Thr Val Met Val Thr Asp Ala Ala Ala
65                  70                  75                  80


Val Gln Ala Val Glu Ala Thr Gly Ala Lys Ala Asp Val Val Ser Tyr
                85                  90                  95


Gly Ile Asp Gly Leu Asp Thr Ile Ile Asp Asp Leu Asn Glu Ala Asp
            100                 105                 110


Ala Pro Glu Gly Val Val Gly Trp Tyr Pro Asp Ile Asp Ser Asp Thr
        115                 120                 125
```

```
Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Asp Ala Leu
    130                 135                 140


Leu Ala Glu Ala Gly Val Asp Ala Ser Ala Val Lys Val Glu Ser Thr
145                 150                 155                 160


Thr Glu Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu Ala Tyr
                165                 170                 175


Tyr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn Ala Ser
            180                 185                 190


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


Gln Val Thr Ile Gly Asn Gly Arg Gly Val Phe Glu Arg Ser Val Phe
    210                 215                 220


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


Thr Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Ala Thr Val Ser
                245                 250                 255


Gly Ser Ser Val Ala Pro Ile Gly Ser Ser Val Cys Arg Ser Gly Ser
            260                 265                 270


Thr Thr Gly Trp Arg Cys Gly Thr Ile Gln Ala Arg Gly Gln Thr Val
        275                 280                 285


Thr Tyr Pro Gln Gly Thr Ile Tyr Asn Met Thr Arg Thr Ser Ala Cys
    290                 295                 300


Ala Glu Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly Thr Gln Ala
305                 310                 315                 320


Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Trp Gly Gly Thr
                325                 330                 335
```

```
Thr Phe Tyr Gln Glu Val Asn Pro Met Leu Asn Ser Trp Asn Leu Arg
            340                 345                 350


Leu Arg Thr
        355


<210>  56
<211>  406
<212>  PRT
<213>  Saccharothrix australiensis

<400>  56

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


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


Arg Glu Ala Lys Ala Ala Thr Thr Glu Gln Ser Leu Lys Ser Arg Leu
        35                  40                  45


Gly Gly His Tyr Ala Gly Ala Trp Leu Asn Glu Gly Ala Thr Glu Leu
    50                  55                  60


Val Val Ala Val Thr Asp Ala Ala Gln Ala Lys Val Val Glu Asp Ala
65                  70                  75                  80


Gly Ala Thr Pro Lys Val Val Gln Arg Ser Gln Ile Gln Leu Asp Glu
                85                  90                  95


Leu Lys Ala Lys Leu Asp Ala Asn Lys Asn Ala Pro Lys Asp Val Pro
            100                 105                 110


Ala Trp Tyr Val Asp Val Lys Thr Asn Ser Val Val Val Leu Ala Arg
        115                 120                 125


Asn Thr Ala Ser Ala Lys Ala Phe Ala Arg Ala Ser Gly Leu Ser Glu
    130                 135                 140


Ala Asp Val Arg Ile Glu Gln Ser Thr Glu Asp Pro Arg Pro Leu Ile
```

```
145                 150                 155                 160

Asp Val Ile Gly Gly Asn Ala Tyr Tyr Met Gly Ser Gly Gly Arg Cys
                165                 170                 175

Ser Val Gly Phe Ser Val Asn Gly Gly Phe Val Thr Ala Gly His Cys
            180                 185                 190

Gly Arg Val Gly Thr Thr Thr Thr Gln Pro Ser Gly Thr Phe Ala Gly
        195                 200                 205

Ser Thr Phe Pro Gly Arg Asp Tyr Ala Trp Val Arg Val Ser Ser Gly
    210                 215                 220

Asn Thr Met Arg Gly Leu Val Asn Arg Tyr Pro Gly Thr Val Pro Val
225                 230                 235                 240

Lys Gly Ser Asn Glu Ser Ser Val Gly Ala Ser Val Cys Arg Ser Gly
                245                 250                 255

Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Gln Lys Asn Thr Ser
            260                 265                 270

Val Thr Tyr Pro Glu Gly Thr Ile Ser Gly Val Thr Arg Thr Asn Ala
        275                 280                 285

Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Trp Leu Thr Gly Asp Gln
    290                 295                 300

Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ser Gly Gly
305                 310                 315                 320

Thr Thr Tyr Phe Gln Pro Val Asn Pro Ile Leu Gln Ala Tyr Gly Leu
                325                 330                 335

Gln Leu Val Ile Glu Gly Gly Pro Thr Gly Thr Thr Gly Pro Thr Thr
            340                 345                 350

Thr Ser Ser Asn Pro Gly Gly Thr Thr Trp Gln Pro Gly Val Ala Tyr
```

```
        355                 360                 365


Thr Ala Gly Thr Thr Val Thr Tyr Glu Gly Val Gly Tyr Glu Cys Leu
    370                 375                 380


Gln Gly His Thr Ser Gln Ile Gly Trp Glu Pro Ser Ala Val Pro Ala
385                 390                 395                 400


Leu Trp Glu Arg Val Gly
                405


<210>  57
<211>  346
<212>  PRT
<213>  Nocardiopsis baichengensis

<400>  57

Asp Ala Phe Pro Glu Gly Thr Glu Pro Leu Ala Glu Ala Ile Glu Arg
1               5                   10                  15


Asp Leu Gly Val Ala Ser Gly Gln Ala Asp Glu Leu Leu Thr Ala Glu
            20                  25                  30


Glu Ser Ala Arg Ser Leu Glu Lys Glu Ala Glu Lys Ala Ala Gly Glu
        35                  40                  45


Ala Phe Ala Gly Ala Val Phe Asp Thr Glu Thr His Glu Leu Thr Val
    50                  55                  60


Ser Val Ala Asp Pro Ser Ala Val Glu Ala Val Glu Ala Thr Gly Ala
65                  70                  75                  80


Glu Thr Arg Val Val Glu Ala Ser Gln Asp Glu Leu Asp Ala Ala Met
                85                  90                  95


Ala Asp Leu Asp Ala Ala Ser Glu Asp Gly Val Ser Glu Glu Val Thr
            100                 105                 110


Gly Trp His Val Asp Leu Glu Ser Asn Thr Val Val Val Glu Ala Leu
        115                 120                 125
```

```
Glu Gly Ser Glu Asp Ala Ala Glu Asp Leu Ile Ala Asp Ala Gly Leu
    130                 135                 140


Asp Ser Ala Pro Val Val Val Glu Lys Ala Asp Ala Gln Pro Glu Thr
145                 150                 155                 160


Phe Gly Ala Ile Val Gly Gly Asp Ala Tyr Tyr Pro Gly Asn Ser Arg
                165                 170                 175


Cys Ser Ile Gly Phe Ser Val Arg Gly Gly Phe Val Thr Ala Gly His
            180                 185                 190


Cys Gly Ser Thr Gly Thr Ser Val Ser Gly Ser Ala Gly Glu Ser Gly
        195                 200                 205


Arg Val Ala Gly Ser Val Phe Pro Gly Arg Asp Met Gly Tyr Val Arg
    210                 215                 220


Ala Asn Ser Gly Trp Thr Pro Ser Pro Tyr Val Asn Asn Tyr Arg Gly
225                 230                 235                 240


Gly Arg Val Ala Val Arg Gly Ser Asn Glu Ala Ser Val Gly Ala Ser
                245                 250                 255


Val Cys Arg Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln
            260                 265                 270


Ala Lys Asn Gln Thr Val Asn Tyr Pro Gln Gly Thr Val Arg Gly Leu
        275                 280                 285


Thr Arg Thr Thr Ala Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Trp
    290                 295                 300


Leu Ser Gly Asn Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn
305                 310                 315                 320


Cys Ser Trp Gly Gly Thr Thr Phe Phe Gln Pro Val Asn Pro Ile Leu
                325                 330                 335
```

```
Ser Gln Trp Gly Leu Ser Leu Thr Thr Thr
            340                 345


<210>  58
<211>  353
<212>  PRT
<213>  Streptomyces sp.

<400>  58

Asn Asp Thr Leu Thr Glu Arg Ala Asp Ala Ala Val Ala Glu Leu Pro
1               5                   10                  15


Ala Gly Val Leu Asp Ala Met Glu Arg Asp Leu Gly Leu Ser Glu Gln
            20                  25                  30


Glu Ala Gly Leu Gln Leu Val Ala Gln Tyr Asp Ala Ser Leu Leu Gly
        35                  40                  45


Glu Thr Leu Ser Ala Asp Leu Asp Ala Tyr Ala Gly Ser Trp Leu Ala
    50                  55                  60


Asp Gly Thr Asp Leu Val Val Ala Thr Thr Asp Arg Ala Glu Ala Ala
65                  70                  75                  80


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


Thr Glu Leu Glu Ser Val Lys Ala Ala Leu Asp Glu Ala Ala Glu Ser
            100                 105                 110


Tyr Asp Thr Thr Asp Ala Pro Val Trp Tyr Val Asp Ile Thr Thr Asn
        115                 120                 125


Asp Val Val Leu Leu Thr Ser Asp Thr Ala Glu Ala Lys Gly Phe Val
    130                 135                 140


Glu Ala Ala Gly Val Asp Ala Gly Ala Val Ser Ile Gln Thr Ser Asp
145                 150                 155                 160
```

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


Met Gly Gly Gly Arg Cys Ser Val Gly Phe Ser Val Thr Gln Gly Ser
            180                 185                 190


Thr Pro Gly Phe Ala Thr Ala Gly His Cys Gly Thr Val Gly Thr Ser
        195                 200                 205


Thr Thr Gly Phe Asn Gln Ala Ala Gln Gly Thr Phe Glu Glu Ser Ser
    210                 215                 220


Phe Pro Gly Asp Asp Met Ala Trp Val Ser Val Asn Ser Asn Trp Asn
225                 230                 235                 240


Thr Thr Pro Thr Val Asn Asp Gly Ala Val Thr Val Ser Gly Ser Thr
                245                 250                 255


Gln Gly Ala Val Gly Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly
            260                 265                 270


Trp His Cys Gly Thr Ile Glu Gln His Asn Thr Ser Val Thr Tyr Pro
        275                 280                 285


Glu Gly Thr Ile Thr Gly Val Thr Arg Thr Ser Val Cys Ala Glu Pro
    290                 295                 300


Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Ser Gln Ala Gln Gly Val
305                 310                 315                 320


Thr Ser Gly Gly Ser Gly Asn Cys Thr Ser Gly Gly Thr Thr Tyr His
                325                 330                 335


Gln Pro Ile Asn Pro Leu Leu Ser Ala Tyr Gly Leu Asp Leu Val Thr
            340                 345                 350


Gly
```

```
<210>  59
<211>  353
<212>  PRT
<213>  Actinoalloteichus spitiensis

<400>  59

Asp Thr Pro Ser Pro Asp Gly Ala Asp Ala Thr Val Ala Ser Pro Glu
1               5                   10                  15


Met Leu Ser Ala Met Gln Arg Asp Leu Gly Leu Thr Glu Gln Glu Ala
            20                  25                  30


Leu Thr Arg Val Ala Val Glu Ala Thr Ala Val Glu Thr Glu Asp Glu
        35                  40                  45


Leu Arg Ala Ser Leu Gly Pro Ala Phe Gly Gly Ala His Phe Asp Gly
    50                  55                  60


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


Glu Val Arg Ala Ala Gly Ala Thr Pro Glu Val Val Ala Phe Ser Ala
                85                  90                  95


Asp Thr Leu Asp Gly Val Val Ser Thr Leu Asn Glu Thr Ser Glu Val
            100                 105                 110


Pro Asp Gly Val Thr Gly Trp Tyr Val Asp Thr Ala Asp Asn Thr Val
        115                 120                 125


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


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


Glu Gln Pro Arg Thr Leu Tyr Asp Ile Ile Gly Gly Asp Ala Tyr Tyr
                165                 170                 175
```

```
Phe Gly Gly Ser Arg Cys Ser Val Gly Phe Ser Val Ser Val Gly Tyr
            180                 185                 190


Val Thr Ala Gly His Cys Gly Gly Val Gly Thr Ala Thr Gln Gly Tyr
        195                 200                 205


Asn Arg Val Ser Ser Gly Gln Val Ala Gly Ser Val Phe Pro Gly Ser
    210                 215                 220


Asp Met Gly Tyr Val Arg Thr Asn Ala Asn Trp Thr Pro Arg Pro Leu
225                 230                 235                 240


Val Asn Arg Tyr Ser Gly Gly Ala Thr Val Thr Val Ser Gly Ser Asn
                245                 250                 255


Glu Ala Ala Val Gly Ala Ser Ile Cys Arg Ser Gly Ser Thr Thr Gly
            260                 265                 270


Trp Arg Cys Gly Thr Val Gln Ala Lys Asn Gln Thr Val Phe Tyr Ala
        275                 280                 285


Gln Gly Ala Val Ser Gly Leu Thr Arg Thr Asn Ala Cys Ala Glu Gly
    290                 295                 300


Gly Asp Ser Gly Gly Ser Trp Leu Ser Gly Ser Gln Ala Gln Gly Val
305                 310                 315                 320


Thr Ser Gly Gly Ser Gly Asn Cys Thr Trp Gly Gly Thr Thr Tyr Phe
                325                 330                 335


Gln Pro Leu Asn Pro Ile Leu Ser Arg Trp Gly Leu Ser Leu Thr Arg
            340                 345                 350


Gly



<210>  60
<211>  338
<212>  PRT
<213>  Byssochlamys verrucosa
```

```
<400>  60

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


Thr Leu Ser Gln Val Ser Asn Thr Leu Ile Lys Ala Val Val Gln Asn
            20                  25                  30


Thr Gly Arg Gly Glu Val Ser Phe Ile His Leu Asn Phe Phe Lys Asp
        35                  40                  45


Asp Ala Pro Val Lys Lys Val Ala Val Tyr Arg Asn Gly Ser Glu Val
    50                  55                  60


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


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


Asp Ile Ala Ser Thr Cys Asp Leu Ile Ser Gly Gly Pro Val Thr Ile
            100                 105                 110


Arg Ser Glu Gly Val Val Pro Tyr Ala Thr Ala Asn Gly Ile Asp Ile
        115                 120                 125


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


Gly Ala Ile Ala Ser Thr Val Ser Lys Ala Ile Ala Pro Leu Asn Arg
145                 150                 155                 160


Arg Thr Asn Ile Ser Ser Cys Ser Gly Ser Glu Gln Ser Thr Leu Thr
                165                 170                 175


Met Ala Leu Lys Asn Ala Ala Ser Leu Ala His Ala Ala Ala Asp Ala
            180                 185                 190


Ala Glu Ser Gly Ser Ala Ser Lys Phe Ser Glu Tyr Phe Lys Thr Thr
```

```
        195                 200                 205

Ala Ser Ser Thr Arg Lys Thr Val Ala Ala Arg Leu Arg Ala Val Ala
    210                 215                 220

Gln Glu Ala Ser Ser Ser Ser Ser Gly Ser Thr Thr Tyr Tyr Cys Asn
225                 230                 235                 240

Asp Ala Tyr Gly Tyr Cys Thr Thr Asn Val Leu Ala Tyr Thr Leu Pro
                245                 250                 255

Ser His Asn Thr Ile Ala Thr Cys Asp Leu Tyr Tyr Thr Asn Leu Ser
            260                 265                 270

Ala Leu Thr Arg Thr Cys His Ala Gln Asp Gln Ala Thr Thr Ser Leu
        275                 280                 285

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

Leu Ala Tyr Gly Tyr Ala Ser Ser Thr Ser Leu Ser Ser Ser Gln Ala
305                 310                 315                 320

Val Met Asn Ala Asp Ser Tyr Ala Leu Tyr Ala Asn Ala Ile Tyr Val
                325                 330                 335

Gly Cys



<210>  61
<211>  339
<212>  PRT
<213>  Hamigera terricola

<400>  61

Ser Pro Val Asn Val Asn Val Gly Arg Glu Glu Leu Pro Ala Leu Asp
1               5                   10                  15

Val Thr Leu Ser Gln Ile Gly Asn Thr Gln Ile Lys Ala Val Val Lys
            20                  25                  30
```

```
Asn Thr Gly Ser Glu Asp Val Thr Phe Met His Leu Asn Phe Phe Thr
        35                  40                  45


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


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


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


Phe Asp Ile Ala Thr Thr Thr Asp Leu Ala Ser Gly Gly Ala Val Thr
            100                 105                 110


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


Val Thr Gly Tyr Ala Arg Tyr Thr Ser Asn Glu Leu His Leu Asp Val
    130                 135                 140


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


Arg Arg Thr Arg Leu Ser Ser Cys Ser Gly Ser Arg Ser Ser Ala Leu
                165                 170                 175


Gln Thr Ala Leu Arg Asn Thr Val Ser Leu Ala Asn Ala Ala Ala Asn
            180                 185                 190


Ala Ala Arg Ser Gly Ser Ala Ser Lys Phe Ser Glu Tyr Phe Lys Thr
        195                 200                 205


Thr Ser Ser Ser Val Arg Ser Thr Val Ala Ala Arg Leu Ser Ala Val
    210                 215                 220


Ala Ser Glu Ala Ser Ser Thr Ser Ser Gly Ser Thr Thr Tyr Tyr Cys
225                 230                 235                 240
```

```
Asn Asp Pro Tyr Gly Tyr Cys Ser Thr Asp Val Leu Ala Tyr Thr Leu
                245                 250                 255


Pro Ser Tyr Asn Ile Ile Ala Asn Cys Asp Ile Tyr Tyr Ser Tyr Leu
            260                 265                 270


Pro Ala Leu Thr Gly Ser Cys His Ala Gln Asp Gln Ala Thr Thr Thr
        275                 280                 285


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


Asp Tyr Gly Tyr Gly Tyr Asn Ala Ala Thr Ser Leu Ser Ser Ser Gln
305                 310                 315                 320


Ala Val Leu Asn Ala Asp Ser Tyr Ala Leu Tyr Ala Asn Ala Ile Tyr
                325                 330                 335


Leu Gly Cys



<210>  62
<211>  334
<212>  PRT
<213>  Aspergillus tamarii

<400>  62

Ile Pro Val Glu Val Pro Ala Ser Ala Pro Gly Leu Asp Val Thr Leu
1               5                   10                  15


Ser Gln Val Gly Asn Thr Arg Ile Lys Ala Val Val Lys Asn Thr Gly
            20                  25                  30


Ser Glu Glu Val Thr Phe Val His Leu Asn Phe Phe Lys Asp Ala Ala
        35                  40                  45


Pro Val Gln Lys Val Ser Leu Phe Arg Asn Ala Thr Glu Val Gln Phe
    50                  55                  60
```

```
Gln Gly Ile Lys Gln Arg Leu Ile Thr Glu Gly Leu Ser Asp Glu Ala
65                  70                  75                  80


Leu Thr Thr Leu Ala Pro Gly Ala Thr Ile Glu Asp Glu Phe Asp Ile
                85                  90                  95


Ala Ser Thr Ser Asp Leu Ser Glu Gly Gly Thr Ile Thr Ile Asn Ser
            100                 105                 110


Asn Gly Leu Val Pro Ile Thr Thr Glu Asn Lys Val Thr Gly Tyr Ile
        115                 120                 125


Pro Phe Ala Ser Asn Glu Leu Ser Ile Asp Val Asp Ala Ala Glu Ala
    130                 135                 140


Ala Thr Val Ser Gln Ala Val Lys Ile Leu Asp Arg Arg Thr Lys Val
145                 150                 155                 160


Thr Ser Cys Ser Gly Ser Arg Ser Ser Ala Leu Gln Thr Ala Leu Arg
                165                 170                 175


Asn Thr Val Ser Leu Ala Arg Ala Ala Ala Ser Ala Ala Gln Ser Gly
            180                 185                 190


Ser Ser Ser Arg Phe Gln Glu Tyr Phe Lys Thr Thr Ser Ser Ser Thr
        195                 200                 205


Arg Ser Thr Val Ala Ala Arg Leu Asn Ala Val Ala Asn Glu Ala Ala
    210                 215                 220


Ser Thr Ala Ser Gly Ser Thr Thr Tyr Tyr Cys Ser Asp Val Tyr Gly
225                 230                 235                 240


Tyr Cys Ser Ser Asn Val Leu Ala Tyr Thr Leu Pro Ala Tyr Asn Ile
                245                 250                 255


Ile Ala Asn Cys Asp Leu Tyr Tyr Ser Tyr Leu Pro Ala Leu Thr Ser
            260                 265                 270
```

```
Thr Cys His Ala Gln Asp Gln Ala Thr Thr Thr Leu His Glu Phe Thr
        275                 280                 285


His Ala Pro Gly Val Tyr Ser Pro Gly Thr Asp Asp Leu Gly Tyr Gly
    290                 295                 300


Tyr Ser Ala Ala Thr Ala Leu Ser Ala Ser Gln Ala Leu Leu Asn Ala
305                 310                 315                 320


Asp Thr Tyr Ala Leu Phe Ala Asn Ala Val Asn Leu Asn Cys
                325                 330


<210>  63
<211>  334
<212>  PRT
<213>  Aspergillus niveus

<400>  63

Leu Pro Ala Lys Thr Gly Glu Gln Leu Gln Lys Leu Asp Val Ala Leu
1               5                   10                  15


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


Ser Glu Asp Ile Thr Phe Val His Leu Asn Phe Phe Arg Asp Thr Ala
        35                  40                  45


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


His Gly Ile Lys Gln Arg Leu Arg Ser Asp Gly Leu Ser Ala Asp Ala
65                  70                  75                  80


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


Ala Ala Thr Ser Asp Leu Ser Glu Gly Gly Ser Ile Thr Ile Ser Ala
            100                 105                 110
```

```
Asp Gly Phe Val Pro Ile Ala Ser Gly Asn Lys Ile Thr Gly Tyr Val
        115                 120                 125


Pro Phe Ser Ser Asn Glu Leu Ser Val Glu Val Asp Ala Ala Gln Ala
    130                 135                 140


Ala Ser Val Ala Ser Ala Val Lys Pro Leu Asp Arg Arg Thr Lys Val
145                 150                 155                 160


Ala Ser Cys Ser Gly Ser Arg Ser Ser Ala Leu Thr Gln Ala Leu Arg
                165                 170                 175


Asn Thr Val Ser Leu Ala Asn Ala Ala Ala Ser Ala Ala Gln Ser Gly
            180                 185                 190


Ser Ser Thr Arg Phe Gln Glu Tyr Phe Lys Thr Thr Ser Ser Ser Val
        195                 200                 205


Arg Ser Ser Val Ala Ala Arg Phe Arg Ala Val Ala Ser Glu Ala Ser
    210                 215                 220


Ser Thr Ser Ala Gly Ser Thr Thr Tyr Tyr Cys Thr Asp Val Tyr Gly
225                 230                 235                 240


Tyr Cys Ser Ser Asn Val Leu Ala Tyr Thr Leu Pro Ala Tyr Asn Ile
                245                 250                 255


Ile Ala Asn Cys Asp Ile Tyr Tyr Thr Tyr Leu Pro Ala Leu Thr Ser
            260                 265                 270


Thr Cys His Ala Gln Asp Gln Ala Thr Thr Thr Leu His Glu Phe Thr
        275                 280                 285


His Ala Pro Gly Val Tyr Ser Pro Gly Thr Asp Asp Leu Gly Tyr Gly
    290                 295                 300


Tyr Asp Ala Ala Thr Ala Leu Ser Ser Ser Gln Ala Leu Asn Asn Ala
305                 310                 315                 320
```

```
Asp Ser Tyr Ala Leu Phe Ala Asn Ala Val Asn Leu Asn Cys
                325                 330


<210>  64
<211>  372
<212>  PRT
<213>  Penicillium sclerotiorum

<400>  64

Ile Pro Thr Gly Gly Lys Lys Ser Ser Phe Ser Val Asp Gln Val Ala
1               5                   10                  15


Ile Pro Ala Thr Lys Thr Lys Asn Phe Ala Asp Thr Tyr Ala Arg Ala
            20                  25                  30


Ile Ser Lys Phe Gly Gly Asn Val Pro Ser His Val Arg Ala Ala Ala
        35                  40                  45


Gln Gln Ser Gly Ala Ala Thr Thr Thr Pro Glu Ala Asn Asp Glu Glu
    50                  55                  60


Tyr Leu Thr Pro Val Asn Val Gly Gly Thr Thr Leu Asn Leu Asp Phe
65                  70                  75                  80


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


Ser Glu Gln Ser Gly His Ser Val Tyr Lys Pro Asn Asn Gly Thr Lys
            100                 105                 110


Leu Ser Gly Ala Thr Trp Ser Ile Ser Tyr Gly Asp Gly Ser Ser Ala
        115                 120                 125


Ser Gly Asp Val Tyr Lys Asp Thr Val Ser Val Gly Pro Val Lys Ala
    130                 135                 140


Thr Gly Gln Ala Val Glu Ala Ala Ser Lys Ile Ser Ala Gln Phe Thr
145                 150                 155                 160


Arg Asp Ser Asn Asn Asp Gly Leu Leu Gly Leu Ala Phe Ser Ser Ile
```

```
                165                 170                 175

Asn Thr Val Lys Pro Lys Ala Gln Thr Thr Phe Phe Asp Thr Val Lys
            180                 185                 190

Ser Ser Leu Ala Ser Pro Leu Phe Ala Val Thr Leu Lys His Asn Ala
        195                 200                 205

Pro Gly Thr Tyr Asp Phe Gly Phe Val Asp Ser Ser Lys Tyr Thr Gly
    210                 215                 220

Ser Leu Ala Tyr Thr Asp Val Asp Asn Ser Gln Gly Phe Trp Glu Phe
225                 230                 235                 240

Thr Ala Asp Ser Tyr Lys Val Gly Ser Gln Ser Gly Ser Ser Ile Lys
                245                 250                 255

Gly Ile Ala Asp Thr Gly Thr Thr Leu Leu Leu Leu Asp Asp Glu Val
            260                 265                 270

Val Ser Ala Tyr Tyr Lys Gln Val Ser Gly Ala Ser Asp Ser Gln Ser
        275                 280                 285

Ala Gly Gly Tyr Thr Phe Asp Cys Ser Ala Asp Leu Pro Asp Phe Thr
    290                 295                 300

Val Thr Ile Ser Gly Tyr Asp Ala Val Val Pro Gly Ser Leu Ile Asn
305                 310                 315                 320

Tyr Ala Pro Val Ser Asp Gly Ser Ser Thr Cys Leu Gly Gly Ile Gln
                325                 330                 335

Ser Asn Ser Gly Ile Gly Phe Ser Ile Phe Gly Asp Ile Phe Leu Lys
            340                 345                 350

Ser Gln Tyr Val Val Phe Asp Ser Asn Gly Pro Arg Leu Gly Phe Ala
        355                 360                 365

Ala Gln Ser Ser
```

```
    370


<210>  65
<211>  371
<212>  PRT
<213>  Penicillium bilaiae

<400>  65

Val Pro Thr Gly Gly Lys Lys Ser Phe Ser Ile Asn Gln Val Ala Ile
1               5                   10                  15


Pro Ala Thr Lys Thr Lys Asn Phe Ala Gly Asn Tyr Ala His Ala Ile
            20                  25                  30


Ala Lys Tyr Gly Gly Asn Val Pro Ser His Val Glu Ala Ala Ala Gln
        35                  40                  45


Gln Ser Gly Ala Ala Thr Thr Thr Pro Glu Ser Asn Asp Glu Glu Tyr
    50                  55                  60


Leu Thr Pro Val Asn Val Gly Gly Thr Thr Leu Asn Leu Asp Phe Asp
65                  70                  75                  80


Thr Gly Ser Ala Asp Leu Trp Val Phe Ser Ala Glu Leu Pro Ser Ala
                85                  90                  95


Glu Gln Ser Gly His Ala Leu Tyr Lys Pro Ser Asn Gly Thr Lys Leu
            100                 105                 110


Ser Gly Ala Ser Trp Ser Ile Ser Tyr Gly Asp Gly Ser Ser Ala Ser
        115                 120                 125


Gly Asp Val Tyr Lys Asp Thr Val Ser Val Gly Ser Val Lys Ala Thr
    130                 135                 140


Gly Gln Ala Val Glu Ala Ala Ser Lys Ile Ser Ala Gln Phe Thr Lys
145                 150                 155                 160


Asp Lys Asn Asn Asp Gly Leu Leu Gly Leu Ala Phe Ser Ser Ile Asn
                165                 170                 175
```

```
Thr Val Lys Pro Lys Ala Gln Thr Thr Phe Phe Asp Thr Val Lys Ser
            180                 185                 190


Ser Leu Ala Ser Pro Leu Phe Ala Val Thr Leu Lys His Asn Ala Pro
        195                 200                 205


Gly Thr Tyr Asp Phe Gly Phe Ile Asp Lys Ser Lys Tyr Thr Gly Ser
    210                 215                 220


Leu Ala Tyr Ala Asp Val Asp Asn Ser Gln Gly Phe Trp Glu Phe Thr
225                 230                 235                 240


Ala Asp Ser Tyr Ser Val Gly Ser Ser Lys Gly Ser Ser Ile Lys Gly
                245                 250                 255


Ile Ala Asp Thr Gly Thr Thr Leu Leu Leu Leu Asp Asp Glu Val Val
            260                 265                 270


Ser Ala Tyr Tyr Lys Gln Val Gln Gly Ala Gln Gln Asp Ser Ser Ala
        275                 280                 285


Gly Gly Tyr Thr Phe Asp Cys Ser Ser Lys Leu Pro Asp Phe Thr Val
    290                 295                 300


Thr Ile Ser Gly Tyr Asp Ala Val Val Pro Gly Asp Leu Ile Asn Phe
305                 310                 315                 320


Ala Pro Ala Ser Glu Gly Ser Ser Thr Cys Leu Gly Gly Ile Gln Ser
                325                 330                 335


Asn Ser Gly Ile Gly Phe Ser Ile Phe Gly Asp Ile Phe Leu Lys Ser
            340                 345                 350


Gln Tyr Val Val Phe Asp Ser Asn Gly Pro Arg Leu Gly Phe Ala Ala
        355                 360                 365


Gln Ser Ser
    370
```

```
<210>  66
<211>  373
<212>  PRT
<213>  Penicillium antarticum

<400>  66

Ser Pro Leu Val Thr Pro Arg Lys Gly Phe Thr Ile Asn Gln Glu Thr
1               5                   10                  15


Arg Ala Val Thr Lys Ser Lys Thr Val Asn Leu Pro Gly Val Tyr Ala
            20                  25                  30


Gln Ala Leu Ser Lys Tyr Gly Ala Thr Val Pro Gln His Val His Ala
        35                  40                  45


Ala Ala Val Ser Gly Ser Ala Val Thr Thr Pro Glu Glu Ser Asp Val
    50                  55                  60


Glu Tyr Leu Thr Pro Val Asn Val Gly Gly Thr Thr Leu Asn Leu Asp
65                  70                  75                  80


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


Ser Ser Gln Gln Ser Gly His Ser Ile Tyr Lys Pro Ser Ser Ser Ala
            100                 105                 110


Thr Lys Leu Ser Gly Ser Ser Trp Ser Ile Ser Tyr Gly Asp Gly Ser
        115                 120                 125


Ser Ala Ser Gly Asp Val Tyr Lys Asp Thr Val Thr Val Gly Gly Val
    130                 135                 140


Lys Ala Thr Gly Gln Ala Val Glu Ala Ala Ser Lys Ile Ser Ser Ala
145                 150                 155                 160


Phe Leu Gln Asp Val Asn Asn Asp Gly Leu Leu Gly Leu Ala Phe Ser
                165                 170                 175
```

```
Ser Ile Asn Thr Val Ser Pro Arg Ala Gln Thr Thr Phe Phe Asp Thr
            180                 185                 190

Val Lys Ser Gln Leu Asp Ser Pro Leu Phe Ala Val Thr Leu Lys His
        195                 200                 205

Asn Ala Pro Gly Ser Tyr Asp Phe Gly Tyr Ile Asp Lys Ser Lys Tyr
    210                 215                 220

Thr Gly Ser Leu Thr Tyr Ala Asn Val Asp Asp Ser Gln Gly Phe Trp
225                 230                 235                 240

Ser Phe Thr Ala Ser Ser Tyr Lys Ile Gly Thr Thr Thr Gly Gly Ser
                245                 250                 255

Ile Thr Gly Ile Ala Asp Thr Gly Thr Thr Leu Leu Leu Leu Pro Asp
            260                 265                 270

Ser Val Val Ser Ala Tyr Tyr Lys Lys Val Ser Gly Ser Gln Asn Ser
        275                 280                 285

Asn Tyr Tyr Gly Gly Tyr Val Phe Pro Cys Ser Ala Thr Leu Pro Asp
    290                 295                 300

Phe Thr Val Thr Ile Asn Gly Tyr Asn Ala Val Val Pro Gly Asn Leu
305                 310                 315                 320

Ile Asn Phe Ala Gln Ala Thr Thr Gly Ser Ser Thr Cys Tyr Gly Gly
                325                 330                 335

Ile Gln Ser Asn Ser Gly Ile Gly Phe Ser Ile Phe Gly Asp Ile Phe
            340                 345                 350

Leu Lys Ser Gln Tyr Val Val Phe Asp Ser Glu Gly Pro Arg Leu Gly
        355                 360                 365

Phe Ala Ala Gln Ala
    370
```

```
<210>  67
<211>  370
<212>  PRT
<213>  Penicillium sumatrense

<400>  67

Val Pro Thr Asn Asn Val Ala Ser Lys Phe Ser Val Asn Gln Val Ser
1               5                   10                  15


Arg Pro Ala Thr Lys Thr Thr Asn Phe Ala Ala Asn Tyr Gly Arg Ala
            20                  25                  30


Leu Ser Lys Tyr Gly Ala Gly Val Pro Ser His Val Glu Ala Ala Ala
        35                  40                  45


Ala Ala Ser Gly Ser Ala Val Thr Thr Pro Glu Ser Asn Asp Val Glu
    50                  55                  60


Tyr Leu Thr Pro Val Ser Ile Gly Gly Thr Thr Leu Asn Leu Asp Phe
65                  70                  75                  80


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


Ser Glu Gln Ser Gly His Ser Val Tyr Asn Pro Ser Lys Ser Gly Lys
            100                 105                 110


Lys Ile Ser Gly Ala Ser Trp Asp Ile Ser Tyr Gly Asp Gly Ser Gly
        115                 120                 125


Ala Ser Gly Asp Val Tyr Thr Asp Thr Val Thr Val Gly Gly Val Thr
    130                 135                 140


Ala Ser Lys Gln Ala Val Glu Ala Ala Lys Gln Ile Ser Ser Gln Phe
145                 150                 155                 160


Gln Gln Asp Thr Asp Asn Asp Gly Leu Leu Gly Leu Ala Phe Ser Ser
                165                 170                 175
```

```
Ile Asn Thr Val Ser Pro Thr Pro Gln Lys Thr Phe Phe Asp Asn Val
            180                 185                 190


Lys Ser Ser Leu Ser Gln Pro Leu Phe Ala Val Ala Leu Lys His Asn
        195                 200                 205


Ala Pro Gly Val Tyr Asp Phe Gly Phe Ile Asp Ser Ser Lys His Thr
    210                 215                 220


Gly Ser Ile Ala Tyr Thr Ser Val Asp Ser Ser Gln Gly Phe Trp Ser
225                 230                 235                 240


Phe Thr Val Asp Gly Tyr Lys Val Gly Ser Lys Ser Gly Ala Gly Phe
                245                 250                 255


Asp Gly Ile Ala Asp Thr Gly Thr Thr Leu Leu Leu Leu Asp Asp Ser
            260                 265                 270


Val Val Ser Ala Tyr Tyr Ser Gln Val Ser Gly Ala Lys Asn Asp Asn
        275                 280                 285


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


Ser Val Thr Ile Gly Ser Tyr Thr Ala Thr Val Pro Gly Ser Leu Ile
305                 310                 315                 320


Asn Tyr Gly Asp Ser Gly Asp Asn Ser Cys Ile Gly Gly Ile Gln Ser
                325                 330                 335


Asn Ser Gly Ile Gly Phe Ser Ile Phe Gly Asp Ile Phe Leu Lys Ser
            340                 345                 350


Gln Tyr Val Val Phe Asn Ala Asn Gly Pro Lys Leu Gly Phe Ala Pro
        355                 360                 365


Gln Ala
    370
```

```
<210>  68
<211>  384
<212>  PRT
<213>  Trichoderma lixii

<400>  68

Leu Pro Thr Glu Gly Gln Lys Thr Ala Ser Ile Glu Val Thr Tyr Asn
1               5                   10                  15


Lys Asn Tyr Val Ala His Gly Pro Thr Ala Leu Phe Lys Ala Lys Arg
            20                  25                  30


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


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


Ser Asp Ser Ala Asp Asp Glu Tyr Ile Thr Ser Val Ser Ile Gly Thr
65                  70                  75                  80


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


Trp Val Phe Ser Ser Glu Thr Pro Lys Ser Ser Ala Ser Gly His Val
            100                 105                 110


Thr Tyr Ser Pro Ser Lys Ser Ser Thr Ala Lys Lys Leu Ser Gly Ser
        115                 120                 125


Thr Trp Ser Ile Thr Tyr Gly Asp His Ser Ser Ser Ser Gly Asp Val
    130                 135                 140


Tyr Thr Asp Val Val Ser Ile Gly Gly Phe Ser Val Lys Thr Gln Ala
145                 150                 155                 160


Ile Glu Ser Ala Thr Lys Val Ser Thr Gln Phe Val Gln Asp Thr Val
                165                 170                 175


Ile Ser Gly Leu Val Gly Leu Gly Phe Asp Val Gly Asn Thr Val Lys
```

```
            180                 185                 190

Pro Arg Ala Gln Lys Thr Trp Phe Ser Asn Ala Ala Ser Ser Leu Ala
        195                 200                 205

Glu Pro Leu Phe Thr Ala Asp Leu Arg His Gln Glu Thr Gly Ser Tyr
    210                 215                 220

Asn Phe Gly Phe Ile Asp Asn Ser Leu Ala Lys Gly Thr Ile Gly Tyr
225                 230                 235                 240

Thr Pro Ala Asp Gly Ser Glu Gly Tyr Trp Gly Phe Thr Ala Thr Gly
                245                 250                 255

Tyr Ser Val Gly Gly Ala Lys Leu Gly Arg Ser Ser Ile Thr Gly Ile
            260                 265                 270

Ala Asp Thr Gly Thr Thr Leu Leu Leu Leu Pro Asp Asn Val Val Asp
        275                 280                 285

Ala Tyr Tyr Asn Asn Val Glu Ser Ala Gln Tyr Asp Asp Ser Gln Glu
    290                 295                 300

Gly Val Val Phe Asp Cys Ser Glu Asp Leu Pro Ser Phe Ser Phe Gly
305                 310                 315                 320

Val Gly Gly Gln Thr Ile Thr Ile Ser Gly Asp Leu Leu Asn Leu Thr
                325                 330                 335

Pro Ile Glu Glu Gly Ser Ser Thr Cys Phe Gly Gly Leu Gln Ser Ser
            340                 345                 350

Ala Asp Ile Gly Ile Asn Ile Phe Gly Asp Val Ala Leu Lys Ala Ala
        355                 360                 365

Leu Val Val Phe Asp Leu Gly Asn Glu Arg Leu Gly Phe Ala Gln Lys
    370                 375                 380

<210>  69
```

```
<211>  384
<212>  PRT
<213>  Trichoderma brevicompactum

<400>  69

Leu Pro Thr Glu Gly Gln Lys Thr Ala Ser Val Glu Val Thr Tyr Asn
1               5                   10                  15


Gln Asn Tyr Ala Ala His Gly Pro Thr Gln Leu Tyr Lys Ala Lys Arg
            20                  25                  30


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


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


Ser Asp Ser Ala Asp Asp Glu Tyr Ile Thr Asn Val Ser Ile Gly Thr
65                  70                  75                  80


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


Trp Val Phe Ser Ser Glu Thr Pro Lys Ser Ser Ala Ser Gly His Thr
            100                 105                 110


Ile Tyr Thr Pro Ser Lys Ser Ser Thr Ser Lys Lys Leu Ser Gly Ala
        115                 120                 125


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


Tyr Thr Asp Lys Val Thr Val Gly Gly Phe Ser Val Ser Thr Gln Ala
145                 150                 155                 160


Val Glu Ser Ala Thr Lys Val Ser Ala Gln Phe Val Gln Asp Thr Ala
                165                 170                 175


Asn Ser Gly Leu Leu Gly Leu Ala Phe Asp Ser Ile Asn Thr Val Ser
            180                 185                 190
```

```
Pro Arg Gln Gln Lys Thr Trp Phe Ser Asn Ala Ala Asn Ser Leu Ala
        195                 200                 205


Gln Pro Leu Phe Thr Ala Asn Leu Asn His Gln Ala Thr Gly Ser Tyr
    210                 215                 220


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


Val Pro Val Asp Asn Ser Gln Gly Phe Trp Gly Phe Thr Ala Ser Gly
                245                 250                 255


Tyr Ser Val Gly Gly Gly Lys Leu Asn Arg Ser Ser Leu Ser Gly Ile
            260                 265                 270


Ala Asp Thr Gly Thr Thr Leu Leu Leu Leu Pro Asp Ala Val Val Asn
        275                 280                 285


Ala Tyr Tyr Ala Asn Val Glu Ser Ala Glu Tyr Asp Asp Glu Gln Glu
    290                 295                 300


Gly Val Val Phe Asp Cys Ser Glu Asp Leu Pro Thr Phe Ser Phe Gly
305                 310                 315                 320


Val Gly Ser Gly Thr Ile Thr Ile Pro Gly Asp Leu Leu Asn Leu Thr
                325                 330                 335


Pro Ile Asp Ser Ser Gly Gln Thr Cys Tyr Gly Gly Leu Gln Ser Ser
            340                 345                 350


Ser Asp Ile Gly Ile Asn Ile Phe Gly Asp Val Ala Leu Lys Ala Ala
        355                 360                 365


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


<210>  70
<211>  379
```

```
<212>  PRT
<213>  Penicillium cinnamopurpureum

<400>  70

Ile Pro Thr Gly Val Pro Asn Arg Lys Gly Phe Thr Val Asn Gln Gln
1               5                   10                  15


Val Arg Pro Val Thr Asn Gly Thr Lys Ser Lys Thr Leu Asn Leu Pro
            20                  25                  30


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


Asn Ile Lys Ala Ala Ala Glu Ser Gly Thr Ala Thr Thr Thr Pro Glu
    50                  55                  60


Asp Asn Asp Ile Glu Tyr Leu Thr Pro Val Asp Val Gly Gly Thr Thr
65                  70                  75                  80


Leu Asn Leu Asp Phe Asp Thr Gly Ser Ala Asp Leu Trp Val Phe Ser
                85                  90                  95


Ser Glu Leu Pro Ser Ser Glu Ser Ser Gly His Ser Ile Tyr Lys Pro
            100                 105                 110


Ser Gln Ser Gly Lys Lys Leu Asp Gly Tyr Ser Trp Lys Ile Ser Tyr
        115                 120                 125


Gly Asp Ser Ser Ser Ala Ser Gly Asp Val Tyr Thr Asp Thr Val Thr
    130                 135                 140


Val Gly Gly Val Thr Ala Asp Gly Gln Ala Val Glu Ala Ala Lys Lys
145                 150                 155                 160


Ile Ser Gln Gln Phe Val Gln Asp Lys Asn Asn Asp Gly Leu Leu Gly
                165                 170                 175


Leu Ala Phe Ser Ser Ile Asn Thr Val Gln Pro Lys Ala Gln Thr Thr
            180                 185                 190
```

```
Phe Phe Asp Thr Val Lys Asp Gln Leu Asp Ser Pro Leu Phe Ala Val
        195                 200                 205


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


Lys Ser Lys Tyr Thr Gly Ser Leu Thr Tyr Ala Asp Val Asp Lys Ser
225                 230                 235                 240


Asp Gly Phe Trp Ala Phe Thr Ala Asp Gly Tyr Ser Val Gly Ser Gly
                245                 250                 255


Ser Ser Ser Ser Ser Arg Ile Lys Gly Ile Ala Asp Thr Gly Thr Thr
            260                 265                 270


Leu Leu Leu Ile Asp Asp Glu Ile Val Ser Ala Tyr Tyr Lys Gln Val
        275                 280                 285


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


Ser Thr Lys Leu Pro Asp Phe Asn Ile Lys Ile Gly Asp Tyr Thr Ala
305                 310                 315                 320


Val Ile Pro Gly Asp Val Ile Asn Tyr Ala Pro Val Gln Gln Gly Ser
                325                 330                 335


Ser Thr Cys Phe Gly Gly Ile Gln Ser Asn Ser Gly Leu Pro Phe Ser
            340                 345                 350


Ile Phe Gly Asp Ile Phe Leu Lys Ser Gln Tyr Val Val Phe Asp Ala
        355                 360                 365


Asn Gly Pro Arg Leu Gly Phe Ala Ala Gln Ala
    370                 375


<210>  71
<211>  350
<212>  PRT
```

```
<213>  Bacillus lichenformis

<400>  71

Ala Gln Pro Ala Lys Asn Val Glu Lys Asp Tyr Ile Val Gly Phe Lys
1               5                   10                  15


Ser Gly Val Lys Thr Ala Ser Val Lys Lys Asp Ile Ile Lys Glu Ser
            20                  25                  30


Gly Gly Lys Val Asp Lys Gln Phe Arg Ile Ile Asn Ala Ala Lys Ala
        35                  40                  45


Lys Leu Asp Lys Glu Ala Leu Lys Glu Val Lys Asn Asp Pro Asp Val
    50                  55                  60


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


Pro Tyr Gly Ile Pro Leu Ile Lys Ala Asp Lys Val Gln Ala Gln Gly
                85                  90                  95


Phe Lys Gly Ala Asn Val Lys Val Ala Val Leu Asp Thr Gly Ile Gln
            100                 105                 110


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


Gly Glu Ala Tyr Asn Thr Asp Gly Asn Gly His Gly Thr His Val Ala
    130                 135                 140


Gly Thr Val Ala Ala Leu Asp Asn Thr Thr Gly Val Leu Gly Val Ala
145                 150                 155                 160


Pro Ser Val Ser Leu Tyr Ala Val Lys Val Leu Asn Ser Ser Gly Ser
                165                 170                 175


Gly Ser Tyr Ser Gly Ile Val Ser Gly Ile Glu Trp Ala Thr Thr Asn
            180                 185                 190
```

```
Gly Met Asp Val Ile Asn Met Ser Leu Gly Gly Ala Ser Gly Ser Thr
        195                 200                 205


Ala Met Lys Gln Ala Val Asp Asn Ala Tyr Ala Arg Gly Val Val Val
    210                 215                 220


Val Ala Ala Ala Gly Asn Ser Gly Ser Ser Gly Asn Thr Asn Thr Ile
225                 230                 235                 240


Gly Tyr Pro Ala Lys Tyr Asp Ser Val Ile Ala Val Gly Ala Val Asp
                245                 250                 255


Ser Asn Ser Asn Arg Ala Ser Phe Ser Ser Val Gly Ala Glu Leu Glu
            260                 265                 270


Val Met Ala Pro Gly Ala Gly Val Tyr Ser Thr Tyr Pro Thr Asn Thr
        275                 280                 285


Tyr Ala Thr Leu Asn Gly Thr Ser Met Ala Ser Pro His Val Ala Gly
    290                 295                 300


Ala Ala Ala Leu Ile Leu Ser Lys His Pro Asn Leu Ser Ala Ser Gln
305                 310                 315                 320


Val Arg Asn Arg Leu Ser Ser Thr Ala Thr Tyr Leu Gly Ser Ser Phe
                325                 330                 335


Tyr Tyr Gly Lys Gly Leu Ile Asn Val Glu Ala Ala Ala Gln
            340                 345                 350


<210>  72
<211>  360
<212>  PRT
<213>  Bacillus subtilis

<400>  72

Phe Ser Asn Met Ser Ala Gln Ala Ala Gly Lys Ser Ser Thr Glu Lys
1               5                   10                  15


Lys Tyr Ile Val Gly Phe Lys Gln Thr Met Ser Ala Met Ser Ser Ala
```

```
            20                  25                  30

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

Phe Lys Tyr Val Asn Ala Ala Ala Ala Thr Leu Asp Glu Lys Ala Val
    50                  55                  60

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

Ile Ala His Glu Tyr Ala Gln Ser Val Pro Tyr Gly Ile Ser Gln Ile
                85                  90                  95

Lys Ala Pro Ala Leu His Ser Gln Gly Tyr Thr Gly Ser Asn Val Lys
            100                 105                 110

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

Val Arg Gly Gly Ala Ser Phe Val Pro Ser Glu Thr Asn Pro Tyr Gln
    130                 135                 140

Asp Gly Ser Ser His Gly Thr His Val Ala Gly Thr Ile Ala Ala Leu
145                 150                 155                 160

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

Ala Val Lys Val Leu Asp Ser Thr Gly Ser Gly Gln Tyr Ser Trp Ile
            180                 185                 190

Ile Asn Gly Ile Glu Trp Ala Ile Ser Asn Asn Met Asp Val Ile Asn
        195                 200                 205

Met Ser Leu Gly Gly Pro Thr Gly Ser Thr Ala Leu Lys Thr Val Val
    210                 215                 220

Asp Lys Ala Val Ser Ser Gly Ile Val Val Ala Ala Ala Ala Gly Asn
```

```
225                 230                 235                 240


Glu Gly Ser Ser Gly Ser Thr Ser Thr Val Gly Tyr Pro Ala Lys Tyr
                245                 250                 255


Pro Ser Thr Ile Ala Val Gly Ala Val Asn Ser Ser Asn Gln Arg Ala
            260                 265                 270


Ser Phe Ser Ser Ala Gly Ser Glu Leu Asp Val Met Ala Pro Gly Val
        275                 280                 285


Ser Ile Gln Ser Thr Leu Pro Gly Gly Thr Tyr Gly Ala Tyr Asn Gly
    290                 295                 300


Thr Ser Met Ala Thr Pro His Val Ala Gly Ala Ala Ala Leu Ile Leu
305                 310                 315                 320


Ser Lys His Pro Thr Trp Thr Asn Ala Gln Val Arg Asp Arg Leu Glu
                325                 330                 335


Ser Thr Ala Thr Tyr Leu Gly Ser Ser Phe Tyr Tyr Gly Lys Gly Leu
            340                 345                 350


Ile Asn Val Gln Ala Ala Ala Gln
        355                 360


<210>  73
<211>  548
<212>  PRT
<213>  Trametes cf versicol

<400>  73

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


Pro Ala Gly Phe Ser Leu Ser Gly Ala Ala Ser Pro Asp Thr Thr Leu
            20                  25                  30


Lys Leu Arg Leu Ala Leu Val Gln Ser Asn Phe Ala Glu Leu Glu Asp
        35                  40                  45
```

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

Leu Ser Lys Glu Glu Val Glu Gln Leu Val Ala Pro Ser Ala Glu Ser
65 70 75 80

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

Thr Ile Ser Pro Ala Gly Asp Trp Leu Ala Phe Glu Val Pro Val Ser
100 105 110

Lys Ala Asn Glu Leu Phe Asp Ala Asp Phe Ser Val Phe Thr His Asp
115 120 125

Glu Ser Gly Leu Lys Ala Val Arg Thr Leu Ala Tyr Ser Ile Pro Ala
130 135 140

Glu Leu Gln Gly His Leu Asp Leu Val His Pro Thr Ile Thr Phe Pro
145 150 155 160

Asn Pro Asn Ser His Leu Pro Val Val Arg Ser Pro Val Lys Pro Val
165 170 175

Gln Asn Leu Thr Ser Arg Ala Val Pro Ala Ser Cys Ala Ser Thr Ile
180 185 190

Thr Pro Ala Cys Leu Gln Ala Leu Tyr Gly Ile Pro Thr Thr Lys Ala
195 200 205

Thr Gln Ser Ser Asn Lys Leu Ala Val Ser Gly Phe Ile Asp Gln Phe
210 215 220

Ala Asn Ser Ala Asp Leu Lys Thr Phe Leu Gly Lys Phe Arg Thr Asp
225 230 235 240

Ile Ser Ser Ser Thr Thr Phe Thr Leu Gln Thr Leu Asp Gly Gly Ser
245 250 255

```
Asn Ser Gln Ser Ser Ser Gln Ala Gly Val Glu Ala Asn Leu Asp Ile
            260                 265                 270


Gln Tyr Thr Val Gly Leu Ala Ser Ala Val Pro Thr Ile Phe Ile Ser
        275                 280                 285


Val Gly Asp Asp Phe Gln Asp Gly Asp Leu Glu Gly Phe Leu Asp Ile
    290                 295                 300


Ile Asn Phe Leu Leu Asn Glu Ser Ala Pro Pro Gln Val Leu Thr Thr
305                 310                 315                 320


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


Leu Cys Asn Ala Tyr Ala Gln Leu Gly Ala Arg Gly Thr Ser Ile Leu
            340                 345                 350


Phe Ala Ser Gly Asp Gly Gly Val Ser Gly Ser Gln Ser Ser Ser Cys
        355                 360                 365


Ser Lys Phe Val Pro Thr Phe Pro Ser Gly Cys Pro Phe Met Thr Ser
    370                 375                 380


Val Gly Ala Thr Gln Gly Ile Asn Pro Glu Thr Ala Ala Asp Phe Ser
385                 390                 395                 400


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


Ala Val Ser Ser Tyr Leu Thr Ala Leu Gly Ser Thr Asn Ser Gly Lys
            420                 425                 430


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


Asp Phe Glu Ile Val Val Ser Gly Arg Thr Glu Gly Val Asp Gly Thr
    450                 455                 460
```

```
Ser Cys Ala Ser Pro Thr Leu Ala Ala Ile Ile Ser Leu Leu Asn Asp
465                 470                 475                 480


Arg Leu Ile Ala Ala Gly Lys Ser Pro Leu Gly Phe Leu Asn Pro Phe
                485                 490                 495


Leu Tyr Ser Ala Ala Gly Thr Ala Ala Leu Thr Asp Ile Thr Ser Gly
            500                 505                 510


Ser Asn Pro Gly Cys Asn Thr Asn Gly Phe Pro Ala Lys Ala Gly Trp
        515                 520                 525


Asp Pro Val Thr Gly Leu Gly Thr Pro Asn Phe Ala Lys Leu Leu Thr
    530                 535                 540


Ala Val Gly Leu
545


<210>  74
<211>  439
<212>  PRT
<213>  Bos taurus

<400>  74

Met Ala Lys Glu Tyr Phe Pro Phe Thr Gly Lys Ile Pro Phe Glu Gly
1               5                   10                  15


Lys Asp Ser Lys Asn Val Met Ala Phe His Tyr Tyr Glu Pro Glu Lys
            20                  25                  30


Val Val Met Gly Lys Lys Met Lys Asp Trp Leu Lys Phe Ala Met Ala
        35                  40                  45


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


Thr Arg Ser Tyr Glu Trp Asp Lys Ala Glu Cys Pro Val Gln Arg Ala
65                  70                  75                  80
```

```
Lys Asp Lys Met Asp Ala Gly Phe Glu Ile Met Asp Lys Leu Gly Ile
                85                  90                  95


Glu Tyr Phe Cys Phe His Asp Val Asp Leu Val Glu Glu Ala Pro Thr
            100                 105                 110


Ile Ala Glu Tyr Glu Glu Arg Met Lys Ala Ile Thr Asp Tyr Ala Gln
        115                 120                 125


Glu Lys Met Lys Gln Phe Pro Asn Ile Lys Leu Leu Trp Gly Thr Ala
    130                 135                 140


Asn Val Phe Gly Asn Lys Arg Tyr Ala Asn Gly Ala Ser Thr Asn Pro
145                 150                 155                 160


Asp Phe Asp Val Val Ala Arg Ala Ile Val Gln Ile Lys Asn Ser Ile
                165                 170                 175


Asp Ala Thr Ile Lys Leu Gly Gly Thr Asn Tyr Val Phe Trp Gly Gly
            180                 185                 190


Arg Glu Gly Tyr Met Ser Leu Leu Asn Thr Asp Gln Lys Arg Glu Lys
        195                 200                 205


Glu His Met Ala Thr Met Leu Gly Met Ala Arg Asp Tyr Ala Arg Ala
    210                 215                 220


Lys Gly Phe Lys Gly Thr Phe Leu Ile Glu Pro Lys Pro Met Glu Pro
225                 230                 235                 240


Ser Lys His Gln Tyr Asp Val Asp Thr Glu Thr Val Ile Gly Phe Leu
                245                 250                 255


Lys Ala His Gly Leu Asp Lys Asp Phe Lys Val Asn Ile Glu Val Asn
            260                 265                 270


His Ala Thr Leu Ala Gly His Thr Phe Glu His Glu Leu Ala Cys Ala
        275                 280                 285
```

```
Val Asp Ala Gly Met Leu Gly Ser Ile Asp Ala Asn Arg Gly Asp Ala
    290                 295                 300


Gln Asn Gly Trp Asp Thr Asp Gln Phe Pro Ile Asp Asn Phe Glu Leu
305                 310                 315                 320


Thr Gln Ala Met Leu Glu Ile Ile Arg Asn Gly Gly Leu Gly Asn Gly
                325                 330                 335


Gly Thr Asn Phe Asp Ala Lys Ile Arg Arg Asn Ser Thr Asp Leu Glu
            340                 345                 350


Asp Leu Phe Ile Ala His Ile Ser Gly Met Asp Ala Met Ala Arg Ala
        355                 360                 365


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


Lys Lys Ala Arg Tyr Ala Ser Phe Asp Ser Gly Ile Gly Lys Asp Phe
385                 390                 395                 400


Glu Asp Gly Lys Leu Thr Phe Glu Gln Val Tyr Glu Tyr Gly Lys Lys
                405                 410                 415


Val Glu Glu Pro Lys Gln Thr Ser Gly Lys Gln Glu Lys Tyr Glu Thr
            420                 425                 430


Ile Val Ala Leu His Cys Lys
        435


<210>  75
<211>  591
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  75

Met Leu Cys Ser Val Ile Gln Arg Gln Thr Arg Glu Val Ser Asn Thr
1               5                   10                  15
```

```
Met Ser Leu Asp Ser Tyr Tyr Leu Gly Phe Asp Leu Ser Thr Gln Gln
            20                  25                  30


Leu Lys Cys Leu Ala Ile Asn Gln Asp Leu Lys Ile Val His Ser Glu
        35                  40                  45


Thr Val Glu Phe Glu Lys Asp Leu Pro His Tyr His Thr Lys Lys Gly
    50                  55                  60


Val Tyr Ile His Gly Asp Thr Ile Glu Cys Pro Val Ala Met Trp Leu
65                  70                  75                  80


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


Leu Asn Lys Val Met Ala Val Ser Gly Ser Cys Gln Gln His Gly Ser
            100                 105                 110


Val Tyr Trp Ser Ser Gln Ala Glu Ser Leu Leu Glu Gln Leu Asn Lys
        115                 120                 125


Lys Pro Glu Lys Asp Leu Leu His Tyr Val Ser Ser Val Ala Phe Ala
    130                 135                 140


Arg Gln Thr Ala Pro Asn Trp Gln Asp His Ser Thr Ala Lys Gln Cys
145                 150                 155                 160


Gln Glu Phe Glu Glu Cys Ile Gly Gly Pro Glu Lys Met Ala Gln Leu
                165                 170                 175


Thr Gly Ser Arg Ala His Phe Arg Phe Thr Gly Pro Gln Ile Leu Lys
            180                 185                 190


Ile Ala Gln Leu Glu Pro Glu Ala Tyr Glu Lys Thr Lys Thr Ile Ser
        195                 200                 205


Leu Val Ser Asn Phe Leu Thr Ser Ile Leu Val Gly His Leu Val Glu
    210                 215                 220
```

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


Arg Lys Phe Met Tyr Glu Leu Leu His Leu Ile Asp Ser Ser Ser Lys
                245                 250                 255


Asp Lys Thr Ile Arg Gln Lys Leu Met Arg Ala Pro Met Lys Asn Leu
            260                 265                 270


Ile Ala Gly Thr Ile Cys Lys Tyr Phe Ile Glu Lys Tyr Gly Phe Asn
        275                 280                 285


Thr Asn Cys Lys Val Ser Pro Met Thr Gly Asp Asn Leu Ala Thr Ile
    290                 295                 300


Cys Ser Leu Pro Leu Arg Lys Asn Asp Val Leu Val Ser Leu Gly Thr
305                 310                 315                 320


Ser Thr Thr Val Leu Leu Val Thr Asp Lys Tyr His Pro Ser Pro Asn
                325                 330                 335


Tyr His Leu Phe Ile His Pro Thr Leu Pro Asn His Tyr Met Gly Met
            340                 345                 350


Ile Cys Tyr Cys Asn Gly Ser Leu Ala Arg Glu Arg Ile Arg Asp Glu
        355                 360                 365


Leu Asn Lys Glu Arg Glu Asn Asn Tyr Glu Lys Thr Asn Asp Trp Thr
    370                 375                 380


Leu Phe Asn Gln Ala Val Leu Asp Asp Ser Glu Ser Ser Glu Asn Glu
385                 390                 395                 400


Leu Gly Val Tyr Phe Pro Leu Gly Glu Ile Val Pro Ser Val Lys Ala
                405                 410                 415


Ile Asn Lys Arg Val Ile Phe Asn Pro Lys Thr Gly Met Ile Glu Arg
            420                 425                 430
```

```
Glu Val Ala Lys Phe Lys Asp Lys Arg His Asp Ala Lys Asn Ile Val
        435                 440                 445


Glu Ser Gln Ala Leu Ser Cys Arg Val Arg Ile Ser Pro Leu Leu Ser
    450                 455                 460


Asp Ser Asn Ala Ser Ser Gln Gln Arg Leu Asn Glu Asp Thr Ile Val
465                 470                 475                 480


Lys Phe Asp Tyr Asp Glu Ser Pro Leu Arg Asp Tyr Leu Asn Lys Arg
                485                 490                 495


Pro Glu Arg Thr Phe Phe Val Gly Gly Ala Ser Lys Asn Asp Ala Ile
            500                 505                 510


Val Lys Lys Phe Ala Gln Val Ile Gly Ala Thr Lys Gly Asn Phe Arg
        515                 520                 525


Leu Glu Thr Pro Asn Ser Cys Ala Leu Gly Gly Cys Tyr Lys Ala Met
    530                 535                 540


Trp Ser Leu Leu Tyr Asp Ser Asn Lys Ile Ala Val Pro Phe Asp Lys
545                 550                 555                 560


Phe Leu Asn Asp Asn Phe Pro Trp His Val Met Glu Ser Ile Ser Asp
                565                 570                 575


Val Asp Asn Glu Asn Trp Ile Ala Ile Ile Pro Arg Leu Ser Pro
            580                 585                 590


<210>  76
<211>  444
<212>  PRT
<213>  Bacillus subtilis

<400>  76

Glu Thr Ala Asn Lys Ser Asn Glu Leu Thr Ala Pro Ser Ile Lys Ser
1               5                   10                  15


Gly Thr Ile Leu His Ala Trp Asn Trp Ser Phe Asn Thr Leu Lys His
```

```
            20                  25                  30

Asn Met Lys Asp Ile His Asp Ala Gly Tyr Thr Ala Ile Gln Thr Ser
        35                  40                  45

Pro Ile Asn Gln Val Lys Glu Gly Asn Gln Gly Asp Lys Ser Met Ser
    50                  55                  60

Asn Trp Tyr Trp Leu Tyr Gln Pro Thr Ser Tyr Gln Ile Gly Asn Arg
65                  70                  75                  80

Tyr Leu Gly Thr Glu Gln Glu Phe Lys Glu Met Cys Ala Ala Ala Glu
                85                  90                  95

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

Phe Asp Tyr Ala Ala Ile Ser Asn Glu Val Lys Ser Ile Pro Asn Trp
        115                 120                 125

Thr His Gly Asn Thr Gln Ile Lys Asn Trp Ser Asp Arg Trp Asp Val
    130                 135                 140

Thr Gln Asn Ser Leu Leu Gly Leu Tyr Asp Trp Asn Thr Gln Asn Thr
145                 150                 155                 160

Gln Val Gln Ser Tyr Leu Lys Arg Phe Leu Glu Arg Ala Leu Asn Asp
                165                 170                 175

Gly Ala Asp Gly Phe Arg Phe Asp Ala Ala Lys His Ile Glu Leu Pro
            180                 185                 190

Asp Asp Gly Ser Tyr Gly Ser Gln Phe Trp Pro Asn Ile Thr Asn Thr
        195                 200                 205

Ser Ala Glu Phe Gln Tyr Gly Glu Ile Leu Gln Asp Ser Ala Ser Arg
    210                 215                 220

Asp Ala Ala Tyr Ala Asn Tyr Met Asp Val Thr Ala Ser Asn Tyr Gly
```

```
225                 230                 235                 240

His Ser Ile Arg Ser Ala Leu Lys Asn Arg Asn Leu Gly Val Ser Asn
                245                 250                 255

Ile Ser His Tyr Ala Tyr Asp Val Ser Ala Asp Lys Leu Val Thr Trp
            260                 265                 270

Val Glu Ser His Asp Thr Tyr Ala Asn Asp Asp Glu Glu Ser Thr Trp
        275                 280                 285

Met Ser Asp Asp Asp Ile Arg Leu Gly Trp Ala Val Ile Ala Ser Arg
    290                 295                 300

Ser Gly Ser Thr Pro Leu Phe Phe Ser Arg Pro Glu Gly Gly Gly Asn
305                 310                 315                 320

Gly Val Arg Phe Pro Gly Lys Ser Gln Ile Gly Asp Arg Gly Ser Ala
                325                 330                 335

Leu Phe Glu Asp Gln Ser Ile Thr Ala Val Asn Arg Phe His Asn Val
            340                 345                 350

Met Ala Gly Gln Pro Glu Glu Leu Ser Asn Pro Asn Gly Asn Asn Gln
        355                 360                 365

Ile Phe Met Asn Gln Arg Gly Ser His Gly Val Val Leu Ala Asn Ala
    370                 375                 380

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

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

Lys Leu Thr Gly Thr Ile Asn Ala Arg Ser Val Ala Val Leu Tyr Pro
            420                 425                 430

Asp Asp Ile Glu Ile Arg Cys Asn Thr Phe Phe Gln
```

```
        435                 440


<210>  77
<211>  476
<212>  PRT
<213>  Saccharomycopsis fibuligera

<400>  77

Gln Pro Val Thr Leu Phe Lys Arg Glu Thr Asn Ala Asp Lys Trp Arg
1               5                   10                  15


Ser Gln Ser Ile Tyr Gln Ile Val Thr Asp Arg Phe Ala Arg Thr Asp
            20                  25                  30


Gly Asp Thr Ser Ala Ser Cys Asn Thr Glu Asp Arg Leu Tyr Cys Gly
        35                  40                  45


Gly Ser Phe Gln Gly Ile Ile Lys Lys Leu Asp Tyr Ile Lys Asp Met
    50                  55                  60


Gly Phe Thr Ala Ile Trp Ile Ser Pro Val Val Glu Asn Ile Pro Asp
65                  70                  75                  80


Asn Thr Ala Tyr Gly Tyr Ala Tyr His Gly Tyr Trp Met Lys Asn Ile
                85                  90                  95


Tyr Lys Ile Asn Glu Asn Phe Gly Thr Ala Asp Asp Leu Lys Ser Leu
            100                 105                 110


Ala Gln Glu Leu His Asp Arg Asp Met Leu Leu Met Val Asp Ile Val
        115                 120                 125


Thr Asn His Tyr Gly Ser Asp Gly Ser Gly Asp Ser Ile Asp Tyr Ser
    130                 135                 140


Glu Tyr Thr Pro Phe Asn Asp Gln Lys Tyr Phe His Asn Tyr Cys Leu
145                 150                 155                 160


Ile Ser Asn Tyr Asp Asp Gln Ala Gln Val Gln Ser Cys Trp Glu Gly
                165                 170                 175
```

```
Asp Ser Ser Val Ala Leu Pro Asp Leu Arg Thr Glu Asp Ser Asp Val
            180                 185                 190


Ala Ser Val Phe Asn Ser Trp Val Lys Asp Phe Val Gly Asn Tyr Ser
        195                 200                 205


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


Phe Pro Asp Phe Val Ser Ala Ser Gly Val Tyr Ser Val Gly Glu Val
225                 230                 235                 240


Phe Gln Gly Asp Pro Ala Tyr Thr Cys Pro Tyr Gln Asn Tyr Ile Pro
                245                 250                 255


Gly Val Ser Asn Tyr Pro Leu Tyr Tyr Pro Thr Thr Arg Phe Phe Lys
            260                 265                 270


Thr Thr Asp Ser Ser Ser Ser Glu Leu Thr Gln Met Ile Ser Ser Val
        275                 280                 285


Ala Ser Ser Cys Ser Asp Pro Thr Leu Leu Thr Asn Phe Val Glu Asn
    290                 295                 300


His Asp Asn Glu Arg Phe Ala Ser Met Thr Ser Asp Gln Ser Leu Ile
305                 310                 315                 320


Ser Asn Ala Ile Ala Phe Val Leu Leu Gly Asp Gly Ile Pro Val Ile
                325                 330                 335


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


Arg Glu Ala Leu Trp Leu Ser Gly Tyr Asn Lys Glu Ser Asp Tyr Tyr
        355                 360                 365


Lys Leu Ile Ala Lys Ala Asn Ala Ala Arg Asn Ala Ala Val Tyr Gln
    370                 375                 380
```

```
Asp Ser Ser Tyr Ala Thr Ser Gln Leu Ser Val Ile Phe Ser Asn Asp
385                 390                 395                 400


His Val Ile Ala Thr Lys Arg Gly Ser Val Val Ser Val Phe Asn Asn
                405                 410                 415


Leu Gly Ser Ser Gly Ser Ser Asp Val Thr Ile Ser Asn Thr Gly Tyr
            420                 425                 430


Ser Ser Gly Glu Asp Leu Val Glu Val Leu Thr Cys Ser Thr Val Ser
        435                 440                 445


Gly Ser Ser Asp Leu Gln Val Ser Ile Gln Gly Gly Gln Pro Gln Ile
    450                 455                 460


Phe Val Pro Ala Lys Tyr Ala Ser Asp Ile Cys Ser
465                 470                 475


<210>  78
<211>  487
<212>  PRT
<213>  Debaryomyces occidentalis

<400>  78

Gln Pro Ile Ile Phe Asp Lys Arg Asp Val Gly Ser Ser Ala Asp Lys
1               5                   10                  15


Trp Lys Asp Gln Ser Ile Tyr Gln Ile Val Thr Asp Arg Phe Ala Arg
            20                  25                  30


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


Cys Gly Gly Ser Tyr Lys Gly Ile Ile Asp Lys Leu Asp Tyr Ile Gln
    50                  55                  60


Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Val Val Glu Gln Ile
65                  70                  75                  80
```

```
Pro Asp Asn Thr Ala Tyr Gly Tyr Ala Tyr His Gly Tyr Trp Met Lys
                85                  90                  95


Asn Ile Asp Glu Leu Asn Thr Asn Phe Gly Thr Ala Asp Glu Leu Lys
            100                 105                 110


Gln Leu Ala Ser Glu Leu His Ser Arg Ser Met Leu Leu Met Val Asp
        115                 120                 125


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


Tyr Ser Ser Phe Thr Pro Phe Asn Gln Gln Ser Tyr Phe His Asp Tyr
145                 150                 155                 160


Cys Leu Ile Thr Asn Tyr Asn Asp Gln Thr Asn Val Glu Asp Cys Trp
                165                 170                 175


Glu Gly Asp Thr Glu Val Ser Leu Pro Asp Leu Ser Thr Glu Asp Asn
            180                 185                 190


Glu Val Ile Gly Val Phe Gln Thr Trp Val Ser Asp Phe Val Gln Asn
        195                 200                 205


Tyr Ser Ile Asp Gly Leu Arg Ile Asp Ser Ala Lys His Val Asp Thr
    210                 215                 220


Ala Ser Leu Thr Lys Phe Glu Asp Ala Ser Gly Val Tyr Asn Leu Gly
225                 230                 235                 240


Glu Val Tyr Gln Gly Asp Pro Thr Tyr Thr Cys Pro Tyr Gln Ser Tyr
                245                 250                 255


Met Lys Gly Val Thr Asn Tyr Pro Leu Tyr Tyr Pro Val Tyr Arg Phe
            260                 265                 270


Phe Ser Asp Thr Ser Ala Thr Ser Ser Glu Leu Thr Ser Met Ile Ser
        275                 280                 285
```

```
Thr Leu Gln Ser Ser Cys Ser Asp Val Ser Leu Leu Gly Asn Phe Ile
    290                 295                 300


Glu Asn His Asp Gln Val Arg Phe Pro Ser Val Thr Ser Asp Thr Ser
305                 310                 315                 320


Leu Ile Lys Asn Ala Met Ala Phe Ile Ile Leu Gly Asp Gly Ile Pro
                325                 330                 335


Ile Ile Tyr Tyr Gly Gln Glu Gln Gly Leu Asn Gly Gly Ser Asp Pro
            340                 345                 350


Ala Asn Arg Glu Ala Leu Trp Leu Ser Gly Tyr Asn Thr Asp Ser Glu
        355                 360                 365


Tyr Tyr Glu Leu Ile Ser Lys Leu Asn Gln Ile Arg Asn Gln Ala Ile
    370                 375                 380


Lys Lys Asp Ser Ala Tyr Ser Thr Tyr Lys Ser Ser Val Val Ser Ser
385                 390                 395                 400


Ser Asp His Tyr Ile Ala Thr Arg Lys Gly Ser Asp Ala Asn Gln Leu
                405                 410                 415


Ile Ser Ile Phe Asn Asn Leu Gly Ser Asn Gly Ser Gln Asp Ile Thr
            420                 425                 430


Val Ser Asn Thr Gly Tyr Ser Ser Gly Asp Lys Val Ile Asp Ile Ile
        435                 440                 445


Ser Cys Asn Ser Val Ser Ala Gly Asp Phe Gly Ser Leu Ser Val Ser
    450                 455                 460


Ile Ser Gly Gly Met Pro Gln Val Tyr Ala Pro Ser Ser Val Leu Ser
465                 470                 475                 480


Gly Ser Gly Ile Cys Asn Gln
                485
```

```
<210>  79
<211>  487
<212>  PRT
<213>  Debaryomyces occidentalis

<400>  79

Lys Pro Ile Phe Leu Ser Lys Arg Asp Ala Gly Ser Ser Ala Ala Ala
1               5                   10                  15


Ala Trp Arg Ser Glu Ser Ile Tyr Gln Leu Val Thr Asp Arg Phe Ala
            20                  25                  30


Arg Thr Asp Gly Ser Thr Ser Ala Thr Cys Asn Thr Gly Asp Arg Val
        35                  40                  45


Tyr Cys Gly Gly Thr Phe Gln Gly Ile Ile Asp Lys Leu Asp Tyr Ile
    50                  55                  60


Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Val Val Glu Gln
65                  70                  75                  80


Ile Pro Asp Asp Thr Gly Tyr Gly Tyr Ala Tyr His Gly Tyr Trp Met
                85                  90                  95


Lys Asp Ile Tyr Ala Ile Asn Ser Asn Phe Gly Thr Ala Asp Asp Leu
            100                 105                 110


Lys Asn Leu Ser Asn Glu Leu His Lys Arg Asn Met Lys Leu Met Val
        115                 120                 125


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


Ala Tyr Ser Asn Tyr Asn Pro Phe Asn Gln Gln Ser Tyr Phe His Asp
145                 150                 155                 160


Tyr Cys Leu Ile Thr Asn Tyr Asp Asp Gln Thr Asn Val Glu Asp Cys
                165                 170                 175
```

```
Trp Glu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu Arg Thr Glu Asp
            180                 185                 190


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


Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Ser Ala Lys His Val Asp
    210                 215                 220


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


Gly Glu Val Tyr Asp Gly Asp Pro Ala Tyr Thr Cys Pro Tyr Gln Asn
                245                 250                 255


Tyr Met Ser Gly Val Thr Asn Tyr Pro Leu Tyr Tyr Pro Met Leu Arg
            260                 265                 270


Phe Phe Gln Gly Thr Ser Asn Ser Val Asp Glu Leu Asn Ala Met Ile
        275                 280                 285


Ser Ser Leu Glu Ser Asp Cys Lys Asp Ile Thr Leu Leu Gly Asn Phe
    290                 295                 300


Ile Glu Asn His Asp Gln Pro Arg Leu Pro Ser Tyr Thr Ser Asp Ser
305                 310                 315                 320


Ala Leu Ile Lys Asn Ala Ile Ala Phe Asn Leu Met Ser Asp Gly Ile
                325                 330                 335


Pro Ile Ile Tyr Tyr Gly Gln Glu Gln Gly Tyr Ser Gly Ser Ser Asp
            340                 345                 350


Pro Asn Asn Arg Glu Ala Leu Trp Leu Ser Gly Tyr Ser Thr Ser Asn
        355                 360                 365


Gly Tyr Tyr Lys Leu Ile Ser Ser Val Asn Gln Ile Arg Asn Gln Ala
    370                 375                 380
```

```
Ile Tyr Lys Asp Ser Lys Tyr Thr Thr Tyr Trp Ser Asp Val Leu Tyr
385                 390                 395                 400


Ala Ser Gly His Val Ile Ala Leu Gln Arg Gly Ala Asp Asp Gln Arg
                405                 410                 415


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


Thr Phe Ser Thr Lys Tyr Ser Gly Gly Glu Lys Val Val Asp Val Leu
        435                 440                 445


Thr Cys Gln Thr Ser Tyr Ala Asn Ser Asp Ser Thr Leu Thr Val Ser
    450                 455                 460


Ile Ser Gly Gly Ala Pro Arg Ile Tyr Ala Pro Ala Ser Leu Ile Ala
465                 470                 475                 480


Asn Ser Gly Ile Cys Asn Phe
                485


<210>  80
<211>  570
<212>  PRT
<213>  Lipomyces kononenkoae

<400>  80

Met Cys Gly Ser Thr Leu Ser Ala Ser Leu Tyr Val Tyr Asn Asp Asp
1               5                   10                  15


Tyr Asp Lys Ile Val Thr Leu Tyr Tyr Leu Thr Ser Ser Gly Thr Thr
            20                  25                  30


Gly Ser Thr Leu Ala Leu Ile Leu Pro Val Trp Ser Asn Asn Trp Glu
        35                  40                  45


Leu Trp Thr Leu Ser Ala Ile Ala Ala Gly Ala Val Glu Ile Thr Gly
    50                  55                  60


Ala Ser Tyr Val Asp Ser Asp Thr Ser Val Thr Tyr Thr Thr Ser Leu
```

```
65                  70                  75                  80


Asp Leu Pro Leu Thr Thr Thr Ser Ala Ser Val Pro Thr Gly Thr Ala
                85                  90                  95


Ala Asn Trp Arg Gly Arg Ser Ile Tyr Gln Val Val Thr Asp Arg Phe
            100                 105                 110


Ala Arg Thr Asp Gly Ser Ile Thr Tyr Ser Cys Asp Val Thr Asp Arg
        115                 120                 125


Val Tyr Cys Gly Gly Ser Tyr Arg Gly Ile Ile Asn Met Leu Asp Tyr
    130                 135                 140


Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Ile Val Glu
145                 150                 155                 160


Asn Ile Pro Asp Asp Thr Gly Tyr Gly Tyr Ala Tyr His Gly Tyr Trp
                165                 170                 175


Met Lys Asp Ile Phe Ala Leu Asn Thr Asn Phe Gly Gly Ala Asp Asp
            180                 185                 190


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


Val Asp Ile Val Val Asn His Phe Ala Phe Ser Gly Asn His Ala Asp
    210                 215                 220


Val Asp Tyr Ser Glu Tyr Phe Pro Tyr Ser Ser Gln Asp Tyr Phe His
225                 230                 235                 240


Ser Phe Cys Trp Ile Thr Asp Tyr Ser Asn Gln Thr Asn Val Glu Glu
                245                 250                 255


Cys Trp Leu Gly Asp Asp Ser Val Pro Leu Val Asp Val Asn Thr Gln
            260                 265                 270


Leu Asp Thr Val Lys Ser Glu Tyr Gln Ser Trp Val Lys Gln Leu Ile
```

```
        275                 280                 285


Ala Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val Lys His Val
    290                 295                 300


Gln Met Asp Phe Trp Ala Pro Phe Gln Glu Ala Ala Gly Ile Tyr Thr
305                 310                 315                 320


Val Gly Glu Val Phe Asp Gly Asp Pro Ser Tyr Thr Cys Pro Tyr Gln
                325                 330                 335


Glu Asn Leu Asp Gly Val Leu Asn Tyr Pro Val Tyr Tyr Pro Val Val
            340                 345                 350


Ser Ala Phe Gln Arg Val Gly Gly Ser Ile Ser Ser Leu Val Asp Met
        355                 360                 365


Ile Asp Thr Leu Lys Ser Glu Cys Ile Asp Thr Thr Leu Leu Gly Ser
    370                 375                 380


Phe Leu Glu Asn Gln Asp Asn Pro Arg Phe Pro Ser Tyr Thr Ser Asp
385                 390                 395                 400


Glu Ser Leu Ile Lys Asn Ala Ile Ala Phe Thr Ile Leu Ser Asp Gly
                405                 410                 415


Ile Pro Ile Ile Tyr Tyr Gly Gln Glu Gln Gly Leu Asn Gly Gly Asn
            420                 425                 430


Asp Pro Tyr Asn Arg Glu Ala Leu Trp Pro Thr Gly Tyr Ser Thr Thr
        435                 440                 445


Ser Thr Phe Tyr Glu Tyr Ile Ala Ser Leu Asn Gln Ile Arg Asn His
    450                 455                 460


Ala Ile Tyr Ile Asp Asp Thr Tyr Leu Thr Tyr Gln Asn Trp Val Ile
465                 470                 475                 480


Tyr Ser Asp Ser Thr Thr Ile Ala Met Arg Lys Gly Phe Thr Gly Asn
```

```
                485                 490                 495


Gln Ile Ile Thr Val Leu Ser Asn Leu Gly Ser Ser Gly Ser Ser Tyr
            500                 505                 510


Thr Leu Thr Leu Ser Asn Thr Gly Tyr Thr Ala Ser Ser Val Val Tyr
        515                 520                 525


Glu Ile Leu Thr Cys Thr Ala Val Thr Val Asp Leu Ser Gly Asn Leu
    530                 535                 540


Ala Val Pro Met Ser Gly Gly Leu Pro Arg Val Phe Tyr Pro Glu Ser
545                 550                 555                 560


Gln Leu Val Gly Ser Gly Ile Cys Ser Met
                565                 570


<210>  81
<211>  476
<212>  PRT
<213>  Lipomyces kononenkoae

<400>  81

Lys Thr Ala Ala Glu Trp Lys Glu Leu Ser Ile Tyr Gln Val Ile Thr
1               5                   10                  15


Asp Arg Phe Ala Thr Thr Asn Leu Thr Ala Pro Asp Cys Trp Ile Arg
            20                  25                  30


Ala Tyr Cys Gly Gly Thr Trp Lys Gly Leu Glu Arg Lys Leu Asp Tyr
        35                  40                  45


Ile Gln Asn Met Gly Phe Asp Ala Val Trp Ile Ser Pro Val Ile His
    50                  55                  60


Asn Ile Glu Val Asn Thr Thr Trp Gly Phe Ala Phe His Gly Tyr Trp
65                  70                  75                  80


Gly Asp Asp Pro Tyr Arg Leu Asn Glu His Phe Gly Thr Ala Ala Asp
                85                  90                  95
```

```
Leu Lys Ser Leu Ser Asp Ser Leu His Ala Arg Gly Met Ser Leu Met
            100                 105                 110


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


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


His Gln Pro Cys Pro Ile Asp Phe Ser Asn Gln Ser Ser Ile Glu Asp
145                 150                 155                 160


Cys Trp Leu Val Thr Glu Pro Ala Pro Ala Leu Val Asp Leu Lys Asn
                165                 170                 175


Glu Asp Gln Val Ile Leu Asp Ala Leu Ile Asn Ser Val Val Asp Leu
            180                 185                 190


Val Glu Thr Tyr Asp Ile Asp Gly Ile Arg Leu Asp Thr Ala Arg His
        195                 200                 205


Val Pro Lys Pro Ser Leu Ala Lys Phe Gln Glu Lys Val Gly Val Phe
    210                 215                 220


Val Thr Gly Glu Ala Leu Asn Gln Ser Val Pro Tyr Val Ala Gln Tyr
225                 230                 235                 240


Gln Gly Pro Leu Asn Ser Ala Ile Asn Tyr Pro Leu Trp Tyr Ala Leu
                245                 250                 255


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


Val Lys Ser Glu Gln Ala Thr Phe Ser Asp Ala His Ala Leu Thr Asn
        275                 280                 285


Phe Leu Asp Asn Gln Asp Gln Pro Arg Phe Ala Ser Tyr Leu Gly Asp
    290                 295                 300
```

```
Gly Asn Gly Asp Asp Val Leu Arg Asp Glu Asn Ala Ala Thr Phe Leu
305                 310                 315                 320


Phe Phe Val Ser Gly Ile Pro Val Ile Tyr Tyr Gly Phe Glu Gln Arg
                325                 330                 335


Phe Asp Gly Gly Phe Asp Pro Val Asn Arg Glu Pro Met Trp Thr Ser
            340                 345                 350


Gly Tyr Asn Thr Ser Thr Pro Leu Tyr Asn Tyr Leu Ala Arg Leu Asn
        355                 360                 365


Ala Ile Arg Lys Tyr Ala Ala Ser Ile Thr Gly Thr Gln Val Phe Tyr
    370                 375                 380


Ser Asp Asp Thr Val Phe Leu Gly Ser Gly Val Ser His Met Ala Met
385                 390                 395                 400


Gln Arg Gly Pro Leu Val Ile Val Leu Thr Asn Val Gly Gln His Ile
                405                 410                 415


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


Asp Ser Leu Thr Asp Leu Val Ser Cys Thr Lys Val Lys Val Val Gly
        435                 440                 445


Ala Asn Gly Thr Phe Thr Ser Pro Ser Asn Gly Gly Lys Ala Arg Ile
    450                 455                 460


Trp Ile Lys Ser Lys Tyr Ala Gly Lys Phe Cys Ser
465                 470                 475


<210>  82
<211>  626
<212>  PRT
<213>  Bacillus subtilis

<400>  82
```

```
Glu Thr Ala Asn Lys Ser Asn Glu Leu Thr Ala Pro Ser Ile Lys Ser
1               5                   10                  15


Gly Thr Ile Leu His Ala Trp Asn Trp Ser Phe Asn Thr Leu Lys His
            20                  25                  30


Asn Met Lys Asp Ile His Asp Ala Gly Tyr Thr Ala Ile Gln Thr Ser
        35                  40                  45


Pro Ile Asn Gln Val Lys Glu Gly Asn Gln Gly Asp Lys Ser Met Ser
    50                  55                  60


Asn Trp Tyr Trp Leu Tyr Gln Pro Thr Ser Tyr Gln Ile Gly Asn Arg
65                  70                  75                  80


Tyr Leu Gly Thr Glu Gln Glu Phe Lys Glu Met Cys Ala Ala Ala Glu
                85                  90                  95


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


Ser Asp Tyr Ala Ala Ile Ser Asn Glu Val Lys Ser Ile Pro Asn Trp
        115                 120                 125


Thr His Gly Asn Thr Gln Ile Lys Asn Trp Ser Asp Arg Trp Asp Val
    130                 135                 140


Thr Gln Asn Ser Leu Leu Gly Leu Tyr Asp Trp Asn Thr Gln Asn Thr
145                 150                 155                 160


Gln Val Gln Ser Tyr Leu Lys Arg Phe Leu Asp Arg Ala Leu Asn Asp
                165                 170                 175


Gly Ala Asp Gly Phe Arg Phe Asp Ala Ala Lys His Ile Glu Leu Pro
            180                 185                 190


Asp Asp Gly Ser Tyr Gly Ser Gln Phe Trp Pro Asn Ile Thr Asn Thr
        195                 200                 205
```

```
Ser Ala Glu Phe Gln Tyr Gly Glu Ile Leu Gln Asp Ser Ala Ser Arg
    210                 215                 220


Asp Ala Ala Tyr Ala Asn Tyr Met Asp Val Thr Ala Ser Asn Tyr Gly
225                 230                 235                 240


His Ser Ile Arg Ser Ala Leu Lys Asn Arg Asn Leu Gly Val Ser Asn
                245                 250                 255


Ile Ser His Tyr Ala Ser Asp Val Ser Ala Asp Lys Leu Val Thr Trp
            260                 265                 270


Val Glu Ser His Asp Thr Tyr Ala Asn Asp Asp Glu Glu Ser Thr Trp
        275                 280                 285


Met Ser Asp Asp Asp Ile Arg Leu Gly Trp Ala Val Ile Ala Ser Arg
    290                 295                 300


Ser Gly Ser Thr Pro Leu Phe Phe Ser Arg Pro Glu Gly Gly Gly Asn
305                 310                 315                 320


Gly Val Arg Phe Pro Gly Lys Ser Gln Ile Gly Asp Arg Gly Ser Ala
                325                 330                 335


Leu Phe Glu Asp Gln Ala Ile Thr Ala Val Asn Arg Phe His Asn Val
            340                 345                 350


Met Ala Gly Gln Pro Glu Glu Leu Ser Asn Pro Asn Gly Asn Asn Gln
        355                 360                 365


Ile Phe Met Asn Gln Arg Gly Ser His Gly Val Val Leu Ala Asn Ala
    370                 375                 380


Gly Ser Ser Ser Val Ser Ile Asn Thr Ala Thr Lys Leu Pro Asp Gly
385                 390                 395                 400


Arg Tyr Asp Asn Lys Ala Gly Ala Gly Ser Phe Gln Val Asn Asp Gly
                405                 410                 415
```

```
Lys Leu Thr Gly Thr Ile Asn Ala Arg Ser Val Ala Val Leu Tyr Pro
            420                 425                 430


Asp Asp Ile Ala Lys Ala Pro His Val Phe Leu Glu Asn Tyr Lys Thr
        435                 440                 445


Gly Val Thr His Ser Phe Asn Asp Gln Leu Thr Ile Thr Leu Arg Ala
    450                 455                 460


Asp Ala Asn Thr Thr Lys Ala Val Tyr Gln Ile Asn Asn Gly Pro Glu
465                 470                 475                 480


Thr Ala Phe Lys Asp Gly Asp Gln Phe Thr Ile Gly Lys Gly Asp Pro
                485                 490                 495


Phe Gly Lys Thr Tyr Thr Ile Met Leu Lys Gly Thr Asn Ser Asp Gly
            500                 505                 510


Val Thr Arg Thr Glu Lys Tyr Ser Phe Val Lys Arg Asp Pro Ala Ser
        515                 520                 525


Ala Lys Thr Ile Gly Tyr Gln Asn Pro Asn His Trp Ser Gln Val Asn
    530                 535                 540


Ala Tyr Ile Tyr Lys His Asp Gly Ser Arg Val Ile Glu Leu Thr Gly
545                 550                 555                 560


Ser Trp Pro Gly Lys Pro Met Thr Lys Asn Ala Asp Gly Ile Tyr Thr
                565                 570                 575


Leu Thr Leu Pro Ala Asp Thr Asp Thr Thr Asn Ala Lys Val Ile Phe
            580                 585                 590


Asn Asn Gly Ser Ala Gln Val Pro Gly Gln Asn Gln Pro Gly Phe Asp
        595                 600                 605


Tyr Val Leu Asn Gly Leu Tyr Asn Asp Ser Gly Leu Ser Gly Ser Leu
    610                 615                 620
```

```
Pro His
625


<210>  83
<211>  483
<212>  PRT
<213>  Bacillus subtilis

<400>  83

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


Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
            20                  25                  30


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


Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
    50                  55                  60


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


Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85                  90                  95


Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110


Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
        115                 120                 125


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


Gly Asn Thr Tyr Ser Asp Phe Lys Trp His Trp Tyr His Phe Asp Gly
145                 150                 155                 160
```

```
Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175


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


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


Val Ala Glu Thr Lys Lys Trp Gly Asn Trp Tyr Ala Asn Glu Leu Ser
    210                 215                 220


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


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


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


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


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


Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                 310                 315                 320


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


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


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

```
Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
    370                 375                 380


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


Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
                405                 410                 415


Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430


Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
        435                 440                 445


Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
    450                 455                 460


Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465                 470                 475                 480


Val Gln Lys



<210>  84
<211>  589
<212>  PRT
<213>  Bacillus subtilis

<400>  84

Met Met Glu Tyr Ala Ala Ile His His Gln Pro Phe Ser Thr Asp Ala
1               5                   10                  15


Tyr Ser Tyr Asp Gly Arg Thr Val His Ile Lys Ile Arg Thr Lys Lys
            20                  25                  30


Gly Asp Ala Asp His Ile Arg Phe Ile Trp Gly Asp Pro Tyr Glu Tyr
        35                  40                  45


Asn Asp Gly Lys Trp Ser Ala Asn Glu Gln Pro Met Arg Lys Ile Ala
```

```
    50                  55                  60

Ala Thr Glu Met His Asp Tyr Trp Phe Ala Glu Val Val Pro Pro Phe
65                  70                  75                  80

Arg Arg Leu Gln Tyr Ala Phe Val Val Thr Asp Asp His Glu Asp Ile
                85                  90                  95

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

Thr Ile His Tyr Tyr Phe Lys Phe Pro Phe Val His Glu Ala Asp Thr
        115                 120                 125

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

Pro Glu Arg Phe Ala Asn Gly Arg Glu Asp Leu Ser Pro Lys Asn Ala
145                 150                 155                 160

Leu Pro Trp Gly Ser Lys Asp Pro Gly Val Asn Asp Phe Phe Gly Gly
                165                 170                 175

Asp Leu Gln Gly Ile Val Asp Lys Leu Asp Tyr Leu Glu Asp Leu Gly
            180                 185                 190

Val Asn Gly Ile Tyr Leu Thr Pro Ile Phe Ser Ala Pro Ser Asn His
        195                 200                 205

Lys Tyr Asp Thr Leu Asp Tyr Phe Ser Ile Asp Pro His Phe Gly Asp
    210                 215                 220

Pro Glu Ile Phe Arg Thr Leu Val Ser Gln Leu His Gln Arg Gly Met
225                 230                 235                 240

Arg Ile Met Leu Asp Ala Val Phe Asn His Ile Gly Ser Ala Ser Pro
                245                 250                 255

Gln Trp Gln Asp Val Val Lys Asn Gly Asp Gln Ser Arg Tyr Lys Asp
```

```
            260                 265                 270

Trp Phe His Ile His Ser Phe Pro Val Thr Asp Asp Asn Tyr Asp Arg
        275                 280                 285

Phe Ala Phe Thr Ala Asp Met Pro Lys Leu Asn Thr Ala Asn Pro Glu
    290                 295                 300

Val Gln Lys Tyr Leu Leu Asp Ile Ala Leu Tyr Trp Ile Arg Glu Phe
305                 310                 315                 320

Asp Ile Asp Gly Trp Arg Leu Asp Val Ala Asn Glu Val Asp His Val
                325                 330                 335

Phe Trp Lys Thr Phe Arg Gln Ala Val Ser Thr Glu Lys Pro Asp Val
            340                 345                 350

Tyr Ile Leu Gly Glu Ile Trp His Ser Ala Glu Pro Trp Leu Arg Gly
        355                 360                 365

Asp Glu Phe His Ala Ala Met Asn Tyr Pro Phe Thr Glu Pro Met Ile
    370                 375                 380

Glu Tyr Phe Ala Asp Gln Thr Ile Ser Ala Ser Arg Met Ala His Arg
385                 390                 395                 400

Val Asn Ala His Leu Met Asn Gly Met Lys Gln Ala Asn Glu Val Met
                405                 410                 415

Phe Asn Leu Leu Asp Ser His Asp Thr Lys Arg Leu Leu Thr Arg Cys
            420                 425                 430

Arg Asn Asp Glu Lys Lys Ala Arg Ala Leu Leu Ala Phe Met Phe Ala
        435                 440                 445

Gln Thr Gly Ser Pro Cys Ile Tyr Tyr Gly Thr Glu Ile Gly Leu Asp
    450                 455                 460

Gly Glu Asn Asp Pro Leu Cys Arg Lys Cys Met Val Trp Glu Lys Glu
```

```
465                 470                 475                 480


Lys Gln Asn Gln Asp Met Leu Gln Phe Met Lys Arg Leu Ile Ala Leu
                485                 490                 495


Arg Lys Gln Glu Asn Thr Leu Leu Thr Glu Gly His Leu Glu Trp Asn
            500                 505                 510


Leu Leu Asp Asp Lys Asn Asp Phe Ile Ser Phe Ser Arg Thr Leu Asp
        515                 520                 525


Glu Lys Ile Leu Ile Tyr Phe Phe Asn Gln Gly Asn Val Val Gln His
    530                 535                 540


Ile Ser Leu Arg Glu Leu Asn Ile Asp Arg Asn Asn Lys Ile Cys Asp
545                 550                 555                 560


Ala Trp Thr Glu Gln Pro Leu His Tyr His Asp Val Ile Ala Val Gln
                565                 570                 575


Pro Gly Glu Phe Leu Ile Leu Ser Ala Ala Ala Pro Val
            580                 585


<210>  85
<211>  483
<212>  PRT
<213>  Bacillus lichenformis

<400>  85

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


Asn Asp Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ser Ala Tyr Leu
            20                  25                  30


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


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

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


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


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


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


Ile Ser Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro
    130                 135                 140


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


Asp Gly Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys
                165                 170                 175


Phe Gln Gly Lys Ala Trp Asp Trp Glu Val Ser Asn Glu Asn Gly Asn
            180                 185                 190


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


Ala Ala Glu Ile Lys Arg Trp Gly Thr Trp Tyr Ala Asn Glu Leu Gln
    210                 215                 220


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


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


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

```
Tyr Leu Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu
        275                 280                 285


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


Arg Lys Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser
305                 310                 315                 320


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


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


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


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


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


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


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


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


Trp His Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser
    450                 455                 460


Glu Gly Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr
465                 470                 475                 480
```

```
Val Gln Arg



<210>  86
<211>  478
<212>  PRT
<213>  Aspergillus niger

<400>  86

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30


Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


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


Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125


Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
    130                 135                 140


Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145                 150                 155                 160
```

```
Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
            180                 185                 190


Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220


Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
            260                 265                 270


Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285


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


Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320


Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335


Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Arg Asn Ala Ile
        355                 360                 365
```

```
Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380


Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Pro Met Arg Lys Gly Thr
385                 390                 395                 400


Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415


Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
            420                 425                 430


Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
        435                 440                 445


Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460


Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser
465                 470                 475


<210>  87
<211>  477
<212>  PRT
<213>  Aspergillus niger

<400>  87

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30


Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60
```

```
Val Thr Ala Gln Leu Pro Gln Thr Thr Ala Tyr Gly Asp Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125


Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
    130                 135                 140


Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
            180                 185                 190


Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220


Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
            260                 265                 270
```

```
Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285

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

Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320

Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335

Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

Pro Thr Asp Ser Glu Leu Tyr Lys Leu Ile Ala Ser Arg Asn Ala Ile
        355                 360                 365

Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380

Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Pro Met Arg Lys Gly Thr
385                 390                 395                 400

Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415

Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
            420                 425                 430

Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
        435                 440                 445

Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460

Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Tyr Gly
465                 470                 475
```

```
<210>  88
<211>  431
<212>  PRT
<213>  Streptomyces avermitilis

<400>  88

Ser Pro Pro Gly Thr Lys Asp Val Thr Ala Val Leu Phe Glu Trp Lys
1               5                   10                  15


Phe Asp Ser Val Ala Arg Glu Cys Thr Asn Thr Leu Gly Pro Ala Gly
            20                  25                  30


Tyr Gly Tyr Val Gln Val Ser Pro Pro Ala Glu His Ile Gln Gly Ser
        35                  40                  45


Gln Trp Trp Thr Ser Tyr Gln Pro Val Ser Tyr Lys Ile Ala Gly Arg
    50                  55                  60


Leu Gly Asp Ala Thr Ala Phe Gln Asn Met Ile Asn Thr Cys His Thr
65                  70                  75                  80


Ala Gly Val Lys Val Val Val Asp Thr Val Val Asn His Met Ser Ala
                85                  90                  95


Gly Ser Gly Thr Gly Thr Gly Gly Ser Ala Tyr Thr Lys Tyr Asn Tyr
            100                 105                 110


Pro Gly Leu Tyr Ser Ser Tyr Asp Met Asp Asp Cys Thr Ala Thr Ile
        115                 120                 125


Thr Asp Tyr Thr Asn Arg Ala Asn Val Gln Asn Cys Glu Leu Val Gly
    130                 135                 140


Leu Ala Asp Leu Asp Thr Gly Glu Glu Tyr Val Arg Lys Thr Ile Ala
145                 150                 155                 160


Gly Tyr Met Asn Thr Leu Leu Gly Tyr Gly Ala Asp Gly Phe Arg Val
                165                 170                 175


Asp Ala Val Lys His Ile Pro Ala Ala Asp Leu Ala Asn Ile Lys Ser
```

```
            180                 185                 190

Arg Leu Thr Asn Pro Ser Val Tyr Trp Lys Gln Glu Val Ile Tyr Ala
        195                 200                 205

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

Gln Glu Phe Arg Tyr Ala Tyr Asp Leu Lys Arg Val Phe Asn Asn Glu
225                 230                 235                 240

Asn Leu Ala Tyr Leu Lys Asn Tyr Gly Glu Gly Trp Gly Tyr Leu Asn
                245                 250                 255

Ser Ser Val Ala Gly Val Phe Val Asp Asn His Asp Thr Glu Arg Asn
            260                 265                 270

Gly Ser Thr Leu Asn Tyr Lys Asp Gly Ala Asn Tyr Thr Leu Ala Asn
        275                 280                 285

Val Phe Met Leu Ala Tyr Pro Tyr Gly Ala Pro Asp Ile Asn Ser Gly
    290                 295                 300

Tyr Glu Trp Ser Asp Ala Asp Ala Gly Pro Pro Gly Gly Gly Thr Val
305                 310                 315                 320

Asn Ala Cys Trp Gln Asp Gly Trp Lys Cys Gln His Ala Trp Pro Glu
                325                 330                 335

Ile Lys Ala Met Val Ala Phe Arg Asn Ala Thr Arg Gly Glu Ser Val
            340                 345                 350

Thr Asn Trp Trp Asp Asn Gly Gly Asp Ala Ile Ala Phe Gly Arg Gly
        355                 360                 365

Ala Lys Gly Tyr Val Ala Ile Asn His Glu Ser Gly Ser Leu Thr Arg
    370                 375                 380

Thr Tyr Gln Thr Ser Leu Thr Ala Gly Thr Tyr Cys Asn Val Gln Asn
```

```
385                 390                 395                 400


Asn Thr Gly Val Thr Val Asp Ser Ser Gly Arg Phe Thr Ala Thr Leu
                405                 410                 415


Gly Ala Asn Thr Ala Leu Ala Leu Tyr Ser Gly Lys Ser Thr Cys
            420                 425                 430


<210>  89
<211>  643
<212>  PRT
<213>  Clostridium phytofermentans

<400>  89

Met Tyr Thr Leu Lys Ser Lys Leu Arg Asp Leu Tyr Arg His Pro Val
1               5                   10                  15


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


Gly Leu Ile Glu Asn Pro Val Ile Gly Ala Leu Pro Leu Ser Phe Leu
        35                  40                  45


Asn Arg Ile Ala Gly Lys Lys Leu Gly Asn Gly Phe Phe Asp Ala Leu
    50                  55                  60


Leu Ala Leu Leu Asn Gln Ser Asn Asp Arg Leu Asp Pro Tyr Ser Ser
65                  70                  75                  80


Lys Asp Lys Lys Ile Thr Pro Thr Trp Trp Lys Glu Ala Val Phe Tyr
                85                  90                  95


Gln Ile Tyr Pro Arg Ser Phe Met Asp Gly Asn Gly Asp Gly Val Gly
            100                 105                 110


Asp Leu Pro Gly Ile Ile Ser Lys Leu Asp Tyr Leu Lys Glu Leu Gly
        115                 120                 125


Val Asp Ala Leu Trp Leu Ser Pro Ile Tyr Asp Ser Pro Gly Asp Asp
    130                 135                 140
```

```
Asn Gly Tyr Asp Ile Arg Asp Tyr Gln Lys Ile Asp Ser Gln Phe Gly
145                 150                 155                 160


Thr Met Glu Asp Phe Asp Leu Leu Leu Thr Glu Leu His Ala Arg Asn
                165                 170                 175


Met Arg Leu Val Met Asp Leu Val Val Asn His Thr Ser Asp Glu His
            180                 185                 190


His Trp Phe Lys Glu Ala Leu Lys Ser Ser Glu Ser Thr Tyr Arg Asp
        195                 200                 205


Tyr Tyr Phe Leu Arg Lys Glu Pro Asn Asn Trp Thr Ser Phe Phe Ser
    210                 215                 220


Gly Ser Ala Trp Asn His Tyr Pro Glu Glu Asp Leu Trp Gly Leu His
225                 230                 235                 240


Leu Phe Ser Lys Lys Gln Met Asp Leu Asn Trp Glu Asn Pro Lys Leu
                245                 250                 255


Arg Gln Asp Ile Tyr Gln Met Ile Arg Trp Trp Leu Glu Lys Gly Val
            260                 265                 270


Asp Gly Phe Arg Leu Asp Val Ile Asn Tyr Ile Ser Lys Glu Thr Gly
        275                 280                 285


Leu Pro Asp Gly Asp Ser Phe Ile Gly Asn Leu Met Gly Phe Thr Gly
    290                 295                 300


Ile Glu His Tyr Phe Tyr Gly Pro Lys Leu His Asn His Leu Gln Glu
305                 310                 315                 320


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


Thr Pro Gly Ile Gly Met Lys Met Gly Lys Leu Leu Thr Asp Asp Ser
            340                 345                 350
```

```
Arg Gly Glu Leu Asn Met Met Phe Ser Phe Asp His Leu Glu Thr Ser
        355                 360                 365

Gly His Ala Arg Phe Asp Gln Tyr Glu Tyr Asp Leu Asn Tyr Tyr Lys
    370                 375                 380

Ser Tyr Ile Met Asp Trp Met Glu Asn Phe Ala Asp Thr Ser Trp Met
385                 390                 395                 400

Ser Leu Phe Tyr Asp Asn His Asp Asn Pro Arg Met Leu Ser Lys Val
                405                 410                 415

Asp His Thr His Thr His Arg Gln Glu Leu Ala Lys Met Leu Ala Met
            420                 425                 430

Ile Gln Met Thr Leu Lys Gly Thr Pro Phe Leu Tyr Gln Gly Gln Glu
        435                 440                 445

Leu Gly Met Ile Asn Lys Asp Phe His Glu Ile Ser Asn Phe Arg Asp
    450                 455                 460

Val Glu Ser Ile Asn Lys Tyr Lys Glu Leu Cys Glu Lys Met Pro Lys
465                 470                 475                 480

Glu Glu Ala Phe Leu Gln Ile Leu Ala Gly Ser Arg Asp His Ala Arg
                485                 490                 495

Thr Pro Met Gln Trp Ser Ala Lys Pro Gly Cys Gly Phe Ser Asn Ala
            500                 505                 510

Val Pro Trp Ile Asp Ser Asp Gly Asp Glu Leu Val Cys Asn Ala Glu
        515                 520                 525

Ile Gln Met Gln Asp Ser Glu Ser Val Leu Ser Phe Tyr Arg Asp Leu
    530                 535                 540

Ile Ala Leu Arg Arg Lys Thr Pro Ala Leu Ile Tyr Gly Asp Ile Glu
545                 550                 555                 560
```

```
Phe Thr His Lys Lys Arg Lys Asp Ile Leu Ile Tyr Thr Arg Tyr Leu
                565                 570                 575


Glu Gly Glu Thr Tyr Leu Ile Ile Cys Asn Leu Ser Asn Asp Glu Gln
            580                 585                 590


Lys Leu Pro Gly Asn Val Pro Val Ser Glu Ser Leu Glu Gly Leu Glu
        595                 600                 605


Ser Leu Ser Ala Ser Ala Asp Glu Arg Lys Gly Leu Val Leu Cys Asn
    610                 615                 620


Tyr Pro Ala Lys Val Met Lys Ser Leu Arg Ala Tyr Glu Gly Arg Val
625                 630                 635                 640


Tyr Arg Ile



<210>  90
<211>  1016
<212>  PRT
<213>  Clostridium phytofermentans

<400>  90

Ala Thr Asp Thr Ile Thr Ile His Tyr His Arg Asp Asp Gly Asp Tyr
1               5                   10                  15


Glu Lys Trp Asn Leu Trp Leu Trp Ala Glu Gly Lys Asp Gly Ala Ala
            20                  25                  30


Tyr Tyr Phe Asp Gly Glu Asp Ala Phe Gly Pro Tyr Val Ser Val Ser
        35                  40                  45


Leu Asp Lys Ser Ala Asp Arg Ile Gly Phe Ile Val Arg Thr Asp Ser
    50                  55                  60


Trp Glu Lys Asp Val Ser Glu Asp Arg Phe Ile Asp Thr Ser Leu Gly
65                  70                  75                  80
```

```
Asp Glu Ile Trp Ile Ser Ser Gly Glu Ser Thr Phe Ser Tyr Glu Ala
                85                  90                  95


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


Leu Asn Tyr Leu Arg Tyr Asp Glu Glu Tyr Thr Asp Ile Ser Phe Arg
        115                 120                 125


Leu Thr Phe Glu Asp Gly Thr Thr Asp Phe Leu Thr Lys Glu His Met
    130                 135                 140


Arg Ile Glu Asn Gly Ile Leu Lys Ala Glu Lys Glu Val Lys Tyr Gly
145                 150                 155                 160


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


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


Glu Met Tyr Trp Met Gln Gly Thr Gly Thr Ile Ser Pro Lys Ala Asp
        195                 200                 205


Phe Ile Lys Arg Ser Lys Glu Ile Glu Ser Ala Leu Ile Thr Ser Met
    210                 215                 220


Lys Glu Ile Thr Val Lys Leu Ser Val Pro Cys Arg Val Asp Asp Ile
225                 230                 235                 240


Lys Gln Asp Gly Phe Lys Leu Ser Pro Lys Leu Ala Val Ser Lys Val
                245                 250                 255


Glu Ala Thr Ser Thr Arg Asp Ser Glu Tyr Lys Thr Ile Lys Glu Gly
            260                 265                 270


Tyr Ala Asp Thr Phe Ile Ile Thr Met Glu Glu Pro Leu Asp Met Ser
        275                 280                 285
```

```
Lys Lys Tyr Ala Leu Ser Lys Thr Asp Tyr Gly Ser Arg Asn Leu Thr
    290                 295                 300


Leu Asp Ser Gly Leu Tyr Thr Ser Glu Glu Phe Glu Ala Ala Tyr Thr
305                 310                 315                 320


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


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


Pro His Gly Glu Ala Lys Asp Gly Glu Lys Pro Glu Ile Thr Tyr Pro
        355                 360                 365


Met Lys Gln Thr Gly Ala Gly Val Trp Gln Ala Glu Ile Glu Gly Asp
    370                 375                 380


Leu Lys Asn Lys Tyr Tyr Val Tyr Gln Val Thr Val Asp Gly Lys Thr
385                 390                 395                 400


Lys Leu Val Val Asp Pro Tyr Ala Lys Ala Ala Gly Val Asn Gly Glu
                405                 410                 415


Arg Gly Met Val Ile Asp Leu Ser Glu Thr Asp Pro Asp Gly Phe Arg
            420                 425                 430


Glu His Ser Ser Pro Glu Phe Lys Asn Pro Val Asp Ala Val Ile Tyr
        435                 440                 445


Glu Ile His Val Arg Asp Leu Ser Met Asn Glu Asn Ser Gly Ile Glu
    450                 455                 460


Asn Lys Gly Lys Phe Leu Gly Phe Thr Glu Thr Gly Thr Thr Asn Ser
465                 470                 475                 480


Ala Gly Leu Ser Thr Gly Leu Asp His Met Lys Glu Leu Gly Val Thr
                485                 490                 495
```

```
His Val His Leu Leu Pro Ser Phe Asp Tyr Lys Thr Ile Asp Glu Ser
            500                 505                 510


Lys Leu Gly Glu Asn Lys Phe Asn Trp Gly Tyr Asp Pro Gln Asn Tyr
        515                 520                 525


Asn Leu Pro Glu Gly Ser Tyr Thr Thr Asp Pro Tyr Gln Gly Glu Val
    530                 535                 540


Arg Val Arg Glu Tyr Lys Glu Met Val Gln Ala Leu His Glu Asn Gly
545                 550                 555                 560


Leu His Val Val Met Asp Val Val Tyr Asn His Thr Tyr Thr Ala Gly
                565                 570                 575


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


Ile Asn Gly Asn Phe Thr Asn Gly Ser Gly Cys Gly Asn Glu Thr Ala
        595                 600                 605


Ser Glu Arg Ala Met Val Arg Lys Phe Ile Val Asp Ser Val Val Tyr
    610                 615                 620


Trp Ala Thr Glu Tyr Lys Val Asp Gly Phe Arg Phe Asp Leu Met Gly
625                 630                 635                 640


Leu His Asp Ile Glu Thr Met Asn Met Val Arg Glu Ala Leu Asp Lys
                645                 650                 655


Ile Asp Pro Ser Ile Leu Leu Tyr Gly Glu Gly Trp Thr Gly Gly Ser
            660                 665                 670


Thr Pro Leu Pro Asp Ser Lys Gln Ala Ile Lys Asn Asn Ala Val Glu
        675                 680                 685


Leu Asn Glu Arg Ile Ala Cys Phe Ser Asp Asp Ile Arg Asp Ala Ile
    690                 695                 700
```

```
Lys Gly Ser Val Phe Asp Ala Ser Asp Thr Gly Phe Ile Asn Ser Gly
705                 710                 715                 720


Lys Arg Asn Val Ser Asn Arg Asp Glu Ser Ile Lys Phe Gly Ile Val
                725                 730                 735


Ala Ser Val Ser His Pro Gln Val Asn Leu Ser Gly Val Pro Tyr Ser
            740                 745                 750


Ser Arg Phe Trp Ala Asn Glu Pro Ser Gln Thr Ile Asn Tyr Ala Ser
        755                 760                 765


Ala His Asp Asn Leu Thr Leu Trp Asp Lys Leu Leu Glu Thr Asn Lys
    770                 775                 780


Met Ala Ser Lys Glu Glu Leu Val Gln Met Asn Lys Leu Ser Ala Ala
785                 790                 795                 800


Ile Val Leu Thr Ser Gln Gly Ile Pro Phe Phe Gln Ala Gly Glu Glu
                805                 810                 815


Met Ala Arg Thr Lys Lys Gly Asn Asp Asn Ser Tyr Gln Ser Pro Asp
            820                 825                 830


Ser Ile Asn Met Leu Asn Trp Asp Asn Lys Thr Glu Tyr Lys Asp Leu
        835                 840                 845


Phe Glu Tyr Tyr Lys Gly Leu Ile Ala Leu Arg Lys Thr Tyr Asp Ala
    850                 855                 860


Phe Arg Met Gln Thr Ala Glu Glu Ile Gln Gln Lys Leu Glu Phe Val
865                 870                 875                 880


Asp Ser Asp Ser Ser Val Ile Ala Tyr Arg Ile His Asp Ala Val Lys
                885                 890                 895


Asp Gly Arg Glu Ile Ala Leu Ile Phe Asn Gly Thr Leu Glu Glu Lys
            900                 905                 910
```

```
Glu Val Val Leu Ser Ala Asn Ala Trp Asp Val Leu Val Asn Gln Asp
        915                 920                 925


Thr Ala Gly Thr Asp Val Ile Glu Thr Ile Thr Gly Gly Thr Ile Lys
    930                 935                 940


Val Pro Ala Lys Ser Thr Leu Val Leu Leu Glu Asn Lys Asp Ala Val
945                 950                 955                 960


Ile Lys Gly Asp Lys Asp Ala Val Lys Gly Asp Glu Ile Gln Glu Leu
                965                 970                 975


Pro Thr Asn Met Gln Glu Val Ala Glu Lys Glu Ser Gly Asn Ala Trp
            980                 985                 990


Leu Trp Val Gly Ile Ala Thr Val  Cys Val Leu Ala Gly  Gly Val Leu
        995                 1000                 1005


Phe Trp  Ile Leu Lys Arg Lys  Arg
    1010                 1015


<210>  91
<211>  554
<212>  PRT
<213>  Clostridium phytofermentans

<400>  91

Met Lys Asn Thr Asn Thr Leu His Pro Trp Trp Glu Ser Ala Ala Ala
1               5                   10                  15


Tyr Gln Ile Tyr Pro Arg Ser Phe Met Asp Ser Asn Gly Asp Gly Val
            20                  25                  30


Gly Asp Leu Gln Gly Ile Ile Ser Arg Leu Pro Tyr Leu Ser Glu Leu
        35                  40                  45


Gly Phe Asp Leu Ile Trp Ile Cys Pro Ile Tyr Pro Ser Pro Asn Asp
    50                  55                  60
```

```
Asp Asn Gly Tyr Asp Ile Ser Asp Tyr Gln Asn Ile Gln Lys Glu Tyr
65                  70                  75                  80


Gly Thr Met Glu Asp Phe Glu Glu Leu Leu His Lys Ala His Glu Arg
                85                  90                  95


Gly Ile Arg Val Ile Met Asp Leu Val Val Asn His Thr Ser Ser Ser
            100                 105                 110


His Pro Trp Phe Ile Glu Ser Arg Ser Ser Lys Asp Asn Pro Lys Arg
        115                 120                 125


Asp Trp Tyr Ile Trp Lys Asp Gly Lys Asp Asn Val Glu Pro Asn Asn
    130                 135                 140


Trp Glu Ser Ile Phe Gly Gly Ser Thr Trp Glu Tyr Asp Glu Lys Ser
145                 150                 155                 160


Gly Gln Tyr Phe Leu His Val Phe Gly Lys Thr Met Pro Asp Ile Asn
                165                 170                 175


Trp Glu Asn Thr Gln Val Lys Lys Ala Ile Phe Asp Met Ile Cys Trp
            180                 185                 190


Trp Leu Asp Lys Gly Ile Asp Gly Phe Arg Val Asp Ala Ile Ser His
        195                 200                 205


Ile Lys Lys Pro Asp Phe Asn Asp Met Pro Asn Pro Lys Asn Glu Arg
    210                 215                 220


Tyr Val Ser Ser Phe Asp Lys His Met Asn Gln Ser Gly Ile Leu Asp
225                 230                 235                 240


Leu Leu Asn Glu Leu Lys Glu Asn Ala Phe Ser Lys Tyr Asp Ile Phe
                245                 250                 255


Thr Val Ala Glu Ala Asn Gly Val Arg Ile Glu Glu Ile Glu Glu Trp
            260                 265                 270
```

```
Val Ser Ser Glu Lys Gly Ile Phe Asn Ser Leu Phe Gln Phe Asp His
        275                 280                 285


Leu Asn Leu Trp Asn Val Gly Ser Glu Glu Gly Lys Ile Ser Ile Lys
    290                 295                 300


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


Gly Asn Val Ala Leu Val Met Glu Asn His Asp Leu Val Arg Ser Ile
                325                 330                 335


Ser Arg Phe Gly Ser Glu Asp Lys Tyr Trp Lys Glu Ser Ala Lys Cys
            340                 345                 350


Leu Ala Leu Met Tyr Tyr Met Gln Lys Gly Val Pro Phe Ile Tyr Gln
        355                 360                 365


Gly Gln Glu Ile Gly Met Leu Asn Ala Asp Tyr Glu Ser His Leu Asp
    370                 375                 380


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


Gly Met Ser Pro Ala Glu Ser Leu Gln Val Leu Lys Lys Ser Ser Arg
                405                 410                 415


Asp Asn Ser Arg Thr Pro Met Gln Trp Asp Ala Ser Pro His Ala Gly
            420                 425                 430


Phe Thr Thr Gly Thr Pro Trp Met Lys Val Asn Gln Asn Tyr His Trp
        435                 440                 445


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


Tyr Lys Lys Leu Ile Lys Ile Lys Lys Glu Thr Thr Gly Leu Ile Tyr
465                 470                 475                 480
```

```
Gly Asp Tyr Lys Leu Leu Met Glu Glu Ser Glu Ser Ile Tyr Ala Tyr
                485                 490                 495


Thr Arg Glu Tyr Glu Glu Lys Asn Tyr Leu Val Val Cys Asn Leu Ser
            500                 505                 510


Glu Glu Leu Ser Glu Leu Gln Ile Asp Leu Asp Ile Thr Lys Gly Glu
        515                 520                 525


Ile Leu Ile Ser Asn Tyr Glu Asp Arg Asn Ser Lys Glu Met Leu Leu
    530                 535                 540


Lys Pro Tyr Glu Cys Arg Leu Tyr Ser Leu
545                 550


<210>  92
<211>  538
<212>  PRT
<213>  Clostridium phytofermentans

<400>  92

Met Val Lys Lys Trp Trp His Ser Ser Val Val Tyr Gln Ile Tyr Pro
1               5                   10                  15


Arg Ser Phe Asn Asp Ser Asn Gly Asp Gly Ile Gly Asp Leu Lys Gly
            20                  25                  30


Ile Ile Glu Lys Leu Asp Tyr Leu Lys Asn Leu Gly Ile Asp Val Ile
        35                  40                  45


Trp Leu Ser Pro Val Phe Lys Ser Pro Asn Asp Asp Asn Gly Tyr Asp
    50                  55                  60


Ile Ser Asp Tyr Glu Asp Ile Met Asp Glu Phe Gly Thr Leu Glu Asp
65                  70                  75                  80


Met Glu Leu Leu Leu Lys Glu Ala Asn Asn Arg Gly Ile Lys Ile Leu
                85                  90                  95


Met Asp Leu Val Ala Asn His Thr Ser Asp Glu His Lys Trp Phe Ile
```

```
            100                 105                 110


Glu Ser Arg Lys Ser Lys Asp Asn Ala Tyr Arg Asp Tyr Tyr Ile Trp
        115                 120                 125


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


Ser Gly Ser Ala Trp Glu Trp Asp Glu Ala Thr Gly Gln Tyr Tyr Leu
145                 150                 155                 160


His Leu Phe Ser Lys Lys Gln Pro Asp Leu Asn Trp Glu Asn Pro Ile
                165                 170                 175


Val Arg Glu Glu Val Trp Lys Ser Met Asn Phe Trp Ile Asp Lys Gly
            180                 185                 190


Ile Gly Gly Phe Arg Met Asp Val Ile Glu Leu Leu Gly Lys Ile Pro
        195                 200                 205


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


Glu Met Asn Arg Asn Ser Phe Gly Asp Lys Asp Leu Leu Thr Val Gly
225                 230                 235                 240


Glu Cys Trp Gly Ala Thr Pro Glu Ile Ala Lys Met Tyr Ser Asn Pro
                245                 250                 255


Asp Gly Ser Glu Leu Ser Met Val Phe Gln Phe Glu His Ile Gly Leu
            260                 265                 270


Asp Gln Ile Pro Gly Lys Asp Lys Trp Asp Leu Gln Pro Leu Asn Leu
        275                 280                 285


Ile Asp Leu Lys Asn Val Phe His Lys Trp Gln Thr Cys Phe His Asp
    290                 295                 300


Asp Gly Trp Asn Ser Leu Phe Trp Asn Asn His Asp Thr Pro Arg Ile
```

```
305                 310                 315                 320

Val Ser Arg Trp Gly Asn Asp Lys Val Tyr Lys Ile Glu Ser Ala Lys
                325                 330                 335

Met Leu Ala Thr Leu Leu His Gly Leu Lys Gly Thr Pro Tyr Ile Tyr
            340                 345                 350

Gln Gly Glu Glu Leu Gly Met Ala Asn Ile Lys Phe Lys Asp Ile Asn
        355                 360                 365

Gln Tyr Lys Asp Ile Glu Thr Leu Asn Met Tyr Lys Asp Arg Leu Asn
    370                 375                 380

Lys Gly Tyr Lys His Glu Asp Ile Met Glu Ser Ile Tyr Ala Lys Gly
385                 390                 395                 400

Arg Asp Asn Ala Arg Thr Pro Met Gln Trp Ser Asp Glu Ile Asp Gly
                405                 410                 415

Gly Phe Thr Thr Gly Thr Pro Trp Ile Glu Val Asn Pro Asn Phe Thr
            420                 425                 430

Glu Ile Asn Ala Lys Glu Gln Val Ser Asn Pro Asn Ser Ile Tyr Asn
        435                 440                 445

Tyr Tyr Lys Lys Leu Ile Glu Ile Arg Lys Asn Asn Glu Val Ile Val
    450                 455                 460

Tyr Gly Asp Phe Glu Met Leu Leu Pro Glu Asp Lys Asn Ile Phe Ala
465                 470                 475                 480

Tyr Val Arg Thr Leu Lys Asp Ser Lys Ile Val Val Val Cys Asn Phe
                485                 490                 495

Tyr Glu Asn Glu Val Glu Tyr Asn Ile Pro Lys Glu Tyr Glu Glu Lys
            500                 505                 510

Lys Glu Val Leu Ile Ser Asn Tyr Gly Leu Ser Leu Thr Gly Arg Leu
```

```
        515                 520                 525


Arg Pro Phe Glu Ala Ile Met Tyr Arg Val
    530                 535



<210>  93
<211>  555
<212>  PRT
<213>  Clostridium phytofermentans

<400>  93

Cys Lys Lys Ala Asp Val Asn Gln Asn Pro Ser Glu Leu Asn Gln Asp
1               5                   10                  15


Glu Ser Gln Lys Glu Lys Glu Glu Asn Asp Asp Glu Gly Thr Pro Glu
            20                  25                  30


Val Ser Gln Asp Glu Thr Lys Ala Val Ile Pro Tyr Asp Tyr Val Gln
        35                  40                  45


Asn Leu Asn Ile Ile Asp Asp Asn Tyr Arg Asn Phe Tyr Glu Ile Phe
    50                  55                  60


Val Tyr Ser Phe Tyr Asp Ser Asn Gly Asp Gly Ile Gly Asp Ile Asn
65                  70                  75                  80


Gly Val Ile Ser Lys Leu Asp Tyr Ile Asn Asp Gly Asn Asp Ala Thr
                85                  90                  95


Asp Ser Asp Leu Gly Phe Asn Gly Ile Trp Leu Met Pro Ile Met Pro
            100                 105                 110


Ser Thr Thr Tyr His Lys Tyr Asp Val Thr Asp Tyr Tyr Asn Ile Asp
        115                 120                 125


Pro Gln Tyr Gly Thr Leu Glu Asp Phe Lys Asn Leu Val Ser Glu Cys
    130                 135                 140


His Lys Arg Gly Ile His Leu Ile Ile Asp Phe Val Phe Asn His Thr
145                 150                 155                 160
```

```
Ser Ala Lys His Pro Trp Phe Leu Glu Ala Val Ser Tyr Leu Glu Ser
                165                 170                 175


Leu Lys Glu Gly Glu Glu Pro Asp Leu Glu Lys Cys Pro Tyr Val Gly
            180                 185                 190


Tyr Tyr His Phe Thr Lys Asp Tyr Asn Gly Ser Lys Thr Tyr Tyr Lys
        195                 200                 205


Ala Gly Thr Ser Asn Trp Tyr Tyr Glu Gly Val Phe Trp Asp Gln Met
    210                 215                 220


Pro Asp Leu Ala Leu Glu Asn Glu Asn Val Arg Lys Glu Ile Glu Asp
225                 230                 235                 240


Ile Ala Lys Tyr Trp Leu Asp Leu Gly Val Asp Gly Phe Arg Leu Asp
                245                 250                 255


Ala Ala Lys Glu Tyr Phe Ser Gly Glu Lys Glu Arg Asn Ile Glu Val
            260                 265                 270


Leu Lys Trp Phe Ser Asp Tyr Val Lys Ser Val Lys Glu Asp Ala Asp
        275                 280                 285


Ile Val Ala Glu Val Trp Asp Glu Glu Gly Thr Ile Ala Ala Tyr Tyr
    290                 295                 300


Glu Ser Gly Ile Pro Ser Leu Phe Asn Phe Pro Leu Ser Gln His Asn
305                 310                 315                 320


Gly Leu Ile Thr Asn Thr Ala Arg Lys Leu Gly Thr Ser Ser Gly Lys
                325                 330                 335


Asn Phe Ala Lys Thr Leu Leu Arg Leu Asp Glu Lys Tyr Lys Glu Gly
            340                 345                 350


Asn Pro Lys Tyr Ile Asp Ala Pro Phe Ile Ser Asn His Asp Thr Thr
        355                 360                 365
```

```
Arg Ile Ser Ala Gln Cys Val Asn Asp Glu Asp Gln Met Lys Met Ser
    370                 375                 380


Ala Gly Met Leu Leu Thr Met Asn Gly Ser Pro Tyr Val Tyr Tyr Gly
385                 390                 395                 400


Glu Glu Ile Gly Met Asn Ser Lys Gly Thr Lys Asp Glu Asn Lys Arg
                405                 410                 415


Leu Pro Met Gln Trp Ser Ala Thr Asp Thr Thr Gly Ile Thr Thr Pro
            420                 425                 430


Pro Ala Asn Ala Asp Ser Val Glu Gln Lys Phe Pro Pro Val Asp Glu
        435                 440                 445


Gln Met Lys Asp Pro Leu Ser Leu Tyr Asn Tyr Tyr Lys Arg Ala Val
    450                 455                 460


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


Ile Glu Glu Leu Cys Thr Lys Asp Ile Ser Ala Ile Lys Lys Val Tyr
                485                 490                 495


Gln Gly Ser Glu Ile Val Ile Leu Tyr Asn Ile Asn Thr Glu Ser Ala
            500                 505                 510


Asn Ile Leu Leu Lys Asp Ala Gly Leu Thr Glu Leu Asn Ile Arg Gly
        515                 520                 525


Tyr Leu Ser Val Asp Gly Asn Ala Val Thr Met Ser Asp Gly Val Val
    530                 535                 540


Ser Met Pro Lys Tyr Ser Ile Val Ile Leu Lys
545                 550                 555


<210>  94
<211>  583
```

```
<212>  PRT
<213>  Clostridium phytofermentans

<400>  94

Met Lys Phe Glu Ala Ile Tyr His Arg Thr Ser Asp Asn Tyr Cys Tyr
1               5                   10                  15


Pro Leu Asn Glu Glu Asp Leu Ile Ile Asn Ile Lys Thr Gly His Asp
            20                  25                  30


Ile Glu Arg Val Phe Ile Tyr Tyr Gly Asp Pro Phe Glu Gly Gly Ile
        35                  40                  45


Leu Gly Gly Asn Trp Thr Trp Asn Gly Val Glu Glu Glu Leu Ile Tyr
    50                  55                  60


Lys Lys Asn Leu Thr His His Ile Trp Trp Thr Thr Thr Val Lys Pro
65                  70                  75                  80


Lys Phe Lys Arg Cys Lys Tyr Tyr Phe Lys Leu Val Ala Asn Asp Thr
                85                  90                  95


Ser Tyr Tyr Tyr Phe Glu Asp Gly Phe Tyr Thr Glu Ala Glu Met Asn
            100                 105                 110


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


Ile Asp Ile Asn Lys Thr Pro Asp Trp Val Asn Asp Thr Val Trp Tyr
    130                 135                 140


Gln Ile Phe Pro Glu Arg Phe Asn Asn Gly Asp Lys Glu Asn Asp Pro
145                 150                 155                 160


Lys Asn Val Lys Ala Trp Gly Phe His Thr Val Ser Asn Asp Glu Phe
                165                 170                 175


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

```
Asp Ile Gly Ile Ser Gly Ile Tyr Leu Thr Pro Ile Phe Glu Ala Asn
        195                 200                 205

Thr Ser His Lys Tyr Asp Thr Lys Asp Tyr Met Lys Ile Asp Pro His
    210                 215                 220

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

Lys Gly Ile Arg Ile Met Leu Asp Gly Val Phe Asn His Cys Gly Asn
                245                 250                 255

Gln Phe Ala Pro Trp Leu Asp Val Leu Lys Asn Gly Pro Asp Ser Lys
            260                 265                 270

Tyr Phe Asn Trp Phe Met Ile Asn Lys Trp Pro Phe Asn Lys Glu Asp
        275                 280                 285

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

Met Pro Lys Leu Asn Thr Asn Asn Pro Glu Val Ile Lys Tyr Leu Leu
305                 310                 315                 320

Asp Val Val Glu Tyr Trp Val Lys Asn Phe Asp Ile Asp Gly Ile Arg
                325                 330                 335

Leu Asp Val Ala Asn Glu Ile Ser His Arg Phe Cys Lys Asp Leu Arg
            340                 345                 350

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

Trp His Asp Ala Ile Thr Trp Leu His Gly Asp Glu Phe Asp Gly Val
    370                 375                 380

Met Asn Tyr Pro Leu Ala Thr Ser Leu Ala Asp Tyr Trp Val Tyr Pro
385                 390                 395                 400
```

```
Glu Lys Thr Asn Tyr Asp Phe Glu Cys Ala Ile Asn His Asn Phe Thr
                405                 410                 415


Met Tyr Met Gln Gln Thr Asn Asp Val Leu Phe Asn Leu Leu Asp Ser
            420                 425                 430


His Asp Thr Asn Arg Leu Ile Asp Lys Val Lys Asp Ile Asp Ile Phe
        435                 440                 445


Tyr Gln Gln Leu Ala Val Leu Phe Thr Met Pro Gly Ser Pro Cys Ile
    450                 455                 460


Tyr Tyr Gly Thr Glu Ile Ala Met Glu Gly Ser Tyr Asp Pro Asp Cys
465                 470                 475                 480


Arg Arg Cys Met Pro Trp Glu Asp Ile Asp Ala Gly Leu Phe Lys Asp
                485                 490                 495


Arg Ile Glu Ile Ile Lys Ala Leu Ile His Leu Arg Lys Thr Asn Asn
            500                 505                 510


Ala Phe Lys Ser Arg His Tyr His Phe Ile Glu Asp Lys Asn Asn Asn
        515                 520                 525


Arg Val Ile His Tyr Ile Lys Thr Asp Glu Asp His Lys Gln Val Glu
    530                 535                 540


Val Ile Leu Asn Cys Ser Lys Asp Ser Ile Val Val Gln Arg Lys Gly
545                 550                 555                 560


Asn Glu Leu Phe Ser Leu Leu Asn Glu Asp Thr Ile Leu Lys Pro Lys
                565                 570                 575


Gly Val Phe Ile Gln Gln Ile
            580


<210>  95
<211>  575
<212>  PRT
```

```
<213>  Clostridium thermocellum

<400>  95

Met Lys Leu Glu Ala Ile Tyr His Lys Pro Tyr Ser Glu Phe Ala Phe
1               5                   10                  15


Pro Val Ala Pro Asp Thr Leu Val Ile Arg Leu Arg Thr Ala Lys Asn
            20                  25                  30


Asp Val Asn Thr Cys Ile Leu Ile Tyr His Glu Lys Tyr Asp Thr Ser
        35                  40                  45


Gln Arg Gly Lys Val Lys Met Asp Lys Val Ala Ser Asp Gly Met Phe
    50                  55                  60


Asp Tyr Tyr Glu Val Glu Leu Asn Val Gly Ile Lys Arg Ile Lys Tyr
65                  70                  75                  80


Met Phe Tyr Leu Glu Asp Asn Tyr Ser Ile Lys Trp Tyr Ser Ser Asp
                85                  90                  95


Gly Phe Phe Asp Tyr Met Pro Gln Trp Gly His Phe Thr Tyr Ser Tyr
            100                 105                 110


Ile Cys Lys Asp Asp Ile Phe His Glu Val Glu Trp Phe Arg Asn Ser
        115                 120                 125


Thr Ile Tyr Gln Ile Phe Pro Asp Arg Phe Ala Lys Phe Pro Pro Asp
    130                 135                 140


Thr Glu Asn Ser Gly Lys Arg Thr Ile His Gly Gly Asn Ile Lys Gly
145                 150                 155                 160


Ile Ile Asp Arg Phe Asp His Leu Val Lys Leu Gly Val Asp Val Val
                165                 170                 175


Tyr Leu Asn Pro Ile Phe Lys Ser Glu Ser Tyr His Arg Tyr Asp Val
            180                 185                 190
```

```
Val Asp Tyr Tyr Glu Ile Asp Pro Met Phe Gly Ser Lys Glu Glu Leu
        195                 200                 205


Arg Glu Leu Met Asp Leu Cys His Lys Asn Gly Ile Lys Val Ile Phe
    210                 215                 220


Asp Gly Val Phe Asn His Ser Gly Asp Lys Phe Phe Ala Phe Arg Asp
225                 230                 235                 240


Val Val Glu Lys Gly Glu Lys Ser Lys Tyr Ala Asn Trp Tyr Phe Ile
                245                 250                 255


Asn Ser Phe Pro Val Gln Gly Tyr Pro Arg Pro Asn Tyr Glu Cys Phe
            260                 265                 270


Ser Phe Tyr Gly Gly Met Pro Lys Leu Asn Thr Gly Asn Pro Glu Thr
        275                 280                 285


Ala Lys Tyr Phe Leu Asp Val Val Lys Tyr Trp Thr Val Glu Phe Gly
    290                 295                 300


Val Asp Gly Trp Arg Leu Asp Ala Ala Asp Glu Val Asp Arg Lys Phe
305                 310                 315                 320


Trp Arg Lys Leu Arg Asp Met Leu Lys Asp Leu Asn Lys Asp Val Val
                325                 330                 335


Leu Ile Gly Glu Ile Phe Asp Glu Ala Ser Ser Trp Leu Trp Gly Asp
            340                 345                 350


Gln Phe Asp Ser Val Ile Asn Tyr Pro Leu Lys Ala Met Ile Asn Asp
        355                 360                 365


Leu Phe Ala Tyr Arg Ser Ile Asp Val Glu Thr Phe Arg Asn Arg Ile
    370                 375                 380


Ser Gly Tyr Ile Met Lys Phe Asn Lys Lys Val Leu Ser Ser Leu Val
385                 390                 395                 400
```

```
Asn Ile Ile Ser Thr His Asp Thr Pro Arg Phe Leu Thr Leu Cys Asn
                405                 410                 415


Gly Asp Glu Lys Arg Phe Glu Met Ala Val Val Phe Gln Phe Thr Phe
            420                 425                 430


Pro Gly Val Pro Leu Ile Tyr Tyr Gly Asp Glu Ile Gly Met Glu Gly
        435                 440                 445


Glu Gly Asp Pro Asp Cys Arg Arg Pro Met Ile Trp Asp Glu Ala Lys
    450                 455                 460


Trp Asn Lys Lys Thr Leu Glu Leu Tyr Lys Phe Leu Ile Gly Leu Arg
465                 470                 475                 480


Lys Arg Phe Asp Ala Leu Arg Thr Gly Glu Tyr Gly Glu Leu Pro Val
                485                 490                 495


Thr Gly Cys Asn Gly Ile Leu Ala Tyr Arg Arg Gly Arg Gly Glu Asn
            500                 505                 510


Gly Ile Ile Val Ala Met Asn Thr Leu Asp Arg Lys Glu Asn Val Val
        515                 520                 525


Val Glu Thr Gly Asp Ser Phe Asp Thr Val Lys Ala Phe Glu Ser Leu
    530                 535                 540


Lys Asp Glu Glu Arg Leu Asn Val Asp Lys Lys Arg Ile Asn Ile Cys
545                 550                 555                 560


Leu Asn Pro Phe Glu Trp Arg Ile Tyr Lys Ala Cys Gly Glu Leu
                565                 570                 575


<210>  96
<211>  655
<212>  PRT
<213>  Thermobifida fusca

<400>  96

Met Ile Gly Arg Phe Pro Ile Leu Asp Val Ser Pro Val Val Asp Ile
```

```
1               5                   10                  15

Gly Thr Ala Lys Ala Val Val Gly Glu Thr Phe Pro Val Arg Ala Thr
            20                  25                  30

Val Phe Arg Glu Gly His Glu Ala Leu Gly Ala Gly Val Val Leu Tyr
        35                  40                  45

Thr Pro Glu Gly Gln Arg Gln Pro Leu Val Pro Leu Arg Glu Ile Ala
    50                  55                  60

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

Leu Trp His Phe Ala Ile Glu Ala Trp Ser Asp Pro Tyr Ala Thr Trp
                85                  90                  95

Cys His Asp Ala Arg Ile Lys Ile Pro Ala Gly Gln Asp Val Glu Leu
            100                 105                 110

Met Leu Glu Glu Gly Ala Arg Leu Leu Glu Arg Ala Ala Arg Arg Val
        115                 120                 125

Pro Arg Arg Pro Ala Leu Ala Glu Ile Ala Ala Ala Met Arg Asp Gly
    130                 135                 140

Ser Arg Ser Ala His Glu Arg Leu Asp Leu Ala Leu Ser Asp Leu Val
145                 150                 155                 160

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

Gln Arg Phe Pro Val Met Val Ser Arg Arg Arg Ala Leu Phe Gly Ser
            180                 185                 190

Trp Tyr Glu Phe Phe Pro Arg Ser Glu Gly Ala Val Leu Asp Thr Glu
        195                 200                 205

Asp Gly Glu Pro Arg Ser Gly Thr Phe Ala Thr Ala Ala Arg Arg Leu
```

```
    210                 215                 220


Pro Ala Ile Ala Asp Met Gly Phe Asp Val Val Tyr Ile Pro Pro Ile
225                 230                 235                 240


His Pro Val Gly Tyr Ser Phe Arg Lys Gly Arg Asn Asn Ser Thr Val
                245                 250                 255


Ala Gln Pro Gly Asp Pro Gly Ser Val Trp Ala Ile Gly Ser His Glu
            260                 265                 270


Gly Gly His Asp Ala Ile His Pro Asp Leu Gly Thr Ile Asp Asp Phe
        275                 280                 285


Asp Ala Phe Val Ala Arg Ala Arg Glu Leu Gly Leu Glu Ile Ala Met
    290                 295                 300


Asp Leu Ala Leu Gln Ala Ser Pro Asp His Pro Trp Val Lys Glu His
305                 310                 315                 320


Pro Glu Trp Phe Thr Val Arg Ala Asp Gly Ser Ile Ala Tyr Ala Glu
                325                 330                 335


Asn Pro Pro Lys Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Lys
            340                 345                 350


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


Met Ser His Gly Val Arg Ile Phe Arg Val Asp Asn Pro His Thr Lys
    370                 375                 380


Pro Val Ala Phe Trp Glu Arg Leu Leu Ala Asp Ile Ala Ala Thr Asp
385                 390                 395                 400


Pro Asp Val Ile Phe Leu Ser Glu Ala Phe Thr Arg Pro Ala Met Met
                405                 410                 415


His Thr Leu Ala Lys Ile Gly Phe His Gln Ser Tyr Thr Tyr Phe Thr
```

```
            420                 425                 430

Trp Arg Asn Thr Lys Gln Glu Leu Glu Glu Tyr Leu Thr Glu Leu Thr
        435                 440                 445

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

Asp Ile Leu His Ala Tyr Leu Gln His Gly Gly Arg Pro Ala Phe Glu
465                 470                 475                 480

Val Arg Ala Ile Leu Ala Ala Thr Leu Ser Pro Thr Trp Gly Met Tyr
                485                 490                 495

Ser Gly Tyr Glu Leu Cys Glu Asn Arg Ala Leu Lys Pro Gly Ser Glu
            500                 505                 510

Glu Tyr Leu Asp Ser Glu Lys Tyr Gln Tyr Lys Pro Arg Asp Trp Glu
        515                 520                 525

Ala Ala Glu Ala Ala Gly Ile Thr Ile Thr Pro Leu Ile Arg Lys Leu
    530                 535                 540

Asn Ser Leu Arg Arg Ser His Pro Ala Leu Gln Glu Leu Arg Asn Leu
545                 550                 555                 560

Arg Phe His Tyr Ala Asp Gln Pro Glu Ile Ile Cys Tyr Ser Lys Arg
                565                 570                 575

Leu Ala Gly Ala Asn His Gly Ala Asp Asp Thr Ile Leu Val Val Ala
            580                 585                 590

Asn Leu Asp Pro His His Thr Arg Glu Ala Thr Val Trp Leu Asp Met
        595                 600                 605

Pro Ala Leu Gly Phe Ala Pro Gly Asp His Ile Thr Val Thr Asp Gln
    610                 615                 620

Leu Ser Gly His Ser Tyr His Trp Val Glu Ala Asn Tyr Val Arg Leu
```

```
625                 630                 635                 640


Asp Pro His Val Gln Thr Ala His Ile Phe Thr Val Ala Pro Ala
                645                 650                 655


<210>  97
<211>  572
<212>  PRT
<213>  Thermobifida fusca

<400>  97

Ala Pro Ser Gly Asn Arg Asp Val Ile Val His Leu Phe Gln Trp Arg
1               5                   10                  15


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


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


Ala Glu Asp Tyr Pro Trp Trp Gln Asp Tyr Gln Pro Val Ser Tyr Lys
    50                  55                  60


Leu Asp Gln Thr Arg Arg Gly Ser Arg Ala Asp Phe Ile Asp Met Val
65                  70                  75                  80


Asn Thr Cys Arg Glu Ala Gly Val Lys Ile Tyr Val Asp Ala Val Ile
                85                  90                  95


Asn His Met Thr Gly Thr Gly Ser Ala Gly Ala Gly Pro Gly Ser Ala
            100                 105                 110


Gly Ser Ser Tyr Ser Lys Tyr Asp Tyr Pro Gly Ile Tyr Gln Ser Gln
        115                 120                 125


Asp Phe Asn Asp Cys Arg Arg Asp Ile Thr Asn Trp Asn Asp Lys Trp
    130                 135                 140


Glu Val Gln His Cys Glu Leu Val Gly Leu Ala Asp Leu Lys Thr Ser
145                 150                 155                 160
```

```
Ser Pro Tyr Val Gln Asp Arg Ile Ala Ala Tyr Leu Asn Glu Leu Ile
                165                 170                 175

Asp Leu Gly Val Ala Gly Phe Arg Ile Asp Ala Ala Lys His Ile Pro
            180                 185                 190

Glu Gly Asp Leu Gln Ala Ile Leu Ser Arg Leu Lys Asn Val His Pro
        195                 200                 205

Ala Trp Gly Gly Gly Lys Pro Tyr Ile Phe Gln Glu Val Ile Ala Asp
    210                 215                 220

Ser Thr Ile Ser Thr Gly Ser Tyr Thr His Leu Gly Ser Val Thr Glu
225                 230                 235                 240

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

Ala His Leu Thr Gly Leu Gly Ser Gly Leu Thr Pro Ser Asp Lys Ala
            260                 265                 270

Val Val Phe Val Val Asn His Asp Thr Gln Arg Tyr Glu Pro Ile Leu
        275                 280                 285

Thr His Thr Asp Gly Ala Arg Tyr Asp Leu Ala Gln Lys Phe Met Leu
    290                 295                 300

Ala His Pro Tyr Gly Thr Pro Lys Val Met Ser Ser Tyr Thr Trp Ser
305                 310                 315                 320

Gly Asp Asp Lys Ala Gly Pro Pro Met His Ser Asp Gly Thr Thr Arg
                325                 330                 335

Pro Thr Asp Cys Ser Ala Asp Arg Trp Leu Cys Glu His Arg Ala Val
            340                 345                 350

Ala Gly Met Val Gly Phe His Asn Ala Val Ala Gly Gln Gly Ile Gly
        355                 360                 365
```

```
Ser Ala Val Thr Asp Gly Asn Gly Arg Leu Ala Phe Ala Arg Gly Ser
    370                 375                 380


Ala Gly Tyr Ala Ala Phe Asn Ala Thr Asn Thr Ala Trp Thr Arg Thr
385                 390                 395                 400


Phe Thr Thr Ser Leu Pro Asp Gly Val Tyr Cys Asp Val Ala Asn Gly
                405                 410                 415


Thr Phe Val Asp Gly Val Cys Asp Gly Pro Ser Tyr Gln Val Ser Gly
            420                 425                 430


Gly Lys Phe Thr Ala Thr Val Pro Ala Asn Gly Ala Val Ala Leu His
        435                 440                 445


Val Glu Ala Pro Gly Ser Cys Gly Pro Asp Gly Cys Gly Thr Pro Pro
    450                 455                 460


Gly Gly Gly Asp Asp Cys Thr Thr Val Thr Ala Arg Phe His Ala Thr
465                 470                 475                 480


Val Thr Thr Trp Tyr Gly Gln Glu Val Ala Val Val Gly Ser Ile Pro
                485                 490                 495


Glu Leu Gly Ser Trp Gln Pro Ala Gln Gly Val Arg Leu Arg Thr Asp
            500                 505                 510


Ser Gly Thr Tyr Pro Val Trp Ser Gly Ala Val Asp Leu Pro Ala Gly
        515                 520                 525


Val Gly Phe Glu Tyr Lys Tyr Val Lys Leu Asn Pro Asp Gly Thr Val
    530                 535                 540


Glu Trp Glu Gln Gly Gly Asn Arg Ile Ala Thr Val Asp Asp Ser Gly
545                 550                 555                 560


Gly Gly Cys Ser Gln Asn Phe Tyr Asp Ser Trp Arg
                565                 570
```

```
<210>  98
<211>  825
<212>  PRT
<213>  Anaerocellum thermophilum

<400>  98

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


Leu Ser Gln Met Val His Ser Val Lys Lys Glu Asp Phe Lys Val Phe
            20                  25                  30


Leu Asn Glu Glu Glu Ile Asp Ile Glu Lys Ile Asp Lys Ile Ile Pro
        35                  40                  45


His Ser Asp Asn Pro Ala Glu Ala Glu Thr Arg Gly Tyr Glu Ile Cys
    50                  55                  60


Glu Gln Lys Gly Lys Ile Arg Phe Val Leu Lys Glu Gly His Phe Asp
65                  70                  75                  80


Tyr His Arg Lys Pro Tyr Lys Lys Pro Val Phe Val Ile Gly Glu Met
                85                  90                  95


Asn Asp Trp Gln Ile Ser Pro Glu Trp Glu Met Thr Tyr Ser Lys Leu
            100                 105                 110


Arg Gly Arg Tyr Glu Leu Ile Lys Asp Leu Lys Glu Ile Lys Ile Gly
        115                 120                 125


Gln Lys Phe Lys Phe Ala Glu Gly Ala Ser Gln Lys Leu Trp Tyr Pro
    130                 135                 140


Pro Gly Phe Gly Asn Asp Ile Val Ile Thr Glu Tyr Phe Asp Arg Glu
145                 150                 155                 160


Thr Ala Phe Thr Asn Met Ile Arg Ile Ile Pro Ser Asn Arg Leu Leu
                165                 170                 175
```

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


Arg Pro Arg Glu Ile Leu Thr Arg Pro Glu Phe Phe Tyr Pro Gly Glu
        195                 200                 205


Leu Gly Ile Lys Tyr Glu Pro Tyr Gly Thr Tyr Phe Lys Leu Trp Ala
    210                 215                 220


Pro Thr Ala Tyr Lys Val Lys Val Lys Val Phe Asp Glu Ser Glu Asn
225                 230                 235                 240


Phe Arg Phe Glu Lys Glu Met Ala Arg Ser Glu Asn Gly Thr Trp Asn
                245                 250                 255


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


Trp His Tyr Asn Tyr Asp Glu Asp Glu Gly Phe Ile Val Tyr Glu Val
        275                 280                 285


Pro Asp Pro Tyr Ser Lys Ala Ser Ser Ser Asn Ser Gln Lys Ser Phe
    290                 295                 300


Ile Phe Asp Pro Ala Asp Thr Leu Ile Glu Gly Trp Gln Gln Asp Glu
305                 310                 315                 320


Phe Val Lys Thr Ile Glu Lys Gln Gln Asp Ala Ile Ile Tyr Glu Met
                325                 330                 335


His Val Arg Asp Phe Thr Ile Asp Lys Asn Ser Gly Val Asp Glu Lys
            340                 345                 350


Phe Arg Gly Lys Phe Leu Gly Leu Cys Gln Lys Ser Phe Tyr Lys Glu
        355                 360                 365


Lys Phe Ser Thr Gly Leu Leu His Leu Lys Glu Leu Gly Ile Thr His
    370                 375                 380
```

```
Ile His Leu Leu Pro Ile Ser Asp Phe Gly Ser Val Asp Asp Lys Asn
385                 390                 395                 400


Pro Asp Lys Lys Tyr Asn Trp Gly Tyr Asp Pro Val Leu Tyr Gln Cys
                405                 410                 415


Pro Glu Tyr Trp Tyr Ser Thr Lys Ser Gly Gly Ile Glu Ala Leu Lys
            420                 425                 430


Glu Leu Lys Thr Met Ile Lys Thr Leu His Gln Asn Gly Ile Gly Val
        435                 440                 445


Val Met Asp Val Val Phe Asn His Thr Tyr His Thr Lys Gly Gly Lys
    450                 455                 460


Phe Ser Ile Phe Asp Lys Ile Val Pro Gly Tyr Phe Tyr Arg Ile Asp
465                 470                 475                 480


Asp Tyr Gly Asp Tyr Ser Asn Ala Thr Gly Cys Gly Asn Glu Ile Ala
                485                 490                 495


Thr Glu Lys Pro Met Val Arg Lys Phe Ile Leu Asp Thr Ile Ile Tyr
            500                 505                 510


Trp Thr Glu Asp Phe His Ile Asp Gly Phe Arg Phe Asp Leu Met Gly
        515                 520                 525


Leu Ile Asp Thr Leu Thr Met Arg Met Ile Ala Lys Glu Val Arg Lys
    530                 535                 540


Arg Asn Pro Tyr Ala Leu Ile Tyr Gly Glu Gly Trp Val Met Gly Asp
545                 550                 555                 560


Ser Met Cys Leu Leu Glu Glu Arg Ala Thr Ile Glu Ser Thr Ala His
                565                 570                 575


His Gly Tyr Ser Ile Gly Leu Phe Asn Asp Arg Ile Arg Asp Ser Ile
            580                 585                 590
```

```
Arg Gly Asp Leu Asp Gly Phe Lys Thr Gly Tyr Met His Gly Asn Leu
        595                 600                 605


Ser Asp Ile Glu Arg Leu Lys Gln Gly Ile Arg Ala Ala Ile Asp Asp
    610                 615                 620


Phe Ala Lys Glu Pro Asp Glu Cys Val Asn Tyr Val Ser Cys His Asp
625                 630                 635                 640


Asn Leu Thr Leu Phe Asp Lys Ala Gln Lys Thr Met Val Gly Glu Asp
                645                 650                 655


Ile Phe Trp Ile Asp Arg Val Cys Arg Leu Ala Asn Ala Ile Ile Leu
            660                 665                 670


Thr Ser Gln Gly Ile Pro Phe Leu His Gly Gly Val Glu Phe Asn Arg
        675                 680                 685


Ser Lys Gly Gly His Pro Asn Thr Tyr Asn Ala Gly Asp Asn Ile Asn
    690                 695                 700


Lys Ile Asp Trp Ser Leu Lys Glu Lys Phe Tyr Asp Thr Phe Lys Phe
705                 710                 715                 720


Tyr Cys Asp Leu Ile Lys Leu Arg Lys Glu His Val Ala Phe Arg Met
                725                 730                 735


Arg Ser Ser Gly Glu Ile Arg Lys Tyr Leu Lys Phe Leu Pro Ala Pro
            740                 745                 750


Asp Gly Ile Val Ala Phe Leu Ile Ser Tyr Pro Tyr Asp Ala Trp Lys
        755                 760                 765


Lys Ile Ile Val Ala Tyr Asn Pro Phe Lys Glu Lys Lys Val Ile Thr
    770                 775                 780


Leu Pro Glu Gly Val Trp Lys Ile Lys Ala Asn Asp Gly Ile Ile Phe
785                 790                 795                 800
```

```
Ser Glu Glu Asn Glu Leu Glu Ala Ile Gly Ser Phe Glu Ile Ser Pro
                805                 810                 815


Val Ser Leu Phe Ile Ala Tyr Gln Lys
            820                 825


<210>  99
<211>  1104
<212>  PRT
<213>  Anaerocellum thermophilum

<400>  99

Asp Glu Lys Thr Thr Leu Ile Ile His Tyr Tyr Arg Tyr Asn Glu Asp
1               5                   10                  15


Tyr Gln Gly Trp Asn Leu Trp Ile Trp Pro Val Glu Pro Val Gly Ala
            20                  25                  30


Glu Gly Lys Ala Tyr Glu Phe Thr Ser Lys Asp Asp Phe Gly Val Lys
        35                  40                  45


Ala Val Val Glu Leu Pro Gly Lys Val Thr Lys Val Gly Ile Ile Val
    50                  55                  60


Arg Lys Gly Asn Trp Glu Ala Lys Asp Val Ala Val Asp Arg Phe Ile
65                  70                  75                  80


Ser Gly Ile Ser Gly Ser Lys Glu Val Trp Leu Ile Glu Gly Glu Glu
                85                  90                  95


Gln Ile Tyr Thr Ser Gln Pro Gln Lys Thr Pro Lys Met Thr Ala Phe
            100                 105                 110


Ile Asp Gly Leu Asn Thr Ile Val Val Lys Leu Ala Lys Lys Ala Asp
        115                 120                 125


Ile Leu Ser Asn Asn Arg Thr Gln Gly Phe Lys Val Thr Ala Phe Tyr
    130                 135                 140
```

```
Glu Glu Val Pro Ile Lys Lys Val Glu Pro Val Leu Pro Lys Ile Asn
145                 150                 155                 160


Lys Asn Phe Lys Pro Glu Glu Ala Gly Tyr Glu Leu Ile Asp Gly Gly
                165                 170                 175


Thr Lys Val Lys Phe Ile Leu Lys Pro Gly Ala Gly Asp Phe Lys Phe
            180                 185                 190


Thr Asp Thr Ser Gly Lys Leu Asp Val Tyr Val Ser Gly Thr Met Asn
        195                 200                 205


Asp Trp Gly Gly Thr Ala Ser Ser Glu Gly Lys Tyr Lys Pro Leu Pro
    210                 215                 220


Ala Trp Lys Met Thr Trp Asn Ala Glu Lys Gly Tyr Tyr Glu Leu Val
225                 230                 235                 240


Lys Glu Leu Gly Lys Asp Gly Val Val Ile Gly Ala Lys Phe Lys Phe
                245                 250                 255


Thr Ser Trp Asp Gly Thr Ser Ala Lys Trp Tyr Pro Asp Gly Met Gly
            260                 265                 270


Asn Asp Lys Val Ile Glu Glu Leu Tyr Thr Gly Asn Glu Lys Ile Thr
        275                 280                 285


Lys Val Asp Thr Phe Lys Ile Thr Thr Glu Asp Glu Leu Glu Pro Gln
    290                 295                 300


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


Ala Arg Asn Ile Leu Asp Asn Pro Lys Tyr Tyr Tyr Lys Gly Asn Asp
                325                 330                 335


Leu Gly Cys Thr Tyr Thr Lys Ala Tyr Ser Ala Phe Arg Leu Trp Ala
            340                 345                 350
```

```
Pro Thr Ala Ile Gly Val Ile Leu Arg Leu Tyr Asp Asp Tyr Lys Thr
        355                 360                 365


Thr Lys Tyr Lys Glu Tyr Glu Met Gln Gln Ser Phe Asn Gly Thr Trp
    370                 375                 380


Tyr Leu Lys Ile Asn Gly Asp Leu Lys Gly Lys Tyr Tyr Gln Tyr Glu
385                 390                 395                 400


Val Trp His Ala Ser Asn Ser Ile Thr Asp Asp Thr Ile Arg Lys Tyr
                405                 410                 415


Val Val Pro Asp Pro Tyr Ser Arg Ala Thr Ser Ala Asn Ser Glu Arg
            420                 425                 430


Thr Leu Ile Phe Asp Pro Lys Asp Thr Asn Pro Val Gly Trp Glu Lys
        435                 440                 445


Asp Thr Phe Val Thr Leu Lys Asn Gln Glu Asp Ala Ile Ile Tyr Glu
    450                 455                 460


Thr His Val Arg Asp Phe Thr Ile Asp Ala Ser Ser Gly Val Arg Pro
465                 470                 475                 480


Glu Phe Arg Gly Lys Tyr Leu Gly Phe Thr Gln Thr Gly Ala Lys Gly
                485                 490                 495


Pro Asn Gly Val Lys Thr Gly Ile Asp His Leu Lys Glu Leu Gly Ile
            500                 505                 510


Thr His Val His Leu Leu Pro Thr Tyr Asp Phe Gly Ser Ile Asp Glu
        515                 520                 525


Thr Asn Pro Asp Lys Gly Tyr Asn Trp Gly Tyr Asp Pro Val Leu Tyr
    530                 535                 540


Gln Asn Val Glu Gly Ser Tyr Ala Thr Asn Pro Asn Thr Ile Val Arg
545                 550                 555                 560
```

```
Ile Lys Glu Tyr Lys Gln Met Val Met Ala Leu His Lys Ala Gly Ile
                565                 570                 575


Gly Ile Ile Gln Asp Val Val Phe Asn His Thr Phe Gln Ile Gly Asp
            580                 585                 590


Ala Lys Phe Ser Ile Phe Asp Lys Ile Val Pro Gly Tyr Phe Tyr Arg
        595                 600                 605


Lys Asp Lys Asp Gly Asn Tyr Ser Asn Ala Ser Gly Cys Gly Asn Glu
    610                 615                 620


Ile Ala Thr Glu Lys Pro Met Val Arg Lys Phe Ile Ile Asp Thr Leu
625                 630                 635                 640


Thr Tyr Leu Thr Lys Glu Tyr His Ile Asp Gly Phe Arg Phe Asp Leu
                645                 650                 655


Met Ala Ala Ile Asp Arg Val Thr Met Ala Lys Ala Gln Glu Glu Val
            660                 665                 670


Arg Lys Ile Asn Pro Ser Ala Val Ile Tyr Gly Glu Gly Trp Leu Ala
        675                 680                 685


Gly Ser Thr Pro Leu Asp Ser Ser Leu Arg Met Glu Ile Gly Ser Phe
    690                 695                 700


Asn Gln Ala Gly Leu His Ile Gly Leu Phe Asn Asp Arg Ile Arg Glu
705                 710                 715                 720


Ala Ile Arg Gly Asn Leu Asp Asn Glu Ser Lys Gly Phe Met Gln Gly
                725                 730                 735


Asn Tyr Ser Phe Arg Leu Glu Asp Leu Lys Arg Gly Ile Gln Gly Gly
            740                 745                 750


Leu Gly Asp Phe Ala Ala Asp Pro Asp Glu Cys Ile Asn Tyr Val Ser
        755                 760                 765
```

```
Ala His Asp Asn Leu Thr Leu Trp Asp Lys Leu Gln Lys Ser Val Pro
    770                 775                 780


Asn Glu Pro Asp Tyr Ile Lys Asp Lys Met Gly Arg Leu Ala Asn Ala
785                 790                 795                 800


Ile Val Leu Thr Ala Gln Gly Val Pro Phe Leu His Gly Gly Val Glu
                805                 810                 815


Phe Asn Arg Thr Lys Tyr Met Asn His Asn Ser Tyr Asn Ala Gly Asp
            820                 825                 830


Lys Ile Asn Lys Tyr Asn Trp Asn Leu Lys Val Lys Trp Tyr Asn Thr
        835                 840                 845


Phe Lys Tyr Tyr Gln Gly Leu Ile Ala Leu Arg Lys Ala His Pro Ala
    850                 855                 860


Phe Arg Met Thr Thr Ala Glu Asp Ile Gln Lys Tyr Leu Thr Phe Ile
865                 870                 875                 880


Gln Thr Pro Lys Gly Thr Leu Gly Phe Arg Leu Thr Tyr Pro Lys Asp
                885                 890                 895


Thr Trp Asn Asp Ile Ile Val Val Tyr Asn Ser Thr Lys Lys Val Gln
            900                 905                 910


Glu Val Thr Leu Pro Glu Gly Asn Trp Val Val Val Ala Asn Gly Asp
        915                 920                 925


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


Lys Ala Leu Val Ala Pro Ile Ser Met Phe Val Ala Tyr Lys Ser Asn
945                 950                 955                 960


Glu Phe Pro Gln Gly Phe Thr Lys Val Thr Gly Lys Asp Pro Val Ser
                965                 970                 975
```

```
Leu Glu Ser Ser Ser Thr Val Thr Val Pro Lys Val Tyr Gly Asn Gly
            980                 985                 990


Asn Ile Glu Val Thr Phe Lys Val  Lys Val Pro His Gly  Thr Asp Asp
        995                 1000                1005


Asp Val  Ile Tyr Leu Ala Gly  Ser Phe Gly Lys Ala  Gly Leu Ser
    1010                 1015                 1020


Asp Trp  Asn Pro Gly Asp Lys  Asp Gly Ala Ile Glu  Leu Val Arg
    1025                 1030                 1035


Leu Gln  Asp Gly Thr Tyr Thr  Val Thr Val Lys Leu  Asn Ala Gly
    1040                 1045                 1050


Glu Thr  Phe Glu Tyr Lys Tyr  Thr Arg Gly Ser Trp  Thr Thr Val
    1055                 1060                 1065


Glu Lys  Gly Ala Asn Lys Glu  Glu Ile Glu Asn Arg  Lys Leu Thr
    1070                 1075                 1080


Val Lys  Asp Glu Gly Gly Gly  Lys Met Ile Val Ser  Asp Thr Val
    1085                 1090                 1095


Leu Asn  Trp Ala Asp Lys
    1100


<210>  100
<211>  611
<212>  PRT
<213>  Anaerocellum thermophilum

<400>  100

Met Arg Lys Pro His Ile Ile Glu Ala Ile Ile Gly Asn Thr Lys Val
1               5                   10                  15


Leu Gly Gln Leu Asp Ser Asn Gly Ile Leu Gln Arg Phe Tyr Trp Pro
            20                  25                  30


Ala Val Asp Tyr Tyr Gln Gln Leu Lys Leu Phe Leu Ala Ala Val Phe
```

```
        35                  40                  45

Leu Asp Gly Leu Val Phe Phe Glu Asp Glu Asn Phe Lys Ile Lys Ser
    50                  55                  60

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

Lys Thr Ile Phe Gln Leu Asp Phe Val Asp Phe Glu Thr Asp Ser Leu
                85                  90                  95

Val Arg Leu Trp Glu Thr Gly Phe Glu Asp Phe Tyr Val Phe Leu Glu
            100                 105                 110

Pro Met Ile Asn Ser Ser Ser Leu Phe Asn Ala Ala Lys Val Asp Lys
        115                 120                 125

Glu Asn Glu Ile Val Tyr Ala Tyr Phe Lys Gly Thr Tyr Ile Gly Leu
    130                 135                 140

Ala Phe Glu Asn Lys Ile Lys Ser Phe Thr Val Lys Asn Gly Ile Asp
145                 150                 155                 160

Asp Ala Asn Asp Asn Gln Leu Glu Gly Trp Asn Glu Ala Thr Asn Pro
                165                 170                 175

Gln Ile Ala Val Lys Leu Lys Asn Thr Gly Lys Val Val Cys Phe Leu
            180                 185                 190

Ala Phe Gly Asn Ser Lys Asp Glu Ile Tyr Gln Lys Leu Ser Tyr Leu
        195                 200                 205

Lys Gln Lys Gly Tyr Asp Glu Val Tyr Arg Gln Asn Lys Ala Phe Trp
    210                 215                 220

Glu Lys Lys Phe Ser Lys Val Lys Leu Ile Cys Thr Gln Asp Pro Lys
225                 230                 235                 240

Asp Met Gln Leu Gln Lys Arg Ser Ala Tyr Val Phe Tyr Val Leu Gln
```

```
                245                 250                 255

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

Phe Phe His Cys Gly Gly Tyr Gly Phe Val Trp Gly Arg Asp Ala Ala
        275                 280                 285

Phe Ile Val Ser Ala Met Asp Glu Leu Gly Leu Ser Arg Glu Val Glu
    290                 295                 300

Lys Phe Phe Gly Phe Lys Phe Ser Cys Gln Glu Lys Glu Gly Phe Trp
305                 310                 315                 320

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

Gln Ile Asp Glu Thr Ala Ser Val Val Trp Gly Phe Leu Glu His Cys
            340                 345                 350

Glu Lys Gln Asn Ser Leu His Leu Ile Asp Leu His Lys Glu Gln Leu
        355                 360                 365

Lys Lys Ala Leu Leu Phe Leu Ile Ala Ala Val Asp Ser Glu Lys Gly
    370                 375                 380

Val Ile Phe Arg Ser Phe Asp Leu Trp Glu Glu Arg Glu Gly Ile His
385                 390                 395                 400

Leu Tyr Ser Asn Ala Ser Ile Tyr Ala Ala Leu Lys Lys Ala Lys Lys
                405                 410                 415

Tyr Phe Pro Glu Leu Glu Ser Glu Ile Glu Lys Lys Leu Lys Ala Ile
            420                 425                 430

Lys Asn Gln Met Ala Thr Arg Phe Tyr Ser Pro Lys Leu Ser Arg Tyr
        435                 440                 445

Val Arg Ser Thr Asp Val Arg Ile Pro His Glu Glu Phe Leu Lys Leu
```

```
    450                 455                 460

Pro Glu Glu Asn Arg Tyr Met Gln Lys Asp Glu Arg Tyr Glu Ile Thr
465                 470                 475                 480

Tyr Tyr Phe Lys Lys Gln Asp Glu Val Val Asp Ile Ser Met Leu Gly
                485                 490                 495

Ile Tyr Tyr Pro Phe Glu Met Val Asp Ser Ser Asp Lys Ala Phe Lys
            500                 505                 510

Ala Thr Ile Leu Ala Ile Glu Arg Glu Cys Gln Asn Ser Ile Val Gly
        515                 520                 525

Gly Tyr Lys Arg Tyr Ser Asp Asp Arg Tyr Ile Gly Gly Asn Pro Trp
    530                 535                 540

Ile Leu Thr Thr Leu Trp Leu Ala Ile Tyr Tyr Lys Lys Thr Gly Gln
545                 550                 555                 560

Ile Asp Arg Ala Glu Lys Leu Phe Glu Trp Ala Lys Ala His Ser Leu
                565                 570                 575

Pro Asn Gly Leu Phe Pro Glu Gln Val Asp Arg Ile Thr Gly Lys Pro
            580                 585                 590

Ala Trp Val Val Pro Leu Ala Trp Ser His Ala Met Tyr Val Leu Tyr
        595                 600                 605

Leu Tyr Glu
    610


<210>  101
<211>  529
<212>  PRT
<213>  Streptomyces avermitilis

<400>  101

Met Thr Ser Phe Arg Pro Ala Pro Ala Trp Leu Ala Asp Ala Val Phe
1               5                   10                  15
```

```
Tyr Gln Ile Tyr Pro Gln Ser Phe Ala Asp Ser Asp Gly Asp Gly Ile
            20                  25                  30

Gly Asp Phe Asn Gly Ile Val Gln Arg Leu Asp His Leu Val Trp Leu
        35                  40                  45

Gly Val Thr Ala Val Trp Leu Asn Pro Cys Phe Val Ser Pro Phe Arg
    50                  55                  60

Asp Ala Gly Tyr Asp Val Ser Asp Tyr Leu Asn Val Ala Pro Arg Tyr
65                  70                  75                  80

Gly Ser Ala Asp Asp Leu Ala Glu Leu Val Asp Glu Ala Gly Arg Arg
                85                  90                  95

Gly Ile Arg Val Leu Leu Asp Leu Val Ala Gly His Thr Ser Asp Glu
            100                 105                 110

His Pro Trp Phe Thr Ala Ser Ala Asn Asp Pro Asp Asp His Arg Tyr
        115                 120                 125

Ile Trp Ala Pro Glu Gly Arg Pro Asp Gly Phe Val Thr Ser Pro Gly
    130                 135                 140

Thr Arg Pro Gly Ala Tyr Leu Pro Asn Phe Phe Asp Thr Gln Pro Ala
145                 150                 155                 160

Leu Asn Phe Gly Tyr Gly Arg Lys Asn Pro Ala Glu Pro Trp Arg Gln
                165                 170                 175

Pro Val Asp Ala Ala Gly Pro Arg Ala Asn Arg Glu Ala Leu Arg Thr
            180                 185                 190

Ile Met Asp His Trp Leu Gly Leu Gly Leu Ala Gly Phe Arg Val Asp
        195                 200                 205

Met Ala Ala Ser Leu Val Lys Asp Asp Pro Gly Arg Thr Glu Thr Ala
    210                 215                 220
```

```
Arg Ile Trp Thr Glu Leu Arg His Trp Leu Asp Thr Ala His Pro Asp
225                 230                 235                 240


Ala Val Leu Leu Ser Glu Trp Gly Glu Pro Glu Val Ser Val Pro Ala
                245                 250                 255


Gly Phe His Thr Asp Phe Phe Leu Gln Phe Gly Gly Ala Thr Asp Gly
            260                 265                 270


Leu Pro Leu Arg Ser Leu Trp Ser Asn Gly Asp Gly Thr Val Asn Glu
        275                 280                 285


Ala Trp Asp Pro Leu Asp Cys Phe Phe Asp Ala Ser Gly Lys Gly Ser
    290                 295                 300


Pro Arg Pro Phe Val Glu Ala Trp Arg Lys Ala Ser Asp Ala Val Gly
305                 310                 315                 320


Ala Thr Gly Phe Val Ser Leu Pro Thr Ala Asn His Asp Phe Ser Arg
                325                 330                 335


Leu Asn Cys Gly Pro Arg Thr Ala Glu Gln Leu Pro Ala Ala Phe Ala
            340                 345                 350


Phe Gln Leu Thr Trp Pro Thr Leu Pro Ala Ile Tyr Tyr Gly Asp Glu
        355                 360                 365


Ile Gly Met Arg Tyr Val Gly Gly Leu Pro Asp Lys Glu Gly Ser Val
    370                 375                 380


Leu Gly Pro Arg Tyr Asn Arg Ala Gly Ser Arg Thr Pro Met Gln Trp
385                 390                 395                 400


Asp Asp Gly Pro Gly Ala Gly Phe Ser Thr Ala Pro Ala Asp Arg Leu
                405                 410                 415


Tyr Leu Pro Leu Asp Pro Ser Pro Asp Arg Pro Thr Val Ala Ala Gln
            420                 425                 430
```

```
Arg Ala Asp Asp Gly Ser Leu Leu His Leu Val Arg Arg Leu Val Ala
        435                 440                 445


Leu Arg Ala Ser Thr Pro Ala Leu Gly Ser Gly Gly Ser Val Glu Val
    450                 455                 460


Leu His Thr Gly Tyr Pro Phe Val Tyr Val Arg Gly Gly Arg Tyr Leu
465                 470                 475                 480


Val Val Val Asn Pro Gln Arg Asn Glu Val Arg Cys Pro Tyr Asp Ala
                485                 490                 495


Thr Arg Glu Ala Arg Ala Leu Glu Ala Ser Gly Val Arg Val Gly Asn
            500                 505                 510


Gly Thr Ile Glu Ala Glu Gly Phe Ser Tyr Gly Val Phe Asp Leu Gly
        515                 520                 525


Arg



<210>  102
<211>  431
<212>  PRT
<213>  Streptomyces avermitilis

<400>  102

Ser Pro Pro Gly Thr Lys Asp Val Thr Ala Val Leu Phe Glu Trp Lys
1               5                   10                  15


Phe Asp Ser Val Ala Arg Glu Cys Thr Asn Thr Leu Gly Pro Ala Gly
            20                  25                  30


Tyr Gly Tyr Val Gln Val Ser Pro Pro Ala Glu His Ile Gln Gly Ser
        35                  40                  45


Gln Trp Trp Thr Ser Tyr Gln Pro Val Ser Tyr Lys Ile Ala Gly Arg
    50                  55                  60
```

```
Leu Gly Asp Ala Thr Ala Phe Gln Asn Met Ile Asn Thr Cys His Thr
65                  70                  75                  80


Ala Gly Val Lys Val Val Val Asp Thr Val Val Asn His Met Ser Ala
                85                  90                  95


Gly Ser Gly Thr Gly Thr Gly Gly Ser Ala Tyr Thr Lys Tyr Asn Tyr
            100                 105                 110


Pro Gly Leu Tyr Ser Ser Tyr Asp Met Asp Asp Cys Thr Ala Thr Ile
        115                 120                 125


Thr Asp Tyr Thr Asn Arg Ala Asn Val Gln Asn Cys Glu Leu Val Gly
    130                 135                 140


Leu Ala Asp Leu Asp Thr Gly Glu Glu Tyr Val Arg Lys Thr Ile Ala
145                 150                 155                 160


Gly Tyr Met Asn Thr Leu Leu Gly Tyr Gly Ala Asp Gly Phe Arg Val
                165                 170                 175


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


Arg Leu Thr Asn Pro Ser Val Tyr Trp Lys Gln Glu Val Ile Tyr Ala
        195                 200                 205


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


Gln Glu Phe Arg Tyr Ala Tyr Asp Leu Lys Arg Val Phe Asn Asn Glu
225                 230                 235                 240


Asn Leu Ala Tyr Leu Lys Asn Tyr Gly Glu Gly Trp Gly Tyr Leu Asn
                245                 250                 255


Ser Ser Val Ala Gly Val Phe Val Asp Asn His Asp Thr Glu Arg Asn
            260                 265                 270
```

Gly Ser Thr Leu Asn Tyr Lys Asp Gly Ala Asn Tyr Thr Leu Ala Asn
        275   280   285

Val Phe Met Leu Ala Tyr Pro Tyr Gly Ala Pro Asp Ile Asn Ser Gly
    290   295   300

Tyr Glu Trp Ser Asp Ala Asp Ala Gly Pro Pro Gly Gly Gly Thr Val
305   310   315   320

Asn Ala Cys Trp Gln Asp Gly Trp Lys Cys Gln His Ala Trp Pro Glu
                325   330   335

Ile Lys Ala Met Val Ala Phe Arg Asn Ala Thr Arg Gly Glu Ser Val
            340   345   350

Thr Asn Trp Trp Asp Asn Gly Gly Asp Ala Ile Ala Phe Gly Arg Gly
        355   360   365

Ala Lys Gly Tyr Val Ala Ile Asn His Glu Ser Gly Ser Leu Thr Arg
    370   375   380

Thr Tyr Gln Thr Ser Leu Thr Ala Gly Thr Tyr Cys Asn Val Gln Asn
385   390   395   400

Asn Thr Gly Val Thr Val Asp Ser Ser Gly Arg Phe Thr Ala Thr Leu
                405   410   415

Gly Ala Asn Thr Ala Leu Ala Leu Tyr Ser Gly Lys Ser Thr Cys
            420   425   430

<210> 103
<211> 503
<212> PRT
<213> Saccharomycopsis fibuligera

<400> 103

Leu Pro Leu Gln Glu Gly Pro Leu Asn Lys Arg Ala Tyr Pro Ser Phe
1   5   10   15

```
Glu Ala Tyr Ser Asn Tyr Lys Val Asp Arg Thr Asp Leu Glu Thr Phe
            20                  25                  30


Leu Asp Lys Gln Lys Asp Val Ser Leu Tyr Tyr Leu Leu Gln Asn Ile
        35                  40                  45


Ala Tyr Pro Glu Gly Gln Phe Asn Asp Gly Val Pro Gly Thr Val Ile
    50                  55                  60


Ala Ser Pro Ser Thr Ser Asn Pro Asp Tyr Tyr Tyr Gln Trp Thr Arg
65                  70                  75                  80


Asp Ser Ala Ile Thr Phe Leu Thr Val Leu Ser Glu Leu Glu Asp Asn
                85                  90                  95


Asn Phe Asn Thr Thr Leu Ala Lys Ala Val Glu Tyr Tyr Ile Asn Thr
            100                 105                 110


Ser Tyr Asn Leu Gln Arg Thr Ser Asn Pro Ser Gly Ser Phe Asp Asp
        115                 120                 125


Glu Asn His Lys Gly Leu Gly Glu Pro Lys Phe Asn Thr Asp Gly Ser
    130                 135                 140


Ala Tyr Thr Gly Ala Trp Gly Arg Pro Gln Asn Asp Gly Pro Ala Leu
145                 150                 155                 160


Arg Ala Tyr Ala Ile Ser Arg Tyr Leu Asn Asp Val Asn Ser Leu Asn
                165                 170                 175


Lys Gly Lys Leu Val Leu Thr Asp Ser Gly Asp Ile Asn Phe Ser Ser
            180                 185                 190


Thr Glu Asp Ile Tyr Lys Asn Ile Ile Lys Pro Asp Leu Glu Tyr Val
        195                 200                 205


Ile Gly Tyr Trp Asp Ser Thr Gly Phe Asp Leu Trp Glu Glu Asn Gln
    210                 215                 220
```

```
Gly Arg His Phe Phe Thr Ser Leu Val Gln Gln Lys Ala Leu Ala Tyr
225                 230                 235                 240


Ala Val Asp Ile Ala Lys Ser Phe Asp Asp Gly Asp Phe Ala Asn Thr
                245                 250                 255


Leu Ser Ser Thr Ala Ser Thr Leu Glu Ser Tyr Leu Ser Gly Ser Asp
            260                 265                 270


Gly Gly Phe Val Asn Thr Asp Val Asn His Ile Val Glu Asn Pro Asp
        275                 280                 285


Leu Leu Gln Gln Asn Ser Arg Gln Gly Leu Asp Ser Ala Thr Tyr Ile
    290                 295                 300


Gly Pro Leu Leu Thr His Asp Ile Gly Glu Ser Ser Ser Thr Pro Phe
305                 310                 315                 320


Asp Val Asp Asn Glu Tyr Val Leu Gln Ser Tyr Tyr Leu Leu Leu Glu
                325                 330                 335


Asp Asn Lys Asp Arg Tyr Ser Val Asn Ser Ala Tyr Ser Ala Gly Ala
            340                 345                 350


Ala Ile Gly Arg Tyr Pro Glu Asp Val Tyr Asn Gly Asp Gly Ser Ser
        355                 360                 365


Glu Gly Asn Pro Trp Phe Leu Ala Thr Ala Tyr Ala Ala Gln Val Pro
    370                 375                 380


Tyr Lys Leu Val Tyr Asp Ala Lys Ser Ala Ser Asn Asp Ile Thr Ile
385                 390                 395                 400


Asn Lys Ile Asn Tyr Asp Phe Phe Asn Lys Tyr Ile Val Asp Leu Ser
                405                 410                 415


Thr Ile Asn Ser Gly Tyr Gln Ser Ser Asp Ser Val Thr Ile Lys Ser
            420                 425                 430
```

```
Gly Ser Asp Glu Phe Asn Thr Val Ala Asp Asn Leu Val Thr Phe Gly
        435                 440                 445


Asp Ser Phe Leu Gln Val Ile Leu Asp His Ile Asn Asp Asp Gly Ser
    450                 455                 460


Leu Asn Glu Gln Leu Asn Arg Asn Thr Gly Tyr Ser Thr Ser Ala Tyr
465                 470                 475                 480


Ser Leu Thr Trp Ser Ser Gly Ala Leu Leu Glu Ala Ile Arg Leu Arg
                485                 490                 495


Asn Lys Val Lys Ala Leu Ala
            500


<210>  104
<211>  497
<212>  PRT
<213>  Saccharomycopsis fibuligera

<400>  104

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


Ser Gly Tyr Thr Val Ala Arg Ser Asn Phe Thr Gln Trp Ile His Glu
            20                  25                  30


Gln Pro Ala Val Ser Trp Tyr Tyr Leu Leu Gln Asn Ile Asp Tyr Pro
        35                  40                  45


Glu Gly Gln Phe Lys Ser Ala Lys Pro Gly Val Val Val Ala Ser Pro
    50                  55                  60


Ser Thr Ser Glu Pro Asp Tyr Phe Tyr Gln Trp Thr Arg Asp Thr Ala
65                  70                  75                  80


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


Asn Thr Thr Leu Ala Lys Val Val Glu Tyr Tyr Ile Ser Asn Thr Tyr
```

```
            100                 105                 110

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

His Asp Gly Leu Gly Glu Pro Lys Phe Asn Val Asp Asp Thr Ala Tyr
    130                 135                 140

Thr Ala Ser Trp Gly Arg Pro Gln Asn Asp Gly Pro Ala Leu Arg Ala
145                 150                 155                 160

Tyr Ala Ile Ser Arg Tyr Leu Asn Ala Val Ala Lys His Asn Asn Gly
                165                 170                 175

Lys Leu Leu Leu Ala Gly Gln Asn Gly Ile Pro Tyr Ser Ser Ala Ser
            180                 185                 190

Asp Ile Tyr Trp Lys Ile Ile Lys Pro Asp Leu Gln His Val Ser Thr
        195                 200                 205

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

His Phe Phe Thr Ala Leu Val Gln Leu Lys Ala Leu Ser Tyr Gly Ile
225                 230                 235                 240

Pro Leu Ser Lys Thr Tyr Asn Asp Pro Gly Phe Thr Ser Trp Leu Glu
                245                 250                 255

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

Asn Ser Gly Lys Lys His Ile Val Glu Ser Pro Gln Leu Ser Ser Arg
        275                 280                 285

Gly Gly Leu Asp Ser Ala Thr Tyr Ile Ala Ala Leu Ile Thr His Asp
    290                 295                 300

Ile Gly Asp Asp Asp Thr Tyr Thr Pro Phe Asn Val Asp Asn Ser Tyr
```

305   310   315   320

Val Leu Asn Ser Leu Tyr Tyr Leu Leu Val Asp Asn Lys Asn Arg Tyr
                325   330   335

Lys Ile Asn Gly Asn Tyr Lys Ala Gly Ala Ala Val Gly Arg Tyr Pro
            340   345   350

Glu Asp Val Tyr Asn Gly Val Gly Thr Ser Glu Gly Asn Pro Trp Gln
        355   360   365

Leu Ala Thr Ala Tyr Ala Gly Gln Thr Phe Tyr Thr Leu Ala Tyr Asn
    370   375   380

Ser Leu Lys Asn Lys Lys Asn Leu Val Ile Glu Lys Leu Asn Tyr Asp
385   390   395   400

Leu Tyr Asn Ser Phe Ile Ala Asp Leu Ser Lys Ile Asp Ser Ser Tyr
                405   410   415

Ala Ser Lys Asp Ser Leu Thr Leu Thr Tyr Gly Ser Asp Asn Tyr Lys
            420   425   430

Asn Val Ile Lys Ser Leu Leu Gln Phe Gly Asp Ser Phe Leu Lys Val
        435   440   445

Leu Leu Asp His Ile Asp Asp Asn Gly Gln Leu Thr Glu Glu Ile Asn
    450   455   460

Arg Tyr Thr Gly Phe Gln Ala Gly Ala Val Ser Leu Thr Trp Ser Ser
465   470   475   480

Gly Ser Leu Leu Ser Ala Asn Arg Ala Arg Asn Lys Leu Ile Glu Leu
                485   490   495

Leu

<210> 105

```
<211>  747
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  105

Phe Pro Thr Ala Leu Val Pro Arg Gly Ser Ser Ser Ser Asn Ile Thr
1               5                   10                  15


Ser Ser Gly Pro Ser Ser Thr Pro Phe Ser Ser Ala Thr Glu Ser Phe
            20                  25                  30


Ser Thr Gly Thr Thr Val Thr Pro Ser Ser Ser Lys Tyr Pro Gly Ser
        35                  40                  45


Lys Thr Glu Thr Ser Val Ser Ser Thr Thr Glu Thr Thr Ile Val Pro
    50                  55                  60


Thr Thr Thr Thr Thr Ser Val Ile Thr Pro Ser Thr Thr Thr Ile Thr
65                  70                  75                  80


Thr Thr Val Cys Ser Thr Gly Thr Asn Ser Ala Gly Glu Thr Thr Ser
                85                  90                  95


Gly Cys Ser Pro Lys Thr Ile Thr Thr Thr Val Pro Cys Ser Thr Ser
            100                 105                 110


Pro Ser Glu Thr Ala Ser Glu Ser Thr Thr Thr Ser Pro Thr Thr Pro
        115                 120                 125


Val Thr Thr Val Val Ser Thr Thr Val Val Thr Thr Glu Tyr Ala Ser
    130                 135                 140


Thr Ser Thr Lys Gln Gly Gly Glu Ile Thr Thr Thr Phe Val Thr Lys
145                 150                 155                 160


Asn Ile Pro Thr Thr Tyr Leu Thr Thr Ile Ala Pro Thr Ser Ser Val
                165                 170                 175


Thr Thr Val Thr Asn Phe Thr Pro Thr Thr Ile Thr Thr Thr Val Cys
            180                 185                 190
```

```
Ser Thr Gly Thr Asn Ser Ala Gly Glu Thr Thr Ser Gly Cys Ser Pro
        195                 200                 205


Lys Thr Val Thr Thr Thr Val Pro Cys Ser Thr Gly Thr Gly Glu Tyr
    210                 215                 220


Thr Thr Glu Ala Thr Ala Pro Val Thr Thr Ala Val Thr Thr Thr Val
225                 230                 235                 240


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


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


Gly Lys Gly Ile Leu Asp Gln Ser Cys Gly Gly Val Phe Ser Asn Asn
        275                 280                 285


Gly Ser Ser Gln Val Gln Leu Arg Asp Val Val Leu Met Asn Gly Thr
    290                 295                 300


Val Val Tyr Asp Ser Asn Gly Ala Trp Asp Ser Ser Pro Leu Glu Glu
305                 310                 315                 320


Trp Leu Gln Arg Gln Lys Lys Val Ser Ile Glu Arg Ile Phe Glu Asn
                325                 330                 335


Ile Gly Pro Ser Ala Val Tyr Pro Ser Ile Leu Pro Gly Val Val Ile
            340                 345                 350


Ala Ser Pro Ser Gln Thr His Pro Asp Tyr Phe Tyr Gln Trp Ile Arg
        355                 360                 365


Asp Ser Ala Leu Thr Ile Asn Ser Ile Val Ser His Ser Ala Asp Pro
    370                 375                 380


Ala Ile Glu Thr Leu Leu Gln Tyr Leu Asn Val Ser Phe His Leu Gln
385                 390                 395                 400
```

```
Arg Thr Asn Asn Thr Leu Gly Ala Gly Ile Gly Tyr Thr Asn Asp Thr
                405                 410                 415

Val Ala Leu Gly Asp Pro Lys Trp Asn Val Asp Asn Thr Ala Phe Thr
            420                 425                 430

Glu Pro Trp Gly Arg Pro Gln Asn Asp Gly Pro Ala Leu Arg Ser Ile
        435                 440                 445

Ala Ile Leu Lys Ile Ile Asp Tyr Ile Lys Gln Ser Gly Thr Asp Leu
    450                 455                 460

Gly Ala Lys Tyr Pro Phe Gln Ser Thr Ala Asp Ile Phe Asp Asp Ile
465                 470                 475                 480

Val Arg Trp Asp Leu Arg Phe Ile Ile Asp His Trp Asn Ser Ser Gly
                485                 490                 495

Phe Asp Leu Trp Glu Glu Val Asn Gly Met His Phe Phe Thr Leu Leu
            500                 505                 510

Val Gln Leu Ser Ala Val Asp Arg Ser Leu Ser Tyr Phe Asn Ala Ser
        515                 520                 525

Glu Arg Ser Ser Pro Phe Val Glu Glu Leu Arg Gln Thr Arg Arg Asp
    530                 535                 540

Ile Ser Lys Phe Leu Val Asp Pro Ala Asn Gly Phe Ile Asn Gly Lys
545                 550                 555                 560

Tyr Asn Tyr Ile Val Glu Thr Pro Met Ile Ala Asp Thr Leu Arg Ser
                565                 570                 575

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

Pro Ser Ala Ser His Leu Pro Phe Asp Ile Asp Asp Pro Ala Val Leu
        595                 600                 605
```

```
Asn Thr Leu His His Leu Met Leu His Met Arg Ser Ile Tyr Pro Ile
    610                 615                 620


Asn Asp Ser Ser Lys Asn Ala Thr Gly Ile Ala Leu Gly Arg Tyr Pro
625                 630                 635                 640


Glu Asp Val Tyr Asp Gly Tyr Gly Val Gly Glu Gly Asn Pro Trp Val
                645                 650                 655


Leu Ala Thr Cys Ala Ala Ser Thr Thr Leu Tyr Gln Leu Ile Tyr Arg
            660                 665                 670


His Ile Ser Glu Gln His Asp Leu Val Val Pro Met Asn Asn Asp Cys
        675                 680                 685


Ser Asn Ala Phe Trp Ser Glu Leu Val Phe Ser Asn Leu Thr Thr Leu
    690                 695                 700


Gly Asn Asp Glu Gly Tyr Leu Ile Leu Glu Phe Asn Thr Pro Ala Phe
705                 710                 715                 720


Asn Gln Thr Ile Gln Lys Ile Phe Gln Leu Ala Asp Ser Phe Leu Val
                725                 730                 735


Lys Leu Lys Ala Thr Trp Glu Gln Thr Gly Asn
            740                 745


<210>  106
<211>  621
<212>  PRT
<213>  Aspergillus niger

<400>  106

Asn Val Ile Ser Lys Arg Ala Thr Trp Asp Ser Trp Leu Ser Asn Glu
1               5                   10                  15


Ala Thr Val Ala Arg Thr Ala Ile Leu Asn Asn Ile Gly Ala Asp Gly
            20                  25                  30
```

```
Ala Trp Val Ser Gly Ala Asp Ser Gly Ile Val Val Ala Ser Pro Ser
        35                  40                  45


Thr Asp Asn Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser Gly Leu
    50                  55                  60


Val Leu Lys Thr Leu Val Asp Leu Phe Arg Asn Gly Asp Thr Ser Leu
65                  70                  75                  80


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


Ile Ser Asn Pro Ser Gly Asp Leu Ser Ser Gly Ala Gly Leu Gly Glu
            100                 105                 110


Pro Lys Phe Asn Val Asp Glu Thr Ala Tyr Thr Gly Ser Trp Gly Arg
        115                 120                 125


Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile Gly Phe
    130                 135                 140


Gly Gln Trp Leu Leu Asp Asn Gly Tyr Thr Ser Thr Ala Thr Asp Ile
145                 150                 155                 160


Val Trp Pro Leu Val Arg Asn Asp Leu Ser Tyr Val Ala Gln Tyr Trp
                165                 170                 175


Asn Gln Thr Gly Tyr Asp Leu Trp Glu Val Asn Gly Ser Ser Phe Phe
            180                 185                 190


Thr Ile Ala Val Gln His Arg Ala Leu Val Glu Gly Ser Ala Phe Ala
        195                 200                 205


Thr Ala Val Gly Ser Ser Cys Ser Trp Cys Asp Ser Gln Ala Pro Glu
    210                 215                 220


Ile Leu Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Phe Ile Leu Ala
225                 230                 235                 240
```

```
Asn Phe Asp Ser Ser Arg Ser Ala Lys Asp Ala Asn Thr Leu Leu Leu
                245                 250                 255


Gly Ser Ile His Thr Phe Asp Pro Glu Ala Ala Cys Asp Asp Ser Thr
            260                 265                 270


Phe Gln Pro Cys Ser Pro Arg Ala Leu Ala Asn His Lys Glu Val Val
        275                 280                 285


Asp Ser Phe Arg Ser Ile Tyr Thr Leu Asn Asp Gly Leu Ser Asp Ser
    290                 295                 300


Glu Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Thr Tyr Tyr Asn Gly
305                 310                 315                 320


Asn Pro Trp Phe Leu Cys Thr Leu Ala Ala Ala Glu Gln Leu Tyr Asp
                325                 330                 335


Ala Leu Tyr Gln Trp Asp Lys Gln Gly Ser Leu Glu Val Thr Asp Val
            340                 345                 350


Ser Leu Asp Phe Phe Lys Ala Leu Tyr Ser Asp Ala Thr Gly Thr Tyr
        355                 360                 365


Ser Ser Ser Ser Ser Thr Tyr Ser Ser Ile Val Asp Ala Val Lys Thr
    370                 375                 380


Phe Ala Asp Gly Phe Val Ser Ile Val Glu Thr His Ala Ala Ser Asn
385                 390                 395                 400


Gly Ser Met Ser Glu Gln Tyr Asp Lys Ser Asp Gly Glu Gln Leu Ser
                405                 410                 415


Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr Ala Asn Asn
            420                 425                 430


Arg Arg Asn Val Val Pro Ser Ala Ser Trp Gly Glu Thr Ser Ala Ser
        435                 440                 445
```

```
Ser Val Pro Gly Thr Cys Ala Ala Thr Ser Ala Ile Gly Thr Tyr Ser
    450                 455                 460


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


Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr Ser Thr Ser
                485                 490                 495


Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr Ser Ser Thr
            500                 505                 510


Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu Thr Ala
        515                 520                 525


Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln
    530                 535                 540


Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys
545                 550                 555                 560


Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu Pro Ala
                565                 570                 575


Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser
            580                 585                 590


Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala
        595                 600                 605


Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
    610                 615                 620


<210>  107
<211>  593
<212>  PRT
<213>  Aspergillus oryzae

<400>  107
```

```
Val Gln Pro Val Leu Arg Gln Ala Thr Gly Leu Asp Thr Trp Leu Ser
1               5                   10                  15


Thr Glu Ala Asn Phe Ser Arg Gln Ala Ile Leu Asn Asn Ile Gly Ala
            20                  25                  30


Asp Gly Gln Ser Ala Gln Gly Ala Ser Pro Gly Val Val Ile Ala Ser
        35                  40                  45


Pro Ser Lys Ser Asp Pro Asp Tyr Phe Tyr Thr Trp Thr Arg Asp Ser
    50                  55                  60


Gly Leu Val Met Lys Thr Leu Val Asp Leu Phe Arg Gly Gly Asp Ala
65                  70                  75                  80


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


Gln Gly Ile Ser Asn Pro Ser Gly Ala Leu Ser Ser Gly Gly Leu Gly
            100                 105                 110


Glu Pro Lys Phe Asn Val Asp Glu Thr Ala Phe Thr Gly Ala Trp Gly
        115                 120                 125


Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr Ala Met Ile Ser
    130                 135                 140


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


Leu Val Trp Pro Val Val Arg Asn Asp Leu Ser Tyr Val Ala Gln Tyr
                165                 170                 175


Trp Ser Gln Ser Gly Phe Asp Leu Trp Glu Glu Val Gln Gly Thr Ser
            180                 185                 190


Phe Phe Thr Val Ala Val Ser His Arg Ala Leu Val Glu Gly Ser Ser
        195                 200                 205
```

```
Phe Ala Lys Thr Val Gly Ser Ser Cys Pro Tyr Cys Asp Ser Gln Ala
    210                 215                 220


Pro Gln Val Arg Cys Tyr Leu Gln Ser Phe Trp Thr Gly Ser Tyr Ile
225                 230                 235                 240


Gln Ala Asn Phe Gly Gly Gly Arg Ser Gly Lys Asp Ile Asn Thr Val
                245                 250                 255


Leu Gly Ser Ile His Thr Phe Asp Pro Gln Ala Thr Cys Asp Asp Ala
            260                 265                 270


Thr Phe Gln Pro Cys Ser Ala Arg Ala Leu Ala Asn His Lys Val Val
        275                 280                 285


Thr Asp Ser Phe Arg Ser Ile Tyr Ala Ile Asn Ser Gly Arg Ala Glu
    290                 295                 300


Asn Gln Ala Val Ala Val Gly Arg Tyr Pro Glu Asp Ser Tyr Tyr Asn
305                 310                 315                 320


Gly Asn Pro Trp Phe Leu Thr Thr Leu Ala Ala Ala Glu Gln Leu Tyr
                325                 330                 335


Asp Ala Leu Tyr Gln Trp Asp Lys Ile Gly Ser Leu Ala Ile Thr Asp
            340                 345                 350


Val Ser Leu Pro Phe Phe Lys Ala Leu Tyr Ser Ser Ala Ala Thr Gly
        355                 360                 365


Thr Tyr Ala Ser Ser Thr Thr Val Tyr Lys Asp Ile Val Ser Ala Val
    370                 375                 380


Lys Ala Tyr Ala Asp Gly Tyr Val Gln Ile Val Gln Thr Tyr Ala Ala
385                 390                 395                 400


Ser Thr Gly Ser Met Ala Glu Gln Tyr Thr Lys Thr Asp Gly Ser Gln
                405                 410                 415
```

```
Thr Ser Ala Arg Asp Leu Thr Trp Ser Tyr Ala Ala Leu Leu Thr Ala
            420                 425                 430


Asn Asn Arg Arg Asn Ala Val Val Pro Ala Pro Trp Gly Glu Thr Ala
        435                 440                 445


Ala Thr Ser Ile Pro Ser Ala Cys Ser Thr Thr Ser Ala Ser Gly Thr
    450                 455                 460


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


Gly Ala Pro Asp Ser Pro Cys Gln Val Pro Thr Thr Val Ser Val Thr
                485                 490                 495


Phe Ala Val Lys Ala Thr Thr Val Tyr Gly Glu Ser Ile Lys Ile Val
            500                 505                 510


Gly Ser Ile Ser Gln Leu Gly Ser Trp Asn Pro Ser Ser Ala Thr Ala
        515                 520                 525


Leu Asn Ala Asp Ser Tyr Thr Thr Asp Asn Pro Leu Trp Thr Gly Thr
    530                 535                 540


Ile Asn Leu Pro Ala Gly Gln Ser Phe Glu Tyr Lys Phe Ile Arg Val
545                 550                 555                 560


Gln Asn Gly Ala Val Thr Trp Glu Ser Asp Pro Asn Arg Lys Tyr Thr
                565                 570                 575


Val Pro Ser Thr Cys Gly Val Lys Ser Ala Val Gln Ser Asp Val Trp
            580                 585                 590


Arg



<210>  108
<211>  579
<212>  PRT
<213>  Rhizopus oryzae
```

```
<400>  108

Ala Ser Ile Pro Ser Ser Ala Ser Val Gln Leu Asp Ser Tyr Asn Tyr
1               5                   10                  15


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


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


Asn Asn Gly Asn Thr Ile Ala Ala Ser Tyr Ser Ala Pro Ile Ser Gly
    50                  55                  60


Ser Asn Tyr Glu Tyr Trp Thr Phe Ser Ala Ser Ile Asn Gly Ile Lys
65                  70                  75                  80


Glu Phe Tyr Ile Lys Tyr Glu Val Ser Gly Lys Thr Tyr Tyr Asp Asn
                85                  90                  95


Asn Asn Ser Ala Asn Tyr Gln Val Ser Thr Ser Lys Pro Thr Thr Thr
            100                 105                 110


Thr Ala Thr Ala Thr Thr Thr Thr Ala Pro Ser Thr Ser Thr Thr Thr
        115                 120                 125


Pro Pro Ser Arg Ser Glu Pro Ala Thr Phe Pro Thr Gly Asn Ser Thr
    130                 135                 140


Ile Ser Ser Trp Ile Lys Lys Gln Glu Gly Ile Ser Arg Phe Ala Met
145                 150                 155                 160


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


Ser Leu Ser Thr Ala Gly Pro Asp Tyr Tyr Tyr Ala Trp Thr Arg Asp
            180                 185                 190


Ala Ala Leu Thr Ser Asn Val Ile Val Tyr Glu Tyr Asn Thr Thr Leu
```

```
        195                 200                 205

Ser Gly Asn Lys Thr Ile Leu Asn Val Leu Lys Asp Tyr Val Thr Phe
    210                 215                 220

Ser Val Lys Thr Gln Ser Thr Ser Thr Val Cys Asn Cys Leu Gly Glu
225                 230                 235                 240

Pro Lys Phe Asn Pro Asp Ala Ser Gly Tyr Thr Gly Ala Trp Gly Arg
                245                 250                 255

Pro Gln Asn Asp Gly Pro Ala Glu Arg Ala Thr Thr Phe Ile Leu Phe
            260                 265                 270

Ala Asp Ser Tyr Leu Thr Gln Thr Lys Asp Ala Ser Tyr Val Thr Gly
        275                 280                 285

Thr Leu Lys Pro Ala Ile Phe Lys Asp Leu Asp Tyr Val Val Asn Val
    290                 295                 300

Trp Ser Asn Gly Cys Phe Asp Leu Trp Glu Glu Val Asn Gly Val His
305                 310                 315                 320

Phe Tyr Thr Leu Met Val Met Arg Lys Gly Leu Leu Leu Gly Ala Asp
                325                 330                 335

Phe Ala Lys Arg Asn Gly Asp Ser Thr Arg Ala Ser Thr Tyr Ser Ser
            340                 345                 350

Thr Ala Ser Thr Ile Ala Asn Lys Ile Ser Ser Phe Trp Val Ser Ser
        355                 360                 365

Asn Asn Trp Ile Gln Val Ser Gln Ser Val Thr Gly Gly Val Ser Lys
    370                 375                 380

Lys Gly Leu Asp Val Ser Thr Leu Leu Ala Ala Asn Leu Gly Ser Val
385                 390                 395                 400

Asp Asp Gly Phe Phe Thr Pro Gly Ser Glu Lys Ile Leu Ala Thr Ala
```

```
                405                 410                 415


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


Leu Pro Ser Tyr Leu Gly Asn Ser Ile Gly Arg Tyr Pro Glu Asp Thr
        435                 440                 445


Tyr Asn Gly Asn Gly Asn Ser Gln Gly Asn Ser Trp Phe Leu Ala Val
    450                 455                 460


Thr Gly Tyr Ala Glu Leu Tyr Tyr Arg Ala Ile Lys Glu Trp Ile Gly
465                 470                 475                 480


Asn Gly Gly Val Thr Val Ser Ser Ile Ser Leu Pro Phe Phe Lys Lys
                485                 490                 495


Phe Asp Ser Ser Ala Thr Ser Gly Lys Lys Tyr Thr Val Gly Thr Ser
            500                 505                 510


Asp Phe Asn Asn Leu Ala Gln Asn Ile Ala Leu Ala Ala Asp Arg Phe
        515                 520                 525


Leu Ser Thr Val Gln Leu His Ala His Asn Asn Gly Ser Leu Ala Glu
    530                 535                 540


Glu Phe Asp Arg Thr Thr Gly Leu Ser Thr Gly Ala Arg Asp Leu Thr
545                 550                 555                 560


Trp Ser His Ala Ser Leu Ile Thr Ala Ser Tyr Ala Lys Ala Gly Ala
                565                 570                 575


Pro Ala Ala


<210>  109
<211>  644
<212>  PRT
<213>  Clostridium thermocellum
```

```
<400>  109

Met Ala Asn Thr Tyr Phe Asn Asp Ala Ile Ile Gly Asn Ser Gly Met
1               5                   10                  15


Leu Val Cys Leu Thr Arg Asn Gly Glu Leu Thr Arg Leu Phe Trp Pro
            20                  25                  30


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


Tyr Thr Gly Gln Lys Asn Ser Thr Ser Trp Phe Tyr Glu Asp Asn Trp
    50                  55                  60


His His Thr Gln Tyr Tyr Val Glu Asp Thr Asn Ile Leu Lys Thr Ile
65                  70                  75                  80


Cys Glu Asp Gly Gly Arg Gly Leu Arg Val Glu Gln Thr Asp Phe Val
                85                  90                  95


Leu Lys Asp Arg Asp Val Met Val Arg Arg Tyr Val Ile Glu Asn Ile
            100                 105                 110


Gly Pro Asn Glu Val Asp Leu Gly Phe Val Gln Tyr Ser Ser Thr Val
        115                 120                 125


Ser Thr Thr Pro Glu Leu Arg Ser Thr Leu Phe Asp Phe Asn Val Asp
    130                 135                 140


Ala Leu Ile His Tyr Arg His Asn Tyr Tyr Ile Ser Ile Ser Ser Asp
145                 150                 155                 160


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


Arg Tyr Thr Glu Leu Tyr Gly Tyr Asp Ser Ile Gly Met Met Lys Asp
            180                 185                 190


Gly Ala Met Ser Phe Asn Ile Gly Lys Ile Glu Pro Gly Gly Lys Lys
        195                 200                 205
```

```
Thr Phe Asn Leu Phe Ile Cys Ala Ser His Thr Leu Lys Gly Val Lys
    210                 215                 220

Glu Leu Val Arg Trp Cys Arg Lys Met Asn Val Asp Glu Glu Tyr Glu
225                 230                 235                 240

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

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

Val Phe Lys Leu Met Ser Asp Glu Arg Thr Gly Gly Leu Leu Ala Ser
        275                 280                 285

Ala Glu Ile Asp Glu Gly Phe Thr Arg Cys Gly Arg Tyr Ala Tyr Cys
    290                 295                 300

Trp Gly Arg Asp Ala Ala Phe Ile Thr Gly Ala Leu Asp Thr Ala Gly
305                 310                 315                 320

Leu Thr Glu Ala Val Asp Lys Phe Tyr Gln Trp Ala Val Met Thr Gln
                325                 330                 335

Asp Asp Asp Gly Ser Trp Gln Gln Arg Tyr His Met Asp Gly Asn Leu
            340                 345                 350

Ala Pro Ser Trp Gly Leu Gln Ile Asp Glu Thr Gly Thr Leu Ile Trp
        355                 360                 365

Gly Met Leu Lys His Tyr Glu Val Thr Lys Asn Ile Asp Phe Leu Lys
    370                 375                 380

Ser Met Trp Glu Ser Ile Lys Lys Gly Val Glu Phe Leu Thr Arg Phe
385                 390                 395                 400

Ile Asp Ser Asp Thr Gly Leu Pro Ala Pro Ser Tyr Asp Leu Trp Glu
                405                 410                 415
```

```
Glu Arg Val Gly Glu His Thr Tyr Ser Ser Ala Ala Val Tyr Ala Gly
            420                 425                 430

Ile Lys Ala Gly Ala Glu Ala Ala Arg Ile Leu Gly Ala Ser Glu Glu
        435                 440                 445

Leu Ile Glu Lys Trp Glu Lys Ala Ala Ser Asp Met Lys Ala Ser Ile
    450                 455                 460

Glu Lys Asn Phe Trp Arg Asp Glu Ala Gly Arg Phe Ile Arg Ser Val
465                 470                 475                 480

Arg Thr Lys Leu Asn Pro Trp Gly Ser Glu His Ser Pro Tyr Thr Thr
                485                 490                 495

Val Ile Lys Val Asn Glu Lys Gly Tyr Phe Arg Asp Val Thr Leu Glu
            500                 505                 510

Asp Trp Thr Ile Asp Val Ser Leu Leu Gly Val Ser Ile Pro Phe Gly
        515                 520                 525

Val Phe Asp Val His Asp Glu Arg Val Lys Lys Thr Val Glu Ala Ile
    530                 535                 540

Glu Arg Ala Leu Thr Ser His Pro Val Gly Gly Ile Lys Arg Tyr Glu
545                 550                 555                 560

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

Val Ala Leu Tyr Tyr Ile Glu Ile Lys Glu Tyr Glu Lys Ala Lys Asp
            580                 585                 590

Tyr Leu Arg Trp Ala Thr Lys Ser Cys Thr Ala Leu Gly Leu Leu Pro
        595                 600                 605

Glu Gln Val Ser Lys Asp Asn Gly Glu Pro Cys Trp Val Ile Pro Leu
    610                 615                 620
```

```
Thr Trp Ser His Ala Met Tyr Val Leu Val Leu Ala Gly Leu Lys Glu
625                 630                 635                 640


Ala Gly Val Leu



<210>  110
<211>  644
<212>  PRT
<213>  Clostridium thermocellum

<400>  110

Met Gln Lys Ser Tyr Tyr Asn Asn Ala Ile Thr Gly Asn Ser Ser Met
1               5                   10                  15


Leu Ala Cys Phe Ser Glu Arg Ala Glu Leu Leu Arg Leu Phe Trp Pro
            20                  25                  30


Asp Ile Asp Tyr Ile Gln Asn Leu Asp Lys Met Phe Leu Gly Leu Phe
        35                  40                  45


Glu Lys Asn Lys Thr Gly Ser Thr Val Trp Leu Asn Asp Ile Arg Cys
    50                  55                  60


Glu His His Gln Glu Tyr Leu Pro Asp Ser Asn Ile Ile Lys Asn Met
65                  70                  75                  80


Val Thr Asn Phe Phe Asp Gly Tyr Lys Val Val Leu Tyr Asp Phe Val
                85                  90                  95


His Pro Glu Met Asp Val Leu Val Arg Arg Phe Glu Ile Glu Asn Leu
            100                 105                 110


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


Ser Ser Asp Ser Glu Val Ala Cys Ser Leu Phe Asp Phe Met Asn Glu
    130                 135                 140
```

```
Ala Leu Val His Tyr Lys Pro Asp Ser Tyr Ile Ala Val Thr Ser Asp
145                 150                 155                 160


Ile Pro Val Tyr Gln Phe Gln Ile Gly Asn Asn Ala Asn Asp Ala Ala
                165                 170                 175


Val Asn Thr Tyr Leu Tyr Gly Lys Asp Asp Ile Gly Met Met Lys Asp
            180                 185                 190


Ala Ala Ile Ser Trp Asp Leu Gly Val Phe Gln Pro His Ala Val Lys
        195                 200                 205


Thr Thr Asn Val Tyr Leu Cys Ala Ala Asp Thr Leu Lys Ser Cys Lys
    210                 215                 220


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


Glu Thr Gly Arg Tyr Trp Lys Asp Tyr Leu Glu Lys Thr Thr Lys Leu
                245                 250                 255


Lys Ser Gly Asn Thr Leu Leu Asp Asp Leu Tyr Lys Arg Ser Leu Leu
            260                 265                 270


Val Phe Arg Leu Met Tyr Ser Lys Lys Ser Gly Gly Leu Met Ala Ala
        275                 280                 285


Pro Glu Val Asp Glu Tyr Phe Thr Lys Cys Gly Lys Tyr Ala Tyr Cys
    290                 295                 300


Trp Gly Arg Asp Ala Ala Phe Ile Thr Gly Ala Leu Asp Ile Gly Gly
305                 310                 315                 320


Leu Cys Glu Ser Val Asp His Phe Tyr Lys Trp Ala Val Asn Val Gln
                325                 330                 335


Asp Glu Asp Gly Ser Trp Gln Gln Arg Tyr His Met Asn Gly Asn Leu
            340                 345                 350
```

```
Gly Pro Cys Trp Gly Leu Gln Val Asp Glu Thr Gly Thr Ile Ile Trp
        355                 360                 365


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


Ser Val Trp Asp Ser Val Lys Ala Ala Ala Asp Phe Leu Val Arg Phe
385                 390                 395                 400


Ile Asp Ser Glu Thr Gly Leu Pro Arg Pro Ser Phe Asp Leu Trp Glu
                405                 410                 415


Glu Arg Tyr Gly Glu His Ala Tyr Ser Ser Ala Ser Val Cys Ala Gly
            420                 425                 430


Leu Lys Ser Ala Ser Glu Met Ala Arg Ile Leu Gly Lys Pro Ser Gln
        435                 440                 445


Glu Tyr Ile Gln Trp Glu Thr Thr Ala Asp Ser Ile Lys Lys Ala Ile
    450                 455                 460


Val Lys Tyr Phe Trp Lys Glu Asp Tyr Arg Arg Phe Ile Arg Ser Ile
465                 470                 475                 480


Arg Val Lys Leu Asn Gly Phe Gly Gln Glu Pro Ser Ser Asp Thr Met
                485                 490                 495


Leu Ile Lys Val Asn Pro Lys Gly Tyr Val Arg Asp Val Thr Lys Glu
            500                 505                 510


Asp Trp Ile Val Asp Val Ser Leu Val Gly Leu Gly Ile Pro Phe Glu
        515                 520                 525


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


Glu Gln Val Leu Thr Ala Gln Gly Val Gly Gly Ile Lys Arg Tyr Glu
545                 550                 555                 560
```

```
Asn Asp Thr Tyr Ile Gly Gly Asn Pro Trp Ile Leu Thr Thr Leu Trp
                565                 570                 575


Ile Ala Leu Tyr His Ala Lys Ser Gly Asn Tyr Lys Lys Ala Lys Glu
            580                 585                 590


Tyr Leu Ile Trp Ala Ala Ser Gly Lys Thr Glu Leu Gly Leu Leu Pro
        595                 600                 605


Glu Gln Ile Asn Arg Asp Thr Gly Lys Pro Glu Trp Ile Ile Pro Leu
    610                 615                 620


Thr Trp Ser His Ala Met Tyr Val His Val Tyr Ser Glu Leu Ile Asn
625                 630                 635                 640


Ala Gly Val Leu



<210>  111
<211>  608
<212>  PRT
<213>  Arxula adeninivorans

<400>  111

Asp Ser Cys His Thr Phe Thr Leu Ala Asn Ser Pro Pro Asp Asp Lys
1               5                   10                  15


Ala Val Ala Leu Ser Ser Tyr Ser Tyr Cys Gly Gly Tyr Leu Ser Ala
            20                  25                  30


Ser Ala Phe Val Lys Asn Leu Ser Tyr Asp Lys Leu Val Thr Leu Tyr
        35                  40                  45


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


Asp Tyr Val Lys Ala Ala Ser Asp Asp Gln Ser Trp Glu Leu Trp Ser
65                  70                  75                  80
```

```
Leu Asn Val Thr Thr Val Pro Asp Gly Val Asp Ala Leu Leu Asn Ile
                85                  90                  95

Thr Tyr Val Ala Ala Ser Ile Gly Lys Thr Asn Ser Gln Gln Leu Asn
            100                 105                 110

Val Gln Val Glu Ala Thr Gly Asp Pro Ile Pro Thr Pro Gln Ile Pro
        115                 120                 125

Thr Ile Tyr Lys Pro Tyr Ala Ser Pro Ser Asp Phe Ser Asp Asp Ile
    130                 135                 140

Thr Asn Trp Leu Lys Pro Ser Asn Asp Ser Gln Thr Gly Ile Ala Lys
145                 150                 155                 160

Ser Phe Leu Phe Asn Asn Ile Asn Ile Pro Gly Ala Ala Pro Gly Thr
                165                 170                 175

Val Ile Ala Ala Gln Ser Tyr Ser Glu Pro Asp Tyr Ala Tyr Thr Trp
            180                 185                 190

Val Arg Asp Ala Ser Leu Val Met Asp Val Val Asn Arg Leu Tyr Ser
        195                 200                 205

Ser Ala Lys Ser Glu Glu Lys Arg Gln Leu Tyr Glu Lys Ile Leu Phe
    210                 215                 220

Gln Tyr Ala Lys Ala Gly Ala Gln Glu Gln Asn Asp Pro Thr Ala Ile
225                 230                 235                 240

Ser Gly Met Gly Glu Pro Lys Phe Tyr Leu Asn Asn Thr Ala Phe Thr
                245                 250                 255

Gly Ser Trp Gly Arg Pro Gln Asn Asp Gly Pro Ala Thr Arg Ala Ile
            260                 265                 270

Thr Leu Ile Glu Phe Ala Asn Ala Tyr Leu Ala Asn Gly Gly Ser Gln
        275                 280                 285
```

```
Asp Thr Val Arg Glu Gln Leu Tyr Asp Ser Asp Lys Tyr Pro Gln Val
    290                 295                 300

Ala Pro Ile Lys Lys Asp Leu Gln Phe Val Ala Ser Asn Trp Ser Ser
305                 310                 315                 320

Pro Ser Phe Asp Leu Trp Glu Glu Glu Glu Ser Ala His Phe Tyr Thr
                325                 330                 335

Arg Leu Val Gln Arg Lys Ala Leu Leu Leu Gly Ala Asp Phe Ala Asn
            340                 345                 350

Asp Met Gly Asp His Glu Leu Ser Asp Lys Leu Lys Thr Gln Ala Ser
        355                 360                 365

Lys Leu Ser Asp Thr Leu Pro Glu Phe Trp Asp Ser Ala Arg Gln Leu
    370                 375                 380

Ile Leu Tyr Glu Tyr Gly Pro Val Leu Arg Gly Lys Tyr Ser Tyr Lys
385                 390                 395                 400

Asp Ile Ser Val Val Leu Gly Val Met His Gly Tyr Ala Asn Asp Asn
                405                 410                 415

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

Ser Thr Ser Phe Leu Asp Val Tyr Lys Val Ala Asn Thr Thr Ser Asp
        435                 440                 445

Glu Ser Gly Lys Pro Leu Gly Ile Pro Val Gly Arg Tyr Pro Glu Asp
    450                 455                 460

Val Tyr Asp Gly Val Gly Thr Ser Gln Gly Asn Pro Trp Tyr Leu Thr
465                 470                 475                 480

Thr Met Ala Met Ala Glu Phe Leu Tyr Arg Ser Val Gln Glu Phe Glu
                485                 490                 495
```

```
Asp Ala Gly Ser Ile Ile Ile Ser Asp Thr Ser Leu Pro Phe Trp Lys
            500                 505                 510


Tyr Phe Ala Ser Ser Val Asp His Lys Ala Gly Ala Lys Tyr Asn Lys
        515                 520                 525


Asn Asp Gln Ser Phe Lys Thr Ser Leu Lys Ser Leu Thr Gly Trp Gly
    530                 535                 540


Asp Ala Phe Met Arg Arg Ala Lys Tyr His Thr Pro Ser Ser Gly His
545                 550                 555                 560


Met Ser Glu Glu Phe Asn Arg Thr Thr Gly Glu Pro Arg Gly Ala Lys
                565                 570                 575


Asp Leu Thr Trp Ser Tyr Ala Ser Leu Leu Ser Ala Ala Phe Ala Arg
            580                 585                 590


Glu Glu Leu Arg Asn Gln Lys Asn Tyr Leu Thr Asn Val Ala Asp Leu
        595                 600                 605


<210>  112
<211>  595
<212>  PRT
<213>  Hormoconis resinae

<400>  112

Ala Pro Thr Glu Leu Lys Ala Arg Asp Leu Ser Ser Phe Ile Ala Ser
1               5                   10                  15


Glu Arg Ala Ile Ala Leu Gln Gly Ala Leu Asn Asn Ile Gly Pro Asp
            20                  25                  30


Gly Ser Ala Val Pro Gly Ala Gly Ala Gly Phe Val Val Ala Ser Pro
        35                  40                  45


Ser Lys Ala Asn Pro Asp Tyr Phe Tyr Thr Trp Ser Arg Asp Ser Ala
    50                  55                  60


Leu Thr Leu Lys Met Ile Ile Asp Glu Phe Ile Leu Gly Asn Thr Thr
```

```
65                  70                  75                  80

Leu Gln Thr Ile Ile Glu Gln Tyr Ile His Ala Gln Ala Val Leu Gln
                85                  90                  95

Thr Val Ser Asn Pro Ser Gly Thr Phe Leu Pro Asp Gly Val Gly Leu
            100                 105                 110

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

Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Ile Ala Leu Met
    130                 135                 140

Thr Tyr Ser Asn Trp Leu Ile Lys Asn Gly Gln Phe Ala Glu Ala Lys
145                 150                 155                 160

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

Tyr Trp Asn Gln Ser Gly Phe Asp Leu Trp Glu Glu Thr Tyr Ala Ser
            180                 185                 190

Ser Phe Phe Thr Ile Gln Asn Gln His Arg Ala Leu Val Glu Gly Ala
        195                 200                 205

Gln Leu Ala His Asp Leu Gly Val Thr Cys Thr Gly Cys Asp Gln Ala
    210                 215                 220

Pro Glu Val Leu Cys Phe Leu Gln Ser Phe Trp Asn Gly Lys Tyr Ile
225                 230                 235                 240

Val Ser Asn Ile Asn Val Asn Asn Gly Arg Thr Gly Leu Asp Gly Asn
                245                 250                 255

Ser Ile Leu Gly Ala Ile Ser Thr Phe Asp Ile Asp Ala Tyr Cys Asp
            260                 265                 270

Ser Pro Thr Leu Gln Pro Cys His Ser Gln Ser Leu Ala Asn Phe Lys
```

```
        275                 280                 285


Val Leu Thr Asp Thr Phe Arg Asn Leu Tyr Thr Ile Asn Ala Gly Ile
    290                 295                 300


Pro Glu Gly Gln Gly Val Ala Val Gly Arg Tyr Ala Glu Asp Val Tyr
305                 310                 315                 320


Met Gly Gly Asn Pro Trp Tyr Leu Ile Thr Thr Ala Ala Ala Glu Phe
                325                 330                 335


Leu Tyr Asp Ala Val Ala Gln Trp Lys Ala Arg His Val Leu Thr Val
            340                 345                 350


Asp Glu Thr Ser Leu Ala Phe Phe Lys Asp Ile Tyr Pro Glu Val Thr
        355                 360                 365


Val Arg Glu Tyr Lys Ser Gly Asn Ala Asn Ser Pro Phe Ala Gln Ile
    370                 375                 380


Met Asp Ala Val Thr Ala Tyr Ala Asp Ser Tyr Val Ala Ile Ala Glu
385                 390                 395                 400


Lys Tyr Ile Pro Ser Asn Gly Ser Leu Ser Glu Gln Phe Asn Arg Asp
                405                 410                 415


Thr Gly Thr Pro Leu Ser Ala Ile Asp Leu Thr Trp Ser Tyr Ala Ala
            420                 425                 430


Phe Ile Thr Met Ser Gln Arg Arg Ala Gly Gln Tyr Pro Ser Ser Trp
        435                 440                 445


Gly Ser Arg Asn Ala Leu Pro Pro Pro Thr Thr Cys Ser Ala Ser Ser
    450                 455                 460


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


Thr Ser Ser Cys Gln Val Ser Ile Thr Phe Asn Ile Asn Ala Thr Thr
```

```
                485                 490                 495


Tyr Tyr Gly Glu Asn Leu Tyr Val Ile Gly Asn Ser Ser Asp Leu Gly
            500                 505                 510


Ala Trp Asn Ile Ala Asp Ala Tyr Pro Leu Ser Ala Ser Ala Tyr Thr
        515                 520                 525


Gln Asp Arg Pro Leu Trp Ser Ala Ala Ile Pro Leu Asn Ala Gly Glu
    530                 535                 540


Val Ile Ser Tyr Gln Tyr Val Arg Gln Glu Asp Cys Asp Gln Pro Tyr
545                 550                 555                 560


Ile Tyr Glu Thr Val Asn Arg Thr Leu Thr Val Pro Ala Cys Gly Gly
                565                 570                 575


Ala Ala Val Thr Thr Asp Asp Ala Trp Met Gly Pro Val Gly Ser Ser
            580                 585                 590


Gly Asn Cys
        595


<210>  113
<211>  601
<212>  PRT
<213>  Aureobasidium pullulans

<400>  113

Leu Pro Ser Pro Glu Ser Ile Gln Glu Arg Ala Thr Gly Ser Leu Ser
1               5                   10                  15


Ser Trp Leu Ser Ser Glu Asn Thr Val Ala Leu Gln Gly Val Leu Asn
            20                  25                  30


Asn Ile Gly Ala Ser Gly Ser Lys Ala Ser Gly Ala Ser Ala Gly Val
        35                  40                  45


Val Val Ala Ser Pro Ser Lys Ser Asn Pro Asp Tyr Phe Tyr Thr Trp
    50                  55                  60
```

```
Thr Arg Asp Ser Ala Leu Val Phe Lys Ala Leu Val Asp Gln Leu Ile
65                  70                  75                  80


Ala Gly Asn Lys Ser Leu Glu Pro Leu Ile Gln Gln Tyr Ile Ser Ala
                85                  90                  95


Gln Ala Lys Leu Gln Thr Val Asn Asn Pro Ser Gly Gly Leu Cys Ser
            100                 105                 110


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


Gly Ala Trp Gly Arg Pro Gln Arg Asp Gly Pro Ala Leu Arg Ala Thr
    130                 135                 140


Ala Met Ile Ala Tyr Ser Arg Tyr Leu Ile Ala Asn Gly Asn Thr Thr
145                 150                 155                 160


Thr Val Asn Asn Ile Ile Trp Pro Ile Val Gln Asn Asp Leu Ser Tyr
                165                 170                 175


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


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


Glu Gly Asn Asn Leu Ala Thr Gln Leu Gly Lys Ser Cys Pro Asn Cys
    210                 215                 220


Val Ser Gln Ala Pro Leu Val Leu Cys Phe Leu Gln Ser Tyr Trp Thr
225                 230                 235                 240


Gly Ser Tyr Ala Leu Ser Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp
                245                 250                 255


Ala Asn Ser Ile Leu Thr Ser Ile His Ile Phe Asp Pro Ala Ala Ser
            260                 265                 270
```

```
Cys Asp Ser Thr Thr Phe Gln Pro Cys Ser Asp Lys Ala Leu Ala Asn
        275                 280                 285


His Lys Val Val Thr Asp Ser Phe Arg Ser Ile Tyr Ser Ile Asn Gln
    290                 295                 300


Gly Ile Ala Gln Gly Ser Gly Val Ala Val Gly Arg Tyr Pro Glu Asp
305                 310                 315                 320


Ser Tyr Tyr Asn Gly Asn Pro Trp Tyr Leu Asn Thr Phe Ala Ala Ala
                325                 330                 335


Glu Gln Leu Tyr Asp Ala Val Tyr Gln Trp Lys Lys Ile Gly Ser Ile
            340                 345                 350


Ser Ile Thr Ser Ile Ser Leu Pro Phe Phe Lys Asp Val Tyr Ser Ser
        355                 360                 365


Ala Ala Val Gly Thr Tyr Ser Ser Ser Thr Val Thr Phe Thr Ser Ile
    370                 375                 380


Val Asn Ala Val Gln Thr Tyr Ala Asp Ser Tyr Met Ser Ile Ala Gln
385                 390                 395                 400


Lys Tyr Thr Pro Ser Asn Gly Ala Leu Ser Glu Gln Tyr Asn Arg Ala
                405                 410                 415


Asp Gly Thr Pro Leu Ser Ala Val Asp Leu Thr Trp Ser Tyr Ala Ala
            420                 425                 430


Phe Leu Thr Ala Tyr Asn Ala Arg Ala Asn Val Leu Pro Ala Ser Trp
        435                 440                 445


Gly Ala Ser Ser Ala Lys Leu Pro Asn Ser Cys Ser Ser Gly Ser Ala
    450                 455                 460


Thr Gly Pro Cys Ala Ala Ala Thr Asn Thr Asn Trp Gly Asn Pro Gly
465                 470                 475                 480
```

```
Ser Pro Ser Thr Gly Thr Pro Thr Thr Thr Thr Gly Gly Ser Cys Thr
                485                 490                 495

Thr Pro Thr Ser Ile Ala Val Thr Phe Asn Glu Gln Lys Thr Thr Ser
            500                 505                 510

Tyr Gly Glu Asn Ile Tyr Ile Val Gly Ser Ile Pro Ala Leu Gly Asn
        515                 520                 525

Trp Asn Thr Ala Asn Ala Val Ala Leu Ser Ala Ser Lys Tyr Thr Ser
    530                 535                 540

Ser Asn Pro Leu Trp Thr Val Thr Ile Asn Phe Ala Thr Gly Thr Ser
545                 550                 555                 560

Phe Asn Tyr Lys Tyr Ile Lys Lys Ala Gln Asp Gly Ser Val Thr Trp
                565                 570                 575

Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Thr Gly Asn Cys Ala Gly
            580                 585                 590

Thr Ala Thr Glu Asn Asp Ser Trp Arg
        595                 600


<210>  114
<211>  718
<212>  PRT
<213>  Bacillus subtilis

<400>  114

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

Ile Ile Thr Val Leu Ile Pro Ala Glu Gln Lys Glu Ile Met Thr Pro
            20                  25                  30

Pro Phe Arg Leu Glu Thr Glu Ile Thr Asp Phe Pro Leu Ala Val Arg
        35                  40                  45
```

```
Glu Glu Tyr Ser Leu Glu Ala Lys Tyr Lys Tyr Val Cys Val Ser Asp
    50                  55                  60


His Pro Val Thr Phe Gly Lys Ile His Cys Val Arg Ala Ser Ser Gly
65                  70                  75                  80


His Lys Thr Asp Leu Gln Ile Gly Ala Val Ile Arg Thr Ala Ala Phe
                85                  90                  95


Asp Asp Glu Phe Tyr Tyr Asp Gly Glu Leu Gly Ala Val Tyr Thr Ala
            100                 105                 110


Asp His Thr Val Phe Lys Val Trp Ala Pro Ala Ala Thr Ser Ala Ala
        115                 120                 125


Val Lys Leu Ser His Pro Asn Lys Ser Gly Arg Thr Phe Gln Met Thr
    130                 135                 140


Arg Leu Glu Lys Gly Val Tyr Ala Val Thr Val Thr Gly Asp Leu His
145                 150                 155                 160


Gly Tyr Glu Tyr Leu Phe Cys Ile Cys Asn Asn Ser Glu Trp Met Glu
                165                 170                 175


Thr Val Asp Gln Tyr Ala Lys Ala Val Thr Val Asn Gly Glu Lys Gly
            180                 185                 190


Val Val Leu Arg Pro Asp Gln Met Lys Trp Thr Ala Pro Leu Lys Pro
        195                 200                 205


Phe Ser His Pro Val Asp Ala Val Ile Tyr Glu Thr His Leu Arg Asp
    210                 215                 220


Phe Ser Ile His Glu Asn Ser Gly Met Ile Asn Lys Gly Lys Tyr Leu
225                 230                 235                 240


Ala Leu Thr Glu Thr Asp Thr Gln Thr Ala Asn Gly Ser Ser Ser Gly
                245                 250                 255
```

```
Leu Ala Tyr Val Lys Glu Leu Gly Val Thr His Val Glu Leu Leu Pro
            260                 265                 270


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


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


Ala Ser Asn Pro His Asp Pro Gln Thr Arg Lys Thr Glu Leu Lys Gln
305                 310                 315                 320


Met Ile Asn Thr Leu His Gln His Gly Leu Arg Val Ile Leu Asp Val
                325                 330                 335


Val Phe Asn His Val Tyr Lys Arg Glu Asn Ser Pro Phe Glu Lys Thr
            340                 345                 350


Val Pro Gly Tyr Phe Phe Arg His Asp Glu Cys Gly Met Pro Ser Asn
        355                 360                 365


Gly Thr Gly Val Gly Asn Asp Ile Ala Ser Glu Arg Arg Met Ala Arg
    370                 375                 380


Lys Phe Ile Ala Asp Cys Val Val Tyr Trp Leu Glu Glu Tyr Asn Val
385                 390                 395                 400


Asp Gly Phe Arg Phe Asp Leu Leu Gly Ile Leu Asp Ile Asp Thr Val
                405                 410                 415


Leu Tyr Met Lys Glu Lys Ala Thr Lys Ala Lys Pro Gly Ile Leu Leu
            420                 425                 430


Phe Gly Glu Gly Trp Asp Leu Ala Thr Pro Leu Pro His Glu Gln Lys
        435                 440                 445


Ala Ala Leu Ala Asn Ala Pro Arg Met Pro Gly Ile Gly Phe Phe Asn
    450                 455                 460
```

```
Asp Met Phe Arg Asp Ala Val Lys Gly Asn Thr Phe His Leu Lys Ala
465                 470                 475                 480


Thr Gly Phe Ala Leu Gly Asn Gly Glu Ser Ala Gln Ala Val Met His
                485                 490                 495


Gly Ile Ala Gly Ser Ser Gly Trp Lys Ala Leu Ala Pro Ile Val Pro
            500                 505                 510


Glu Pro Ser Gln Ser Ile Asn Tyr Val Glu Ser His Asp Asn His Thr
        515                 520                 525


Phe Trp Asp Lys Met Ser Phe Ala Leu Pro Gln Glu Asn Asp Ser Arg
    530                 535                 540


Lys Arg Ser Arg Gln Arg Leu Ala Ala Ala Ile Ile Leu Leu Ala Gln
545                 550                 555                 560


Gly Val Pro Phe Ile His Ser Gly Gln Glu Phe Phe Arg Thr Lys Gln
                565                 570                 575


Gly Val Glu Asn Ser Tyr Gln Ser Ser Asp Ser Ile Asn Gln Leu Asp
            580                 585                 590


Trp Asp Arg Arg Glu Thr Phe Lys Glu Asp Val His Tyr Ile Arg Arg
        595                 600                 605


Leu Ile Ser Leu Arg Lys Ala His Pro Ala Phe Arg Leu Arg Ser Ala
    610                 615                 620


Ala Asp Ile Gln Arg His Leu Glu Cys Leu Thr Leu Lys Glu His Leu
625                 630                 635                 640


Ile Ala Tyr Arg Leu Tyr Asp Leu Asp Glu Val Asp Glu Trp Lys Asp
                645                 650                 655


Ile Ile Val Ile His His Ala Ser Pro Asp Ser Val Glu Trp Arg Leu
            660                 665                 670
```

```
Pro Asn Asp Ile Pro Tyr Arg Leu Leu Cys Asp Pro Ser Gly Phe Gln
        675                 680                 685


Glu Asp Pro Thr Glu Ile Lys Lys Thr Val Ala Val Asn Gly Ile Gly
    690                 695                 700


Thr Val Ile Leu Tyr Leu Ala Ser Asp Leu Lys Ser Phe Ala
705                 710                 715


<210>  115
<211>  710
<212>  PRT
<213>  Bacillus licheniformis

<400>  115

Met Pro Gly Ile Ser Arg Pro Phe Glu Ala Tyr Leu Asp Glu Met Arg
1               5                   10                  15


Thr Ile Thr Val Leu Val Pro Lys Ser Arg Ala Ser Ser Cys Ser Pro
            20                  25                  30


Pro Phe Leu Leu Glu Asp Asp Gln Gly Glu Arg Ile Glu Leu Ser Val
        35                  40                  45


Lys Ala Gln Val Glu Leu Glu Glu Gln Phe Lys Tyr Val Leu Glu Ser
    50                  55                  60


Ser Cys Thr Val Pro Phe Gly Arg Val His Lys Val Cys Cys Glu Glu
65                  70                  75                  80


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


Phe Asp Lys Ala Phe Phe Tyr Asp Gly Arg Leu Gly Ala Phe Tyr Ser
            100                 105                 110


Lys Gly Ser Thr Leu Phe Lys Val Trp Ala Pro Thr Ala Ser Ala Ala
        115                 120                 125
```

```
Ala Ile Lys Leu Glu Asp Pro Asp Ser Leu Gln Thr Asn Thr Phe Gln
    130                 135                 140


Met Met Arg Arg Lys Lys Gly Val Phe Glu Val Thr Val Glu Gly Asp
145                 150                 155                 160


Leu Asn Gly Trp Ser Tyr Leu Tyr Glu Leu Tyr Val Asn Gly Lys Pro
                165                 170                 175


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


Lys Gly Val Val Leu Asp Pro Glu Glu Val Lys Val Glu Lys His Arg
        195                 200                 205


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


Ile Arg Asp Phe Ser Ile His Glu Asp Ser Gly Met Arg His Lys Gly
225                 230                 235                 240


Lys Tyr Val Ala Phe Thr Glu Asp Gly Thr Glu Thr Ser Gly Gly Phe
                245                 250                 255


Ser Thr Gly Ile Ala Tyr Leu Lys Glu Leu Gly Val Thr His Ile Glu
            260                 265                 270


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


Gln Ser Tyr Asn Trp Gly Tyr Asn Pro Leu His Phe Asn Ala Pro Glu
    290                 295                 300


Gly Ser Tyr Ser Leu Asp Pro Gln Asn Pro Lys Cys Arg Ile Thr Glu
305                 310                 315                 320


Leu Lys Thr Met Ile Gln Ser Leu His Lys His Gly Phe Ser Val Ile
                325                 330                 335
```

```
Met Asp Ala Val Tyr Asn His Val Tyr Lys Arg Glu Thr Ser Pro Phe
            340                 345                 350


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


Pro Ser Asp Gly Thr Gly Val Gly Asn Asp Ile Ala Ser Glu Arg Leu
    370                 375                 380


Met Val Arg Lys Tyr Ile Leu Asp Ser Val Arg Tyr Trp Leu Glu Glu
385                 390                 395                 400


Tyr Asp Val Asp Gly Ile Arg Phe Asp Leu Met Gly Ile Leu Asp Ile
                405                 410                 415


Glu Thr Val Arg Gln Ile Ser Thr Leu Ala Glu Asn Val Lys Pro Gly
            420                 425                 430


Val Pro Leu Phe Gly Glu Gly Trp Asp Leu Asn Thr Pro Leu Asp Ser
        435                 440                 445


Gly Gln Lys Ala Thr Leu Gln Asn Ala Gly Lys Val Pro Ala Val Gly
    450                 455                 460


Phe Phe Asn Asp Arg Phe Arg Asn Ala Val Lys Gly Ser Thr Phe Glu
465                 470                 475                 480


Leu Ser Asp Arg Gly Tyr Ala Leu Gly Asp Thr Gly Lys Lys Ala Ala
                485                 490                 495


Leu Gln His Gly Ile Ala Gly Ser Pro Gly Phe Leu Gln Pro Ala Gln
            500                 505                 510


Ser Ile Asn Tyr Val Glu Cys His Asp Asn His Thr Phe Trp Asp Lys
        515                 520                 525


Met Ala Leu Cys Phe Glu Glu Asp Ala Asp Thr Lys Arg Leu Arg Gln
    530                 535                 540
```

```
Arg Leu Ala Val Ser Ile Val Leu Leu Ser Gln Gly Val Pro Phe Leu
545                 550                 555                 560


His Ala Gly Gln Glu Phe Cys Arg Thr Lys Asn Gly Asp Ser Asn Ser
                565                 570                 575


Tyr Arg Ser Gly Asp Asp Ile Asn Lys Leu Asp Trp Glu Lys Arg Ala
            580                 585                 590


Glu Leu Cys Glu Asp Val Glu Tyr Val Arg Gln Leu Ile Arg Leu Arg
        595                 600                 605


Arg Ser His Pro Ala Phe Arg Leu Gln Lys Glu Glu Glu Val Lys Glu
    610                 615                 620


His Leu Ser Phe Met Asp Gly Thr Gly Glu Val Thr Ala Tyr Lys Leu
625                 630                 635                 640


Lys Asn Ile Ala Ala Ile Asp Pro Trp Asn Glu Ile Ile Val Val His
                645                 650                 655


Cys Pro Phe Ala Lys Lys Glu Thr Leu Lys Leu Pro Asp Gln Lys Gln
            660                 665                 670


Tyr Leu Leu His Cys Asp Pro Phe Thr Phe Phe Asn Gly Lys Val Gln
        675                 680                 685


Ala Glu Lys Arg Leu Arg Leu Asn Gly Ile Gly Thr Tyr Val Leu Tyr
    690                 695                 700


Glu Pro Lys Gly Ile Phe
705                 710


<210>  116
<211>  918
<212>  PRT
<213>  Oryza sativa

<400>  116

Met Ala Val Gly Glu Glu Cys Ala Ala Ala Val Ala Ser Gln Gly Phe
```

```
1               5                   10                  15


Val Ser Asp Ala Arg Ala Tyr Trp Val Thr Arg Ser Leu Ile Ala Trp
            20                  25                  30


Asn Val Asn Asp Gln Asp Thr Ser Leu Phe Leu Tyr Ala Ser Arg Asp
        35                  40                  45


Ala Thr Met His Val Ser Asp Gly Ala Ile His Gly Tyr Asp Ser Lys
    50                  55                  60


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


Lys Phe Pro Phe Ile Arg Ser Tyr Arg Thr Phe Arg Val Pro Ser Ser
                85                  90                  95


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


Asp Ala His Gly Arg His Gln Asp Val Thr Gly Leu Gln Leu Pro Gly
        115                 120                 125


Val Leu Asp Asp Met Phe Ala Tyr Thr Gly Pro Leu Gly Ala Val Phe
    130                 135                 140


Ser Asp Lys Asp Val Asp Leu Tyr Leu Trp Ala Pro Thr Ala Gln Asp
145                 150                 155                 160


Val Arg Val Cys Phe Tyr Asp Gly Pro Ala Gly Pro Leu Leu Gln Thr
                165                 170                 175


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


Tyr Arg Glu Asn Gln Tyr Tyr Leu Tyr Glu Val Lys Val Tyr His Pro
        195                 200                 205


Ser Thr Ser Gln Val Glu Lys Cys Leu Ala Asp Asp Pro Tyr Ala Arg
```

```
    210                 215                 220


Gly Leu Ser Ala Asn Gly Thr Arg Thr Trp Leu Val Asp Ile Asn Ser
225                 230                 235                 240


Glu Thr Leu Lys Pro Ala Ser Trp Asp Glu Leu Ser Asp Glu Lys Pro
                245                 250                 255


Asn Leu Glu Ser Phe Ser Asp Ile Ser Ile Tyr Glu Leu His Ile Arg
            260                 265                 270


Asp Phe Ser Ala His Asp Ser Thr Val Asp Cys Asn Ser Arg Gly Gly
        275                 280                 285


Phe Arg Ala Phe Thr Phe Gln Asp Ser Ala Gly Ile Arg His Leu Arg
    290                 295                 300


Lys Leu Ser Ala Ala Gly Leu Thr His Val His Leu Leu Pro Ser Phe
305                 310                 315                 320


His Phe Ala Ser Val Asp Asp Asn Lys Ser Asn Trp Lys Phe Val Asp
                325                 330                 335


Glu Ala Gln Leu Ala Lys Leu Pro Pro Gly Ser Asp Glu Gln Gln Ala
            340                 345                 350


Ala Ile Val Ser Ile Gln Gln Glu Asp Pro Tyr Asn Trp Gly Tyr Asp
        355                 360                 365


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


Gly Pro Ser Arg Ile Ile Glu Tyr Arg Gln Met Val Gln Ala Leu Asn
385                 390                 395                 400


Arg Ile Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Asp
                405                 410                 415


Ser Ser Gly Pro Phe Gly Val Ser Ser Val Leu Asp Lys Ile Val Pro
```

```
            420                 425                 430

Gly Tyr Tyr Leu Arg Arg Asn Val Asn Gly Gln Ile Glu Asn Ser Ala
        435                 440                 445

Ala Met Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile
    450                 455                 460

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

Arg Phe Asp Leu Met Gly His Ile Met Lys Ser Thr Met Phe Thr Val
                485                 490                 495

Met Ser Ile Cys Thr Ile Ser Thr Ile Ile Lys Ile Lys Asp Val Phe
            500                 505                 510

Ala Asp Thr Leu Ile Arg Ala Lys Ser Ala Ile Arg Ser Leu Thr Arg
        515                 520                 525

Asp Val His Gly Val Asp Gly Ser Lys Ile Tyr Leu Tyr Gly Glu Gly
    530                 535                 540

Trp Asp Phe Gly Glu Val Ala Gln Asn Lys Arg Gly Ile Asn Ala Ser
545                 550                 555                 560

Gln Ile Asn Met Ser Gly Thr Gly Ile Gly Ser Phe Asn Asp Arg Ile
                565                 570                 575

Arg Asp Ser Val Asn Gly Gly Asn Pro Phe Gly Asn Pro Leu Gln Gln
            580                 585                 590

Gly Phe Ser Thr Gly Leu Phe Leu Glu Pro Asn Gly Tyr Tyr Gln Gly
        595                 600                 605

Asn Glu Ala Asp Thr Arg Arg Glu Leu Ala Thr Tyr Ala Asp His Ile
    610                 615                 620

Gln Ile Gly Leu Ala Gly Asn Leu Lys Asp Tyr Val Leu Arg Thr His
```

```
625                 630                 635                 640

Thr Gly Glu Ala Lys Lys Gly Ser Asp Ile Tyr Thr Phe Asp Gly Ser
                645                 650                 655

Pro Val Gly Tyr Thr Ser Ser Pro Val Glu Thr Ile Asn Tyr Val Ser
            660                 665                 670

Ala His Asp Asn Glu Thr Leu Phe Asp Ile Val Ser Ile Lys Thr Pro
        675                 680                 685

Ile Gly Leu Ser Ile Asp Glu Lys Cys Arg Ile Asn His Leu Ala Ser
    690                 695                 700

Ser Met Ile Ala Leu Ser Gln Gly Ile Pro Phe Phe His Ala Gly Asp
705                 710                 715                 720

Glu Ile Leu Arg Ser Lys Ser Leu Asp Arg Asp Ser Tyr Asn Ser Gly
                725                 730                 735

Asp Trp Phe Asn Lys Leu Asp Phe Thr Tyr Glu Thr Asn Asn Trp Gly
            740                 745                 750

Val Gly Leu Pro Pro Arg Asp Lys Asn Glu Glu Asn Trp His Leu Ile
        755                 760                 765

Lys Pro Arg Leu Glu Asn Pro Ser Phe Arg Pro Leu Lys Asn His Ile
    770                 775                 780

Leu Ser Val Phe Asp Asn Phe Val Asp Ile Leu Lys Ile Arg Tyr Ser
785                 790                 795                 800

Ser Pro Leu Phe Arg Leu Ser Thr Ala Ser Asp Ile Glu Gln Arg Val
                805                 810                 815

Arg Phe His Asn Thr Gly Pro Ser Met Val Pro Gly Val Ile Val Met
            820                 825                 830

Ser Ile Lys Asp Ala Gln Asn Glu Lys Cys Lys Met Ala Gln Leu Asp
```

```
        835                 840                 845


Lys Asn Phe Ser Tyr Val Val Thr Ile Phe Asn Val Cys Pro His Glu
    850                 855                 860


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


Pro Ile Gln Val Asn Ser Ser Asp Ala Leu Val Arg Gln Ser Ala Tyr
                885                 890                 895


Glu Ala Ser Lys Gly Arg Phe Thr Val Pro Arg Arg Thr Thr Ala Val
            900                 905                 910


Phe Val Gln Pro Arg Cys
        915


<210>  117
<211>  963
<212>  PRT
<213>  Triticum aestivum

<400>  117

Met Pro Met Pro Met Arg Thr Met Leu Leu Arg His Leu Ser Pro Ala
1               5                   10                  15


Pro Ala Leu Pro Asn Pro Arg Arg Ser Ser Ala Ser Ser Pro Gln Arg
            20                  25                  30


Arg Pro Ala Arg Ala Arg Pro Pro Pro Leu His Ser Ala Arg Ala Thr
        35                  40                  45


Ala Leu Arg Ala Arg Arg Thr Pro Met Ala Ala Gly Glu Thr Gly Ala
    50                  55                  60


Ser Val Ser Val Ser Ala Ala Glu Ala Glu Ala Glu Ala Thr Gln Ala
65                  70                  75                  80


Phe Met Pro Asp Ala Arg Ala Tyr Trp Val Thr Ser Asp Leu Ile Ala
                85                  90                  95
```

```
Trp Asn Val Ser Glu Gln Glu Ala Ala Ser Val Tyr Leu Tyr Ala Ser
            100                 105                 110

Arg Thr Ala Ala Met Gly Leu Ser Pro Ser Asn Gly Gly Ile Gln Gly
        115                 120                 125

Tyr Asp Ser Lys Val Glu Leu Gln Pro Glu Ser Ala Gly Leu Pro Glu
    130                 135                 140

Thr Val Thr Gln Lys Phe Pro Phe Ile Ser Ser Tyr Arg Ala Phe Arg
145                 150                 155                 160

Val Pro Ser Ser Val Asp Val Ala Ser Leu Val Lys Cys Gln Leu Val
                165                 170                 175

Ile Ala Ser Phe Gly Ala Asp Gly Lys His Val Asp Val Thr Gly Leu
            180                 185                 190

Gln Leu Pro Gly Val Leu Asp Asp Ile Phe Ala Tyr Thr Gly Pro Leu
        195                 200                 205

Gly Ala Val Phe Arg Glu Asp Ser Val Ser Leu His Leu Trp Ala Pro
    210                 215                 220

Thr Ala Gln Asp Val Ser Val Cys Phe Phe Asp Gly Pro Ala Gly Pro
225                 230                 235                 240

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

Thr Gly Pro Arg Glu Trp Glu Asn Arg Tyr Tyr Leu Tyr Glu Val Asp
            260                 265                 270

Val Tyr His Pro Thr Lys Ala Gln Val Leu Lys Cys Leu Ala Gly Asp
        275                 280                 285

Pro Tyr Ala Arg Gly Leu Ser Ala Asn Gly Ala Arg Thr Trp Leu Val
    290                 295                 300
```

```
Asp Ile Asn Asn Glu Thr Leu Lys Pro Ala Ser Trp Asp Glu Leu Ala
305                 310                 315                 320


Asp Glu Lys Pro Lys Leu Asp Ser Phe Ser Asp Ile Thr Ile Tyr Glu
                325                 330                 335


Leu His Ile Arg Asp Phe Ser Ala His Asp Gly Thr Val Asp Ser Asp
            340                 345                 350


Ser Cys Gly Gly Phe Arg Ala Phe Ala Tyr Gln Ala Ser Ala Gly Met
        355                 360                 365


Gln His Leu Arg Lys Leu Ser Asp Ala Gly Leu Thr His Val His Leu
    370                 375                 380


Leu Pro Ser Phe His Phe Ala Gly Val Asp Asp Ile Lys Ser Asn Trp
385                 390                 395                 400


Lys Phe Val Asp Glu Cys Lys Leu Ala Thr Phe Pro Pro Gly Ser Asp
                405                 410                 415


Met Gln Gln Glu Ala Val Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn
            420                 425                 430


Trp Gly Tyr Asn Pro Val Leu Trp Gly Val Pro Lys Gly Ser Tyr Ala
        435                 440                 445


Ser Asp Pro Asp Gly Pro Ser Arg Ile Ile Glu Tyr Arg Gln Met Val
    450                 455                 460


Gln Ala Leu Asn Arg Ile Gly Leu Arg Val Val Met Asp Val Val Tyr
465                 470                 475                 480


Asn His Leu Asp Ser Ser Gly Pro Cys Gly Ile Ser Ser Val Leu Asp
                485                 490                 495


Lys Ile Val Pro Gly Tyr Tyr Val Arg Arg Asp Thr Asn Gly Gln Ile
            500                 505                 510
```

```
Glu Asn Ser Ala Ala Met Asn Asn Thr Ala Ser Glu His Phe Met Val
        515                 520                 525

Asp Arg Leu Ile Val Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys
    530                 535                 540

Ile Asp Gly Phe Arg Phe Asp Leu Met Gly His Ile Met Lys His Thr
545                 550                 555                 560

Met Met Arg Ala Lys Ala Ala Leu Gln Ser Leu Thr Arg Asp Ala His
                565                 570                 575

Gly Val Asp Gly Ser Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asp Phe
            580                 585                 590

Ala Glu Val Ala Arg Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn
        595                 600                 605

Met Ser Gly Thr Gly Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala
    610                 615                 620

Val Asn Gly Gly Asn Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Asn
625                 630                 635                 640

Thr Gly Leu Phe Leu Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Ala
                645                 650                 655

Asp Thr Arg Arg Ser Leu Ala Thr Tyr Ala Asp Gln Ile Gln Ile Gly
            660                 665                 670

Leu Ala Gly Asn Leu Arg Asp Tyr Val Leu Ile Thr His Thr Gly Glu
        675                 680                 685

Thr Lys Lys Gly Ser Glu Ile His Thr Phe Asp Gly Leu Pro Val Gly
    690                 695                 700

Tyr Thr Ser Ser Pro Ile Glu Ile Ile Asn Tyr Val Ser Ala His Asp
705                 710                 715                 720
```

```
Asn Glu Thr Leu Phe Asp Val Ile Ser Val Lys Thr Pro Met Asn Leu
                725                 730                 735


Ser Val Asp Glu Arg Cys Arg Ile Asn His Leu Ala Ser Ser Met Met
            740                 745                 750


Ala Leu Ser Gln Gly Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu
        755                 760                 765


Arg Ser Lys Ser Ile Asp Arg Asp Ser Tyr Asn Ser Gly Asp Trp Phe
    770                 775                 780


Asn Lys Leu Asp Phe Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu
785                 790                 795                 800


Pro Pro Ser Glu Lys Asn Glu Asp Asn Trp Pro Leu Met Lys Pro Arg
                805                 810                 815


Leu Glu Asn Pro Ser Phe Lys Pro Ala Lys Gly His Ile Leu Ala Ala
            820                 825                 830


Leu Asp Ser Phe Val Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu
        835                 840                 845


Phe Arg Leu Ser Thr Ala Ser Asp Ile Lys Gln Arg Val His Phe His
    850                 855                 860


Asn Thr Gly Pro Ser Ser Val Pro Gly Val Ile Val Met Gly Ile Glu
865                 870                 875                 880


Asp Ala Arg Asp Glu Lys Pro Glu Met Ala Gln Leu Asp Ala Asn Phe
                885                 890                 895


Ser Tyr Val Val Thr Val Phe Asn Val Cys Pro His Glu Val Ser Met
            900                 905                 910


Asp Ile Pro Ala Leu Ala Ser Met Arg Leu Glu Leu His Pro Val Gln
        915                 920                 925
```

```
Val Asn Ser Ser Asp Ala Leu Val Gly Lys Ser Val Tyr Glu Ala Ala
    930                 935                 940


Thr Gly Arg Phe Thr Val Pro Arg Arg Thr Val Ser Val Phe Val Glu
945                 950                 955                 960


Pro Arg Cys




<210>  118
<211>  647
<212>  PRT
<213>  Clostridium phytofermentans

<400>  118

Met Asp Glu Phe Trp Asn Ser Ile Asp Gly Glu Lys Gln Tyr Tyr Tyr
1               5                   10                  15


Asp Gly Asn Asp Leu Gly Cys Thr Tyr Thr Asn Arg Ser Thr Lys Leu
            20                  25                  30


Lys Val Trp Ala Pro Thr Ala Ser Met Val Val Val Asn Leu Tyr Gln
        35                  40                  45


Asn Gly Asn Ala Gly Lys Pro Tyr Ile Thr Glu Ile Met Lys Lys Glu
    50                  55                  60


Glu Ser Gly Ile Trp Ser Val Cys Leu Leu Gly Asp Leu Glu Gly Val
65                  70                  75                  80


Tyr Tyr Thr Tyr Leu Val Thr Val Asp Gly Gln Thr Lys Glu Ala Val
                85                  90                  95


Asp Pro Tyr Ala Arg Thr Thr Gly Leu Asn Gly Lys Arg Ala Met Ile
            100                 105                 110


Leu Asp Leu Glu Lys Thr Asn Pro Thr Gly Phe Leu Glu Asp Thr Lys
        115                 120                 125
```

```
Pro Lys Phe Asp Ser Phe Leu Asp Ala Val Ile Tyr Glu Leu His Ile
    130                 135                 140


Arg Asp Leu Ser Met Glu Ser Asp Ser Gly Ile Lys Glu Lys Gly Lys
145                 150                 155                 160


Leu Leu Gly Leu Thr Glu Leu Asn Thr Arg Asn Ser Asp Gly Leu Thr
                165                 170                 175


Thr Gly Leu Ser His Ile Leu Asp Leu Gly Val Thr His Ile His Leu
            180                 185                 190


Leu Pro Cys Phe Asp Tyr Ala Ser Val Asp Glu Glu Asn Ser Ser Ile
        195                 200                 205


Phe Asn Trp Gly Tyr Asp Pro Glu Asn Tyr Asn Val Val Glu Gly Ser
    210                 215                 220


Tyr Ser Thr Asn Pro Tyr Asp Gly Ala Val Arg Val Lys Glu Phe Lys
225                 230                 235                 240


Thr Leu Val Gln Ser Leu His Glu Asn Gly Leu Arg Val Ile Met Asp
                245                 250                 255


Val Val Tyr Asn His Thr Met Lys Thr Glu Glu Ser Asn Phe Asn Lys
            260                 265                 270


Ile Val Pro Asp Tyr Tyr Tyr Arg Lys Val Gly Asp Lys Phe Ser Asp
        275                 280                 285


Ala Ser Ala Cys Gly Asn Glu Thr Ala Ser Glu Arg Leu Met Val Arg
    290                 295                 300


Lys Phe Ile Val Asp Ser Ile Ile Tyr Trp Ala Lys Glu Tyr His Ile
305                 310                 315                 320


Asp Gly Phe Arg Phe Asp Leu Met Gly Ile His Asp Ile Glu Thr Met
                325                 330                 335
```

```
Asn Glu Val Arg Lys Val Leu Asp Gln Ile Asp Pro Ser Ile Ile Leu
            340                 345                 350


Tyr Gly Glu Gly Trp Val Gly Gly Asp Ser Pro Leu Pro Ala Gly Gln
        355                 360                 365


Arg Ala Met Lys Ala Asn Met Ser Met Leu Pro Gly Ile Ala Ala Phe
    370                 375                 380


Ser Asp Asp Phe Arg Asp Gly Leu Lys Gly Ser Val Phe Leu Ala Glu
385                 390                 395                 400


Glu Lys Gly Phe Ala Thr Gly Asp Ser Asp Lys Lys Glu Ser Val Lys
                405                 410                 415


Phe Gly Val Val Ala Ser Thr Leu His Pro Gln Ile Asp Tyr Lys Lys
            420                 425                 430


Val Asn Tyr Ser Asp Ser Pro Trp Ala Leu Glu Pro Ala Gln Cys Ile
        435                 440                 445


Asn Tyr Val Ser Ala His Asp Asn Tyr Thr Leu Trp Asp Lys Ile Ala
    450                 455                 460


Cys Ser Cys Lys Glu Asp Thr Tyr Glu Ile Arg Val Lys Lys Asn Lys
465                 470                 475                 480


Leu Cys Ala Ala Ile Val Phe Thr Ser Gln Gly Ile Pro Phe Leu Gln
                485                 490                 495


Ala Gly Glu Glu Met Leu Arg Asn Lys Pro Ser Ser Glu Ile Ala Gly
            500                 505                 510


Glu Phe Val Glu Asn Ser Tyr Asn Ser Ser Asp Ser Val Asn Cys Ile
        515                 520                 525


Lys Trp Ser Asn Lys Ala Asn Val Ile Asp Val Val Ser Tyr Tyr Glu
    530                 535                 540
```

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

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

Asp Val Ile Ser Tyr Leu Ile Gln Gly Asp Leu Val Asp Lys Thr Leu
            580   585   590

Cys Val Ile Tyr Asn Ser Ser Glu Glu Lys Val Thr Ile Arg Leu Pro
        595   600   605

Glu Ser Asp Trp Thr Val Tyr Ile Asp Gly Asn Asn Ser Gly Val Glu
    610   615   620

Pro Leu Tyr Glu Val Lys Gly Thr Thr Val Glu Val Glu Pro Ile Ser
625   630   635   640

Cys Met Val Leu Val Lys Asp
                645

<210> 119
<211> 1764
<212> PRT
<213> Streptomyces avermitilis

<400> 119

Ala Thr Pro Pro Ala Pro Pro Ser Asp Ala Lys Leu Ala Ala Glu Pro
1   5   10   15

Ala Arg His Asp Ala Thr Arg Glu Gln Phe Tyr Phe Val Met Pro Asp
            20   25   30

Arg Phe Ala Asn Gly Asp Thr Ser Asn Asp Lys Gly Gly Leu Thr Gly
        35   40   45

Ser Arg Leu Ser Thr Gly Tyr Asp Pro Thr Asp Lys Gly Phe Tyr Gln
    50   55   60

```
Gly Gly Asp Leu Lys Gly Leu Thr Arg Lys Leu Asp Tyr Ile Lys Gly
65                  70                  75                  80


Leu Gly Thr Thr Ser Ile Trp Leu Ala Pro Ile Phe Lys Asn Gln Pro
                85                  90                  95


Val Gln Gly Thr Gly Lys Asp Ala Ser Ala Gly Tyr His Gly Tyr Trp
            100                 105                 110


Ile Thr Asp Phe Thr Lys Val Asp Pro His Phe Gly Thr Asn Lys Asp
        115                 120                 125


Leu Glu Thr Leu Ile Ser Lys Ala His Ala Lys Gly Met Lys Val Phe
    130                 135                 140


Phe Asp Val Ile Thr Asn His Thr Ala Asp Val Val Asp Tyr Glu Glu
145                 150                 155                 160


Lys Ser Tyr Gly Tyr Leu Ser Lys Gly Ala Phe Pro Tyr Leu Thr Lys
                165                 170                 175


Asp Gly Arg Pro Phe Asp Asp Ala Gly Tyr Thr Asp Gly Pro Arg Lys
            180                 185                 190


Phe Pro Ala Val Asp Gly Asp Ser Phe Pro Arg Thr Pro Ala Val Ala
        195                 200                 205


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


Met Tyr His Asn Arg Gly Asp Ser Thr Phe Ala Gly Glu Ser Ser Thr
225                 230                 235                 240


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


Val Val Arg Gly Met Glu Lys Ile Tyr Glu Lys Trp Val Arg Asp Phe
            260                 265                 270
```

```
Gly Ile Asp Gly Phe Arg Ile Asp Thr Val Lys His Val Asn Thr Glu
        275                 280                 285


Phe Trp Thr Gln Trp Ala Thr Ala Leu Asp Ala Tyr Ala Lys Lys Arg
    290                 295                 300


Gly Lys Asp Asp Phe Phe Met Phe Gly Glu Val Tyr Ser Ala Asp Thr
305                 310                 315                 320


Ser Val Thr Ser Pro Tyr Val Thr Gln Gly Arg Leu Asp Ser Thr Leu
                325                 330                 335


Asp Phe Pro Phe Gln Asp Ala Ala Arg Ser Tyr Ala Ser Gln Gly Gly
            340                 345                 350


Ser Ala Lys Lys Leu Ala Ser Val Phe Gly Asp Asp Tyr Lys Tyr Thr
        355                 360                 365


Thr Asp Lys Ala Asn Ala Tyr Glu Gln Val Thr Phe Leu Gly Asn His
    370                 375                 380


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


Thr Asp Ala Glu Leu Leu Arg Lys Asp Arg Leu Ala Asn Glu Leu Met
                405                 410                 415


Phe Leu Ser Arg Gly Asn Pro Val Val Tyr Tyr Gly Asp Glu Gln Gly
            420                 425                 430


Phe Thr Gly Ser Gly Gly Asp Lys Asp Ala Arg Gln Thr Met Phe Ala
        435                 440                 445


Ser Lys Val Ala Asp Tyr Leu Asp Asp Asp Glu Ile Gly Thr Asp Arg
    450                 455                 460


Gly His Ala Ser Asp Ala Tyr Asp Thr Ser Ala Pro Leu Tyr Lys Glu
465                 470                 475                 480
```

```
Ile Ala Ala Leu Ser Lys Leu Arg Lys Asp Asn Pro Ala Leu Ala Asp
                485                 490                 495


Gly Ile Gln Thr Glu Arg Tyr Ala Ala Asp Gly Ala Gly Val Tyr Ala
            500                 505                 510


Phe Ser Arg Thr Asp Ala Arg Thr Gly Thr Glu Tyr Val Val Ala Val
        515                 520                 525


Asn Asn Ala Asp Lys Ala Ser Ala Ala Thr Phe Ala Thr Gly Ser Ala
    530                 535                 540


Asp Thr Ala Phe Lys Gly Ile His Gly Thr Asp Asp Val Leu Lys Ser
545                 550                 555                 560


Asp Ala Asp Lys Lys Ile Thr Val Thr Val Pro Ala Gly Ala Ala Val
                565                 570                 575


Val Leu Lys Ala Ala Gly Arg Pro Gly Thr Pro Ala Ala Lys Pro Ser
            580                 585                 590


Leu Thr Leu Lys Ala Pro Asp Ala Gly Ala Thr Gly Thr Val Glu Leu
        595                 600                 605


Ser Ala Asp Val Asp Gly Gly Arg Leu Asn Arg Val Val Phe Ala Ala
    610                 615                 620


Gln Val Gly Asn Ala Lys Trp Arg Thr Leu Gly Ser Ala Asp His Ala
625                 630                 635                 640


Pro Tyr Arg Val Thr Gln Thr Ile Gly Lys Asp Val Pro Ala Gly Thr
                645                 650                 655


Ala Leu Arg Tyr Lys Ala Val Val Ile Asp Ala Ala Gly Arg Thr Ala
            660                 665                 670


Ser Ala Thr Ala Ala Ser Thr Thr Gly Thr Pro Pro Ala Ala Glu Thr
        675                 680                 685
```

```
Pro Thr Ala Ser Ser Arg Asp Tyr Ala Ile Val His Tyr Lys Arg Pro
    690                 695                 700


Asp Gly Asp Tyr Thr Asp Trp Arg Leu Tyr Ala Trp Gly Asp Leu Ala
705                 710                 715                 720


Asp Gly Glu Ser Thr Thr Trp Pro Ala Gly His Asp Phe Val Gly Arg
                725                 730                 735


Asp Ala Tyr Gly Ala Phe Ala Tyr Val Lys Leu Lys Pro Gly Ala Ser
            740                 745                 750


Thr Val Asn Phe Leu Val Ile Asp Lys Asp Gly Asp Lys Asp Val Ser
        755                 760                 765


Ala Asp Arg Thr Ile Asp Val Thr Lys Ala Gly Glu Val Trp Val Glu
    770                 775                 780


Gln Gly Lys Glu Thr Val Arg Thr Glu Arg Pro Asp Tyr Pro Ala Gln
785                 790                 795                 800


Asp Lys Thr Lys Ala Val Ile His Tyr His Arg Ala Asp Gly Asp Leu
                805                 810                 815


Thr Gly Trp Gly Leu His Val Trp Thr Gly Ala Ala Thr Pro Thr Asp
            820                 825                 830


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


Phe Glu Val Pro Leu Thr Asp Gly Ala Thr Ser Leu Ser Tyr Ile Ile
    850                 855                 860


His Lys Gly Asp Glu Lys Asp Leu Ser Ala Asp Arg Ser Leu Asp Leu
865                 870                 875                 880


Thr Ala Asp Gly His Glu Val Trp Leu Leu Asn Gly Gln Glu Asn His
                885                 890                 895
```

```
Leu Leu Pro Gln Pro Ala Gly Ser Ala Ala Ala Leu Asp Leu Thr Thr
            900                 905                 910


Ser Lys Ala Val Trp Ile Asp Arg Asn Thr Val Ala Trp Asn Gly Ser
        915                 920                 925


Asp Ala Ala Ala Ser Thr Gln Leu Leu Ser Ser Arg Asp Gly Ser Ile
    930                 935                 940


Ala Val Lys Asp Gly Ser Leu Thr Ser Asp Asp Glu Arg Trp Leu Arg
945                 950                 955                 960


Leu Ser Lys Thr Ser Leu Thr Asp Ala Gln Lys Ala Ala Phe Pro His
                965                 970                 975


Leu Lys Ser Tyr Thr Ala Trp Ser Val Asp Pro Arg Asp Arg Asp Arg
            980                 985                 990


Val Arg Glu Ala Leu Ala Gly Gln  Val Val Ala Ser Gln  Arg Ala Ala
        995                 1000                 1005


Asn Gly  Ala Val Leu Ala Ala  Thr Gly Val Gln Leu  Ala Gly Val
    1010                 1015                 1020


Leu Asp  Asp Leu Tyr Asp Ala  Thr Lys Ala Asp Leu  Gly Pro Thr
    1025                 1030                 1035


Phe Arg  Gly Gly His Pro Thr  Leu Ala Val Trp Ala  Pro Thr Ala
    1040                 1045                 1050


Gln Ser  Val Ser Leu Glu Leu  Asp Gly Ala His Val  Arg Met Lys
    1055                 1060                 1065


Arg Asn  Asn Ala Thr Gly Val  Trp Ser Val Thr Gly  Pro Ala Ser
    1070                 1075                 1080


Trp Lys  Gly Lys Pro Tyr Arg  Tyr Val Val Lys Val  Trp Ala Pro
    1085                 1090                 1095
```

```
Thr Val  Arg Lys Val Val Thr  Asn Lys Val Thr Asp  Pro Tyr Ser
    1100                 1105                 1110


Val Ala  Leu Thr Thr Asp Ser  Glu Arg Ser Leu Val  Val Asp Leu
    1115                 1120                 1125


Asp Asp  Arg Ser Leu Ala Pro  Ser Gly Trp Ser Ser  Leu Lys Lys
    1130                 1135                 1140


Pro Lys  Ala Val Pro Leu Arg  Asp Ala Glu Ile Gln  Glu Leu His
    1145                 1150                 1155


Ile Arg  Asp Phe Ser Val Ala  Asp Arg Thr Val Pro  Ala Lys Asp
    1160                 1165                 1170


Arg Gly  Thr Tyr Leu Ala Phe  Thr Asp Lys Asn Ser  Asp Gly Ser
    1175                 1180                 1185


Arg His  Leu Arg Gln Leu Ala  Glu Ser Gly Thr Ser  Tyr Val His
    1190                 1195                 1200


Leu Leu  Pro Ala Phe Asp Ile  Ala Thr Ile Ala Glu  Lys Lys Ser
    1205                 1210                 1215


Gly Gln  Gln Ala Thr Asp Cys  Asp Leu Ala Ser Tyr  Ala Ala Asp
    1220                 1225                 1230


Ser Glu  Lys Gln Gln Glu Cys  Leu Thr Ala Val Ala  Ala Lys Asp
    1235                 1240                 1245


Ala Tyr  Asn Trp Gly Tyr Asp  Pro Tyr His Tyr Thr  Val Pro Glu
    1250                 1255                 1260


Gly Ser  Tyr Ala Thr Asp Ala  Asn Gly Thr Arg Arg  Thr Val Glu
    1265                 1270                 1275


Phe Arg  Arg Met Val Lys Ser  Leu Asn Gln Asp Gly  Leu Arg Val
    1280                 1285                 1290
```

```
Val Met  Asp Val Val Tyr Asn  His Thr Ala Ala Ala  Gly Gln Ala
    1295                 1300                 1305


Gly Thr  Ser Val Leu Asp Arg  Ile Val Pro Gly Tyr  Tyr Gln Arg
    1310                 1315                 1320


Leu Leu  Ala Asp Gly Ser Val  Ala Thr Ser Thr Cys  Cys Ala Asn
    1325                 1330                 1335


Thr Ala  Thr Glu Asn Ala Met  Met Gly Lys Leu Val  Val Asp Ser
    1340                 1345                 1350


Leu Val  Thr Trp Ala Lys Glu  Tyr Lys Val Asp Gly  Phe Arg Phe
    1355                 1360                 1365


Asp Leu  Met Gly His Gln Pro  Lys Ala Asn Ile Leu  Ala Val Arg
    1370                 1375                 1380


Lys Ala  Leu Asp Ala Leu Thr  Val Ala Lys Asp Gly  Val Asp Gly
    1385                 1390                 1395


Lys Lys  Ile Ile Leu Tyr Gly  Glu Gly Trp Asn Phe  Gly Glu Val
    1400                 1405                 1410


Ala Asp  Asp Ala Arg Phe Val  Gln Ala Thr Gln Lys  Asn Met Ala
    1415                 1420                 1425


Gly Thr  Gly Ile Ala Thr Phe  Ser Asp Arg Ala Arg  Asp Ala Val
    1430                 1435                 1440


Arg Gly  Gly Gly Pro Phe Asp  Ala Asp Pro Gly Val  Gln Gly Phe
    1445                 1450                 1455


Gly Ser  Gly Leu Tyr Thr Asp  Pro Asn Ser Ser Asp  Ala Asn Gly
    1460                 1465                 1470


Thr Pro  Ala Glu Gln Lys Ala  Arg Leu Leu His Tyr  Gln Asp Leu
    1475                 1480                 1485
```

```
Ile Lys  Val Gly Leu Ser Gly  Asn Leu Ala Lys Tyr  Arg Phe Thr
    1490                 1495                 1500


Asp Ser  Ser Gly Lys Glu Val  Thr Gly Ser Glu Val  Asp Tyr Asn
    1505                 1510                 1515


Gly Thr  Gly Ala Gly Tyr Ala  Asp Ala Pro Gly Asp  Ala Leu Ala
    1520                 1525                 1530


Tyr Ala  Asp Ala His Asp Asn  Glu Ser Leu Tyr Asp  Ala Leu Thr
    1535                 1540                 1545


Tyr Lys  Leu Pro Lys Gly Thr  Pro Ala Gly Asp Arg  Ala Arg Met
    1550                 1555                 1560


Gln Val  Leu Ala Met Ala Thr  Ala Ala Leu Ala Gln  Gly Pro Ser
    1565                 1570                 1575


Leu Ser  Gln Ala Gly Ser Asp  Leu Leu Arg Ser Lys  Ser Leu Asp
    1580                 1585                 1590


Arg Asn  Ser Tyr Asp Ser Gly  Asp Trp Phe Asn Ala  Ile His Trp
    1595                 1600                 1605


Asn Cys  Gln Asp Gly Asn Gly  Phe Gly Arg Gly Leu  Pro Met Ala
    1610                 1615                 1620


Ala Asp  Asn Lys Ser Lys Trp  Pro Tyr Ala Thr Pro  Leu Leu Thr
    1625                 1630                 1635


Ser Val  Lys Val Gly Cys Asp  Gln Ile Glu Gly Thr  Ser Ala Gly
    1640                 1645                 1650


Tyr Gln  Asp Leu Leu Arg Ile  Arg Thr Thr Glu Pro  Asp Phe Ser
    1655                 1660                 1665


Leu Ser  Thr Ala Gly Gln Val  Gln Ser Lys Leu Thr  Phe Pro Leu
    1670                 1675                 1680
```

```
Ser Gly  Lys Asp Glu Thr Pro  Gly Val Ile Thr Met  Lys Leu Gly
    1685                 1690                 1695


Asp Leu  Val Val Val Phe Asn  Ala Thr Pro Asp Gln  Gln Glu Gln
    1700                 1705                 1710


Thr Val  Ala Ala Leu Ala Gly  Lys Asp Tyr Ala Leu  His Pro Val
    1715                 1720                 1725


Gln Ala  Ala Gly Ala Asp Pro  Ile Val Lys Ser Ala  Ser Tyr Thr
    1730                 1735                 1740


Ala Lys  Ser Gly Met Phe Ala  Val Pro Gly Arg Thr  Val Ala Ile
    1745                 1750                 1755


Phe Ser  Gln Val Ala Arg
    1760


<210>  120
<211>  1079
<212>  PRT
<213>  Klebsiella pneumoniae

<400>  120

Ser Ser Ser Ser Pro Ser Gly Ser Pro Gly Ser Pro Gly Asn Pro Gly
1               5                   10                  15


Asn Pro Gly Thr Pro Gly Thr Pro Asp Pro Gln Asp Val Val Val Arg
            20                  25                  30


Leu Pro Asp Val Ala Val Pro Gly Glu Ala Ala Gln Ala Ser Ala Asn
        35                  40                  45


Gln Ala Val Ile His Leu Val Asp Ile Ala Gly Ile Thr Ser Ser Thr
    50                  55                  60


Pro Ala Asp Tyr Ala Thr Lys Asn Leu Tyr Leu Trp Asn Asn Glu Thr
65                  70                  75                  80


Cys Asp Ala Leu Ser Ala Pro Val Ala Asp Trp Asn Asp Val Ser Thr
```

```
                85                  90                  95

Thr Pro Thr Gly Ser Asp Lys Tyr Gly Pro Tyr Trp Val Ile Pro Leu
            100                 105                 110

Thr Lys Glu Ser Gly Cys Ile Asn Val Ile Val Arg Asp Gly Thr Asn
        115                 120                 125

Lys Leu Ile Asp Ser Asp Leu Arg Val Ser Phe Gly Asp Phe Thr Asp
    130                 135                 140

Arg Thr Val Ser Val Ile Ala Gly Asn Ser Ala Val Tyr Asp Ser Arg
145                 150                 155                 160

Ala Asp Ala Phe Arg Ala Ala Phe Gly Val Ala Leu Ala Asp Ala His
                165                 170                 175

Trp Val Asp Lys Thr Thr Leu Leu Trp Pro Gly Gly Glu Asn Lys Pro
            180                 185                 190

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

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

Ser Gln Gln Val Ser Met Arg Phe Pro His Leu Ala Ser Tyr Pro Ala
225                 230                 235                 240

Phe Lys Leu Pro Asp Asp Val Asn Val Asp Glu Leu Leu Gln Gly Glu
                245                 250                 255

Thr Val Ala Ile Ser Ala Glu Ser Asp Gly Ile Leu Ser Ser Ala Thr
            260                 265                 270

Gln Val Gln Thr Ala Gly Val Leu Asp Asp Thr Tyr Ala Ala Ala Ala
        275                 280                 285

Glu Ala Leu Ser Tyr Gly Ala Gln Leu Thr Asp Ser Gly Val Thr Phe
```

290 295 300

Arg Val Trp Ala Pro Thr Ala Gln Gln Val Glu Leu Val Val Tyr Ser
305 310 315 320

Ala Asp Lys Lys Val Val Ala Ser His Pro Met Thr Arg Asp Ser Ala
325 330 335

Ser Gly Ala Trp Ser Trp Gln Gly Gly Ser Asp Leu Lys Gly Ala Phe
340 345 350

Tyr Arg Tyr Ala Met Thr Val Tyr His Pro Gln Ser Arg Lys Val Glu
355 360 365

Gln Tyr Glu Val Thr Asp Pro Tyr Ala His Ser Leu Ser Thr Asn Ser
370 375 380

Glu Tyr Ser Gln Val Val Asp Leu Asn Asp Ser Ala Leu Lys Pro Glu
385 390 395 400

Gly Trp Asp Gly Leu Thr Met Pro His Ala Gln Lys Thr Lys Ala Asp
405 410 415

Leu Ala Lys Met Thr Ile His Glu Ser His Ile Arg Asp Leu Ser Ala
420 425 430

Trp Asp Gln Thr Val Pro Ala Glu Leu Arg Gly Lys Tyr Leu Ala Leu
435 440 445

Thr Ala Gln Glu Ser Asn Met Val Gln His Leu Lys Gln Leu Ser Ala
450 455 460

Ser Gly Val Thr His Ile Glu Leu Leu Pro Val Phe Asp Leu Ala Thr
465 470 475 480

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

Arg Leu Cys Glu Ile Asn Ser Ala Val Lys Ser Ser Glu Phe Ala Gly

```
            500                 505                 510


Tyr Cys Asp Ser Gly Ser Thr Val Glu Glu Val Leu Thr Gln Leu Lys
        515                 520                 525


Gln Asn Asp Ser Lys Asp Asn Pro Gln Val Gln Ala Leu Asn Thr Leu
    530                 535                 540


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


Thr Val Pro Glu Gly Ser Tyr Ala Thr Asp Pro Glu Gly Thr Ala Arg
                565                 570                 575


Ile Lys Glu Phe Arg Thr Met Ile Gln Ala Ile Lys Gln Asp Leu Gly
            580                 585                 590


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


Pro Thr Asp Arg Thr Ser Val Leu Asp Lys Ile Val Pro Trp Tyr Tyr
    610                 615                 620


Gln Arg Leu Asn Glu Thr Thr Gly Ser Val Glu Ser Ala Thr Cys Cys
625                 630                 635                 640


Ser Asp Ser Ala Pro Glu His Arg Met Phe Ala Lys Leu Ile Ala Asp
                645                 650                 655


Ser Leu Ala Val Trp Thr Thr Asp Tyr Lys Ile Asp Gly Phe Arg Phe
            660                 665                 670


Asp Leu Met Gly Tyr His Pro Lys Ala Gln Ile Leu Ser Ala Trp Glu
        675                 680                 685


Arg Ile Lys Ala Leu Asn Pro Asp Ile Tyr Phe Phe Gly Glu Gly Trp
    690                 695                 700


Asp Ser Asn Gln Ser Asp Arg Phe Glu Ile Ala Ser Gln Ile Asn Leu
```

```
705                 710                 715                 720


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


Arg Gly Gly Gly Pro Phe Asp Ser Gly Asp Ala Leu Arg Gln Asn Gln
            740                 745                 750


Gly Val Gly Ser Gly Ala Gly Val Leu Pro Asn Glu Leu Thr Ser Met
        755                 760                 765


Thr Asp Asp Gln Ala Arg His Leu Ala Asp Leu Thr Arg Leu Gly Met
    770                 775                 780


Ala Gly Asn Leu Ala Asp Phe Val Leu Ile Asp Lys Asp Gly Ala Val
785                 790                 795                 800


Lys Lys Gly Ser Glu Ile Asp Tyr Asn Gly Ala Pro Gly Gly Tyr Ala
                805                 810                 815


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


Thr Leu Trp Asp Met Ile Ser Tyr Lys Ala Ala Gln Glu Ala Asp Leu
        835                 840                 845


Asp Thr Arg Val Arg Met Gln Ala Val Ser Leu Ala Thr Val Met Leu
    850                 855                 860


Gly Gln Gly Ile Ala Phe Asp Gln Gln Gly Ser Glu Leu Leu Arg Ser
865                 870                 875                 880


Lys Ser Phe Thr Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Arg
                885                 890                 895


Val Asp Tyr Ser Leu Gln Asp Asn Asn Tyr Asn Val Gly Met Pro Arg
            900                 905                 910


Ser Ser Asp Asp Gly Ser Asn Tyr Asp Ile Ile Ala Arg Val Lys Asp
```

```
        915                 920                 925


Ala Val Ala Thr Pro Gly Glu Thr Glu Leu Lys Gln Met Thr Ala Phe
    930                 935                 940


Tyr Gln Glu Leu Thr Ala Leu Arg Lys Ser Ser Pro Leu Phe Thr Leu
945                 950                 955                 960


Gly Asp Gly Ala Thr Val Met Gln Arg Val Asp Phe Arg Asn Thr Gly
                965                 970                 975


Ala Asp Gln Gln Thr Gly Leu Leu Val Met Thr Ile Asp Asp Gly Met
            980                 985                 990


Gln Ala Gly Ala Ser Leu Asp Ser  Arg Val Asp Gly Ile  Val Val Ala
        995                 1000                1005


Ile Asn  Ala Ala Pro Glu Ser  Arg Thr Leu Gln Asp  Phe Ala Gly
    1010                1015                1020


Thr Ser  Leu Gln Leu Ser Ala  Ile Gln Gln Ala Ala  Gly Asp Arg
    1025                1030                1035


Ser Leu  Ala Ser Gly Val Gln  Val Ala Ala Asp Gly  Ser Val Thr
    1040                1045                1050


Leu Pro  Ala Trp Ser Val Ala  Val Leu Glu Leu Pro  Gln Gly Glu
    1055                1060                1065


Ser Gln  Gly Ala Gly Leu Pro  Val Ser Ser Lys
    1070                1075


<210>  121
<211>  546
<212>  PRT
<213>  Rhizomucor pusillus

<400>  121

Ala Thr Ser Asp Asp Trp Lys Gly Lys Ala Ile Tyr Gln Leu Leu Thr
1               5                   10                  15
```

```
Asp Arg Phe Gly Arg Ala Asp Asp Ser Thr Ser Asn Cys Ser Asn Leu
            20                  25                  30

Ser Asn Tyr Cys Gly Gly Thr Tyr Glu Gly Ile Thr Lys His Leu Asp
        35                  40                  45

Tyr Ile Ser Gly Met Gly Phe Asp Ala Ile Trp Ile Ser Pro Ile Pro
    50                  55                  60

Lys Asn Ser Asp Gly Gly Tyr His Gly Tyr Trp Ala Thr Asp Phe Tyr
65                  70                  75                  80

Gln Leu Asn Ser Asn Phe Gly Asp Glu Ser Gln Leu Lys Ala Leu Ile
                85                  90                  95

Gln Ala Ala His Glu Arg Asp Met Tyr Val Met Leu Asp Val Val Ala
            100                 105                 110

Asn His Ala Gly Pro Thr Ser Asn Gly Tyr Ser Gly Tyr Thr Phe Asp
        115                 120                 125

Asp Ala Ser Leu Tyr His Pro Lys Cys Thr Ile Asp Tyr Asn Asn Gln
    130                 135                 140

Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Glu Leu Pro Asp Ile Asp
145                 150                 155                 160

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

Trp Val Gly Asn Tyr Ser Phe Asp Gly Ile Arg Ile Asp Thr Val Lys
            180                 185                 190

His Ile Arg Lys Asp Phe Trp Thr Gly Tyr Ala Glu Ala Ala Gly Val
        195                 200                 205

Phe Ala Thr Gly Glu Val Phe Asn Gly Asp Pro Ala Tyr Val Gly Pro
    210                 215                 220
```

```
Tyr Gln Lys Tyr Leu Pro Ser Leu Ile Asn Tyr Pro Met Tyr Tyr Ala
225                 230                 235                 240


Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg Ile Ser
                245                 250                 255


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


Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn Ser Gln
        275                 280                 285


Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu Leu Gly
    290                 295                 300


Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe Ser Gly
305                 310                 315                 320


Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Thr Asn Tyr Asp
                325                 330                 335


Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser Val Arg
            340                 345                 350


Met Lys Ser Asn Lys Ala Val Tyr Met Asp Ile Tyr Val Gly Asp Asn
        355                 360                 365


Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn Asn Tyr
    370                 375                 380


Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly Lys Phe
385                 390                 395                 400


Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr Thr Thr
                405                 410                 415


Val Ser Ser Asp Gly Thr Val Thr Phe Asn Leu Lys Asp Gly Leu Pro
            420                 425                 430
```

```
Ala Ile Phe Thr Ser Ala Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly
        435                 440                 445


Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln
    450                 455                 460


Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro
465                 470                 475                 480


Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala
                485                 490                 495


Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn
            500                 505                 510


Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu
        515                 520                 525


Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp
    530                 535                 540


Glu Ser
545


<210>  122
<211>  481
<212>  PRT
<213>  Bacillus licheniformis

<400>  122

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


Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
            20                  25                  30


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

```
Gln Ala Asp Val Gly Tyr Gly Ala Tyr Asp Leu Tyr Asp Leu Gly Glu
    50                  55                  60


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


Leu Gln Ser Ala Ile Lys Ser Leu His Ser Arg Asp Ile Asn Val Tyr
                85                  90                  95


Gly Asp Val Val Ile Asn His Lys Gly Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110


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


Gly Glu His Leu Ile Lys Ala Trp Thr His Phe His Phe Pro Gly Arg
    130                 135                 140


Gly Ser Thr Tyr Ser Asp Phe Lys Trp Tyr Trp Tyr His Phe Asp Gly
145                 150                 155                 160


Thr Asp Trp Asp Glu Ser Arg Lys Leu Asn Arg Ile Tyr Lys Phe Gln
                165                 170                 175


Gly Lys Thr Trp Asp Trp Glu Val Ser Asn Glu Phe Gly Asn Tyr Asp
            180                 185                 190


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


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


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


Asp Trp Val Asn His Val Arg Glu Lys Thr Gly Lys Glu Met Phe Thr
                245                 250                 255
```

```
Val Ala Glu Tyr Trp Ser Asn Asp Leu Gly Ala Leu Glu Asn Tyr Leu
            260                 265                 270


Asn Lys Thr Asn Phe Asn His Ser Val Phe Asp Val Pro Leu His Tyr
        275                 280                 285


Gln Phe His Ala Ala Ser Thr Gln Gly Gly Gly Tyr Asp Met Arg Lys
    290                 295                 300


Leu Leu Asn Gly Thr Val Val Ser Lys His Pro Leu Lys Ser Val Thr
305                 310                 315                 320


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


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


Glu Ser Gly Tyr Pro Gln Val Phe Tyr Gly Asp Met Tyr Gly Thr Lys
        355                 360                 365


Gly Asp Ser Gln Arg Glu Ile Pro Ala Leu Lys His Lys Ile Glu Pro
    370                 375                 380


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


Phe Asp His His Asp Ile Val Gly Trp Thr Arg Glu Gly Asp Ser Ser
                405                 410                 415


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


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


Asp Ile Thr Gly Asn Arg Ser Glu Pro Val Val Ile Asn Ser Glu Gly
    450                 455                 460
```

```
Trp Gly Glu Phe His Val Asn Gly Gly Ser Val Ser Ile Tyr Val Gln
465                 470                 475                 480


Arg




<210>  123
<211>  484
<212>  PRT
<213>  Aspergillus niger

<400>  123

Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30


Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60


Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
        115                 120                 125


Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140
```

```
Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160


Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175


Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190


Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205


Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
225                 230                 235                 240


Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255


Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270


Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285


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


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350
```

```
Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365


Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
    370                 375                 380


Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400


Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
            420                 425                 430


Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
        435                 440                 445


Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
    450                 455                 460


Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465                 470                 475                 480


Leu Tyr Val Glu



<210>  124
<211>  586
<212>  PRT
<213>  Aspergillus tamarii

<400>  124

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Ala Cys Asn Thr
            20                  25                  30


Glu Asp Arg Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
```

        35   40   45

Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50   55   60

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

Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85   90   95

Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100   105   110

Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115   120   125

Gly Ala Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Asn Ser Gln Glu
    130   135   140

Tyr Phe His Ser Phe Cys Leu Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145   150   155   160

Val Glu Asn Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
                165   170   175

Asp Thr Thr Lys Asp Glu Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
            180   185   190

Thr Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Val Asp Thr Val
        195   200   205

Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210   215   220

Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225   230   235   240

Pro Tyr Gln Asp Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr

```
                245                 250                 255

Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asn Asp Leu
            260                 265                 270

Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285

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

Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320

Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335

Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

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

Arg Ser His Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380

Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

Asp Gly Ser Gln Val Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415

Asp Ser Tyr Thr Leu Ser Leu Gly Asp Thr Gly Tyr Lys Ala Gly Gln
            420                 425                 430

Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
        435                 440                 445

Gly Lys Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
```

```
    450                 455                 460


Pro Thr Glu Lys Leu Ala Asp Ser Lys Ile Cys Ser Ser Ser Gly Ala
465                 470                 475                 480


Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val
                485                 490                 495


Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val
            500                 505                 510


Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser
        515                 520                 525


Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr
    530                 535                 540


Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp
545                 550                 555                 560


Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr
                565                 570                 575


Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  125
<211>  603
<212>  PRT
<213>  Acidomyces richmondensis

<400>  125

Leu Thr Pro Ala Glu Trp Arg Ala Gln Ser Ile Tyr Gln Val Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Leu Thr Asn Gly Ser Thr Thr Ala Pro Cys Asn Leu
            20                  25                  30


Asn Glu Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asn Lys Leu Asp
        35                  40                  45
```

```
Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Val Val
    50                  55                  60


Glu Asn Ile Pro Ala Ser Asp Asn Thr Ala Asp Gly Glu Ser Tyr His
65                  70                  75                  80


Gly Tyr Trp Ala Gln Arg Ile Tyr Glu Val Asn Pro Asn Phe Gly Ser
                85                  90                  95


Ala Ala Asp Leu Glu Ala Leu Ser Glu Ala Ile His Ala Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Ile Val Thr Asn His Met Gly Tyr Asp Gly Cys
        115                 120                 125


Gly Thr Cys Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Asn Gln Ser
    130                 135                 140


Tyr Phe His Pro Phe Cys Leu Ile Asn Tyr Asn Asn Ala Thr Ser Ile
145                 150                 155                 160


Gln Val Cys Trp Glu Gly Asp Asn Ile Val Ser Leu Pro Asp Leu Arg
                165                 170                 175


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


Leu Val Ala Asn Tyr Ser Ile Asp Gly Leu Arg Val Asp Ser Met Gln
        195                 200                 205


Gln Val Asp Gln Ala Phe Trp Gln Pro Phe Met Ser Ala Ala Gly Asp
    210                 215                 220


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


Pro Tyr Gln Gln Tyr Leu Pro Gly Val Leu Asn Tyr Pro Ala Tyr Tyr
                245                 250                 255
```

```
Trp Ile Thr Gln Ala Phe Glu Ser Thr Ser Gly Ser Ile Gly Asn Leu
            260                 265                 270

Val Asn Gly Ile Asn Glu Met Lys Asn Asp Cys Leu Asp Thr Thr Leu
        275                 280                 285

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

Thr Ser Asp Tyr Ser Leu Asp Lys Asn Ala Ile Ala Phe Ala Met Leu
305                 310                 315                 320

Gln Asp Gly Ile Pro Ile Val Tyr Glu Gly Gln Glu Gln His Tyr Ser
                325                 330                 335

Gly Gly Ser Val Pro Asn Asn Arg Glu Asp Ile Trp Ser Ser Gly Tyr
            340                 345                 350

Ser Thr Thr Ser Glu Leu Tyr Thr Phe Ile Lys Ile Ile Asn Ala Ile
        355                 360                 365

Arg Thr Gln Ala Leu Thr Lys Asp Ser Ser Tyr Leu Thr Tyr Lys Ala
    370                 375                 380

Tyr Pro Val Tyr Ser Asp Ser Gln Thr Ile Ala Met Arg Lys Gly Glu
385                 390                 395                 400

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

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

Gln Ser Ile Thr Glu Leu Leu Thr Cys Thr Val Ser Thr Thr Asp Ser
        435                 440                 445

Gly Gly Asn Leu Val Val Asn Ile Ser Ser Gly Leu Pro Arg Val Tyr
    450                 455                 460
```

```
Tyr Pro Thr Ser Ala Ile Ser Gly Ser Thr Val Cys Ala Glu Ser Thr
465                 470                 475                 480


Ser Thr Leu Thr Ile Ser Ser Pro Ile Ser Thr Ser Thr Ser Asp Cys
                485                 490                 495


Thr Thr Ala Ser Ser Val Ala Val Thr Phe Asp Glu Thr Val Thr Thr
            500                 505                 510


Thr Tyr Gly Glu Thr Ile Lys Leu Ser Gly Ser Ile Ser Gln Leu Gly
        515                 520                 525


Asp Trp Asn Thr Gln Asp Ala Ile Leu Leu Ser Ala Ala Asp Tyr Lys
    530                 535                 540


Ser Thr Asp Asn Val Trp Phe Val Thr Ile Asn Leu Pro Ala Gly Ile
545                 550                 555                 560


Val Phe Gln Tyr Lys Tyr Ile Asn Val Asp Ser Asp Gly Asp Val Thr
                565                 570                 575


Trp Glu Ala Asp Pro Asn His Thr Tyr Thr Val Ser Ala Thr Cys Ala
            580                 585                 590


Thr Ala Ala Thr Ile His Asp Thr Trp Gln Asn
        595                 600


<210>  126
<211>  588
<212>  PRT
<213>  Aspergillus bombycis

<400>  126

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30
```

```
Glu Asp Arg Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Gly Gln Leu Pro Gln Asp Thr Ala Tyr Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Asp Ile Tyr Ala Leu Asn Glu Asn His Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125


Gly Ala Ser Val Asp Tyr Ser Val Phe Asn Pro Phe Ser Ser Gln Asp
    130                 135                 140


Tyr Phe His Ser Phe Cys Leu Ile Glu Asn Tyr Asp Asp Gln Thr Gln
145                 150                 155                 160


Ser Glu Asn Cys Trp Leu Gly Asp Asn Ser Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Lys Asp Glu Val Lys Asn Glu Trp Tyr Glu Trp Val Gly
            180                 185                 190


Asn Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Val Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Glu Ala Ala Gly
    210                 215                 220


Val Tyr Cys Ile Gly Glu Val Leu Asn Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240
```

```
Pro Tyr Gln Asp Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asn Asp Leu
            260                 265                 270


Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285


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


Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320


Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335


Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


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


Arg Asn His Ala Val Ser Thr Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380


Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400


Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415


Asp Ala Tyr Thr Leu Ser Leu Gly Asn Thr Gly Tyr Thr Ala Gly Gln
            420                 425                 430


Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Leu Thr Val Gly Ser Asp
        435                 440                 445
```

```
Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460


Pro Thr Glu Lys Leu Gly Asp Ser Lys Ile Cys Ser Ser Ser Gly Arg
465                 470                 475                 480


Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
                485                 490                 495


Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
            500                 505                 510


Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525


Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
    530                 535                 540


Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545                 550                 555                 560


Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
                565                 570                 575


Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  127
<211>  570
<212>  PRT
<213>  Alternaria sp.

<400>  127

Ala Asp Thr Ser Ala Trp Lys Ser Arg Ser Ile Tyr Phe Val Leu Thr
1               5                   10                  15


Asp Arg Ile Ala Arg Ser Ser Ser Asp Thr Gly Gly Gly Ser Cys Ser
            20                  25                  30
```

```
Asn Leu Gly Asn Tyr Cys Gly Gly Thr Phe Lys Gly Leu Glu Ser Lys
        35                  40                  45


Leu Asp Tyr Ile Lys Asn Leu Gly Phe Asp Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Val Ala Asn Ser Ala Gly Gly Tyr His Gly Tyr Trp Ala Gln Asp
65                  70                  75                  80


Leu Tyr Ala Val Asn Ser Asn Tyr Gly Thr Ala Ala Asp Leu Lys Ser
                85                  90                  95


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


Val Ala Asn His Met Gly Gln Gly Ala Ile Ser Gly Asn Arg Pro Glu
        115                 120                 125


Pro Leu Asn Gln Asp Ser Ser Tyr His Ser Ala Cys Asp Ile Asn Tyr
    130                 135                 140


Ser Ser Gln Thr Ser Ile Glu Gln Cys Arg Ile Ala Asn Leu Pro Asp
145                 150                 155                 160


Leu Asn Thr Gln Ser Ser Gln Ile Arg Ser Leu Leu Asn Thr Trp Ile
                165                 170                 175


Ser Trp Leu Val Asn Glu Tyr Ser Phe Asp Gly Val Arg Ile Asp Thr
            180                 185                 190


Val Lys His Val Glu Lys Asp Phe Trp Pro Gly Phe Ala Ser Ala Ala
        195                 200                 205


Gly Val Tyr Ser Ile Gly Glu Val Trp Asp Gly Asn Pro Thr Tyr Leu
    210                 215                 220


Ala Glu Tyr Ala Arg Leu Met Pro Gly Leu Leu Asn Tyr Ala Thr Tyr
225                 230                 235                 240
```

```
Tyr Pro Met Asn Asn Phe Tyr Gln Gln Lys Gly Ser Ser Gln Ala Leu
                245                 250                 255


Val Asp Met Met Asn Thr Val Arg Asp Thr Phe Pro Asp Pro Ser Ala
            260                 265                 270


Leu Gly Thr Phe Leu Asp Asn His Asp Asn Asn Arg Trp Leu Asn Gln
        275                 280                 285


Lys Asn Asp Val Thr Leu Leu Lys Asn Ala Leu Ala Phe Val Ile Leu
    290                 295                 300


Ser Arg Gly Ile Pro Ile Val Tyr Tyr Gly Thr Glu Gln Gly Tyr Ala
305                 310                 315                 320


Gly Gly Ala Asp Pro Ala Asn Arg Glu Asp Leu Trp Arg Ser Ser Phe
                325                 330                 335


Asn Thr Asn Ala Asp Leu Tyr Gln Ala Ile Lys Lys Leu Asn Ala Ala
            340                 345                 350


Arg Thr Ser Ala Gly Gly Leu Ala Gly Asn Asp His Thr His Leu Tyr
        355                 360                 365


Val Ser Ser Asn Ala Tyr Ala Trp Ser Arg Ala Asn Gly Asn Leu Val
    370                 375                 380


Val Leu Thr Thr Asn Ala Gly Ser Gly Ser Asn Ala Gln His Cys Phe
385                 390                 395                 400


Asn Thr Gln Lys Ala Asn Gly Arg Trp Thr Asn Val Tyr Gly Asn Gly
                405                 410                 415


Ala Thr Val Thr Ala Asp Gly Ser Gly Asn Ile Cys Val Asn Val Ala
            420                 425                 430


Asn Gly Glu Pro Val Val Leu Leu Val Ser Thr Ala Thr Pro Thr Ser
        435                 440                 445
```

```
Ala Thr Pro Thr Ser Asn Pro Ser Pro Thr Thr Leu Leu Thr Thr Ser
    450                 455                 460


Thr Ala Cys Pro Thr Ser Val Ser Val Ser Phe Thr His Arg Val Thr
465                 470                 475                 480


Thr Val Phe Gly Asp Thr Ile Lys Ile Thr Gly Asn Thr Ala Gln Leu
                485                 490                 495


Gly Asn Trp Asn Pro Ser Asn Gly Val Ala Leu Ser Ala Ala Ser Tyr
            500                 505                 510


Thr Ser Ser Asn Pro Ile Trp Thr Leu Thr Leu Pro Leu Pro Ala Gly
        515                 520                 525


Ser Ala Ile Gln Tyr Lys Phe Val Lys Val Ser Ser Gly Gly Thr Val
    530                 535                 540


Thr Trp Glu Ser Asp Pro Asn Arg Ser Tyr Ser Val Pro Gly Cys Gln
545                 550                 555                 560


Ala Ser Ala Ser Val Ser Ser Gln Trp Gln
                565                 570


<210>  128
<211>  551
<212>  PRT
<213>  Rhizopus microsporus

<400>  128

Ser Pro Ile Thr Ile Arg Ser Gln Asn Ser Asn Asp Trp Ser Ser Arg
1               5                   10                  15


Val Ile Tyr Gln Leu Leu Thr Asp Arg Phe Ala Lys Thr Val Asp Asp
            20                  25                  30


Gln Ser Pro Cys Ser Asp Leu Gly Asn Tyr Cys Gly Gly Ser Phe Gln
        35                  40                  45


Gly Ile Ile Asn His Leu Asp Tyr Ile Ala Gly Met Gly Phe Asp Ala
```

```
    50                  55                  60


Ile Trp Ile Ser Pro Ile Pro Gln Asn Ala Gln Gly Gly Tyr His Gly
65                  70                  75                  80


Tyr Trp Ala Thr Asn Phe Ser Ala Ile Asn Ser Asn Phe Gly Ser Ser
                85                  90                  95


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


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


Asn Asn Tyr Asn Gly Tyr Thr Phe Asn Gln Gly Ser Tyr Tyr His Ser
    130                 135                 140


Tyr Cys Asp Ile Asn Tyr Asn Asp Gln Thr Ser Val Glu Gln Cys Trp
145                 150                 155                 160


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


Thr Leu Tyr Ser Thr Val Ser Asn Trp Ile Ser Glu Tyr Gly Phe Asp
            180                 185                 190


Gly Ile Arg Ile Asp Thr Val Lys His Val Arg Lys Asp Phe Trp Asp
        195                 200                 205


Gly Tyr Val Lys Ala Ala Gly Val Phe Ala Thr Gly Glu Val Leu His
    210                 215                 220


Gly Ser Val Ser Tyr Val Ala Pro Tyr Gln Ser His Val Pro Ser Leu
225                 230                 235                 240


Ile Asn Tyr Pro Leu Tyr Tyr Pro Ile Tyr Asp Val Phe Thr Lys Ala
                245                 250                 255


Ala Thr Met Thr Arg Leu Lys Ser Gly Tyr Asn Asp Ile Gln Ser Gly
```

```
            260                 265                 270

Gly Phe Ser Asn Leu Asn Leu Leu Leu Asn Phe Ile Asp Asn His Asp
        275                 280                 285

Asn Pro Arg Leu Leu Ser Lys Ala Asp Gln Ser Leu Val Lys Asn Ala
    290                 295                 300

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

Thr Glu Gln Ser Tyr Lys Gly Gly Asn Asp Pro Asn Asn Arg Glu Pro
                325                 330                 335

Leu Trp Thr Ser Gly Tyr Ser Ser Ser Ser Glu Met Tyr Gln Phe Ile
            340                 345                 350

Lys Gln Val Ile Gln Ile Arg Lys Gly Ser Asn Ala Thr Val Thr Met
        355                 360                 365

Asp Ile Asp Gln Ala Asp Asn Val Tyr Val Phe Gln Arg Gly Asn Tyr
    370                 375                 380

Leu Ala Val Val Asn Asn Tyr Gly Gln Gly Ser Thr Asn Ser Val Thr
385                 390                 395                 400

Val Lys Ser Gly Ser Phe Ala Asp Gly Thr Val Leu Lys Asp Val Phe
                405                 410                 415

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

Gln Asn Gly Asn Pro Ala Val Phe Ser Pro Gln Gly Ala Thr Ser Pro
        435                 440                 445

Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr
    450                 455                 460

Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu
```

```
465                 470                 475                 480


Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr
                485                 490                 495


Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln
            500                 505                 510


Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala
        515                 520                 525


Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu
    530                 535                 540


Lys Asp Thr Trp Asp Glu Ser
545                 550


<210>  129
<211>  565
<212>  PRT
<213>  Syncephalastrum racemosum

<400>  129

Val Pro Leu Ser Ile Ile Asp Lys Arg Ala Gly Val Thr Thr Leu Ser
1               5                   10                  15


Lys Arg Ala Ala Ala Asp Asp Trp Lys Ser Arg Ser Ile Tyr Gln Ile
            20                  25                  30


Val Thr Asp Arg Phe Ala Arg Ser Asp Gly Ser Thr Ser Gly Cys Gly
        35                  40                  45


Asp Leu Ser Asn Tyr Cys Gly Gly Asp Tyr Lys Gly Ile Gln Asn Gln
    50                  55                  60


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


Ile Pro Glu Asn Thr Asp Gly Gly Tyr His Gly Tyr Trp Ala Lys Asn
                85                  90                  95
```

```
Phe Glu Ala Leu Asn Thr Asn Phe Gly Ser Ala Asp Asp Leu Lys Ala
            100                 105                 110


Leu Val Thr Ala Ala His Gly Lys Gly Met Tyr Val Met Leu Asp Val
        115                 120                 125


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


Thr Phe Asp Ser Ala Ser Asn Tyr His Ala Gln Cys Asp Ile Asp Tyr
145                 150                 155                 160


Glu Asn Gln Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Asn Leu Pro
                165                 170                 175


Asp Ile Asn Thr Glu Asp Asp Thr Ile Val Ser Lys Leu His Ser Ile
            180                 185                 190


Val Ser Asp Trp Val Thr Thr Tyr Asp Phe Asp Gly Ile Arg Ile Asp
        195                 200                 205


Thr Val Lys His Ile Arg Lys Asp Phe Trp Ser Gly Tyr Glu Glu Ala
    210                 215                 220


Ala Gly Val Phe Ala Thr Gly Glu Val Phe Asp Gly Asp Ala Ala Tyr
225                 230                 235                 240


Val Gly Pro Tyr Gln Asp Gln Leu Ser Ser Leu Ile Asn Tyr Pro Leu
                245                 250                 255


Tyr Tyr Ala Ile Arg Asp Val Phe Thr Ala Gly Ser Gly Phe Ser Arg
            260                 265                 270


Ile Ser Asp Met Leu Ser Ser Ile Asn Ser Asn Phe Lys Asp Pro Ser
        275                 280                 285


Val Leu Thr Thr Phe Val Asp Asn Gln Asp Asn Ala Arg Phe Leu Ser
    290                 295                 300
```

```
Val Lys Ser Asp Thr Ser Leu Tyr Lys Asn Ala Leu Ala Phe Thr Ile
305                 310                 315                 320


Leu Thr Glu Gly Ile Pro Val Val Tyr Tyr Gly Thr Glu Gln Gly Phe
                325                 330                 335


Lys Gly Gly Asn Asp Pro Asn Asn Arg Glu Val Leu Trp Thr Ser Asn
            340                 345                 350


Tyr Asp Thr Ser Ser Asp Leu Tyr Lys Phe Ile Lys Ile Val Asn Asp
        355                 360                 365


Gln Val Arg Gln Lys Ser Asn Lys Thr Val Lys Leu Asn Val Asp Val
    370                 375                 380


Gly Thr Asn Thr Tyr Ala Phe Thr His Gly Lys Asn Leu Ile Val Val
385                 390                 395                 400


Asn Asn Tyr Gly Ser Gly Ser Thr Ala Ser Val Thr Val Lys Val Gly
                405                 410                 415


Asp Ser Ile Ala Asp Gly Thr Lys Leu Val Asp Ala Val Ser Asn Ile
            420                 425                 430


Thr Ala Thr Val Ser Gly Gly Ser Ile Thr Phe Ser Leu Asn Asn Gly
        435                 440                 445


Leu Pro Ala Leu Phe Val Pro Ser Ser Gly Ala Thr Ser Pro Gly Gly
    450                 455                 460


Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val
465                 470                 475                 480


Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn
                485                 490                 495


Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr
            500                 505                 510
```

Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys
515 520 525

Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser
530 535 540

Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp
545 550 555 560

Thr Trp Asp Glu Ser
565

<210> 130
<211> 583
<212> PRT
<213> Rhizomucor pusillus

<400> 130

Ala Thr Ser Asp Asp Trp Lys Gly Lys Ala Ile Tyr Gln Leu Leu Thr
1 5 10 15

Asp Arg Phe Gly Arg Ala Asp Asp Ser Thr Ser Asn Cys Ser Asn Leu
20 25 30

Ser Asn Tyr Cys Gly Gly Thr Tyr Glu Gly Ile Thr Lys His Leu Asp
35 40 45

Tyr Ile Ser Gly Met Gly Phe Asp Ala Ile Trp Ile Ser Pro Ile Pro
50 55 60

Lys Asn Ser Asp Gly Gly Tyr His Gly Tyr Trp Ala Thr Asp Phe Tyr
65 70 75 80

Gln Leu Asn Ser Asn Phe Gly Asp Glu Ser Gln Leu Lys Ala Leu Ile
85 90 95

Gln Ala Ala His Glu Arg Asp Met Tyr Val Met Leu Asp Val Val Ala
100 105 110

```
Asn His Ala Gly Pro Thr Ser Asn Gly Tyr Ser Gly Tyr Thr Phe Asp
        115                 120                 125


Asp Ala Ser Leu Tyr His Pro Lys Cys Thr Ile Asp Tyr Asn Asn Gln
    130                 135                 140


Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Glu Leu Pro Asp Ile Asp
145                 150                 155                 160


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


Trp Val Gly Asn Tyr Ser Phe Asp Gly Ile Arg Ile Asp Thr Val Lys
            180                 185                 190


His Ile Arg Lys Asp Phe Trp Thr Gly Tyr Ala Glu Ala Ala Gly Val
        195                 200                 205


Phe Ala Thr Gly Glu Val Phe Asn Gly Asp Pro Ala Tyr Val Gly Pro
    210                 215                 220


Tyr Gln Lys Tyr Leu Pro Ser Leu Ile Asn Tyr Pro Met Tyr Tyr Ala
225                 230                 235                 240


Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg Ile Ser
                245                 250                 255


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


Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn Ser Gln
        275                 280                 285


Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu Leu Gly
    290                 295                 300


Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe Ser Gly
305                 310                 315                 320
```

```
Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Thr Asn Tyr Asp
                325                 330                 335


Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser Val Arg
            340                 345                 350


Met Lys Ser Asn Lys Ala Val Tyr Met Asp Ile Tyr Val Gly Asp Asn
        355                 360                 365


Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn Asn Tyr
    370                 375                 380


Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly Lys Phe
385                 390                 395                 400


Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr Thr Thr
                405                 410                 415


Val Ser Ser Asp Gly Thr Val Thr Phe Asn Leu Lys Asp Gly Leu Pro
            420                 425                 430


Ala Ile Phe Thr Ser Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Pro
        435                 440                 445


Thr Gly Ser Gly Ser Val Thr Ser Thr Ser Lys Thr Thr Ala Thr Ala
    450                 455                 460


Ser Lys Thr Ser Thr Ser Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr
465                 470                 475                 480


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


Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly Asp Trp Glu Thr
            500                 505                 510


Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr Ser Ser Asp Pro
        515                 520                 525
```

```
Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu Ser Phe Glu Tyr
    530                 535                 540


Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu Trp Glu Ser Asp
545                 550                 555                 560


Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly Thr Ser Thr Ala
                565                 570                 575


Thr Val Thr Asp Thr Trp Arg
            580


<210>  131
<211>  553
<212>  PRT
<213>  Dichotomocladium hesseltinei

<400>  131

Gln Pro Val Asn Ile Thr Lys Arg Ala Ser Ala Ala Asp Trp Arg Ser
1               5                   10                  15


Arg Ala Ile Tyr Gln Val Leu Thr Asp Arg Phe Ala Arg Thr Asp Gly
            20                  25                  30


Ser Thr Ser Gly Cys Ser Asn Leu Ser Asn Tyr Cys Gly Gly Thr Phe
        35                  40                  45


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


Ala Ile Trp Ile Ser Pro Ile Pro Thr Asn Ser Pro Gly Gly Tyr His
65                  70                  75                  80


Gly Tyr Trp Ala Thr Asp Phe Tyr Gly Ile Asn Ser Asn Phe Gly Ser
                85                  90                  95


Ser Asn Asp Leu Lys Glu Leu Val Asn Ala Ala His Ala Lys Gly Met
            100                 105                 110
```

```
Tyr Val Met Leu Asp Val Val Ala Asn His Ala Gly Pro Thr Ser Asn
        115                 120                 125


Gly Asp Tyr Ser Gly Tyr Thr Phe Gly Ser Ser Gly Leu Tyr His Asn
    130                 135                 140


Arg Cys Ser Ile Asn Tyr Asn Asp Gln Arg Ser Ile Glu Gln Cys Trp
145                 150                 155                 160


Val Ala Asp Asp Leu Pro Asp Ile Asn Thr Glu Asn Asn Asp Asn Val
                165                 170                 175


Asn Lys Pro Asn Asn Ile Val Ser Thr Trp Val Lys Thr Tyr Gly Phe
            180                 185                 190


Asp Ala Ile Arg Ile Asp Thr Val Lys His Val Arg Lys Asp Phe Trp
        195                 200                 205


Pro Gly Tyr Thr Ser Ala Ala Gly Val Phe Ala Thr Gly Glu Val Phe
    210                 215                 220


Asp Gly Asn Pro Ser Tyr Val Ala Asp Tyr Gln Asn Tyr Met Glu Ser
225                 230                 235                 240


Leu Ile Asn Tyr Pro Leu Tyr Tyr Ala Leu Asn Asp Val Phe Ala Ser
                245                 250                 255


Gly Tyr Ser Phe Ser Arg Leu Ser Asn Gln Arg Val Ala Asn Tyr His
            260                 265                 270


Ala Phe Lys Asp Val Ser Val Leu Pro Ile Phe Ile Asp Asn His Asp
        275                 280                 285


Asn Pro Arg Phe Leu Asn Lys Lys Asn Asp Ile Ala Gln Phe Lys Asn
    290                 295                 300


Ala Leu Thr Tyr Val Leu Leu Gly Glu Gly Ile Pro Val Val Tyr Tyr
305                 310                 315                 320
```

```
Gly Ser Glu Gln Ala Tyr Ala Gly Gly Ala Asp Pro Ala Asn Arg Glu
                325                 330                 335


Ala Leu Trp Ser Ser Gly Phe Ser Thr Asn Ser Asp Met Tyr Gln Phe
            340                 345                 350


Ile Ala Lys Leu Asn Arg Val Arg Gln Lys Ser Asn Lys Ser Val Tyr
        355                 360                 365


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


Ser Leu Val Val Leu Asn Asn Phe Gly Asn Gly Ala Ser Arg Gln Val
385                 390                 395                 400


Thr Val Asn Val Gly Ala Gln Val Ala Ser Asn Thr Arg Leu Thr Asp
                405                 410                 415


Val Val Ser Gly Thr Ser Val Thr Val Ser Gly Ser Ser Val Thr Phe
            420                 425                 430


Thr Ile Asn Asn Gly Leu Pro Ala Val Phe Thr Val Ser Gly Ala Thr
        435                 440                 445


Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val Tyr
    450                 455                 460


Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser
465                 470                 475                 480


Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser Ala
                485                 490                 495


Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr
            500                 505                 510


Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp Glu
        515                 520                 525
```

```
Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr
    530                 535                 540


Thr Glu Lys Asp Thr Trp Asp Glu Ser
545                 550


<210>  132
<211>  552
<212>  PRT
<213>  Lichtheimia ramosa

<400>  132

Arg Pro Phe Val Lys Arg Ala Thr Ala Asp Asp Trp Arg Asp Arg Ala
1               5                   10                  15


Ile Tyr Gln Ile Leu Thr Asp Arg Phe Ala Arg Ser Asp Gly Ser Thr
            20                  25                  30


Asp Asn Cys Ser Asp Leu Ser Asn Tyr Cys Gly Gly Asn Tyr Gln Gly
        35                  40                  45


Ile Ile Gln Gln Leu Asp Tyr Ile Glu Gly Met Gly Phe Asp Ala Ile
    50                  55                  60


Trp Ile Ser Pro Ile Pro Ala Asn Ala Asp Gly Gly Tyr His Gly Tyr
65                  70                  75                  80


Trp Ala Thr Asp Phe Glu Ser Leu Asn Asp His Phe Gly Ser Gln Asp
                85                  90                  95


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


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


Tyr Ser Gly Tyr Thr Phe Gly Ser Ser Asp Leu Tyr His Pro Gln Cys
    130                 135                 140


Ser Ile Asp Tyr Ser Asn Gln Asn Ser Ile Glu Gln Cys Trp Val Ala
```

```
145                 150                 155                 160

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

Leu His Asp Ile Val Ser Thr Trp Val Ser Thr Tyr Gly Phe Asp Gly
            180                 185                 190

Ile Arg Ile Asp Thr Val Lys His Val Arg Lys Asp Phe Trp Pro Gly
        195                 200                 205

Tyr Ala Ser Ala Ala Gly Val Phe Ala Thr Gly Glu Val Tyr Asp Gly
    210                 215                 220

Asp Gln Thr Tyr Val Gly Ala Tyr Gln Asp Tyr Leu Asp Ser Leu Leu
225                 230                 235                 240

Asn Tyr Pro Leu Tyr Tyr Ala Leu Asn Asp Val Phe Ala Ser Gly Gln
                245                 250                 255

Gly Phe Gln Arg Leu Ser Asn Gln Arg Asn Ala Ile Met Ser Ala Phe
            260                 265                 270

Lys Asp Val Ser Val Leu Thr Ser Phe Val Asp Asn His Asp Val Ala
        275                 280                 285

Arg Phe Leu Ser Thr Lys Asn Asp Gln Ala Leu Phe Lys Asn Ala Leu
    290                 295                 300

Ala Phe Val Leu Leu Gly Glu Thr Ile Pro Val Val Tyr Tyr Gly Ser
305                 310                 315                 320

Glu Gln Gly Phe Ala Gly Gly Ala Asp Pro Ala Asn Arg Glu Ala Leu
                325                 330                 335

Trp Ser Ser Gly Tyr Asp Thr Ser Ser Asp Leu Tyr Gln Phe Ile Ala
            340                 345                 350

Thr Ile Asn Asn Asn Val Arg Gln Lys Ser Gly Lys Lys Val Tyr Met
```

```
        355                 360                 365


Asp Leu Asp Val Gln Asp Asn Val Tyr Ala Phe Met His Gly Asp Ala
    370                 375                 380


Leu Val Val Leu Asn Asn Tyr Gly Ser Gly Ala Ser Asn Gln Val Ser
385                 390                 395                 400


Val Asn Val Gly Ala Gln Val Ala Glu Ser Thr Ser Phe Thr Asp Ala
                405                 410                 415


Ile Ser Gly Thr Ser Ile Thr Val Ser Ser Gly Ser Val Thr Phe Thr
            420                 425                 430


Leu Asp Asn Gly Asn Pro Ala Ile Phe Val Pro Ala Gly Ala Thr Ser
        435                 440                 445


Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala
    450                 455                 460


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


Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn
                485                 490                 495


Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile
            500                 505                 510


Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp
        515                 520                 525


Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr
    530                 535                 540


Glu Lys Asp Thr Trp Asp Glu Ser
545                 550


<210>  133
```

```
<211>  587
<212>  PRT
<213>  Penicillium aethiopicum

<400>  133

Ala Arg Thr Ala Asp Trp Lys Pro Arg Ser Ile Tyr Gln Thr Met Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ser Pro Cys Asn Thr
            20                  25                  30


Lys Ala Gly Leu Tyr Cys Gly Gly Thr Trp Arg Gly Thr Ile Asp His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Asp Ala Val Met Ile Ser Pro
    50                  55                  60


Ile Ile Glu Asn Ile Glu Gly Arg Val Asp Tyr Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Pro Leu Asn Leu Asp Asn Leu Asn Ser His Phe Gly Thr
                85                  90                  95


His Gln Asp Leu Leu Asp Leu Ser Asp Ala Leu His Ser Arg Gly Met
            100                 105                 110


Tyr Phe Met Met Asp Thr Val Ile Asn Asn Met Ala Tyr Ile Thr Asn
        115                 120                 125


Gly Ser Asp Pro Ala Thr Asp Ile Asp Tyr Ser Val Phe Thr Pro Phe
    130                 135                 140


Asn Asn Ala Asp Tyr Phe His Pro Tyr Cys Thr Met Asn Trp Ser Val
145                 150                 155                 160


Pro Ala Ile Ala Gln Arg Cys Asn Thr Gly Asp Asp Thr Val Ala Leu
                165                 170                 175


Pro Asp Leu Phe Thr Glu His Glu Asp Val Gln Gln Leu Leu Ile Lys
            180                 185                 190
```

```
Trp Ala Asn Lys Ala Ile Lys Thr Tyr Ser Ile Asp Gly Leu Arg Ile
        195                 200                 205

Asp Ala Ala Lys His Val Asn Pro Asp Phe Leu Arg Lys Phe Ser Asp
    210                 215                 220

Gly Val Asp Ile Phe Met Thr Gly Glu Val Leu Glu Gly Ser Val Ser
225                 230                 235                 240

Ile Met Glu Asp Tyr Gln Ser Asn Tyr Ile Asn Ser Leu Pro Asn Tyr
                245                 250                 255

Pro Ile Tyr Phe Glu Ile Leu Ser Ala Phe Thr Asn Gly Asn Thr Ser
            260                 265                 270

Gln Leu Ala Ile Ala Val Glu Asn Met Arg Val Ala Ile Pro Asp Val
        275                 280                 285

Asn Ala Met Ala Ser Phe Ser Glu Asn His Asp Lys Pro Arg Ile Ala
    290                 295                 300

Ser Tyr Asn Asp Asp Met Ser Ile Ala Lys Asn Val Leu Val Phe Thr
305                 310                 315                 320

Met Leu Phe Asp Gly Ile Pro Met Ile Tyr Gln Gly Gln Glu Gln His
                325                 330                 335

Leu Lys Gly Asp Gly Val Pro His Asn Arg Glu Ala Ile Trp Leu Ser
            340                 345                 350

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

Arg Ile Arg Asn His Ala Gly Tyr Leu Gly Ser Asp Tyr Phe Glu Asp
    370                 375                 380

Ala Thr His Pro Ile Tyr Gln Gly Ser Ser Glu Leu Ala Phe Thr Lys
385                 390                 395                 400
```

```
Gly Val Gln Gly Arg Gln Val Val Met Val Leu Ser Asn Gln Pro Ser
                405                 410                 415


Thr Ser Gly Arg Tyr Ala Leu Asp Leu Ala Val Ser Tyr Asn Ala Gly
            420                 425                 430


Thr Glu Leu Met Asp Val Leu Asn Cys Asn Asn Tyr Thr Val Asp Asn
        435                 440                 445


Gln Gly Val Leu Arg Val Asp Met Asp Lys Gly Glu Pro Arg Val Phe
    450                 455                 460


Phe Pro Arg Lys Tyr Met Glu Gly Ser Gly Leu Cys Gly Tyr Ser Gly
465                 470                 475                 480


Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp
                485                 490                 495


Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp
            500                 505                 510


Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser
        515                 520                 525


Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp
    530                 535                 540


Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile
545                 550                 555                 560


Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly
                565                 570                 575


Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  134
<211>  597
```

```
<212>  PRT
<213>  Subulispora sp.

<400>  134

Leu Thr Pro Ala Glu Trp Gly Ser Gln Ser Ile Tyr Gln Val Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Leu Thr Asp Gly Ser Thr Thr Ala Ser Cys Asp Leu
            20                  25                  30


Asn Thr Tyr Cys Gly Gly Thr Trp Leu Gly Ile Gln Asn His Leu Asp
        35                  40                  45


Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Ile Val
    50                  55                  60


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


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


Asp Leu Ile Asn Leu Ser Ala Ala Leu His Glu Arg Gly Met Tyr Leu
            100                 105                 110


Met Val Asp Val Val Asn Asn His Met Gly Tyr Leu Gly Cys Gly Thr
        115                 120                 125


Cys Val Asp Tyr Ser Glu Tyr Thr Pro Phe Asn Glu Glu Ser Tyr Tyr
    130                 135                 140


His Pro Tyr Cys Pro Thr Asp Tyr Ser Asn Leu Thr Ser Ile Gln Val
145                 150                 155                 160


Cys Trp Glu Gly Asp Asn Ile Val Ser Leu Pro Asp Leu Arg Thr Glu
                165                 170                 175


Asp Ser Asp Val Arg Ser Met Trp Tyr Asp Trp Ile Thr Pro Leu Val
            180                 185                 190
```

```
Ala Lys Tyr Ser Ile Asp Gly Leu Arg Met Asp Ser Ala Glu His Val
        195                 200                 205


Glu Lys Ser Phe Trp Pro Gly Trp Val Ser Ala Ser Gly Val Tyr Asn
    210                 215                 220


Val Gly Glu Val Asp Glu Gly Asp Pro Thr Ile Phe Pro Asp Trp Leu
225                 230                 235                 240


Asn Tyr Ile Asp Gly Thr Leu Asn Tyr Pro Ala Tyr Tyr Trp Ile Thr
                245                 250                 255


Gln Ala Phe Gln Ser Thr Ser Gly Ser Ile Ser Asn Leu Val Thr Gly
            260                 265                 270


Val Asn Gln Leu Lys Ala Ser Met Lys Thr Ser Thr Phe Gly Ser Phe
        275                 280                 285


Leu Glu Asn His Asp Gln Pro Arg Phe Pro Ser Leu Thr Ser Asp Thr
    290                 295                 300


Asp Leu Ala Lys Asn Ala Ile Ala Phe Ala Met Leu Ala Asp Gly Val
305                 310                 315                 320


Pro Ile Val Tyr Tyr Gly Gln Glu Gln Gly Tyr Ser Gly Gly Gly Val
                325                 330                 335


Pro Asn Asp Arg Glu Pro Leu Trp Thr Ser Gly Tyr Ser Thr Thr Ser
            340                 345                 350


Ala Gly Tyr Thr Phe Ile Lys Thr Ile Asn Ala Val Arg His Leu Ala
        355                 360                 365


Val Thr Gln Asp Thr Ala Tyr Val Ala Tyr Gln Ala Tyr Pro Ile Tyr
    370                 375                 380


Ser Asp Ser Arg Val Ile Ala Met Lys Lys Ser Ser Val Leu Ala Val
385                 390                 395                 400
```

```
Phe Ser Asn Ile Gly Ser Ser Gly Ser Gly Tyr Ser Ile Thr Leu Pro
                405                 410                 415


Ala Gly Ala Phe Ala Ala Ser Gln Ala Leu Thr Asp Ala Val Ser Cys
            420                 425                 430


Gln Thr Tyr Thr Ala Asp Ala Ser Gly Gly Leu Thr Phe Thr Phe Gly
        435                 440                 445


Gln Ala Pro Ser Val Phe Tyr Ala Thr Ala Ser Leu Ala Gly Ser Gly
    450                 455                 460


Leu Cys Gly Thr Thr Gly Thr Gly Gly Ser Thr Gly Thr Thr Thr Ala
465                 470                 475                 480


Ser Glu Thr Gly Gly Ser Ser Pro Thr Ser Thr Ala Cys Ala Ser Val
                485                 490                 495


Pro Val Thr Phe Asn Glu Lys Val Thr Thr Val Val Gly Glu Thr Ile
            500                 505                 510


Lys Ile Ser Gly Ser Val Ala Ala Leu Gly Asp Trp Ala Thr Gly Ser
        515                 520                 525


Ala Val Ala Leu Ser Ala Ala Ser Tyr Thr Ser Ser Asn Pro Gln Trp
    530                 535                 540


Asp Val Thr Ile Ser Phe Ala Pro Gly Thr Val Ile Glu Tyr Lys Tyr
545                 550                 555                 560


Ile Asn Val Ala Ser Ser Gly Ala Val Thr Trp Glu Ala Asp Pro Asn
                565                 570                 575


His Thr Tyr Thr Val Pro Ala Ser Cys Ala Thr Ala Ala Val Val Ser
            580                 585                 590


Asp Thr Trp Gln Thr
        595
```

```
<210>  135
<211>  601
<212>  PRT
<213>  Trichoderma paraviridescens

<400>  135

Leu Thr Ala Ala Gln Trp Arg Ser Gln Ser Ile Tyr Gln Val Leu Thr
1               5                   10                  15


Asp Arg Phe Ser Gln Thr Asn Gly Ala Thr Asn Ser Ala Cys Asn Ala
            20                  25                  30


Gly Asn Gln Val Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Lys Asn
        35                  40                  45


Leu Asp Tyr Ile Lys Ser Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60


Val Val Glu Asn Leu Ala Gly Asn Ser Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Ala Gln Asp Ile Tyr Gln Val Asn Thr Asn Phe Gly Ser
                85                  90                  95


Ala Ala Asp Leu Arg Ala Leu Ser Glu Ala Leu His Asn Ala Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Ile Val Thr Asn His Met Gly Tyr Leu Gly Cys
        115                 120                 125


Gly Thr Cys Val Gln Tyr Asn Thr Phe Asn Pro Phe Asn Ser Gln Ser
    130                 135                 140


Tyr Tyr His Pro Phe Cys Leu Ile Asn Phe Asn Ser Ser Asn Met Thr
145                 150                 155                 160


Gln Ile Gln Asn Cys Trp Glu Gly Asp Asn Thr Val Ser Leu Pro Asp
                165                 170                 175
```

```
Leu Ala Thr Glu Asn Ala Asn Val Leu Ser Met Trp Gln Thr Trp Ile
            180                 185                 190


Thr Gln Leu Val Ala Asn Tyr Thr Ile Asp Gly Leu Arg Met Asp Ser
        195                 200                 205


Cys Phe Glu Leu Asn Tyr Gly Tyr Phe Glu Pro Phe Gln Ser Ser Ala
    210                 215                 220


Asn Val Tyr Ile Val Gly Glu Val Asp Asn Gly Asp Pro Ala Ile Val
225                 230                 235                 240


Cys Pro Tyr Gln Lys Asn Tyr Gly Leu Asn Thr Leu Asn Tyr Pro Ala
                245                 250                 255


Tyr Tyr Trp Ile Thr Gln Ala Phe Gln Ser Thr Ser Gly Ser Ile Ser
            260                 265                 270


Asn Leu Val Asn Gly Leu Asn Thr Met Lys Ser Glu Cys Ser Asp Thr
        275                 280                 285


Thr Leu Leu Gly Ser Phe Met Glu Asn His Asp Asn Pro Arg Phe Pro
    290                 295                 300


Ser Leu Thr Ser Asp Ile Ser Leu Ala Lys Asn Ala Ile Ala Phe Thr
305                 310                 315                 320


Met Leu Ala Asp Gly Ile Pro Ile Ile Tyr Glu Gly Gln Glu Gln His
                325                 330                 335


Leu Asn Gly Gly Gly Val Pro Asn Asn Arg Glu Ala Ile Trp Leu Ser
            340                 345                 350


Gly Tyr Ser Thr Ser Ala Val Leu Tyr Thr His Ile Lys Ala Leu Asn
        355                 360                 365


Gln Ile Arg Ser Gln Ala Ile Lys Gln Asn Ser Ala Tyr Val Thr Thr
    370                 375                 380
```

```
Gln Ala Ala Val Thr Tyr Ser Asp Ser Ser Thr Ile Val Thr Arg Lys
385                 390                 395                 400


Gly Ser Thr Gly Ser Gln Ile Val Gly Val Phe Ser Asn Lys Gly Ala
                405                 410                 415


Asn Gly Asn Ser Tyr Thr Leu Thr Leu Pro Ser Ala Asp Thr Gly Phe
            420                 425                 430


Thr Ser Asn Glu Gln Val Val Glu Ile Leu Ser Cys Thr Ala Tyr Thr
        435                 440                 445


Thr Asp Ser Ser Gly Asn Leu Ala Val Ala Met Ala Gly Gly Leu Pro
    450                 455                 460


Arg Val Phe Tyr Ala Arg Ser Ser Leu Ser Gly Ser Gly Ile Cys Pro
465                 470                 475                 480


Asn Leu Gly Ser Gly Gly Gly Thr Pro Thr Ser Thr Pro Pro Thr Ser
                485                 490                 495


Cys Thr Ala Ile Pro Val Thr Phe Asp Glu Lys Val Thr Thr Thr Phe
            500                 505                 510


Gly Gln Thr Ile Lys Ile Ala Gly Asp Ile Ser Ala Leu Gly Asn Trp
        515                 520                 525


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


Asn Pro Leu Trp Ala Ile Thr Leu Asn Leu Ala Pro Gly Gln Val Val
545                 550                 555                 560


Glu Tyr Lys Tyr Ile Asn Val Ala Gln Asn Gly Gly Val Thr Trp Glu
                565                 570                 575


Ala Asp Pro Asn His Thr Tyr Thr Val Pro Ser Ala Cys Thr Ala Gln
            580                 585                 590
```

```
Pro Thr Val Ala Asn Thr Trp Gln Gly
        595                 600


<210>  136
<211>  598
<212>  PRT
<213>  Byssoascus striatosporus

<400>  136

Leu Ser Ala Asp Asp Trp Arg Ala Gln Ser Ile Tyr Gln Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Leu Thr Asn Gly Ser Thr Thr Ala Pro Cys Asp Thr
            20                  25                  30


Glu Glu Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60


Val Val Glu Asn Leu Ser Gly Asp Ser Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Ala Gln Asn Val Tyr Glu Val Asn Pro Asn Phe Gly Ala
                85                  90                  95


Thr Ser Asp Leu Val Ala Leu Ser Gln Val Val His Asp Lys Gly Met
            100                 105                 110


Tyr Leu Met Leu Asp Val Val Thr Asn His Met Gly Tyr Leu Gly Cys
        115                 120                 125


Gly Thr Cys Val Asp Tyr Ser Val Phe Asn Pro Phe Asn Glu Glu Ser
    130                 135                 140


Tyr Tyr His Pro Phe Cys Leu Ile Asp Tyr Asp Asn Thr Thr Ser Ile
145                 150                 155                 160


Glu Val Cys Trp Glu Gly Asp Asn Ile Val Ser Leu Pro Asp Leu Arg
```

```
                165                 170                 175


Thr Glu Asp Ser Asp Val Leu Ser Thr Trp Glu Ser Trp Val Thr Glu
            180                 185                 190


Leu Val Ser Asn Tyr Thr Val Asp Gly Ile Arg Leu Asp Ser Thr Glu
        195                 200                 205


Glu Leu Asp Gln Ala Phe Leu Pro Pro Phe Glu Ser Ala Ala Gly Val
    210                 215                 220


Tyr Ile Val Gly Glu Val Asp Asn Gly Asp Pro Ala Val Val Cys Pro
225                 230                 235                 240


Tyr Gln Glu Tyr Val Ser Gly Val Leu Asn Tyr Pro Ala Tyr Tyr Trp
                245                 250                 255


Ile Thr Gln Ala Phe Glu Ser Thr Ser Gly Ser Ile Gly Asn Leu Val
            260                 265                 270


Asn Gly Ile Asn Thr Met Lys Ser Asp Cys Ser Asp Thr Ser Leu Leu
        275                 280                 285


Gly Ser Phe Leu Glu Asn His Asp Gln Pro Arg Phe Ala Ser Leu Thr
    290                 295                 300


Ser Asp Ile Ser Leu Ala Lys Asn Ala Ile Ala Phe Ser Met Leu Gln
305                 310                 315                 320


Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser Gly
                325                 330                 335


Gly Ala Val Pro Asn Asp Arg Glu Ala Leu Trp Leu Ser Gly Tyr Pro
            340                 345                 350


Thr Ser Ser Thr Leu Tyr Thr Trp Ile Thr Ser Leu Asn Gln Ile Arg
        355                 360                 365


Ser His Ala Ile Ala Thr Asn Ser Ser Tyr Leu Thr Tyr Asn Ala Tyr
```

```
    370                 375                 380

Pro Val Tyr Ser Asp Asp Ser Thr Ile Val Met Arg Lys Gly Phe Ala
385                 390                 395                 400

Asp Asn Gln Ile Val Ser Val Tyr Thr Asn Gln Gly Ala Asp Ala Thr
                405                 410                 415

Ala Tyr Thr Leu Asp Leu Pro Ser Thr Asp Thr Gly Phe Thr Ala Ser
            420                 425                 430

Gln Ser Leu Val Glu Ile Gly Gly Cys Thr Thr Thr Ala Thr Asp Asp
        435                 440                 445

Ser Gly Asn Leu Ala Val Ala Met Ala Ser Gly Leu Pro Arg Ile Tyr
    450                 455                 460

Tyr Pro Ala Ala Gly Leu Ser Gly Ser Gly Val Cys Gly Gln Leu Gly
465                 470                 475                 480

Ser Gly Gly Gly Thr Pro Thr Ser Thr Pro Pro Thr Ser Cys Thr Ala
                485                 490                 495

Ile Pro Val Thr Phe Asp Glu Lys Val Thr Thr Thr Phe Gly Gln Thr
            500                 505                 510

Ile Lys Ile Ala Gly Asp Ile Ser Ala Leu Gly Asn Trp Asn Thr Ala
        515                 520                 525

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

Trp Ala Ile Thr Leu Asn Leu Ala Pro Gly Gln Val Val Glu Tyr Lys
545                 550                 555                 560

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

Asn His Thr Tyr Thr Val Pro Ser Ala Cys Thr Ala Gln Pro Thr Val
```

```
            580                 585                 590


Ala Asn Thr Trp Gln Gly
        595



<210>  137
<211>  615
<212>  PRT
<213>  Aspergillus brasiliensis

<400>  137

Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30


Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60


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


Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110


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


Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140


Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160
```

```
Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175


Asn Thr Thr Glu Thr Val Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190


Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205


Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
225                 230                 235                 240


Pro Tyr Gln Asp Tyr Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255


Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asp Leu
            260                 265                 270


Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285


Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Tyr Tyr
    290                 295                 300


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Asp Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365
```

```
Arg Lys Leu Ala Ile Ala Ala Asp Ser Ser Tyr Ile Thr Tyr Ala Asn
    370                 375                 380


Asp Pro Ile Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400


Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
            420                 425                 430


Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Asn
        435                 440                 445


Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
    450                 455                 460


Pro Ala Ser Val Val Asp Asp Ser Ser Leu Cys Gly Gly Ser Gly Ser
465                 470                 475                 480


Ser Thr Ser Thr Thr Thr Ser Thr Ala Thr Ala Thr Thr Thr Ser Lys
                485                 490                 495


Thr Ser Thr Thr Ser Ser Ser Ser Ser Ser Ser Ser Cys Thr Ala Ser
            500                 505                 510


Ala Thr Ala Ile Pro Ile Thr Phe Glu Glu Leu Val Thr Thr Thr Tyr
        515                 520                 525


Gly Glu Glu Ile Tyr Leu Ser Gly Ser Ile Ser Gln Leu Gly Asp Trp
    530                 535                 540


Asp Thr Ser Asp Ala Val Lys Leu Ser Ala Asp Asp Tyr Thr Ser Ser
545                 550                 555                 560


Asn Pro Glu Trp Ser Val Thr Val Thr Leu Pro Val Gly Thr Thr Phe
                565                 570                 575
```

```
Glu Tyr Lys Phe Ile Lys Val Glu Ser Gly Gly Ser Val Thr Trp Glu
            580                 585                 590


Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro Glu Cys Gly Ser Gly Glu
        595                 600                 605


Thr Val Val Asp Thr Trp Arg
    610                 615


<210>  138
<211>  604
<212>  PRT
<213>  Penicillium subspinulosum

<400>  138

Ala Leu Ser Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30


Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Val Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60


Ile Thr Glu Gln Leu Ser Gly Asp Thr Ser Asp Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Lys Ile Tyr Asn Val Asn Ser Asn Phe Gly Thr
                85                  90                  95


Ala Asp Asp Leu Val Ala Leu Ser Asp Ala Leu His Ala Arg Asp Met
            100                 105                 110


Tyr Leu Met Leu Asp Val Val Pro Asn His Met Gly Tyr Asp Gly Asp
        115                 120                 125
```

```
Gly Asp Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140


Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Tyr Asp Asp Ile Glu Met
145                 150                 155                 160


Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175


Asn Thr Thr Glu Thr Val Val Gln Asp Ile Trp Tyr Ala Trp Val Ala
            180                 185                 190


Asp Leu Val Ala Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205


Leu Glu Val Gln Pro Ala Phe Phe Pro Ala Tyr Gln Ser Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asp Pro Thr Leu Asp Cys
225                 230                 235                 240


Pro Tyr Gln Asp Tyr Leu Asp Gly Ile Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asp Leu
            260                 265                 270


Tyr Asp Met Ile Asn Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285


Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Tyr Tyr
    290                 295                 300


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Ala Ser Phe Ile Phe Leu
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335
```

```
Gly Gly Asp Val Pro Tyr Asp Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


Ser Thr Thr Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ser Ile
        355                 360                 365


Arg Lys Leu Ala Ile Ser Leu Asp Asp Asp Tyr Ile Thr Tyr Val Asn
    370                 375                 380


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


Ser Gly Leu Gln Val Ile Thr Val Leu Ser Asn Leu Gly Ala Asp Gly
                405                 410                 415


Ser Ala Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Asp Ser Gly Thr
            420                 425                 430


Asp Leu Ile Glu Val Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
        435                 440                 445


Gly Asp Ile Ala Val Pro Met Glu Ser Gly Leu Pro Arg Val Phe Leu
    450                 455                 460


Pro Glu Ser Ser Ile Lys Asp Ser Asp Leu Cys Ser Gly Thr Thr Thr
465                 470                 475                 480


Thr Thr Thr Ser Thr Ala Ala Thr Ala Thr Ala Thr Ser Thr Ser Thr
                485                 490                 495


Cys Thr Ala Ala Thr Glu Val Ser Ile Ile Phe Glu Glu Leu Val Thr
            500                 505                 510


Thr Thr Tyr Gly Glu Glu Ile Tyr Leu Ser Gly Ser Ile Ser Glu Leu
        515                 520                 525


Gly Ser Trp Asp Thr Ser Asp Ala Leu Glu Leu Ser Ala Ala Asn Tyr
    530                 535                 540
```

```
Thr Ser Ser Asn Pro Glu Trp Tyr Leu Glu Val Thr Leu Pro Val Gly
545                 550                 555                 560


Thr Ser Phe Glu Tyr Lys Phe Ile Met Ile Glu Ser Asp Gly Thr Val
                565                 570                 575


Val Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Ser Ala Cys
            580                 585                 590


Ser Gly Ala Val Glu Thr Val Val Asp Thr Trp Arg
        595                 600


<210>  139
<211>  606
<212>  PRT
<213>  Penicillium antarcticum

<400>  139

Leu Thr Pro Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Met Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Ser Asp Asn Ser Thr Thr Ala Ala Cys Asn Val
            20                  25                  30


Ser Asp Arg Thr Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Glu Gln Leu Pro Gln Asp Thr Gly Asp Gly Glu Ala Tyr His
65                  70                  75                  80


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


Ala Ala Asp Leu Leu Ala Leu Ser Glu Ala Leu His Ala Arg Gly Met
            100                 105                 110
```

```
Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Ala Gly Ala
        115                 120                 125


Gly Ser Ser Val Glu Tyr Ser Val Phe His Pro Phe Ser Ser Ser Ser
    130                 135                 140


Tyr Phe His Ser Tyr Cys Leu Ile Ser Asn Tyr Asp Asp Gln Ser Asn
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Thr Ile Val Ser Leu Pro Asp Val
                165                 170                 175


Asp Thr Thr Gln Thr Ala Val Gln Thr Leu Trp Tyr Asp Trp Ile Gly
            180                 185                 190


Asp Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Ser Phe Trp Pro Gly Tyr Asn Asp Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Ile Phe Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240


Asp Tyr Gln Asn Tyr Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


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


Tyr Asp Met Ile Asn Ser Val Lys Ser Asp Cys Ala Asp Pro Thr Leu
        275                 280                 285


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


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Ile Ser Phe Leu Phe Leu
305                 310                 315                 320
```

```
Ser Asp Gly Ile Pro Ile Ile Tyr Ser Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Ala Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


Ser Thr Thr Ala Glu Leu Tyr Lys Tyr Ile Ala Thr Thr Asn Arg Ile
        355                 360                 365


Arg Lys Ala Ala Val Ser Ala Asp Ser Ser Tyr Ile Thr Thr Lys Asn
    370                 375                 380


Val Pro Phe Tyr Gln Asp Ser His Thr Leu Ala Met Lys Lys Gly Ser
385                 390                 395                 400


Ser Ala Ser Pro Val Ile Thr Val Leu Ser Asn Tyr Gly Ser Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Ser Leu Ser Gly Ser Gly Tyr Ser Ser Gly Thr
            420                 425                 430


Asn Leu Met Glu Met Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
        435                 440                 445


Gly Asn Ile Ala Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Met
    450                 455                 460


Leu Ala Ser Ser Ala Ser Ser Ile Cys Ala Ser Ser Thr Thr Thr Ser
465                 470                 475                 480


Thr Ala Thr Val Ala Thr Gln Thr Thr Thr Leu Thr Thr Thr Gly Thr
                485                 490                 495


Ser Cys Thr Gln Ala Thr Val Leu Pro Val Leu Phe Lys Glu Leu Val
            500                 505                 510


Thr Thr Thr Tyr Gly Gln Asn Val Tyr Ile Ser Gly Ser Ile Ser Gln
        515                 520                 525
```

```
Leu Gly Ser Trp Asp Thr Ser Ser Ala Ile Ala Leu Ser Ala Ser Ser
    530                 535                 540


Tyr Asn Ser Ser Asn Pro Leu Trp Gln Val Ala Ile Thr Leu Pro Val
545                 550                 555                 560


Gly Thr Ser Phe Gln Tyr Lys Phe Leu Glu Lys Thr Thr Gly Ser Thr
                565                 570                 575


Thr Ile Gln Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Thr
            580                 585                 590


Gly Cys Val Gly Thr Thr Ala Thr Ala Ile Ala Thr Trp Arg
        595                 600                 605


<210>  140
<211>  609
<212>  PRT
<213>  Penicillium coprophilum

<400>  140

Leu Thr Pro Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asn Ser Val Thr Ala Asn Cys Asn Val
            20                  25                  30


Asn Asp Arg Val Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asn Gln
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


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


Gly Tyr Trp Gln Gln Asp Ile Tyr Asn Val Asn Pro Asn His Gly Thr
                85                  90                  95


Ser Asp Asp Leu Leu Ala Leu Ser Lys Ala Leu His Ala Arg Gly Met
```

```
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Ala Gly Ala
        115                 120                 125


Gly Asn Asn Val Asp Tyr Ser Val Phe Thr Pro Phe Asn Ser Ala Ser
    130                 135                 140


Tyr Phe His Ser Tyr Cys Leu Ile Ser Asn Tyr Asn Asp Gln Ser Asn
145                 150                 155                 160


Val Glu Asn Cys Trp Leu Gly Asp Thr Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Gln Ser Ser Val Gln Thr Leu Trp Asn Asn Trp Ile Ser
            180                 185                 190


Asp Leu Val Ser Lys Tyr Ser Ile Asp Gly Leu Arg Val Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Ser Phe Trp Pro Ala Phe Asn Arg Ala Ala Gly
    210                 215                 220


Val Tyr Ser Val Gly Glu Val Phe Asp Gly Ser Pro Ser Tyr Thr Cys
225                 230                 235                 240


Asp Tyr Gln Lys Tyr Met Asp Gly Val Leu Asn Tyr Pro Met Tyr Tyr
                245                 250                 255


Pro Leu Leu Arg Ala Phe Gln Ser Thr Ser Gly Ser Ile Ser Asp Leu
            260                 265                 270


Tyr Asn Met Ile Gly Thr Leu Ser Ser Thr Cys Ala Asp Ser Thr Leu
        275                 280                 285


Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Pro Ser Tyr
    290                 295                 300


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Phe Leu Phe Leu
```

```
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Val Tyr Ser Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Ser Asp Pro Ala Asn Arg Glu Ala Leu Trp Leu Ser Lys Tyr
            340                 345                 350


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


Arg Lys Ala Ala Val Ala Ala Asp Ser Ser Tyr Ile Thr Ser Lys Asn
    370                 375                 380


Val Ala Phe Tyr Gln Asp Ser His Thr Leu Ala Met Lys Lys Gly Ser
385                 390                 395                 400


Gly Ser Ser Pro Val Ile Thr Val Leu Ser Asn Ala Gly Ser Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Tyr Leu Ser Gly Ser Gly Tyr Ser Ser Gly Thr
            420                 425                 430


Gln Leu Met Glu Leu Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
        435                 440                 445


Asn Lys Ile Ala Val Pro Met Ala Ser Gly Leu Pro Arg Val Phe Val
    450                 455                 460


Leu Ala Ser Ser Val Ser Asn Ser Gly Leu Cys Gly Ser Ser Thr Pro
465                 470                 475                 480


Thr Thr Thr Ala Thr Thr Ala Thr Thr Ala Thr Gln Thr Thr Thr Ala
                485                 490                 495


Thr Thr Thr Ala Gly Gly Cys Thr Gln Ala Thr Ala Leu Pro Val Leu
            500                 505                 510


Phe Lys Glu Leu Val Thr Thr Ser Tyr Gly Gln Asp Ile Tyr Ile Ser
```

```
        515                 520                 525


Gly Ser Ile Ser Gln Leu Gly Thr Trp Asp Thr Ser Lys Ala Val Ala
    530                 535                 540


Leu Ser Ala Asp Ser Tyr Thr Ser Ser Asn Pro Leu Trp Gln Ala Thr
545                 550                 555                 560


Ile Thr Leu Pro Val Gly Thr Thr Phe Gln Tyr Lys Phe Ile Lys Lys
                565                 570                 575


Ala Asn Gly Ala Ile Thr Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr
            580                 585                 590


Val Pro Thr Gly Cys Ser Gly Ser Thr Ala Thr Val Thr Ala Ser Trp
        595                 600                 605


Lys



<210>  141
<211>  602
<212>  PRT
<213>  Penicillium olsonii

<400>  141

Leu Thr Pro Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Asp Asp Asn Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30


Gly Asp Arg Thr Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asn Gln
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Glu Gln Leu Ser Ala Asn Thr Gly Tyr Gly Thr Ala Tyr His
65                  70                  75                  80
```

```
Gly Tyr Trp Gln Gln Asp Ile Tyr Glu Val Asn Pro Asn His Gly Ser
                85                  90                  95

Ser Ala Asp Leu Lys Ala Leu Ser Ala Ala Leu His Ala Arg Gly Met
            100                 105                 110

Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asn Gly Ile
        115                 120                 125

Gly Ser Ser Val Asp Tyr Ser Val Phe Asn Pro Phe Ser Ser Ser Ser
    130                 135                 140

Tyr Phe His Ser Tyr Cys Leu Ile Ser Asn Tyr Asn Asp Gln Ser Asn
145                 150                 155                 160

Val Glu Asn Cys Trp Leu Gly Asp Thr Thr Val Ser Leu Pro Asp Leu
                165                 170                 175

Asp Thr Thr Gln Thr Ala Val Gln Thr Ile Trp Asn Glu Trp Ile Thr
            180                 185                 190

Asp Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205

Lys His Val Gln Lys Ser Phe Trp Pro Gly Phe Asn Asp Ala Ala Gly
    210                 215                 220

Val Tyr Ser Val Gly Glu Ile Phe Asp Gly Asn Pro Ser Tyr Thr Cys
225                 230                 235                 240

Asp Tyr Gln Asn Tyr Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255

Pro Leu Leu Tyr Ala Phe Gln Ser Thr Ser Gly Ser Ile Ser Asp Leu
            260                 265                 270

Tyr Asn Met Ile Asn Thr Val Ala Ser Asp Cys Ala Asp Ser Thr Leu
        275                 280                 285
```

```
Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Pro Ser Tyr
    290                 295                 300

Thr Gly Asp Tyr Ser Gln Ala Lys Asn Val Ile Ser Tyr Leu Phe Leu
305                 310                 315                 320

Ser Asp Gly Ile Pro Ile Ile Tyr Ser Gly Gln Glu Gln His Tyr Ser
                325                 330                 335

Gly Ala Ser Asp Pro Ala Asn Arg Glu Ala Leu Trp Leu Ser Gly Tyr
            340                 345                 350

Ser Thr Thr Ala Glu Leu Tyr Lys Trp Ile Ala Thr Thr Asn Lys Ile
        355                 360                 365

Arg Lys Leu Ala Val Ser Ala Asp Ser Ser Tyr Ile Thr Ser Lys Asn
    370                 375                 380

Ser Pro Phe Tyr Gln Asp Ser His Thr Leu Gly Met Lys Lys Gly Ser
385                 390                 395                 400

Val Ile Thr Ile Leu Ser Asn Asn Gly Ala Ser Gly Ser Ser Tyr Thr
                405                 410                 415

Leu Ser Leu Ser Gly Ser Gly Tyr Ser Ser Gly Thr Lys Leu Met Glu
            420                 425                 430

Leu Tyr Thr Cys Thr Ser Ile Thr Val Asp Ser Ser Gly Asn Ile Pro
        435                 440                 445

Val Pro Met Val Ser Gly Leu Pro Arg Ala Leu Ile Pro Ala Ser Ser
    450                 455                 460

Ile Gly Ser Asn Gly Leu Cys Gly Ser Thr Thr Ser Pro Thr Thr Thr
465                 470                 475                 480

Ala Ala Thr Gln Thr Thr Thr Ala Thr Thr Thr Gly Thr Cys Thr Gln
                485                 490                 495
```

```
Ala Thr Ala Leu Pro Val Leu Phe Lys Glu Leu Val Thr Thr Ser Tyr
            500                 505                 510


Gly Gln Asn Val Tyr Ile Ser Gly Ser Ile Ser Gln Leu Gly Asn Trp
        515                 520                 525


Asp Ala Ser Ser Ala Ile Ala Leu Ser Ala Ser Ser Tyr Thr Ser Ser
    530                 535                 540


Asn Pro Leu Trp Gln Val Thr Ile Thr Leu Pro Val Gly Thr Lys Phe
545                 550                 555                 560


Glu Tyr Lys Phe Ile Glu Lys Ser Ser Gly Ser Ala Thr Ala Thr Trp
                565                 570                 575


Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Thr Gly Cys Ala Gly
            580                 585                 590


Thr Thr Ala Thr Val Thr Ala Thr Trp Arg
        595                 600


<210>  142
<211>  621
<212>  PRT
<213>  Penicillium vasconiae

<400>  142

Leu Thr Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Ser Val
            20                  25                  30


Ser Asp Arg Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60
```

```
Val Thr Glu Gln Leu Ser Gln Asp Thr Gly Asp Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Glu Ile Tyr Asn Val Asn Thr Asn Tyr Gly Thr
                85                  90                  95


Ala Ala Asp Leu Leu Ala Leu Ser Lys Ala Leu His Ser Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125


Gly Asn Thr Val Asp Tyr Ser Val Phe Asn Pro Phe Asp Ser Ser Ser
    130                 135                 140


Tyr Phe His Ser Tyr Cys Glu Ile Ser Asp Tyr Ser Asn Gln Thr Asn
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Thr Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Leu Ser Ser Val Gln Thr Ile Trp Tyr Asn Trp Val Thr
            180                 185                 190


Glu Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Ser Phe Trp Pro Gly Tyr Asn Ser Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Val Phe Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Ser Tyr Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Gln Leu Leu Tyr Ala Phe Glu Ser Thr Ser Gly Ser Ile Ser Ser Leu
            260                 265                 270
```

```
Tyr Asn Met Ile Asn Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285


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


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Ile Ser Phe Ile Phe Phe
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Ser Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


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


Arg Ser Leu Ala Ile Ser Lys Asp Thr Ala Tyr Ile Thr Ser Lys Asn
    370                 375                 380


Asn Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Lys Lys Gly Ser
385                 390                 395                 400


Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Arg Gly Ser Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Ser Ser Gly Thr
            420                 425                 430


Gln Leu Met Glu Met Tyr Thr Cys Thr Ala Val Thr Val Asp Ser Ser
        435                 440                 445


Gly Asn Ile Ala Val Pro Met Ala Ser Gly Leu Pro Arg Ile Tyr Met
    450                 455                 460


Leu Ala Ser Ser Ala Cys Ser Ile Cys Ser Ser Ser Cys Ser Thr Thr
465                 470                 475                 480
```

```
Thr Thr Thr Ser Thr Thr Ser Thr Ser Thr Thr Thr Ala Ser Thr Leu
                485                 490                 495


Lys Thr Thr Thr Ser Thr Thr Ser Ala Thr Ser Thr Thr Ser Thr Ser
            500                 505                 510


Cys Thr Gln Ala Thr Ala Leu Pro Val Leu Phe Lys Glu Ile Val Thr
        515                 520                 525


Thr Ser Tyr Gly Gln Asn Ile Tyr Ile Ser Gly Ser Ile Ser Gln Leu
    530                 535                 540


Gly Ser Trp Asp Thr Ser Asn Ala Val Ala Leu Ser Ala Asp Gln Tyr
545                 550                 555                 560


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


Thr Ser Phe Glu Tyr Lys Phe Ile Glu Glu Thr Ser Gly Ser Ser Thr
            580                 585                 590


Ile Thr Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Thr Gly
        595                 600                 605


Cys Ala Gly Ser Thr Ala Thr Val Thr Ala Thr Trp Arg
    610                 615                 620


<210>  143
<211>  615
<212>  PRT
<213>  Penicillium sp.

<400>  143

Leu Thr Ala Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asn Val
            20                  25                  30
```

```
Ser Asp Arg Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


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


Gly Tyr Trp Gln Gln Glu Ile Tyr Asn Val Asn Thr Asn Tyr Gly Thr
                85                  90                  95


Ala Ala Asp Leu Leu Ala Leu Ser Lys Ala Leu His Ser Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125


Gly Asn Thr Val Asp Tyr Ser Val Phe Asn Pro Phe Asp Ser Ser Ser
    130                 135                 140


Tyr Phe His Ser Tyr Cys Glu Ile Thr Asp Tyr Ser Asn Gln Thr Asn
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Thr Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asn Thr Thr Leu Ser Ser Val Gln Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190


Ala Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205


Lys His Val Gln Glu Ser Phe Trp Pro Glu Tyr Asn Ser Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Val Phe Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240
```

```
Pro Tyr Gln Asn Tyr Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Gln Leu Leu Tyr Ala Phe Glu Ser Thr Ser Gly Ser Ile Ser Asp Leu
            260                 265                 270


Tyr Asn Met Ile Asn Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285


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


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Phe Ile Phe Phe
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Ser Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


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


Arg Ser Leu Ala Val Ser Lys Asp Thr Ala Tyr Ile Thr Ser Lys Asn
    370                 375                 380


Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Lys Lys Gly Ser
385                 390                 395                 400


Gly Gly Ser Gln Val Val Thr Val Leu Ser Asn Arg Gly Ser Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Ser Ser Gly Thr
            420                 425                 430


Lys Leu Met Glu Met Tyr Thr Cys Thr Ala Val Thr Val Asp Ser Ser
        435                 440                 445
```

```
Gly Asn Ile Ala Val Pro Met Ala Ser Gly Leu Pro Arg Val Tyr Met
    450                 455                 460


Leu Ala Ser Ser Ala Cys Ser Ile Cys Ser Ser Ala Cys Ser Thr Thr
465                 470                 475                 480


Thr Thr Ser Ser Thr Thr Ser Thr Ala Thr Thr Thr Ser Thr Thr Leu
                485                 490                 495


Lys Thr Thr Thr Thr Thr Thr Ser Thr Ser Cys Thr Gln Ala Thr Ala
            500                 505                 510


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


Ile Tyr Ile Ser Gly Ser Ile Ser Glu Leu Gly Asp Trp Asp Thr Ser
    530                 535                 540


Asn Ala Val Ala Leu Ser Ala Asp Gln Tyr Thr Ser Ser Asn Asn Leu
545                 550                 555                 560


Trp Tyr Val Val Val Thr Ile Pro Val Gly Thr Ser Phe Glu Tyr Lys
                565                 570                 575


Phe Ile Glu Glu Thr Ser Gly Ser Ser Ser Ile Thr Trp Glu Ser Asp
            580                 585                 590


Pro Asn Arg Ser Tyr Thr Val Pro Thr Gly Cys Ala Gly Ser Thr Ala
        595                 600                 605


Thr Val Thr Ala Thr Trp Arg
    610                 615


<210>  144
<211>  606
<212>  PRT
<213>  Heterocephalum aurantiacum

<400>  144

Leu Thr Ala Ala Glu Trp Arg Gln Gln Ser Ile Tyr Phe Leu Leu Thr
```

```
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Ala Cys Asn Leu
            20                  25                  30


Ser Gln Arg Ala Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Lys Gln Ile Glu Ala Ser Thr Ser Asp Gly Thr Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Asp Ile Tyr Asn Ile Asn Ser His Tyr Gly Thr
                85                  90                  95


Ala Asp Asp Leu Arg Ala Leu Ser Ser Ala Leu His Ser Arg Gly Met
            100                 105                 110


Tyr Leu Met Ile Asp Val Val Ala Asn His Met Gly Tyr Pro Gly Ala
        115                 120                 125


Gly Thr Ser Val Asp Tyr Ser Ile Phe Thr Pro Phe Gly Ser Ser Ser
    130                 135                 140


Tyr Phe His Ser Tyr Cys Gln Ile Thr Asp Tyr Asp Asn Gln Ser Asn
145                 150                 155                 160


Val Glu Asn Cys Trp Leu Gly Asp Asn Val Val Ser Leu Pro Asp Leu
                165                 170                 175


Asn Thr Gln Asn Ser Asn Val Arg Asn Leu Trp Tyr Asp Trp Val Glu
            180                 185                 190


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


Lys His Val Glu Lys Asp Phe Trp Pro Ser Tyr Asn Ala Ala Ala Gly
```

```
    210                 215                 220

Val Tyr Cys Val Gly Glu Val Phe His Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240

Pro Tyr Gln Asn Tyr Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255

Gln Leu Leu Tyr Ala Phe Gln Ser Ser Ser Gly Ser Ile Thr Asp Leu
            260                 265                 270

Tyr Asn Met Ile Asn Ser Val Ala Ser Asp Cys Lys Asp Pro Thr Thr
        275                 280                 285

Leu Gly Asn Phe Ile Glu Asn His Asp Asn Pro Arg Phe Pro Ser Tyr
    290                 295                 300

Thr Ser Asp Met Ser Gln Ala Lys Ser Val Ile Ala Phe Leu Phe Leu
305                 310                 315                 320

Ser Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335

Gly Gly Ala Asp Pro Asn Asn Arg Glu Ala Ile Trp Leu Ser Gly Tyr
            340                 345                 350

Ser Thr Ser Ser Thr Leu Tyr Gln Phe Ile Ser Ser Thr Asn Ser Ile
        355                 360                 365

Arg Lys Leu Ala Ile Ser Lys Asp Ser Ser Tyr Leu Thr Ser Arg Asn
    370                 375                 380

Asn Pro Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Ser
385                 390                 395                 400

Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
                405                 410                 415

Asn Ser Tyr Thr Leu Thr Leu Thr Asn His Gly Tyr Ser Ser Gly Ala
```

```
            420                 425                 430

Gln Leu Thr Glu Leu Tyr Thr Cys Ser Ser Ile Gln Val Ala Ser Ser
        435                 440                 445

Gly Gly Leu Ala Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Val
    450                 455                 460

Pro Ser Ser Trp Ile Gln Gly Ser Gly Leu Cys Gly Gly Gly Ser Thr
465                 470                 475                 480

Thr Thr Thr Thr Thr Ala Thr Thr Thr Thr Thr Thr Thr Thr Ser Thr
                485                 490                 495

Ser Ser Cys Ala Ala Ala Thr Ser Leu Ala Val Val Phe Asn Glu Leu
            500                 505                 510

Val Thr Thr Tyr Tyr Gly Glu Asn Ile Phe Ile Ala Gly Ser Ile Ser
        515                 520                 525

Gln Leu Gly Ser Trp Asp Thr Gly Lys Ser Val Ala Leu Ser Ala Ser
    530                 535                 540

Gln Tyr Thr Ser Ser Asn Pro Leu Trp Thr Ala Thr Val Ser Leu Pro
545                 550                 555                 560

Val Gly Thr Ser Phe Gln Tyr Lys Phe Ile Lys Lys Glu Pro Asp Gly
                565                 570                 575

Gln Val Val Trp Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Ala
            580                 585                 590

Gly Cys Ala Gly Thr Thr Gln Thr Val Asn Thr Ser Trp Arg
        595                 600                 605


<210>  145
<211>  602
<212>  PRT
<213>  Neosartorya massa
```

```
<400>  145

Leu Thr Pro Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Glu Asp Asn Ser Thr Thr Ala Ala Cys Asp Val
            20                  25                  30


Thr Gln Arg Leu Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Glu Gln Phe Tyr Glu Asp Thr Gly Asp Gly Thr Ser Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Asn Ile Tyr Glu Val Asn Tyr Asn Tyr Gly Thr
                85                  90                  95


Ala Gln Asp Leu Lys Asn Leu Ala Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125


Gly Asn Thr Val Asp Tyr Ser Val Phe Thr Pro Phe Asp Ser Ser Ser
    130                 135                 140


Tyr Phe His Pro Tyr Cys Leu Ile Ser Asp Tyr Ser Asn Gln Thr Asn
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Thr Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Asp Thr Thr Val Arg Thr Ile Trp Tyr Asp Trp Val Lys
            180                 185                 190


Gly Leu Val Ala Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205
```

```
Lys His Val Glu Lys Asp Phe Trp Pro Gly Tyr Asn Asp Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Val Phe Ser Gly Asp Pro Thr Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Asn Tyr Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Gln Leu Leu Tyr Ala Phe Glu Ser Thr Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270


Tyr Asp Met Ile Asn Ser Val Ala Ser Asp Cys Ala Asp Pro Thr Leu
        275                 280                 285


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


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Ile Ser Phe Ile Phe Phe
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Ala Asp Pro Ala Asn Arg Glu Ala Val Trp Leu Ser Gly Tyr
            340                 345                 350


Ser Thr Ser Ala Thr Leu Tyr Ser Trp Ile Ala Ser Thr Asn Arg Ile
        355                 360                 365


Arg Lys Leu Ala Ile Ser Lys Asp Ala Ala Tyr Ile Thr Ser Lys Asn
    370                 375                 380


Asn Pro Phe Tyr Tyr Asp Ser Asn Thr Leu Ala Met Arg Lys Gly Ser
385                 390                 395                 400


Ile Ala Gly Ala Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser
                405                 410                 415
```

```
Gly Ser Ser Tyr Thr Leu Ser Leu Ser Gly Thr Gly Tyr Ser Ala Gly
            420                 425                 430


Ala Ser Leu Val Glu Met Tyr Thr Cys Thr Thr Leu Thr Val Asp Ser
        435                 440                 445


Ser Gly Asn Leu Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu
    450                 455                 460


Val Pro Ser Ser Trp Val Ser Gly Ser Gly Leu Cys Gly Ser Gly Ser
465                 470                 475                 480


Thr Thr Thr Thr Thr Thr Thr Ala Thr Ala Thr Thr Thr Ala Cys Thr
                485                 490                 495


Ser Ala Thr Ala Leu Pro Ile Val Phe Glu Glu Val Val Thr Thr Thr
            500                 505                 510


Tyr Gly Glu Asn Val Tyr Leu Thr Gly Ser Ile Ser Gln Leu Gly Asn
        515                 520                 525


Trp Asp Thr Ser Ser Ala Ile Ala Leu Ser Ala Ser Lys Tyr Thr Ser
    530                 535                 540


Ser Asn Pro Glu Trp Tyr Val Thr Val Thr Leu Pro Val Gly Thr Ser
545                 550                 555                 560


Phe Gln Tyr Lys Phe Phe Lys Lys Glu Ser Asp Gly Ser Ile Val Trp
                565                 570                 575


Glu Ser Asp Pro Asn Arg Ser Tyr Thr Val Pro Thr Gly Cys Ala Gly
            580                 585                 590


Thr Thr Val Thr Val Ser Asp Thr Trp Arg
        595                 600


<210>  146
<211>  588
```

```
<212>  PRT
<213>  Penicillium janthinellum

<400>  146

Ala Thr Pro Ala Gln Trp Arg Ser Gln Ser Ile Tyr Phe Met Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Pro Cys Asp Thr
            20                  25                  30


Ser Gln Arg Ala Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Gly Gln Leu Asp Gly Asp Thr Gly Asp Gly Thr Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Ser Asn Tyr Gly Thr
                85                  90                  95


Ala Ser Asp Leu Lys Ala Leu Ala Ser Ala Leu His Ala Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asn Gly Ala
        115                 120                 125


Gly Asn Thr Val Asp Tyr Ser Val Phe Asp Ala Phe Asn Ser Asn Gln
    130                 135                 140


Tyr Phe His Ser Tyr Cys Glu Val Thr Asn Tyr Ser Asn Gln Thr Asn
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Thr Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asn Thr Glu Leu Ser Ser Val Gln Ser Ile Trp Tyr Asn Trp Val Gly
            180                 185                 190
```

```
Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Val Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Val Phe Asp Gly Asp Ala Ser Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Glu Val Met Asp Gly Val Leu Asn Tyr Pro Met Tyr Tyr
                245                 250                 255


Pro Leu Leu Arg Ala Phe Gln Ser Thr Ser Gly Ser Met Ser Asp Leu
            260                 265                 270


Tyr Asn Met Ile Asn Thr Val Lys Ser Thr Cys Ser Asp Ser Thr Leu
        275                 280                 285


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


Thr Asn Asp Met Ser Leu Ala Lys Asn Val Ala Ala Phe Thr Ile Met
305                 310                 315                 320


Ala Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Ser Asp Pro Ala Asn Arg Glu Ala Val Trp Leu Ser Gly Tyr
            340                 345                 350


Asn Thr Asp Ser Ala Leu Tyr Lys Leu Ile Ala Lys Val Asn Ala Ile
        355                 360                 365


Arg Ser Tyr Ala Ile Ser Gln Ser Ala Ser Tyr Val Thr Tyr Lys Asn
    370                 375                 380


Tyr Pro Ile Tyr Gln Asp Ala Ser Thr Leu Ala Met Arg Lys Gly Ser
385                 390                 395                 400
```

```
Ser Gly Thr Gln Thr Ile Thr Val Leu Ser Asn Arg Gly Ala Ser Gly
                405                 410                 415


Ser Gln Tyr Thr Leu Ser Leu Gly Asn Thr Gly Tyr Ser Thr Gly Thr
            420                 425                 430


Thr Leu Thr Glu Ile Ile Thr Cys Ala Lys Ile Thr Val Asp Ser Ser
        435                 440                 445


Gly Asn Val Pro Val Pro Met Ala Ser Gly Glu Pro Arg Ile Leu Tyr
    450                 455                 460


Pro Ser Ser Ser Ile Lys Gly Ser Ala Ile Cys Ala Ser Ser Gly Arg
465                 470                 475                 480


Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
                485                 490                 495


Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
            500                 505                 510


Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525


Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
    530                 535                 540


Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545                 550                 555                 560


Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
                565                 570                 575


Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  147
<211>  589
<212>  PRT
```

```
<213>  Aspergillus brasiliensis

<400>  147

Ala Thr Pro Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Asn Ser Thr Thr Ala Ser Cys Asp Leu
            20                  25                  30


Ser Ala Arg Gln Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn Gln
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Val Thr Pro
    50                  55                  60


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


Gly Tyr Trp Gln Gln Asp Ala Tyr Ala Leu Asn Ser His Tyr Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ala Leu Ala Thr Ala Leu His Ser Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly His Asn Gly Thr
        115                 120                 125


Gly Ser Ser Val Glu Tyr Ser Val Tyr Asn Pro Phe Asn Ala Lys Lys
    130                 135                 140


Tyr Phe His Asn Leu Cys Trp Ile Ser Asn Tyr Asp Asn Gln Thr Asn
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ala Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Arg Thr Asp Val Lys Asn Met Trp Tyr Asp Trp Val Lys
            180                 185                 190
```

```
Ser Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Val Asp Thr Val
        195                 200                 205


Lys Asn Val Gln Lys Asn Phe Trp Pro Gly Tyr Asn Asn Ala Ser Gly
    210                 215                 220


Val Tyr Cys Ile Gly Glu Val Phe Asp Gly Asp Ala Ser Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Asp Asp Leu Asp Gly Val Leu Asn Tyr Pro Met Tyr Tyr
                245                 250                 255


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


Tyr Asn Met Ile Asn Thr Val Lys Ser Thr Cys Lys Asp Ser Thr Leu
        275                 280                 285


Leu Gly Thr Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Asn Tyr
    290                 295                 300


Thr Ser Asp Met Ser Leu Ala Lys Asn Val Ala Thr Phe Thr Ile Leu
305                 310                 315                 320


Ala Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Asn Asp Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


Lys Thr Thr Ser Glu Leu Tyr Thr His Ile Ala Ala Ser Asn Lys Ile
        355                 360                 365


Arg Thr His Ala Ile Lys Gln Asp Ser Gly Tyr Leu Thr Tyr Lys Asn
    370                 375                 380


Tyr Pro Ile Tyr Gln Asp Thr Ser Thr Leu Ala Met Arg Lys Gly Tyr
385                 390                 395                 400
```

```
Asn Gly Thr Gln Thr Ile Thr Val Leu Ser Asn Leu Gly Ala Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Ser Leu Pro Gly Thr Gly Tyr Thr Ala Gly Gln
            420                 425                 430


Lys Ile Thr Glu Ile Tyr Thr Cys Thr Asn Leu Thr Val Asn Ser Asn
        435                 440                 445


Gly Ser Val Pro Val Pro Met Lys Ser Gly Leu Pro Arg Ile Leu Tyr
    450                 455                 460


Pro Thr Asp Lys Leu Val Asn Gly Ser Ser Phe Cys Ser Ser Ser Gly
465                 470                 475                 480


Arg Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr
                485                 490                 495


Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr
            500                 505                 510


Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala
        515                 520                 525


Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro
    530                 535                 540


Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr
545                 550                 555                 560


Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala
                565                 570                 575


Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  148
<211>  588
<212>  PRT
<213>  Aspergillus westerdijkiae
```

```
<400>  148

Ala Thr Pro Ala Gln Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Asp Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30


Glu Asp Arg Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Gln
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Ala Gln Leu Thr Glu Asp Thr Lys Tyr Gly Asp Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ala Leu Ala Asp Ala Leu His Glu Arg Asp Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Ala Gly Ala
        115                 120                 125


Gly Asp Ser Val Asp Tyr Ser Val Phe Asn Pro Phe Asn Ser Gln Asp
    130                 135                 140


Tyr Phe His Ser Phe Cys Leu Ile Gln Asp Tyr Asn Asp Gln Thr Gln
145                 150                 155                 160


Ser Glu Asp Cys Trp Leu Gly Asp Asn Ser Val Ser Leu Pro Asp Leu
                165                 170                 175


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


Gly Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
```

```
        195                 200                 205

Lys His Val Gln Lys Glu Phe Trp Pro Gly Tyr Asn Asp Ala Ala Gly
    210                 215                 220

Val Tyr Cys Ile Gly Glu Ile Leu Asp Gly Asp Ala Ser Tyr Thr Cys
225                 230                 235                 240

Pro Tyr Gln Glu Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255

Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Ile Ser Asp Leu
            260                 265                 270

Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285

Met Gly Thr Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300

Thr Asp Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Thr Ile Leu
305                 310                 315                 320

Ala Asp Gly Ile Pro Ile Val Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335

Gly Gly Glu Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Gly Lys Tyr
            340                 345                 350

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

Arg Asn His Ala Ile Ser Thr Asp Lys Glu Tyr Val Asn Tyr Lys Asn
    370                 375                 380

Tyr Pro Ile Tyr Lys Asp Asp Ser Thr Ile Ala Met Arg Lys Gly Phe
385                 390                 395                 400

Asp Gly Ala Gln Ile Ile Thr Val Leu Ser Asn Gln Gly Ser Ser Gly
```

```
                405                 410                 415

Ser Ser Tyr Thr Leu Ser Leu Gly Asp Thr Gly Phe Ser Ser Gly Asp
            420                 425                 430

Lys Leu Thr Glu Ile Tyr Thr Cys Thr Ala Val Thr Val Asp Ser Asp
        435                 440                 445

Gly Lys Val Pro Val Pro Met Asp Gly Gly Ala Pro Arg Ala Leu Phe
    450                 455                 460

Pro Thr Glu Lys Leu Ser Gly Ser Ser Leu Cys Ser Gly Ser Gly Arg
465                 470                 475                 480

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
                485                 490                 495

Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
            500                 505                 510

Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525

Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
    530                 535                 540

Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545                 550                 555                 560

Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
                565                 570                 575

Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  149
<211>  476
<212>  PRT
<213>  Hamigera avellanea
```

```
<400>  149

Ala Thr Pro Ala Asp Trp Arg Ser Arg Ser Ile Tyr Phe Ile Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Glu Cys Asp Thr
            20                  25                  30


Ser Ala Arg Ala Tyr Cys Gly Gly Thr Trp Arg Gly Ile Ile Asn Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Asn Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


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


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


Ala Asp Asp Leu Arg Ala Leu Ala Ser Ala Leu His Glu Arg Asn Met
            100                 105                 110


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


Gly Asp Ser Val Asp Tyr Ser Val Phe Asn Pro Phe Asp Ser Ala Asp
    130                 135                 140


Tyr Phe His Pro Tyr Cys Leu Ile Ser Asn Tyr Glu Asp Gln Thr Glu
145                 150                 155                 160


Val Glu Asn Cys Trp Leu Gly Asp Thr Asn Val Ala Leu Val Asp Leu
                165                 170                 175


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


Ser Leu Val Gly Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205
```

```
Arg His Val Gln Lys Asp Phe Trp Pro Gly Phe Asn Asp Ala Ala Gly
    210                 215                 220


Val Tyr Ser Val Gly Glu Val Phe Ser Gly Asp Thr Ala Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Glu Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Pro Leu Leu Arg Ala Phe Gln Ser Thr Ser Gly Ser Ile Asn Asp Leu
            260                 265                 270


Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Ala Asp Ser Thr Leu
        275                 280                 285


Met Gly Thr Phe Leu Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300


Thr Ser Asp Val Ala Leu Ala Lys Asn Ala Ile Ala Phe Thr Ile Leu
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Val Trp Leu Ser Gly Tyr
            340                 345                 350


Ser Thr Asp Ser Glu Leu Tyr Ser Phe Val Ala Val Thr Asn Gln Ile
        355                 360                 365


Arg Asn Tyr Ala Ile Ser Gln Asp Gln Gly Tyr Val Thr Trp Lys Asn
    370                 375                 380


Val Pro Ile Tyr Gln Asp Thr Ser Thr Leu Ala Met Arg Lys Gly Thr
385                 390                 395                 400


Asp Gly Ser Gln Val Ile Thr Val Leu Ser Asn Leu Gly Ala Ser Gly
                405                 410                 415
```

```
Ser Ser Tyr Thr Leu Thr Leu Gly Gly Ser Gly Tyr Ser Ser Gly Gln
            420                 425                 430


Gln Leu Thr Glu Ile Phe Ser Cys Ala Thr Val Thr Val Asp Ser Ser
        435                 440                 445


Gly Asn Ile Pro Val Pro Met Gly Ser Gly Gln Pro Lys Val Phe Tyr
    450                 455                 460


Pro Thr Ala Gly Leu Gly Gly Ser Gly Ile Cys Gln
465                 470                 475


<210>  150
<211>  586
<212>  PRT
<213>  Hamigera avellanea

<400>  150

Ala Thr Pro Ala Asp Trp Arg Ser Arg Ser Ile Tyr Phe Ile Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Glu Cys Asp Thr
            20                  25                  30


Ser Ala Arg Ala Tyr Cys Gly Gly Thr Trp Arg Gly Ile Ile Asn Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Asn Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


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


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


Ala Asp Asp Leu Arg Ala Leu Ala Ser Ala Leu His Glu Arg Asn Met
            100                 105                 110
```

```
Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Trp Ala Gly Ser
        115                 120                 125


Gly Asp Ser Val Asp Tyr Ser Val Phe Asn Pro Phe Asp Ser Ala Asp
    130                 135                 140


Tyr Phe His Pro Tyr Cys Leu Ile Ser Asn Tyr Glu Asp Gln Thr Glu
145                 150                 155                 160


Val Glu Asn Cys Trp Leu Gly Asp Thr Asn Val Ala Leu Val Asp Leu
                165                 170                 175


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


Ser Leu Val Gly Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205


Arg His Val Gln Lys Asp Phe Trp Pro Gly Phe Asn Asp Ala Ala Gly
    210                 215                 220


Val Tyr Ser Val Gly Glu Val Phe Ser Gly Asp Thr Ala Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Glu Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Pro Leu Leu Arg Ala Phe Gln Ser Thr Ser Gly Ser Ile Asn Asp Leu
            260                 265                 270


Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Ala Asp Ser Thr Leu
        275                 280                 285


Met Gly Thr Phe Leu Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr
    290                 295                 300


Thr Ser Asp Val Ala Leu Ala Lys Asn Ala Ile Ala Phe Thr Ile Leu
305                 310                 315                 320
```

```
Ser Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Val Trp Leu Ser Gly Tyr
            340                 345                 350


Ser Thr Asp Ser Glu Leu Tyr Ser Phe Val Ala Val Thr Asn Gln Ile
        355                 360                 365


Arg Asn Tyr Ala Ile Ser Gln Asp Gln Gly Tyr Val Thr Trp Lys Asn
    370                 375                 380


Val Pro Ile Tyr Gln Asp Thr Ser Thr Leu Ala Met Arg Lys Gly Thr
385                 390                 395                 400


Asp Gly Ser Gln Val Ile Thr Val Leu Ser Asn Leu Gly Ala Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Thr Leu Gly Gly Ser Gly Tyr Ser Ser Gly Gln
            420                 425                 430


Gln Leu Thr Glu Ile Phe Ser Cys Ala Thr Val Thr Val Asp Ser Ser
        435                 440                 445


Gly Asn Ile Pro Val Pro Met Gly Ser Gly Gln Pro Lys Val Phe Tyr
    450                 455                 460


Pro Thr Ala Gly Leu Gly Gly Ser Gly Ile Cys Gln Ser Ser Gly Ala
465                 470                 475                 480


Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val
                485                 490                 495


Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val
            500                 505                 510


Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser
        515                 520                 525
```

```
Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr
    530                 535                 540


Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp
545                 550                 555                 560


Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr
                565                 570                 575


Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  151
<211>  576
<212>  PRT
<213>  Meripilus giganteus

<400>  151

Arg Pro Thr Val Phe Asp Ala Gly Ala Asp Ala His Ser Leu His Ala
1               5                   10                  15


Arg Ala Pro Ser Gly Ser Lys Asp Val Ile Ile Gln Met Phe Glu Trp
            20                  25                  30


Asn Trp Asp Ser Val Ala Ala Glu Cys Thr Asn Phe Ile Gly Pro Ala
        35                  40                  45


Gly Tyr Gly Phe Val Gln Val Ser Pro Pro Gln Glu Thr Ile Gln Gly
    50                  55                  60


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


Lys Arg Gly Asp Arg Ser Gln Phe Ala Asn Met Ile Thr Thr Cys His
                85                  90                  95


Ala Ala Gly Val Gly Val Ile Val Asp Thr Ile Trp Asn His Met Ala
            100                 105                 110
```

```
Gly Val Asp Ser Gly Thr Gly Thr Ala Gly Ser Ser Phe Thr His Tyr
        115                 120                 125


Asn Tyr Pro Gly Ile Tyr Gln Asn Gln Asp Phe His His Cys Gly Leu
    130                 135                 140


Glu Pro Gly Asp Asp Ile Val Asn Tyr Asp Asn Ala Val Glu Val Gln
145                 150                 155                 160


Thr Cys Glu Leu Val Asn Leu Ala Asp Leu Ala Thr Asp Thr Glu Tyr
                165                 170                 175


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


Ala Asp Gly Leu Arg Leu Asp Ala Ser Lys His Ile Pro Val Gly Asp
        195                 200                 205


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


Glu Val Ile Phe Gly Ala Gly Glu Pro Ile Thr Pro Asn Gln Tyr Thr
225                 230                 235                 240


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


Ala Phe Leu Ser Ser Gly Ile Ser Asn Leu Gln Asp Phe Glu Asn Arg
            260                 265                 270


Gly Trp Val Pro Gly Ser Gly Ala Asn Val Phe Val Val Asn His Asp
        275                 280                 285


Thr Glu Arg Asn Gly Ala Ser Leu Asn Asn Asn Ser Pro Ser Asn Thr
    290                 295                 300


Tyr Val Thr Ala Thr Ile Phe Ser Leu Ala His Pro Tyr Gly Thr Pro
305                 310                 315                 320
```

```
Thr Ile Leu Ser Ser Tyr Asp Gly Phe Thr Asn Thr Asp Ala Gly Ala
                325                 330                 335


Pro Asn Asn Asn Val Gly Thr Cys Ser Thr Ser Gly Gly Ala Asn Gly
            340                 345                 350


Trp Leu Cys Gln His Arg Trp Thr Ala Ile Ala Gly Met Val Gly Phe
        355                 360                 365


Arg Asn Asn Val Gly Ser Ala Ala Leu Asn Asn Trp Gln Ala Pro Gln
    370                 375                 380


Ser Gln Gln Ile Ala Phe Gly Arg Gly Ala Leu Gly Phe Val Ala Ile
385                 390                 395                 400


Asn Asn Ala Asp Ser Ala Trp Ser Thr Thr Phe Thr Thr Ser Leu Pro
                405                 410                 415


Asp Gly Ser Tyr Cys Asp Val Ile Ser Gly Lys Ala Ser Gly Ser Ser
            420                 425                 430


Cys Thr Gly Ser Ser Phe Thr Val Ser Gly Gly Lys Leu Thr Ala Thr
        435                 440                 445


Val Pro Ala Arg Ser Ala Ile Ala Val His Thr Gly Gln Lys Gly Ser
    450                 455                 460


Gly Gly Ala Thr Pro Thr Ser Ala Pro Ser Thr Thr Pro Thr Ser Gly
465                 470                 475                 480


Thr Val Ser Met Thr Phe Ala Glu Gln Ala Thr Thr Thr Phe Gly Glu
                485                 490                 495


Asn Ile Phe Leu Val Gly Ser Ile Ser Gln Leu Gly Asn Trp Asn Pro
            500                 505                 510


Ala Ser Ala Ile Ala Leu Ser Ser Ala Ala Tyr Pro Thr Trp Ser Val
        515                 520                 525
```

Ser Val Asn Ile Pro Ala Gly Thr Thr Phe Gln Tyr Lys Phe Ile Arg
530 535 540

Lys Glu Thr Asp Gly Ser Val Val Trp Glu Ser Asp Pro Asn Arg Gln
545 550 555 560

Ala Thr Ala Pro Ala Ser Gly Thr Thr Thr Leu Thr Ser Ser Trp Arg
565 570 575

<210> 152
<211> 575
<212> PRT
<213> Cerrena unicolor

<400> 152

Arg Pro Leu Asn Ala Ser Asn Ala Leu Asp Ala Arg Ala Pro Ser Gly
1 5 10 15

Ala Lys Ser Val Ile Ile Gln Met Phe Glu Trp Thr Trp Asp Ser Val
20 25 30

Ala Ala Glu Cys Thr Asn Phe Ile Gly Pro Ala Gly Tyr Gly Phe Val
35 40 45

Gln Val Ser Pro Pro Gln Glu Thr Ile Gln Gly Asp Gln Trp Trp Thr
50 55 60

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

Asp Gln Phe Ala Ala Met Ile Asp Thr Cys His Asp Ala Gly Val Lys
85 90 95

Val Ile Val Asp Thr Ile Trp Asn His Met Ala Gly Val Glu Ser Gly
100 105 110

Thr Gly Val Ala Gly Ser Ser Phe Thr His Tyr Asn Tyr Pro Gly Ile
115 120 125

Tyr Gln Asn Gln Asp Phe His His Cys Gly Leu Glu Ser Gly Asp Asp

```
    130                 135                 140


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


Asn Leu Ala Asp Leu Ala Thr Glu Thr Asp Tyr Val Arg Gly Arg Leu
                165                 170                 175


Ala Glu Tyr Gly Asn Asp Leu Leu Ser Leu Gly Ala Asp Gly Leu Arg
            180                 185                 190


Leu Asp Ala Ala Lys His Ile Ala Val Gly Asp Leu Ala Asn Ile Ile
        195                 200                 205


Gly Arg Leu Asn Ser Thr Pro Tyr Ile Thr Gln Glu Val Ile Phe Gly
    210                 215                 220


Ser Gly Glu Pro Ile Thr Pro Asn Gln Tyr Thr Gly Asn Gly Asp Val
225                 230                 235                 240


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


Asp Ile Ser Ser Leu Gln Asp Phe Glu Asn Arg Gly Trp Val Ala Gly
            260                 265                 270


Ser Gly Ala Asn Val Phe Val Thr Asn His Asp Thr Glu Arg Asn Gly
        275                 280                 285


Asn Ser Leu Asn Asn Asn Ser Pro Asn Asn Ala Tyr Thr Leu Ala Met
    290                 295                 300


Ile Phe Ser Leu Ala His Pro Tyr Gly Thr Pro Ser Ile Leu Ser Ser
305                 310                 315                 320


Tyr Ser Gly Phe Thr Asp Thr Asp Ala Gly Ala Pro Asn Gly Gly Ala
                325                 330                 335


Gly Thr Cys Ser Gly Ser Gly Gly Ser Asn Gly Trp Leu Cys Gln His
```

```
            340                 345                 350

Arg Trp Thr Ala Val Ala Gly Met Val Gly Phe Arg Asn Thr Val Gly
        355                 360                 365

Ser Ala Ala Leu Asn Asn Trp Val Ser Pro Gln Ser Ser Gln Ile Ala
    370                 375                 380

Phe Gly Arg Gly Ala Leu Gly Phe Val Ala Ile Asn Asn Gly Asp Ser
385                 390                 395                 400

Thr Trp Ser Thr Thr Phe Thr Thr Ser Leu Pro Asp Gly Thr Tyr Cys
                405                 410                 415

Asp Val Ile Thr Gly Thr Ser Ser Ser Gly Ser Cys Thr Gly Ser Ser
            420                 425                 430

Phe Thr Val Ser Gly Gly Thr Phe Thr Ala Asn Val Ala Ala Arg Asp
        435                 440                 445

Ala Val Ala Ile His Thr Gly Ala Thr Gly Thr Gly Ser Gly Ser Gly
    450                 455                 460

Asn Thr Ser Thr Gly Ser Gly Gly Thr Thr Ser Asp Thr Val Ser Val
465                 470                 475                 480

Ser Phe Ala Glu Thr Ala Thr Thr Thr Phe Gly Glu Asn Ile Phe Leu
                485                 490                 495

Val Gly Ser Ile Ser Gln Leu Gly Ala Trp Asp Pro Ala Ser Ala Ile
            500                 505                 510

Ala Leu Ser Ser Ala Ser Tyr Pro Thr Trp Thr Val Thr Val Thr Leu
        515                 520                 525

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

Gly Ser Val Val Trp Glu Ser Asp Pro Asn Arg Gln Ala Thr Thr Pro
```

```
545                 550                 555                 560


Ser Ser Ser Asp Ala Ala Thr Thr Thr Leu Ser Thr Ser Trp Arg
                565                 570                 575



<210>  153
<211>  562
<212>  PRT
<213>  Physalacria cryptomeriae

<400>  153

Ala Pro Phe Leu Glu Leu Gln Val Arg Ala Pro Ser Ser Thr Lys Gln
1               5                   10                  15


Val Ile Ile Gln Met Phe Glu Trp Thr Trp Asp Ser Val Ala Ala Glu
            20                  25                  30


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


Pro Pro Ala Glu His Ile Thr Gly Asp Gln Trp Trp Thr Asp Tyr Gln
    50                  55                  60


Pro Val Ser Tyr Ile Leu Thr Ser Lys Arg Gly Asn Arg Ser Gln Phe
65                  70                  75                  80


Ala Asn Met Val Thr Thr Cys His Thr Ala Gly Val Leu Val Ile Ala
                85                  90                  95


Asp Ala Leu Phe Asn His Met Ala Gly Ile Glu Ser Gly Thr Gly Thr
            100                 105                 110


Ala Gly Ser Ser Phe Thr His Tyr Asp Tyr Pro Gly Ile Tyr Gln Thr
        115                 120                 125


Gln Asp Phe His His Cys Gly Leu Thr Ser Gly Asp Asp Ile Ser Asp
    130                 135                 140


Tyr Ser Ser Gln Ala Gln Val Gln Thr Cys Glu Leu Val Asn Leu Ala
145                 150                 155                 160
```

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

Ala Asn Asp Leu Ile Ser Leu Gly Val Asn Gly Leu Arg Leu Asp Ala
            180                 185                 190

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

Ser Ser Thr Val Tyr Ile Thr Gln Glu Val Ile Phe Gly Ser Gly Glu
    210                 215                 220

Pro Val Thr Pro Ser Met Tyr Thr Gln Asn Gly Asp Val Gln Glu Phe
225                 230                 235                 240

Arg Tyr Thr Ser Thr Leu Gln Ser Ala Phe Ser Gly Gly Asp Ile Ser
                245                 250                 255

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

Asn Val Phe Val Ala Asn His Asp Thr Glu Arg Gly Gly Ser Ser Leu
        275                 280                 285

Asn Tyr Lys Ser Ser Ser Asn Thr Tyr Val Thr Ala Thr Ile Phe Ser
    290                 295                 300

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

Ser Asp Thr Asp Ala Gly Ser Pro Asn Gly Gly Ala Gly Thr Cys Ser
                325                 330                 335

Thr Thr Gly Gly Ala Asn Gly Trp Leu Cys Gln His Arg Trp Val Ala
            340                 345                 350

Phe Ser Gly Met Val Gly Phe His Asn Asn Val Gly Thr Ala Ser Leu
        355                 360                 365
```

```
Thr Asn Trp Val Ser Pro Gln Ser Asn Gln Ile Ala Phe Glu Arg Ser
    370                 375                 380


Gly Lys Gly Phe Val Ala Ile Asn Asn Ala Asp Ser Ala Trp Thr Ala
385                 390                 395                 400


Thr Phe Thr Thr Ser Leu Ala Ala Gly Ser Tyr Cys Asp Val Ile Thr
                405                 410                 415


Gly Thr Ser Asn Gly Ser Ala Cys Ser Gly Thr Ser Tyr Thr Val Ser
            420                 425                 430


Gly Gly Ser Phe Ser Ala Thr Val Ala Ala Arg Ser Ala Val Ala Ile
        435                 440                 445


His Thr Gly Ala Thr Gly Ser Gly Ser Gly Gly Gly Gly Gly Ser Thr
    450                 455                 460


Gly Ser Val Ala Ile Thr Phe Gln Glu Thr Ala Thr Thr Thr Leu Gly
465                 470                 475                 480


Glu Asn Ile Phe Leu Val Gly Ser Ile Ser Gln Leu Arg Thr Trp Ala
                485                 490                 495


Pro Ala Ser Ala Ile Ala Leu Ser Ser Ala Ser Tyr Pro Thr Trp Ser
            500                 505                 510


Val Thr Val Ser Ile Pro Ala Gly Thr Thr Phe Glu Tyr Lys Phe Ile
        515                 520                 525


Arg Lys Glu Ser Asp Gly Ser Val Val Trp Glu Ser Asp Pro Asn Arg
    530                 535                 540


Ser Ala Thr Ala Ser Ser Ser Ala Ser Thr Gln Thr Ile Leu Thr Ser
545                 550                 555                 560


Trp Arg
```

```
<210>  154
<211>  578
<212>  PRT
<213>  Lenzites betulinus

<400>  154

Arg Pro Ala Ser Thr Val Phe His Gly Ala Glu Thr Arg Ser Leu Asp
1               5                   10                  15


Ala Arg Ala Pro Ser Gly Ser Lys Asp Val Ile Ile Gln Met Phe Glu
            20                  25                  30


Trp Thr Trp Asp Ser Val Ala Ala Glu Cys Thr Asn Phe Ile Gly Pro
        35                  40                  45


Ala Gly Tyr Gly Phe Val Gln Gly Ser Pro Pro Gln Glu His Ile Gln
    50                  55                  60


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


Ser Lys Arg Gly Asp Arg Thr Ser Phe Ala Asn Met Ile Gln Thr Cys
                85                  90                  95


His Thr Ala Gly Val Gly Val Ile Val Asp Thr Leu Phe Asn His Met
            100                 105                 110


Ala Gly Val Asp Ser Gly Thr Gly Val Ala Gly Ser Ser Phe Thr His
        115                 120                 125


Tyr Asn Tyr Pro Gly Ile Tyr Gln Asn Gln Asp Phe His His Cys Gly
    130                 135                 140


Leu Glu Pro Gly Asp Asp Ile Val Asn Tyr Asp Asn Ala Val Glu Val
145                 150                 155                 160


Gln Thr Cys Glu Leu Asp Asn Leu Ala Asp Leu Ala Thr Glu Thr Glu
                165                 170                 175
```

```
Tyr Val Arg Gly Arg Leu Ala Gln Tyr Gly Asn Asp Leu Leu Ser Leu
                180                 185                 190

Gly Ala Asp Gly Met Arg Leu Asp Ala Ala Lys His Ile Ala Val Gly
        195                 200                 205

Asp Ile Ala Asn Ile Leu Ser Arg Leu Asn Arg Thr Val Tyr Ile Thr
    210                 215                 220

Gln Glu Val Ile Phe Gly Ala Gly Glu Pro Ile Thr Pro Asn Gln Tyr
225                 230                 235                 240

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

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

Arg Gly Trp Val Pro Gly Ser Gly Ala Asn Val Phe Val Thr Asn His
        275                 280                 285

Asp Thr Glu Arg Asn Gly Ala Ser Leu Asn Asn Asn Ser Pro Ser Asn
    290                 295                 300

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

Pro Ser Ile Leu Ser Ser Tyr Ser Gly Phe Thr Asp Thr Asp Ala Gly
            325                 330                 335

Ala Pro Asn Gly Gly Val Gly Thr Cys Ser Gly Ser Gly Gly Thr Asn
                340                 345                 350

Gly Trp Leu Cys Gln His Arg Trp Thr Ala Val Ala Gly Met Val Gly
        355                 360                 365

Phe Arg Asn Gln Val Gly Ser Ala Ala Leu Gly Asn Trp Gln Ser Pro
    370                 375                 380
```

```
Gln Ser Gln Gln Ile Ala Phe Gly Arg Gly Ala Leu Gly Phe Val Ala
385                 390                 395                 400


Ile Asn Asn Ala Asp Ser Ala Trp Ser Ala Thr Phe Thr Thr Ser Leu
                405                 410                 415


Pro Asp Gly Ser Tyr Cys Asp Val Ile Ser Gly Gln Thr Ser Gly Ser
            420                 425                 430


Thr Cys Thr Gly Ser Ser Phe Thr Val Ser Gly Gly Ser Leu Ser Ala
        435                 440                 445


Thr Val Pro Ala Arg Ser Ala Ile Ala Val His Thr Gly Gln Lys Gly
    450                 455                 460


Thr Gly Ser Gly Ser Gly Thr Gly Thr Gly Gly Gly Gly Ser Thr Gly
465                 470                 475                 480


Ser Gly Asn Val Ala Val Asn Phe Ala Glu Thr Ala Thr Thr Thr Phe
                485                 490                 495


Gly Glu Asn Ile Phe Val Val Gly Ser Ile Ser Gln Leu Gly Thr Trp
            500                 505                 510


Asn Thr Ala Asn Ala Ile Ala Leu Ser Ser Pro Ser Tyr Pro Thr Trp
        515                 520                 525


Thr Val Ser Ile Ser Ile Pro Ala Gly Thr Thr Phe Gln Tyr Lys Phe
    530                 535                 540


Ile Arg Lys Glu Thr Asp Gly Ser Val Val Trp Glu Ser Asp Pro Asn
545                 550                 555                 560


Arg Gln Ala Thr Ala Pro Ala Ser Gly Ser Thr Thr Leu Ser Thr Ser
                565                 570                 575


Trp Arg
```

```
<210>  155
<211>  571
<212>  PRT
<213>  Trametes ljubarskyi

<400>  155

Arg Pro Ala Thr Phe Asp Ala Ala Asp Ala Arg Ser Val Gln Pro Arg
1               5                   10                  15


Ala Pro Ser Gly Ser Lys Asp Val Ile Ile Gln Met Phe Glu Trp Thr
            20                  25                  30


Trp Asp Ser Val Ala Ala Glu Cys Thr Asn Phe Ile Gly Pro Ala Gly
        35                  40                  45


Tyr Gly Phe Val Gln Gly Asn Pro Pro Gln Glu His Ile Gln Gly Asp
    50                  55                  60


Gln Trp Trp Thr Asp Tyr Gln Pro Val Ser Tyr Ile Leu Thr Ser Lys
65                  70                  75                  80


Arg Gly Asp Arg Thr Ala Phe Ala Asn Met Ile Ser Thr Cys His Ala
                85                  90                  95


Ala Gly Val Gly Val Ile Val Asp Thr Ile Phe Asn His Met Ser Gly
            100                 105                 110


Val Asp Ser Gly Thr Gly Val Ala Gly Ser Ser Phe Thr His Tyr Asn
        115                 120                 125


Tyr Pro Gly Ile Tyr Gln Asn Gln Asp Phe His His Cys Gly Leu Glu
    130                 135                 140


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


Cys Glu Leu Glu Asn Leu Ala Asp Leu Ala Thr Asp Thr Glu Tyr Val
                165                 170                 175
```

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


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


Ala Asn Ile Leu Ser Arg Leu Asn Arg Ser Val Tyr Ile Thr Gln Glu
    210                 215                 220


Val Ile Tyr Gly Asp Gly Glu Pro Ile Thr Pro Asn Gln Tyr Thr Gly
225                 230                 235                 240


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


Phe Leu Gly Gly Gly Ile Ser Ser Leu Gln Ser Phe Asp Asn Leu Gly
            260                 265                 270


Trp Val Pro Gly Thr Gly Ala Asn Val Phe Val Thr Asn His Asp Thr
        275                 280                 285


Glu Arg Asn Gly Asn Ser Leu Asn Asn Asn Ser Pro Ser Asn Thr Tyr
    290                 295                 300


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


Ile Leu Ser Ser Tyr Ser Gly Phe Thr Asn Thr Asp Ala Gly Ala Pro
                325                 330                 335


Asn Gly Gly Thr Gly Thr Cys Ser Gly Ser Gly Gly Ala Asn Gly Trp
            340                 345                 350


Leu Cys Gln His Arg Trp Thr Ala Val Ala Gly Met Val Gly Phe Arg
        355                 360                 365


Asn Asn Val Gly Ser Ala Ala Leu Thr Asn Trp Gln Ser Pro Gln Ser
    370                 375                 380
```

```
Gln Gln Ile Ala Phe Gly Arg Gly Ala Leu Gly Phe Val Ala Ile Asn
385                 390                 395                 400


Asn Ala Asp Ser Ala Trp Ser Thr Thr Phe Thr Thr Ser Leu Pro Asp
                405                 410                 415


Gly Ser Tyr Cys Asp Val Val Ser Gly Thr Ser Ser Asn Gly Gly Cys
            420                 425                 430


Thr Gly Ser Ser Phe Ser Val Ser Gly Gly Ser Leu Thr Ala Thr Val
        435                 440                 445


Pro Ala Arg Ser Ala Ile Ala Ile His Thr Gly Glu Thr Gly Ser Gly
    450                 455                 460


Ser Asn Ser Gly Gly Gly Ser Gly Gly Ser Gly Thr Val Thr Ile Asn
465                 470                 475                 480


Phe Ala Glu Thr Ala Thr Thr Thr Phe Gly Glu Asn Ile Phe Val Val
                485                 490                 495


Gly Ser Ile Pro Gln Leu Gly Ser Trp Asn Pro Ala Asn Ala Ile Ala
            500                 505                 510


Leu Ser Ser Ala Ser Tyr Pro Thr Trp Thr Val Ser Val Ser Val Pro
        515                 520                 525


Ala Gly Thr Thr Phe Glu Tyr Lys Phe Ile Arg Lys Glu Thr Asp Gly
    530                 535                 540


Ser Val Val Trp Glu Ser Asp Pro Asn Arg Ser Asp Thr Ala Pro Ala
545                 550                 555                 560


Ser Gly Thr Gln Thr Ile Thr Thr Ser Trp Arg
                565                 570


<210>  156
<211>  451
<212>  PRT
<213>  Bacillus subtilis
```

```
<400>  156

Gly Pro Ala Ala Ala Ser Ala Glu Thr Ala Asn Lys Ser Asn Glu Leu
1               5                   10                  15


Thr Ala Pro Ser Ile Lys Ser Gly Thr Ile Leu His Ala Trp Asn Trp
            20                  25                  30


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


Tyr Thr Ala Ile Gln Thr Ser Pro Ile Asn Gln Val Lys Glu Gly Asn
    50                  55                  60


Gln Gly Asp Lys Ser Met Ser Asn Trp Tyr Trp Leu Tyr Gln Pro Thr
65                  70                  75                  80


Ser Tyr Gln Ile Gly Asn Arg Tyr Leu Gly Thr Glu Gln Glu Phe Lys
                85                  90                  95


Glu Met Cys Ala Ala Ala Glu Glu Tyr Gly Ile Lys Val Ile Val Asp
            100                 105                 110


Ala Val Ile Asn His Thr Thr Phe Asp Tyr Ala Ala Ile Ser Asn Glu
        115                 120                 125


Val Lys Ser Ile Pro Asn Trp Thr His Gly Asn Thr Gln Ile Lys Asn
    130                 135                 140


Trp Ser Asp Arg Trp Asp Val Thr Gln Asn Ser Leu Leu Gly Leu Tyr
145                 150                 155                 160


Asp Trp Asn Thr Gln Asn Thr Gln Val Gln Ser Tyr Leu Lys Arg Phe
                165                 170                 175


Leu Glu Arg Ala Leu Asn Asp Gly Ala Asp Gly Phe Arg Phe Asp Ala
            180                 185                 190


Ala Lys His Ile Glu Leu Pro Asp Asp Gly Ser Tyr Gly Ser Gln Phe
```

        195   200   205

Trp Pro Asn Ile Thr Asn Thr Ser Ala Glu Phe Gln Tyr Gly Glu Ile
    210   215   220

Leu Gln Asp Ser Ala Ser Arg Asp Ala Ala Tyr Ala Asn Tyr Met Asp
225   230   235   240

Val Thr Ala Ser Asn Tyr Gly His Ser Ile Arg Ser Ala Leu Lys Asn
                245   250   255

Arg Asn Leu Gly Val Ser Asn Ile Ser His Tyr Ala Tyr Asp Val Ser
            260   265   270

Ala Asp Lys Leu Val Thr Trp Val Glu Ser His Asp Thr Tyr Ala Asn
        275   280   285

Asp Asp Glu Glu Ser Thr Trp Met Ser Asp Asp Asp Ile Arg Leu Gly
    290   295   300

Trp Ala Val Ile Ala Ser Arg Ser Gly Ser Thr Pro Leu Phe Phe Ser
305   310   315   320

Arg Pro Glu Gly Gly Gly Asn Gly Val Arg Phe Pro Gly Lys Ser Gln
                325   330   335

Ile Gly Asp Arg Gly Ser Ala Leu Phe Glu Asp Gln Ser Ile Thr Ala
            340   345   350

Val Asn Arg Phe His Asn Val Met Ala Gly Gln Pro Glu Glu Leu Ser
        355   360   365

Asn Pro Asn Gly Asn Asn Gln Ile Phe Met Asn Gln Arg Gly Ser His
    370   375   380

Gly Val Val Leu Ala Asn Ala Gly Ser Ser Ser Val Ser Ile Asn Thr
385   390   395   400

Pro Thr Lys Leu Pro Asp Gly Arg Tyr Asp Asn Lys Ala Gly Ala Gly

```
                405                 410                 415


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


Ser Val Ala Val Leu Tyr Pro Asp Asp Ile Glu Ile Arg Cys Asn Thr
        435                 440                 445


Phe Phe Gln
    450


<210>  157
<211>  633
<212>  PRT
<213>  Bacillus subtilis

<400>  157

Gly Pro Ala Ala Ala Ser Ala Glu Thr Ala Asn Lys Ser Asn Glu Leu
1               5                   10                  15


Thr Ala Pro Ser Ile Lys Ser Gly Thr Ile Leu His Ala Trp Asn Trp
            20                  25                  30


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


Tyr Thr Ala Ile Gln Thr Ser Pro Ile Asn Gln Val Lys Glu Gly Asn
    50                  55                  60


Gln Gly Asp Lys Ser Met Ser Asn Trp Tyr Trp Leu Tyr Gln Pro Thr
65                  70                  75                  80


Ser Tyr Gln Ile Gly Asn Arg Tyr Leu Gly Thr Glu Gln Glu Phe Lys
                85                  90                  95


Glu Met Cys Ala Ala Ala Glu Glu Tyr Gly Ile Lys Val Ile Val Asp
            100                 105                 110


Ala Val Ile Asn His Thr Thr Ser Asp Tyr Ala Ala Ile Ser Asn Glu
        115                 120                 125
```

```
Val Lys Ser Ile Pro Asn Trp Thr His Gly Asn Thr Gln Ile Lys Asn
    130                 135                 140

Trp Ser Asp Arg Trp Asp Val Thr Gln Asn Ser Leu Leu Gly Leu Tyr
145                 150                 155                 160

Asp Trp Asn Thr Gln Asn Thr Gln Val Gln Ser Tyr Leu Lys Arg Phe
                165                 170                 175

Leu Asp Arg Ala Leu Asn Asp Gly Ala Asp Gly Phe Arg Phe Asp Ala
            180                 185                 190

Ala Lys His Ile Glu Leu Pro Asp Asp Gly Ser Tyr Gly Ser Gln Phe
        195                 200                 205

Trp Pro Asn Ile Thr Asn Thr Ser Ala Glu Phe Gln Tyr Gly Glu Ile
    210                 215                 220

Leu Gln Asp Ser Ala Ser Arg Asp Ala Ala Tyr Ala Asn Tyr Met Asp
225                 230                 235                 240

Val Thr Ala Ser Asn Tyr Gly His Ser Ile Arg Ser Ala Leu Lys Asn
                245                 250                 255

Arg Asn Leu Gly Val Ser Asn Ile Ser His Tyr Ala Ser Asp Val Ser
            260                 265                 270

Ala Asp Lys Leu Val Thr Trp Val Glu Ser His Asp Thr Tyr Ala Asn
        275                 280                 285

Asp Asp Glu Glu Ser Thr Trp Met Ser Asp Asp Asp Ile Arg Leu Gly
    290                 295                 300

Trp Ala Val Ile Ala Ser Arg Ser Gly Ser Thr Pro Leu Phe Phe Ser
305                 310                 315                 320

Arg Pro Glu Gly Gly Gly Asn Gly Val Arg Phe Pro Gly Lys Ser Gln
                325                 330                 335
```

```
Ile Gly Asp Arg Gly Ser Ala Leu Phe Glu Asp Gln Ala Ile Thr Ala
            340                 345                 350

Val Asn Arg Phe His Asn Val Met Ala Gly Gln Pro Glu Glu Leu Ser
        355                 360                 365

Asn Pro Asn Gly Asn Asn Gln Ile Phe Met Asn Gln Arg Gly Ser His
    370                 375                 380

Gly Val Val Leu Ala Asn Ala Gly Ser Ser Ser Val Ser Ile Asn Thr
385                 390                 395                 400

Ala Thr Lys Leu Pro Asp Gly Arg Tyr Asp Asn Lys Ala Gly Ala Gly
                405                 410                 415

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

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

Phe Leu Glu Asn Tyr Lys Thr Gly Val Thr His Ser Phe Asn Asp Gln
    450                 455                 460

Leu Thr Ile Thr Leu Arg Ala Asp Ala Asn Thr Thr Lys Ala Val Tyr
465                 470                 475                 480

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

Thr Ile Gly Lys Gly Asp Pro Phe Gly Lys Thr Tyr Thr Ile Met Leu
            500                 505                 510

Lys Gly Thr Asn Ser Asp Gly Val Thr Arg Thr Glu Lys Tyr Ser Phe
        515                 520                 525

Val Lys Arg Asp Pro Ala Ser Ala Lys Thr Ile Gly Tyr Gln Asn Pro
    530                 535                 540
```

```
Asn His Trp Ser Gln Val Asn Ala Tyr Ile Tyr Lys His Asp Gly Ser
545                 550                 555                 560


Arg Val Ile Glu Leu Thr Gly Ser Trp Pro Gly Lys Pro Met Thr Lys
                565                 570                 575


Asn Ala Asp Gly Ile Tyr Thr Leu Thr Leu Pro Ala Asp Thr Asp Thr
            580                 585                 590


Thr Asn Ala Lys Val Ile Phe Asn Asn Gly Ser Ala Gln Val Pro Gly
        595                 600                 605


Gln Asn Gln Pro Gly Phe Asp Tyr Val Leu Asn Gly Leu Tyr Asn Asp
    610                 615                 620


Ser Gly Leu Ser Gly Ser Leu Pro His
625                 630


<210>  158
<211>  487
<212>  PRT
<213>  Schwanniomyces occidentalis

<400>  158

Lys Pro Ile Phe Leu Ser Lys Arg Asp Ala Gly Ser Ser Ala Ala Ala
1               5                   10                  15


Ala Trp Arg Ser Glu Ser Ile Tyr Gln Leu Val Thr Asp Arg Phe Ala
            20                  25                  30


Arg Thr Asp Gly Ser Thr Ser Ala Thr Cys Asn Thr Gly Asp Arg Val
        35                  40                  45


Tyr Cys Gly Gly Thr Phe Gln Gly Ile Ile Asp Lys Leu Asp Tyr Ile
    50                  55                  60


Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Val Val Glu Gln
65                  70                  75                  80
```

```
Ile Pro Asp Asp Thr Gly Tyr Gly Tyr Ala Tyr His Gly Tyr Trp Met
                85                  90                  95


Lys Asp Ile Tyr Ala Ile Asn Ser Asn Phe Gly Thr Ala Asp Asp Leu
            100                 105                 110


Lys Asn Leu Ser Asn Glu Leu His Lys Arg Asn Met Lys Leu Met Val
        115                 120                 125


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


Ala Tyr Ser Asn Tyr Asn Pro Phe Asn Gln Gln Ser Tyr Phe His Asp
145                 150                 155                 160


Tyr Cys Leu Ile Thr Asn Tyr Asp Asp Gln Thr Asn Val Glu Asp Cys
                165                 170                 175


Trp Glu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu Arg Thr Glu Asp
            180                 185                 190


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


Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Ser Ala Lys His Val Asp
    210                 215                 220


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


Gly Glu Val Tyr Asp Gly Asp Pro Ala Tyr Thr Cys Pro Tyr Gln Asn
                245                 250                 255


Tyr Met Ser Gly Val Thr Asn Tyr Pro Leu Tyr Tyr Pro Met Leu Arg
            260                 265                 270


Phe Phe Gln Gly Thr Ser Asn Ser Val Asp Glu Leu Asn Ala Met Ile
        275                 280                 285
```

```
Ser Ser Leu Glu Ser Asp Cys Lys Asp Ile Thr Leu Leu Gly Asn Phe
    290                 295                 300


Ile Glu Asn His Asp Gln Pro Arg Leu Pro Ser Tyr Thr Ser Asp Ser
305                 310                 315                 320


Ala Leu Ile Lys Asn Ala Ile Ala Phe Asn Leu Met Ser Asp Gly Ile
                325                 330                 335


Pro Ile Ile Tyr Tyr Gly Gln Glu Gln Gly Tyr Ser Gly Ser Ser Asp
            340                 345                 350


Pro Asn Asn Arg Glu Ala Leu Trp Leu Ser Gly Tyr Ser Thr Ser Asn
        355                 360                 365


Gly Tyr Tyr Lys Leu Ile Ser Ser Val Asn Gln Ile Arg Asn Gln Ala
    370                 375                 380


Ile Tyr Lys Asp Ser Lys Tyr Thr Thr Tyr Trp Ser Asp Val Leu Tyr
385                 390                 395                 400


Ala Ser Gly His Val Ile Ala Leu Gln Arg Gly Ala Asp Asp Gln Arg
                405                 410                 415


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


Thr Phe Ser Thr Lys Tyr Ser Gly Gly Glu Lys Val Val Asp Val Leu
        435                 440                 445


Thr Cys Gln Thr Ser Tyr Ala Asn Ser Asp Ser Thr Leu Thr Val Ser
    450                 455                 460


Ile Ser Gly Gly Ala Pro Arg Ile Tyr Ala Pro Ala Ser Leu Ile Ala
465                 470                 475                 480


Asn Ser Gly Ile Cys Asn Phe
                485
```

```
<210>  159
<211>  583
<212>  PRT
<213>  Rhizomucor pusillus

<400>  159

Ala Thr Ser Asp Asp Trp Lys Gly Lys Ala Ile Tyr Gln Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Ala Asp Asp Ser Thr Ser Asn Cys Ser Asn Leu
            20                  25                  30


Ser Asn Tyr Cys Gly Gly Thr Tyr Glu Gly Ile Thr Lys His Leu Asp
        35                  40                  45


Tyr Ile Ser Gly Met Gly Phe Asp Ala Ile Trp Ile Ser Pro Ile Pro
    50                  55                  60


Lys Asn Ser Asp Gly Gly Tyr His Gly Tyr Trp Ala Thr Asp Phe Tyr
65                  70                  75                  80


Gln Leu Asn Ser Asn Phe Gly Asp Glu Ser Gln Leu Lys Ala Leu Ile
                85                  90                  95


Gln Ala Ala His Glu Arg Asp Met Tyr Val Met Leu Asp Val Val Ala
            100                 105                 110


Asn His Ala Gly Pro Thr Ser Asn Gly Tyr Ser Gly Tyr Thr Phe Gly
        115                 120                 125


Asp Ala Ser Leu Tyr His Pro Lys Cys Thr Ile Asp Tyr Asn Asp Gln
    130                 135                 140


Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Glu Leu Pro Asp Ile Asp
145                 150                 155                 160


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

```
Trp Val Gly Asn Tyr Ser Phe Asp Gly Ile Arg Ile Asp Thr Val Lys
            180                 185                 190


His Ile Arg Lys Asp Phe Trp Thr Gly Tyr Ala Glu Ala Ala Gly Val
        195                 200                 205


Phe Ala Thr Gly Glu Val Phe Asn Gly Asp Pro Ala Tyr Val Gly Pro
    210                 215                 220


Tyr Gln Lys Tyr Leu Pro Ser Leu Ile Asn Tyr Pro Met Tyr Tyr Ala
225                 230                 235                 240


Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg Ile Ser
                245                 250                 255


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


Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn Ser Gln
        275                 280                 285


Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu Leu Gly
    290                 295                 300


Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe Ser Gly
305                 310                 315                 320


Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Thr Asn Tyr Asp
                325                 330                 335


Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser Val Arg
            340                 345                 350


Met Lys Ser Asn Lys Ala Val Tyr Met Asp Ile Tyr Val Gly Asp Asn
        355                 360                 365


Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn Asn Tyr
    370                 375                 380
```

```
Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly Lys Phe
385                 390                 395                 400


Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr Thr Thr
                405                 410                 415


Val Ser Ser Asp Gly Thr Val Thr Phe Asn Leu Lys Asp Gly Leu Pro
            420                 425                 430


Ala Ile Phe Thr Ser Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Pro
        435                 440                 445


Thr Gly Ser Gly Ser Val Thr Ser Thr Ser Lys Thr Thr Ala Thr Ala
    450                 455                 460


Ser Lys Thr Ser Thr Ser Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr
465                 470                 475                 480


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


Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly Asp Trp Glu Thr
            500                 505                 510


Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr Ser Ser Asp Pro
        515                 520                 525


Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu Ser Phe Glu Tyr
    530                 535                 540


Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu Trp Glu Ser Asp
545                 550                 555                 560


Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly Thr Ser Thr Ala
                565                 570                 575


Thr Val Thr Asp Thr Trp Arg
            580
```

```
<210>  160
<211>  616
<212>  PRT
<213>  Aspergillus niger

<400>  160

Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr Asp Arg Phe
1               5                   10                  15


Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr Gly Asp Gln
            20                  25                  30


Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His Leu Asp Tyr
        35                  40                  45


Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro Ile Thr Glu
    50                  55                  60


Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His Gly Tyr Trp
65                  70                  75                  80


Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr Ala Asp Asp
                85                  90                  95


Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met Tyr Leu Met
            100                 105                 110


Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn Gly Asn Asp
        115                 120                 125


Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser Tyr Phe His
    130                 135                 140


Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met Val Gln Asp
145                 150                 155                 160


Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu Asn Thr Thr
                165                 170                 175


Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala Asp Leu Val
```

```
            180                 185                 190

Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val Leu Glu Val
        195                 200                 205

Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly Val Tyr Cys
    210                 215                 220

Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys Pro Tyr Gln
225                 230                 235                 240

Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp Gln Leu Leu
                245                 250                 255

Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu Tyr Asn Met
            260                 265                 270

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

Phe Ile Glu Asn His Asp Asn Pro Arg Phe Ala Ser Tyr Thr Ser Asp
    290                 295                 300

Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu Ser Asp Gly
305                 310                 315                 320

Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser Gly Gly Lys
                325                 330                 335

Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr Asp Thr Ser
            340                 345                 350

Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile Arg Lys Leu
        355                 360                 365

Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn Asp Ala Phe
    370                 375                 380

Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr Ser Gly Ser
```

```
385                 390                 395                 400


Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly Ser Ser Tyr
                405                 410                 415


Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr Lys Leu Ile
            420                 425                 430


Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser Gly Asp Ile
        435                 440                 445


Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu Pro Ala Ser
    450                 455                 460


Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg Thr Thr Thr
465                 470                 475                 480


Thr Thr Thr Ala Ala Thr Ser Thr Ser Lys Ala Thr Thr Ser Ser Ser
                485                 490                 495


Ser Ser Ser Ala Ala Ala Thr Thr Ser Ser Ser Cys Thr Ala Thr Ser
            500                 505                 510


Thr Thr Leu Pro Ile Thr Phe Glu Glu Leu Val Thr Thr Thr Tyr Gly
        515                 520                 525


Glu Glu Val Tyr Leu Ser Gly Ser Ile Ser Gln Leu Gly Glu Trp Asp
    530                 535                 540


Thr Ser Asp Ala Val Lys Leu Ser Ala Asp Asp Tyr Thr Ser Ser Asn
545                 550                 555                 560


Pro Glu Trp Ser Val Thr Val Ser Leu Pro Val Gly Thr Thr Phe Glu
                565                 570                 575


Tyr Lys Phe Ile Lys Val Asp Glu Gly Gly Ser Val Thr Trp Glu Ser
            580                 585                 590


Asp Pro Asn Arg Glu Tyr Thr Val Pro Glu Cys Gly Asn Gly Ser Gly
```

595 600 605

Glu Thr Val Val Asp Thr Trp Arg
610 615

<210> 161
<211> 512
<212> PRT
<213> Bacillus stearothermophilus

<400> 161

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

Asp Asp Gly Thr Leu Trp Thr Lys Val Ala Asn Glu Ala Asn Asn Leu
20 25 30

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

Thr Ser Arg Ser Asp Val Gly Tyr Gly Val Tyr Asp Leu Tyr Asp Leu
50 55 60

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

Ala Gln Tyr Leu Gln Ala Ile Gln Ala Ala His Ala Ala Gly Met Gln
85 90 95

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

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

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

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

```
Asp Gly Val Asp Trp Asp Glu Ser Arg Lys Leu Ser Arg Ile Tyr Lys
                165                 170                 175

Phe Arg Gly Lys Ala Trp Asp Trp Glu Val Asp Thr Glu Phe Gly Asn
            180                 185                 190

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

Val Thr Glu Leu Lys Asn Trp Gly Lys Trp Tyr Val Asn Thr Thr Asn
    210                 215                 220

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

Phe Pro Asp Trp Leu Ser Tyr Val Arg Ser Gln Thr Gly Lys Pro Leu
                245                 250                 255

Phe Thr Val Gly Glu Tyr Trp Ser Tyr Asp Ile Asn Lys Leu His Asn
            260                 265                 270

Tyr Ile Thr Lys Thr Asp Gly Thr Met Ser Leu Phe Asp Ala Pro Leu
        275                 280                 285

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

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

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

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

Thr Arg Gln Glu Gly Tyr Pro Cys Val Phe Tyr Gly Asp Tyr Tyr Gly
        355                 360                 365
```

```
Ile Pro Gln Tyr Asn Ile Pro Ser Leu Lys Ser Lys Ile Asp Pro Leu
    370                 375                 380


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


Asp His Ser Asp Ile Ile Gly Trp Thr Arg Glu Gly Gly Thr Glu Lys
                405                 410                 415


Pro Gly Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro Gly Gly Ser
            420                 425                 430


Lys Trp Met Tyr Val Gly Lys Gln His Ala Gly Lys Val Phe Tyr Asp
        435                 440                 445


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


Gly Glu Phe Lys Val Asn Gly Gly Ser Val Ser Val Trp Val Pro Arg
465                 470                 475                 480


Lys Thr Thr Val Ser Thr Ile Ala Arg Pro Ile Thr Thr Arg Pro Trp
                485                 490                 495


Thr Gly Glu Phe Val Arg Trp Thr Glu Pro Arg Leu Val Ala Trp Pro
            500                 505                 510


<210>  162
<211>  483
<212>  PRT
<213>  Bacillus halmapalus

<400>  162

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


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

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


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


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


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


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


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


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


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


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


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


Asn Gly Asn Tyr Asp Tyr Leu Met Tyr Ala Asp Val Asp Met Asp His
        195                 200                 205


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


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

```
Tyr Ser Phe Thr Arg Asp Trp Leu Thr His Val Arg Asn Ala Thr Gly
                245                 250                 255


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


Leu Glu Asn Tyr Leu Asn Lys Thr Asn Trp Asn His Ser Val Phe Asp
        275                 280                 285


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


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


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


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


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


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


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


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


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


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

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


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


Val Lys Arg




<210>  163
<211>  478
<212>  PRT
<213>  Aspergillus oryzae

<400>  163

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30


Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


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


Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125
```

```
Gly Ser Ser Val Asp Tyr Ser Val Phe Lys Pro Phe Ser Ser Gln Asp
    130                 135                 140


Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Tyr Glu Asp Gln Thr Gln
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
            180                 185                 190


Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220


Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240


Pro Tyr Gln Asn Val Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
            260                 265                 270


Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285


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


Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320


Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
                325                 330                 335
```

```
Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


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


Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380


Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400


Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
                405                 410                 415


Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
            420                 425                 430


Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Gly Ser Asp
        435                 440                 445


Gly Asn Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460


Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser
465                 470                 475


<210>  164
<211>  483
<212>  PRT
<213>  Bacillus amyloliquefaciens

<400>  164

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


Gly Gln His Trp Lys Arg Leu Gln Asn Asp Ala Glu His Leu Ser Asp
            20                  25                  30


Ile Gly Ile Thr Ala Val Trp Ile Pro Pro Ala Tyr Lys Gly Leu Ser
```

```
        35                  40                  45

Gln Ser Asp Asn Gly Tyr Gly Pro Tyr Asp Leu Tyr Asp Leu Gly Glu
    50                  55                  60

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

Leu Gln Asp Ala Ile Gly Ser Leu His Ser Arg Asn Val Gln Val Tyr
                85                  90                  95

Gly Asp Val Val Leu Asn His Lys Ala Gly Ala Asp Ala Thr Glu Asp
            100                 105                 110

Val Thr Ala Val Glu Val Asn Pro Ala Asn Arg Asn Gln Glu Thr Ser
        115                 120                 125

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

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

Ala Asp Trp Asp Glu Ser Arg Lys Ile Ser Arg Ile Phe Lys Phe Arg
                165                 170                 175

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

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

Val Ala Glu Thr Lys Lys Trp Gly Ile Trp Tyr Ala Asn Glu Leu Ser
    210                 215                 220

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

Leu Arg Asp Trp Val Gln Ala Val Arg Gln Ala Thr Gly Lys Glu Met
```

```
                245                 250                 255

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

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

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

Arg Arg Leu Leu Asp Gly Thr Val Val Ser Arg His Pro Glu Lys Ala
305                 310                 315                 320

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

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

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

Thr Lys Gly Thr Ser Pro Lys Glu Ile Pro Ser Leu Lys Asp Asn Ile
    370                 375                 380

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

Asp Tyr Ile Asp His Pro Asp Val Ile Gly Trp Thr Arg Glu Gly Asp
                405                 410                 415

Ser Ser Ala Ala Lys Ser Gly Leu Ala Ala Leu Ile Thr Asp Gly Pro
            420                 425                 430

Gly Gly Ser Lys Arg Met Tyr Ala Gly Leu Lys Asn Ala Gly Glu Thr
        435                 440                 445

Trp Tyr Asp Ile Thr Gly Asn Arg Ser Asp Thr Val Lys Ile Gly Ser
```

```
    450                 455                 460


Asp Gly Trp Gly Glu Phe His Val Asn Asp Gly Ser Val Ser Ile Tyr
465                 470                 475                 480


Val Gln Lys




<210>  165
<211>  583
<212>  PRT
<213>  Rhizomucor pusillus

<400>  165

Ala Thr Ser Asp Asp Trp Lys Gly Lys Ala Ile Tyr Gln Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Ala Asp Asp Ser Thr Ser Asn Cys Ser Asn Leu
            20                  25                  30


Ser Asn Tyr Cys Gly Gly Thr Tyr Glu Gly Ile Thr Lys His Leu Asp
        35                  40                  45


Tyr Ile Ser Gly Met Gly Phe Asp Ala Ile Trp Ile Ser Pro Ile Pro
    50                  55                  60


Lys Asn Ser Asp Gly Gly Tyr His Gly Tyr Trp Ala Thr Asp Phe Tyr
65                  70                  75                  80


Gln Leu Asn Ser Asn Phe Gly Asp Glu Ser Gln Leu Lys Ala Leu Ile
                85                  90                  95


Gln Ala Ala His Glu Arg Asp Met Tyr Val Met Leu Asp Val Val Ala
            100                 105                 110


Asn His Ala Gly Pro Thr Ser Asn Gly Tyr Ser Gly Tyr Thr Phe Asp
        115                 120                 125


Asp Ala Ser Leu Tyr His Pro Lys Cys Thr Ile Asp Tyr Asn Asn Gln
    130                 135                 140
```

```
Thr Ser Ile Glu Gln Cys Trp Val Ala Asp Glu Leu Pro Asp Ile Asp
145                 150                 155                 160


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


Trp Val Gly Asn Tyr Ser Phe Asp Gly Ile Arg Ile Asp Thr Val Lys
            180                 185                 190


His Ile Arg Lys Asp Phe Trp Thr Gly Tyr Ala Glu Ala Ala Gly Val
        195                 200                 205


Phe Ala Thr Gly Glu Val Phe Asn Gly Asp Pro Ala Tyr Val Gly Pro
    210                 215                 220


Tyr Gln Lys Tyr Leu Pro Ser Leu Ile Asn Tyr Pro Met Tyr Tyr Ala
225                 230                 235                 240


Leu Asn Asp Val Phe Val Ser Lys Ser Lys Gly Phe Ser Arg Ile Ser
                245                 250                 255


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


Thr Thr Phe Val Asp Asn His Asp Asn Pro Arg Phe Leu Asn Ser Gln
        275                 280                 285


Ser Asp Lys Ala Leu Phe Lys Asn Ala Leu Thr Tyr Val Leu Leu Gly
    290                 295                 300


Glu Gly Ile Pro Ile Val Tyr Tyr Gly Ser Glu Gln Gly Phe Ser Gly
305                 310                 315                 320


Gly Ala Asp Pro Ala Asn Arg Glu Val Leu Trp Thr Thr Asn Tyr Asp
                325                 330                 335


Thr Ser Ser Asp Leu Tyr Gln Phe Ile Lys Thr Val Asn Ser Val Arg
            340                 345                 350
```

```
Met Lys Ser Asn Lys Ala Val Tyr Met Asp Ile Tyr Val Gly Asp Asn
        355                 360                 365

Ala Tyr Ala Phe Lys His Gly Asp Ala Leu Val Val Leu Asn Asn Tyr
    370                 375                 380

Gly Ser Gly Ser Thr Asn Gln Val Ser Phe Ser Val Ser Gly Lys Phe
385                 390                 395                 400

Asp Ser Gly Ala Ser Leu Met Asp Ile Val Ser Asn Ile Thr Thr Thr
                405                 410                 415

Val Ser Ser Asp Gly Thr Val Thr Phe Asn Leu Lys Asp Gly Leu Pro
            420                 425                 430

Ala Ile Phe Thr Ser Ala Thr Gly Gly Thr Thr Thr Thr Ala Thr Pro
        435                 440                 445

Thr Gly Ser Gly Ser Val Thr Ser Thr Ser Lys Thr Thr Ala Thr Ala
    450                 455                 460

Ser Lys Thr Ser Thr Ser Thr Ser Ser Thr Ser Cys Thr Thr Pro Thr
465                 470                 475                 480

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

Asn Ile Tyr Leu Val Gly Ser Ile Ser Gln Leu Gly Asp Trp Glu Thr
            500                 505                 510

Ser Asp Gly Ile Ala Leu Ser Ala Asp Lys Tyr Thr Ser Ser Asp Pro
        515                 520                 525

Leu Trp Tyr Val Thr Val Thr Leu Pro Ala Gly Glu Ser Phe Glu Tyr
    530                 535                 540

Lys Phe Ile Arg Ile Glu Ser Asp Asp Ser Val Glu Trp Glu Ser Asp
545                 550                 555                 560
```

```
Pro Asn Arg Glu Tyr Thr Val Pro Gln Ala Cys Gly Thr Ser Thr Ala
                565                 570                 575


Thr Val Thr Asp Thr Trp Arg
            580



<210>  166
<211>  623
<212>  PRT
<213>  Kionochaeta ivoriensis

<400>  166

Leu Ser Pro Ala Gly Trp Arg Gln Gln Ser Ile Tyr Gln Val Met Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Ile Ala Ser Cys Asp Thr
            20                  25                  30


Ser Gln Gln Ala Tyr Cys Gly Gly Thr Trp Gln Gly Leu Ile Asn Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Val Trp Ile Ser Pro
    50                  55                  60


Met Val His Gln Met Ala Gly Ala Thr Ser Asp Gly Glu Ser Tyr His
65                  70                  75                  80


Gly Tyr Trp Ala Gln Asp Ile Asn Thr Val Asn Ser Ala Phe Gly Thr
                85                  90                  95


Ala Ala Asp Leu Lys Ala Leu Ser Ala Ala Leu His Ala Arg Gly Met
            100                 105                 110


Tyr Leu Met Leu Asp Val Val Thr Asn His Phe Ala Tyr Asp Gly Cys
        115                 120                 125


Gly Thr Cys Val Asp Tyr Ser Ile Phe Asn Pro Phe Asn Ser Glu Ser
    130                 135                 140
```

```
Tyr Phe His Pro Phe Cys Leu Ile Asp Tyr Ser Asn Thr Thr Ser Ile
145                 150                 155                 160

Gln Val Cys Trp Glu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu Arg
                165                 170                 175

Thr Glu Asp Ser Asp Val Arg Ser Ile Trp Asn Ser Trp Ile Ser Ser
            180                 185                 190

Val Ile Ser Thr Tyr Gly Val Asp Gly Leu Arg Val Asp Ser Ala Gln
        195                 200                 205

Gln Val Glu Thr Ser Phe Trp Ala Gly Phe Glu Ala Ala Ala Gly Val
    210                 215                 220

Tyr Met Val Gly Glu Val Phe Asn Gly Asp Pro Thr Tyr Val Thr Pro
225                 230                 235                 240

Phe Gln Asp Tyr Met Asp Gly Val Leu Asn Tyr Pro Ala Tyr Tyr Trp
                245                 250                 255

Ile Thr Gln Ala Phe Glu Ser Thr Ser Gly Ser Ile Ser Asn Leu Ala
            260                 265                 270

Asn Gly Met Asn Thr Met Lys Ser Leu Ala Lys Asn Thr Ser Leu Leu
        275                 280                 285

Gly Ser Phe Leu Glu Asn His Asp Asn Pro Arg Phe Pro Ser Leu Thr
    290                 295                 300

Ser Asp Met Ser Leu Ala Gln Asn Ala Ile Ala Phe Thr Met Leu Met
305                 310                 315                 320

Asp Gly Ile Pro Ile Ile Tyr Gln Gly Gln Glu Gln His Phe Ser Gly
                325                 330                 335

Gly Gly Val Pro Ser Asp Arg Glu Ala Val Trp Leu Ser Gly Tyr Pro
            340                 345                 350
```

```
Asn Asp Thr Thr Leu Tyr Ala Trp Ile Thr Lys Leu Asn Ala Val Arg
        355                 360                 365


Ser Trp Ala Ile Ala Lys Asp Ser Ser Tyr Leu Ala Tyr Met Ala Tyr
    370                 375                 380


Pro Val Tyr Thr Asp Thr His Thr Ile Ala Met Arg Lys Gly Asp Thr
385                 390                 395                 400


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


Ser Tyr Ser Val Thr Leu Thr Ser Ala Asp Thr Gly Phe Thr Ala Ser
            420                 425                 430


Gln Ser Val Val Asp Leu Val Gly Cys Lys Thr Tyr Thr Ala Asp Ser
        435                 440                 445


Thr Gly Ser Leu Ser Leu Ser Leu Thr Gly Gly Ile Pro Ile Ile Leu
    450                 455                 460


Tyr Pro Ala Ala Ser Leu Thr Gly Asn Thr Ile Cys Thr Ser Thr Gly
465                 470                 475                 480


Gly Thr Thr Thr Thr Ala Thr Pro Thr Gly Ser Gly Ser Val Thr Ser
                485                 490                 495


Thr Ser Lys Thr Thr Ala Thr Ala Ser Lys Thr Ser Thr Ser Thr Ser
            500                 505                 510


Ser Thr Ser Cys Thr Thr Pro Thr Ala Val Ala Val Thr Phe Asp Leu
        515                 520                 525


Thr Ala Thr Thr Thr Tyr Gly Glu Asn Ile Tyr Leu Val Gly Ser Ile
    530                 535                 540


Ser Gln Leu Gly Asp Trp Glu Thr Ser Asp Gly Ile Ala Leu Ser Ala
545                 550                 555                 560
```

```
Asp Lys Tyr Thr Ser Ser Asp Pro Leu Trp Tyr Val Thr Val Thr Leu
                565                 570                 575


Pro Ala Gly Glu Ser Phe Glu Tyr Lys Phe Ile Arg Ile Glu Ser Asp
            580                 585                 590


Asp Ser Val Glu Trp Glu Ser Asp Pro Asn Arg Glu Tyr Thr Val Pro
        595                 600                 605


Gln Ala Cys Gly Thr Ser Thr Ala Thr Val Thr Asp Thr Trp Arg
    610                 615                 620


<210>  167
<211>  588
<212>  PRT
<213>  Aspergillus niger

<400>  167

Leu Ser Ala Ala Glu Trp Arg Thr Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Thr Cys Asp Thr
            20                  25                  30


Gly Asp Gln Ile Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Ser Pro
    50                  55                  60


Ile Thr Glu Gln Leu Pro Gln Asp Thr Ala Asp Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Lys Ile Tyr Asp Val Asn Ser Asn Phe Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ser Leu Ser Asp Ala Leu His Ala Arg Gly Met
            100                 105                 110
```

```
Tyr Leu Met Val Asp Val Val Pro Asn His Met Gly Tyr Ala Gly Asn
        115                 120                 125


Gly Asn Asp Val Asp Tyr Ser Val Phe Asp Pro Phe Asp Ser Ser Ser
    130                 135                 140


Tyr Phe His Pro Tyr Cys Leu Ile Thr Asp Trp Asp Asn Leu Thr Met
145                 150                 155                 160


Val Gln Asp Cys Trp Glu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175


Asn Thr Thr Glu Thr Ala Val Arg Thr Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190


Asp Leu Val Ser Asn Tyr Ser Val Asp Gly Leu Arg Ile Asp Ser Val
        195                 200                 205


Leu Glu Val Glu Pro Asp Phe Phe Pro Gly Tyr Gln Glu Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Val Asp Asn Gly Asn Pro Ala Leu Asp Cys
225                 230                 235                 240


Pro Tyr Gln Lys Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Trp
                245                 250                 255


Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asn Leu
            260                 265                 270


Tyr Asn Met Ile Lys Ser Val Ala Ser Asp Cys Ser Asp Pro Thr Leu
        275                 280                 285


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


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Leu Ser Tyr Ile Phe Leu
305                 310                 315                 320
```

```
Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Glu Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Lys Val Pro Tyr Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350


Asp Thr Ser Ala Glu Leu Tyr Thr Trp Ile Ala Thr Thr Asn Ala Ile
        355                 360                 365


Arg Lys Leu Ala Ile Ser Ala Asp Ser Ala Tyr Ile Thr Tyr Ala Asn
    370                 375                 380


Asp Ala Phe Tyr Thr Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400


Ser Gly Ser Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ser Ser Gly
                405                 410                 415


Ser Ser Tyr Thr Leu Thr Leu Ser Gly Ser Gly Tyr Thr Ser Gly Thr
            420                 425                 430


Lys Leu Ile Glu Ala Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser
        435                 440                 445


Gly Asp Ile Pro Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Leu
    450                 455                 460


Pro Ala Ser Val Val Asp Ser Ser Ser Leu Cys Gly Gly Ser Gly Arg
465                 470                 475                 480


Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
                485                 490                 495


Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
            500                 505                 510


Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525
```

```
Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
    530                 535                 540


Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545                 550                 555                 560


Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
                565                 570                 575


Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  168
<211>  588
<212>  PRT
<213>  Aspergillus oryzae

<400>  168

Ala Thr Pro Ala Asp Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Thr Ala Thr Cys Asn Thr
            20                  25                  30


Ala Asp Gln Lys Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asp Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


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


Gly Tyr Trp Gln Gln Asp Ile Tyr Ser Leu Asn Glu Asn Tyr Gly Thr
                85                  90                  95


Ala Asp Asp Leu Lys Ala Leu Ser Ser Ala Leu His Glu Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Pro
```

```
        115                 120                 125

Gly Ser Ser Val Asp Tyr Ser Val Phe Val Pro Phe Asn Ser Ala Ser
    130                 135                 140

Tyr Phe His Pro Phe Cys Phe Ile Gln Asn Trp Asp Asn Gln Thr Gln
145                 150                 155                 160

Val Glu Asp Cys Trp Leu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu
                165                 170                 175

Asp Thr Thr Lys Asp Val Val Lys Asn Glu Trp Tyr Asp Trp Val Gly
            180                 185                 190

Ser Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205

Lys His Val Gln Lys Asp Phe Trp Pro Gly Tyr Asn Lys Ala Ala Gly
    210                 215                 220

Val Tyr Cys Ile Gly Glu Val Leu Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240

Pro Tyr Gln Glu Val Leu Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255

Pro Leu Leu Asn Ala Phe Lys Ser Thr Ser Gly Ser Met Asp Asp Leu
            260                 265                 270

Tyr Asn Met Ile Asn Thr Val Lys Ser Asp Cys Pro Asp Ser Thr Leu
        275                 280                 285

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

Thr Asn Asp Ile Ala Leu Ala Lys Asn Val Ala Ala Phe Ile Ile Leu
305                 310                 315                 320

Asn Asp Gly Ile Pro Ile Ile Tyr Ala Gly Gln Glu Gln His Tyr Ala
```

```
            325                 330                 335

Gly Gly Asn Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
        340                 345                 350

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

Arg Asn Tyr Ala Ile Ser Lys Asp Thr Gly Phe Val Thr Tyr Lys Asn
    370                 375                 380

Trp Pro Ile Tyr Lys Asp Asp Thr Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

Asp Gly Ser Gln Ile Val Thr Ile Leu Ser Asn Lys Gly Ala Ser Gly
            405                 410                 415

Asp Ser Tyr Thr Leu Ser Leu Ser Gly Ala Gly Tyr Thr Ala Gly Gln
        420                 425                 430

Gln Leu Thr Glu Val Ile Gly Cys Thr Thr Val Thr Val Asp Ser Ser
        435                 440                 445

Gly Asp Val Pro Val Pro Met Ala Gly Gly Leu Pro Arg Val Leu Tyr
    450                 455                 460

Pro Thr Glu Lys Leu Ala Gly Ser Lys Ile Cys Ser Ser Ser Gly Arg
465                 470                 475                 480

Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe
            485                 490                 495

Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly
        500                 505                 510

Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu
        515                 520                 525

Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala
```

```
    530                 535                 540


Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val
545                 550                 555                 560


Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser
                565                 570                 575


Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  169
<211>  583
<212>  PRT
<213>  Penicillium canescens

<400>  169

Leu Thr Pro Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Met Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Ser Asp Asn Ser Thr Thr Ala Ala Cys Asn Val
            20                  25                  30


Ser Asp Arg Thr Tyr Cys Gly Gly Thr Trp Gln Gly Ile Ile Asn His
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Glu Gln Leu Pro Gln Asp Thr Gly Asp Gly Glu Ala Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Asn Ile Tyr Glu Ile Asp Ser Lys Leu Gly Thr
                85                  90                  95


Ala Ala Asp Leu Leu Ala Leu Ser Lys Ala Leu His Ala Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Ala Gly Ser
        115                 120                 125
```

```
Gly Asn Ser Val Asp Tyr Ser Val Phe Asn Pro Phe Ser Ser Ser Ser
    130                 135                 140


Tyr Phe His Ser Tyr Cys Leu Ile Ser Asn Tyr Asp Asp Gln Ser Asn
145                 150                 155                 160


Val Glu Asn Cys Trp Leu Gly Asp Thr Ile Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Gln Thr Ala Val Gln Thr Ile Trp Tyr Asp Trp Ile Ala
            180                 185                 190


Asp Leu Val Ser Asn Tyr Ser Ile Asp Gly Leu Arg Ile Asp Thr Val
        195                 200                 205


Lys His Val Gln Lys Ser Phe Trp Pro Gly Tyr Asn Asp Ala Ala Gly
    210                 215                 220


Val Tyr Cys Val Gly Glu Ile Phe Asp Gly Asp Pro Ala Tyr Thr Cys
225                 230                 235                 240


Asp Tyr Gln Asn Tyr Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


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


Tyr Asn Met Ile Asn Ser Val Lys Ser Asp Cys Ala Asp Ser Thr Leu
        275                 280                 285


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


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Ile Ser Phe Leu Phe Leu
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Ile Tyr Ser Gly Gln Glu Gln His Tyr Ser
                325                 330                 335
```

```
Gly Gly Ala Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
            340                 345                 350

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

Arg Lys Leu Ala Val Ser Asp Ser Ser Tyr Leu Thr Thr Lys Asn Val
    370                 375                 380

Pro Phe Tyr Gln Asp Ser His Thr Leu Ala Met Lys Lys Gly Ser Ser
385                 390                 395                 400

Ala Ser Pro Val Ile Thr Val Leu Ser Asn Tyr Gly Ser Ser Gly Ser
                405                 410                 415

Ser Tyr Thr Leu Ser Leu Ser Gly Ser Gly Tyr Ser Ser Gly Thr Lys
            420                 425                 430

Leu Met Glu Met Tyr Thr Cys Thr Ser Val Thr Val Asp Ser Ser Gly
        435                 440                 445

Asn Ile Ala Val Pro Met Ala Ser Gly Leu Pro Arg Val Leu Met Leu
    450                 455                 460

Ala Ser Ser Ala Asn Ser Leu Cys Gly Ser Ser Gly Ala Thr Ser Pro
465                 470                 475                 480

Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr
                485                 490                 495

Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu
            500                 505                 510

Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr
        515                 520                 525

Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln
    530                 535                 540
```

```
Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala
545                 550                 555                 560


Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu
                565                 570                 575


Lys Asp Thr Trp Asp Glu Ser
            580


<210>  170
<211>  583
<212>  PRT
<213>  Acidomyces acidothermus

<400>  170

Leu Thr Pro Ala Gln Trp Arg Gly Gln Ser Ile Tyr Gln Val Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asp Ser Thr Thr Ala Ala Cys Asp Val
            20                  25                  30


Asn Asp Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn His Leu Asp
        35                  40                  45


Tyr Ile Gln Asp Met Gly Phe Ser Ala Ile Trp Ile Ser Pro Val Val
    50                  55                  60


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


Trp Ala Gln Asn Ile Tyr Ala Leu Asn Pro Asn Phe Gly Thr Val Ser
                85                  90                  95


Asp Leu Val Ala Leu Ser Ala Ala Leu His Gln Arg Gly Met Tyr Leu
            100                 105                 110


Met Val Asp Val Val Thr Asn His Met Gly Tyr Asp Gly Cys Gly Asp
        115                 120                 125
```

```
Cys Val Asp Tyr Ser Val Phe Thr Pro Phe Asn Ser Gln Ser Tyr Phe
    130                 135                 140


His Pro Phe Cys Leu Ile Asp Tyr Asn Asn Ser Thr Ser Ile Lys Val
145                 150                 155                 160


Cys Trp Glu Gly Asp Asn Ile Val Ser Leu Pro Asp Met Arg Thr Glu
                165                 170                 175


Asp Ser Asp Val Ala Thr Glu Trp Asn Thr Trp Ile Ser Glu Leu Val
            180                 185                 190


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


Asp Asn Ala Phe Phe Pro Pro Phe Gln Ala Ala Ala Gly Gly Ile His
    210                 215                 220


Val Leu Gly Glu Val Phe Asn Gly Asp Pro Asn Tyr Val Cys Pro Tyr
225                 230                 235                 240


Gln Asp Phe Met Ser Gly Val Leu Asn Tyr Pro Ala Tyr Tyr Tyr Ile
                245                 250                 255


Thr Gln Ala Phe Gln Ser Thr Ser Gly Ser Ile Ser Asn Leu Val Asn
            260                 265                 270


Gly Ile Asn Gln Met Lys Ser Thr Cys Thr Asp Thr Thr Leu Leu Gly
        275                 280                 285


Ser Phe Leu Glu Asn His Asp Asn Pro Arg Phe Pro Ser Tyr Thr Ser
    290                 295                 300


Asp Leu Ser Leu Asp Lys Asn Ala Ile Thr Phe Thr Ile Leu Gln Asp
305                 310                 315                 320


Gly Ile Pro Ile Ile Tyr Glu Gly Gln Glu Gln His Tyr Ser Gly Gly
                325                 330                 335
```

```
Thr Val Pro Asn Asn Arg Glu Ala Ile Trp Leu Ser Gly Tyr Asp Lys
            340                 345                 350


Ser Ala Pro Leu Tyr Thr Trp Ile Ala Ser Val Asn Gln Ile Arg Asn
        355                 360                 365


Gln Ala Ile Phe Lys Asp Ser Asn Tyr Leu Thr Tyr Met Ala Trp Pro
    370                 375                 380


Ile Tyr Ser Asp Ala Ser Thr Ile Ala Met Arg Lys Gly Phe Asp Gly
385                 390                 395                 400


Leu Gln Ile Ile Ser Val Tyr Ser Asn Lys Gly Ala Ser Ala Ala Ser
                405                 410                 415


Tyr Thr Ile Ser Leu Glu Ser Ser Thr Thr Gly Phe Thr Ala Asn Glu
            420                 425                 430


Ala Leu Val Glu Val Met Ser Cys Thr Thr Tyr Thr Thr Asp Gly Ser
        435                 440                 445


Gly Asn Leu Ala Val Thr Ile Ser Gly Gly Leu Pro Ala Val Phe Tyr
    450                 455                 460


Pro Lys Ala Gln Leu Ala Gly Ser Gly Ile Cys Gly Ala Thr Ser Pro
465                 470                 475                 480


Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr
                485                 490                 495


Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu
            500                 505                 510


Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr
        515                 520                 525


Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln
    530                 535                 540
```

```
Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala
545                 550                 555                 560


Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu
                565                 570                 575


Lys Asp Thr Trp Asp Glu Ser
            580


<210>  171
<211>  586
<212>  PRT
<213>  Kinochaeta ivoriensis

<400>  171

Leu Ser Pro Ala Gly Trp Arg Gln Gln Ser Ile Tyr Gln Val Met Thr
1               5                   10                  15


Asp Arg Phe Ala Arg Thr Asp Gly Ser Thr Ile Ala Ser Cys Asp Thr
            20                  25                  30


Ser Gln Gln Ala Tyr Cys Gly Gly Thr Trp Gln Gly Leu Ile Asn Lys
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Val Trp Ile Ser Pro
    50                  55                  60


Met Val His Gln Met Ala Gly Ala Thr Ser Asp Gly Glu Ser Tyr His
65                  70                  75                  80


Gly Tyr Trp Ala Gln Asp Ile Asn Thr Val Asn Ser Ala Phe Gly Thr
                85                  90                  95


Ala Ala Asp Leu Lys Ala Leu Ser Ala Ala Leu His Ala Arg Gly Met
            100                 105                 110


Tyr Leu Met Leu Asp Val Val Thr Asn His Phe Ala Tyr Asp Gly Cys
        115                 120                 125
```

```
Gly Thr Cys Val Asp Tyr Ser Ile Phe Asn Pro Phe Asn Ser Glu Ser
    130                 135                 140


Tyr Phe His Pro Phe Cys Leu Ile Asp Tyr Ser Asn Thr Thr Ser Ile
145                 150                 155                 160


Gln Val Cys Trp Glu Gly Asp Asn Thr Val Ser Leu Pro Asp Leu Arg
                165                 170                 175


Thr Glu Asp Ser Asp Val Arg Ser Ile Trp Asn Ser Trp Ile Ser Ser
            180                 185                 190


Val Ile Ser Thr Tyr Gly Val Asp Gly Leu Arg Val Asp Ser Ala Gln
        195                 200                 205


Gln Val Glu Thr Ser Phe Trp Ala Gly Phe Glu Ala Ala Ala Gly Val
    210                 215                 220


Tyr Met Val Gly Glu Val Phe Asn Gly Asp Pro Thr Tyr Val Thr Pro
225                 230                 235                 240


Phe Gln Asp Tyr Met Asp Gly Val Leu Asn Tyr Pro Ala Tyr Tyr Trp
                245                 250                 255


Ile Thr Gln Ala Phe Glu Ser Thr Ser Gly Ser Ile Ser Asn Leu Ala
            260                 265                 270


Asn Gly Met Asn Thr Met Lys Ser Leu Ala Lys Asn Thr Ser Leu Leu
        275                 280                 285


Gly Ser Phe Leu Glu Asn His Asp Asn Pro Arg Phe Pro Ser Leu Thr
    290                 295                 300


Ser Asp Met Ser Leu Ala Gln Asn Ala Ile Ala Phe Thr Met Leu Met
305                 310                 315                 320


Asp Gly Ile Pro Ile Ile Tyr Gln Gly Gln Glu Gln His Phe Ser Gly
                325                 330                 335
```

```
Gly Gly Val Pro Ser Asp Arg Glu Ala Val Trp Leu Ser Gly Tyr Pro
            340                 345                 350


Asn Asp Thr Thr Leu Tyr Ala Trp Ile Thr Lys Leu Asn Ala Val Arg
        355                 360                 365


Ser Trp Ala Ile Ala Lys Asp Ser Ser Tyr Leu Ala Tyr Met Ala Tyr
    370                 375                 380


Pro Val Tyr Thr Asp Thr His Thr Ile Ala Met Arg Lys Gly Asp Thr
385                 390                 395                 400


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


Ser Tyr Ser Val Thr Leu Thr Ser Ala Asp Thr Gly Phe Thr Ala Ser
            420                 425                 430


Gln Ser Val Val Asp Leu Val Gly Cys Lys Thr Tyr Thr Ala Asp Ser
        435                 440                 445


Thr Gly Ser Leu Ser Leu Ser Leu Thr Gly Gly Ile Pro Ile Ile Leu
    450                 455                 460


Tyr Pro Ala Ala Ser Leu Thr Gly Asn Thr Ile Cys Thr Ser Gly Ala
465                 470                 475                 480


Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val
                485                 490                 495


Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val
            500                 505                 510


Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser
        515                 520                 525


Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr
    530                 535                 540
```

```
Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp
545                 550                 555                 560


Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr
                565                 570                 575


Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580                 585


<210>  172
<211>  585
<212>  PRT
<213>  Aspergillus terreus

<400>  172

Leu Thr Pro Ala Glu Trp Arg Ser Gln Ser Ile Tyr Phe Leu Leu Thr
1               5                   10                  15


Asp Arg Phe Gly Arg Thr Asp Asn Ser Thr Thr Ala Ala Cys Asp Thr
            20                  25                  30


Ser Asp Arg Val Tyr Cys Gly Gly Ser Trp Gln Gly Ile Ile Asn Gln
        35                  40                  45


Leu Asp Tyr Ile Gln Gly Met Gly Phe Thr Ala Ile Trp Ile Thr Pro
    50                  55                  60


Val Thr Gly Gln Phe Tyr Glu Asn Thr Gly Asp Gly Thr Ser Tyr His
65                  70                  75                  80


Gly Tyr Trp Gln Gln Asp Ile Tyr Asp Leu Asn Tyr Asn Tyr Gly Thr
                85                  90                  95


Ala Gln Asp Leu Lys Asn Leu Ala Asn Ala Leu His Glu Arg Gly Met
            100                 105                 110


Tyr Leu Met Val Asp Val Val Ala Asn His Met Gly Tyr Asp Gly Ala
        115                 120                 125


Gly Asn Thr Val Asp Tyr Ser Val Phe Asn Pro Phe Ser Ser Ser Ser
```

```
    130                 135                 140


Tyr Phe His Pro Tyr Cys Leu Ile Ser Asn Tyr Asp Asn Gln Thr Asn
145                 150                 155                 160


Val Glu Asp Cys Trp Leu Gly Asp Thr Thr Val Ser Leu Pro Asp Leu
                165                 170                 175


Asp Thr Thr Ser Thr Ala Val Arg Asn Ile Trp Tyr Asp Trp Val Ala
            180                 185                 190


Asp Leu Val Ala Asn Tyr Ser Ile Asp Gly Leu Arg Val Asp Thr Val
        195                 200                 205


Lys His Val Glu Lys Asp Phe Trp Pro Gly Tyr Asn Ser Ala Ala Gly
    210                 215                 220


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


Pro Tyr Gln Asn Tyr Met Asp Gly Val Leu Asn Tyr Pro Ile Tyr Tyr
                245                 250                 255


Gln Leu Leu Tyr Ala Phe Glu Ser Ser Ser Gly Ser Ile Ser Asp Leu
            260                 265                 270


Tyr Asn Met Ile Ser Ser Val Ala Ser Ser Cys Lys Asp Pro Thr Leu
        275                 280                 285


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


Thr Ser Asp Tyr Ser Gln Ala Lys Asn Val Ile Thr Phe Ile Phe Leu
305                 310                 315                 320


Ser Asp Gly Ile Pro Ile Val Tyr Ala Gly Gln Glu Gln His Tyr Ser
                325                 330                 335


Gly Gly Ser Asp Pro Ala Asn Arg Glu Ala Thr Trp Leu Ser Gly Tyr
```

```
            340                 345                 350

Ser Thr Ser Ala Thr Leu Tyr Thr Trp Ile Ala Thr Thr Asn Gln Ile
        355                 360                 365

Arg Ser Leu Ala Ile Ser Lys Asp Ala Gly Tyr Val Gln Ala Lys Asn
    370                 375                 380

Asn Pro Phe Tyr Ser Asp Ser Asn Thr Ile Ala Met Arg Lys Gly Thr
385                 390                 395                 400

Thr Ala Gly Ala Gln Val Ile Thr Val Leu Ser Asn Lys Gly Ala Ser
                405                 410                 415

Gly Ser Ser Tyr Thr Leu Ser Leu Ser Gly Thr Gly Tyr Ser Ala Gly
            420                 425                 430

Val Thr Leu Val Glu Thr Tyr Thr Cys Thr Thr Val Thr Val Asp Ser
        435                 440                 445

Ser Gly Asn Leu Pro Val Pro Met Thr Ser Gly Leu Pro Arg Val Phe
    450                 455                 460

Val Pro Ser Ser Trp Val Asn Gly Ser Ala Leu Cys Asn Gly Ala Thr
465                 470                 475                 480

Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val Tyr
                485                 490                 495

Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser
            500                 505                 510

Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser Ala
        515                 520                 525

Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr
    530                 535                 540

Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp Glu
```

545   550   555   560

Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr
                565   570   575

Thr Glu Lys Asp Thr Trp Asp Glu Ser
            580   585

<210> 173
<211> 565
<212> PRT
<213> Thamnidium elegans

<400> 173

Val Pro Leu Ser Val Leu Asp Lys Arg Asn Gly Val Thr Thr Leu Ser
1   5   10   15

Lys Arg Ala Ala Ala Ala Asp Trp Lys Ser Arg Ser Ile Tyr Gln Leu
            20   25   30

Val Thr Asp Arg Phe Gly Arg Ser Asp Gly Ser Thr Ser Ala Cys Gly
        35   40   45

Asp Leu Ser Asn Tyr Cys Gly Gly Asp Tyr Lys Gly Ile Gln Asn Gln
    50   55   60

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

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

Phe Glu Lys Leu Asn Thr Asn Phe Gly Ser Ala Asp Asp Leu Lys Ala
            100   105   110

Leu Val Thr Ala Ala His Gly Lys Gly Met Tyr Val Met Leu Asp Val
        115   120   125

Val Ala Asn His Ala Gly Pro Ala Ser Gly Gly Asp Tyr Ser Gly Phe
    130   135   140

```
Thr Phe Ser Ser Ala Ser Asn Tyr His Pro Gln Cys Thr Ile Asp Tyr
145                 150                 155                 160


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


Asp Ile Asn Thr Glu Asp Asp Thr Ile Val Ser Lys Leu His Ser Ile
            180                 185                 190


Val Ser Asp Trp Val Thr Thr Tyr Asp Phe Asp Gly Ile Arg Ile Asp
        195                 200                 205


Thr Val Lys His Ile Arg Lys Asp Phe Trp Ser Gly Tyr Glu Glu Ala
    210                 215                 220


Ala Gly Val Phe Ala Thr Gly Glu Val Phe Asp Gly Asp Ala Ala Tyr
225                 230                 235                 240


Val Gly Pro Tyr Gln Asp Gln Leu Ser Ser Leu Ile Asn Tyr Pro Leu
                245                 250                 255


Tyr Tyr Ala Ile Arg Asp Val Phe Ser Ala Gly Ser Gly Phe Ser Arg
            260                 265                 270


Ile Ser Asp Met Leu Ser Thr Ile Lys Ser Asn Phe Lys Asp Pro Ser
        275                 280                 285


Val Leu Thr Thr Phe Val Asp Asn Gln Asp Asn Ala Arg Phe Leu Ser
    290                 295                 300


Val Lys Ser Asp Met Ser Leu Tyr Lys Asn Ala Leu Ala Phe Thr Ile
305                 310                 315                 320


Leu Thr Glu Gly Ile Pro Val Val Tyr Tyr Gly Thr Glu Gln Gly Phe
                325                 330                 335


Lys Gly Gly Asp Asp Pro Lys Asn Arg Glu Val Leu Trp Thr Ser Asn
            340                 345                 350
```

```
Tyr Asp Thr Ser Ser Asp Leu Tyr Lys Phe Ile Lys Ile Val Asn Asn
        355                 360                 365

Asp Val Arg Gln Lys Ser Asp Lys Thr Val Thr Leu Asp Val Asp Val
    370                 375                 380

Gly Thr Asn Thr Tyr Ala Phe Thr His Gly Lys Asn Leu Ile Val Val
385                 390                 395                 400

Asn Asn Tyr Gly Ser Gly Ser Thr Glu Ser Val Thr Val Lys Val Gly
                405                 410                 415

Asp Ser Val Ala Asp Gly Thr Lys Leu Val Asp Ala Val Ser Asn Ile
            420                 425                 430

Thr Ala Thr Val Ser Gly Gly Ser Ile Thr Phe Ser Leu Lys Asp Gly
        435                 440                 445

Leu Pro Ala Leu Phe Val Pro Ser Ser Gly Ala Thr Ser Pro Gly Gly
    450                 455                 460

Ser Ser Gly Ser Val Glu Val Thr Phe Asp Val Tyr Ala Thr Thr Val
465                 470                 475                 480

Tyr Gly Gln Asn Ile Tyr Ile Thr Gly Asp Val Ser Glu Leu Gly Asn
                485                 490                 495

Trp Thr Pro Ala Asn Gly Val Ala Leu Ser Ser Ala Asn Tyr Pro Thr
            500                 505                 510

Trp Ser Ala Thr Ile Ala Leu Pro Ala Asp Thr Thr Ile Gln Tyr Lys
        515                 520                 525

Tyr Val Asn Ile Asp Gly Ser Thr Val Ile Trp Glu Asp Ala Ile Ser
    530                 535                 540

Asn Arg Glu Ile Thr Thr Pro Ala Ser Gly Thr Tyr Thr Glu Lys Asp
545                 550                 555                 560
```

```
Thr Trp Asp Glu Ser
                565


<210>  174
<211>  574
<212>  PRT
<213>  Meripilus giganteus

<400>  174

Arg Pro Thr Val Phe Asp Ala Gly Ala Asp Ala His Ser Leu His Ala
1               5                   10                  15


Arg Ala Pro Ser Gly Ser Lys Asp Val Ile Ile Gln Met Phe Glu Trp
            20                  25                  30


Asn Trp Asp Ser Val Ala Ala Glu Cys Thr Asn Phe Ile Gly Pro Ala
        35                  40                  45


Gly Tyr Gly Phe Val Gln Val Ser Pro Pro Gln Glu Thr Ile Gln Gly
    50                  55                  60


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


Lys Arg Gly Asp Arg Ser Gln Phe Ala Asn Met Ile Thr Thr Cys His
                85                  90                  95


Ala Ala Gly Val Gly Val Ile Val Asp Thr Ile Trp Asn His Met Ala
            100                 105                 110


Gly Val Asp Ser Gly Thr Gly Thr Ala Gly Ser Ser Phe Thr His Tyr
        115                 120                 125


Asn Tyr Pro Gly Ile Tyr Gln Asn Gln Asp Phe His His Cys Gly Leu
    130                 135                 140


Glu Pro Gly Asp Asp Ile Val Asn Tyr Asp Asn Ala Val Glu Val Gln
145                 150                 155                 160
```

```
Thr Cys Glu Leu Val Asn Leu Ala Asp Leu Ala Thr Asp Thr Glu Tyr
                165                 170                 175

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

Ala Asp Gly Leu Arg Leu Asp Ala Ser Lys His Ile Pro Val Gly Asp
        195                 200                 205

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

Glu Val Ile Phe Gly Ala Gly Glu Pro Ile Thr Pro Asn Gln Tyr Thr
225                 230                 235                 240

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

Ala Phe Leu Ser Ser Gly Ile Ser Asn Leu Gln Asp Phe Glu Asn Arg
            260                 265                 270

Gly Trp Val Pro Gly Ser Gly Ala Asn Val Phe Val Val Asn His Asp
        275                 280                 285

Thr Glu Arg Asn Gly Ala Ser Leu Asn Asn Asn Ser Pro Ser Asn Thr
    290                 295                 300

Tyr Val Thr Ala Thr Ile Phe Ser Leu Ala His Pro Tyr Gly Thr Pro
305                 310                 315                 320

Thr Ile Leu Ser Ser Tyr Asp Gly Phe Thr Asn Thr Asp Ala Gly Ala
                325                 330                 335

Pro Asn Asn Asn Val Gly Thr Cys Ser Thr Ser Gly Gly Ala Asn Gly
            340                 345                 350

Trp Leu Cys Gln His Arg Trp Thr Ala Ile Ala Gly Met Val Gly Phe
        355                 360                 365
```

```
Arg Asn Asn Val Gly Ser Ala Ala Leu Asn Asn Trp Gln Ala Pro Gln
    370                 375                 380


Ser Gln Gln Ile Ala Phe Gly Arg Gly Ala Leu Gly Phe Val Ala Ile
385                 390                 395                 400


Asn Asn Ala Asp Ser Ala Trp Ser Thr Thr Phe Thr Thr Ser Leu Pro
                405                 410                 415


Asp Gly Ser Tyr Cys Asp Val Ile Ser Gly Lys Ala Ser Gly Ser Ser
            420                 425                 430


Cys Thr Gly Ser Ser Phe Thr Val Ser Gly Gly Lys Leu Thr Ala Thr
        435                 440                 445


Val Pro Ala Arg Ser Ala Ile Ala Val His Thr Gly Gln Lys Gly Ser
    450                 455                 460


Gly Gly Gly Ala Thr Ser Pro Gly Gly Ser Ser Gly Ser Val Glu Val
465                 470                 475                 480


Thr Phe Asp Val Tyr Ala Thr Thr Val Tyr Gly Gln Asn Ile Tyr Ile
                485                 490                 495


Thr Gly Asp Val Ser Glu Leu Gly Asn Trp Thr Pro Ala Asn Gly Val
            500                 505                 510


Ala Leu Ser Ser Ala Asn Tyr Pro Thr Trp Ser Ala Thr Ile Ala Leu
        515                 520                 525


Pro Ala Asp Thr Thr Ile Gln Tyr Lys Tyr Val Asn Ile Asp Gly Ser
    530                 535                 540


Thr Val Ile Trp Glu Asp Ala Ile Ser Asn Arg Glu Ile Thr Thr Pro
545                 550                 555                 560


Ala Ser Gly Thr Tyr Thr Glu Lys Asp Thr Trp Asp Glu Ser
                565                 570
```

```
<210>  175
<211>  671
<212>  PRT
<213>  Chaetomium megalocarpum

<400>  175

Leu Tyr Ile Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys Gln Gly Glu Ile Leu Lys Ala Ile Glu Leu Ala Arg Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Val Asp Glu
        35                  40                  45


Val Ile Ala Ala Phe Ser Arg Leu Ser Gln Pro Leu Ser Asn Asn Ser
    50                  55                  60


Glu Leu Thr Ala Phe Leu Ala Glu Asn Phe Ala Pro Ala Gly Gly Glu
65                  70                  75                  80


Leu Glu Glu Val Pro Ile Ser Glu Leu Glu Thr Asp Pro Ser Phe Leu
                85                  90                  95


Asn Lys Leu Glu Asp Val Asp Ile Lys Glu Phe Val Gly Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Gly Asn Cys
        115                 120                 125


Ser Gln Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160


Leu Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr Gln Ile Ser Lys
                165                 170                 175
```

```
Asn Met Ile Glu Asn Phe Leu Asp Phe Val Glu Thr Ile Gly Phe Val
            180                 185                 190


Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205


Leu Thr Leu Met Val Lys Thr Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220


Ile Leu Glu Arg Ala Leu Pro Leu Leu Val Lys Glu Tyr Glu Phe Trp
225                 230                 235                 240


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


Thr Leu Asn Arg Tyr Ser Val Asn Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Tyr Arg Glu Asp Tyr Val Thr Ala Asn Asn Ala Ser Tyr Tyr Ala Gln
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Glu Thr Glu Lys
    290                 295                 300


Ala Glu Leu Tyr Ser Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320


Tyr Thr Ala Arg Trp Leu Lys Thr Pro Asp Asp Ala Ala Arg Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Val Arg Ser Ile Val Ser Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Ile Ser Glu Tyr Leu
        355                 360                 365


Glu Gln Ala Gly Asn Ser Ser Glu Ala Lys Arg Phe Ala Asp Ala Ala
    370                 375                 380
```

```
Glu Gln Arg Ser Glu Ala Met Tyr Ala Leu Met Trp Asn Ala Thr His
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Asp Asn Ser Gln Arg Val Phe
                405                 410                 415


Val Pro Ala Asp Ala Asp Thr Ala Pro Ser Asp Gln Thr Ala Ala Pro
            420                 425                 430


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


Thr Gly Ala Ala Pro Ala Ser Leu Lys Ala Asn Pro Leu Ala Val Gln
    450                 455                 460


Asn Ala Tyr Ala Arg Val Ala Arg Met Leu Asp Thr Lys Ala Gly Ala
465                 470                 475                 480


Ile Ala Ala Thr Asn Leu Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Ile Leu Met Lys Gly Leu Leu Asn Thr
            500                 505                 510


Pro Ala Thr Phe Gly Thr Glu Asp Pro Ala Tyr Ala His Thr Gln Asp
        515                 520                 525


Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Ala Thr Pro Gln Leu Gln Gly
545                 550                 555                 560


Ala Ala Pro Gly Ala Thr Gly Thr Met Phe Glu Lys Tyr Ala Asp Asp
                565                 570                 575


Ala Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590
```

```
Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Gly
        595                 600                 605


Asp Arg Leu Val Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala His Thr
    610                 615                 620


His Ser Ser Glu Lys Arg Thr Val Ala Gly Ala Ser Arg Pro Asp Ala
625                 630                 635                 640


Gly Ala Ser Gly Val Arg Arg Glu Arg Arg Ala Val Glu Leu Asp Pro
                645                 650                 655


Trp Asp Ala Ala Trp Thr Lys Met Phe Gly Arg Ser Lys Leu Arg
            660                 665                 670


<210>  176
<211>  662
<212>  PRT
<213>  Lecanicillium psalliotae

<400>  176

Leu Tyr Gln Asn Gly Ser Val Ile Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys His Gly Asp Ile Leu Lys Glu Val Glu Leu Ala Arg Pro Phe Thr
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Ala Lys Lys Pro Leu Ala Glu
        35                  40                  45


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


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


Leu Lys Ala Val Ser Lys Asp Lys Leu Lys Thr Asp Ala Lys Phe Val
                85                  90                  95


Asp Lys Leu Asn Asp Thr Val Ile Lys Glu Phe Val Asn Lys Val Ile
```

```
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Glu Tyr Ala Gly Ser Ala Thr Asn
        115                 120                 125


Cys Thr Asn Cys Pro Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val
    130                 135                 140


Val Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp
145                 150                 155                 160


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


Lys Asn Thr Ile Glu Asn Phe Leu Asp Leu Ile Glu Gln Phe Gly Phe
            180                 185                 190


Ile Pro Asn Gly Ala Arg Leu Tyr Tyr Leu Asn Arg Ser Gln Pro Pro
        195                 200                 205


Leu Leu Ser Gln Met Val Lys Asn Tyr Ile Ser Tyr Thr Asn Asp Thr
    210                 215                 220


Asp Ile Leu Lys Arg Ala Leu Pro Ile Leu Val Lys Glu His Glu Phe
225                 230                 235                 240


Phe Met Asn Asn Arg Ser Val Glu Ile Thr Val Glu Asn Lys Thr Tyr
                245                 250                 255


Thr Leu Asn Arg Tyr Ala Val Ser Asn Thr Gln Pro Arg Pro Glu Ser
            260                 265                 270


Phe Arg Glu Asp Tyr Asn Thr Val Asn Asn Asn Ser Tyr Tyr Ala Ala
        275                 280                 285


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


Ala Thr Leu Tyr Ala Asn Leu Ala Ser Gly Ala Glu Ser Gly Leu Asp
```

```
305                 310                 315                 320


Tyr Thr Thr Ala Lys Trp Ser Thr Asn Pro Arg Asp Ser Met Glu Asp
                325                 330                 335


Ile Tyr Phe Pro Leu Arg Ser Leu Asn Ile Met Asn Ile Val Pro Val
            340                 345                 350


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


Tyr Asn Ile Thr Gly Asn Ser Ser Glu Ala Asp Ser Trp Ser Lys Lys
    370                 375                 380


Ala Ala Glu Arg Gln Glu Ala Ile Gln Ala Val Phe Trp Asn Glu Thr
385                 390                 395                 400


Leu Tyr Ser Tyr Phe Asp Tyr Asn Arg Thr Ser Ser Ser Gln His Ile
                405                 410                 415


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


Pro Ala Gly Met Gln Glu Val Phe Thr Val Thr Gln Phe Tyr Pro Phe
        435                 440                 445


Trp Met Gly Ala Ala Pro Asp Tyr Ile Arg Asn Asn Pro His Ala Val
    450                 455                 460


Lys Thr Ala Tyr Ser Arg Ile Ala Lys Tyr Leu Glu Leu Lys Pro Gly
465                 470                 475                 480


Gly Ile Pro Ser Ser Asn Leu Arg Ser Gly Gln Gln Trp Asp Gln Pro
                485                 490                 495


Ser Val Trp Pro Pro Leu Met His Val Leu Met Lys Gly Leu Val Asn
            500                 505                 510


Thr Pro Ala Thr Phe Gly Lys Glu Asp Pro Ala Tyr Lys Asp Val His
```

```
        515                 520                 525


Lys Leu Ala Leu Thr Leu Gly Gln Arg Tyr Leu Asp Ser Thr Phe Cys
    530                 535                 540


Thr Trp Tyr Ala Thr Gly Gly Ser Thr Ser Glu Thr Pro Gln Leu Ser
545                 550                 555                 560


Gly Leu Ser Asp Ser Asp Val Gly Ile Met Phe Glu Lys Tyr Asp Asp
                565                 570                 575


Thr Ser Ile Asn His Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu
            580                 585                 590


Gly Phe Gly Trp Ser Asn Gly Val Leu Met Trp Val Ala Asp Thr Phe
        595                 600                 605


Gly Asn Glu Leu Lys Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala Asn
    610                 615                 620


Val His Pro Gly Lys Arg Ser Val Ser Ala Val Glu Leu Ser Ser Arg
625                 630                 635                 640


Asp Ala Gln Arg Val Lys Lys Phe Gly Arg Arg Ala Glu Gly Arg Met
                645                 650                 655


Lys Val Pro Gly Val Leu
            660


<210>  177
<211>  637
<212>  PRT
<213>  Doratomyces sp.

<400>  177

Leu Tyr Thr Asn Gly Ser Ile Ile Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys His Gly Asp Ile Leu His Gln Val Gln Leu Ala His Pro Phe Pro
            20                  25                  30
```

```
Asp Ser Lys Thr Phe Val Asp Met Pro Ala Ile Lys Ser Val Asp Glu
        35                  40                  45

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

Ala Leu Gln Asn Phe Leu Ala Glu Asn Phe Ala Glu Ala Gly His Glu
65                  70                  75                  80

Leu Ala Glu Val Asp Pro Ser Glu Leu Ser Thr Asp Pro Arg Phe Leu
                85                  90                  95

Asp Lys Val Ser Asp Thr Val Ile His Glu Phe Thr Gln Lys Val Ile
            100                 105                 110

Asp Ile Trp Pro Asp Leu Thr Arg Ser Tyr Ser Pro Ser Gly Ala Gly
        115                 120                 125

Ser Asp Cys Pro Asp Cys Pro Asn Ser Phe Leu Pro Val Asn Arg Thr
    130                 135                 140

Phe Val Val Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser
145                 150                 155                 160

Tyr Trp Ile Val Glu Gly Leu Leu Arg Thr Gly Gly Asp Phe Leu Gly
                165                 170                 175

Val Ser Arg Asn Ile Ile Glu Asn Phe Leu Asp Phe Val Asp Asp Phe
            180                 185                 190

Gly Phe Val Pro Asn Gly Ala Arg Arg Tyr Tyr Leu Asn Arg Ser Gln
        195                 200                 205

Pro Pro Leu Leu Ser Leu Met Val Lys Ser Tyr Val Glu Gln Thr Asn
    210                 215                 220

Asp Thr Glu Ile Leu Asp Arg Ala Val Pro Leu Leu Ile Lys Glu Tyr
225                 230                 235                 240
```

```
Glu Phe Trp Thr Lys Asn Arg Thr Val Glu Val Pro Phe Gly Asn Glu
                245                 250                 255

Thr Ile Thr Leu Asn Gln Tyr Asn Val Asp Asn Thr Gln Pro Arg Pro
            260                 265                 270

Glu Ser Tyr Arg Glu Asp Tyr Ile Thr Ala Thr Asn Ala Ser Tyr Tyr
        275                 280                 285

Ser Ala Ser Gly Glu Val Tyr Glu Glu Val Glu Lys Leu Asn Glu Thr
    290                 295                 300

Gln Arg Ala Thr Val Tyr Arg Asn Leu Ala Thr Gly Ala Glu Ser Gly
305                 310                 315                 320

Trp Asp Tyr Thr Ser Arg Trp Met Ala Arg Pro Arg Asp Ala Val Glu
                325                 330                 335

Asp Val Tyr Phe Pro Leu Arg Ser Leu Asn Ile Ile Glu Ile Val Pro
            340                 345                 350

Val Asp Leu Asn Ser Ile Leu Tyr Ala Asn Glu Leu Ala Ile Ala Glu
        355                 360                 365

Phe Val Arg Leu Ala Gly Ala Asp Asp Cys Glu Glu Glu Ala Ala Ala
    370                 375                 380

Trp Glu Ala Leu Ala Glu Lys Arg Ser Ala Asp Met His Arg Leu Met
385                 390                 395                 400

Trp Asn Asp Thr Leu His Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ser
                405                 410                 415

Ser Gln Asn Val Tyr Val Pro Ala Asp Asn Asp Thr Ala Pro Phe Glu
            420                 425                 430

Arg Pro Gly Gly Thr Pro Glu Gly Ser Gln Val Phe Phe Ser Ala Ala
        435                 440                 445
```

```
Gln Phe Tyr Pro Phe Trp Thr Gly Ala Ala Pro Ser Ser Leu Arg Asp
    450                 455                 460


Asp Pro Ala Ala Val Gln Leu Ala Tyr Ser Arg Val Ala Ser Tyr Leu
465                 470                 475                 480


Asp Leu Arg Ala Gly Gly Ile Pro Ala Thr Asn Leu Arg Thr Gly Gln
                485                 490                 495


Gln Trp Asp Gln Pro Ser Val Trp Pro Pro Leu Met His Ile Leu Thr
            500                 505                 510


Ser Gly Leu Leu Asn Thr Ser Pro Ala Ser Ala Ser Asp Asp Asp Asp
        515                 520                 525


Pro Ser Tyr Ala Pro Thr Arg Asp Leu Ala Leu Ser Leu Ala Gln Arg
    530                 535                 540


Tyr Leu Asp Ser Thr Phe Cys Thr Trp Tyr Ala Thr Gly Gly Ser Thr
545                 550                 555                 560


Ser Glu Thr Pro Gln Leu Asp Gly Phe Thr Asp Glu Asp Lys Gly Ala
                565                 570                 575


Met Phe Glu Lys Tyr Asp Asp Ser Ala Thr Asn Val Ala Gly Gly Gly
            580                 585                 590


Gly Glu Tyr Glu Val Val Glu Gly Phe Gly Trp Thr Asn Gly Val Leu
        595                 600                 605


Ile Trp Met Val Asp Thr Phe Gly Asp Glu Leu Ser Arg Pro Asp Cys
    610                 615                 620


Gly Asp Ile Glu Ala Ala Asn Ala His Pro Ala Arg Lys
625                 630                 635


<210>  178
<211>  601
```

```
<212>  PRT
<213>  Mucor moelleri

<400>  178

Ile Gln Asn His Thr Ser Phe Ser Cys Asp Ser Pro Ile Tyr Cys Glu
1               5                   10                  15


Gly Asp Ile Leu His Thr Val Gln Leu Ala Lys Ile Phe Ser Asp Ser
            20                  25                  30


Lys Thr Phe Val Asp Met Pro Thr Ser Lys Ser Glu Ser Gln Val Ile
        35                  40                  45


Glu Ala Phe Lys Ala Ile Gly Gly Arg Asn Ala Thr Ile Ala Gln Val
    50                  55                  60


Gln Gln Phe Leu Asn Glu Asn Phe Leu Thr Ala Gly Thr Glu Val Lys
65                  70                  75                  80


Arg Leu Thr Asn Ile Thr Ile Pro Glu Leu Asn Trp Ile Asp Asn Ile
                85                  90                  95


Thr Asp Pro Asp Tyr Arg Gly Trp Ile Ser Lys Leu Asn Gln Ala Trp
            100                 105                 110


Ser Asn Leu Thr Phe Thr Phe Asp Thr Ser Val Leu Cys Gln Asp Cys
        115                 120                 125


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


Arg Phe Arg Glu Phe Tyr Tyr Trp Asp Ser Phe Phe Val Ile Lys Gly
145                 150                 155                 160


Leu Leu Leu Ser Asp Gln Val Glu Leu Ala Lys Asn Met Ile Leu Asn
                165                 170                 175


Phe Phe Asp Phe Ile Asp Thr Tyr Gly Phe Ile Pro Asn Gly Ala Arg
            180                 185                 190
```

```
Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Phe Leu Thr Gln Met Val
        195                 200                 205


Glu Ala Phe Trp Glu Lys Thr Ser Asp Lys Glu Phe Met Thr Asn Ala
    210                 215                 220


Leu Pro Phe Leu Asp Lys Glu Tyr Asn Phe Trp Met Thr Asn Asn Ser
225                 230                 235                 240


Ile Ser Val Pro Asp Pro Lys Asn Pro Ser Lys Lys Tyr Lys Met Asn
                245                 250                 255


His Tyr Val Thr Leu Asn Thr Ser Pro Arg Pro Glu Ser Tyr Val Glu
            260                 265                 270


Asp Tyr Asn Thr Val Asn Asn Gly Thr Asp Tyr Ser Gln Ala Val Lys
        275                 280                 285


Leu Gln Leu Tyr Ala Asp Ile Ala Ala Gly Ala Glu Thr Gly Trp Asp
    290                 295                 300


Tyr Ser Ser Arg Trp Thr Arg Gln Lys His Pro Ala Pro Asn Gln Thr
305                 310                 315                 320


Glu Gly Tyr Glu Met Leu Arg Ser Ile Asn Thr Ala Asn Ile Val Pro
                325                 330                 335


Ile Asp Leu Asn Ser Leu Leu Trp Asn Thr Glu Thr Met Leu Ala Glu
            340                 345                 350


Trp His Asp Arg Phe Gly Glu Lys Ser Lys Ser Lys Lys Lys Ser Ala
        355                 360                 365


Tyr Tyr Gln Thr Gln Ala Lys Lys Arg Leu Asp Ala Met Glu Lys Leu
    370                 375                 380


Met Trp Asn Pro Thr Asp Tyr Thr Tyr Tyr Asp Tyr Asn Leu Thr Ser
385                 390                 395                 400
```

```
Ser Ser Gln Asn Leu Glu Phe Thr Pro Ala Asn Leu Phe Pro Ile Trp
                405                 410                 415

Leu Gly Ala Leu Pro Asn Lys Val Met Lys Asn Lys Thr Glu Leu Ala
            420                 425                 430

Arg Val Phe Asp Glu Thr Glu Asn Ala Leu Arg Lys Tyr Pro Gly Ile
        435                 440                 445

Leu Thr Thr Ser Tyr Tyr Asn Thr Thr Met Gln Trp Asp Trp Pro Asn
    450                 455                 460

Gly Trp Pro Pro Leu Ser Tyr Val Ala Met Glu Gly Met Asn Lys Val
465                 470                 475                 480

Glu Glu Ser Leu Asn Gly Lys Lys Gly Ser Lys Gln Asp Gly Lys Thr
                485                 490                 495

Tyr Thr Thr Ser Arg Gly Thr Ser Leu Ala Arg Leu Ser Phe Thr Leu
            500                 505                 510

Ala Glu Arg Tyr Ala Ala Ser Ala Tyr Cys Gly Trp Tyr Lys Thr Gly
        515                 520                 525

Gly Ser Ile Pro Gly Ile Leu Asn Lys Ile Asp Gly Val Ala Asp Asp
    530                 535                 540

Gly His Met Phe Glu Lys Phe Asp Val Asn Thr Ile Gly Ile Ser Gly
545                 550                 555                 560

Ser Gln Gly Glu Tyr Val Ser Gln Thr Gly Phe Gly Trp Thr Asn Gly
                565                 570                 575

Ile Ala Leu Trp Ile Phe Asp Thr Tyr Ala Asn Leu Thr Ala Pro Asp
            580                 585                 590

Cys Asn Gln Thr Ile Thr Leu Asn Ile
        595                 600
```

```
<210>  179
<211>  650
<212>  PRT
<213>  Phialophora cyclaminis

<400>  179

Leu Tyr Ile Asn Gly Ser Val Ile Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys His Gly Glu Leu Leu Lys Ala Ile Glu Leu Ala Arg Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Arg Lys Pro Val Asp Glu
        35                  40                  45


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


Lys Leu Gly Glu Phe Leu Gln Ala Asn Phe Leu Pro Ala Gly Gly Asp
65                  70                  75                  80


Leu Ser Asp Phe Pro Pro Gly Ser Leu Glu Thr Asp Pro Lys Phe Leu
                85                  90                  95


Asp Asn Ile Asn Asp Thr Val Ile Arg Glu Phe Thr Glu Ala Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Val Gly Ala Ser Asn Cys
        115                 120                 125


Thr Gly Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160


Ile Glu Gly Leu Leu Arg Thr Gly Gly Asn Phe Val Gln Ile Ser Lys
                165                 170                 175
```

```
Asn Ile Ile Glu Asn Phe Leu Asp Phe Val Glu Thr Ile Gly Phe Val
            180                 185                 190


Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205


Leu Thr Ala Met Val Lys Ala Tyr Leu Glu His Thr Asn Asp Thr Lys
    210                 215                 220


Ile Leu Asp Arg Ala Val Pro Leu Leu Ile Lys Glu Tyr Asn Phe Trp
225                 230                 235                 240


Ile Thr Asn Arg Ser Val Thr Leu Thr Gly Pro Asp Gly Asn Glu Tyr
                245                 250                 255


Thr Leu Gln Arg Tyr Ser Val Asn Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Tyr Arg Glu Asp Tyr Asn Thr Ala Asn Asn Lys Ser Tyr Tyr Ser Thr
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Glu Asn Val Ser Leu Asn Asp Ser Glu Lys
    290                 295                 300


Lys Glu Leu Tyr Ala Asn Leu Ala Thr Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320


Tyr Gly Thr Arg Trp Leu Ser Arg Pro Ala Asp Ala Leu Arg Asp Val
                325                 330                 335


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


Leu Asn Ala Ile Leu Tyr Gln Asn Glu Ala Ser Ile Ser Ser Phe Leu
        355                 360                 365


Tyr Ile Gln Gly Asn Asp Thr Gly Ala Ala His Phe Ala Lys Leu Ala
    370                 375                 380
```

```
Ala Ala Arg Gln Lys Ala Met Thr Ala Val Leu Trp Asn Ala Thr Leu
385                 390                 395                 400


Phe Ser Tyr Phe Asp Tyr Asn Met Thr Ser Ser Ser His Phe Ser Phe
                405                 410                 415


Ile Pro Val Asp Asp Asp Ala Thr Ser Ile Glu Thr Ala Thr Ala Pro
            420                 425                 430


Arg Gly Phe Gln Gln Ile Phe His Val Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Ala Ser Leu Arg Glu Asn Pro Leu Ala Val Gln
    450                 455                 460


Arg Ala Phe Ser Arg Val Ser Gln Met Leu Glu Glu Lys Ala Gly Ser
465                 470                 475                 480


Ile Pro Ala Thr Asn Phe Tyr Thr Gly Gln Gln Trp Asp Glu Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Ile Ile Met Glu Gly Leu Arg Asn Thr
            500                 505                 510


Pro Ala Thr Phe Gly Glu Asp Asp Pro Ile Tyr Gln Gly Val Gln Asp
        515                 520                 525


Leu Ala Leu Arg Val Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Leu Thr Pro Lys Leu Ala Gly
545                 550                 555                 560


Leu Thr Asp Asn Ala Lys Gly Ile Met Phe Glu Lys Tyr Gly Asp Asn
                565                 570                 575


Ser Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590
```

```
Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Val Asp Thr Phe Gly
        595                 600                 605


Asn Lys Leu Lys Arg Pro Asp Cys Gly Asp Ile Gln Pro Ala His Val
    610                 615                 620


Glu Ala Arg Gly Leu Gln Arg Arg Ala Val Glu Leu Asp Lys Trp Asp
625                 630                 635                 640


Ala Gln Trp Val Lys Arg Phe Gly Ala Lys
                645                 650


<210>  180
<211>  654
<212>  PRT
<213>  Thielavia arenaria

<400>  180

Leu Tyr Ile Asn Gly Ser Val Ile Ala Pro Cys Asp Ser Pro Leu Tyr
1               5                   10                  15


Cys His Gly Asp Ile Leu Lys Ala Ile Glu Leu Ala Arg Pro Phe Gln
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Arg Pro Val Glu Glu
        35                  40                  45


Val Ile Ala Ala Phe Asn Arg Leu Ser Gln Pro Leu Ser Asn Asn Ser
    50                  55                  60


Glu Leu Asn Ala Phe Leu Gln Ala Asn Phe Ala Pro Ala Gly Gly Glu
65                  70                  75                  80


Leu Glu Glu Val Pro Glu Ser Glu Leu Ser Thr Asn Pro Val Phe Leu
                85                  90                  95


Asp Lys Leu Asn Asp Thr Val Ile Lys Glu Phe Val Ala Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Gly Asn Cys
```

```
        115                 120                 125


Ser Glu Cys Ala Asp Ser Phe Ile Pro Val Asn Arg Thr Phe Val Ile
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Phe Trp Ile
145                 150                 155                 160


Leu Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr Glu Ile Ser Lys
                165                 170                 175


Asn Met Ile Glu Asn Phe Leu Asp Phe Val Glu Thr Ile Gly His Ile
            180                 185                 190


Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205


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


Ile Leu Glu Arg Ala Leu Pro Leu Leu Ile Lys Glu Tyr Glu Phe Trp
225                 230                 235                 240


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


Thr Leu His Arg Tyr Asn Val Asn Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Tyr Arg Glu Asp Trp Ile Thr Ala Asn Asn Ala Ser Tyr Tyr Ala Ala
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Glu Ser Glu Lys
    290                 295                 300


Ala Ala Leu Tyr Ser Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320


Tyr Gly Thr Arg Phe Leu Met Arg Pro Glu Asp Ala Ala Arg Asp Ile
```

```
                325                 330                 335

Tyr Phe Pro Leu Arg His Leu Asn Val Arg Asp Met Val Thr Val Asp
            340                 345                 350

Leu Asn Ala Ile Leu Tyr Gln Asn Glu Val Ile Ile Ser Glu Tyr Leu
        355                 360                 365

Glu Gln Ala Gly Asn Asn Thr Glu Ala Glu Arg Phe Ala Ser Ala Ala
    370                 375                 380

Arg Gln Arg Ser Glu Ala Met Tyr Ala Leu Met Trp Asn Glu Thr Leu
385                 390                 395                 400

Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Asn Ser Gln Tyr Thr Phe
                405                 410                 415

Ile Pro Ala Asp Val Asn Ala Thr Ala Ala Glu Lys Ala Asn Ala Pro
            420                 425                 430

Glu Gly Gln Lys Val Ile Phe His Ile Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445

Thr Gly Ala Ala Pro Asp Gln Leu Lys Asn Asn Pro Leu Ala Val Gln
    450                 455                 460

Lys Ala Tyr Ser Arg Val Ala Glu Met Leu Asp Ile Lys Pro Gly Ala
465                 470                 475                 480

Ile Pro Ala Thr Asn Phe Ile Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495

Val Trp Pro Pro Leu Met His Val Leu Met Ala Gly Leu Leu Asn Thr
            500                 505                 510

Pro Pro Thr Phe Gly Glu Asp Asp Pro Ala Tyr Gln Ala Val Gln Ala
        515                 520                 525

Leu Ala Leu Arg Leu Gly Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
```

```
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Glu Thr Ser Gln Thr Pro Arg Leu Gln Gly
545                 550                 555                 560


Val Ser Pro Asp Ala Thr Gly Thr Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575


Ala Ile Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Ala
        595                 600                 605


Asn Gly Leu Lys Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala His Thr
    610                 615                 620


His Asn Gly Ala Lys Arg Ala Val Glu Leu His Pro Arg Asp Ala Ala
625                 630                 635                 640


Trp Thr Lys Lys Phe Gly Lys Arg Ala Leu Lys Lys Arg Ala
                645                 650


<210>  181
<211>  661
<212>  PRT
<213>  Thielavia antarctica

<400>  181

Leu Tyr Val Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Leu Tyr
1               5                   10                  15


Cys Gln Gly Glu Ile Leu Lys Ala Ile Glu Leu Ala Arg Pro Phe Ala
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Leu Arg Pro Leu Asp Asp
        35                  40                  45


Val Ile Ala Ala Phe Arg Lys Leu Ser Gln Pro Leu Ser Asn Ser Ser
    50                  55                  60
```

```
Glu Leu Asn Ala Phe Leu Ala Ala Asn Phe Ala Pro Ala Gly Gly Glu
65                  70                  75                  80


Leu Glu Glu Val Pro Lys Ser Glu Leu Arg Thr Lys Pro Ala Phe Leu
                85                  90                  95


Asp Lys Val Glu Asp Val Val Ile Lys Glu Phe Val Gly Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Gly Asn Cys
        115                 120                 125


Thr Glu Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160


Leu Glu Gly Leu Leu Arg Thr Gly Gly Asp Phe Thr Lys Ile Ser Arg
                165                 170                 175


Asn Ile Ile Glu Asn Phe Leu Asp Phe Val Asp Thr Ile Gly Phe Val
            180                 185                 190


Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Val
        195                 200                 205


Leu Thr Leu Met Val Lys Thr Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220


Ile Leu Glu Arg Ala Leu Pro Leu Leu Ile Lys Glu His Glu Phe Trp
225                 230                 235                 240


Thr Thr Asn Arg Ser Val Ser Val Glu Val Asp Gly Lys Thr His Thr
                245                 250                 255


Leu Asn Arg Tyr Phe Val Asn Asn Asn Gln Pro Arg Pro Glu Ser Tyr
            260                 265                 270
```

```
Arg Glu Asp Trp Ile Thr Ala Asn Asn Ala Ser Tyr Tyr Ala Ala Ser
        275                 280                 285

Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Gly Thr Gln Gln Ala
    290                 295                 300

Glu Leu Tyr Ala Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp Tyr
305                 310                 315                 320

Thr Ser Arg Trp Leu Lys Thr Pro Ser Asp Ala Ala Arg Asp Val Tyr
                325                 330                 335

Phe Pro Leu Arg Ser Leu Asn Val Ile Asn Thr Ile Pro Val Asp Leu
            340                 345                 350

Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Ile Ser Glu Tyr Leu Glu
        355                 360                 365

Gln Ala Gly Asn Lys Ser Gly Ala Glu Lys Phe Ser Asp Ala Ala Arg
    370                 375                 380

Gln Arg Ser Glu Ala Met Tyr Ala Leu Met Trp Asn Ala Thr Asn Trp
385                 390                 395                 400

Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ser Gly Gln Asn Thr His Phe
                405                 410                 415

Pro Ala Asp Ala Asp Ala Thr Ala Ala Glu Thr Thr Ser Ser Pro Ala
            420                 425                 430

Gly Thr Gln Leu Leu Phe Ser Val Ser Gln Leu Tyr Pro Phe Trp Thr
        435                 440                 445

Gly Ala Ala Pro Gln Gln Leu Lys Ser Asn Pro Leu Ala Val Thr Gln
    450                 455                 460

Ala Tyr Ala Arg Val Ala Ala Met Leu Asp Ala Lys Ala Gly Ala Ile
465                 470                 475                 480
```

```
Pro Ala Thr Asn Leu Leu Thr Gly Gln Gln Trp Asp Glu Pro Asn Val
                485                 490                 495

Trp Pro Pro Leu Gln His Val Leu Met Gln Gly Leu Leu Asn Thr Pro
            500                 505                 510

Ala Thr Phe Gly Ala Asp Asp Pro Ala Tyr Gln Ala Thr Gln Ala Leu
        515                 520                 525

Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr Trp
    530                 535                 540

Tyr Ala Thr Gly Gly Ser Thr Ser Ala Thr Pro Arg Leu Ala Gly Val
545                 550                 555                 560

Ser Ala Gly Ala Glu Gly Ser Met Phe Glu Lys Tyr Gly Asp Asp Ser
                565                 570                 575

Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly Phe
            580                 585                 590

Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Ala Gly
        595                 600                 605

Lys Leu Gln Arg Pro Glu Cys Gly Asp Ile Glu Ala Ala Gln Thr His
    610                 615                 620

Gly Gly Ala Ala Arg Arg Gly Leu Gly Met Glu Arg Arg Ala Ile Glu
625                 630                 635                 640

Leu Asp Pro Trp Asp Ala Arg Trp Thr Lys Ala Phe Gly Lys Arg Ala
                645                 650                 655

Leu Arg Arg Arg Ala
            660


<210>  182
<211>  667
```

```
<212>  PRT
<213>  Chaetomium sp.

<400>  182

Leu Tyr Ile Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Leu Tyr
1               5                   10                  15


Cys Gln Gly Glu Ile Leu Lys Ala Ile Glu Leu Ala Arg Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Val Asp Asp
        35                  40                  45


Val Ile Ala Ala Phe Ser Arg Leu Ser Gln Pro Leu Ser Asn Asn Ser
    50                  55                  60


Glu Leu Asn Ala Phe Leu Ala Glu Asn Phe Ala Pro Ala Gly Gly Glu
65                  70                  75                  80


Leu Glu Glu Val Pro Glu Ser Glu Leu Glu Thr Asp Pro Ala Phe Leu
                85                  90                  95


Asp Lys Leu Glu Asp Thr Thr Ile Lys Glu Phe Val Thr Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Gly Asn Cys
        115                 120                 125


Ser Lys Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160


Leu Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr Glu Ile Ser Lys
                165                 170                 175


Asn Ile Ile Glu Asn Phe Leu Asp Phe Val Asp Thr Ile Gly Phe Ile
            180                 185                 190
```

```
Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205


Leu Thr Leu Met Val Lys Thr Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220


Ile Leu Glu Arg Ala Leu Pro Leu Leu Ile Lys Glu His Glu Phe Trp
225                 230                 235                 240


Thr Asn Asn Arg Ser Val Ala Ile Thr Ala Ala Asp Gly Lys Lys Tyr
                245                 250                 255


Thr Leu Gln Arg Tyr Tyr Val Asn Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Phe Arg Glu Asp Tyr Ile Thr Ala Asn Asn Ala Ser Tyr Tyr Ala Ala
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Glu Thr Glu Lys
    290                 295                 300


Ala Glu Leu Tyr Ser Asn Leu Ala Ser Gly Ala Glu Ala Gly Trp Asp
305                 310                 315                 320


Tyr Thr Ala Arg Trp Leu Lys Thr Pro Asn Asp Ala Ala Arg Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Val Ile Gly Met Val Pro Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Ile Ala Glu Tyr Leu
        355                 360                 365


Gln Gln Ala Gly Asn Ser Ser Glu Ala Arg Arg Phe Ala Thr Ala Ala
    370                 375                 380


Glu Lys Arg Ser Glu Ala Met Tyr Ala Leu Met Trp Asn Ser Thr His
385                 390                 395                 400
```

```
Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Asn Ser Gln Arg Ile Phe
                405                 410                 415


Val Pro Thr Asp Ala Asp Ala Asp Pro Val Asp Gln Thr Asn Ala Pro
            420                 425                 430


Pro Gly His Gln Val Leu Phe Asp Ile Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Ala Ser Leu Lys Asn Asn Pro Leu Ala Val Gln
    450                 455                 460


Leu Ala Tyr Ala Arg Val Ala His Met Leu Asp Thr Lys Ala Gly Ala
465                 470                 475                 480


Ile Pro Gly Thr Asn Phe Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Val Leu Met Lys Gly Leu Leu Asn Thr
            500                 505                 510


Pro Pro Thr Phe Gly Glu Ala Asp Pro Ala Tyr Gln Glu Val Gln Arg
        515                 520                 525


Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Asp Met Pro Gln Leu Gln Gly
545                 550                 555                 560


Val Asn Pro Gly Ala Thr Gly Thr Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575


Ala Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Gly
        595                 600                 605
```

```
Glu Gly Leu Thr Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala His Thr
    610                 615                 620


His Ser Gly Ala Lys Arg Gly Leu Asp Gly Gly Glu Gly Gly Ala Gly
625                 630                 635                 640


Gly Leu Trp Gly Arg Arg Ala Val Glu Leu Asp Pro Trp Asp Ala Arg
                645                 650                 655


Trp Thr Lys Met Phe Gly Arg Arg Lys Arg Glu
            660                 665


<210>  183
<211>  671
<212>  PRT
<213>  Chaetomium nigricolor

<400>  183

Leu Tyr Ile Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Leu Tyr
1               5                   10                  15


Cys Gln Gly Glu Ile Leu Arg Ala Ile Glu Leu Ala Arg Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Leu Glu Glu
        35                  40                  45


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


Glu Leu Asn Thr Phe Leu Ala Glu Asn Phe Ala Pro Ala Gly Gly Glu
65                  70                  75                  80


Leu Glu Glu Val Pro Lys Asp Glu Leu Asn Thr Asp Pro Gly Phe Leu
                85                  90                  95


Asp Lys Leu Asn Asp Thr Thr Ile Arg Glu Phe Val Ala Lys Val Ile
            100                 105                 110
```

```
Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Gly Gly Asn Cys
        115                 120                 125

Ser Glu Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140

Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160

Leu Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Ile Glu Ile Ser Lys
                165                 170                 175

Asn Ile Ile Glu Asn Phe Leu Asp Phe Val Glu Thr Ile Gly Phe Ile
            180                 185                 190

Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205

Leu Thr Leu Met Val Lys Thr Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220

Ile Leu Glu Arg Ala Leu Pro Leu Leu Ile Lys Glu His Glu Phe Trp
225                 230                 235                 240

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

Thr Leu Asn Arg Tyr His Val Asn Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270

Tyr Arg Glu Asp Tyr Ile Thr Ala Asn Asn Gly Ser Tyr Tyr Ala Ala
        275                 280                 285

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

Ala Glu Leu Tyr Ala Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320
```

```
Tyr Thr Ala Arg Trp Leu Lys Thr Pro Asn Asp Ala Ala Asn Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Val Arg Gly Leu Val Pro Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Ile Ala Glu Tyr Leu
        355                 360                 365


Gln Gln Ala Gly Asn Leu Ser Leu Ala Gln Arg Phe Ala Glu Ala Ala
    370                 375                 380


Glu Gln Arg Ser Glu Ala Met Tyr Ala Leu Met Trp Asn Ala Thr Tyr
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Asn Ser Gln Arg Ile Phe
                405                 410                 415


Val Pro Leu Asp Ala Asp Ser Arg Thr Ile Glu Thr Val Gly Ala Pro
            420                 425                 430


Pro Gly His Gln Val Leu Phe Asp Ile Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Ala Asn Leu Lys Asn Asn Pro Leu Ala Val Gln
    450                 455                 460


Gln Ala Tyr Ser Arg Val Ala Ser Met Leu Asp Ala Lys Ala Gly Ala
465                 470                 475                 480


Ile Pro Ala Thr Asn Phe Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Ile Leu Met Gln Gly Leu Leu Asn Thr
            500                 505                 510


Pro Pro Thr Phe Gly Asp Ser Asp Pro Ala Tyr Gln His Val Arg Asp
        515                 520                 525
```

```
Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Asp Met Pro Gln Leu Gln Gly
545                 550                 555                 560


Val Ser Pro Asp Ala Thr Gly Thr Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575


Ala Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Gly
        595                 600                 605


Asp Ala Leu Lys Arg Pro Asp Cys Gly Asp Ile Glu Ala Ala His Thr
    610                 615                 620


His Gln Ala Lys Lys Arg Asp Val Glu Gly Leu Glu Arg Arg Ala Val
625                 630                 635                 640


Glu Leu Asp Pro Trp Asp Ala Ala Trp Thr Lys Met Phe Gly Arg Ser
                645                 650                 655


Lys Leu Arg Lys Arg Gly Ala Gly Gly Gln Lys Arg Trp Val Ser
            660                 665                 670


<210>  184
<211>  666
<212>  PRT
<213>  Chaetomium jodhpurense

<400>  184

Leu Tyr Phe Asn Gly Ser Val Ile Ala Pro Cys Asp Ser Pro Leu Tyr
1               5                   10                  15


Cys Gln Gly Glu Ile Leu Lys Ala Ile Glu Leu Ala Arg Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Val Asp Glu
```

```
        35                  40                  45

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

Glu Leu Asn Ala Phe Leu Ala Glu Asn Phe Ala Pro Ala Gly Gly Glu
65                  70                  75                  80

Leu Glu Glu Val Pro Lys Asp Glu Leu Asn Thr Asp Pro Lys Phe Leu
                85                  90                  95

Asp Lys Leu Glu Asp Ala Thr Ile Lys Glu Phe Val Ala Lys Val Ile
            100                 105                 110

Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Ala Ser Asn Cys
        115                 120                 125

Ser Glu Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Ile
    130                 135                 140

Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160

Leu Glu Gly Leu Leu Arg Thr Gly Gly Ala Tyr Thr Gln Ile Ser Arg
                165                 170                 175

Asn Met Leu Glu Asn Phe Leu Asp Phe Val Glu Thr Ile Gly Phe Ile
            180                 185                 190

Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205

Leu Ala Met Met Ile Lys Asn Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220

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

Ile Asn Asn Arg Ser Val Ser Ile Thr Ala Ala Asp Gly Lys Gln Tyr
```

```
                245                 250                 255


Thr Leu His Arg Tyr Asn Val Asn Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Tyr Arg Glu Asp Tyr Ile Thr Ala Asn Asn Ala Ser Tyr Tyr Ala Ala
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Glu Ser Glu Lys
    290                 295                 300


Ala Glu Leu Tyr Ala Asn Leu Ala Thr Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320


Tyr Thr Ala Arg Trp Leu Lys Thr Pro Asn Asp Ala Ala Lys Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Val Arg Gly Met Val Ser Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Ile Ala Glu Tyr Leu
        355                 360                 365


Glu Arg Ala Gly Asn Ile Ser Glu Ala Glu Arg Phe Ala Ala Met Ala
    370                 375                 380


Gln Gln Arg Ser Glu Ala Met Tyr Ala Leu Met Trp Asn Ser Thr His
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Asn Ser Gln Arg Ile Phe
                405                 410                 415


Val Pro Leu Asp Asp Asp Ser Ser Thr Ala Glu Gln Ala Asn Ser Pro
            420                 425                 430


Pro Gly His Gln Val Leu Phe Asp Ile Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Glu Ser Leu Lys Ser Asn Pro Leu Ala Val Gln
```

```
    450                 455                 460


Leu Ala Tyr Ser Arg Val Ala Arg Met Leu Asp Thr Lys Ala Gly Ala
465                 470                 475                 480


Ile Pro Ala Thr Asn Phe Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Val Leu Met Ala Gly Leu Leu Asn Thr
            500                 505                 510


Pro Pro Thr Phe Gly Glu Ser Asp Pro Ala Tyr Gln Asn Val Arg Ala
        515                 520                 525


Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Glu Thr Ser Gln Thr Pro Arg Leu Gln Gly
545                 550                 555                 560


Val Ser Pro Asp Ala Thr Gly Thr Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575


Ala Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Ala
        595                 600                 605


Asp Gly Leu Lys Lys Pro Asp Cys Gly Asn Ile Thr Ala Ala His Thr
    610                 615                 620


His Ser Ala Lys Arg Gly Leu Glu Arg Arg Ala Val Glu Leu Asp Pro
625                 630                 635                 640


Trp Asp Ala Ala Trp Thr Lys Met Phe Gly Arg Ser Lys Leu Arg Lys
                645                 650                 655


Arg Glu Glu Gly Arg Lys Arg Trp Leu Ser
```

```
            660                 665


<210>  185
<211>  670
<212>  PRT
<213>  Chaetomium piluliferum

<400>  185

Leu Tyr Ile Asn Gly Ser Val Ile Ala Pro Cys Asp Ser Pro Leu Tyr
1               5                   10                  15


Cys His Gly Glu Ile Leu Lys Ala Ile Glu Leu Ala Arg Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Leu Asp Glu
        35                  40                  45


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


Glu Leu Asn Ala Phe Leu Ala Glu Asn Phe Ala Pro Ala Gly Gly Glu
65                  70                  75                  80


Leu Glu Glu Val Ser Lys Asp Glu Leu Gln Thr Asp Pro Thr Phe Leu
                85                  90                  95


Asp Lys Leu Asp Asp Thr Thr Ile Lys Glu Phe Val Ser Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Glu Leu Thr Arg Arg Tyr Val Gly Ser Ser Asp Cys
        115                 120                 125


Ser Gly Cys Ala Asn Ser Phe Ile Pro Ile Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160


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

```
Asn Ile Ile Glu Asn Phe Leu Asp Phe Val Glu Thr Ile Gly Phe Val
            180                 185                 190

Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205

Leu Thr Leu Met Val Lys Thr Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220

Ile Leu Glu Arg Ala Leu Pro Leu Leu Val Lys Glu His Glu Phe Trp
225                 230                 235                 240

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

Leu Asn Arg Tyr Ser Val Asn Asn Asn Gln Pro Arg Pro Glu Ser Tyr
            260                 265                 270

Arg Glu Asp Tyr Ile Thr Ala Ser Asn Glu Ser Tyr Tyr Ala Glu Ser
        275                 280                 285

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

Glu Leu Tyr Ser Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp Tyr
305                 310                 315                 320

Thr Ser Arg Trp Leu Lys Thr Pro Asn Asp Ala Ala Asn Asp Val Tyr
                325                 330                 335

Phe Pro Leu Arg Ser Leu Asn Val Leu Gly Leu Val Pro Val Asp Leu
            340                 345                 350

Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Leu Ala Glu Tyr Phe Glu
        355                 360                 365

Gln Ala Gly Asn Ser Ser Glu Ala Glu Arg Phe Ala Ala Ala Ala Glu
    370                 375                 380
```

```
Gln Arg Ser Glu Ala Met Tyr Asp Leu Met Trp Asn Ala Thr His Trp
385                 390                 395                 400


Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ser Ser Gln Arg Ile Phe Val
                405                 410                 415


Pro Leu Asp Asp Gly Ala Ser Thr Gln Glu Gln Ser Thr Ser Pro Pro
            420                 425                 430


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


Gly Ala Ala Pro Ala Ala Leu Lys Ser Asn Pro Leu Ala Val Gln His
    450                 455                 460


Ala Tyr Ser Arg Val Ala Asp Met Leu Asn Thr Lys Ala Gly Ala Ile
465                 470                 475                 480


Pro Ala Thr Asn Phe Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn Val
                485                 490                 495


Trp Pro Pro Leu Gln His Ile Ile Met Gln Gly Leu Leu Asn Thr Pro
            500                 505                 510


Pro Thr Phe Gly Glu Ser Asp Pro Ala Tyr Glu Asn Thr Gln Ser Leu
        515                 520                 525


Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr Trp
    530                 535                 540


Tyr Ala Thr Gly Gly Ser Thr Ser Asp Met Pro Pro Leu Gln Gly Val
545                 550                 555                 560


Ser Ala Gly Ala Thr Gly Thr Met Phe Glu Lys Tyr Ala Asp Asp Ala
                565                 570                 575


Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly Phe
            580                 585                 590
```

Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Gly Asp
595 600 605

Ala Leu Lys Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala Ser Thr His
610 615 620

Glu Gly Ala Thr Lys Arg Asp Leu Arg Gly Leu Gly Arg Arg Ala Val
625 630 635 640

Glu Leu Asp Pro Trp Asp Ala Ala Trp Thr Lys Met Phe Gly Arg Ala
645 650 655

Lys Leu Arg Lys Arg Glu Gln Gly Arg Glu Thr Trp Val Asn
660 665 670

<210> 186
<211> 674
<212> PRT
<213> Myceliophthora hinnulea

<400> 186

Leu Tyr Ile Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Ile Tyr
1 5 10 15

Cys His Gly Glu Leu Leu Lys Gly Val Glu Leu Ala His Pro Phe Val
20 25 30

Asp Ser Lys Thr Phe Val Asp Met Pro Thr Leu Lys Pro Val Asp Glu
35 40 45

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

Glu Leu Asn Asn Phe Leu Ala Glu Tyr Phe Ala Pro Ala Gly His Glu
65 70 75 80

Leu Glu Glu Val Pro Asp Ser Glu Leu Gln Thr Asp Pro Lys Phe Leu
85 90 95

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


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Gly Asp Cys
        115                 120                 125


Ser Asp Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160


Leu Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr Gln Ile Ser Lys
                165                 170                 175


Asn Ile Ile Glu Asn Phe Leu Asp Phe Ile Asp Thr Ile Gly Phe Ile
            180                 185                 190


Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205


Leu Thr Arg Met Val Lys Ser Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220


Ile Leu Glu Arg Ala Leu Pro Leu Leu Ile Lys Glu His Asp Phe Phe
225                 230                 235                 240


Thr Asn Asn Arg Ser Val Ser Val Thr Ala Ser Asn Gly Lys Thr Tyr
                245                 250                 255


Thr Leu His Arg Tyr His Val Glu Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Tyr Arg Glu Asp Tyr Ile Thr Ala Asn Asn Gly Ser Tyr Tyr Ala Ala
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Glu Thr Glu Lys
    290                 295                 300
```

```
Ala Val Leu Tyr Ser Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320

Tyr Thr Ala Arg Trp Leu Arg Val Pro Asp Asp Ala Ala Arg Asp Val
                325                 330                 335

Tyr Phe Pro Leu Arg Ser Leu Asn Val Arg Glu Ile Val Pro Val Asp
            340                 345                 350

Leu Asn Ser Ile Leu Tyr Glu Asn Glu Val Ile Ile Ala Gly Tyr Leu
        355                 360                 365

Glu Lys Ala Gly Asn Ser Ser Glu Ala Lys Arg Phe Ala Ser Ala Ala
    370                 375                 380

Lys Gln Arg Ser Glu Ala Met Tyr Asn Leu Met Trp Asn Ala Thr His
385                 390                 395                 400

Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Asn Ala Gln Asn Ile Phe
                405                 410                 415

Ile Pro Ala Asp Glu Asp Thr Ala Pro Phe Asp Arg Thr Ala Ala Pro
            420                 425                 430

Pro Gly Lys Gln Val Leu Phe His Ile Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445

Thr Gly Ala Ala Pro Ala His Leu Lys Ser Asn Pro Leu Ala Val Gln
    450                 455                 460

Lys Ala Tyr Ala Arg Val Ser Arg Met Leu Asp Ser Lys Lys Gly Ala
465                 470                 475                 480

Ile Ala Ala Thr Asn Tyr Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495

Val Trp Pro Pro Leu Gln His Val Leu Met Gln Gly Leu Leu Asn Thr
            500                 505                 510
```

```
Pro Ala Thr Phe Gly Glu Ser Asp Pro Ala Tyr Gln Gly Val Gln Lys
        515                 520                 525


Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Asp Phe Pro Gln Leu Gln Gly
545                 550                 555                 560


Val Ser Pro Asp Ala Thr Gly Ile Met Phe Glu Lys Tyr Ala Asp Ser
                565                 570                 575


Ala Ile Asn Val Ala Gly Ser Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Gly
        595                 600                 605


Asn Lys Leu Lys Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala His Thr
    610                 615                 620


His Ser Glu Ala Lys Arg Ser Leu Gly Asp Gly Gly Leu Ala Arg Arg
625                 630                 635                 640


Ala Val Glu Leu Asp Pro Trp Asp Ala Ala Trp Thr Lys Met Phe Gly
                645                 650                 655


Arg Ser Lys Leu Arg Arg Arg Glu Ala Glu Asp Val Arg Lys Arg Trp
            660                 665                 670


Ser Ser



<210>  187
<211>  659
<212>  PRT
<213>  Chloridium virescens

<400>  187
```

```
Leu Tyr Ile Asn Gly Ser Val Ile Ala Pro Cys Asp Ser Pro Leu Tyr
1               5                   10                  15


Cys Gln Gly Asp Ile Leu Lys Ala Ile Gln Leu Ala Gln Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Thr Gln Pro Val Asp Gln
        35                  40                  45


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


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


Leu Thr Glu Val Pro Lys Asp Gln Leu Gln Thr Asn Pro Met Phe Leu
                85                  90                  95


Asn Lys Leu Asn Asp Thr Val Ile Arg Glu Phe Val Thr Ala Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Thr Tyr Thr Gly Ala Ser Asn Cys
        115                 120                 125


Thr Gly Cys Ser Asp Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Phe Trp Ile
145                 150                 155                 160


Leu Gln Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr Gln Ile Ser Lys
                165                 170                 175


Asn Ile Ile Glu Asn Phe Leu Asp Leu Val Asp Gln Phe Gly Phe Val
            180                 185                 190


Pro Asn Gly Ala Arg Val Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Val
        195                 200                 205
```

```
Leu Ser Glu Met Val Arg Thr Tyr Val Ala Tyr Thr Asn Asp Thr Ser
    210                 215                 220


Ile Leu Ala Arg Ala Ile Pro Thr Leu Ile Lys Glu His Asn Phe Trp
225                 230                 235                 240


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


Thr Leu Asn Gln Tyr His Val Glu Asn Thr Gln Pro Arg Pro Glu Ser
            260                 265                 270


Tyr Thr Glu Asp Tyr Ile Thr Ala Asn Asn His Ser Tyr Tyr Ala Thr
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Glu Thr Lys Pro Leu Asn Asp Ser Glu Ile
    290                 295                 300


Ala Asn Leu Tyr Ala Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320


Tyr Gly Ser Arg Tyr Leu Ala Arg Pro Asn Asp Ala Ala Gln Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Val Leu Asn Ile Val Pro Leu Asp
            340                 345                 350


Leu Asn Ser Leu Leu Tyr Gln Ser Glu Gln Asn Ile Ala Leu Phe Leu
        355                 360                 365


Gln Ala Thr Gly Asn Ser Ser Glu Ala Glu Gln Trp Thr Ser Leu Ala
    370                 375                 380


Ala Gln Arg Gln Thr Ala Ile His Ala Leu Met Trp Asn Glu Thr Leu
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Asn Gly Gln Asn Ile Tyr
                405                 410                 415
```

```
Val Pro Ala Asp Lys Asp Ala Thr Pro Ala Asp Thr Ala Ser Ala Pro
            420                 425                 430


Pro Gly Tyr Gln Val Leu Phe Asp Val Ala Gln Phe Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Thr Asp Glu Leu Arg Arg Asn Pro Leu Ala Val Arg
    450                 455                 460


Gln Ala Phe Thr Arg Val Asp Ala Tyr Leu Thr Ala Lys Ala Gly Gly
465                 470                 475                 480


Ile Pro Ala Thr Asn Leu Met Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Met His Val Leu Met Gln Ser Leu Leu Asp Thr
            500                 505                 510


Pro Ala Thr Phe Gly Ala Ala Asp Pro Ser Tyr Ala Ala Leu Gln Gly
        515                 520                 525


Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Met Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Gln Thr Pro Lys Leu Gln Gly
545                 550                 555                 560


Leu Gly Pro Asp Ala Val Gly Thr Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575


Ala Thr Asn Ile Ala Gly Ser Gly Gly Glu Tyr Thr Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Thr Phe Gly
        595                 600                 605


Ala Gln Leu Thr Arg Pro Asn Cys Gly Asn Ile Thr Ala Ala His Val
    610                 615                 620
```

```
Thr Pro Gly Lys Arg Ser Val Gly Leu Gly Arg Arg Ala Val Glu Leu
625                 630                 635                 640


His Glu Ser Asp Ala Arg Trp Val Lys Met Phe Gly Ser Arg Ala Trp
                645                 650                 655


Arg Asn Ala




<210>  188
<211>  662
<212>  PRT
<213>  Gelasinospora cratophora

<400>  188

Leu Tyr Val Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


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


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Val Asp Glu
        35                  40                  45


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


Glu Leu His Glu Phe Leu Asn Thr Tyr Phe Gly Pro Ala Gly Gly Glu
65                  70                  75                  80


Leu Glu Ala Val Pro Thr Asp Gln Leu His Val Ser Pro Thr Phe Leu
                85                  90                  95


Asp Asn Val Ser Asp Asp Val Val Lys Gln Phe Val Asn Ser Val Ile
            100                 105                 110


Asn Ile Trp Pro Asp Leu Thr Arg Lys Tyr Val Gly Ala Gly Glu Ile
        115                 120                 125


Cys Thr Gly Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val
```

```
    130                 135                 140

Val Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Phe Trp
145                 150                 155                 160

Ile Leu Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr Glu Ile Ser
                165                 170                 175

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

Val Pro Asn Gly Ala Arg Leu Tyr Tyr Leu Asn Arg Ser Gln Pro Pro
        195                 200                 205

Leu Leu Thr Gln Met Val Arg Ile Tyr Val Glu His Thr Asn Asp Thr
    210                 215                 220

Ser Ile Leu Glu Arg Ala Val Pro Ile Leu Lys Lys Glu Trp Glu Trp
225                 230                 235                 240

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

Ser Leu Gln Arg Tyr His Val Asp Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270

Tyr Ser Glu Asp Tyr Ile Thr Ala Asn Asn Asn Ser Tyr Tyr Ala Thr
        275                 280                 285

Ser Gly Ile Ile Tyr Pro Glu Thr Thr Pro Leu Asn Asp Thr Gln Lys
    290                 295                 300

Ala Gln Leu Tyr Ala Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320

Tyr Ser Thr Arg Trp Leu Lys Asn Pro Asn Asp Ala Ala Arg Asp Val
                325                 330                 335

Tyr Phe Pro Leu Arg Ser Leu Asn Val Leu Glu Ile Val Pro Val Asp
```

```
            340                 345                 350

Leu Asn Ser Ile Leu Tyr Gln Asn Glu Val Thr Ile Gly Lys Phe Leu
        355                 360                 365

Ala Gln Gln Gly Asn Lys Asp Glu Ala Glu Glu Trp Ala Lys Lys Ala
    370                 375                 380

Glu Gln Arg Ser Glu Ala Met Tyr Lys Leu Met Trp Asn Ser Thr Leu
385                 390                 395                 400

Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ser Ser Gln Asn Ile Tyr
                405                 410                 415

Val Pro Ala Asp Pro Gln Val Phe Pro Phe Glu Lys Pro Ser Gly Thr
            420                 425                 430

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

Trp Thr Gly Ala Ala Pro Asp Gln Leu Lys Ala Asn Pro Leu Ala Val
    450                 455                 460

Lys Leu Thr Phe Asp Arg Val Lys Asn Tyr Leu Asp Asn Lys Ala Gly
465                 470                 475                 480

Gly Ile Pro Ala Thr Asn Phe Val Thr Gly Gln Gln Trp Asp Glu Pro
                485                 490                 495

Asn Val Trp Pro Pro Leu Met His Val Leu Met Asp Gly Leu Leu Asn
            500                 505                 510

Thr Pro Ala Thr Phe Gly Glu Asp Asp Pro Ala Tyr Gln Glu Thr Gln
        515                 520                 525

Asn Leu Ala Leu Arg Leu Ala Gln Arg Tyr Val Asp Ser Thr Phe Cys
    530                 535                 540

Thr Trp Trp Ala Thr Gly Gly Ser Thr Ser Glu Thr Pro Lys Leu Gln
```

```
545                 550                 555                 560


Gly Leu Gly Ser Asp Ala Lys Gly Ile Met Phe Glu Lys Tyr Ala Asp
                565                 570                 575


Asn Ser Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu
            580                 585                 590


Gly Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Lys Phe
        595                 600                 605


Gly Asp Lys Leu Lys Arg Pro Asn Cys Gly Asp Leu Thr Pro Ala Asn
    610                 615                 620


Val Gly Lys Arg Ala Val Glu Leu Asp Ala Phe Asp Ala Lys Phe Thr
625                 630                 635                 640


Lys Lys Phe Ala Arg Lys Gly Lys Leu Glu Lys Leu Lys Ala Lys Phe
                645                 650                 655


Lys Arg Arg Ala Ala Ile
            660


<210>  189
<211>  543
<212>  PRT
<213>  Acidobacteriaceae bacterium

<400>  189

Gln Thr Thr Thr Thr Ser Ala Gly Leu His Asp Thr Leu Ala Tyr Ile
1               5                   10                  15


Lys Arg Thr Trp His Thr Leu Glu Arg Ser Asn Lys Thr Leu Leu Lys
            20                  25                  30


Ser Ala Asp Asp Val Lys Val Gly Gln Ala Gly Thr Leu Thr Leu Tyr
        35                  40                  45


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

```
Glu Leu Pro Pro Ala Asp Lys Lys Arg Ile Val Val Arg Gln Leu Pro
65                  70                  75                  80


Glu His Pro Glu Ala Val Glu Pro Ala Gly Leu Leu Tyr Leu Pro Tyr
                85                  90                  95


Pro Tyr Val Val Pro Gly Gly Arg Phe Asn Glu Met Tyr Gly Trp Asp
            100                 105                 110


Ser Tyr Phe Ile Leu Leu Gly Leu Val His Asp Asp Glu Leu Ala Leu
        115                 120                 125


Ala Lys Asn Met Thr Asp Asn Phe Ile Tyr Glu Ile Glu His Tyr Gly
    130                 135                 140


Met Ile Leu Asn Ala Asn Arg Thr Tyr Tyr Leu Thr Arg Ser Gln Pro
145                 150                 155                 160


Pro Phe Leu Thr Gln Met Ile Leu Glu Val Tyr Arg Arg Thr Gly Asp
                165                 170                 175


Gly Lys Trp Leu Ala Ser Thr Leu Pro Ala Ile Glu Lys Tyr Tyr Ala
            180                 185                 190


Tyr Trp Met Arg Glu Pro His Leu Thr Pro Glu Thr Gly Leu Ser Arg
        195                 200                 205


Tyr Trp Gly Gly Ala Asp Thr Pro Ala Pro Glu Val Val His Gly Glu
    210                 215                 220


Lys Asp Ala Ala Gly His Asn Gln Tyr Asp Arg Val Arg Glu Tyr Tyr
225                 230                 235                 240


Arg Thr His Asn Val Thr Ala Tyr Asp Val Ser Gln Tyr Tyr Asp Lys
                245                 250                 255


Ala Thr Asp Arg Leu Lys Pro Leu Phe Tyr Ile Ala Asp Arg Ala Met
            260                 265                 270
```

```
Arg Glu Ser Gly Phe Asp Pro Ser Ser Arg Tyr Gly Pro Phe Ser Ala
        275                 280                 285

Asp Ile Ile His Tyr Asp Pro Val Cys Leu Asn Ser Leu Leu Tyr Arg
    290                 295                 300

Met Glu Ser Asp Thr Ala Thr Ile Leu Lys Gln Leu Asn Arg Thr Ser
305                 310                 315                 320

Glu Ala Arg Val Trp Glu Lys Arg Ala Thr Gln Arg Ala Glu Leu Val
                325                 330                 335

Asn Arg Leu Met Trp Asn Glu Glu Lys Gly Leu Tyr Phe Asp Tyr Asp
            340                 345                 350

Phe Ile Thr Arg Arg Gln Ser Asn Tyr His Phe Val Thr Thr Phe Tyr
        355                 360                 365

Pro Leu Trp Ala Gly Ile Ala Ser Arg Gln Gln Ala Asp Arg Val Arg
    370                 375                 380

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

Tyr Ile Ser Gly Ser Gln Trp Asp Ala Pro Phe Gly Trp Ala Pro Leu
                405                 410                 415

Gln Ile Met Thr Val Glu Gly Leu Arg Arg Tyr Gly Phe Asn Glu Asp
            420                 425                 430

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

Glu Glu His Gly Thr Ile Lys Glu Lys Tyr Asp Val Val Ile Gly Lys
    450                 455                 460

Ser Asp Leu Ala Ala Gly Leu Lys Phe Gly Tyr Thr Ser Asn Glu Ala
465                 470                 475                 480
```

```
Gly Phe Gly Trp Thr Asn Ala Ala Val Val Leu Phe Ile Glu Glu Leu
                485                 490                 495


Ala Gly Glu Arg Pro Leu Ala Ala Ser Leu Asp Arg Glu Ser Met Pro
            500                 505                 510


Met Leu Arg Gln Arg His Leu Ser Pro Gln Pro Ser Val Trp Pro Pro
        515                 520                 525


Phe Ser Pro Gln Ala Pro Gln Tyr Arg Arg Arg Asp Pro Tyr Arg
    530                 535                 540


<210>  190
<211>  532
<212>  PRT
<213>  Acidobacterium capsulatum

<400>  190

Gly Ala Arg Ser Ser Leu Ser Pro His Ala Val Ala Gly Pro Gln Pro
1               5                   10                  15


Ile Asp Ala Tyr Ile His Thr Ala Trp Ser Thr Leu Thr Arg Ser Met
            20                  25                  30


Ser Asp Cys Lys Ser Val Ala Asp Pro Lys Leu Lys Ser Thr Pro Val
        35                  40                  45


Leu Tyr Leu Pro Arg Asp Leu Ala Val Pro Ala Asn Val Ala Ala Met
    50                  55                  60


Gln Lys Gln Cys His Val Arg Val Leu Arg Leu Pro Ile Val Ile Thr
65                  70                  75                  80


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


Tyr Leu Pro His Pro Tyr Val Val Pro Gly Gly Arg Phe Asn Glu Met
            100                 105                 110
```

```
Tyr Gly Trp Asp Ser Phe Phe Ile Leu Lys Gly Leu Leu Asp Asp His
        115                 120                 125


His Ile Ala Leu Ala Arg Gly Ile Val Glu Asn Phe Phe Phe Glu Ile
    130                 135                 140


Ala His Tyr Gly Gly Ile Leu Asn Ala Asn Arg Thr Tyr Tyr Phe Thr
145                 150                 155                 160


Arg Ser Gln Pro Pro Phe Leu Ser Ser Met Ile Arg Ala Ile Tyr Ala
                165                 170                 175


Ala Glu Val Ala Glu Gly His Thr Gln Ala Ala His Ala Trp Leu Val
            180                 185                 190


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


Ile His Gln Ala Gly Asn Thr Gly Leu Ala Arg Tyr Phe Asp Thr Gly
    210                 215                 220


Gln Gly Pro Val Pro Glu Met Ala Asp Asp Ser Thr Tyr Tyr Gln Asp
225                 230                 235                 240


Val Ile Arg Trp Leu Leu Ala His Pro Gly Leu His Thr Gly Tyr Leu
                245                 250                 255


Met His Gly Ser Pro His Leu Asp Ala Ala Ala Arg Glu Arg Leu Ala
            260                 265                 270


Gln Leu Ser Cys Asp Pro Thr Leu Ser Lys Val Cys Ala Arg Ala His
        275                 280                 285


Val His Gly Tyr Trp Leu Thr Arg Ser Phe Tyr Lys Gly Asp Arg Ala
    290                 295                 300


Met Arg Glu Ser Gly Phe Asp Thr Thr Phe Arg Phe Gly Pro Phe Ser
305                 310                 315                 320
```

```
Gly Ser Thr Gln His Phe Ala Pro Val Gly Leu Asn Ala Leu Leu Tyr
                325                 330                 335


Lys Tyr Glu Arg Asp Leu Ala Trp Met Ala Ala Gln Leu Gly Lys Pro
            340                 345                 350


Gly Glu Ala Ala Lys Trp Asn Ser Glu Ala Glu Thr Arg Arg Ala Glu
        355                 360                 365


Met Asn His Tyr Leu Trp Asn Ala Gln Lys Lys Met Tyr Phe Asp Tyr
    370                 375                 380


Asn Phe Glu Thr His Arg Gln Ser Ser Tyr Ala Phe Ile Thr Thr Phe
385                 390                 395                 400


Tyr Pro Leu Trp Ala Gly Ala Ala Asp Lys Ala Gln Gln Gln Gly Val
                405                 410                 415


Ile Ala Ser Leu Pro Leu Phe Glu His Pro Gly Gly Leu Ala Ile Ser
            420                 425                 430


Asn His Asp Ser Gly Val Gln Trp Asp Leu Pro Tyr Gly Trp Ala Pro
        435                 440                 445


Thr Glu Trp Met Ala Val Gln Gly Leu Leu Arg Ala Asp Asp Gln His
    450                 455                 460


Asp Ala Arg Arg Ile Ala Ser Glu Phe Asn Arg Thr Val Arg Thr Thr
465                 470                 475                 480


Tyr Gln His Asp His Ala Ile Tyr Glu Lys Tyr Asp Val Val Asn Arg
                485                 490                 495


Ser Asn Asp Phe Arg Val Thr Ala Gly Tyr Thr Gln Asn Val Val Gly
            500                 505                 510


Phe Gly Trp Thr Asn Ala Val Tyr Leu Glu Phe Gln Ser Leu Leu Ala
        515                 520                 525
```

```
His Pro Gly Gln
    530


<210>  191
<211>  568
<212>  PRT
<213>  Acidovorax wautersii

<400>  191

Ala Ala Ala Val Ser Ser Gly Leu Arg Ile Ser Glu Arg His Pro Ala
1               5                   10                  15


Tyr Ser Thr Asn Pro Ala Arg Val Gln Val Pro Gly Ala Pro Gly Ala
            20                  25                  30


Pro Pro Ser Asp His Cys Thr Pro Ala Asp Arg Tyr Gln Glu Leu Phe
        35                  40                  45


Val Ala Val Gln Ser Gln Gln Ile Phe Glu Asp Ser Lys Thr Phe Val
    50                  55                  60


Asp Cys Gly Pro Ile Gly Glu Pro Glu Asp Ile Leu Ala Ala Tyr Arg
65                  70                  75                  80


Ala Glu His Ala Gln Pro Asp Phe Asp Leu Ala Arg Phe Val Ala Gln
                85                  90                  95


His Phe Thr Ala Pro Gln Val Ala Ala Asn Asp Tyr Val Gly Ala Pro
            100                 105                 110


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


Arg Lys Pro Glu Asp His Pro Val Arg Gly Ser Ala Leu Pro Leu Ala
    130                 135                 140


His Pro Tyr Val Val Pro Gly Gly Arg Phe Ala Glu Leu Tyr Tyr Trp
145                 150                 155                 160
```

```
Asp Ser Tyr Phe Thr Met Leu Gly Leu Ala Ala Thr Gly Arg Ser Glu
                165                 170                 175


Leu Val Gln Cys Met Thr Asp Asn Phe Ala Arg Leu Ile Asp Ala Phe
            180                 185                 190


Gly Phe Val Pro Asn Gly Thr Arg Thr Tyr Tyr Leu Ser Arg Ser Gln
        195                 200                 205


Pro Pro Leu Phe Ala Ala Met Ala Glu Leu Gly Ala Leu Val Gly Gly
    210                 215                 220


Pro Pro Val Ser His Tyr Leu Pro Gln Leu Leu Gln Glu His Ala Trp
225                 230                 235                 240


Trp Met Asp Gly Leu His Val Leu His Pro Gly Glu Ala Arg Arg Arg
                245                 250                 255


Val Val Ala Leu Pro Gly Gly Glu Ile Leu Asn Arg Tyr Trp Asp Asp
            260                 265                 270


Arg Asp Thr Pro Arg Glu Glu Ser Trp Arg Glu Asp Ile Glu Thr Ala
        275                 280                 285


Ser Ala Val Asp Arg Pro Ser Ala Asp Val Tyr Arg Asp Leu Arg Ala
    290                 295                 300


Ala Ala Glu Ser Gly Trp Asp Phe Ser Thr Arg Trp Leu Arg Ala Pro
305                 310                 315                 320


Asp Ala Ala Asn Pro Ala Ser Leu His Leu Ser Gln Ile Cys Thr Thr
                325                 330                 335


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


Ser Ile Ala Lys Ala Ser Gln Ser Ala Gly Asp Arg Ala Thr Ala Thr
        355                 360                 365
```

```
His Phe His Asp Leu Ala Ala His Arg Arg Glu Ala Val Asn Arg Leu
    370                 375                 380


Met Trp Asn Glu Ala Glu Gly Ala Tyr Phe Asp Tyr Asp Trp Arg Arg
385                 390                 395                 400


Gly Glu Leu Arg Gly Cys Leu Thr Ala Ala Thr Val Val Pro Leu Tyr
                405                 410                 415


Ala Gly Met Ala Thr Glu Ala Gln Ala Ala Ala Val Ala Arg Ala Val
            420                 425                 430


Arg Thr His Leu Leu Ala Ala Gly Gly Leu Ala Thr Thr Val Cys Ser
        435                 440                 445


Ser Asp Gln Gln Trp Asp Arg Pro Asn Gly Trp Ala Pro Leu Gln Trp
    450                 455                 460


Met Ala Val Arg Gly Leu Glu Arg Tyr Gly His Lys Asp Leu Ala Leu
465                 470                 475                 480


Glu Val Arg Gln Arg Trp Ile Glu Thr Val Arg Ser Val Tyr Gln Arg
                485                 490                 495


Glu Gly Lys Leu Val Glu Lys Tyr Ala Val Gly Asn Gly Asp Gly Ala
            500                 505                 510


Pro Leu Cys Gly Gly Gly Gly Gly Glu Tyr Pro Leu Gln Asp Gly Phe
        515                 520                 525


Gly Trp Thr Asn Gly Val Val Gln Cys Trp Leu Asp Pro Arg Tyr Asp
    530                 535                 540


Thr Tyr Ala Ala Ala Gln Thr Val Tyr Tyr Gly Pro Thr Asp Asp Gly
545                 550                 555                 560


Thr Ala Asp Ser Leu Pro Glu Ala
                565
```

```
<210>  192
<211>  529
<212>  PRT
<213>  Xanthomonas arboricola

<400>  192

Ala Pro Met Asp Thr Pro Val Val Asn Ala Pro Ala Ala Thr Pro Pro
1               5                   10                  15


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


Glu Leu Phe Asp Asp Gln Lys His Phe Val Asp Phe Leu Pro Leu Arg
        35                  40                  45


Asp Pro Ala Leu Ile Asn Ala Asp Tyr Leu Ala Gln His Asp His Pro
    50                  55                  60


Gly Phe Asp Leu Arg Lys Phe Val Asp Ala Asn Phe Glu Glu Ser Pro
65                  70                  75                  80


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


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


Pro Tyr Ser Ser Leu Leu Ala Leu Pro His Pro Tyr Val Val Pro Gly
        115                 120                 125


Gly Arg Phe Arg Glu Val Tyr Tyr Trp Asp Ser Tyr Phe Thr Met Leu
    130                 135                 140


Gly Leu Val Lys Ser Gly Glu Thr Thr Leu Ser Arg Gln Met Leu Asp
145                 150                 155                 160


Asn Phe Ala Tyr Leu Ile Asp Thr Tyr Gly His Ile Pro Asn Gly Asn
                165                 170                 175


Arg Ser Tyr Tyr Leu Ser Arg Ser Gln Pro Pro Phe Phe Ser Tyr Met
```

```
            180                 185                 190

Val Glu Leu Gln Ala Gly Val Glu Gly Glu Ala Val Tyr Gln Arg Tyr
        195                 200                 205

Leu Pro Gln Leu Arg Lys Glu Tyr Ala Tyr Trp Met Gln Gly Ser Glu
    210                 215                 220

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

Gly Ser Leu Leu Asn Arg Tyr Trp Asp Glu Arg Asp Thr Pro Arg Pro
                245                 250                 255

Glu Ala Trp Leu His Asp Thr Arg Thr Ala Ala Glu Ala Gly Asp Arg
            260                 265                 270

Pro Ala Ala Glu Val Tyr Arg Asp Leu Arg Ala Gly Ala Glu Ser Gly
        275                 280                 285

Trp Asp Tyr Thr Ser Arg Trp Leu Ala Asp Gly Gln Asn Leu Arg Thr
    290                 295                 300

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

His Leu Glu Arg Thr Leu Ala Gln Ala Cys Ala Gln Pro Gly Ala Glu
                325                 330                 335

Cys Ala Gln Asp Tyr Ala Ala Leu Ala Leu Arg Arg Lys Gln Ala Ile
            340                 345                 350

Asp Ala His Leu Trp Asn Ala Ala Gly Tyr Tyr Ala Asp Tyr Asp Trp
        355                 360                 365

Gln Thr Arg Lys Leu Ser Asp Gln Val Thr Ala Ala Ala Leu Tyr Pro
    370                 375                 380

Leu Phe Thr Gly Leu Ala Thr Asp Ala His Ala Lys Arg Thr Ala Ser
```

```
385                 390                 395                 400


Thr Val Arg Ala Arg Leu Leu Arg Pro Gly Gly Leu Ala Thr Thr Ala
                405                 410                 415


Val Lys Thr Gly Gln Gln Trp Asp Glu Pro Asn Gly Trp Ala Pro Leu
            420                 425                 430


Gln Trp Val Ala Val Asp Gly Leu Arg Arg Tyr Gly Glu Asp Ala Leu
        435                 440                 445


Ala Arg Thr Ile Gly Glu Arg Phe Leu Thr Gln Val Gln Ala Leu Phe
    450                 455                 460


Ala Arg Glu His Lys Leu Val Glu Lys Tyr Gly Leu Glu Ala Asp Ala
465                 470                 475                 480


Ala Gly Gly Gly Gly Gly Glu Tyr Ala Leu Gln Asp Gly Phe Gly Trp
                485                 490                 495


Thr Asn Gly Val Thr Leu Met Leu Leu Asn Leu Tyr Pro Asp Thr Ala
            500                 505                 510


Thr Lys Pro Ala Pro Ala Lys Arg Ala Arg Lys Pro Glu Ala Ala Ala
        515                 520                 525


Arg



<210>  193
<211>  540
<212>  PRT
<213>  Kosakonia sacchari

<400>  193

Ala Glu Ala Gln Asn Thr Pro Gln Pro Pro Asp Ile Leu Leu Gly Pro
1               5                   10                  15


Leu Phe Ser Asp Val Gln Thr Ala Lys Leu Phe Pro Asp Gln Lys Thr
            20                  25                  30
```

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

Tyr Arg Met Gln Arg Met Gln Thr Ser Phe Asp Leu Arg His Phe Val
    50                  55                  60

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

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

Thr Arg Thr Thr Asp Ser Ala Gly Lys Trp Asp Ser Leu Leu Pro Leu
            100                 105                 110

Pro Lys Pro Tyr Val Val Pro Gly Gly Arg Phe Arg Glu Val Tyr Tyr
        115                 120                 125

Trp Asp Ser Tyr Phe Thr Met Leu Gly Leu Ala Glu Ser Gly His Trp
    130                 135                 140

Asp Lys Ile Glu Asp Met Val Thr Asn Phe Ala His Glu Ile Asp Thr
145                 150                 155                 160

Trp Gly His Ile Pro Asn Gly Asn Arg Ser Tyr Tyr Leu Ser Arg Ser
                165                 170                 175

Gln Pro Pro Phe Phe Ser Leu Met Val Glu Leu Leu Ala Thr His Asp
            180                 185                 190

Gly Asp Glu Ala Leu Lys Thr Trp Leu Pro Gln Met Glu Lys Glu Tyr
        195                 200                 205

Gln Tyr Trp Met Glu Gly Ala Asp Thr Leu Gln Pro Gly Gln Ala Asn
    210                 215                 220

Lys Arg Val Val Lys Leu Ser Asp Gly Ser Val Leu Asn Arg Tyr Trp
225                 230                 235                 240
```

```
Asp Asp Arg Asp Thr Pro Arg Pro Glu Ser Trp Leu Asp Asp Val Thr
                245                 250                 255


Thr Ala Lys Asn Asn Pro Asn Arg Pro Ala Thr Glu Ile Tyr Arg Asp
            260                 265                 270


Leu Arg Ser Ala Ala Ala Ser Gly Trp Asp Phe Ser Ser Arg Trp Met
        275                 280                 285


Asp Asp Pro Asn Gln Leu Gly Thr Ile Arg Thr Thr Ser Ile Val Pro
    290                 295                 300


Val Asp Leu Asn Ala Leu Met Phe Lys Met Glu Lys Met Leu Ala Arg
305                 310                 315                 320


Gly Tyr Gln Ala Ala Gly Asp Ser Ala Lys Ala Ser Gln Tyr Asp Ala
                325                 330                 335


Leu Ala Asn Ala Arg Gln Lys Gly Ile Glu Ala Asn Leu Trp Asn Glu
            340                 345                 350


Lys Glu Gly Trp Tyr Ala Asp Tyr Asp Leu Lys Thr Lys Lys Val Arg
        355                 360                 365


Asn Gln Leu Thr Ala Ala Ala Leu Tyr Pro Leu Phe Val Asn Ala Ala
    370                 375                 380


Ala Lys Asp Arg Ala Asp Lys Val Ala Ser Ala Ala Lys Glu Arg Leu
385                 390                 395                 400


Leu Lys Pro Gly Gly Ile Ala Thr Thr Thr Val Asn Ser Gly Gln Gln
                405                 410                 415


Trp Asp Ala Pro Asn Gly Trp Ala Pro Leu Gln Trp Val Ala Thr Ala
            420                 425                 430


Gly Leu Gln Asn Tyr Asp Gln Gln Lys Leu Ala Met Glu Val Ser Trp
        435                 440                 445
```

```
Arg Phe Leu Thr Asn Val Gln His Thr Tyr Asp Arg Glu Lys Lys Leu
    450                 455                 460


Val Glu Lys Tyr Asp Val Ser Thr Thr Gly Thr Gly Gly Gly Gly Gly
465                 470                 475                 480


Glu Tyr Pro Leu Gln Asp Gly Phe Gly Trp Thr Asn Gly Val Thr Leu
                485                 490                 495


Lys Met Leu Asp Gln Ile Cys Pro Lys Glu Lys Pro Cys Asp Ser Val
            500                 505                 510


Pro Gln Thr Gln Pro Ala Gln Gln Pro Ala Ala Lys Val Glu Pro Thr
        515                 520                 525


Ser Gln Pro Ser Lys Gln Gln Gln Ala Val Ala Gln
    530                 535                 540



<210>  194
<211>  532
<212>  PRT
<213>  Enterobacter sp.

<400>  194

Asp Glu Gln Pro Ala Phe Gln Lys Asn Ser Pro Asp Ile Leu Leu Gly
1               5                   10                  15


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


Thr Phe Ala Asp Ala Val Pro Lys Ser Asp Pro Leu Met Ile Leu Ala
        35                  40                  45


Asp Tyr Arg Met Gln His Thr Gln Ser Ser Phe Asp Leu Arg His Phe
    50                  55                  60


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

```
Pro Ala Gly Gln Ser Leu Arg Glu His Ile Asp Asp Leu Trp Pro Val
                85                  90                  95


Leu Thr Arg Thr Thr Asp Lys Ala Ser Asn Lys Trp Asp Ser Leu Leu
            100                 105                 110


Pro Leu Pro Lys Pro Tyr Val Val Pro Gly Gly Arg Phe Arg Glu Val
        115                 120                 125


Tyr Tyr Trp Asp Ser Tyr Phe Thr Met Leu Gly Leu Ala Glu Ser Gly
    130                 135                 140


His Trp Asp Lys Ile Ser Asp Met Val Asp Asn Phe Ala Trp Glu Ile
145                 150                 155                 160


Asp Thr Phe Gly His Ile Pro Asn Gly Asn Arg Ser Tyr Tyr Leu Ser
                165                 170                 175


Arg Ser Gln Pro Pro Phe Phe Ser Met Met Val Glu Leu Leu Ala Thr
            180                 185                 190


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


Tyr Ala Tyr Trp Met Glu Gly Val Asp Ser Leu Gln Pro Gly Gln Ala
    210                 215                 220


Asn Gln Arg Val Val Lys Leu Asp Asp Gly Ser Val Leu Asn Arg Tyr
225                 230                 235                 240


Trp Asp Asp Arg Asp Thr Pro Arg Pro Glu Ser Trp Leu Asp Asp Val
                245                 250                 255


Asn Thr Ala Lys Asn Asn Pro Asn Arg Pro Ala Thr Glu Ile Tyr Arg
            260                 265                 270


Asp Leu Arg Ser Ala Ala Ala Ser Gly Trp Asp Phe Ser Ser Arg Trp
        275                 280                 285
```

```
Met Asp Asp Pro Gln Lys Leu Gly Thr Ile Arg Thr Thr Ser Ile Val
    290                 295                 300


Pro Val Asp Leu Asn Ala Leu Met Phe Lys Met Glu Lys Leu Leu Ala
305                 310                 315                 320


Arg Ala Ser Gln Glu Ala Gly Asp Ser Ala Ala Ala Ser Lys Tyr Glu
                325                 330                 335


Ala Leu Ala Thr Ala Arg Gln Lys Ala Ile Glu Asn His Leu Trp Asn
            340                 345                 350


Asp Lys Glu Gly Trp Tyr Ala Asp Tyr Asp Leu Lys Ser Lys Lys Val
        355                 360                 365


Arg Asn Gln Leu Thr Ala Ala Ala Leu Phe Pro Leu Tyr Val Lys Ala
    370                 375                 380


Ala Ser Gln Glu Arg Ala Asp Lys Val Ala Ala Ala Thr Ser Ala Arg
385                 390                 395                 400


Leu Leu Lys Pro Gly Gly Ile Thr Thr Thr Thr Ile Asn Ser Gly Gln
                405                 410                 415


Gln Trp Asp Ala Pro Asn Gly Trp Ala Pro Leu Gln Trp Val Ala Thr
            420                 425                 430


Glu Gly Leu Gln Asn Tyr Gly Gln Asn Lys Val Ala Met Asp Val Thr
        435                 440                 445


Trp Arg Phe Leu Lys Asn Val Gln His Thr Tyr Asp Arg Glu Lys Lys
    450                 455                 460


Leu Val Glu Lys Tyr Asp Val Ser Thr Thr Gly Thr Gly Gly Gly Gly
465                 470                 475                 480


Gly Glu Tyr Pro Leu Gln Asp Gly Phe Gly Trp Ser Asn Gly Val Thr
                485                 490                 495
```

```
Leu Lys Met Leu Asp Leu Val Cys Pro Lys Glu Lys Pro Cys Asp Ser
            500                 505                 510


Val Pro Glu Asn Gln Pro Ala Ala Asn Asp Glu Ala Ala Pro Val Lys
        515                 520                 525


Ala Ser Ala Gln
    530


<210>  195
<211>  720
<212>  PRT
<213>  Saitozyma flava

<400>  195

Gln Asn Pro Ala Ser Ser Ser Ser Phe Ser Pro Thr Pro Val Thr Thr
1               5                   10                  15


Met Val Pro Ser Pro Thr Ala Ala Leu Asn Ala Thr Val Pro Gly Gln
            20                  25                  30


Gly Val Tyr Pro Pro Leu Gln Ala Trp Cys Asn Asn Gly Gly Asn Asp
        35                  40                  45


Thr Phe Cys Pro Gly Val Leu Leu Gln Asp Val Gln Leu Ser Gly Ile
    50                  55                  60


Phe Pro Asp Ser Lys Thr Phe Val Asp Lys Pro Thr Arg Gly Thr Leu
65                  70                  75                  80


Asn Glu Thr Leu Arg Thr Phe Ala Ser Leu Gly Asn Asn Leu Thr Val
                85                  90                  95


Gly Gln Ile Glu Gly Phe Val Asn Asn Ser Phe Lys Gly Glu Gly Leu
            100                 105                 110


Glu Leu Ser Gln Val Ala Leu Glu Gly Phe Asn Pro Asn Pro Ala Phe
        115                 120                 125
```

```
Leu Asp Thr Ile Ser Asp Pro Ile Tyr Gln Gly Trp Met Ser Val Val
    130                 135                 140


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


Cys Asn Gly Asp Cys Glu Ser Ser Leu Ile Pro Leu Asn Asn Thr Ile
                165                 170                 175


Val Val Pro Gly Gly Arg Tyr Arg Glu Ile Tyr Tyr Trp Asp Ser Tyr
            180                 185                 190


Trp Ile Leu Ile Gly Leu Leu Glu Ser Glu Leu Thr Ala Tyr Ala Thr
        195                 200                 205


Asp Leu Ile Ser Asn Phe Met Asp Phe Ile Gln Thr Tyr Gly Phe Ile
    210                 215                 220


Pro Asn Gly Gly Arg Lys Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Val
225                 230                 235                 240


Phe Thr Gln Met Leu Asn Thr Tyr Val Gln Arg Thr Gly Asn Thr Ser
                245                 250                 255


Ile Leu Ala Arg Gly Leu Pro Leu Ala His Gln Glu Leu Val Trp Trp
            260                 265                 270


Glu Asn Asn Arg Val Ile Ser Val Thr Ser Pro Tyr Ser Asn Ile Thr
        275                 280                 285


Arg Arg Val Ala His Phe Ala Val Asn Asn Thr Ala Pro Arg Pro Glu
    290                 295                 300


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


Asn Glu Thr Ala Arg Gly Gln Leu Tyr Ser Asp Leu Ala Ala Gly Ala
                325                 330                 335
```

```
Glu Ser Gly Trp Asp Tyr Ser Ser Arg Trp Cys Lys Gln Pro Val Ile
            340                 345                 350

Asn Leu Thr Asp Asn Phe Pro Ala Leu Arg Thr Ile Asn Thr Ala Lys
        355                 360                 365

Ile Ile Pro Val Asp Leu Asn Ser Leu Leu Ala Gly Asp His Thr Leu
    370                 375                 380

Leu Ala Asn Leu Tyr Glu Leu Tyr Gly Asn Ser Ser Asn Ala Asn Thr
385                 390                 395                 400

Ser Val Thr Ser Asn Ser Ser Gln Leu Val Pro Tyr His Arg Gln Leu
                405                 410                 415

Ala Lys Asn Tyr Ser Asp Ala Val Leu Asp Leu His Trp Asp Ala Gln
            420                 425                 430

Lys Ala Trp Phe Tyr Asp Phe Asn Leu Thr Ala Asn Ala Arg Ala Asp
        435                 440                 445

Ile Tyr His Pro Gly Gly Thr Phe Ala Leu Trp Gln Asn Ile Thr Pro
    450                 455                 460

Pro Ala Val Ala Ser Asn Glu Thr Tyr Ala Leu Glu Val Val Ser Gly
465                 470                 475                 480

Ala Arg Phe Leu Leu Gly Lys Tyr Thr Ser Ile Pro Ser Val Ser Thr
                485                 490                 495

Leu Ile Glu Thr Gly Leu Asn Trp Asp Phe Pro Asn Ser Trp Pro Pro
            500                 505                 510

His Val Tyr Ser Ser Ile Lys Ala Phe Glu Thr Leu Gly Arg Ala Phe
        515                 520                 525

Pro Asn Ala Ser Val Leu Ser Asn Ile Ser Ile Pro Phe Ser Asp Val
    530                 535                 540
```

```
Gln Lys Asn Gln Leu Gly Leu Asp Glu Ser Ala Ile Pro Ala Gln Pro
545                 550                 555                 560


Ala Ser Thr Ile Gly Asn Ser Thr Ser Gln Ile Ala Glu Ala Gln Gly
                565                 570                 575


Lys Pro Trp Pro Gln Ala Leu Ser Ile Glu Tyr Ala Asn Arg Tyr Met
            580                 585                 590


Gln Ala Ala Phe Cys Ser Trp Tyr Ser Thr Gly Gly Ser Ile Asp Gly
        595                 600                 605


Leu Leu Thr Gln Leu Pro Leu Ser Glu Leu Asn Met Thr Gly Thr Phe
    610                 615                 620


Gln Ala Gly Thr Thr Gly Val Met Phe Glu Lys Phe Asn Val Thr Asp
625                 630                 635                 640


Leu Asp Ala Ala Gly Gly Gly Gly Glu Tyr Lys Val Gln Ile Gly Phe
                645                 650                 655


Gly Trp Thr Asn Gly Val Ala Leu Trp Leu Gly Ala Asn Phe Gly Gln
            660                 665                 670


Tyr Leu Pro Gln Pro Thr Cys Pro Leu Ile Pro Ile Ile Glu Val Gln
        675                 680                 685


Asn Gly Met Asn Ser Ser Val Tyr Gln Asn Gly Thr Met Thr Asn Ser
    690                 695                 700


Thr Lys Thr Gln Ser Tyr Ile Phe Gln Gly His Arg Ile Pro Arg Lys
705                 710                 715                 720


<210>  196
<211>  723
<212>  PRT
<213>  Phaeotremella skinneri

<400>  196

Gln Thr Pro Thr Ser Ser Ser Ser Ser Ser Phe Ser Ala Thr Pro Val
```

```
1               5                   10                  15


Ser Thr Ser Val Pro Ser Pro Thr Val Pro Leu Asn Ser Ser Val Ile
            20                  25                  30


Gly Gln Gly Leu Tyr Pro Pro Ala Gln Ala Trp Cys Asn Gly Gly Met
        35                  40                  45


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


Gly Ile Phe Ala Asp Ser Lys Thr Phe Pro Asp Lys Pro Thr Val Gly
65                  70                  75                  80


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


Thr Val Gly Glu Ile Glu Thr Phe Val Asn Gln Tyr Phe Lys Gly Glu
            100                 105                 110


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


Ala Ile Leu Asn Asn Ile Thr Asp Pro Val Phe Lys Gly Trp Val Ser
    130                 135                 140


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


Ser Leu Cys Asn Glu Thr Ser Cys Ala Ser Ser Leu Ile Pro Leu Asn
                165                 170                 175


His Thr Ile Val Val Pro Gly Gly Arg Tyr Arg Glu Ile Tyr Tyr Trp
            180                 185                 190


Asp Ser Phe Trp Ile Leu Gln Gly Leu Leu Lys Ser Glu Leu Tyr Thr
        195                 200                 205


Tyr Ser Trp Asp Leu Leu Gln Asn Phe Met Asp Leu Ile Glu Thr Tyr
```

```
    210                 215                 220

Gly Phe Leu Pro Asn Gly Gly Arg Lys Tyr Tyr Leu Asn Arg Ser Gln
225                 230                 235                 240

Pro Pro Val Phe Ile Gln Met Leu Asp Ala Tyr Ile Lys Val Thr Gly
                245                 250                 255

Asn Ser Ser Ile Leu Ala Arg Ala Leu Pro Ile Ala Thr Thr Glu Leu
            260                 265                 270

Ala Trp Trp Ser Ser Asn Arg Thr Ile Pro Val Thr Ser Pro Tyr Thr
        275                 280                 285

Gly Ile Thr His Leu Val Ala His Tyr Ala Val Thr Asn Ser Ala Pro
    290                 295                 300

Arg Pro Glu Gly Tyr Val Glu Asp Phe Thr Thr Ala Met Gly Ala Ser
305                 310                 315                 320

Pro Ala Leu Asn Asp Ser Ala Arg Ala Glu Leu Tyr Ser Glu Leu Ala
                325                 330                 335

Ser Gly Ala Glu Thr Gly Trp Asp Tyr Ser Ser Arg Trp Cys Arg Gln
            340                 345                 350

Pro Leu Leu Asn Leu Thr Asp Asn Asn Pro Ala Leu Arg Thr Leu Asn
        355                 360                 365

Val Lys Ala Ile Ile Pro Val Asp Leu Asn Ser Leu Leu Ala Gly Asp
    370                 375                 380

His Ala Leu Leu Ala Asn Leu Tyr Asp Leu Tyr Ser Asn Ser Ser Ser
385                 390                 395                 400

Ser Asn Ser Thr Ser Asn Ser Ser Ser Ile Ser Asn Ser Ser Ser Gln
                405                 410                 415

Ala Ala Tyr His Arg Gln Ala Ala Gln Asn Leu Thr Ala Ala Ile Leu
```

```
            420                 425                 430

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

Ser Ser Asn Ser Gln Ser Asp Ile Tyr Thr Pro Ala Ser Leu Phe Pro
    450                 455                 460

Leu Trp Gln Asn Ile Thr Pro Pro Ala Leu Val Gly Asn Glu Thr Ala
465                 470                 475                 480

Ala Leu Gln Leu Val Ser Gly Val Arg Tyr Leu Leu Gly Lys Tyr Ala
                485                 490                 495

Gly Ile Pro Ser Val Ala Thr Leu Leu Ala Thr Gly Leu Asn Trp Asp
            500                 505                 510

Phe Pro Asn Ser Trp Pro Pro His Val Tyr Thr Ser Ile Lys Ala Phe
        515                 520                 525

Gln Thr Leu Tyr Arg Val Asn Pro Asn Ala Thr Val Leu Ser Asn Leu
    530                 535                 540

Thr Leu Ser Phe Ala Gln Val Gln Ala Gly Gln Leu Gly Leu Ser Glu
545                 550                 555                 560

Thr Gly Phe Gln Ile Gln Pro Ala Ser Thr Val Gly Asn Thr Ser Leu
                565                 570                 575

Glu Thr Ala Glu Ala Lys Gly Lys Pro Trp Pro Val Ala Leu Gly Ile
            580                 585                 590

Glu Tyr Ala Asn Arg Tyr Met Gln Ser Ala Phe Cys Ser Trp Tyr Ser
        595                 600                 605

Thr Gly Gly Glu Ile Ser Gly Val Leu Thr Gln Leu Pro Leu Ser Asp
    610                 615                 620

Leu Asn Ser Thr Gly Thr Phe Thr Ala Gly Gln Thr Gly Val Met Phe
```

```
625                 630                 635                 640


Glu Lys Phe Asn Val Thr Asp Pro Asp Ala Ala Gly Gly Gly Gly Glu
                645                 650                 655


Tyr Thr Val Gln Thr Gly Phe Gly Trp Thr Asn Gly Val Val Leu Trp
            660                 665                 670


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


Ile Pro Ile Ile Glu Ile Ser Gly Ser Ser Asn Ser Ser Ile Tyr Ala
    690                 695                 700


Asn Gly Thr Val Thr Asn Ser Thr Ala Leu Tyr Arg Gly Tyr Lys Ile
705                 710                 715                 720


Pro Arg Lys



<210>  197
<211>  663
<212>  PRT
<213>  Trichoderma asperellum

<400>  197

Leu Tyr Thr Asn Gly Ser Val Ile Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys His Gly Asp Ile Leu Gln Asp Ile Gln Leu Ala His Pro Phe Ser
            20                  25                  30


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


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


Ser Leu Gln Val Phe Leu Glu Thr Tyr Phe Ala Asp Ala Gly Gly Glu
65                  70                  75                  80
```

```
Leu Val Glu Val Pro Arg Ser Ser Leu Thr Thr Asn Pro Ala Phe Leu
                85                  90                  95


Asn Lys Ile Asn Asp Thr Val Ile Arg Glu Phe Val Thr Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ser Gly Ala Val Gly Asn
        115                 120                 125


Cys Ser Thr Cys Pro Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val
    130                 135                 140


Val Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp
145                 150                 155                 160


Ile Ile Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Val Gly Ile Ala
                165                 170                 175


Lys Asn Thr Ile Glu Asn Phe Leu Asp Phe Ile Asp Arg Phe Gly Phe
            180                 185                 190


Ile Pro Asn Gly Ala Arg Leu Tyr Tyr Leu Asn Arg Ser Gln Pro Pro
        195                 200                 205


Leu Leu Ser Gln Met Val Arg Ile Tyr Ile Glu His Thr Asn Asp Thr
    210                 215                 220


Ser Ile Leu Lys Arg Ala Leu Pro Leu Leu Val Lys Glu His Asp Phe
225                 230                 235                 240


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


Thr Leu Gln Gln Tyr Ala Val Gln Asn Thr Gln Pro Arg Pro Glu Ser
            260                 265                 270


Phe Leu Glu Asp Tyr Val Thr Ala Asn Asn Arg Ser Tyr Tyr Ala Thr
        275                 280                 285
```

```
Ser Gly Ile Ile Tyr Pro Glu Asn Lys His Leu Asn Ser Thr Glu Met
    290                 295                 300


Ala Asp Leu Tyr Ala Asn Leu Ala Thr Gly Ala Glu Ser Gly Asn Asp
305                 310                 315                 320


Tyr Thr Ser Arg Trp Leu Ala Asn Pro Ser Asp Ala Ile Asn Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Asn Lys Glu Ile Val Pro Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gly Asn Glu Leu Thr Ile Ser Gln Phe Tyr
        355                 360                 365


Asn Arg Thr Gly Asp Ala Thr Ala Ala Arg Ala Trp Ala Glu Arg Ala
    370                 375                 380


Ala Asn Arg Ser Ala Ala Ile Gln Ala Val Phe Trp Asn Glu Thr Leu
385                 390                 395                 400


Phe Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ser Ser Gln Tyr Val Tyr
                405                 410                 415


Val Pro Ala Asp Lys Asp Thr Ile Ser Leu Asp Arg Gln Thr Ala Pro
            420                 425                 430


Ser Gly Lys Gln Val Phe Phe His Val Gly Gln Phe Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Asp Tyr Val Lys Asn Asn Pro Tyr Ala Val Thr
    450                 455                 460


Arg Ala Tyr Asp Arg Val Thr Gly Tyr Leu Asp Ala Gln Pro Gly Gly
465                 470                 475                 480


Ile Pro Ala Ser Asn Val Gln Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495
```

```
Val Trp Pro Pro His Met His Ile Leu Met Gln Gly Leu Asn Asn Val
            500                 505                 510


Pro Ala Thr Phe Thr Ala Gln Asp Pro Ser Tyr Gln Asp Ile Gln Asn
        515                 520                 525


Leu Ser Leu Arg Leu Gly Gln Arg Tyr Leu Asp Phe Thr Phe Cys Thr
    530                 535                 540


Trp Leu Ala Thr Gly Gly Ser Thr Ser Glu Thr Pro Lys Leu His Gly
545                 550                 555                 560


Leu Ser Asp Gln Asp Val Gly Ile Met Phe Glu Lys Tyr Asp Asp Asn
                565                 570                 575


Ser Thr Asn Ala Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Leu Trp Thr Ala Asp Thr Phe Gly
        595                 600                 605


Asn Lys Leu Lys Arg Pro Gln Cys Gly Asn Ile Thr Ala Gly His Pro
    610                 615                 620


Ala Pro Ala Ser Ser Ser Ser Lys Arg Ser Ala Val Gln Leu Asp Ala
625                 630                 635                 640


Trp Asp Ala Arg Arg Val Lys Lys Phe Gly Lys Arg Thr Glu Gly Arg
                645                 650                 655


Val Lys Arg Pro Phe Leu Phe
            660


<210>  198
<211>  674
<212>  PRT
<213>  Corynascus sepedonium

<400>  198
```

```
Leu Tyr Ile Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15

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

Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Val Asp Glu
        35                  40                  45

Val Leu Ala Ala Phe Ser Lys Leu Ser Leu Pro Leu Ser Asn Asn Ser
    50                  55                  60

Glu Leu Asn Ala Phe Leu Tyr Glu Asn Phe Ala Gln Ala Gly His Glu
65                  70                  75                  80

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

Asp Lys Leu Glu Asp Arg Thr Ile Lys Glu Phe Val Gly Lys Val Ile
            100                 105                 110

Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Ser Asn Cys
        115                 120                 125

Thr Glu Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140

Ala Gly Gly Arg Phe Arg Glu Gly Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160

Val Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr His Ile Ser Lys
                165                 170                 175

Asn Ile Ile Glu Asn Phe Leu Asp Phe Val Asp Thr Ile Gly Phe Ile
            180                 185                 190

Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205
```

```
Leu Thr Leu Met Val Lys Ser Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220


Ile Leu Asp Arg Ala Leu Pro Leu Leu Ile Lys Glu His Glu Phe Phe
225                 230                 235                 240


Met Asn Asn Arg Thr Val Ser Ile Thr Gly Ser Asn Gly Lys Glu Tyr
                245                 250                 255


Thr Leu Asn Arg Tyr His Val Glu Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Phe Arg Glu Asp Tyr Ile Thr Ala Asn Asn Gly Ser Tyr Tyr Ala Ser
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Glu Thr Glu Lys
    290                 295                 300


Ala Ala Leu Tyr Ser Asn Leu Ala Thr Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320


Tyr Thr Ser Arg Trp Leu Gly Val Pro Ser Asp Ala Ala Arg Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Val Arg Asp Ile Val Pro Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Ile Ala Glu Tyr Leu
        355                 360                 365


Glu Lys Ala Gly Asn Ser Ser Ala Ala Lys Arg Phe Ala Thr Ala Ala
    370                 375                 380


Glu Gln Arg Ser Glu Ala Met Tyr Ser Leu Met Trp Asn Ala Thr His
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Asp Asn Thr Gln His Ile Phe
                405                 410                 415
```

```
Val Pro Ala Asp Glu Asp Thr Ala Pro Gln Asp Arg Ile Glu Ala Pro
            420                 425                 430


Pro Gly Gln Gln Val Phe Phe His Ile Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Ala Ser Leu Lys Ala Asn Pro Leu Ala Val Gln
    450                 455                 460


Gln Ala Tyr Ala Arg Val Ala Arg Met Leu Asp Ile Lys Lys Gly Ala
465                 470                 475                 480


Ile Pro Ala Thr Asn Tyr Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Ile Leu Met Lys Gly Leu Leu Asn Thr
            500                 505                 510


Pro Ala Thr Phe Gly Lys Ser Asp Pro Ala Tyr Gln Ser Val Gln Asn
        515                 520                 525


Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Asp Phe Pro Gln Leu Glu Gly
545                 550                 555                 560


Val Thr Pro Gly Ala Thr Gly Val Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575


Ala Thr Asn Val Ala Gly Thr Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Gly
        595                 600                 605


Asn Lys Leu Lys Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala His Thr
    610                 615                 620
```

His Ser Ser Ala Lys Arg Gly Leu Glu Glu Asn Lys Leu Pro Arg Arg
625 630 635 640

Ala Val Glu Leu Asp Pro Trp Asp Ala Ala Trp Thr Lys Met Phe Gly
645 650 655

Arg Ser Lys Leu Arg Arg Arg Glu Ala Glu Asp Val Arg Lys Arg Trp
660 665 670

Met Ser

<210> 199
<211> 674
<212> PRT
<213> Myceliophthora thermophila

<400> 199

Leu Tyr Ile Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Ile Tyr
1 5 10 15

Cys His Gly Glu Leu Leu Lys Gly Val Glu Leu Ala His Pro Phe Val
20 25 30

Asp Ser Lys Thr Phe Val Asp Met Pro Thr Leu Lys Pro Val Asp Glu
35 40 45

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

Glu Leu Asn Asn Phe Leu Ala Glu Tyr Phe Ala Pro Ala Gly His Glu
65 70 75 80

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

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

```
Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Gly Asp Cys
        115                 120                 125


Ser Gly Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160


Leu Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr Gln Ile Ser Lys
                165                 170                 175


Asn Ile Ile Glu Asn Phe Leu Asp Phe Ile Asp Thr Ile Gly Phe Ile
            180                 185                 190


Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205


Leu Thr Arg Met Val Lys Ser Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220


Ile Leu Glu Arg Ala Leu Pro Leu Leu Ile Lys Glu His Asp Phe Phe
225                 230                 235                 240


Thr Asn Asn Arg Ser Val Ser Val Thr Ala Ser Asn Gly Lys Thr Tyr
                245                 250                 255


Thr Leu His Arg Tyr His Val Glu Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Tyr Arg Glu Asp Tyr Ile Thr Ala Asn Asn Gly Ser Tyr Tyr Ala Ala
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Glu Thr Glu Lys
    290                 295                 300


Ala Val Leu Tyr Ser Asn Leu Ala Ser Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320
```

```
Tyr Thr Ala Arg Trp Leu Arg Val Pro Asp Asp Ala Ala Arg Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Val Arg Glu Met Val Pro Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Glu Asn Glu Val Ile Ile Ala Glu Tyr Leu
        355                 360                 365


Glu Lys Ala Gly Asn Ser Ser Glu Ala Lys Arg Phe Ala Ser Ala Ala
    370                 375                 380


Lys Gln Arg Ser Glu Ala Met Tyr Asn Leu Met Trp Asn Ala Thr His
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Asn Ala Gln Asn Ile Phe
                405                 410                 415


Val Pro Ala Asp Glu Asp Thr Ala Ser Phe Asp Arg Tyr Ala Ala Pro
            420                 425                 430


Pro Gly Gln Gln Val Leu Phe His Val Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Ala His Leu Lys Ser Asn Pro Leu Ala Val Gln
    450                 455                 460


Lys Ala Tyr Ala Arg Val Ser Arg Arg Leu Asp Thr Lys Lys Gly Ala
465                 470                 475                 480


Ile Ala Ala Thr Asn Tyr Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Val Leu Met Gln Gly Leu Leu Asn Thr
            500                 505                 510


Pro Ala Thr Phe Gly Glu Ser Asp Pro Ala Tyr Gln Gly Val Gln Lys
        515                 520                 525
```

```
Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Asp Phe Pro Gln Leu Gln Gly
545                 550                 555                 560


Val Ser Pro Asp Ala Thr Gly Ile Met Phe Glu Lys Tyr Ala Asp Ser
                565                 570                 575


Ala Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Gly
        595                 600                 605


Asn Lys Leu Lys Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala His Thr
    610                 615                 620


His Ser Glu Ala Lys Arg Ser Leu Gly Asp Gly Gly Leu Ala Arg Arg
625                 630                 635                 640


Ala Val Glu Leu Asp Pro Trp Asp Ala Ala Trp Thr Lys Met Phe Gly
                645                 650                 655


Arg Ser Lys Leu Arg Arg Arg Glu Ala Glu Asp Val Arg Lys Arg Trp
            660                 665                 670


Ser Ser



<210>  200
<211>  661
<212>  PRT
<213>  reesei GH37

<400>  200

Leu Tyr Ile Asn Gly Ser Val Ile Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys His Gly Asp Ile Leu Arg Glu Ile Glu Leu Ala His Pro Phe Ser
```

```
            20                  25                  30

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

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

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

Leu Ile Gln Val Pro Arg Ala Asn Leu Thr Thr Asn Pro Thr Phe Leu
                85                  90                  95

Ser Lys Ile Asn Asp Thr Val Ile Glu Gln Phe Val Thr Gln Val Ile
            100                 105                 110

Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Asp Ala Ala Val
        115                 120                 125

Lys Asn Cys Ser Ser Cys Pro Asn Ser Phe Ile Pro Val Asn Arg Thr
    130                 135                 140

Phe Val Val Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser
145                 150                 155                 160

Tyr Trp Ile Val Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Val Gly
                165                 170                 175

Ile Ala Arg Asn Thr Ile Asp Asn Phe Leu Asp Phe Ile Glu Arg Phe
            180                 185                 190

Gly Phe Val Pro Asn Gly Ala Arg Leu Tyr Tyr Leu Asn Arg Ser Gln
        195                 200                 205

Pro Pro Leu Leu Ser Arg Met Val Lys Val Tyr Ile Asp His Thr Asn
    210                 215                 220

Asp Thr Ala Ile Leu Arg Arg Ala Leu Pro Leu Leu Val Lys Glu His
```

```
225                 230                 235                 240

Glu Phe Trp Thr Arg Asn Arg Thr Val Asp Val Arg Val Asn Asn Lys
                245                 250                 255

Thr Tyr Val Leu Asn Gln Tyr Ala Val Gln Asn Thr Gln Pro Arg Pro
            260                 265                 270

Glu Ser Phe Arg Glu Asp Phe Gln Thr Ala Asn Asn Arg Ser Tyr Tyr
        275                 280                 285

Ala Ala Ser Gly Ile Ile Tyr Pro Ala Thr Lys Pro Leu Asn Glu Ser
    290                 295                 300

Gln Ile Glu Glu Leu Tyr Ala Asn Leu Ala Ser Gly Ala Glu Ser Gly
305                 310                 315                 320

Asn Asp Tyr Thr Ala Arg Trp Leu Ala Asp Pro Ser Asp Ala Met Arg
                325                 330                 335

Asp Val Tyr Phe Pro Leu Arg Ser Leu Asn Asn Lys Asp Ile Val Pro
            340                 345                 350

Val Asp Leu Asn Ser Ile Leu Tyr Gly Asn Glu Leu Ala Ile Ala Gln
        355                 360                 365

Phe Tyr Asn Gln Thr Gly Asn Thr Thr Ala Ala Arg Glu Trp Ser Ser
    370                 375                 380

Leu Ala Ala Asn Arg Ser Ala Ser Ile Gln Ala Val Phe Trp Asn Glu
385                 390                 395                 400

Thr Leu Phe Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ser Ser Gln Asn
                405                 410                 415

Ile Tyr Val Pro Leu Asp Lys Asp Ala Val Ala Leu Asp Arg Gln Thr
            420                 425                 430

Ala Pro Pro Gly Lys Gln Val Leu Phe His Val Gly Gln Phe Tyr Pro
```

```
        435                 440                 445

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

Val Thr Arg Ile Phe Asp Arg Val Lys Ser Tyr Leu Asp Thr Arg Pro
465                 470                 475                 480

Gly Gly Ile Pro Ala Ser Asn Val Asn Thr Gly Gln Gln Trp Asp Gln
                485                 490                 495

Pro Asn Val Trp Pro Pro His Met His Ile Leu Met Glu Ser Leu Asn
            500                 505                 510

Ser Val Pro Ala Thr Phe Ser Glu Ala Asp Pro Ala Tyr Gln Asp Val
        515                 520                 525

Arg Asn Leu Ser Leu Arg Leu Gly Gln Arg Tyr Leu Asp Phe Thr Phe
    530                 535                 540

Cys Thr Trp Arg Ala Thr Gly Gly Ser Thr Ser Glu Thr Pro Lys Leu
545                 550                 555                 560

Gln Gly Leu Thr Asp Gln Asp Val Gly Ile Met Phe Glu Lys Tyr Asn
                565                 570                 575

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

Glu Gly Phe Gly Trp Thr Asn Gly Val Leu Leu Trp Thr Ala Asp Thr
        595                 600                 605

Phe Gly Ser Gln Leu Lys Arg Pro Gln Cys Gly Asn Ile Met Ala Gly
    610                 615                 620

His Pro Ala Pro Ser Lys Arg Ser Ala Val Gln Leu Asp Met Trp Asp
625                 630                 635                 640

Ala Ser Arg Val Lys Lys Phe Gly Arg Arg Ala Glu Gly Arg Met Gly
```

```
            645                 650                 655


Thr Leu His Ala Trp
            660



<210>  201
<211>  670
<212>  PRT
<213>  Chaetomium virescens

<400>  201

Leu Tyr Ile Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Leu Tyr
1               5                   10                  15


Cys Gln Gly Glu Ile Leu Lys Ala Ile Glu Leu Ala Arg Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Leu Glu Glu
        35                  40                  45


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


Glu Leu Thr Ala Phe Leu Ala Glu Asn Phe Ala Pro Ala Gly Gly Glu
65                  70                  75                  80


Leu Glu Glu Val Pro Lys Ser Glu Leu His Thr Asp Pro Val Phe Leu
                85                  90                  95


Asn Lys Leu Asp Asp Ala Val Val Lys Glu Phe Val Gly Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Gly Asn Cys
        115                 120                 125


Ser Asn Cys Glu Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160
```

```
Val Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Val Gly Ile Thr Lys
                165                 170                 175

Asn Ile Leu Glu Asn Phe Leu Asp Phe Ile Glu Thr Ile Gly Phe Val
            180                 185                 190

Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205

Leu Thr Lys Met Ile Lys Ile Tyr Val Asp His Thr Lys Asp Thr Ser
    210                 215                 220

Ile Leu Gln Arg Ala Leu Pro Leu Leu Ile Lys Glu His Glu Trp Trp
225                 230                 235                 240

Thr Asn Asn Arg Ser Val Thr Val Thr Gly Pro Asn Gly Lys Thr Tyr
                245                 250                 255

Thr Leu Asn Arg Tyr His Val Asn Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270

Phe Arg Glu Asp Tyr Ile Thr Ala Asn Asn Gly Ser Tyr Tyr Ala Thr
        275                 280                 285

Ser Gly Ile Ile Tyr Pro Val Lys Ser Pro Leu Asn Glu Thr Glu Lys
    290                 295                 300

Asp Glu Thr Tyr Ala Asn Leu Ala Thr Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320

Tyr Thr Ala Arg Trp Leu Arg Thr Pro Asn Asp Ala Ala Lys Asp Val
                325                 330                 335

Tyr Phe Pro Leu Arg Ser Leu Asn Val Arg Asn Met Ile Pro Val Asp
            340                 345                 350

Leu Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Ile Gly Glu Tyr Leu
        355                 360                 365
```

```
Glu Gln Ala Gly Asn Lys Ser Glu Ala Gln Arg Trp Phe Gln Ala Ala
    370                 375                 380


Asn Gln Arg Ser Glu Ala Met Tyr Ala Leu Met Trp Asn Ala Thr His
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Asn Ser Gln Tyr Ile Phe
                405                 410                 415


Ile Ala Asn Asp Glu Asp Ala Thr Thr Ala Glu Gln Ala Asn Ser Pro
            420                 425                 430


Pro Gly Gln Gln Val Leu Phe Ser Ile Ser Gln Leu Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Asp Gln Leu Lys Lys Asn Pro Leu Ala Val Gln
    450                 455                 460


Gln Ala Tyr Tyr Arg Ile Glu Arg Met Leu Asn Glu Lys Ala Gly Ala
465                 470                 475                 480


Ile Pro Ser Thr Asn Phe Arg Thr Gly Gln Gln Trp Asp Glu Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Ile Leu Met Gln Gly Leu Leu Asn Thr
            500                 505                 510


Pro Ala Thr Phe Gly Thr Ala Asp Pro Ala Tyr Ala Ala Val Gln Asn
        515                 520                 525


Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Gln Thr Pro Gln Leu Gln Gly
545                 550                 555                 560


Val Ser Pro Gly Ala Thr Gly Ile Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575
```

```
Ala Thr Asn Val Ala Gly Ser Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Glu Thr Phe Gly
        595                 600                 605


Asn Lys Leu Lys Arg Pro Asp Cys Gly Asp Ile Gln Ala Ala His Thr
    610                 615                 620


His Thr Asp Lys Lys Lys Arg Trp Ser Val Asp Gly Glu Val Arg Ala
625                 630                 635                 640


Arg Glu Arg Met Ala Val Glu Leu Asp Pro Trp Asp Ala Lys Trp Thr
                645                 650                 655


Lys Met Phe Gly Gln Ala Lys Gly Arg Val Gly Arg Arg Ser
            660                 665                 670


<210>  202
<211>  508
<212>  PRT
<213>  Rhodothermus marinus

<400>  202

Gln Asp Arg Val Ala Cys Gln Val Pro Leu Pro Ser Val Glu Arg Ile
1               5                   10                  15


Glu Ala Val Arg Ala Tyr Ile Arg Gln Ser Trp Asp Val Leu Thr Arg
            20                  25                  30


Ser His Arg Asp Leu Leu Ala Ala Val Gln Asp Pro Lys Ile Glu His
        35                  40                  45


Glu Pro Gly Thr Pro Trp Pro Leu Tyr Ile Ala Ala Thr Glu Asp Ser
    50                  55                  60


Val Ala Val Trp His Arg Leu Gln Gln Glu Leu Pro Asp Ser Val Leu
65                  70                  75                  80
```

```
Gln Gln Ile Val Leu Arg Val Leu Pro Glu Asp Pro Val Ala His Leu
                85                  90                  95


Asp Glu Ile His Pro His Gly Leu Leu Tyr Leu Pro Glu Pro Tyr Val
            100                 105                 110


Val Pro Gly Gly Arg Phe Asn Glu Met Tyr Gly Trp Asp Ser Tyr Phe
        115                 120                 125


Ile Val Val Gly Leu Leu Arg Asp Gly Arg Val Asp Leu Ala Lys Ala
    130                 135                 140


Met Thr Asp Asn His Leu Tyr Gln Val Arg His Tyr Gly Lys Val Leu
145                 150                 155                 160


Asn Ala Asn Arg Thr Tyr Tyr Leu Thr Arg Ser Gln Pro Pro Phe Leu
                165                 170                 175


Ser Ala Met Val Leu Ala Val Tyr Ala His Thr Gln Asp Arg Asp Trp
            180                 185                 190


Leu Ala Ala Ala Val Pro Leu Ile Glu Arg Tyr Tyr Ala Tyr Trp Thr
        195                 200                 205


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


Leu Gly Glu Gly Pro Ala Pro Glu Val Val Ala Gly Glu Arg Asp Ala
225                 230                 235                 240


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


Glu Val Thr Ala Tyr Asp Glu Ser Leu Tyr Tyr Val Ala Glu Ala Asp
            260                 265                 270


Ser Leu Thr Pro Leu Phe Tyr Lys Gly Asp Arg Ser Met Arg Glu Ser
        275                 280                 285
```

```
Gly Phe Asp Pro Ser Asn Arg Phe Gly Pro Phe Ser Val Asp Ile Ile
    290                 295                 300


His Tyr Ala Pro Val Gly Leu Asn Ala Leu Leu Tyr Arg Met Glu Thr
305                 310                 315                 320


Asp Leu Ala Arg Ile His Glu Ile Leu Gly Asp Thr Ala Ala Ala Ala
                325                 330                 335


Ala Trp Arg Ala Arg Ala Glu Ala Arg Arg Glu Arg Val Asp Arg Tyr
            340                 345                 350


Leu Trp Asp Ser Glu Arg Gly Leu Tyr Phe Asp Tyr Asn Phe Arg Thr
        355                 360                 365


Gly Arg Arg Ser Asp Tyr Val Phe Ala Thr Thr Phe Tyr Pro Leu Trp
    370                 375                 380


Val Gly Met Ala Ser Pro Glu Gln Ala Ala Arg Val Ala Ala Asn Leu
385                 390                 395                 400


Tyr Leu Leu Glu Ala Pro Gly Gly Leu Leu Thr Ser Thr His Ile Ser
                405                 410                 415


Gly Ser Gln Trp Asp Ala Pro Tyr Gly Trp Ala Pro Leu Tyr Leu Ile
            420                 425                 430


Ala Val Glu Gly Leu Arg Arg Tyr Gly Tyr Asp Glu Ala Ala Asp Arg
        435                 440                 445


Leu Thr Ala Lys Phe Val Ser Met Ile Val Glu Asp Phe Glu Arg Thr
    450                 455                 460


Gly Val Ile Leu Glu Lys Tyr Asp Val Val Gln Arg Arg Ser Asp Val
465                 470                 475                 480


Ala Leu Arg Tyr Gly Tyr Thr Ser Asn Glu Ile Gly Phe Gly Trp Thr
                485                 490                 495
```

```
Asn Ala Val Phe Ala Glu Leu Leu Ala Gln Met Asp
            500                 505


<210>  203
<211>  674
<212>  PRT
<213>  Myceliophthora sepedonium

<400>  203

Leu Tyr Ile Asn Gly Ser Val Thr Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


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


Asp Ser Lys Thr Phe Val Asp Met Pro Thr Ile Lys Pro Val Asp Glu
        35                  40                  45


Val Leu Ala Ala Phe Ser Lys Leu Ser Leu Pro Leu Ser Asn Asn Ser
    50                  55                  60


Glu Leu Asn Ala Phe Leu Tyr Glu Asn Phe Ala Gln Ala Gly His Glu
65                  70                  75                  80


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


Asp Lys Leu Glu Asp Arg Thr Ile Lys Glu Phe Val Gly Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ala Gly Pro Ser Asn Cys
        115                 120                 125


Thr Glu Cys Ala Asn Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp Ile
145                 150                 155                 160
```

```
Val Glu Gly Leu Leu Arg Thr Gly Gly Ala Phe Thr His Ile Ser Lys
                165                 170                 175


Asn Ile Ile Glu Asn Phe Leu Asp Phe Val Asp Thr Ile Gly Phe Ile
            180                 185                 190


Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205


Leu Thr Leu Met Val Lys Ser Tyr Val Asp Tyr Thr Asn Asp Thr Ser
    210                 215                 220


Ile Leu Asp Arg Ala Leu Pro Leu Leu Ile Lys Glu His Glu Phe Phe
225                 230                 235                 240


Met Asn Asn Arg Thr Val Ser Ile Thr Gly Ser Asn Gly Lys Glu Tyr
                245                 250                 255


Thr Leu Asn Arg Tyr His Val Glu Asn Asn Gln Pro Arg Pro Glu Ser
            260                 265                 270


Phe Arg Glu Asp Tyr Ile Thr Ala Asn Asn Gly Ser Tyr Tyr Ala Ser
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Val Lys Thr Pro Leu Asn Glu Thr Glu Lys
    290                 295                 300


Ala Ala Leu Tyr Ser Asn Leu Ala Thr Gly Ala Glu Ser Gly Trp Asp
305                 310                 315                 320


Tyr Thr Ser Arg Trp Leu Gly Val Pro Ser Asp Ala Ala Arg Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Ser Leu Asn Val Arg Asp Ile Val Pro Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gln Asn Glu Val Ile Ile Ala Glu Tyr Leu
        355                 360                 365
```

```
Glu Lys Ala Gly Asn Ser Ser Ala Ala Lys Arg Phe Ala Thr Ala Ala
    370                 375                 380


Glu Gln Arg Ser Glu Ala Met Tyr Ser Leu Met Trp Asn Ala Thr His
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Asp Asn Thr Gln His Ile Phe
                405                 410                 415


Val Pro Ala Asp Glu Asp Thr Ala Pro Gln Asp Arg Ile Glu Ala Pro
            420                 425                 430


Pro Gly Gln Gln Val Phe Phe His Ile Ala Gln Leu Tyr Pro Phe Trp
        435                 440                 445


Thr Gly Ala Ala Pro Ala Ser Leu Lys Ala Asn Pro Leu Ala Val Gln
    450                 455                 460


Gln Ala Tyr Ala Arg Val Ala Arg Met Leu Asp Ile Lys Lys Gly Ala
465                 470                 475                 480


Ile Pro Ala Thr Asn Tyr Arg Thr Gly Gln Gln Trp Asp Gln Pro Asn
                485                 490                 495


Val Trp Pro Pro Leu Gln His Ile Leu Met Lys Gly Leu Leu Asn Thr
            500                 505                 510


Pro Ala Thr Phe Gly Lys Ser Asp Pro Ala Tyr Gln Ser Val Gln Asn
        515                 520                 525


Leu Ala Leu Arg Leu Ala Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540


Trp Tyr Ala Thr Gly Gly Ser Thr Ser Asp Phe Pro Gln Leu Glu Gly
545                 550                 555                 560


Val Thr Pro Gly Ala Thr Gly Val Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575
```

```
Ala Thr Asn Val Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp Val Phe Gly
        595                 600                 605


Asn Lys Leu Lys Arg Pro Asp Cys Gly Asn Ile Thr Ala Ala His Thr
    610                 615                 620


His Ser Ser Ala Lys Arg Gly Leu Glu Glu Asn Lys Leu Pro Arg Arg
625                 630                 635                 640


Ala Val Glu Leu Asp Pro Trp Asp Ala Ala Trp Thr Lys Met Phe Gly
                645                 650                 655


Arg Ser Lys Leu Arg Arg Arg Glu Ala Glu Asp Val Arg Lys Arg Trp
            660                 665                 670


Met Ser



<210>  204
<211>  657
<212>  PRT
<213>  Moelleriella libera

<400>  204

Leu His Thr Asn Gly Ser Leu Ile Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys Tyr Gly Asp Ile Leu Lys Gln Val Glu Leu Ala Arg Pro Phe Ala
            20                  25                  30


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


Ile Gln Ala Ala Phe Asp Lys Leu Glu Lys Pro Leu Arg Asn Asn Thr
    50                  55                  60


Ala Leu Gln Asp Phe Leu Lys Thr Tyr Phe Ala Asp Ala Gly Gln Glu
```

```
65                  70                  75                  80

Leu Gln Glu Val Pro Lys Ser Glu Leu Lys Thr Asp Pro Gln Phe Leu
                85                  90                  95

Lys Thr Leu Asn Asp Thr Val Ile Arg Glu Phe Val Thr Lys Val Ile
            100                 105                 110

Asp Ile Trp Pro Asp Leu Thr Arg Ser Tyr Lys Gly Ser Asn Thr Asn
        115                 120                 125

Cys Thr Asp Cys Pro Asn Ser Phe Ile Pro Ile Asn Arg Thr Phe Val
    130                 135                 140

Ile Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp
145                 150                 155                 160

Ile Leu Glu Gly Leu Leu Arg Thr Arg Gly Ser Phe Thr Gln Ile Ala
                165                 170                 175

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

Val Pro Asn Gly Ala Arg Ile Tyr Phe Leu Asn Arg Ser Gln Pro Pro
        195                 200                 205

Met Leu Ser Gln Met Val Lys Leu Tyr Ile Asp His Thr Asn Asp Thr
    210                 215                 220

Ala Ile Leu Gln Arg Ala Leu Pro Leu Leu Val Lys Glu His Ala Trp
225                 230                 235                 240

Trp Met Asn Asn Arg Thr Val Asp Val Gln Val Gly Gly Lys Thr Tyr
                245                 250                 255

Lys Leu Asn Arg Tyr Ala Val Ser Asn Thr Glu Pro Arg Pro Glu Ser
            260                 265                 270

Tyr Arg Glu Asp Phe Glu Thr Ala Ser Asn Ser Ser Tyr Tyr Ala Gln
```

```
        275                 280                 285


Ser Gly Ile Ile Tyr Pro Glu Thr Lys Lys Leu Asn Asp Ser Gln Arg
    290                 295                 300


Ala Val Leu Tyr Ala Asn Met Ala Thr Gly Gly Glu Asn Gly Trp Asp
305                 310                 315                 320


Phe Ser Ser Arg Trp Ile Ala Asn Pro Ser Asp Ser Val Arg Asp Val
                325                 330                 335


Tyr Phe Pro Leu Arg Thr Asn Asn Ala Gln Asn Val Val Pro Val Cys
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gly Asn Glu Met Thr Ile Gly Gly Phe Phe
        355                 360                 365


Asn Ser Thr Gly Asn Thr Thr Ala Gly Gln Glu Trp Ala Ala Lys Ala
    370                 375                 380


Lys Ala Arg Ser Glu Ala Met His Ala Thr Met Trp Asn Glu Thr His
385                 390                 395                 400


Phe Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ser Ala Gln Asp Val Tyr
                405                 410                 415


Thr Leu Ala Asp Asp Asp Thr Ser Ile Tyr Asp Asn Gly Thr Leu Thr
            420                 425                 430


Gly Ala Pro Pro Gly Tyr Gln Val Ala Phe Asn Gly Ala Gln Phe Tyr
        435                 440                 445


Pro Phe Trp Gln Gly Ala Ala Pro Thr Tyr Leu Lys Glu Asn Pro Gln
    450                 455                 460


Ala Val Lys Thr Ala Tyr Ala Arg Val Ala Gln Tyr Leu Lys Val Arg
465                 470                 475                 480


Lys Gly Gly Ile Pro Ala Thr Asn Leu Lys Ala Arg Glu Gln Trp Asp
```

```
                485                 490                 495

Gln Pro Asn Val Trp Pro Pro Leu Met His Ile Leu Met Gln Gly Leu
            500                 505                 510

Leu Asn Thr Pro Pro Thr Phe Gly Ser Ser Asp Pro Ser Tyr Lys Ser
        515                 520                 525

Val Arg Ser Met Ala Leu Thr Leu Ala Gln Arg Tyr Leu Asp Ser Thr
    530                 535                 540

Phe Cys Thr Trp Tyr Ala Thr Gly Gly Ser Thr Ser Glu Thr Pro Lys
545                 550                 555                 560

Arg Pro Gly Leu Pro Glu Lys Asp Lys Gly Ile Met Phe Glu Lys Tyr
                565                 570                 575

Ala Asp Asn Ser Ile Asp Ile Ala Gly Ser Gly Gly Glu Tyr Glu Val
            580                 585                 590

Val Glu Gly Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Ala Asp
        595                 600                 605

Thr Phe Ala Asn Glu Leu Lys Arg Pro Asp Cys Gly Asn Gly Ser Ser
    610                 615                 620

Ser Ser Ser Thr Ser Ser Ala Ala Lys Arg Gly Leu Ser Ala Val Glu
625                 630                 635                 640

Leu His Pro Ala Asp Ala Ser Arg Ile Lys Arg Phe Gly Ser Ser Lys
                645                 650                 655

Gly


<210>  205
<211>  660
<212>  PRT
<213>  Acremonium dichromosporum
```

```
<400>  205

Ile Tyr Val Asp Gly Asn Ile Thr Ala Pro Cys Asp Ser Pro Val Tyr
1               5                   10                  15


Cys Tyr Gly Glu Met Leu His Gln Ile Gln Leu Ala Lys Pro Phe Asp
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Ala Leu Lys Pro Leu Ser Gln
        35                  40                  45


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


Ala Leu Asn Asn Phe Leu Asp Glu Phe Phe Ala Asp Ala Gly Gly Glu
65                  70                  75                  80


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


Asp Lys Ile Asp Asp Glu Val Val Lys Glu Phe Thr Asn Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Ser Gly Ala Ala Ala Ser
        115                 120                 125


Asn Cys Thr Asn Cys Pro Ser Ser Phe Ile Pro Leu Asn Arg Thr Phe
    130                 135                 140


Val Val Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Thr Tyr
145                 150                 155                 160


Trp Ile Ile Glu Gly Leu Leu Arg Thr Gly Gly Ser Phe Thr Asp Ile
                165                 170                 175


Ser Arg Asp Ile Ile Glu Asn Phe Leu Asp Phe Val Asp Gln Phe Gly
            180                 185                 190


Phe Val Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro
        195                 200                 205
```

```
Pro Val Leu Ser Arg Met Val Gln Ala Tyr Ile Glu His Thr Asn Asp
    210                 215                 220


Thr Asp Ile Leu Asp Arg Ala Leu Pro Leu Leu Met Lys Glu His Glu
225                 230                 235                 240


Phe Phe Ser Glu Asn Arg Thr Ile Asp Ile Glu Gly Pro Asn Gly Thr
                245                 250                 255


Thr Tyr Thr Leu Asn Arg Tyr Asp Val Arg Asn Asn Gln Pro Arg Pro
            260                 265                 270


Glu Ser Tyr Ser Glu Asp Tyr Glu Thr Ala Thr Asn Thr Ser Tyr Tyr
        275                 280                 285


Ser His Asp Ser Gly Ile Ile Tyr Pro Glu Thr Glu Pro Leu Asn Asp
    290                 295                 300


Thr Glu Arg Ala Asn Leu Tyr Ser Ala Leu Ala Ser Gly Ala Glu Ser
305                 310                 315                 320


Gly Trp Asp Tyr Ser Ser Arg Trp Ile Ala Arg Pro Arg Asp Ala Ala
                325                 330                 335


Glu Asp Val Tyr Phe Pro Leu Arg Ser Leu Asn Thr Asn Asn Ile Val
            340                 345                 350


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


Gly Phe Leu Asn Gln Thr Gly Asn Ala Ser Ala Ala Ala Glu Trp Glu
    370                 375                 380


Glu Leu Ala Tyr Asn Arg Ser Glu Ala Ile His Ala Leu Met Trp Asn
385                 390                 395                 400


Glu Thr Tyr Met Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ala Ala Gln
                405                 410                 415
```

```
His Ile Tyr Val Pro Ala Asp Asp Asp Val Ser Thr Leu Glu Ser Ser
            420                 425                 430


Thr Ala Pro Glu Gly His Met Val Leu Phe Ser Val Ser Gln Phe Tyr
        435                 440                 445


Pro Phe Trp Thr Gly Ala Ala Pro Ser Tyr Ile Lys Asn Asn Pro Phe
    450                 455                 460


Ala Ile Ala Gln Ile Tyr Lys Arg Val Glu Thr Leu Leu Asp Thr Arg
465                 470                 475                 480


Lys Gly Gly Ile Pro Ala Thr Asn Phe Arg Thr Gly Gln Gln Trp Asp
                485                 490                 495


Gln Pro Ser Val Trp Pro Pro Leu Met His Ile Leu Met Ala Gly Leu
            500                 505                 510


Gln Asn Thr Pro Ala Thr Phe Gly Glu Asp Asp Pro Ala Tyr Gln His
        515                 520                 525


Val His Glu Ile Ala Leu Arg Ile Gly Gln Arg Tyr Leu Asp Ser Thr
    530                 535                 540


Phe Cys Thr Trp Arg Ala Thr Gly Gly Ala Thr Ser Glu Thr Pro Gln
545                 550                 555                 560


Leu Glu Gly Phe Thr Asp Arg Asp Val Gly Ile Met Phe Glu Lys Tyr
                565                 570                 575


Ala Asp Asn Ser Thr Asn Ile Ala Gly Gly Gly Gly Glu Tyr Glu Val
            580                 585                 590


Val Glu Gly Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Thr Val Asp
        595                 600                 605


Glu Phe Gly Asn Glu Leu Lys Arg Pro Asp Cys Gly Asp Leu Glu Ala
    610                 615                 620
```

```
Ala Asp Thr Thr Glu Arg Arg Lys Arg Ser Ala Leu Gln Leu Ala Pro
625                 630                 635                 640


Arg Asp Ala Gln Arg Thr Lys Lys Phe Gly Lys Arg Ala Val Glu Arg
                645                 650                 655


Gln Pro Trp Phe
            660


<210>  206
<211>  667
<212>  PRT
<213>  Fusarium sambucinum

<400>  206

Leu Tyr Val Asn Gly Thr Val Val Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys His Gly Asp Ile Leu Glu Gln Val Glu Leu Ala Arg Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Met Pro Ala Ile Arg Pro Leu Ser Glu
        35                  40                  45


Ile Gln Lys Ala Phe Asp Glu Leu Asp Lys Pro Leu Arg Asn Asn Ser
    50                  55                  60


Ala Leu Ala Asp Phe Leu Ser Glu Asn Phe Ala Asp Ala Gly Asn Glu
65                  70                  75                  80


Leu Glu Glu Val Pro Glu Asp Glu Leu Lys Thr Asp Pro Lys Phe Leu
                85                  90                  95


Asp Asn Ile Asn Asp Thr Val Ile Arg Glu Phe Thr Glu Lys Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Asp Gln Asp Ser Lys Asn
        115                 120                 125
```

```
Cys Ser Asp Cys Pro Asn Ser Phe Ile Pro Val Asn Arg Ser Phe Val
    130                 135                 140


Val Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Tyr Trp
145                 150                 155                 160


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


Lys Asn Thr Ile Glu Asn Phe Leu Asp Phe Ile Glu Glu Tyr Gly Phe
            180                 185                 190


Val Pro Asn Gly Ala Arg Ile Tyr Tyr Leu Asn Arg Ser Gln Pro Pro
        195                 200                 205


Leu Leu Ser Gln Met Val Lys Ile Tyr Ile Asp His Thr Asn Asp Thr
    210                 215                 220


Asp Ile Leu Glu Arg Ala Leu Pro Leu Leu Val Lys Glu His Glu Phe
225                 230                 235                 240


Phe Met Lys Asn Arg Ser Val Pro Val Tyr Ile Asn Asp Glu Thr Tyr
                245                 250                 255


Met Leu Asn Thr Tyr Asn Val Ser Asn Thr Gln Pro Arg Pro Glu Ser
            260                 265                 270


Tyr Arg Glu Asp Tyr Ile Thr Ala Thr Asn Lys Ser Tyr Tyr Ser Thr
        275                 280                 285


Ser Gly Glu Val Tyr Ser Gly Gly Glu Glu Leu Ser Phe Lys Gln Lys
    290                 295                 300


Glu Thr Leu Tyr Gly Asn Leu Ala Ser Gly Ala Glu Ser Gly Leu Asp
305                 310                 315                 320


Tyr Thr Ser Lys Trp Ile Ala Arg Pro Glu Asn Ala Ile Arg Asp Asn
                325                 330                 335
```

```
Tyr Phe Pro Leu Arg Tyr Leu Asn Thr Arg Asn Ile Ile Pro Val Asp
            340                 345                 350


Leu Asn Ser Ile Leu Tyr Gly Asn Glu Ile Ala Ile Ala Asp Phe Tyr
        355                 360                 365


Glu Gln Thr Gly Asn Ser Ser Ala Ser Glu Gln Trp Arg Glu Val Ala
    370                 375                 380


Ala Asn Arg Ser Tyr Ala Met His Ala Phe Met Trp Asn Glu Thr Leu
385                 390                 395                 400


Trp Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Lys Ala Gln Gln Ile Tyr
                405                 410                 415


Phe Pro Ala Asp Asn Asn Thr Val Ser Val Asp Thr Glu Asp Ala Pro
            420                 425                 430


Lys Gly Gln Gln Val Phe Phe Ser Pro Thr Gln Phe Tyr Pro Phe Trp
        435                 440                 445


Leu Gly Ala Ala Pro Asp Tyr Leu Lys Asn Asn Pro Tyr Ala Val Leu
    450                 455                 460


Ser Ala Tyr Lys Arg Val Ala Thr Tyr Leu Asp Lys Arg Glu Gly Gly
465                 470                 475                 480


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


Val Trp Pro Pro Met Met His Ile Leu Met Ala Gly Leu Glu Lys Val
            500                 505                 510


Pro Ala Thr Phe Gly Ile Met Asp Pro Ser Phe Ile Glu Ile Arg Lys
        515                 520                 525


Leu Ala Leu Arg Leu Gly Gln Arg Tyr Leu Asp Ser Thr Phe Cys Thr
    530                 535                 540
```

```
Trp Tyr Ala Thr Gly Gly Ser Thr Ser Glu Thr Pro Lys Leu Glu Ser
545                 550                 555                 560


Val Ser Asp Lys Glu Asp Gly Ile Met Phe Glu Lys Tyr Ala Asp Asn
                565                 570                 575


Ala Thr Asn Thr Ala Gly Gly Gly Gly Glu Tyr Glu Val Val Glu Gly
            580                 585                 590


Phe Gly Trp Thr Asn Gly Val Leu Ile Trp Ala Val Glu Glu Phe Gly
        595                 600                 605


Asn Arg Leu Thr Arg Pro Lys Cys Lys Asn Leu Glu Thr Ala His Ser
    610                 615                 620


Ser Asp Lys Arg Asp Thr Ser Ala Val Met Leu His Ala Arg Asp Ala
625                 630                 635                 640


Lys His Val Lys Lys Phe Gly Arg Arg Lys Arg Ala Glu Glu Lys Ala
                645                 650                 655


Ala Lys Lys Arg Ser Ser Arg Leu Phe His Phe
            660                 665


<210>  207
<211>  660
<212>  PRT
<213>  Phoma sp.

<400>  207

Leu Tyr Gln Asn Gly Ser Ile Ile Ala Pro Cys Asp Ser Pro Ile Tyr
1               5                   10                  15


Cys Tyr Gly Asp Leu Leu Arg Glu Ile Glu Leu Ala Gln Pro Phe Ser
            20                  25                  30


Asp Ser Lys Thr Phe Val Asp Leu Pro Thr Ile Arg Pro Leu Asp Glu
        35                  40                  45
```

```
Val Leu Arg Ala Phe Asn Asn Leu Thr Lys Pro Ile Gln Asn Asn Thr
    50                  55                  60


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


Leu Asp Ala Leu Pro Lys Asp Gln Leu Glu Thr Gln Pro Asp Phe Leu
                85                  90                  95


Asp Asn Val Asn Ser Ser Val Ile Val Asn Phe Thr Ser Gln Val Ile
            100                 105                 110


Asp Ile Trp Pro Asp Leu Thr Arg Arg Tyr Val Gly Ala Gly Asn Cys
        115                 120                 125


Thr Gly Cys Val Ser Ser Phe Ile Pro Val Asn Arg Thr Phe Val Val
    130                 135                 140


Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp Asp Ser Phe Trp Ile
145                 150                 155                 160


Ile Glu Gly Leu Leu Arg Thr Lys Gly Ser Phe Thr Gln Ile Ala Glu
                165                 170                 175


Asn Ile Ile Glu Asn Phe Met Asp Leu Val Glu Glu Leu Gly Phe Val
            180                 185                 190


Pro Asn Gly Ala Arg Arg Tyr Tyr Glu Asn Arg Ser Gln Pro Pro Leu
        195                 200                 205


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


Leu Leu Glu Arg Ala Leu Pro Val Leu Glu Gln Glu Tyr Glu Phe Trp
225                 230                 235                 240


Val Asn Asn Arg Ser Val Thr Leu Glu Arg Gly Gly Lys Asn Tyr Thr
                245                 250                 255
```

```
Leu His His Tyr Asn Val Ser Asn Thr Gln Pro Arg Pro Glu Ser Tyr
            260                 265                 270


Arg Glu Asp Tyr Ile Thr Ala Asn Asn Leu Thr Tyr Tyr Asn Glu Asn
        275                 280                 285


Gly Glu Gln Phe Asn Ala Ser His Pro Leu Asn Asp Thr Gln Lys Ala
    290                 295                 300


Leu Leu Tyr Ala Glu Leu Ala Ser Gly Ala Glu Thr Gly Trp Asp Tyr
305                 310                 315                 320


Ser Ser Arg Trp Leu Ala Asn Pro Ser Asp Ala Val Asn Asp Asp Phe
                325                 330                 335


Phe Pro Leu Arg Ser Leu Asn Val Ile Asn Thr Ile Pro Val Asp Leu
            340                 345                 350


Asn Ser Ile Leu Tyr Tyr Asn Glu Ile Thr Ile Ala Glu Phe His Arg
        355                 360                 365


Arg Glu Gly Asn Tyr Cys Ala Ala Arg Gln Trp Ala Glu Leu Ala Arg
    370                 375                 380


Asn Arg Ser Glu Ala Met Thr Ala Leu Leu Trp Asn Ala Glu Tyr Tyr
385                 390                 395                 400


Ser Tyr Phe Asp Tyr Asn Leu Thr Ser Ser Ala Gln Asn Ile Tyr Thr
                405                 410                 415


Leu Ala Asp Asn Thr Ser Thr Pro Leu Ser Leu Ala Gly Ala Pro Ala
            420                 425                 430


Gly Tyr Gln Val Gly Phe Gln Leu Ser Gln Leu Tyr Pro Phe Trp Thr
        435                 440                 445


Gly Ala Ala Pro Asp Ser Ile Lys Gly Asp Pro Thr Ala Ile Arg Arg
    450                 455                 460
```

```
Ala Phe Ala Arg Val Glu Glu Ala Leu Asp Thr Glu Ala Gly Ala Val
465                 470                 475                 480


Ser Ala Thr Asn Leu Phe Thr Gly Gln Gln Trp Asp Glu Pro Asn Val
                485                 490                 495


Trp Pro Pro Leu Gln Tyr Ile Ala Ile Gln Gly Leu Leu Asn Thr Pro
            500                 505                 510


Leu Glu Val Ser Glu Asp Asp Asp Glu Gln Thr Ala Glu Asp Tyr Val
        515                 520                 525


Trp Thr Gln Asn Leu Ala Leu Arg Leu Ala Gln Arg Tyr Thr Asp Ser
    530                 535                 540


Leu Phe Cys Thr Trp Arg Ser Thr Gly Gly Ala Thr Glu Glu Glu Pro
545                 550                 555                 560


Gln Leu Pro Gly Ala Thr Gly Asn Gly Thr Ile Phe Glu Lys Tyr Ser
                565                 570                 575


Asp Glu Ala Ile Asn Ala Arg Gly Gly Gly Gly Glu Tyr Thr Val Val
            580                 585                 590


Glu Gly Phe Gly Trp Ser Asn Gly Val Leu Ile Trp Ala Val Asp Asn
        595                 600                 605


Phe Gly Gln Lys Leu Thr Thr Pro Asp Cys Gly Asn Ile Thr Ala Ala
    610                 615                 620


Ala Pro Pro Ser Thr Ala Ser Lys Arg Lys Arg Ser Ala Val Glu Ile
625                 630                 635                 640


His Gln Arg Asp Ala Ala Trp Ile Lys Gly Thr Lys Glu Asn Lys Met
                645                 650                 655


Phe Gly Lys Lys
            660
```

```
<210>  208
<211>  737
<212>  PRT
<213>  Lentinus similis

<400>  208

Leu Pro Gln Ala Val Thr Pro Ser Ser Thr Ser Val Ser Ser Gln Thr
1               5                   10                  15


Val Ser Thr Ala Val Pro Ser Pro Thr Ala Ser Leu Thr Ser Thr Leu
            20                  25                  30


Pro Ser Gln Ile Pro Leu Pro Pro Lys Gln Asp Trp Cys Pro Ser Glu
        35                  40                  45


Ile Phe Cys Ala Gly Glu Leu Leu Gln Thr Val Asn Val Ala Gln Leu
    50                  55                  60


Tyr Pro Asp Pro Lys Thr Phe Val Asp Lys Pro Thr Ala Arg Lys Ser
65                  70                  75                  80


Gln Gln Val Val Ser Asn Phe Gln Asn Ile Gly Gly Asn Ser Ser Asn
                85                  90                  95


Val Thr Val Gly Ala Ile Glu Asp Phe Val Asn Ser Asn Phe Lys Gly
            100                 105                 110


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


Pro Ala Phe Leu Asn Asn Val Ser Asp Pro Leu Val Lys Ala Trp Ser
    130                 135                 140


Gln Ile Val His Gly Tyr Trp Thr Gln Leu Thr Arg Ser Thr Asn Asp
145                 150                 155                 160


Ser Ala Leu Cys Pro Glu Gly Thr Glu Ser Gly Ser Cys Glu Ser Ser
                165                 170                 175


Leu Ile Pro Leu Asn His Thr Phe Val Val Pro Gly Gly Arg Phe Arg
```

```
            180                 185                 190

Glu Gln Tyr Tyr Trp Asp Ser Tyr Trp Ile Val Gln Gly Leu Leu Val
        195                 200                 205

Ser Glu Leu Tyr Asp Ile Val Asn Asp Thr Leu Gln Asn Phe Met Asp
    210                 215                 220

Glu Leu Glu His Ile Gly Phe Ile Pro Asn Gly Gly Arg Ile Tyr Tyr
225                 230                 235                 240

Leu Asn Arg Ser Gln Pro Pro Leu Phe Ile His Met Leu Thr Ser Tyr
                245                 250                 255

Val Gln Ala Ser Gly Asp Thr Ser Ile Leu Lys Arg Ala Leu Pro Leu
            260                 265                 270

Ala Glu Lys Glu Leu Ala Trp Trp Ser Ala Asn Arg Ser Val Gln Val
        275                 280                 285

Lys Ser Pro Tyr Thr Asn Ala Thr His Asn Val Tyr Arg Tyr His Val
    290                 295                 300

Thr Asn Thr Ala Pro Arg Pro Glu Ser Tyr Tyr Thr Asp Tyr Ile Thr
305                 310                 315                 320

Ala Asn Asp Pro Thr Leu Gln Thr Pro Leu Thr Glu Gln Gln Arg Ala
                325                 330                 335

Asp Leu Tyr Ala Glu Leu Ala Thr Gly Ala Glu Ser Gly Trp Asp Tyr
            340                 345                 350

Ser Ser Arg Trp Leu Lys Glu Pro Leu Ala Gly Gly Ser Asn Asn Thr
        355                 360                 365

Ser Pro Ala Leu Arg Ser Leu Asn Ile Arg Ser Leu Val Pro Val Asp
    370                 375                 380

Leu Asn Ser Ile Leu Tyr Lys Ala His Leu Asn Leu Ala Ala Leu Tyr
```

```
385                 390                 395                 400

Asn Asn Glu Ser His Ser Ala Ala Ala Ser Asn His Thr Gln Ala Ala
                405                 410                 415

Ile Ala Leu Arg Glu Ala Ile Leu Asp Leu His Trp Asp Ala Asn Lys
            420                 425                 430

Arg Ala Phe Tyr Asp Phe Asn Ile Thr Ser Asn Ala Arg Asn Asp Ile
        435                 440                 445

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

Glu Ile Leu Ser Asp Gly Ser Gly Ala Thr Ala Phe Gly Ala Phe Ala
465                 470                 475                 480

Ala Val Asn Met Val Leu Asn Arg Tyr Asn Gly Thr Phe Pro Val Thr
                485                 490                 495

Phe Leu Glu Thr Gly Leu Gln Trp Asp Ala Pro Asn Ala Trp Pro Pro
            500                 505                 510

His Gln Phe Ile Ile Ile Glu Ala Leu Arg Asn Leu Pro Ser Asn Ile
        515                 520                 525

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

Leu Ile Pro Ala Gly Gln Val Gly Ile Ala Glu Gly Asp Leu Pro Gly
545                 550                 555                 560

Gln Ile Leu Ser Pro Gly Gln Asn Ala Thr Lys Thr Gly Pro Ala Ala
                565                 570                 575

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

Ser Gly Glu Gly Trp Ala Ala Val Leu Gln Arg Glu Leu Ala Asn Arg
```

```
        595                 600                 605


Tyr Ile Ala Ser Ala Leu Cys Ser Trp His Ala Thr Gly Gly Glu Val
    610                 615                 620


Pro Asn Leu Leu Pro Arg Leu Ser Asp Ser Gln Leu Gln Ile Thr Gln
625                 630                 635                 640


Ser Gln Asn Asn Thr Gly Asn Met Phe Glu Lys Phe Ser Ile Asn Asp
                645                 650                 655


Ile Asp Ser Ala Gly Arg Gly Gly Glu Tyr Thr Val Gln Ala Gly Phe
            660                 665                 670


Gly Trp Thr Asn Gly Val Val Leu Tyr Leu Thr His Val Phe Gly Asp
        675                 680                 685


Lys Leu Val Ala Pro Ser Cys Pro Asn Leu Val Ala Leu Ser Ser Asn
    690                 695                 700


Thr Ala Thr Thr Ser Gly Ala Val Ala Gln Met Thr Leu Pro Ser Ser
705                 710                 715                 720


Leu Ala Val Thr Val Gly Ala Val Val Leu Gly Phe Val Gly Leu Val
                725                 730                 735


Leu



<210>  209
<211>  683
<212>  PRT
<213>  Diaporthe nobilis

<400>  209

Gln Thr Leu Asp Gly Ile Tyr Tyr Asp Gly Asp Asn Ile Ala Pro Cys
1               5                   10                  15


Ser Ser Ala Leu Tyr Cys Tyr Gly Asp Ile Leu Asp Ser Ile Gln Arg
            20                  25                  30
```

```
Ala Lys Pro Phe Ala Asp Ser Lys Thr Phe Val Asp Met Pro Thr Arg
        35                  40                  45

Val Pro Leu Glu Glu Val Arg Ala Ala Tyr Asp Gln Leu Thr Lys Pro
    50                  55                  60

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

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

Asn Ala Ser Phe Leu Gly Gly Ile Ala Asn Ala Val Asn Arg Glu Phe
            100                 105                 110

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

Glu Ser Ala Val Cys Ala Glu Cys Asp Asn Ser Leu Leu Ser Ile Lys
    130                 135                 140

Arg Pro Phe Ile Val Ala Gly Gly Arg Phe Arg Glu Pro Tyr Tyr Trp
145                 150                 155                 160

Asp Ser Tyr Trp Ile Leu His Gly Leu Leu Arg Ser Gly Gly Asn Phe
                165                 170                 175

Thr Arg Ile Ala Arg Asn Gln Ile Glu Asn Phe Leu Asp Phe Val Glu
            180                 185                 190

Asp Tyr Gly Phe Val Pro Asn Gly Ala Arg Val Tyr Tyr Leu Asn Arg
        195                 200                 205

Ser Gln Pro Pro Leu Leu Ala Gln Met Val Arg Ile Tyr Ile Glu Gln
    210                 215                 220

Thr Gly Asp Ala Thr Ile Leu Asp Arg Ala Ile Pro Leu Leu Ile Arg
225                 230                 235                 240
```

```
Glu His Asp Phe Phe Met Ser Asn Arg Thr Val His Val Ser Val Gly
                245                 250                 255


Ser Arg Asn Tyr Thr Leu Asn Arg Tyr Asn Val Ala Asn Thr Glu Pro
            260                 265                 270


Arg Pro Glu Ser Tyr Tyr Glu Asp Tyr Thr Gln Val Asn Asn Ala Ser
        275                 280                 285


Tyr Tyr Ala Asn Asp Gly Arg Val Phe Pro Thr Arg Asn Thr Thr Gln
    290                 295                 300


Ala Glu Lys Asp Leu Gln Tyr Lys Asn Leu Ala Ser Gly Ala Glu Ser
305                 310                 315                 320


Gly Trp Asp Phe Ser Thr Arg Phe Met Arg Asp Pro Thr Ile Ala Ala
                325                 330                 335


Asn Asp Thr Tyr Phe Pro Leu Ala Ser Tyr Asn Ile Ile Asn Ile Ile
            340                 345                 350


Pro Val Glu Leu Asn Ser Ile Leu Tyr Trp Asn Glu Val Thr Ile Ala
        355                 360                 365


Ala Phe Leu Arg Gln Gln Gln Gln Gln Val Pro Asn Ala Thr Ala Glu
    370                 375                 380


Ala Asp Ala Asp Ala Trp Asp Ala Arg Ala Ala Ser Arg Ser Glu Ala
385                 390                 395                 400


Met Tyr Ser Val Met Trp Asn Glu Thr Leu Gly Gly Tyr Phe Asp Phe
                405                 410                 415


Asn Leu Thr Ser Gly Ser Gln Asp Val Phe Trp Ala Arg Asp Ala Asp
            420                 425                 430


Ser Leu Pro Thr Glu Gln Ala Gly Thr Glu Pro Gly Gln Gln Val Val
        435                 440                 445
```

```
Phe Asn Ile Gly Gln Leu Ser Pro Phe Trp Thr Gly Ala Ala Pro Arg
    450                 455                 460


Ser Leu Ala Gly Asp Pro Ala Ala Val Arg Arg Ala Phe Ser Arg Val
465                 470                 475                 480


Asp Glu Tyr Leu Gly Ser Arg Lys Gly Gly Ile Ala Pro Thr Asn Phe
                485                 490                 495


Val Ser Gly Gln Gln Trp Asp Gln Pro Ser Val Trp Pro Pro His Met
            500                 505                 510


His Ile Leu Met Glu Ala Leu Leu Arg Thr Ala Glu Ala Gly Gly Glu
        515                 520                 525


Ser Glu Gly Gly Ser Glu Asp Trp Ala Trp Ala Gln Asp Leu Ala Leu
    530                 535                 540


Arg Leu Gly Gln Arg Tyr Phe Asp Ser Ala Tyr Cys Thr Trp Arg Ala
545                 550                 555                 560


Thr Gly Gly Gly Thr Pro Ser Ser Pro Pro Leu Ala Asn Pro Pro Gln
                565                 570                 575


Asp Leu Gly Gly Gln Met Phe Glu Lys Tyr Ser Asp Gln Ser Leu Asn
            580                 585                 590


Glu Ala Gly Ser Gly Gly Glu Tyr Val Val Val Val Gly Phe Gly Trp
        595                 600                 605


Ser Asn Gly Val Leu Ile Trp Val Ala Asp Thr Phe Arg Asp Arg Leu
    610                 615                 620


Gln Thr Pro Ala Cys Gly Asp Leu Thr Thr Arg Gly Glu Ala Gly Lys
625                 630                 635                 640


Met Arg Glu Lys Arg Met Ser Glu Asn Gly Arg His Gly Asp Gly Ser
                645                 650                 655
```

```
Asn Ala Ile Ser Ala Val Lys Leu Asp Tyr Phe Asp Ala Ala Trp Thr
            660                 665                 670


Ser Glu Asn Val Gly Gly Leu His Gly Val Arg
        675                 680



<210>  210
<211>  763
<212>  PRT
<213>  Solicoccozyma terricola

<400>  210

Gln Gly Asn Ser Ser Met Ser Ala Ser Asn Ala Thr Ser Ser Ser Thr
1               5                   10                  15


Gly Thr Gly Thr Ser Ser Ser Ala Ala Ala Val Met Thr Ala Val Pro
            20                  25                  30


Met Pro Thr Ala Pro Leu Ser Ser Pro Val Glu Met Leu Pro Leu Pro
        35                  40                  45


Pro Val Gln Pro Trp Cys Asn Gly Gly Glu Asn Ala Thr Tyr Cys Pro
    50                  55                  60


Gly Ser Leu Met Gln Leu Val Gln Leu Ser Gly Ile Tyr Asn Asp Ser
65                  70                  75                  80


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


Gln Ala Phe Asp Ala Leu Pro Val Asn Ala Thr Val Gly Asp Val Glu
            100                 105                 110


Thr Phe Val Glu Lys Tyr Phe Lys Gly Glu Gly Gln Glu Leu Glu Thr
        115                 120                 125


Val Gln Ile Gln Asn Phe Thr Gln Asn Pro Thr Phe Leu Asn Val Ile
    130                 135                 140
```

```
Asp Asp Glu Leu Tyr Lys Gly Phe Val Ser Thr Val Asn Gly Tyr Trp
145                 150                 155                 160


Ser Leu Leu Val Arg Gln Thr Asn Glu Ser Ala Leu Cys Thr Asn Gly
                165                 170                 175


Ala Cys Glu Ser Ser Leu Ile Pro Leu Asn Arg Ser Phe Ile Val Pro
            180                 185                 190


Gly Gly Arg Tyr Arg Glu Ile Tyr Tyr Trp Asp Ser Phe Trp Ile Leu
        195                 200                 205


Glu Gly Leu Leu Lys Ser Glu Leu Tyr Leu Tyr Ala Tyr Asn Leu Leu
    210                 215                 220


Glu Asn Phe Met Asp Leu Ile Glu Lys Phe Gly Phe Leu Pro Asn Gly
225                 230                 235                 240


Gly Arg Ser Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Val Phe Val Gln
                245                 250                 255


Met Leu Asn Ala Tyr Ile Gln Val Thr Gly Asn Val Ser Ile Leu Thr
            260                 265                 270


Arg Ala Leu Pro Ile Ala Glu Thr Glu Leu Gln Trp Trp Arg Thr Asn
        275                 280                 285


Arg Thr Ile Ser Val Thr Ser Pro Tyr Thr Gly Thr Asn Tyr Ser Val
    290                 295                 300


Ala Arg Tyr Phe Val Thr Asn Ser Ala Pro Arg Pro Glu Gly Tyr Val
305                 310                 315                 320


Glu Asp Ile Thr Thr Ala Phe Gly Gly Asn Pro Ala Leu Asn Glu Ser
                325                 330                 335


Ala Arg Ser Ala Leu Tyr Ala Glu Leu Ala Ser Gly Ala Glu Thr Gly
            340                 345                 350
```

```
Trp Asp Tyr Ser Ser Arg Trp Cys Lys Gln Pro Leu Leu Asn Leu Thr
        355                 360                 365


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


Val Asp Leu Asn Ser Leu Leu Cys Gly Asp His Val Leu Leu Ala Asn
385                 390                 395                 400


Leu Tyr Glu Phe Tyr Met Asn Ser Thr Ile Gly Gly Gly Ser Gly Ile
                405                 410                 415


Ser Ser Gly Gly Gly Asn Ser Thr Ile Gly Met Gly Ala Trp Ala Asn
            420                 425                 430


Ser Thr Ser Gly Ser Asn Met Thr Ser Asn Ser Thr Ser Ser Ser Asn
        435                 440                 445


Met Thr Gly Leu Val Gln Ser His Arg Met Ile Ala Lys Glu Phe Glu
    450                 455                 460


Ala Ala Ile Asn Asp Leu Met Trp Asp Lys Gln Lys Leu Trp Trp Tyr
465                 470                 475                 480


Asp Phe Asn Met Thr Ala Asn Ala Arg Ala Asp Val Tyr His Pro Gly
                485                 490                 495


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


Asn Asp Thr Ala Ala Phe Gly Val Phe Ala Gly Val Arg Tyr Met Val
        515                 520                 525


Gly Met Tyr Pro Gly Pro Pro Ala Pro Ala Ser Leu Ile Gln Thr Gly
    530                 535                 540


Leu Asn Trp Asp Ala Pro Asn Val Trp Pro Pro His Val Tyr Thr Gly
545                 550                 555                 560
```

```
Ile Lys Ala Leu Glu Thr Val Leu Arg Ile Asn Pro Asn Ser Ser Val
                565                 570                 575


Val Pro Asn Ile Thr Leu Thr Asp Phe Thr Arg Ile Pro Thr Gly Gln
            580                 585                 590


Leu Gly Leu Asn Gln Ser Gln Leu Pro Pro Gln Pro Ala Ser Ala Leu
        595                 600                 605


Gly Asn Gly Thr Ala Asp Leu Asp Gln Ala Ile Ala Gln Met Gln Lys
    610                 615                 620


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


Leu Gln Ser Ala Phe Cys Ser Trp Tyr Ser Thr Gly Gly Ser Ile Pro
                645                 650                 655


Gly Leu Leu Gln Gln Leu Ser Pro Gln Glu Leu Asn Leu Thr Gly Ser
            660                 665                 670


Leu Thr Thr Gly Ser Gln Ala Met Gly Asn Ile Phe Glu Lys Phe Asn
        675                 680                 685


Leu Thr Asn Val Asp Ala Ala Gly Gly Gly Gly Glu Tyr Thr Val Gln
    690                 695                 700


Ile Gly Phe Gly Trp Ser Asn Gly Val Ile Leu His Thr Ala Gly Glu
705                 710                 715                 720


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


Glu Thr Ala Asn Ala Thr Ser Thr Asn Ala Thr Lys Ser Asn Asn Thr
            740                 745                 750


Met Val Phe Ser Gly Tyr Arg Leu Pro His Asp
        755                 760
```

```
<210>  211
<211>  734
<212>  PRT
<213>  Dioszegia cryoxerica

<400>  211

Gln Ser Ser Ser Ser Ser Ser Phe Ser Pro Thr Pro Val Thr Thr Ala
1               5                   10                  15


Val Pro Ser Ala Thr Ala Ala Leu Asn Gln Thr Val Ser Gly Gln Gly
            20                  25                  30


Val Tyr Pro Pro Leu Gln Pro Trp Cys Asn Ala Gly Glu Asn Ala Thr
        35                  40                  45


Tyr Cys Pro Gly Val Ile Leu Gln Asp Val Gln Leu Ser Gly Leu Phe
    50                  55                  60


Pro Asp Ser Lys Thr Phe Val Asp Lys Pro Thr Asn Gly Thr Gln Asn
65                  70                  75                  80


Ala Thr Gln Gln Ala Phe Gln Gln Leu Gly Asn Asn Ile Thr Leu Gly
                85                  90                  95


Gln Leu Ala Gln Phe Val Asn Thr Ser Phe Arg Gly Glu Gly Leu Glu
            100                 105                 110


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


Asn Lys Val Ser Asn Pro Leu Tyr Arg Gly Trp Val Ser Thr Val Asn
    130                 135                 140


Ser Tyr Trp Ser Leu Leu Ile Arg Glu Thr Asn Gln Ser Ala Val Cys
145                 150                 155                 160


Thr Thr Gln Cys Glu Ser Ser Leu Ile Pro Leu Asn Tyr Thr Ile Val
                165                 170                 175
```

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


Ile Leu Glu Gly Leu Leu Lys Ser Glu Leu Tyr Thr Tyr Ala Trp Asp
        195                 200                 205


Val Leu Gln Asn Phe Met Asp Phe Val Asp Val Tyr Gly Phe Ile Pro
    210                 215                 220


Asn Gly Gly Arg Lys Tyr Tyr Leu Asn Arg Ser Gln Pro Pro Val Phe
225                 230                 235                 240


Ile Gln Met Leu Asp Ala Tyr Val Lys Ala Thr Gly Asn Val Thr Ile
                245                 250                 255


Leu Glu Arg Ala Leu Pro Leu Ala Ser Glu Glu Met Arg Trp Trp Ile
            260                 265                 270


Asn Asn Arg Thr Thr Gln Val Thr Ser Pro Phe Thr Gly Ile Thr Arg
        275                 280                 285


Arg Val Tyr Val Phe Asn Val Thr Asn Ser Ala Pro Arg Pro Glu Gly
    290                 295                 300


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


Glu Ala Gln Arg Gly Ala Leu Tyr Ala Glu Leu Ala Thr Gly Ala Glu
                325                 330                 335


Ser Gly Trp Asp Tyr Ser Ser Arg Trp Cys Lys Gln Pro Val Ile Asn
            340                 345                 350


Val Thr Asp Asn Leu Pro Ala Leu Arg Thr Leu Asn Gly Arg Ser Ile
        355                 360                 365


Val Pro Val Asp Leu Asn Ser Leu Gln Ala Gly Asn His Ala Leu Leu
    370                 375                 380
```

```
Ala Arg Leu Tyr Glu Val Tyr Ile Asn Ala Ser Thr Thr Ser Asn Thr
385                 390                 395                 400


Thr Ala Ala Gln Thr Ile Arg Ala Asn Ala Thr Gln Glu Ile Ala Leu
                405                 410                 415


His Lys Thr Leu Ala Asn Asp Tyr Ser Gln Ala Val Leu Asp Leu His
            420                 425                 430


Trp Asp Pro Ala Arg Ala Trp Phe Tyr Asp Phe Asn Leu Thr Ser Asn
        435                 440                 445


Ser Arg Glu Ser Leu Tyr Thr Pro Ala Gly Thr Phe Ala Leu Trp Gln
    450                 455                 460


Asn Ile Thr Pro Pro Gly Leu Glu Gly Asn Asp Thr Ala Ala Leu Arg
465                 470                 475                 480


Ile Ala Ser Gly Ala Arg Tyr Leu Leu Gly Arg Tyr Gly Gly Ile Gln
                485                 490                 495


Gly Val Ser Ser Leu Leu Val Thr Gly Leu Asn Trp Asp Phe Pro Asn
            500                 505                 510


Ser Trp Pro Pro His Thr Tyr Thr Ser Ile Lys Ala Phe Gln Thr Leu
        515                 520                 525


Gly Arg Leu Val Gly Asn Ala Ser Ile Val Gly Asn Ala Thr Ile Pro
    530                 535                 540


Phe Ser Gln Val Ala Thr Asn Gln Leu Gly Leu Asn Glu Thr Gln Leu
545                 550                 555                 560


Pro Pro Gln Asp Pro Ala Leu Gln Gly Asn Ala Ser Leu Thr Val Pro
                565                 570                 575


Ser Ala Arg Asn Val Ser Trp Pro Leu Ala Leu Glu Ile Glu Tyr Ala
            580                 585                 590
```

```
Ser Arg Tyr Met Gln Gly Ala Phe Cys Ser Trp Tyr Ser Thr Gly Gly
        595                 600                 605


Ser Ile Ser Gly Leu Leu Thr Gln Leu Pro Val Ser Gln Leu Asn Ala
    610                 615                 620


Thr Gly Thr Tyr Gln Ala Gly Gln Thr Gly Gln Met Phe Glu Lys Phe
625                 630                 635                 640


Asn Ala Thr Asp Ile Asp Ala Ala Gly Gly Gly Gly Glu Tyr Thr Val
                645                 650                 655


Gln Ile Gly Phe Gly Trp Thr Asn Gly Val Val Leu Trp Leu Ala Asp
            660                 665                 670


Asn Phe Gly Gln Tyr Leu Pro Gln Pro Thr Cys Pro Leu Val Val Leu
        675                 680                 685


Ser Leu Thr Asn Leu Asn Ser Thr Thr Ala Gly Asn Ser Thr Asn Gly
    690                 695                 700


Thr Ser Pro Ala Ala Pro Gly Asn Ala Thr Ser Leu Val Ala Val Ser
705                 710                 715                 720


Glu Leu Gln Gly Ile Trp Glu Gly Gln Arg Val Ser Arg Asp
                725                 730


<210>  212
<211>  1020
<212>  PRT
<213>  Talaromyces funiculosus

<400>  212

Leu Pro Phe Asn Glu Arg Val Asp Gln Val Leu Arg Ser Tyr Glu Val
1               5                   10                  15


Thr Ser Lys Leu Asp Ser Arg Ser Thr Lys Pro Ser Lys His Gly His
            20                  25                  30


Thr Tyr Gln Thr Gln Phe Leu Gly Val Thr Trp Asp Gln Arg Asn Trp
```

```
        35                  40                  45


Arg Leu Gln Ser Thr Val Leu Asp Gln Gly His Tyr Glu Ser Arg Gly
    50                  55                  60


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


Leu Phe Glu Leu Asp Ser Pro Val Asp Gly Asp Val Ile Asn Gly Trp
                85                  90                  95


Pro Leu Phe Ser Arg Arg Gln Thr Phe Ala Gly Leu Ala Gly Phe Tyr
            100                 105                 110


Asp Leu Gln Pro Arg Thr Asn Gly Thr Asn Phe Pro Trp Leu Ser Gln
        115                 120                 125


Tyr Gly Asp Asp Ser Ala Ile Ser Gly Val Pro His Trp Gly Gly Met
    130                 135                 140


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


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


Leu Ser Trp Asp Tyr Lys Trp Thr Pro Lys Asn Ala Asn Gly Ser Phe
            180                 185                 190


Gly Ile Ser Tyr Lys Ile Phe Ala Asn Lys Leu Asp Val Asn Gln Ala
        195                 200                 205


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


Val Asn Val Ile Asp Gly Tyr Ala Ala Val Arg Thr Asp Phe Val Ser
225                 230                 235                 240


Ser Gly Asn Glu Ser Asp Val Val Tyr Thr Ala Val Lys Pro Asn Gly
```

```
                245                 250                 255


Val Thr Asn Val Thr Ala Trp Ile Tyr Thr Ala Leu Asp Gly Asp Asp
            260                 265                 270


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


His Gln Asn Asp Ser Ser Ile Ala Gln Ser Val Asn Val Thr Phe Thr
    290                 295                 300


Ala Gly Thr Thr Ile Thr Ile Asn Lys Phe Val Gly Ala Ala Ser Thr
305                 310                 315                 320


Asp Ala Phe Pro Asp Pro Gln Ser Thr Ala Arg Glu Ala Ala Leu Ser
                325                 330                 335


Ala Arg Arg Arg Gly Phe Asp Asp Leu Phe Arg Ser His Ile Ser Glu
            340                 345                 350


Trp Ala Gln Val Met Pro Asp Asp Ser Val Asp Asp Phe Thr Leu Ala
        355                 360                 365


Asn Gly Thr Leu Pro Asn Asp Thr Phe Ile Ile Glu Ser Ala Val Met
    370                 375                 380


Ala Val Val Asn Pro Tyr Tyr Leu Leu Gln Asn Thr Val Gly Pro Asn
385                 390                 395                 400


Ala Leu Arg Arg Val Asn Asn Ala Pro Val Asn Asp Trp Ser Ile Pro
                405                 410                 415


Val Gly Gly Leu Thr Ser Asp Ser Tyr Ala Gly Gln Ile Phe Trp Asp
            420                 425                 430


Ala Asp Val Trp Met Gln Pro Gly Leu Val Ala Ala Phe Pro Glu Ser
        435                 440                 445


Ala Lys Arg Ile Thr Asn Tyr Arg Ala Ala Lys Tyr Ser Gln Ala Leu
```

```
    450                 455                 460

Glu Asn Ala Lys Thr Ala Tyr Thr Ser Ser Gln Asn Gln Thr Trp Phe
465                 470                 475                 480

Ser Pro Asp Ala Ala Ile Tyr Ser Trp Thr Ser Gly Arg Val Gly Asn
                485                 490                 495

Cys Thr Ala Thr Gly Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly
            500                 505                 510

Asp Ile Gly Ile Ser Leu Val Asn Glu Trp Val Val Ser Gly Asp Asn
        515                 520                 525

Glu Thr Phe Lys Asn Lys His Phe Pro Ile Tyr Asn Ser Ile Ala Thr
    530                 535                 540

Leu Tyr Gly Asp Leu Leu Lys Lys Asn Gly Ser Tyr Tyr Thr Leu Thr
545                 550                 555                 560

Asn Met Thr Asp Pro Asp Glu Tyr Ala Asn Asn Val Asp Ala Gly Gly
                565                 570                 575

Tyr Thr Met Thr Leu Ile Ser Gln Thr Leu Ser Asn Ala Asn Ala Phe
            580                 585                 590

Arg Lys Gln Phe Gly Met Asn Glu Asn Thr Thr Trp Thr Glu Met Ala
        595                 600                 605

Asp Asn Ile Leu Leu Ile Arg Glu Asn Asp Val Thr Leu Glu Tyr Thr
    610                 615                 620

Thr Met Asn Asn Ser Val Ala Val Lys Gln Ala Asp Val Ile Leu Ser
625                 630                 635                 640

Thr Phe Pro Leu Asp Tyr Thr Lys Asn Tyr Thr Thr Ser Ala Ala Leu
                645                 650                 655

Asn Asp Leu Asp Tyr Tyr Ala Leu Lys Gln Ser Pro Asp Gly Pro Gly
```

```
            660                 665                 670

Met Thr Tyr Ala Ile Phe Ser Ile Val Ala Asn Asp Val Ser Pro Ser
        675                 680                 685

Gly Cys Ser Ala Tyr Thr Tyr Ala Gln Tyr Ser Tyr Asp Pro Tyr Ile
    690                 695                 700

Arg Gly Pro Phe Phe Gln Phe Ser Glu Gln Leu Leu Asp Asp Tyr Thr
705                 710                 715                 720

Ile Asn Gly Gly Thr His Pro Ala Phe Pro Phe Leu Thr Gly His Gly
                725                 730                 735

Gly Ala Asn Gln Val Val Leu Tyr Gly Tyr Leu Gly Leu Arg Leu Leu
            740                 745                 750

Pro Asp Asp Met Leu His Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro
        755                 760                 765

Ser Ile Lys Tyr Arg Thr Phe Tyr Trp Arg Gly Trp Pro Ile Gln Ala
    770                 775                 780

Ala Ser Asn Tyr Thr His Thr Thr Ile Gln Arg Ala Thr Thr Val Ala
785                 790                 795                 800

Pro Leu Ser Thr Ala Asp Pro Thr Tyr Ala Asn Lys Ser Ile His Val
                805                 810                 815

Ser Val Gly His Asn Thr Val Asn Ser Thr Thr Tyr Ser Leu Ser Ala
            820                 825                 830

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

Thr Val Ala Gly Asn Val Val Gln Cys Lys Ser Val Leu Ser Thr Asp
    850                 855                 860

Ala Tyr Gln Lys Gly Gln Tyr Pro Ile Ser Ala Val Asp Gly Ala Ala
```

865 870 875 880

Ser Thr Lys Trp Gln Pro Glu Phe Ala Ala Asn Ile Ser Ser Leu Thr
885 890 895

Val Asp Leu Thr Gly Ser Asn Val Ser Ser Val Ser Gly Phe Tyr Phe
900 905 910

Asp Trp Ala Gln Ala Pro Pro Thr Asn Ile Thr Val Leu Leu His Asn
915 920 925

Ser Ser Ser Ala Ala Leu Ala Ser Ser Gly Asp Lys Pro Gly Ser Ser
930 935 940

Ala Val Thr Leu Asn Ile Thr Ile Ser Asn Pro Tyr Asn Ala Ser Thr
945 950 955 960

Tyr Asn Ala Asn Ile Ile Ala Leu Pro Ser Ser Asn Ser Thr Asn Tyr
965 970 975

Thr Phe Pro Ala Pro Val Pro Lys Pro Arg Tyr Ala Thr Leu Phe Val
980 985 990

Gln Gly Asn Gln Ala Leu Asp Glu Thr Asp Thr Lys Ser Gly Asn Gly
995 1000 1005

Thr Gly Ala Thr Val Ala Glu Trp Ala Ile Leu Ser
1010 1015 1020

<210> 213
<211> 1063
<212> PRT
<213> Hamigera avellanea

<400> 213

Ala Ser Pro Lys Ser Arg Ile Asn Gln Cys Leu Lys Lys His Ala Gly
1 5 10 15

Gln Gly Ser His Asp Asp Glu Thr Ser Ser Asn Val Tyr Gln Thr Arg
20 25 30

```
Phe Pro Gly Val Thr Trp Asp Glu Asp Asn Trp Ser Leu Thr Thr Ser
        35                  40                  45

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

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

Ile Pro Leu Asn Gly Asp Val Ile Asn Gly Trp Pro Leu Tyr Ser Arg
                85                  90                  95

Arg Gln Thr Phe Ala Thr Ile Ser Gly Phe Phe Asp Ser Gln Pro Glu
            100                 105                 110

Thr Asn Gly Thr Asn Phe Gly Trp Leu Asn Gln Tyr Gly Gly Glu Ser
        115                 120                 125

Val Ile Ser Gly Val Pro His Trp Ser Gly Leu Ile Leu Asp Leu Gly
    130                 135                 140

Asp Gly Thr Tyr Leu Asp Ser Thr Val Asp Asn Ala Thr Leu Ser Gly
145                 150                 155                 160

Phe Thr Ser Ser Tyr Asp Phe Lys Ala Gly Val Leu Ser Trp Ser Tyr
                165                 170                 175

Gln Trp Thr Pro Glu Gly Lys His Gly Ser Tyr Asp Ile Thr Tyr Arg
            180                 185                 190

Leu Phe Thr Asn Lys Leu Tyr Val Asn Gln Ala Val Val Asp Met Glu
        195                 200                 205

Ile Val Pro Thr Val Ala Gly Lys Ala Ser Val Val Asn Val Ile Glu
    210                 215                 220

Gly Ser Ser Ala Val Arg Thr Asp Phe Val Glu Ser Gly Glu Asp Asp
225                 230                 235                 240
```

```
Gly Ala Ile Phe Ser Ala Val Arg Pro Trp Gly Ile Ser Asn Val Thr
                245                 250                 255


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


Ser Arg Thr Leu Val Ser Asn Lys Pro Tyr Val Ser Thr Asn Glu Ser
        275                 280                 285


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


Arg Ile Thr Lys Phe Val Gly Ala Ala Ser Thr Asp Ala Phe Ala Asn
305                 310                 315                 320


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


Tyr Leu Lys Ser Leu Asn Ser His Ile Ala Glu Trp Ala Ser Val Met
            340                 345                 350


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


Pro Ala Asp Glu His Ile Ile Glu Ser Ala Ile Ile Ser Val Thr Asn
    370                 375                 380


Thr Tyr Tyr Leu Leu Gln Asn Thr Val Gly Lys Asn Ala Ile Lys Ala
385                 390                 395                 400


Ser Ser Asp Ala Ala Leu Asn Met Asp Ser Ile Ser Val Gly Gly Leu
                405                 410                 415


Thr Ser Asp Ser Tyr Ala Gly Leu Ile Phe Trp Asp Ala Asp Ile Trp
            420                 425                 430


Met Gln Pro Gly Leu Val Ala Ser His Pro Glu Ala Ala Glu Val Phe
        435                 440                 445
```

```
Thr Asn Tyr Arg Val Ala Lys Tyr Pro Gln Ala Val Lys Asn Ile Glu
    450                 455                 460


Thr Ala Phe Ala Ser Ser Lys Asn Gln Thr Asn Phe Ser Pro Ser Ala
465                 470                 475                 480


Ala Ala Tyr Pro Trp Thr Ser Gly Arg Tyr Gly Asn Cys Thr Gly Thr
                485                 490                 495


Gly Pro Cys Phe Asp Tyr Gln Tyr His Leu Asn Gly Asp Ile Gly Leu
            500                 505                 510


Ser Met Ile Asn Gln Trp Val Val Ser Gly Asp Thr Gln Thr Phe Arg
        515                 520                 525


Glu Lys His Phe Pro Ile Tyr Asp Ser Ala Ala Thr Phe Phe Ser Asn
    530                 535                 540


Leu Val Glu Arg Asn Gly Ser Thr Trp Thr Leu Thr Asn Met Thr Asp
545                 550                 555                 560


Pro Asp Glu Tyr Ala Asn His Ile Asp Ala Gly Gly Tyr Thr Met Pro
                565                 570                 575


Leu Ile Ala Glu Thr Leu Leu Tyr Ala Asn Ser Phe Arg Lys Gln Phe
            580                 585                 590


Gly Val Glu Pro Asn Glu Thr Trp Asn Glu Ile Ala Glu Asn Val Leu
        595                 600                 605


Val Leu Arg Thr Asn Gly Val Thr Leu Glu Phe Thr Ser Met Asn Gly
    610                 615                 620


Ser Ala Pro Val Lys Gln Ala Asp Val Val Leu Val Thr Tyr Pro Leu
625                 630                 635                 640


Asp Tyr Asn Asn Asn Tyr Ser Pro Glu Asp Ser Leu Asn Asp Leu Asp
                645                 650                 655
```

```
Tyr Tyr Ala Asn Lys Gln Ser Glu Asp Gly Pro Ala Met Thr Trp Ala
            660                 665                 670


Ile Phe Ser Val Val Ala Asn Glu Ala Ser Pro Ser Gly Cys Ser Ala
        675                 680                 685


Tyr Thr Tyr Ala Gln Tyr Ala Tyr Tyr Pro Tyr Ala Arg Ala Pro Phe
    690                 695                 700


Phe Gln Leu Ser Glu Gln Met Ile Asp Asp Ala Ser Ile Asn Gly Gly
705                 710                 715                 720


Thr His Pro Ala Tyr Pro Phe Leu Thr Gly His Gly Gly Ala Asn Gln
                725                 730                 735


Val Asn Leu Met Gly Tyr Leu Gly Leu Arg Leu Leu Pro Asp Asn Val
            740                 745                 750


Ile His Val Asp Pro Asn Leu Pro Pro Gln Ile Pro His Leu Lys Tyr
        755                 760                 765


Arg Thr Phe Tyr Trp Arg Gly Trp Pro Met Ser Ala Ala Ser Asn Tyr
    770                 775                 780


Thr His Thr Thr Ile Gln Arg Ala Val Asn Val Pro Ala Leu Ser Thr
785                 790                 795                 800


Ala Asp Gln Lys Phe Ala Asn Val Ser Ile Pro Val His Val Gly Pro
                805                 810                 815


Glu Thr Asn Ala Thr Val Tyr Arg Leu Pro Val Asn Gly Thr Leu Thr
            820                 825                 830


Ile Pro Asn Arg Gln Ile Ala Ser Lys Asn Thr Val Ala Gly Asn Leu
        835                 840                 845


Ile Gln Cys Arg Pro Val Glu Ser Gln Asn Asp Phe Gln Pro Gly Gln
    850                 855                 860
```

```
Phe Pro Ile Ser Val Val Asp Gly Ala Ser Ser Thr Arg Trp Gln Pro
865                 870                 875                 880


Lys His Ala Asp Asn Val Ser Ala Val Thr Val Thr Phe Ala Asp Glu
                885                 890                 895


Glu Val Gly Ser Leu Val Ser Gly Phe Tyr Phe Asp Trp Ala Gln Ala
            900                 905                 910


Pro Pro Val Asp Ala Ala Val Ile Phe His Asn Ser Ser Leu Glu Asn
        915                 920                 925


Pro Ala Ser Ala Phe Ser Phe Ala Ser Asn Ser Ser Ser Ser Glu Tyr
    930                 935                 940


Ser Val Ile Thr Thr Leu Lys Asn Val Glu Gln Ser Asp Pro Tyr Asp
945                 950                 955                 960


Pro Glu Ser Asp Lys Leu Asp Ile Ile Ala Ile Pro Thr Gly Asn Thr
                965                 970                 975


Thr Lys Val Thr Leu Pro Ser Ala Val Pro Ala Ala Arg Tyr Ala Thr
            980                 985                 990


Leu Phe Ile Thr Gly Asn Gln Ala  Leu Gly Pro Glu Asp  Ile Ala Ala
        995                 1000                 1005


Lys Asn  Gly Thr Gly Ala Thr  Val Ala Glu Trp Ala  Ile Val Gly
    1010                 1015                 1020


Gln Thr  Ser Ser Ala Thr Ser  Lys Arg Ser Ile Gln  Thr Arg Lys
    1025                 1030                 1035


Leu Gln  Val Arg Ser Gly Ala  Ala Leu Ser Gly Leu  Gly Phe Ala
    1040                 1045                 1050


Gln Arg  Arg Arg Gln Ser Ala  Glu Met Tyr
    1055                 1060
```

```
<210>  214
<211>  1020
<212>  PRT
<213>  Talaromyces ruber

<400>  214

Leu Pro Phe Asn Glu Arg Val Asp His Val Leu Arg Ser His Asp Leu
1               5                   10                  15


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


Thr Tyr Gln Thr Gln Phe Thr Gly Val Thr Trp Asp Gln Arg Asn Trp
        35                  40                  45


Arg Leu Gln Ser Asn Val Leu Asp Gln Gly His Tyr Glu Ser Arg Gly
    50                  55                  60


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


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


Pro Leu Phe Ser Arg Arg Gln Thr Phe Ala Gly Leu Ala Gly Phe Tyr
            100                 105                 110


Asp Leu Gln Pro Thr Thr Asn Gly Ser Asn Phe Pro Trp Leu Asp Gln
        115                 120                 125


Tyr Gly Asp Asp Ser Val Ile Ser Gly Val Pro His Trp Gly Gly Leu
    130                 135                 140


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


Ser Thr Ile Ser Asp Tyr Ser Thr Thr Tyr Asp Tyr Lys Ala Gly Val
                165                 170                 175
```

```
Leu Ser Trp His Tyr Lys Trp Thr Pro Lys Asn Ala Asn Gly Ser Phe
            180                 185                 190


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


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


Ala Asn Val Ile Asp Gly Tyr Ser Ala Val Arg Thr Glu Phe Val Ala
225                 230                 235                 240


Ser Gly Asn Glu Ser Asp Ala Ile Phe Thr Ala Val Lys Pro Val Gly
                245                 250                 255


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


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


His Gln Asn Asp Ser Ser Ile Ala Gln Ser Val Asn Val Thr Phe Thr
    290                 295                 300


Ala Gly Thr Thr Ile Thr Ile Asn Lys Phe Val Gly Ala Ala Ser Thr
305                 310                 315                 320


Asp Ala Phe Pro Asp Pro Gln Ser Thr Ala Arg Glu Ala Ala Leu Lys
                325                 330                 335


Ala Arg Arg Arg Gly Phe Asp Asp Leu Phe Arg Ser His Ile Ser Glu
            340                 345                 350


Trp Ala Gln Val Met Pro Asp Asp Ser Val Asp Asp Phe Thr Leu Ala
        355                 360                 365


Asn Gly Thr Leu Pro Asn Asp Pro Phe Ile Ile Glu Ser Ala Val Met
    370                 375                 380
```

```
Ala Val Val Asn Pro Tyr Tyr Leu Leu Gln Asn Thr Val Gly Pro Asn
385                 390                 395                 400


Ala Leu Arg Arg Val Asn Asn Ala Pro Val Asn Asp Trp Ser Ile Pro
                405                 410                 415


Val Gly Gly Leu Thr Ser Asp Ser Tyr Ala Gly Gln Val Phe Trp Asp
            420                 425                 430


Ala Asp Val Trp Met Gln Pro Gly Leu Val Ala Ala Phe Pro Glu Ser
        435                 440                 445


Ala Lys Arg Ile Thr Asn Tyr Arg Thr Ala Ile Tyr Ser Gln Ala Leu
    450                 455                 460


Glu Asn Ala Lys Thr Ala Tyr Thr Ser Ser Gln Asn Gln Thr Ser Phe
465                 470                 475                 480


Ser Ser Asp Ala Ala Ile Tyr Ser Trp Thr Ser Gly Arg Tyr Gly Asn
                485                 490                 495


Cys Thr Ala Thr Gly Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly
            500                 505                 510


Asp Ile Gly Ile Ser Leu Val Asn Gln Trp Val Val Ser Gly Asp Asn
        515                 520                 525


Asp Thr Phe Lys Asn Thr His Phe Pro Ile Tyr Asn Ser Ile Ala Thr
    530                 535                 540


Leu Tyr Gly Asp Leu Leu Lys Lys Asn Gly Ser Tyr Tyr Thr Leu Thr
545                 550                 555                 560


Asn Met Thr Asp Pro Asp Glu Tyr Ala Asn Asn Val Asp Ala Gly Gly
                565                 570                 575


Tyr Thr Met Thr Leu Ile Ser Gln Thr Leu Ser Asn Ala Asn Ala Phe
            580                 585                 590
```

```
Arg Lys Gln Phe Gly Met Asp Glu Asn Thr Thr Trp Thr Asp Met Ala
        595                 600                 605


Asp Asn Val Leu Leu Ile Arg Glu Asn Asp Val Thr Leu Glu Tyr Thr
    610                 615                 620


Thr Met Asn Asn Ser Val Ala Val Lys Gln Ala Asp Val Ile Leu Ser
625                 630                 635                 640


Thr Tyr Pro Leu Asp Tyr Thr Lys Asn Tyr Thr Thr Ser Ala Ala Leu
                645                 650                 655


Asn Asp Leu Asp Tyr Tyr Ala Leu Lys Gln Ser Pro Asp Gly Pro Gly
            660                 665                 670


Met Thr Tyr Ala Ile Phe Ser Ile Val Ala Asn Asp Val Ser Pro Ser
        675                 680                 685


Gly Cys Ser Ala Tyr Thr Tyr Ala Gln Tyr Ser Tyr Asp Pro Tyr Ile
    690                 695                 700


Arg Gly Pro Phe Phe Gln Phe Ser Glu Gln Leu Leu Asp Asp Tyr Thr
705                 710                 715                 720


Ala Asn Gly Gly Thr His Pro Ala Phe Pro Phe Leu Thr Gly His Gly
                725                 730                 735


Gly Ala Asn Gln Val Val Leu Tyr Gly Tyr Leu Gly Leu Arg Leu Leu
            740                 745                 750


Pro Asp Asn Val Leu His Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro
        755                 760                 765


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


Ala Ser Asn Tyr Thr His Thr Thr Ile Gln Arg Ala Thr Ser Val Ala
785                 790                 795                 800
```

```
Pro Leu Ser Thr Ala Asp Gln Thr Tyr Ala Asn Arg Ser Ile Ser Val
                805                 810                 815


Gln Val Gly Gln Asn Thr Val Asn Ser Thr Thr Tyr Ser Leu Pro Ala
            820                 825                 830


Asn Gly Ser Ala Ile Val Val Pro Asn Arg Gln Ile Gly Ser Ile Asn
        835                 840                 845


Thr Val Ala Gly Asn Ile Ala Gln Cys Lys Ser Val Leu Ser Thr Asp
    850                 855                 860


Ala Tyr Gln Pro Gly Gln Tyr Pro Ile Ser Ala Val Asp Gly Ala Ala
865                 870                 875                 880


Ser Thr Lys Trp Gln Pro Glu Phe Ala Ala Asn Ile Ser Ser Leu Thr
                885                 890                 895


Val Asp Leu Thr Ser Ser Asn Ala Ser Thr Val Ser Gly Phe Tyr Phe
            900                 905                 910


Asp Trp Ala Gln Ala Pro Pro Thr Asn Ile Thr Val Leu Leu His Asn
        915                 920                 925


Ser Ser Asn Ala Pro Leu Thr Ser Ser Asn Ser Asn Gly Gly Asn Ser
    930                 935                 940


Thr Val Ser Leu Asn Val Thr Ile Ser Asn Pro Tyr Asp Ala Ser Ala
945                 950                 955                 960


Tyr Asn Ala Asn Val Ile Thr Leu Ser Ser Ser Asn Thr Thr Asn Tyr
                965                 970                 975


Thr Phe Pro Ala Pro Val Ser Lys Pro Arg Tyr Ala Thr Leu Phe Val
            980                 985                 990


Gln Gly Asn Gln Ala Leu Asp Glu  Thr Asp Leu Lys Ala  Gly Asn Gly
        995                 1000                 1005
```

```
Thr Gly  Ala Thr Val Ala Glu  Trp Ala Val Leu Ser
    1010                 1015                 1020


<210>  215
<211>  1055
<212>  PRT
<213>  Trichoderma lixii

<400>  215

Ala Thr Ser Asn Asn Arg Val Ser Glu Cys Leu Gly Arg Asn Gly Gly
1               5                   10                  15


Ser Ser Thr Gly Val His Phe Ser Lys Asn Val Tyr Lys Thr Asp Phe
            20                  25                  30


Ala Gly Val Thr Trp Asp Glu Asp Asn Trp Leu Leu Ser Thr Thr Glu
        35                  40                  45


Leu Lys Gln Gly Ala Phe Glu Ser Arg Gly Ser Ile Ala Asn Gly Tyr
    50                  55                  60


Leu Gly Ile Asn Val Ala Ser Val Gly Pro Phe Phe Glu Leu Asp Thr
65                  70                  75                  80


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


Gln Ser Phe Ala Thr Ile Ala Gly Phe Trp Asp Ser Gln Pro Val Met
            100                 105                 110


Asn Gly Thr Asn Phe Pro Trp Ile Ser Gln Tyr Gly Ser Asp Thr Ala
        115                 120                 125


Ile Ser Gly Ile Pro His Trp Ser Gly Leu Ile Leu Asp Leu Gly Gly
    130                 135                 140


Asn Thr Tyr Leu Asp Ala Thr Val Asp Asn Arg Thr Ile Ser Asn Phe
145                 150                 155                 160
```

```
Arg Ser Thr Tyr Asp Tyr Lys Ala Gly Val Leu Ser Trp Ser Tyr Lys
                165                 170                 175


Trp Thr Pro Lys Gly Asn Lys Gly Ser Phe Asp Ile Ser Tyr Arg Ile
            180                 185                 190


Phe Ala Asn Lys Leu Tyr Val Asn Gln Ala Val Val Asp Leu Gln Val
        195                 200                 205


Thr Ala Ser Lys Asn Val Glu Ala Ser Ile Val Asn Val Ile Asp Gly
    210                 215                 220


Phe Ala Ala Val Arg Thr Asp Phe Val Glu Ser Gly Glu Asp Gly Asn
225                 230                 235                 240


Ala Ile Phe Ser Ala Val Arg Pro Asn Gly Val Ala Asn Val Thr Ala
                245                 250                 255


Tyr Val Tyr Ala Asp Ile Thr Gly Ser Gly Gly Val Asp Leu Ser Ser
            260                 265                 270


Arg Lys Ile Val His Asn Lys Pro Tyr Val His Ala Asn Ala Ser Ser
        275                 280                 285


Ile Ala Gln Ala Val Pro Val Lys Phe Ser Ala Gly Arg Ala Val Arg
    290                 295                 300


Val Thr Lys Phe Val Gly Gly Ala Ser Ser Asp Ala Phe Lys Asn Pro
305                 310                 315                 320


Lys Gln Ile Ala Lys Ser Ala Ala Ala Thr Ala Leu Lys Asn Gly Tyr
                325                 330                 335


Ser Lys Ser Leu Asn Ser His Val Thr Glu Trp Ala Ala Val Met Pro
            340                 345                 350


Glu Ser Ser Val Asp Ser Phe Ala Asp Pro Lys Thr Gly Lys Leu Pro
        355                 360                 365
```

```
Asn Asp Asn Tyr Ile Ile Asp Ser Ala Ile Ile Ala Val Val Asn Thr
    370                 375                 380


Tyr Tyr Leu Leu Gln Asn Thr Val Gly Lys Asn Gly Ser Lys Ala Ala
385                 390                 395                 400


Asn Gly Ala Pro Val Asn Val Asp Ser Ile Ser Val Gly Gly Leu Thr
                405                 410                 415


Ser Asp Ser Tyr Ala Gly Gln Val Phe Trp Asp Ala Asp Leu Trp Met
            420                 425                 430


Gln Pro Gly Leu Leu Ala Ala His Pro Glu Ala Ala Glu Arg Ile Ile
        435                 440                 445


Asn Tyr Arg Leu Ala Arg Tyr Gly Gln Ala Lys Glu Asn Val Lys Thr
    450                 455                 460


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


Val Phe Pro Trp Thr Ser Gly Arg Tyr Gly Asn Cys Thr Ala Thr Gly
                485                 490                 495


Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly Asp Ile Gly Leu Ala
            500                 505                 510


Leu Val Asn Gln Trp Val Val Asn Gly Asp Thr Lys Asp Phe Glu Lys
        515                 520                 525


Asn Leu Phe Pro Val Tyr Asp Ser Ile Ala Gln Leu Tyr Gly Asn Leu
    530                 535                 540


Leu Lys Pro Asn Gly Thr Ala Trp Thr Leu Thr Asn Met Thr Asp Pro
545                 550                 555                 560


Asp Glu Tyr Ala Asn His Val Asp Ala Gly Gly Tyr Thr Met Pro Phe
                565                 570                 575
```

```
Ile Ala Glu Thr Leu Gln Asn Ala Asn Thr Phe Arg Lys Gln Phe Gly
            580                 585                 590


Ile Glu Gln Asn Lys Thr Trp Asn Asp Met Ala Ser Asn Ala Leu Val
        595                 600                 605


Leu Arg Glu Asn Gly Val Thr Leu Glu Phe Thr Thr Met Asn Gly Ser
    610                 615                 620


Ala Val Val Lys Gln Ala Asp Val Ile Met Val Thr Phe Pro Leu Ser
625                 630                 635                 640


Tyr Thr Thr Asn Tyr Thr Thr Glu Asp Ala Leu Asn Asp Leu Asp Tyr
                645                 650                 655


Tyr Ala Asn Lys Gln Ser Pro Asp Gly Pro Ala Met Thr Tyr Ala Phe
            660                 665                 670


Phe Ser Ile Val Ala Asn Glu Ile Ser Pro Ser Gly Cys Ser Ala Tyr
        675                 680                 685


Thr Tyr Ala Gln Tyr Ala Phe Lys Pro Tyr Val Arg Ala Pro Phe Tyr
    690                 695                 700


Gln Leu Ser Glu Gln Ile Ile Asp Asp Ser Ser Ile Asn Gly Gly Thr
705                 710                 715                 720


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


Val Leu Phe Gly Tyr Leu Gly Leu Arg Leu Val Pro Asp Asp Phe Ile
            740                 745                 750


His Ile Glu Pro Asn Leu Pro Pro Gln Ile Pro Tyr Leu Arg Tyr Arg
        755                 760                 765


Thr Phe Tyr Trp Arg Gly Trp Pro Ile Ser Ala Trp Ser Asn Tyr Thr
    770                 775                 780
```

```
His Thr Thr Ile Ser Arg Ala Ser Gly Val Ala Ala Leu Asp Gly Ala
785                 790                 795                 800


Asp Gln Arg Phe Ala Gly Lys Thr Ile Thr Ile His Ser Gly Pro Glu
                805                 810                 815


Glu Ser Pro Lys Ala Tyr His Leu Pro Val Lys Gly Ser Val Val Val
            820                 825                 830


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


Gln Cys His Ala Ala Ser Ser Pro Ser Asp Tyr Val Pro Gly Gln Phe
    850                 855                 860


Pro Ile Ala Ala Val Asp Gly Ala Thr Ser Thr Lys Trp Gln Pro Ala
865                 870                 875                 880


Ser Ala Asp Lys Leu Ser Ser Ile Thr Val Ser Leu Asp Gln Glu Asp
                885                 890                 895


Val Gly Ser Leu Val Ser Gly Phe His Phe Asp Trp Ala Gln Ala Pro
            900                 905                 910


Pro Val Asn Ala Thr Ile Ile Phe His Asn Glu Ala Ile Asn Asp Pro
        915                 920                 925


Ala Thr Val Leu Lys Ser Gln Lys His Asn Ser Asn Tyr Lys Val Val
    930                 935                 940


Ser Ser Leu Thr Asn Ile Lys Gln Ser Asn Pro Tyr Ile Lys Thr Thr
945                 950                 955                 960


Asp Leu Asp Ile Ile Ala Ile Pro Ile Gly Asn Thr Thr Asn Val Thr
                965                 970                 975


Leu Ser Gln Pro Val Ala Ala Ser Arg Tyr Ala Ser Leu Val Ile Val
            980                 985                 990
```

```
Gly Asn Gln Gly Leu Asp His Ala  Asp Val Val Gly Lys  Asn Gly Thr
        995                 1000                1005


Gly Ala  Thr Val Ala Glu Trp  Ala Ile Ile Gly His  Ser Lys Gly
    1010                1015                1020


His Thr  Gly Ala Pro Gly His  His Gly Lys Arg Lys  Leu Asn Leu
    1025                1030                1035


Arg Ala  Ala Ala Ala Met Ser  Asp Pro Asp Ser Phe  Ala Arg Arg
    1040                1045                1050


Arg Gln
    1055


<210>  216
<211>  1056
<212>  PRT
<213>  Aspergillus cervinus

<400>  216

Ser Thr Phe Ser His Lys Asn Asp Arg Ile Leu Lys Gly Leu Lys Arg
1               5                   10                  15


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


Tyr Gln Thr Lys Phe Asp Gly Val Thr Trp Asp Asp Asp Asn Trp Leu
        35                  40                  45


Leu Thr Thr Thr Ala Leu Asp Gln Gly Asp Phe Arg Ser Arg Gly Ser
    50                  55                  60


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


Phe Glu Leu Asp Thr Ala Glu Asn Gly Asp Val Ile Ser Gly Trp Pro
                85                  90                  95


Leu Phe Ser Arg Arg Gln Thr Phe Ala Thr Ile Ala Gly Phe Phe Asp
```

```
            100                 105                 110

Ser Gln Pro Thr Thr Asn Gly Ser Asn Phe Pro Trp Leu Tyr Gln Tyr
        115                 120                 125

Gly Gly Asp Ser Val Ile Ser Gly Val Pro His Trp Ser Gly Leu Val
    130                 135                 140

Leu Asp Leu Gly Asn Asp Thr Tyr Leu Asp Ser Thr Val Asp Asn Gln
145                 150                 155                 160

Thr Ile Glu Asn Phe Thr Ser Met Tyr Asp Tyr Lys Ser Gly Val Leu
                165                 170                 175

Ser Trp Ser Tyr Thr Trp Val Pro Ala Gly Asn Lys Gly Ser Phe Asp
            180                 185                 190

Ile Val Tyr Arg Leu Phe Ala His Lys Leu Asn Val Asn Gln Ala Val
        195                 200                 205

Val Asp Met Glu Ile Thr Pro Ser Leu Ser Phe Asn Ala Thr Val Val
    210                 215                 220

Asn Ile Leu Asp Gly Tyr Ser Ala Val Arg Thr Asp Phe Val Glu Ser
225                 230                 235                 240

Gly Asn Asp Asn Gly Ala Ile Phe Thr Ala Val Arg Pro Trp Gly Ile
                245                 250                 255

Ser Asn Val Thr Ala Tyr Val Tyr Ala Asn Leu Thr Gly Thr Pro Asn
            260                 265                 270

Val Asp Leu Ser Ser Arg Thr Ile Val Ala Asn Lys Pro Tyr Val His
        275                 280                 285

Thr Asn Ala Ser Ser Ile Ala Gln Ala Val Asn Val Ser Cys Ser Pro
    290                 295                 300

Asn Glu Thr Val Arg Ile Thr Lys Phe Val Gly Ala Ala Ser Ser Asp
```

```
305                 310                 315                 320


Ala Phe Glu Asn Pro Gln Glu Thr Ala Arg Gln Ala Val Ser Ala Ala
                325                 330                 335


Ile Gly Ala Gly Tyr Leu Arg Ser Leu Gly Thr His Ile Ala Glu Trp
            340                 345                 350


Ala Ser Ile Phe Pro Asp Asp Ser Val Asp Arg Phe Thr Asp Pro Ala
        355                 360                 365


Thr Gly Lys Leu Pro Ala Asn Lys His Ile Ile Asn Ser Ala Ile Ile
    370                 375                 380


Ala Val Thr Asn Thr Tyr Tyr Leu Leu Gln Asn Thr Val Gly Lys Asn
385                 390                 395                 400


Ala Ile Gln Ala Val Ser Gly Ala Pro Val Asn Ile Asp Ser Ile Ser
                405                 410                 415


Val Gly Gly Leu Thr Ser Asp Ser Tyr Ala Gly Gln Val Phe Trp Asp
            420                 425                 430


Ala Asp Val Trp Met Gln Pro Gly Leu Ala Ala Ser His Pro Glu Ala
        435                 440                 445


Ala Gln Arg Ile Thr Asn Phe Arg Ala Ala Lys Tyr Pro Gln Ala Leu
    450                 455                 460


Ala Asn Ile Glu Thr Ala Phe Thr Ser Ser Lys Asn Gln Thr Ser Phe
465                 470                 475                 480


Ser Pro Ser Ala Ala Ala Phe Pro Trp Thr Ser Gly Arg Phe Gly Asn
                485                 490                 495


Cys Thr Ala Thr Gly Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly
            500                 505                 510


Asp Ile Gly Leu Ser Leu Met Tyr Gln Trp Ile Ala Ser Gly Asp Thr
```

```
        515                 520                 525

Gln Thr Phe Arg Glu Thr His Phe Pro Ile Tyr Asp Ser Ile Ala Thr
    530                 535                 540

Met Tyr Ser Asn Ile Val Glu Arg Asn Gly Ser Tyr Trp Thr Leu Lys
545                 550                 555                 560

Asn Met Thr Asp Pro Asp Glu Tyr Ala Asn Gln Ile Asp Ala Gly Gly
                565                 570                 575

Phe Thr Met Pro Leu Ile Ser Gln Thr Leu Asn Tyr Ala Asn Ala Phe
            580                 585                 590

Arg Gln Gln Phe Gly Leu Asp Val Asn Gln Thr Trp Ser Glu Ile Ala
        595                 600                 605

Asn Asn Val Leu Val Leu Asn Asp Asn Gly Val Thr Leu Glu Tyr Thr
    610                 615                 620

Thr Met Asn Gly Ser Thr Val Val Lys Gln Ala Asp Val Val Leu Asp
625                 630                 635                 640

Thr Tyr Pro Leu Val Tyr Ser Asn Asn Tyr Thr Ser Gln Asn Ser Leu
                645                 650                 655

Asp Asp Leu Asp Tyr Tyr Ala Asn Gln Gln Ser Pro Asp Gly Pro Ala
            660                 665                 670

Met Thr Trp Ala Ile Phe Ser Ile Val Ala Asn Asp Val Ser Pro Ser
        675                 680                 685

Gly Cys Ser Ala Phe Thr Tyr His Gln Tyr Ser Tyr Asp Pro Tyr Ala
    690                 695                 700

Arg Ala Pro Phe Phe Gln Leu Ser Glu Gln Leu Ile Asp Asp Ala Ser
705                 710                 715                 720

Thr Asn Gly Gly Thr His Pro Ala Phe Pro Phe Leu Thr Gly His Gly
```

```
                725                 730                 735

Gly Ala Asn Gln Val Val Ile Phe Gly Tyr Leu Gly Leu Arg Leu Leu
            740                 745                 750

Pro Asp Glu Ala Ile His Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro
        755                 760                 765

His Val Ala Tyr Arg Thr Phe Tyr Trp Arg Gly Trp Pro Ile Ser Ala
    770                 775                 780

Gln Ser Asn Ser Thr His Thr Thr Ile Ser Arg Ala Met Asn Ala Ser
785                 790                 795                 800

Pro Leu Asp Thr Ala Asp Ser Arg Phe Ala Asn Val Ser Ile Pro Ile
                805                 810                 815

Tyr Val Gly Thr Glu Ser Asn Ala Thr Val Phe Gln Leu Pro Pro Thr
            820                 825                 830

Gly Pro Leu Thr Ile Leu Asn Arg Gln Asn Gly Phe Asn Asn Thr Ile
        835                 840                 845

Pro Gly Asn Val Ala Gln Cys Arg Pro Val Tyr Ser Pro Asp Asp Tyr
    850                 855                 860

Ala Pro Gly Gln Phe Pro Ile Ala Ala Val Asp Gly Ala Thr Ser Thr
865                 870                 875                 880

Arg Trp Gln Pro Ser Ser Ala Asn Thr Ser Ser Val Thr Val Thr Leu
                885                 890                 895

Pro Asp Thr Gln Ile Asn Ser Pro Val Ser Gly Phe Tyr Phe Asn Trp
            900                 905                 910

Trp Gln Leu Pro Pro Val Asn Ala Thr Val Ile Phe His Asp Asp Leu
        915                 920                 925

Leu Glu Asn Pro Ala Ala Thr Ile Ser Ser Ser Gly Asn Ser Ser Ser
```

930 935 940

Tyr Arg Val Val Met Thr Leu Thr Asn Ile Gln Gln Ser Ser Pro Tyr
945 950 955 960

Asn Ala Gln Ile Ala Ala Leu Asp Glu Ile Thr Ile Pro Thr Gly Asn
965 970 975

Thr Thr Thr Val Gln Leu Thr Asn His Ala Gln Thr Ser Arg Tyr Ala
980 985 990

Thr Leu Leu Ile Ser Gly Asn Gln Gly Leu Gly Asp Thr Gln Asp Gly
995 1000 1005

Val Gly Ala Thr Val Ala Glu Trp Val Ile Leu Gly Gln Gly Gln
1010 1015 1020

Gly Ser Ser Ser Ser Asn Ser Asn Gly Lys Arg Lys Leu Gly Ala
1025 1030 1035

Arg Ser Ala Ala Ala Leu Ser Asn Gly Trp Thr Glu Arg Arg Arg
1040 1045 1050

Arg Leu Ile
1055

<210> 217
<211> 1053
<212> PRT
<213> Rasamsonia brevistipitata

<400> 217

Leu Arg Ser Glu Ala Arg Val Ala Gln Val Val Arg Ala Tyr Ser Ser
1 5 10 15

Ser Thr Gly Val Glu Ala Gly His Gly Asn Ala Thr Gln Tyr Glu Thr
20 25 30

Arg Phe Pro Gly Val Thr Trp Asp Gln Arg His Trp Arg Leu Lys Ser
35 40 45

```
Thr Val Leu Asp Gln Gly His Phe Gln Ser Arg Gly Ser Ile Ala Asn
    50                  55                  60

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

Asp Thr Pro Val Asp Gly Asp Val Ile Asn Gly Trp Pro Leu Phe Ser
                85                  90                  95

Arg Arg Gln Thr Phe Ala Thr Ile Ala Gly Phe Tyr Asp Glu Gln Pro
            100                 105                 110

Arg Thr Asn Gly Ser Asn Phe Asp Trp Leu Tyr Gln Asp Gly Gly Glu
        115                 120                 125

Ser Val Ile Ser Gly Val Pro His Trp Ser Gly Leu Ile Leu Asp Leu
    130                 135                 140

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

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

Tyr Lys Trp Thr Pro Lys Ser Ser Lys Gly Ser Phe Lys Ile Ser Tyr
            180                 185                 190

Arg Leu Phe Ala His Lys Leu Asn Ile Asn Gln Ala Val Val Arg Met
        195                 200                 205

Glu Ile Thr Pro Ser Ala Asp Thr Asp Ala Thr Val Val Asn Val Leu
    210                 215                 220

Asp Gly Tyr Ser Ala Val Arg Thr Asp Phe Val Gly Ser Gly Lys Asp
225                 230                 235                 240

Gly Asp Ala Val Tyr Ser Ala Val Ser Pro Trp Glu Val Gln Asn Val
                245                 250                 255
```

```
Thr Ala Tyr Val Tyr Ala Val Leu Asp Gly Ser Asp Gly Val Asp Leu
            260                 265                 270


Ser Thr Leu Ser Leu Val Asn Gly Lys Pro Tyr Val His Thr Asn Glu
        275                 280                 285


Ser Ser Ile Ala Gln Ser Val Asn Val Arg Phe Arg Ala Gly Lys Thr
    290                 295                 300


Val Thr Val Thr Lys Phe Val Gly Ala Ala Ser Thr Asp Ala Phe Pro
305                 310                 315                 320


Asp Pro Gln Gln Thr Ala Arg Glu Ala Ala Leu Ala Ala Lys Glu Glu
                325                 330                 335


Gly Tyr Asp Ala Leu Leu Arg Ser His Val Ala Glu Trp Ala Ala Val
            340                 345                 350


Met Pro Glu Glu Ser Val Asp Asp Phe Thr Tyr His Asn Gly Thr Leu
        355                 360                 365


Pro Gly Asp Asp Phe Ile Val Glu Ser Ala Ile Met Ala Val Val Asn
    370                 375                 380


Pro Tyr Tyr Leu Leu Gln Asn Thr Val Gly Glu Asn Ala Leu Arg Glu
385                 390                 395                 400


Val Ser His Ala Pro Val Asn Glu Trp Ser Ile Ser Val Gly Gly Leu
                405                 410                 415


Thr Ser Asp Ser Tyr Ala Gly Leu Ile Phe Trp Asp Ala Asp Leu Trp
            420                 425                 430


Met His Pro Gly Leu Ala Val Ala Phe Pro Gln Ala Ala Thr Arg Ile
        435                 440                 445


Thr Asn Tyr Arg Val Ala Lys Tyr Glu Gln Ala Arg Gln Asn Ala Lys
    450                 455                 460
```

```
Thr Ser Phe Thr Gly Ser Lys Asn Gln Thr Trp Phe Ser Asp Ser Ala
465                 470                 475                 480

Ala Val Tyr Pro Trp Thr Ser Gly Arg Tyr Gly Asn Cys Thr Gly Thr
                485                 490                 495

Gly Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly Asp Ile Gly Leu
            500                 505                 510

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

Glu Ser Tyr Phe Pro Ile Tyr Asp Ser Ile Ala Thr Leu Tyr Ala Asp
    530                 535                 540

Leu Leu Gln Gln Asn Gly Ser His Trp Thr Leu Thr Asn Met Thr Asp
545                 550                 555                 560

Pro Asp Glu Tyr Ala Asn Ala Val Asp Ala Gly Gly Tyr Thr Met Pro
                565                 570                 575

Leu Ile Ala Gln Thr Leu Leu Tyr Ala Asn Ser Phe Arg Gln Gln Phe
            580                 585                 590

Gly Ala Gln Pro Asn Ser Thr Trp Thr Glu Met Ala Ser Asn Ile Leu
        595                 600                 605

Phe Leu Arg Glu Asn Asp Ile Thr Leu Glu Tyr Thr Thr Met Asn Asn
    610                 615                 620

Ser Val Gln Val Lys Gln Ala Asp Val Val Leu Val Thr Tyr Pro Leu
625                 630                 635                 640

Glu Tyr Thr Thr Asn Tyr Asn Ala Gly Asn Ala Leu Thr Asp Leu Asp
                645                 650                 655

Tyr Tyr Ala Leu Lys Gln Ser Pro Asp Gly Pro Ala Met Thr Tyr Ala
            660                 665                 670
```

```
Ile Phe Ser Ile Val Ala Asn Glu Val Ser Pro Ser Gly Cys Ser Val
        675                 680                 685


Tyr Thr Tyr Ala Gln Tyr Ser Tyr Asp Pro Tyr Val Arg Pro Pro Phe
    690                 695                 700


Phe Gln Leu Ser Glu Gln Leu Val Asp Asp Tyr Thr Leu Asn Gly Gly
705                 710                 715                 720


Thr His Pro Ala Tyr Pro Phe Leu Thr Gly His Gly Gly Ala Asn Gln
                725                 730                 735


Val Val Ile Phe Gly Tyr Leu Gly Leu Arg Leu Leu Pro Asp Asn Val
            740                 745                 750


Ile His Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro Gln Val Lys Tyr
        755                 760                 765


Arg Thr Phe Tyr Trp Arg Gly Trp Pro Ile Gln Ala Tyr Ser Asn Tyr
    770                 775                 780


Thr His Thr Thr Ile Gly Arg Ala Ala Asp Val Leu Ala Leu Asp Thr
785                 790                 795                 800


Ala Asp Gln Arg Phe Ala Asn Thr Thr Ile Pro Val Gln Val Gly Ser
                805                 810                 815


Gly Ser Asn Ala Thr Val Tyr Gln Leu Pro Ile Asp Gly Val Leu Thr
            820                 825                 830


Val Ala Asn Arg Gln Val Ala Ser Thr Asn Thr Val Ala Gly Asn Leu
        835                 840                 845


Ala Gln Cys Gln Pro Val Asp Ser Ser Asp Ser Tyr Val Pro Gly Gln
    850                 855                 860


Tyr Pro Leu Ala Ala Val Asp Gly Ala Ala Ser Thr Lys Trp Gln Pro
865                 870                 875                 880
```

```
Ser Phe Ala Ala Asn Val Ser Ser Val Thr Val Ser Leu Pro Glu Ser
                885                 890                 895


Glu Ser Gly Thr Leu Val Ser Gly Phe Tyr Phe Asp Trp Ala Gln Ala
            900                 905                 910


Pro Pro Val Asn Ala Thr Val Val Phe His Asn Asn Thr Val Glu Asn
        915                 920                 925


Pro Thr Arg Tyr Met Ser Ser Pro Thr Phe Val Thr His Ile Asp Asn
    930                 935                 940


Ile Thr Leu Ser Ser Pro Tyr Asn Ala Glu Ala Asn Pro Ala Ala Thr
945                 950                 955                 960


Ile Leu Leu Pro Ser Ser Asn Thr Thr Asn Val Thr Leu Ala His Pro
                965                 970                 975


Met Pro Val Pro Arg Tyr Ala Thr Leu Phe Ile Thr Gly Asn Gln Ala
            980                 985                 990


Leu Ser Glu Ser Glu Val Gln Ala  Gln Asn Gly Thr Gly  Ala Thr Val
        995                 1000                 1005


Ala Glu  Trp Ala Ile Leu Ala  Ser Asn Pro Glu Thr  Gly Ser Ser
    1010                 1015                 1020


Lys Arg  Asn Leu Gln Leu Arg  Gly Val Gly Arg Ser  Ala Leu Ala
    1025                 1030                 1035


Gly Leu  Pro Arg Arg Ala Asn  Arg Lys Glu Arg Arg  Thr Asp Val
    1040                 1045                 1050


<210>  218
<211>  1034
<212>  PRT
<213>  Acremonium curvulum

<400>  218
```

```
Leu Glu Glu Arg Val Ser Gln Thr Leu Asn Arg His Gly Val Arg Ser
1               5                   10                  15


Ser Tyr Asn Arg Arg Ala Asp Asn Gly Asp Gln Asn Arg Ile Ser Asn
            20                  25                  30


Thr Ser His Pro Tyr Ile Tyr Gln Thr Ser Phe Glu Gly Val Thr Trp
        35                  40                  45


Asp Ser Arg Asn Trp Arg Leu Gln Gly Thr Val Leu Asp Gln Gly His
    50                  55                  60


Tyr Gln Ser Arg Gly Ser Ile Ala Asn Gly Tyr Phe Gly Ile Asn Val
65                  70                  75                  80


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


Val Ile Asn Gly Trp Pro Leu Phe Ser Arg Arg Gln Thr Phe Ala Gly
            100                 105                 110


Leu Ala Gly Phe Trp Ala Thr Gln Pro Thr Thr Asn Gly Thr Asn Phe
        115                 120                 125


Pro Trp Leu Tyr Gln Tyr Gly Asp Glu Ser Pro Ile Ser Gly Ile Pro
    130                 135                 140


His Trp Gly Gly Leu Val Leu Asp Leu Gly Asp Asp Val Tyr Leu Asp
145                 150                 155                 160


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


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


Arg Gly Ser Gly Ser Phe Asp Ile Thr Tyr Ser Leu Phe Ala Asn Lys
        195                 200                 205
```

```
Leu Asp Ile Asn Gln Ala Ala Val Arg Leu Ser Ile Arg Pro Ser Arg
    210                 215                 220


Asp Thr Lys Ala Lys Val Val Asn Val Leu Glu Gly Tyr Ala Ala Val
225                 230                 235                 240


Arg Thr Asp Phe Val Asp Ser Gly Lys Asp Gly Asp Ala Ile Tyr Ser
                245                 250                 255


Ala Val Arg Pro Val Gly Val Asn Asn Val Thr Ala Tyr Val Tyr Ala
            260                 265                 270


Val Leu Asp Ala Asp Ser Ala Val Asp Leu Ser Ser Ala Lys Val Ile
        275                 280                 285


Asp Asp Ala Pro Tyr Leu Tyr Thr Asn Lys Ser Thr Ile Ala Gln Ser
    290                 295                 300


Val Asn Val Glu Phe Lys Ala Asn Gln Asn Val Thr Ile Thr Lys Phe
305                 310                 315                 320


Val Gly Ile Ala Ser Thr Asp Ala Phe Pro Lys Pro Arg Asp Val Ala
                325                 330                 335


Lys Gln Ala Ala Phe Ala Gly Lys Arg Arg Gly Tyr Asp Asp Ala Leu
            340                 345                 350


Arg Ser His Val Ser Glu Trp Ala Gln Val Met Pro Asp Asp Ser Val
        355                 360                 365


Asp Asp Phe Ser Ser Asp Asn Gly Thr Leu Pro Asp Asp Gly Phe Ile
    370                 375                 380


Ile Glu Ser Ser Ile Met Ala Val Val Asn Pro Phe Tyr Leu Leu Gln
385                 390                 395                 400


Asn Thr Val Gly Ala Asn Ala Leu Arg Arg Val Asn Asn Ala Ala Val
                405                 410                 415
```

```
Asn Asp Tyr Ser Ile Ser Val Gly Gly Leu Thr Ser Asp Ser Tyr Ala
            420                 425                 430


Gly Leu Val Phe Trp Asp Ala Asp Ile Trp Met Gln Pro Gly Leu Ala
        435                 440                 445


Ala Ala Phe Pro Glu Ala Ala Gln Arg Ile Thr Asn Tyr Arg Val Ala
    450                 455                 460


Leu Tyr Pro Gln Ala Lys Arg Asn Ile Lys Thr Ala Phe Gln Ser Ser
465                 470                 475                 480


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


Ser Gly Arg Trp Gly Asn Cys Thr Ala Ser Gly Pro Cys Phe Asp Tyr
            500                 505                 510


Glu Tyr His Leu Asn Gly Asp Ile Gly Ile Ala Phe Val Asn Glu Trp
        515                 520                 525


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


Tyr Asp Ser Ile Ala Thr Ala Phe Ala Asn Leu Leu Gln Lys Asn Gly
545                 550                 555                 560


Thr Gln Trp Thr Leu Thr Asn Met Thr Asp Pro Asp Glu Tyr Ala Asn
                565                 570                 575


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


Thr Tyr Ala Asn Leu Phe Arg Lys Lys Phe Gly Lys Glu Glu Asn Asp
        595                 600                 605


Thr Trp Ala Asp Met Ala Glu Asn Val Leu Ile Leu Arg Glu Asn Asp
    610                 615                 620
```

```
Val Thr Leu Glu Tyr Thr Ala Met Asn Asn Ser Val Glu Val Lys Gln
625                 630                 635                 640


Ala Asp Val Val Leu Asn Thr Phe Pro Leu Asp Tyr Thr Arg Asp Tyr
                645                 650                 655


Ala Pro Ser Ala Ala Leu Asn Asp Leu Asp Tyr Tyr Ala Leu Lys Gln
            660                 665                 670


Ser Pro Asp Gly Pro Ala Met Thr Tyr Ala Ile Phe Ser Ile Val Ala
        675                 680                 685


Asn Glu Val Ser Pro Ser Gly Cys Ser Ala Tyr Thr Tyr Ala Gln Tyr
    690                 695                 700


Ser Tyr Ser Pro Tyr Leu Arg Gly Pro Phe His Gln Leu Ser Glu Gln
705                 710                 715                 720


Leu Thr Asp Asp Phe Thr Thr Asn Gly Gly Thr His Pro Ala Tyr Pro
                725                 730                 735


Phe Leu Thr Gly His Gly Gly Ala Asn Gln Val Val Leu Phe Gly Tyr
            740                 745                 750


Leu Gly Leu Arg Ile Val Pro Asp Asp Lys Ile His Val Asp Pro Asn
        755                 760                 765


Leu Pro Pro Gln Ile Pro Gln Val Lys Tyr Arg Thr Phe Tyr Trp His
    770                 775                 780


Gly Trp Pro Ile Ala Ala Lys Ser Asn Tyr Thr His Thr Thr Ile Ser
785                 790                 795                 800


Arg Ala Thr Thr Ile Lys Glu Leu Asp Thr Ala Asn Lys Lys Tyr Ala
                805                 810                 815


Asn Ala Ser Ile Gln Val Val Val Gly Ser Gly Lys Ser Ala Lys Thr
            820                 825                 830
```

```
Tyr Lys Leu Pro Ala Asn Gly Ser Ser Ile Val Val Ala Asn Arg Lys
        835                 840                 845


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


Ala Gln Ser Phe Asp Thr Phe Val Pro Gly Gln Phe Pro Ile Ser Ile
865                 870                 875                 880


Asn Asp Gly Ala Ala Ser Thr Lys Trp Gln Pro Glu Phe Ala Asn Asn
                885                 890                 895


Ile Ser Ala Val Thr Val Thr Val Pro Ala Ser Lys Ser Lys Lys Ile
            900                 905                 910


Ser Gly Phe Tyr Phe Asp Trp Ala Gln Ala Pro Pro Thr Asn Ala Thr
        915                 920                 925


Val Val Leu His Asp Glu Lys Met Asp Asn Pro Thr Met Val Leu Leu
    930                 935                 940


Pro Val Ser Lys Asp Asp Asp Lys Lys Gly Ser Val Ala Arg Val Asn
945                 950                 955                 960


Val Thr Ile Ser Glu Pro Trp Ser Ala Lys Asp Lys Ser Asn Phe Val
                965                 970                 975


Ile Gly Leu Gln Gly Gly Asn Thr Thr Asn Phe Thr Phe Ser Glu Pro
            980                 985                 990


Val Ala Ala Lys Arg Tyr Ala Thr  Leu Phe Ile Gln Gly  Asn Gln Ala
        995                 1000                 1005


Leu Asp  Lys Val Asp Ile Lys  Tyr Lys Asn Gly Thr  Gly Ala Thr
    1010                 1015                 1020


Val Ala  Glu Trp Gly Ile Leu  Ser Asp Asp Ala
    1025                 1030
```

```
<210>  219
<211>  1015
<212>  PRT
<213>  Talaromyces piceae

<400>  219

Ala Arg Val Asp Gln Val Leu Gln Ala Arg Asp Thr His His Pro Ser
1               5                   10                  15


Leu His Ser Ser Ser Ser Tyr Gln Thr Arg Phe Asp Gly Val Thr Trp
            20                  25                  30


Asp Gln Arg Asn Trp Arg Leu Gln Ser Arg Val Leu Asp Gln Gly His
        35                  40                  45


Tyr Gln Ser Arg Gly Ser Val Ala Asn Gly Tyr Leu Gly Ile Asn Val
    50                  55                  60


Ala Ser Ala Gly Pro Phe Phe Glu Leu Asp Thr Pro Val Asp Gly Asp
65                  70                  75                  80


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


Leu Ala Gly Phe Tyr Asp Arg Gln Pro Thr Thr Asn Ser Thr Asn Tyr
            100                 105                 110


Gly Trp Leu Asn Gln Tyr Gly Asp Glu Ser Val Ile Ser Gly Ile Pro
        115                 120                 125


His Trp Ser Gly Leu Val Leu Asp Leu Gly Asp Gly His Tyr Leu Asp
    130                 135                 140


Ala Thr Val Asp Ser Ser Thr Ile Ser Asp Tyr Thr Thr Thr Tyr Asp
145                 150                 155                 160


Phe Lys Ala Gly Val Leu Ser Trp Asp Tyr Asn Trp Ala Pro Arg Gln
                165                 170                 175
```

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

His Lys Leu Asp Ile Asn Gln Ala Val Val Lys Leu Ser Ile Thr Pro
195 200 205

Ser Ala Ser Gly Asn Ala Ser Val Val Asn Val Ile Asp Gly Tyr Ser
210 215 220

Ala Val Arg Thr Glu Phe Val Lys Ser Gly Thr Asp Gly Asp Ala Val
225 230 235 240

Tyr Ser Ala Val Ser Pro Val Gly Val Ser Asn Val Thr Ala Trp Val
245 250 255

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

Leu Val Thr Gly Lys Pro Tyr Val Tyr Gln Asn Asp Ser Ser Ile Ala
275 280 285

Gln Ser Val Asn Val Glu Phe Arg Ala Gly Glu Thr Val Thr Ile Thr
290 295 300

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

Thr Ala Arg Asp Ala Ala Leu Leu Ala Lys Lys Lys Gly Phe Asp Asp
325 330 335

Leu Leu Arg Ser His Val Ser Glu Trp Ala Gln Val Met Pro Asp Gly
340 345 350

Ser Val Asp Asp Phe Thr Arg Glu Asp Gly Thr Leu Pro Asp Asp Glu
355 360 365

Phe Ile Ile Glu Ser Ala Val Thr Ala Val Val Asn Pro Phe Tyr Leu
370 375 380

```
Leu Gln Asn Thr Val Gly Lys Asn Ala Leu Gln Arg Val Ser Asn Ala
385                 390                 395                 400


Pro Val Asn Asp Trp Ser Ile Pro Val Gly Gly Leu Ser Ser Asp Ser
                405                 410                 415


Tyr Ala Gly Leu Ile Phe Trp Asp Ala Asp Val Trp Met Gln Pro Gly
            420                 425                 430


Leu Val Ala Ala Phe Pro Glu Ser Ala Gln Arg Ile Thr Asn Tyr Arg
        435                 440                 445


Ala Ala Met Tyr Arg Gln Ala Arg Ala Asn Ile Gln Ser Ala Phe Ala
    450                 455                 460


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


Trp Thr Ser Gly Arg Tyr Gly Asn Cys Thr Gly Thr Gly Pro Cys Phe
                485                 490                 495


Asp Tyr Glu Tyr His Leu Asn Gly Asp Ile Ala Ile Ser Leu Val Asn
            500                 505                 510


Gln Trp Val Val Ser Gly Asp Thr Glu Thr Phe Lys Asn Glu His Phe
        515                 520                 525


Pro Ile Tyr Asp Ser Ile Ala Thr Met Tyr Ala Asp Val Leu Lys Lys
    530                 535                 540


Asn Gly Ser Phe Tyr Thr Leu Thr Asn Met Thr Asp Pro Asp Glu Tyr
545                 550                 555                 560


Ala Asn Asn Lys Asp Ala Gly Gly Phe Thr Met Pro Leu Ile Ala Lys
                565                 570                 575


Thr Leu Leu Asn Ala Asn Asp Phe Arg Lys Gln Phe Asn Met Glu Glu
            580                 585                 590
```

```
Asn Ser Thr Trp Asn Glu Lys Ala Ala Ser Val Gln Ile Leu Arg Glu
        595                 600                 605


Asn Asp Val Thr Leu Glu Tyr Thr Thr Met Asn Asn Ser Val Ala Val
    610                 615                 620


Lys Gln Ala Asp Val Val Leu Met Thr Phe Pro Leu Asp Tyr Thr Ala
625                 630                 635                 640


Asn Tyr Ser Ser Ser Ser Ala Leu Asn Asp Leu Asp Tyr Tyr Ala Leu
                645                 650                 655


Lys Gln Ser Pro Asp Gly Pro Gly Met Thr Tyr Ala Ile Phe Ser Ile
            660                 665                 670


Val Ala Asn Gln Val Ser Pro Ser Gly Cys Ser Ala Tyr Thr Tyr Ala
        675                 680                 685


Gln Tyr Ser Tyr Tyr Pro Tyr Ala Arg Ala Pro Phe Phe Gln Leu Ser
    690                 695                 700


Glu Gln Leu Leu Asp Asp Tyr Thr Ala Asn Gly Gly Thr His Pro Ala
705                 710                 715                 720


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


Gly Tyr Leu Gly Leu Arg Leu Val Pro Asp Glu Thr Leu Tyr Ile Asp
            740                 745                 750


Pro Asn Leu Pro Pro Gln Ile Pro Gln Val Lys Tyr Arg Thr Phe Tyr
        755                 760                 765


Trp Arg Gly Trp Pro Ile Gln Ala Ala Ser Asn Tyr Thr His Thr Thr
    770                 775                 780


Ile Arg Arg Ala Thr Thr Val Ala Pro Leu Asp Thr Ala Asp Glu Lys
785                 790                 795                 800
```

```
Tyr Thr Asp Glu Ala Ile Thr Leu His Val Gly Gln Gln Ser Asp Gly
                805                 810                 815


Asn Lys Tyr Gln Leu Pro Ala Asp Gly Thr Pro Val Thr Val Ala Asn
            820                 825                 830


Arg Arg Val Ser Ser Val Asn Thr Val Lys Gly Asn Met Ile Gln Cys
        835                 840                 845


Gln Pro Val Gln Ser Thr Ala Ser Ile Gln Pro Gly Gln Phe Pro Ile
    850                 855                 860


Ala Ala Val Asp Gly Ala Ala Ser Thr Lys Trp Gln Pro Glu Phe Ala
865                 870                 875                 880


Ala Asn Ala Ser Ser Leu Thr Val Glu Ile Pro Ser Ser Gly Lys Lys
                885                 890                 895


Arg Lys Thr Val Ser Gly Phe Phe Phe Asp Trp Ala Glu Ala Pro Pro
            900                 905                 910


Thr Asn Ala Thr Val Val Leu His Asn Asn Pro Val Ser Glu Pro Thr
        915                 920                 925


Leu Ser Ser Phe Glu Ala Gly Lys Asp Gly Val Val Leu Arg Ala Phe
    930                 935                 940


Asp Ile Glu Ile Ser Ser Pro Tyr Asn Ala Ser Thr Tyr Ala Asp Glu
945                 950                 955                 960


Ile Ile Ile Pro Gln Gly Asn Ser Thr Asn Tyr Thr Phe Ser His Pro
                965                 970                 975


Val Pro Ala Pro Arg Phe Ala Thr Leu Phe Val Gln Gly Asn Gln Ala
            980                 985                 990


Leu Asp Lys Val Asp Val Glu Asn  Lys Asn Gly Thr Gly  Pro Met Val
        995                 1000                1005
```

```
Ala Glu  Trp Val Ile Leu Glu
    1010                1015


<210>  220
<211>  1022
<212>  PRT
<213>  Penicillium sp.

<400>  220

Leu Pro Leu Glu Glu Arg Val Asp Arg Val Leu Arg Ser Tyr Ser Val
1               5                   10                  15


Gly Ser Gly Leu Glu Ala Arg His Ser Lys Tyr Thr Tyr Gln Thr Gln
            20                  25                  30


Phe Asp Gly Val Thr Trp Asp Gln Gln Asn Trp Arg Leu Glu Ser Thr
        35                  40                  45


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


Tyr Ile Gly Leu Asn Val Ala Gly Ala Gly Pro Phe Phe Glu Leu Asp
65                  70                  75                  80


Ala Pro Val Asp Gly Asp Val Ile Asn Gly Trp Pro Leu Phe Ser Arg
                85                  90                  95


Arg Gln Thr Phe Ala Gly Leu Ser Gly Phe Tyr Asp Val Gln Pro Thr
            100                 105                 110


Thr Asn Gly Ser Asn Tyr Pro Trp Leu Asp Gln Tyr Gly Tyr Asp Ser
        115                 120                 125


Val Ile Ser Gly Ile Pro His Trp Gly Gly Leu Val Leu Asp Leu Gly
    130                 135                 140


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


Tyr Thr Thr Thr Phe Asp Tyr Lys Ala Gly Val Leu Ser Trp Asp Tyr
```

```
                165                 170                 175

Asn Trp Thr Pro Lys Asn Thr Ser Phe Gly Ile Ser Tyr Lys Ile Phe
            180                 185                 190

Ser Ser Lys Leu Asp Ile Asn Gln Ala Val Val Gln Leu Ser Ile Thr
        195                 200                 205

Pro Ser Ala Asn Gly Thr Ala Ser Val Ala Asn Val Ile Asp Gly Tyr
    210                 215                 220

Ala Ala Val Arg Thr Glu Phe Val Thr Ser Gly Asn Asp Ser Asp Ala
225                 230                 235                 240

Leu Phe Thr Ala Val Lys Pro Thr Gly Ile Asn Asn Val Thr Ala Trp
                245                 250                 255

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

Thr Leu Val Asn Asn Lys Pro Tyr Ile Asn Gln Asn Asp Ser Ser Ile
        275                 280                 285

Ala Gln Ala Val Asp Val Glu Phe Thr Ala Asp Ser Thr Val Thr Ile
    290                 295                 300

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

Lys Thr Ala Lys Asp Ala Ala Leu Ala Ala Arg Ile Lys Gly Phe Glu
                325                 330                 335

Asp Leu Leu Arg Ser His Val Ser Glu Trp Ala Gln Val Met Pro Asp
            340                 345                 350

Asp Ser Val Asp Asp Phe Ser Leu Ala Asp Gly Thr Leu Pro Asp Asp
        355                 360                 365

Ile Phe Ile Ile Glu Ser Ser Val Met Ala Val Val Asn Pro Tyr Tyr
```

```
    370                 375                 380


Leu Leu Gln Asn Thr Val Gly Glu Asn Ala Leu Arg Arg Val Asn Asp
385                 390                 395                 400


Ala Pro Val Asn Ile Trp Ser Ile Pro Val Gly Gly Leu Thr Ser Asp
                405                 410                 415


Ser Tyr Ala Gly Gln Ile Phe Trp Asp Ala Asp Leu Trp Met Gln Pro
            420                 425                 430


Gly Leu Val Ala Ala Phe Pro Glu Ser Ala Lys Arg Ile Ser Asn Tyr
        435                 440                 445


Arg Val Ala Lys Tyr Pro Glu Ala Leu Ala Asn Thr Asn Thr Ser Phe
    450                 455                 460


Ala Gly Ser Gln Asn His Thr Thr Phe Ser Ser Asp Ala Ala Ile Tyr
465                 470                 475                 480


Ser Trp Thr Ser Gly Arg Tyr Gly Asn Cys Thr Ala Thr Gly Pro Cys
                485                 490                 495


Trp Asp Tyr Glu Tyr His Leu Asn Gly Asp Ile Gly Ile Ser Leu Val
            500                 505                 510


Asn Gln Trp Val Thr Ser Gly Asp Thr Glu Thr Phe Gln Asn Asp Leu
        515                 520                 525


Phe Pro Ile Tyr Asn Ser Val Ala Thr Leu Tyr Ala Asp Leu Leu Lys
    530                 535                 540


Leu Asn Gly Ser Tyr Tyr Thr Leu Thr Asn Met Thr Asp Pro Asp Glu
545                 550                 555                 560


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


Lys Thr Leu Ser Asn Ala Asn Ala Phe Arg Lys His Phe Gly Leu Asp
```

```
            580                 585                 590

Gln Asn Ser Thr Trp Thr Glu Met Ala Glu Asn Val Leu Val Ile Arg
        595                 600                 605

Glu Asn Asp Val Thr Leu Glu Tyr Thr Thr Met Asn Asn Ser Val Ala
    610                 615                 620

Val Lys Gln Ala Asp Val Val Leu Ser Thr Phe Pro Leu Asp Tyr Thr
625                 630                 635                 640

Met Asn Tyr Thr Thr Ser Asp Ala Val Asn Asp Leu Asp Tyr Tyr Ala
                645                 650                 655

Leu Lys Gln Ala Ser Asp Gly Pro Gly Met Thr Tyr Ala Ile Phe Ser
            660                 665                 670

Ile Val Ala Asp Lys Val Ser Lys Ser Gly Cys Ser Ala Tyr Thr Tyr
        675                 680                 685

Ala Gln Tyr Ser Phe Asp Pro Tyr Ile Arg Ser Pro Phe Phe Gln Phe
    690                 695                 700

Ser Glu Gln Leu Asp Asp Asp Tyr Thr Thr Asn Gly Gly Thr His Pro
705                 710                 715                 720

Ala Phe Pro Phe Leu Thr Gly His Gly Gly Ala Asn Gln Val Val Leu
                725                 730                 735

Tyr Gly Tyr Leu Gly Leu Arg Leu Leu Pro Asp Asn Val Leu His Ile
            740                 745                 750

Asp Pro Asn Leu Pro Pro Gln Ile Pro Ser Val Lys Tyr Arg Thr Phe
        755                 760                 765

Tyr Trp His Gly Trp Pro Ile Gln Ala Asn Ser Asn Tyr Thr His Thr
    770                 775                 780

Thr Ile Arg Arg Ala Thr Thr Thr Ala Pro Leu Ser Thr Ala Asp Gln
```

```
785                 790                 795                 800


Thr Tyr Ser Asn Thr Ser Ile Thr Val Gln Val Gly Thr Ser Asn Gly
                805                 810                 815


Thr Thr Tyr Ser Leu Arg Val Asp Gly Thr Pro Leu Thr Ile Lys Asn
            820                 825                 830


Arg Arg Ile Gly Ser Val Gln Thr Ile Ser Gly Asn Ile Ala Gln Cys
        835                 840                 845


Gln Pro Val Gln Ser Pro Asp Ser Tyr Glu Pro Gly Gln Tyr Pro Leu
    850                 855                 860


Ser Val Val Asp Gly Ala Ser Ser Thr Lys Trp Gln Pro Glu Ser Ala
865                 870                 875                 880


Ala Asn Ile Ser Ser Val Thr Val Thr Leu Gly Ser Ser Tyr Ser Pro
                885                 890                 895


Gly Asn Ser Ser Asn Ala Thr Ala Ser Ser Ile Leu Gly Phe Tyr Phe
            900                 905                 910


Asn Trp Ala Gln Ala Pro Pro Asp Asn Ile Thr Val Val Leu His Asn
        915                 920                 925


Ala Ser Ile Pro Tyr Leu Asn Ala Ser Leu Ser Ser Leu Ser Asn Thr
    930                 935                 940


Thr Thr Thr Thr Ser Leu Asn Ile Thr Val Ser Asn Pro Tyr Asp Ser
945                 950                 955                 960


Ser Ala Asp Glu Lys Ile Ile Val Leu Pro Ser Ser Asn Thr Thr Asn
                965                 970                 975


Tyr Thr Phe Pro Ser Pro Val Pro Val Pro Arg Phe Ala Thr Leu Phe
            980                 985                 990


Ile Gln Gly Asn Gln Gly Leu Asp  Gln Thr Asp Leu Glu  Tyr Gly Asn
```

```
        995                 1000                1005


Gly Thr  Gly Ala Thr Val Ala  Glu Trp Ala Ile Leu  Ser Ala
    1010                 1015                1020


<210>  221
<211>  1020
<212>  PRT
<213>  Talaromyces aurantiacus

<400>  221

Leu Pro Phe Gln Asp Arg Val Asp Gln Val Leu Arg Ser Tyr Ser Ala
1               5                   10                  15


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


Thr Tyr Glu Thr Gln Phe Pro Gly Val Thr Trp Asp Gln Arg Asn Trp
        35                  40                  45


Arg Leu Gln Ser Thr Val Leu Asp Gln Gly His Tyr Glu Ser Arg Gly
    50                  55                  60


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


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


Pro Leu Phe Ser Arg Arg Gln Thr Phe Ala Gly Leu Ala Gly Phe Tyr
            100                 105                 110


Asp Leu Gln Pro Thr Thr Asn Gly Ser Asn Phe Pro Trp Leu Asp Gln
        115                 120                 125


Tyr Gly Asp Asp Ser Ala Ile Ser Gly Val Pro His Trp Gly Gly Leu
    130                 135                 140


Val Leu Asp Leu Gly Asp Gly Gln Tyr Leu Asp Ala Thr Val Asp Asn
145                 150                 155                 160
```

```
Ser Thr Val Ser Asp Tyr Lys Thr Thr Tyr Asp Phe Lys Ala Gly Val
                165                 170                 175

Leu Ser Trp Asp Tyr Lys Trp Thr Pro Lys Ser Ser Asn Val Ser Phe
            180                 185                 190

Gly Ile Ser Tyr Lys Val Phe Ala Asn Lys Leu Asp Val Asn Gln Ala
        195                 200                 205

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

Val Asn Val Ile Asp Gly Tyr Ser Ala Val Arg Thr Asp Phe Val Ser
225                 230                 235                 240

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

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

Ala Phe Asp Phe Ser Ser Ala Thr Ile Val Asn Asn Lys Pro Tyr Val
        275                 280                 285

His Gln Asn Asp Ser Ser Ile Ala Gln Ser Val Asn Val Thr Phe Thr
    290                 295                 300

Ala Gly Thr Thr Val Thr Ile Asn Lys Phe Val Gly Ala Ala Ser Thr
305                 310                 315                 320

Asp Ala Phe Pro Asp Pro Arg Ser Thr Ala Lys Glu Ala Ala Leu Ala
                325                 330                 335

Gly Arg Arg Arg Gly Tyr Asp Asp Ser Phe Arg Ala His Ile Ser Glu
            340                 345                 350

Trp Ala Gln Val Met Pro Asp Asp Ser Val Asp Asp Phe Thr Leu Ala
        355                 360                 365
```

```
Asn Gly Thr Leu Pro Asn Asp Thr Phe Ile Ile Glu Ser Ala Val Met
    370                 375                 380


Ala Val Val Asn Pro Tyr Tyr Leu Leu Gln Asn Thr Val Gly Pro Asn
385                 390                 395                 400


Ala Leu Arg Arg Val Asn Asn Ala Pro Val Asn Asp Trp Ser Ile Ser
                405                 410                 415


Val Gly Gly Leu Thr Ser Asp Ser Tyr Ala Gly Gln Val Phe Trp Asp
            420                 425                 430


Ala Asp Val Trp Met Gln Pro Gly Leu Val Ala Ala Phe Pro Glu Ser
        435                 440                 445


Ala Lys Arg Ile Thr Asn Tyr Arg Ala Ala Ile Tyr Ser Gln Ala Leu
    450                 455                 460


Ala Asn Ala Lys Thr Ala Tyr Thr Ser Ser Gln Asn Gln Thr Ser Phe
465                 470                 475                 480


Ser Ser Asp Ala Ala Ile Tyr Ser Trp Thr Ser Gly Arg Tyr Gly Asn
                485                 490                 495


Cys Thr Ala Thr Gly Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly
            500                 505                 510


Asp Ile Gly Ile Ser Leu Val Asn Gln Trp Val Ala Ser Gly Asp Asn
        515                 520                 525


Glu Thr Phe Lys Asn Thr His Phe Pro Ile Tyr Asn Ser Ile Ala Thr
    530                 535                 540


Leu Tyr Gly Asp Leu Leu Lys Lys Asn Gly Ser Tyr Tyr Thr Leu Thr
545                 550                 555                 560


Asn Met Thr Asp Pro Asp Glu Tyr Ala Asn Asn Val Asp Ala Gly Gly
                565                 570                 575
```

```
Tyr Thr Met Thr Leu Ile Ser Gln Thr Leu Ser Asn Ala Asn Ala Phe
            580                 585                 590


Arg Lys Gln Phe Gly Met Asp Glu Asn Thr Thr Trp Thr Glu Met Ala
        595                 600                 605


Asp Asn Val Leu Leu Ile Arg Glu Asn Asp Ile Thr Leu Glu Tyr Thr
    610                 615                 620


Thr Met Asn Asn Ser Val Ala Val Lys Gln Ala Asp Val Ile Leu Ser
625                 630                 635                 640


Thr Tyr Pro Leu Asp Tyr Thr Lys Asn Tyr Thr Thr Ser Ala Ala Leu
                645                 650                 655


Asn Asp Leu Asp Tyr Tyr Ala Leu Lys Gln Ser Pro Asp Gly Pro Gly
            660                 665                 670


Met Thr Tyr Ala Ile Phe Ser Ile Val Ala Asn Asp Val Ser Pro Ser
        675                 680                 685


Gly Cys Ser Ala Tyr Thr Tyr Ala Gln Tyr Ser Tyr Asp Pro Tyr Ile
    690                 695                 700


Arg Gly Pro Phe Phe Gln Phe Ser Glu Gln Leu Leu Asp Asp Tyr Thr
705                 710                 715                 720


Ala Asn Gly Gly Thr His Pro Ala Phe Pro Phe Leu Thr Gly His Gly
                725                 730                 735


Gly Ala Asn Gln Val Val Leu Tyr Gly Tyr Leu Gly Leu Arg Leu Val
            740                 745                 750


Pro Asp Asp Lys Leu His Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro
        755                 760                 765


Ser Val Lys Tyr Arg Thr Phe Tyr Trp Arg Gly Trp Pro Ile Gln Ala
    770                 775                 780
```

```
Ala Ser Asn Tyr Thr His Thr Thr Ile Gln Arg Ala Thr Arg Val Ala
785                 790                 795                 800


Pro Leu Ser Thr Ala Asp Met Thr Tyr Ala Asn Lys Ser Ile Ser Val
                805                 810                 815


Gln Val Gly Gln Asn Thr Ala Asn Ser Thr Thr Tyr Ser Leu Pro Val
            820                 825                 830


Asn Gly Ser Ala Leu Val Ile Ser Asn Arg Gln Ile Gly Ser Ile Asn
        835                 840                 845


Thr Val Gln Gly Asn Ile Ala Gln Cys Lys Ser Val Gln Ser Met Asn
    850                 855                 860


Gly Tyr Gln Pro Gly Gln Tyr Pro Ile Ser Ala Val Asp Gly Ala Ala
865                 870                 875                 880


Ser Thr Lys Trp Gln Pro Glu Phe Ala Ala Asn Val Ser Ser Leu Thr
                885                 890                 895


Val Asp Leu Thr Ser Ser Asn Ala Ser Ser Val Ser Gly Phe Tyr Phe
            900                 905                 910


Asp Trp Ala Gln Ala Pro Pro Val Asn Val Thr Val Val Leu His Asn
        915                 920                 925


Ser Thr Ser Ala Ser Leu Thr Ser Ser Ala Ala Gln Asn Gly Ser Ser
    930                 935                 940


Thr Val Ser Leu Asn Ile Thr Ile Ser Asn Pro Tyr Asn Ala Ser Ser
945                 950                 955                 960


Tyr Asp Ala Asn Val Ile Glu Leu Ser Ser Ser Asn Thr Thr Asn Tyr
                965                 970                 975


Arg Phe Pro Ala Pro Val Pro Lys Pro Arg Tyr Ala Thr Leu Phe Val
            980                 985                 990
```

```
Gln Gly Ser Gln Ala Leu Asp Glu  Thr Asp Met Lys Ala  Gly Asn Gly
        995                 1000                 1005


Thr Gly  Ala Thr Val Ala Glu  Trp Ala Ile Leu Ser
    1010                 1015                 1020



<210>  222
<211>  1016
<212>  PRT
<213>  Talaromyces pinophilus

<400>  222

Leu Pro Phe Asn Glu Arg Val Asp Gln Val Leu Arg Ser Tyr Ser Pro
1               5                   10                  15


Lys Asn Leu Glu Ser Arg Ser Thr Lys His Gly Asn Ser Tyr Gln Thr
            20                  25                  30


Gln Phe Ser Gly Val Thr Trp Asp Gln Arg Asn Trp Arg Leu Gln Ser
        35                  40                  45


Thr Val Leu Asp Gln Gly His Tyr Glu Ser Arg Gly Ser Ile Ala Asn
    50                  55                  60


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


Asp Thr Ala Val Asp Gly Asp Val Ile Asn Gly Trp Pro Leu Phe Ser
                85                  90                  95


Arg Arg Gln Thr Phe Ala Gly Leu Ala Gly Phe Tyr Asp Leu Gln Pro
            100                 105                 110


Thr Thr Asn Gly Ser Asn Phe Pro Trp Leu Ser Gln Tyr Gly Asp Asp
        115                 120                 125


Ser Ala Ile Ser Gly Val Pro His Trp Gly Gly Leu Ile Leu Asp Leu
    130                 135                 140
```

```
Gly Asp Gly Glu Tyr Leu Asp Ala Thr Val Asp Asn Ser Thr Ile Ser
145                 150                 155                 160


Asp Tyr Thr Thr Thr Tyr Asp Tyr Lys Ala Gly Val Leu Ser Trp Asp
                165                 170                 175


Tyr Lys Trp Thr Pro Lys Asn Ser Lys Ala Ser Phe Gly Ile Asn Tyr
            180                 185                 190


Lys Ile Phe Ala Asn Lys Leu Asp Val Asn Gln Ala Val Val Gln Leu
        195                 200                 205


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


Asp Gly Tyr Ser Ala Val Arg Thr Asp Phe Val Ser Ser Gly Asn Glu
225                 230                 235                 240


Ser Asp Val Ile Tyr Thr Ala Val Lys Pro Val Gly Val Asn Asn Val
                245                 250                 255


Thr Ala Trp Ile Tyr Ala Ala Leu Asp Gly Asp Glu Ala Phe Asp Phe
            260                 265                 270


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


Ser Ser Ile Ala Gln Ser Val Asn Val Ala Phe Thr Ala Gly Thr Thr
    290                 295                 300


Ile Thr Ile Asn Lys Phe Val Gly Ala Ala Ser Thr Asp Ala Phe Pro
305                 310                 315                 320


Asp Pro Gln Ser Thr Ala Arg Glu Ala Ala Met Thr Ala Arg Arg Arg
                325                 330                 335


Gly Phe Asp Asp Leu Phe Arg Ser His Val Ser Glu Trp Ala Gln Val
            340                 345                 350
```

```
Met Pro Asp Asp Ser Val Asp Asp Phe Thr Leu Ala Asn Gly Thr Leu
        355                 360                 365


Pro Asn Asp Thr Phe Ile Ile Glu Ser Ala Val Met Ala Val Val Asn
    370                 375                 380


Pro Tyr Tyr Leu Leu Gln Asn Thr Val Gly Ala Asn Ala Leu Arg Arg
385                 390                 395                 400


Val Asn Asn Ala Pro Val Asn Asp Trp Ser Ile Pro Val Gly Gly Leu
                405                 410                 415


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


Met Gln Pro Gly Leu Val Ala Ala Phe Pro Glu Ser Ala Lys Arg Ile
        435                 440                 445


Thr Asn Tyr Arg Thr Ala Lys Tyr Ser Gln Ala Leu Glu Asn Ala Lys
    450                 455                 460


Thr Ala Tyr Thr Ser Ser Gln Asn Gln Thr Ser Phe Ser Ser Asp Ala
465                 470                 475                 480


Ala Ile Tyr Ser Trp Thr Ser Gly Arg Tyr Gly Asn Cys Thr Ala Thr
                485                 490                 495


Gly Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly Asp Ile Gly Ile
            500                 505                 510


Ser Leu Val Asn Gln Trp Val Val Ser Gly Asp Asn Glu Thr Phe Lys
        515                 520                 525


Asn Thr His Phe Pro Ile Tyr Asn Ser Ile Ala Thr Leu Tyr Gly Asp
    530                 535                 540


Leu Leu Lys Lys Asn Gly Ser Tyr Tyr Thr Leu Thr Asn Met Thr Asp
545                 550                 555                 560
```

```
Pro Asp Glu Tyr Ala Asn Asn Val Asp Ala Gly Gly Tyr Thr Met Thr
                565                 570                 575


Leu Ile Ser Gln Thr Leu Ser Asn Ala Asn Ala Phe Arg Lys Gln Phe
            580                 585                 590


Gly Met Asp Glu Asn Thr Thr Trp Thr Glu Met Ala Asp Asn Ile Leu
        595                 600                 605


Leu Ile Arg Glu Asn Asp Val Thr Leu Glu Tyr Thr Thr Met Asn Asn
    610                 615                 620


Ser Val Ala Val Lys Gln Ala Asp Val Ile Leu Ser Thr Phe Pro Leu
625                 630                 635                 640


Asp Tyr Thr Lys Asn Tyr Thr Thr Ser Ala Ala Leu Asn Asp Leu Asp
                645                 650                 655


Tyr Tyr Ala Leu Lys Gln Ser Pro Asp Gly Pro Gly Met Thr Tyr Ala
            660                 665                 670


Ile Phe Ser Ile Val Ala Asn Asp Val Ser Pro Ser Gly Cys Ser Ala
        675                 680                 685


Tyr Thr Tyr Ala Gln Tyr Ser Tyr Asp Pro Tyr Ile Arg Gly Pro Phe
    690                 695                 700


Phe Gln Phe Ser Glu Gln Leu Leu Asp Asp Tyr Thr Ala Asn Gly Gly
705                 710                 715                 720


Thr His Pro Ala Phe Pro Phe Leu Thr Gly His Gly Gly Ala Asn Gln
                725                 730                 735


Val Val Leu Tyr Gly Tyr Leu Gly Leu Arg Leu Leu Pro Asp Asp Met
            740                 745                 750


Leu His Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro Ser Val Lys Tyr
        755                 760                 765
```

```
Arg Thr Phe Tyr Trp Arg Gly Trp Pro Ile Gln Ala Ala Ser Asn Tyr
    770                 775                 780


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


Ala Asp Pro Ala Tyr Ala Asn Thr Ser Ile Ser Val Ser Val Gly Gln
                805                 810                 815


Asn Thr Ala Asn Ser Thr Thr Tyr Ser Leu Pro Val Asn Gly Ser Ala
            820                 825                 830


Ile Val Val Pro Asn Arg Gln Ile Gly Ser Ile Asn Thr Val Ala Gly
        835                 840                 845


Asn Ile Ala Gln Cys Val Ser Val Leu Ser Thr Asp Ala Tyr Gln Pro
    850                 855                 860


Gly Gln Tyr Pro Ile Ser Ala Val Asp Gly Ala Ala Ser Thr Lys Trp
865                 870                 875                 880


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


Ser Ser Asn Ala Ser Ser Val Ser Gly Phe Tyr Phe Asp Trp Ala Gln
            900                 905                 910


Ala Pro Pro Thr Asn Ile Thr Val Leu Leu His Asn Ser Ser Ser Ala
        915                 920                 925


Ala Leu Thr Ser Ser Ser Thr His Gly Gly Ser Ser Ser Val Ser Leu
    930                 935                 940


Asn Ile Thr Ile Ser Asn Pro Tyr Asp Ala Ser Ser Tyr Asp Ala Asn
945                 950                 955                 960


Val Ile Ala Leu Ser Ser Ser Asn Thr Thr Asn Tyr Thr Phe Ser Ala
                965                 970                 975
```

```
Pro Val Ala Lys Pro Arg Tyr Ala Thr Leu Phe Val Gln Gly Asn Gln
            980                 985                 990


Ala Leu Asp Glu Thr Asp Thr Lys  Ala Gly Asn Gly Thr  Gly Ala Thr
        995                 1000                1005


Val Ala  Glu Trp Ala Ile Leu  Ser
    1010                 1015


<210>  223
<211>  1069
<212>  PRT
<213>  Talaromyces leycettanus

<400>  223

Thr Ser Ala Asn Ala Arg Ile Asn Arg Cys Val Lys Lys His Ala Gly
1               5                   10                  15


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


Pro Gly Val Thr Trp Asp Gln Asp Asn Trp Cys Leu Ser Thr Thr Thr
        35                  40                  45


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


Leu Gly Ile Asn Val Ala Ser Val Gly Pro Phe Phe Glu Phe Asp Thr
65                  70                  75                  80


Pro Val Asp Gly Asp Val Ile Asn Gly Trp Pro Leu Phe Asp Arg Arg
                85                  90                  95


Met Ser Phe Ala Thr Ile Ser Gly Phe Trp Asp Gln Gln Pro Thr Thr
            100                 105                 110


Asn Gly Ser Asn Phe Pro Trp Leu Tyr Gln Tyr Gly Gly Glu Ser Val
        115                 120                 125
```

```
Ile Ser Gly Val Pro His Trp Ser Gly Leu Ile Leu Asp Leu Gly Asp
    130                 135                 140


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


Ser Thr Thr Tyr Asp Phe Lys Ser Gly Val Leu Ser Trp Ser Tyr Gln
                165                 170                 175


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


Phe Ala His Lys Leu Tyr Val Asn Gln Ala Val Val Asp Met Glu Val
        195                 200                 205


Val Ser Ser Thr Glu Ala Lys Ala Thr Val Val Asn Val Ile Asp Gly
    210                 215                 220


Ala Ser Ala Val Arg Thr Asp Phe Val Glu Ser Gly Gln Asp Asp Gly
225                 230                 235                 240


Ala Ile Tyr Thr Ala Val Arg Pro Trp Gly Ile Ala Asn Val Thr Ala
                245                 250                 255


Tyr Ile Tyr Ala Asn Ile Thr Gly Ser Asp Asn Val Asp Met Arg Ser
            260                 265                 270


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


Ile Thr Gln Ala Val Asn Val His Phe Thr Pro Gly Lys Ser Val Arg
    290                 295                 300


Ile Thr Lys Phe Val Gly Gly Ala Ser Ser Asp Ala Phe Ser Asn Pro
305                 310                 315                 320


Gln Gln Ile Ala Lys Gln Ala Cys Ser Thr Ala Gln Ala Asn Gly Tyr
                325                 330                 335
```

```
Val Lys Ser Leu Arg Ser His Val Ala Glu Trp Ala Ser Val Met Pro
            340                 345                 350


Asp Asp Ser Val Asp Asp Phe Thr Phe Pro Ser Asn Gly Thr Leu Pro
        355                 360                 365


Ala Asp Glu Tyr Ile Ile Glu Ser Gln Ile Ile Ser Val Ala Asn Thr
    370                 375                 380


Tyr Tyr Leu Leu Gln Asn Thr Val Gly Lys Asn Ala Ile Asn Ala Ser
385                 390                 395                 400


Ser Ser Thr Glu Leu Asn Lys Asp Ser Ile Ala Val Gly Gly Leu Thr
                405                 410                 415


Ser Glu Ser Tyr Ala Gly Met Ile Phe Trp Asp Ala Asp Val Trp Met
            420                 425                 430


Gln Pro Gly Leu Val Ala Ser His Pro Glu Ala Ala Gln Arg Ile Thr
        435                 440                 445


Asn Tyr Arg Val Ala Lys Tyr Pro Gln Ala Lys Ala Asn Val Ala Thr
    450                 455                 460


Ala Tyr Gln Ser Ser Lys Asn Gln Thr Asn Phe Ser Pro Asp Ala Ala
465                 470                 475                 480


Val Tyr Ser Trp Thr Ser Ala Arg Tyr Gly Asn Cys Thr Ala Thr Gly
                485                 490                 495


Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly Asp Ile Gly Leu Ser
            500                 505                 510


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


Lys Leu Phe Pro Val Phe Asp Ser Val Ala Thr Leu Tyr Ser Asn Ile
    530                 535                 540
```

```
Val Gln Lys Asn Gly Ser Ser Trp Thr Leu Thr Asn Met Thr Asp Pro
545                 550                 555                 560


Asp Glu Tyr Ala Asn Gln Val Asp Ala Gly Gly Tyr Thr Met Pro Leu
                565                 570                 575


Ile Ala Gln Thr Leu Leu Tyr Ala Asn Ser Phe Arg Gln Gln Phe Gly
            580                 585                 590


Leu Glu Thr Asn Asp Thr Trp Asn Glu Ile Ala Gln Asp Val Leu Val
        595                 600                 605


Ile Arg Glu Asn Gly Val Thr Leu Glu Phe Thr Thr Met Asn Gly Ser
    610                 615                 620


Ala Val Val Lys Gln Ala Asp Val Val Leu Asp Thr Tyr Pro Leu Gly
625                 630                 635                 640


Tyr Thr His Asn Tyr Gly Pro Thr Asp Ala Leu Asn Asp Leu Asp Tyr
                645                 650                 655


Tyr Ala Asn Arg Gln Ser Pro Asp Gly Pro Ala Met Thr Trp Ala Ile
            660                 665                 670


Phe Ser Val Val Ala Asn Gln Ile Ser Pro Ser Gly Cys Ser Ala Tyr
        675                 680                 685


Thr Tyr Ala Gln Tyr Ala Phe Ser Pro Tyr Ala Arg Ala Pro Phe Tyr
    690                 695                 700


Gln Leu Ser Glu Gln Leu Ile Asp Asp Ala Ser Leu Asn Gly Gly Thr
705                 710                 715                 720


His Pro Ala Tyr Pro Phe Leu Thr Gly His Gly Gly Ala Leu Gln Val
                725                 730                 735


Asn Leu Phe Gly Tyr Leu Gly Phe Arg Tyr Leu Pro Asp Asn Val Ile
            740                 745                 750
```

```
His Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro His Ile Thr Tyr Arg
        755                 760                 765


Thr Phe Tyr Trp Arg Gly Trp Pro Ile Thr Ala Ala Ser Thr Tyr Thr
    770                 775                 780


His Thr Thr Leu Ser Arg Ala Trp Asn Val Ser Ser Leu Asp Ser Ala
785                 790                 795                 800


Asp Pro Lys Phe Ala Asn Ala Ser Ile Pro Val His Val Gly Leu Glu
                805                 810                 815


Ser Asn Val Thr Val Tyr Arg Leu Pro Val Asn Gly Thr Leu Thr Val
            820                 825                 830


Pro Asn Arg Met Val Gly Ser Lys Asn Thr Leu Ala Gly Asn Met Val
        835                 840                 845


Gln Cys Arg Pro Val Gln Ser Met Asp Gly Tyr Gln Pro Gly Gln Phe
    850                 855                 860


Pro Ile Ser Val Val Asp Gly Ala Ser Ser Thr Lys Trp Gln Pro Leu
865                 870                 875                 880


Tyr Ser Ala Asn Val Ser Ser Val Thr Val Thr Leu Ser Ser Ser Ala
                885                 890                 895


Val Gly Lys Ser Val Asn Gly Phe Tyr Phe Asp Trp Ala Gln Asn Pro
            900                 905                 910


Pro Val Asn Ala Ala Val Val Phe His Asn Ser Ser Phe Ala Gln Asn
        915                 920                 925


Pro Ala Thr Thr Phe Ser Phe Asp Asn Pro Ser Ala Ser Gly Asn Leu
    930                 935                 940


Tyr Ser Val Val Ser Val Leu Lys Asp Ile Gln Leu Ser Asp Pro Tyr
945                 950                 955                 960
```

```
Asp Pro Ala Thr Thr Asp Leu Asp Val Ile Ala Ile Pro Lys Gly Asn
                965                 970                 975


Thr Thr Asn Val Thr Leu Ser Ser Pro Val Pro Ala Ala Arg Tyr Ala
            980                 985                 990


Thr Leu Phe Ile Gln Gly Asn Gln  Ala Asn Ser Pro Ala  Glu Val Ala
        995                 1000                1005


Ala Lys  Asn Gly Thr Gly Ala  Thr Val Ala Glu Trp  Ala Ile Leu
    1010                1015                1020


Gly Gln  Glu Val Gln Asn Asn  Gly Tyr Gly Asp Gln  Ile Glu Ala
    1025                1030                1035


Arg Arg  Leu Asp Val Arg Gly  Ala Ala Ala Leu Ser  Gly Met Gly
    1040                1045                1050


Ser Phe  Thr Gln Arg Arg Lys  Arg Lys Met Ile Leu  Pro Arg Phe
    1055                1060                1065


Asp



<210>  224
<211>  1016
<212>  PRT
<213>  Talaromyces variabilis

<400>  224

Ala Leu Ser Pro Gly Ala Arg Val Asn Gln Val Leu Arg Ala His Asn
1               5                   10                  15


Ser Leu Pro Pro Ser Leu Thr Asp Asn Ser Thr Gly Ser Ser Tyr Lys
            20                  25                  30


Thr Arg Phe Asp Gly Val Thr Trp Asp Gln Arg Asn Trp Arg Leu Gln
        35                  40                  45


Ser Arg Val Leu Asp Gln Gly His Tyr Glu Ala Arg Gly Ser Val Ala
```

```
    50                  55                  60


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


Leu Asp Thr Pro Val Asp Gly Asp Val Ile Asn Gly Trp Pro Leu Phe
                85                  90                  95


Ser Arg Arg Gln Thr Phe Ala Gly Leu Ala Gly Phe Tyr Asp Leu Gln
            100                 105                 110


Pro Thr Thr Asn Ser Thr Asn Tyr Gly Trp Leu Asn Gln Tyr Gly Asp
        115                 120                 125


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


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


Ser Asp Tyr Thr Thr Thr Tyr Asp Tyr Lys Ala Gly Ile Leu Ser Trp
                165                 170                 175


Asp Tyr Lys Trp Thr Pro Arg Gln Asn Ser Ser Ser Phe Arg Ile Ser
            180                 185                 190


Tyr Gln Leu Phe Ala Asn Lys Leu Asp Ile Asn Gln Ala Val Val Lys
        195                 200                 205


Leu Ser Ile Thr Pro Ser Lys Ser Gly Asn Ala Ser Val Val Asn Val
    210                 215                 220


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


Asp Gly Asn Ala Ile Tyr Thr Ala Val Ser Pro Val Gly Val Ser Asn
                245                 250                 255


Val Thr Ala Trp Val Tyr Ala Val Leu Asp Gly Asp Lys Ala Phe Asp
```

```
            260                 265                 270


Leu Ser Ser Pro Ser Arg Val Thr Gly Lys Pro Tyr Ile His Gln Asn
        275                 280                 285


Glu Ser Ser Ile Ala Gln Ala Val Asn Val Glu Phe Ser Ala Gly Lys
    290                 295                 300


Thr Val Thr Ile Ala Lys Phe Val Gly Ala Ala Ser Thr Asp Ala Phe
305                 310                 315                 320


Ser Asn Pro Gln Lys Lys Ala Lys Thr Ala Ala Leu Asp Gly Lys Lys
                325                 330                 335


Lys Gly Phe Glu Asp Leu Leu Arg Ser His Val Ser Glu Trp Ala Gln
            340                 345                 350


Val Met Pro Asp Asp Ser Val Asp Asp Phe Thr Leu Ala Asn Gly Thr
        355                 360                 365


Leu Pro Asp Asp Ser Phe Ile Ile Glu Gln Ala Val Thr Ala Val Val
    370                 375                 380


Asn Pro Tyr Tyr Leu Leu Gln Asn Thr Val Gly Lys Asn Ala Leu Gln
385                 390                 395                 400


Arg Val Asn Asn Ala Pro Val Asn Asp Trp Ser Ile Pro Val Gly Gly
                405                 410                 415


Leu Ser Ser Asp Ser Tyr Ala Gly Met Ile Phe Trp Asp Ala Asp Val
            420                 425                 430


Trp Met Gln Pro Gly Leu Val Ala Ala Phe Pro Glu Ser Ala Lys Arg
        435                 440                 445


Ile Thr Asn Tyr Arg Ala Ala Lys Tyr Gln Gln Ala Ile Ala Asn Val
    450                 455                 460


Lys Thr Ala Tyr Ser Ser Ser Gln Asn Glu Thr Val Phe Ser Pro Asn
```

```
465                 470                 475                 480


Ala Ala Ile Phe Pro Trp Thr Ser Gly Arg Tyr Gly Asn Cys Thr Gly
                485                 490                 495


Thr Gly Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly Asp Ile Ala
            500                 505                 510


Ile Ser Leu Val Asn Gln Trp Val Val Ser Gly Asp Thr Glu Thr Phe
        515                 520                 525


Gln Asn Glu His Phe Pro Ile Tyr Asn Ser Ile Ala Thr Val Tyr Gly
    530                 535                 540


Asp Leu Leu Lys Lys Asn Gly Ser Tyr Tyr Thr Leu Thr Asn Met Thr
545                 550                 555                 560


Asp Pro Asp Glu Tyr Ala Asn Asn Lys Asp Ala Gly Gly Tyr Thr Met
                565                 570                 575


Pro Leu Ile Ala Asn Thr Leu Ile Lys Ala Asn Glu Phe Arg Arg Gln
            580                 585                 590


Phe Gly Met Ala Glu Asn Ala Thr Trp Asn Glu Met Ala Glu Asn Val
        595                 600                 605


Leu Ile Ile Arg Glu Asn Asp Val Thr Leu Glu Tyr Thr Thr Met Asn
    610                 615                 620


Asn Ser Val Ala Val Lys Gln Ala Asp Val Val Leu Arg Thr Phe Pro
625                 630                 635                 640


Leu Asp Tyr Thr Thr Asn Tyr Ser Ser Ser Ala Ala Leu Asn Asp Leu
                645                 650                 655


Asp Tyr Tyr Ala Leu Lys Gln Ser Pro Asp Gly Pro Gly Met Thr Tyr
            660                 665                 670


Ala Ile Phe Ser Ile Val Ala Asn Glu Val Ser Pro Ser Gly Cys Ser
```

```
        675                 680                 685


Ala Tyr Thr Tyr Ala Gln Tyr Ser Tyr Asp Pro Tyr Ala Arg Ala Pro
    690                 695                 700


Phe Phe Gln Leu Ser Glu Gln Leu Ile Asp Asp Tyr Thr Thr Asn Gly
705                 710                 715                 720


Gly Thr His Pro Ala Tyr Pro Phe Leu Thr Gly His Gly Gly Ala Asn
                725                 730                 735


Gln Val Val Leu Tyr Gly Tyr Leu Gly Leu Arg Leu Val Ala Asp Glu
            740                 745                 750


Ile Leu His Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro Gln Val Thr
        755                 760                 765


Tyr Arg Thr Phe Tyr Trp Arg Gly Trp Pro Ile Gln Ala Ala Ser Asn
    770                 775                 780


Tyr Thr His Thr Thr Ile His Arg Ala Thr Thr Val Ala Pro Leu Asp
785                 790                 795                 800


Ser Ala Glu Lys Lys Tyr Ala Lys Ser Ala Ile Ser Val Gln Val Gly
                805                 810                 815


Gln Gln Ala Asn Ser Thr Thr Tyr Lys Leu Pro Ala Asp Gly Thr Pro
            820                 825                 830


Leu Thr Val Ala Asn Arg Lys Val Gly Ser Thr Asn Thr Ile Lys Gly
        835                 840                 845


Asn Ile Ala Gln Cys Gln Ser Val Gln Ser Val Asp Ser Tyr Gln Pro
    850                 855                 860


Gly Gln Tyr Ala Leu Ala Ala Val Asp Gly Ala Ala Ser Thr Lys Trp
865                 870                 875                 880


Gln Pro Glu Phe Ala Ala Asn Val Ser Ser Leu Thr Val Ser Ile Pro
```

```
                885                 890                 895


Ser Gly Lys Thr Ser Val Ser Gly Phe Tyr Phe Asp Trp Ala Gln Ala
            900                 905                 910


Pro Pro Ser Asn Ala Thr Val Val Phe His Asn Asn Ser Val Ser Asn
        915                 920                 925


Pro Thr Phe Ser Ser Phe Gly Ser Arg Lys Gly Ala Arg Ile Thr His
    930                 935                 940


Ile Asp Val Lys Leu Ser Asn Pro Tyr Asn Ala Ser Ser Asn Ala Asp
945                 950                 955                 960


Ala Ile Val Ile Pro Ser Gly Asn Thr Thr Asn Phe Thr Phe Ser Asn
                965                 970                 975


Pro Val Pro Ala Pro Arg Phe Ala Thr Leu Phe Val Gln Gly Asn Gln
            980                 985                 990


Gly Leu Asp Lys Val Asp Val Gln  Asn Gly Asn Gly Thr  Gly Ala Thr
        995                 1000                1005


Val Ala  Glu Trp Ala Ile Leu  Glu
    1010                1015


<210>  225
<211>  1050
<212>  PRT
<213>  Aspergillus niger

<400>  225

Leu Pro Gly Lys Asn Ala Arg Ile Ser Ala Ser Leu Lys Arg His Ala
1               5                   10                  15


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


Thr Lys Phe Ser Gly Val Thr Trp Asp Glu Asp His Trp Leu Leu Thr
        35                  40                  45
```

```
Thr Thr Thr Pro Asp Gln Gly His Tyr Gln Ser Arg Gly Ser Val Ala
    50                  55                  60


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


Leu Asp Glu Pro Val Asn Gly Asp Val Ile Asn Gly Trp Pro Leu Tyr
                85                  90                  95


Ser Arg Arg Gln Ser Phe Ala Thr Ile Ser Gly Phe Trp Asp Arg Gln
            100                 105                 110


Ala His Thr Asn Gly Ser Asn Phe Pro Trp Leu Ser Gln Tyr Gly Asp
        115                 120                 125


Asp Ser Val Ile Ser Gly Val Pro His Trp Ser Gly Leu Ile Leu Asp
    130                 135                 140


Leu Gly Asp Asp Thr Tyr Leu Asp Ala Thr Val Asp Asn Arg Thr Ile
145                 150                 155                 160


Ser Asn Phe Lys Ser Thr Tyr Asp Phe Lys Ser Gly Val Leu Ser Trp
                165                 170                 175


Ser Tyr Thr Trp Thr Pro Gln Gly Asn Lys Gly Ser Tyr Ala Ile Thr
            180                 185                 190


Tyr Arg Leu Phe Ala His Lys Leu Tyr Val Asn Arg Ala Val Val Asp
        195                 200                 205


Met Glu Ile Thr Pro Leu Thr Asn Gly Asn Ala Thr Val Val Asn Val
    210                 215                 220


Leu Asp Gly Tyr Ala Ala Val Arg Thr Asp Phe Val Ala Ser Gly Gln
225                 230                 235                 240


Glu Glu Gly Ala Ile Phe Ser Ala Val Arg Pro Trp Gly Val Asn Asn
                245                 250                 255
```

```
Val Thr Ala Tyr Val Tyr Ala Thr Leu Asp Gly Ser Asp Ser Val Asp
            260                 265                 270


Leu Ser Ser Arg Arg Ile Val Thr Asp Lys Pro Tyr Val Ser Thr Asn
        275                 280                 285


Ser Ser Ser Val Ala Gln Ala Val Asp Val Met Phe Thr Ala Asn Glu
    290                 295                 300


Thr Val Arg Ile Thr Lys Phe Val Gly Gly Ala Thr Thr Asp Tyr Phe
305                 310                 315                 320


Leu Ala Thr Gln Glu Thr Ala Lys Ala Ala Cys Leu Ala Gly Leu Ala
                325                 330                 335


Asp Gly Tyr Val Lys Ser Leu Gln Ser His Val Gly Glu Trp Ala Thr
            340                 345                 350


Ile Met His Asp His Ser Val Asp Arg Phe Thr Asp Pro Ala Thr Gly
        355                 360                 365


Lys Leu Pro Glu Asp Ser His Ile Val Asp Ser Ala Ile Ile Ala Val
    370                 375                 380


Thr Asn Thr Tyr Tyr Leu Leu Gln Asn Thr Ala Gly Thr Asn Ala Ile
385                 390                 395                 400


Val Ala Ala Gly Gly Ile Pro Val Asn Val Asp Ser Cys Ala Pro Gly
                405                 410                 415


Gly Leu Thr Ser Asp Ser Tyr Gly Gly Gln Ile Phe Trp Asp Ala Asp
            420                 425                 430


Leu Trp Met Gln Pro Gly Leu Val Ala Ser His Pro Glu Ser Ala Gln
        435                 440                 445


Arg Phe Thr Asn Tyr Arg Ile Ala Leu His Tyr Gln Ala Gln Ala Asn
    450                 455                 460
```

```
Ile Glu Thr Ala Phe Thr Gly Ser Lys Asn Gln Thr Ser Phe Ser Ser
465                 470                 475                 480


Ser Ala Ala Ile Tyr Pro Trp Thr Ser Gly Arg Phe Gly Asn Cys Thr
                485                 490                 495


Ala Thr Gly Pro Cys Trp Asp Tyr Gln Tyr His Leu Asn Gly Asp Ile
            500                 505                 510


Gly Leu Ala Met Ile Asn Gln Trp Val Ala Ser Gly Asp Thr Ala Trp
        515                 520                 525


Phe Lys Asn Tyr Leu Phe Pro Ile Tyr Asp Ala Ala Ala Thr Leu Tyr
    530                 535                 540


Ser Glu Leu Val Glu Arg Asn Gly Ser Ser Trp Thr Leu Thr Asn Met
545                 550                 555                 560


Thr Asp Pro Asp Glu Tyr Ala Asn Ser Ile Asn Ala Gly Gly Tyr Thr
                565                 570                 575


Met Pro Leu Ile Ala Glu Thr Leu Gln Asn Ala Asn Lys Leu Arg Lys
            580                 585                 590


Gln Phe Gly Leu Glu Pro Asn Glu Thr Trp Asp Glu Ile Ala Glu Asp
        595                 600                 605


Val Leu Ile Leu Arg Glu Asn Gly Val Thr Leu Glu Tyr Thr Ser Met
    610                 615                 620


Asn Gly Ser Ala Val Val Lys Gln Ala Asp Ile Val Leu Asn Thr Phe
625                 630                 635                 640


Pro Leu Thr Tyr Glu Ser Asp Asn Tyr Thr Ala Thr Asn Ser Leu Thr
                645                 650                 655


Asp Leu Asp Tyr Tyr Ala Asn Lys Gln Ser Ala Asp Gly Pro Ala Met
            660                 665                 670
```

```
Thr Tyr Ala Ile Phe Ala Ile Val Ala Ser Asp Val Ser Pro Ser Gly
        675                 680                 685

Cys Ser Ala Phe Thr Tyr His Gln Tyr Ser Tyr Ala Pro Tyr Ala Arg
    690                 695                 700

Gly Pro Trp Tyr Gln Leu Ser Glu Gln Met Ile Asp Asp Ala Ser Ile
705                 710                 715                 720

Asn Gly Gly Thr His Pro Ala Phe Pro Phe Leu Thr Gly His Gly Gly
                725                 730                 735

Ala Asn Gln Val Ala Leu Tyr Gly Tyr Leu Gly Leu Arg Leu His Pro
            740                 745                 750

Asp Asp Thr Ile Tyr Ile Asp Pro Asn Leu Pro Pro Gln Ile Pro His
        755                 760                 765

Ile Thr Tyr Arg Thr Phe Tyr Trp His Gly Trp Pro Ile Ser Ala Trp
    770                 775                 780

Ser Asn Tyr Thr His Thr Thr Ile Gln Arg Asp Ser Ser Leu Ala Pro
785                 790                 795                 800

Leu Ala Ser Ala Asp Leu Leu Phe Ser Asn Val Ser Ile Lys Val Gln
                805                 810                 815

Val Gly Gln Ser Thr Ala Ser Ala Asp Glu Ala Thr Ile Tyr Tyr Leu
            820                 825                 830

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

Asn Thr Thr Pro Gly Asn Gln Val Gln Cys His Pro Val Tyr Ser Pro
    850                 855                 860

Asp Ala Tyr Glu Pro Gly Gln Phe Pro Ile Ser Ala Val Asp Gly Ala
865                 870                 875                 880
```

```
Thr Ser Thr Lys Trp Gln Pro Ser Thr Ser Asp Leu Thr Ser Leu Thr
                885                 890                 895


Val Thr Leu Ser Thr Thr Ala Glu Ala Gly Ala Glu Glu Val Ser Gly
            900                 905                 910


Phe Tyr Phe Asp Trp Ser Gln Ala Pro Pro Glu Asn Leu Thr Val Ile
        915                 920                 925


Phe His Asp Ser Pro Ile Gly Asn Pro Ser Thr Val Phe Ala Ala Ala
    930                 935                 940


Gly Ser Asn Ser Thr Gly Tyr Arg Val Ile Thr Ser Met Ser Asn Ile
945                 950                 955                 960


Val Gln Ser Lys Pro Tyr Asn Ala Ile Ser Ala Glu Glu Leu Asn Val
                965                 970                 975


Val Ser Ile Pro Thr Ala Asn Thr Thr Thr Ile Thr Leu Asp Ala Pro
            980                 985                 990


Val Gln Lys Ala Arg Tyr Ala Thr  Leu Leu Ile Ala Gly  Asn Gln Ala
        995                 1000                 1005


Asn Glu  Thr Ala Gly Ala Thr  Val Ala Glu Trp Val  Ile Leu Gly
    1010                 1015                 1020


Gln Asn  Ser Thr Ser Ser Ser  Ser Ala Gln Ala Lys  Arg Lys Met
    1025                 1030                 1035


Ser Ala  Arg Ser Lys Ala Thr  Leu Ala Gln Leu Ser
    1040                 1045                 1050


<210>  226
<211>  1056
<212>  PRT
<213>  Trichoderma reesei

<400>  226
```

```
Thr Thr Leu Val Asp Arg Val Thr Lys Cys Leu Ser Arg His Asp Gly
1               5                   10                  15


Ser Asp Ala Glu Ser His Phe Ser Lys Asn Val Tyr Lys Thr Asp Phe
            20                  25                  30


Ala Gly Val Thr Trp Asp Glu Asp Asn Trp Leu Leu Ser Thr Thr Gln
        35                  40                  45


Leu Lys Gln Gly Ala Phe Glu Ala Arg Gly Ser Val Ala Asn Gly Tyr
    50                  55                  60


Leu Gly Ile Asn Val Ala Ser Val Gly Pro Phe Phe Glu Val Asp Thr
65                  70                  75                  80


Glu Glu Asp Gly Asp Val Ile Ser Gly Trp Pro Leu Phe Ser Arg Arg
                85                  90                  95


Gln Ser Phe Ala Thr Val Ala Gly Phe Trp Asp Ala Gln Pro Gln Met
            100                 105                 110


Asn Gly Thr Asn Phe Pro Trp Leu Ser Gln Tyr Gly Ser Asp Thr Ala
        115                 120                 125


Ile Ser Gly Ile Pro His Trp Ser Gly Leu Val Leu Asp Leu Gly Gly
    130                 135                 140


Gly Thr Tyr Leu Asp Ala Thr Val Ser Asn Lys Thr Ile Ser His Phe
145                 150                 155                 160


Arg Ser Thr Tyr Asp Tyr Lys Ala Gly Val Leu Ser Trp Ser Tyr Lys
                165                 170                 175


Trp Thr Pro Lys Gly Asn Lys Gly Ser Phe Asp Ile Ser Tyr Arg Leu
            180                 185                 190


Phe Ala Asn Lys Leu His Val Asn Gln Ala Val Val Asp Met Gln Val
        195                 200                 205
```

```
Thr Ala Ser Lys Asn Val Gln Ala Ser Ile Val Asn Val Leu Asp Gly
    210                 215                 220


Phe Ala Ala Val Arg Thr Asp Phe Val Glu Ser Gly Glu Asp Gly Ser
225                 230                 235                 240


Ala Ile Phe Ala Ala Val Arg Pro Asn Gly Val Ala Asn Val Thr Ala
                245                 250                 255


Tyr Val Tyr Ala Asp Ile Thr Gly Ser Gly Gly Val Asn Leu Ser Ser
            260                 265                 270


Arg Lys Ile Val His Asn Lys Pro Tyr Val His Ala Asn Ala Ser Ser
        275                 280                 285


Ile Ala Gln Ala Val Pro Val Lys Phe Ala Ala Gly Arg Thr Val Arg
    290                 295                 300


Val Thr Lys Phe Val Gly Ala Ala Ser Ser Asp Ala Phe Lys Asn Pro
305                 310                 315                 320


Lys Gln Val Ala Lys Lys Ala Ala Ala Ala Gly Leu Ser Asn Gly Tyr
                325                 330                 335


Thr Lys Ser Leu Lys Ala His Val Glu Glu Trp Ala Thr Val Met Pro
            340                 345                 350


Glu Ser Ser Val Asp Ser Phe Ala Asp Pro Lys Thr Gly Lys Leu Pro
        355                 360                 365


Ala Asp Ser His Ile Val Asp Ser Ala Ile Ile Ala Val Thr Asn Thr
    370                 375                 380


Tyr Tyr Leu Leu Gln Asn Thr Val Gly Lys Asn Gly Ile Lys Ala Val
385                 390                 395                 400


Asp Gly Ala Pro Val Asn Val Asp Ser Ile Ser Val Gly Gly Leu Thr
                405                 410                 415
```

```
Ser Asp Ser Tyr Ala Gly Gln Ile Phe Trp Asp Ala Asp Leu Trp Met
            420                 425                 430

Gln Pro Gly Leu Val Ala Ala His Pro Glu Ala Ala Glu Arg Ile Thr
        435                 440                 445

Asn Tyr Arg Leu Ala Arg Tyr Gly Gln Ala Lys Glu Asn Val Lys Thr
    450                 455                 460

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

Val Phe Pro Trp Thr Ser Gly Arg Tyr Gly Asn Cys Thr Ala Thr Gly
                485                 490                 495

Pro Cys Trp Asp Tyr Glu Tyr His Leu Asn Gly Asp Ile Gly Ile Ser
            500                 505                 510

Leu Val Asn Gln Trp Val Val Asn Gly Asp Thr Lys Asp Phe Glu Lys
        515                 520                 525

Asn Leu Phe Pro Val Tyr Asp Ser Val Ala Gln Leu Tyr Gly Asn Leu
    530                 535                 540

Leu Arg Pro Asn Lys Thr Ser Trp Thr Leu Thr Asn Met Thr Asp Pro
545                 550                 555                 560

Asp Glu Tyr Ala Asn His Val Asp Ala Gly Gly Tyr Thr Met Pro Leu
                565                 570                 575

Ile Ala Glu Thr Leu Gln Lys Ala Asn Ser Phe Arg Gln Gln Phe Gly
            580                 585                 590

Ile Glu Gln Asn Lys Thr Trp Asn Asp Met Ala Ser Asn Val Leu Val
        595                 600                 605

Leu Arg Glu Asn Gly Val Thr Leu Glu Phe Thr Ala Met Asn Gly Thr
    610                 615                 620
```

```
Ala Val Val Lys Gln Ala Asp Val Ile Met Leu Thr Tyr Pro Leu Ser
625                 630                 635                 640


Tyr Gly Thr Asn Tyr Ser Ala Gln Asp Ala Leu Asn Asp Leu Asp Tyr
                645                 650                 655


Tyr Ala Asn Lys Gln Ser Pro Asp Gly Pro Ala Met Thr Tyr Ala Phe
            660                 665                 670


Phe Ser Ile Val Ala Asn Glu Ile Ser Pro Ser Gly Cys Ser Ala Tyr
        675                 680                 685


Thr Tyr Ala Gln Asn Ala Phe Lys Pro Tyr Val Arg Ala Pro Phe Tyr
    690                 695                 700


Gln Ile Ser Glu Gln Leu Ile Asp Asp Ala Ser Val Asn Gly Gly Thr
705                 710                 715                 720


His Pro Ala Tyr Pro Phe Leu Thr Gly His Gly Gly Ala His Gln Val
                725                 730                 735


Val Leu Phe Gly Tyr Leu Gly Leu Arg Leu Val Pro Asp Asp Val Ile
            740                 745                 750


His Ile Glu Pro Asn Leu Pro Pro Gln Ile Pro Tyr Leu Arg Tyr Arg
        755                 760                 765


Thr Phe Tyr Trp Arg Gly Trp Pro Ile Ser Ala Trp Ser Asn Tyr Thr
    770                 775                 780


His Thr Thr Leu Ser Arg Ala Ala Gly Val Ala Ala Leu Glu Gly Ala
785                 790                 795                 800


Asp Gln Arg Phe Ala Arg Lys Pro Ile Thr Ile His Ala Gly Pro Glu
                805                 810                 815


Gln Asp Pro Thr Ala Tyr Arg Leu Pro Val Lys Gly Ser Val Val Ile
            820                 825                 830
```

```
Pro Asn Lys Gln Ile Gly Ser Gln Gln Thr Tyr Ala Gly Asn Leu Val
        835                 840                 845


Gln Cys His Ala Ala Ser Ser Pro Asn Asp Tyr Val Pro Gly Gln Phe
    850                 855                 860


Pro Ile Ala Ala Val Asp Gly Ala Thr Ser Thr Lys Trp Gln Pro Ala
865                 870                 875                 880


Ser Ala Asp Lys Val Ser Ser Ile Thr Val Ser Leu Asp Lys Glu Asp
                885                 890                 895


Val Gly Ser Leu Val Ser Gly Phe His Phe Asp Trp Ala Gln Ala Pro
            900                 905                 910


Pro Val Asn Ala Thr Val Ile Phe His Asp Glu Ala Leu Ala Asp Pro
        915                 920                 925


Ala Thr Ala Leu Ala Ser Ala His Lys His Asn Ser Lys Tyr Thr Thr
    930                 935                 940


Val Thr Ser Leu Thr Asn Ile Glu Leu Ser Asp Pro Tyr Val Ser Thr
945                 950                 955                 960


Lys Asp Leu Asn Ala Ile Ala Ile Pro Ile Gly Asn Thr Thr Asn Val
                965                 970                 975


Thr Leu Ser His Pro Val Ala Ala Ser Arg Tyr Ala Ser Leu Leu Ile
            980                 985                 990


Val Gly Asn Gln Gly Leu Asp Pro  Val Asp Val Lys Ala  Lys Asn Gly
        995                 1000                 1005


Thr Gly  Ala Thr Val Ala Glu  Trp Ala Ile Phe Gly  His Gly Lys
    1010                 1015                 1020


Glu His  Ser Gly Lys Pro Ser  Ser His Ser Lys Arg  Arg Leu Asn
    1025                 1030                 1035
```

```
Val Arg  Thr Ala Ala Thr Leu  Ser Asn Pro Arg Ser  Phe Met Arg
    1040                 1045                 1050


Arg Arg  Leu
    1055


<210>  227
<211>  19
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  227

Met Leu Ser Leu Lys Thr Leu Leu Cys Thr Leu Leu Thr Val Ser Ser
1               5                   10                  15


Val Leu Ala




<210>  228
<211>  185
<212>  DNA
<213>  Saccharomyces cerevisiae

<400>  228
agtgctttta actaagaatt attagtcttt tctgcttatt ttttcatcat agtttagaac       60

actttatatt aacgaatagt ttatgaatct atttaggttt aaaaattgat acagttttat      120

aagttacttt ttcaaagact cgtgctgtct attgcataat gcactggaag ggaaaaaaa      180

aggtg                                                                  185


<210>  229
<211>  555
<212>  PRT
<213>  Pycnoporus sanguineus glucoamylase

<400>  229

Gln Ser Ser Ala Val Asp Ala Tyr Val Ala Ser Glu Ser Pro Ile Ala
1               5                   10                  15


Lys Gln Gly Val Leu Asn Asn Ile Gly Pro Asn Gly Ser Lys Ala His
            20                  25                  30
```

```
Gly Ala Lys Ala Gly Ile Val Val Ala Ser Pro Ser Thr Glu Asn Pro
        35                  40                  45

Asp Tyr Leu Tyr Thr Trp Thr Arg Asp Ser Ser Leu Val Phe Lys Leu
    50                  55                  60

Leu Ile Asp Gln Phe Thr Ser Gly Asp Asp Thr Ser Leu Arg Gly Leu
65                  70                  75                  80

Ile Asp Asp Phe Thr Ser Ala Glu Ala Ile Leu Gln Gln Val Ser Asn
                85                  90                  95

Pro Ser Gly Thr Val Ser Thr Gly Gly Leu Gly Glu Pro Lys Phe Asn
            100                 105                 110

Ile Asp Glu Thr Ala Phe Thr Gly Ala Trp Gly Arg Pro Gln Arg Asp
        115                 120                 125

Gly Pro Ala Leu Arg Ala Thr Ser Ile Ile Arg Tyr Ala Asn Trp Leu
    130                 135                 140

Leu Asp Asn Gly Asn Thr Thr Tyr Val Ser Asn Thr Leu Trp Pro Val
145                 150                 155                 160

Ile Gln Leu Asp Leu Asp Tyr Val Ala Asp Asn Trp Asn Gln Ser Thr
                165                 170                 175

Phe Asp Leu Trp Glu Glu Val Asp Ser Ser Ser Phe Phe Thr Thr Ala
            180                 185                 190

Val Gln His Arg Ala Leu Arg Glu Gly Ala Thr Phe Ala Ser Arg Ile
        195                 200                 205

Gly Gln Ser Ser Val Val Ser Gly Tyr Thr Thr Gln Ala Asp Asn Leu
    210                 215                 220

Leu Cys Phe Leu Gln Ser Tyr Trp Asn Pro Ser Gly Gly Tyr Val Thr
225                 230                 235                 240
```

```
Ala Asn Thr Gly Gly Gly Arg Ser Gly Lys Asp Ser Asn Thr Val Leu
                245                 250                 255


Thr Ser Ile His Thr Phe Asp Pro Ala Ala Gly Cys Asp Ala Ala Thr
            260                 265                 270


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


Asp Ala Phe Arg Ser Ile Tyr Thr Ile Asn Asn Gly Ile Ala Ser Asn
    290                 295                 300


Ala Ala Val Ala Thr Gly Arg Tyr Pro Glu Asp Ser Tyr Met Gly Gly
305                 310                 315                 320


Asn Pro Trp Tyr Leu Thr Thr Ser Ala Val Ala Glu Gln Leu Tyr Asp
                325                 330                 335


Ala Leu Tyr Val Trp Asp Gln Leu Gly Gly Leu Asn Val Thr Ser Thr
            340                 345                 350


Ser Leu Ala Phe Phe Gln Gln Phe Ala Ser Gly Leu Ser Thr Gly Thr
        355                 360                 365


Tyr Ser Ala Ser Ser Ser Thr Tyr Ala Thr Leu Thr Ser Ala Ile Arg
    370                 375                 380


Ser Phe Ala Asp Gly Phe Leu Ala Ile Asn Ala Lys Tyr Thr Pro Ala
385                 390                 395                 400


Asp Gly Gly Leu Ala Glu Gln Tyr Ser Arg Asn Asp Gly Thr Pro Leu
                405                 410                 415


Ser Ala Val Asp Leu Thr Trp Ser Tyr Ala Ala Ala Leu Thr Ala Phe
            420                 425                 430


Ala Ala Arg Glu Gly Lys Thr Tyr Gly Ser Trp Gly Ala Ala Gly Leu
        435                 440                 445
```

```
Thr Val Pro Ala Ser Cys Ser Gly Gly Gly Gly Ala Thr Val Ala Val
    450                 455                 460


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


Thr Gly Ser Val Ala Ala Leu Gln Asn Trp Ser Pro Asp Asn Ala Leu
                485                 490                 495


Ile Leu Ser Ala Ala Asn Tyr Pro Thr Trp Ser Ile Thr Val Asn Leu
            500                 505                 510


Pro Ala Asn Thr Val Val Gln Tyr Lys Tyr Ile Arg Lys Phe Asn Gly
        515                 520                 525


Gln Val Thr Trp Glu Ser Asp Pro Asn Asn Gln Ile Thr Thr Pro Ser
    530                 535                 540


Gly Gly Ser Phe Thr Gln Asn Asp Val Trp Arg
545                 550                 555


<210>  230
<211>  599
<212>  PRT
<213>  Trichoderma reesei

<400>  230

Ser Val Asp Asp Phe Ile Ser Thr Glu Thr Pro Ile Ala Leu Asn Asn
1               5                   10                  15


Leu Leu Cys Asn Val Gly Pro Asp Gly Cys Arg Ala Phe Gly Thr Ser
            20                  25                  30


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


Tyr Met Trp Thr Arg Asp Ser Ala Leu Val Phe Lys Asn Leu Ile Asp
    50                  55                  60
```

```
Arg Phe Thr Glu Thr Tyr Asp Ala Gly Leu Gln Arg Arg Ile Glu Gln
65                  70                  75                  80


Tyr Ile Thr Ala Gln Val Thr Leu Gln Gly Leu Ser Asn Pro Ser Gly
                85                  90                  95


Ser Leu Ala Asp Gly Ser Gly Leu Gly Glu Pro Lys Phe Glu Leu Thr
            100                 105                 110


Leu Lys Pro Phe Thr Gly Asn Trp Gly Arg Pro Gln Arg Asp Gly Pro
        115                 120                 125


Ala Leu Arg Ala Ile Ala Leu Ile Gly Tyr Ser Lys Trp Leu Ile Asn
    130                 135                 140


Asn Asn Tyr Gln Ser Thr Val Ser Asn Val Ile Trp Pro Ile Val Arg
145                 150                 155                 160


Asn Asp Leu Asn Tyr Val Ala Gln Tyr Trp Asn Gln Thr Gly Phe Asp
                165                 170                 175


Leu Trp Glu Glu Val Asn Gly Ser Ser Phe Phe Thr Val Ala Asn Gln
            180                 185                 190


His Arg Ala Leu Val Glu Gly Ala Thr Leu Ala Ala Thr Leu Gly Gln
        195                 200                 205


Ser Gly Ser Ala Tyr Ser Ser Val Ala Pro Gln Val Leu Cys Phe Leu
    210                 215                 220


Gln Arg Phe Trp Val Ser Ser Gly Gly Tyr Val Asp Ser Asn Ile Asn
225                 230                 235                 240


Thr Asn Glu Gly Arg Thr Gly Lys Asp Val Asn Ser Val Leu Thr Ser
                245                 250                 255


Ile His Thr Phe Asp Pro Asn Leu Gly Cys Asp Ala Gly Thr Phe Gln
            260                 265                 270
```

```
Pro Cys Ser Asp Lys Ala Leu Ser Asn Leu Lys Val Val Val Asp Ser
        275                 280                 285


Phe Arg Ser Ile Tyr Gly Val Asn Lys Gly Ile Pro Ala Gly Ala Ala
    290                 295                 300


Val Ala Ile Gly Arg Tyr Ala Glu Asp Val Tyr Tyr Asn Gly Asn Pro
305                 310                 315                 320


Trp Tyr Leu Ala Thr Phe Ala Ala Ala Glu Gln Leu Tyr Asp Ala Ile
                325                 330                 335


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


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


Ser Ser Ser Ser Thr Phe Thr Asn Ile Ile Asn Ala Val Ser Thr Tyr
    370                 375                 380


Ala Asp Gly Phe Leu Ser Glu Ala Ala Lys Tyr Val Pro Ala Asp Gly
385                 390                 395                 400


Ser Leu Ala Glu Gln Phe Asp Arg Asn Ser Gly Thr Pro Leu Ser Ala
                405                 410                 415


Val His Leu Thr Trp Ser Tyr Ala Ser Phe Leu Thr Ala Ala Ala Arg
            420                 425                 430


Arg Ala Gly Ile Val Pro Pro Ser Trp Ala Asn Ser Ser Ala Ser Thr
        435                 440                 445


Ile Pro Ser Thr Cys Ser Gly Ala Ser Val Val Gly Ser Tyr Ser Arg
    450                 455                 460


Pro Thr Ala Thr Ser Phe Pro Pro Ser Gln Thr Pro Lys Pro Gly Val
465                 470                 475                 480
```

```
Pro Ser Gly Thr Pro Tyr Thr Pro Leu Pro Cys Ala Thr Pro Thr Ser
                485                 490                 495


Val Ala Val Thr Phe His Glu Leu Val Ser Thr Gln Phe Gly His Thr
            500                 505                 510


Val Lys Val Ala Gly Asn Ala Ala Ala Leu Gly Asn Trp Ser Thr Ser
        515                 520                 525


Ala Ala Val Ala Leu Asp Ala Val Asn Tyr Arg Asp Asn His Pro Leu
    530                 535                 540


Trp Ile Gly Thr Val Asn Leu Glu Ala Gly Asp Val Val Glu Tyr Lys
545                 550                 555                 560


Tyr Ile Ile Val Gly Gln Asp Gly Ser Val Thr Trp Glu Ser Asp Pro
                565                 570                 575


Asn His Thr Tyr Thr Val Pro Ala Val Ala Cys Val Thr Gln Val Val
            580                 585                 590


Lys Glu Asp Thr Trp Gln Ser
        595


<210>  231
<211>  633
<212>  PRT
<213>  Bacillus amyloliquefaciens

<400>  231

Gly Pro Ala Ala Ala Asn Ala Glu Thr Ala Asn Lys Ser Asn Lys Val
1               5                   10                  15


Thr Ala Ser Ser Val Lys Asn Gly Thr Ile Leu His Ala Trp Asn Trp
            20                  25                  30


Ser Phe Asn Thr Leu Thr Gln Asn Met Lys Asp Ile Arg Asp Ala Gly
        35                  40                  45
```

```
Tyr Ala Ala Ile Gln Thr Ser Pro Ile Asn Gln Val Lys Glu Gly Asn
    50                  55                  60


Gln Gly Asp Lys Ser Met Arg Asn Trp Tyr Trp Leu Tyr Gln Pro Thr
65                  70                  75                  80


Ser Tyr Gln Ile Gly Asn Arg Tyr Leu Gly Thr Glu Gln Glu Phe Lys
                85                  90                  95


Asp Met Cys Ala Ala Ala Glu Lys Tyr Gly Val Lys Val Ile Val Asp
            100                 105                 110


Ala Val Ile Asn His Thr Thr Ser Asp Tyr Gly Ala Ile Ser Asp Glu
        115                 120                 125


Ile Lys Arg Ile Pro Asn Trp Thr His Gly Asn Thr Gln Ile Lys Asn
    130                 135                 140


Trp Ser Asp Arg Trp Asp Val Thr Gln Asn Ser Leu Leu Gly Leu Tyr
145                 150                 155                 160


Asp Trp Asn Thr Gln Asn Thr Glu Val Gln Val Tyr Leu Lys Arg Phe
                165                 170                 175


Leu Glu Arg Ala Leu Asn Asp Gly Ala Asp Gly Phe Arg Tyr Asp Ala
            180                 185                 190


Ala Lys His Ile Glu Leu Pro Asp Asp Gly Asn Tyr Gly Ser Gln Phe
        195                 200                 205


Trp Pro Asn Ile Thr Asn Thr Ser Ala Glu Phe Gln Tyr Gly Glu Ile
    210                 215                 220


Leu Gln Asp Ser Ala Ser Arg Asp Thr Ala Tyr Ala Asn Tyr Met Asn
225                 230                 235                 240


Val Thr Ala Ser Asn Tyr Gly His Ser Ile Arg Ser Ala Leu Lys Asn
                245                 250                 255
```

```
Arg Asn Leu Ser Val Ser Asn Ile Ser His Tyr Ala Ser Asp Val Ser
            260                 265                 270


Ala Asp Lys Leu Val Thr Trp Val Glu Ser His Asp Thr Tyr Ala Asn
        275                 280                 285


Asp Asp Glu Glu Ser Thr Trp Met Ser Asp Asp Asp Ile Arg Leu Gly
    290                 295                 300


Trp Ala Val Ile Gly Ser Arg Ser Gly Ser Thr Pro Leu Phe Phe Ser
305                 310                 315                 320


Arg Pro Glu Gly Gly Gly Asn Gly Val Arg Phe Pro Gly Lys Ser Gln
                325                 330                 335


Ile Gly Asp Arg Gly Ser Ala Leu Phe Lys Asp Gln Ala Ile Thr Ala
            340                 345                 350


Val Asn Thr Phe His Asn Val Met Ala Gly Gln Pro Glu Glu Leu Ser
        355                 360                 365


Asn Pro Asn Gly Asn Asn Gln Val Phe Met Asn Gln Arg Gly Ser Lys
    370                 375                 380


Gly Val Val Leu Ala Asn Ala Gly Ser Ser Ser Val Thr Ile Asn Thr
385                 390                 395                 400


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


Ser Phe Gln Val Ala Asn Gly Lys Leu Thr Gly Thr Ile Asn Ala Arg
            420                 425                 430


Ser Ala Ala Val Leu Tyr Pro Asp Asp Ile Gly Asn Ala Pro His Val
        435                 440                 445


Phe Leu Glu Asn Tyr Gln Thr Gly Ala Val His Ser Phe Asn Asp Gln
    450                 455                 460
```

Leu Thr Val Thr Leu Arg Ala Asn Ala Lys Thr Thr Lys Ala Val Tyr
465   470   475   480

Gln Ile Asn Asn Gly Gln Gln Thr Ala Phe Lys Asp Gly Asp Arg Leu
                485   490   495

Thr Ile Gly Lys Gly Asp Pro Ile Gly Thr Thr Tyr Asn Ile Lys Leu
            500   505   510

Thr Gly Thr Asn Gly Glu Gly Ala Ala Arg Thr Gln Glu Tyr Thr Phe
        515   520   525

Val Lys Lys Asp Pro Ser Gln Thr Asn Ile Ile Gly Tyr Gln Asn Pro
    530   535   540

Asp His Trp Gly Gln Val Asn Ala Tyr Ile Tyr Lys His Asp Gly Gly
545   550   555   560

Arg Ala Ile Glu Leu Thr Gly Ser Trp Pro Gly Lys Ala Met Thr Lys
                565   570   575

Asn Ala Asn Gly Met Tyr Thr Leu Thr Leu Pro Glu Asn Thr Asp Thr
            580   585   590

Ala Asn Ala Lys Val Ile Phe Asn Asn Gly Ser Ala Gln Val Pro Gly
        595   600   605

Gln Asn Gln Pro Gly Phe Asp Tyr Val Gln Asn Gly Leu Tyr Asn Asn
    610   615   620

Ser Gly Leu Asn Gly Tyr Leu Pro His
625   630

<210> 232
<211> 700
<212> DNA
<213> Saccharomyces cerevisiae

<400> 232
cacccatgaa ccacacggtt agtccaaaag gggcagttca gattccagat gcgggaatta   60

```
gcttgctgcc accctcacct cactaacgct gcggtgtgcg gatacttcat gctatttata      120

gacgcgcgtg tcggaatcag cacgcgcaag aaccaaatgg gaaaatcgga atgggtccag      180

aactgctttg agtgctggct attggcgtct gatttccgtt ttgggaatcc tttgccgcgc      240

gcccctctca aaactccgca caagtcccag aaagcgggaa agaaataaaa cgccaccaaa      300

aaaaaaaaaa taaaagccaa tcctcgaagc gtgggtggta ggccctggat tatcccgtac      360

aagtatttct caggagtaaa aaaaccgttt gttttggaat ttcccatttc gcggccacct      420

acgccgctat ctttgcaaca actatctgcg ataactcagc aaattttgca tattcgtgtt      480

gcagtattgc gataatggga gtcttacttc caacataacg gcagaaagaa atgtgagaaa      540

attttgcatc ctttgcctcc gttcaagtat ataaagtcgg catgcttgat aatctttctt      600

tccatcctac attgttctaa ttattcttat tctcctttat tctttcctaa cataccaaga      660

aattaatctt ctgtcattcg cttaaacact atatcaataa                            700


<210>  233
<211>  240
<212>  DNA
<213>  Saccharomyces cerevisiae

<400>  233
tcagtactga caataaaaag attcttgttt tcaagaactt gtcatttgta tagtttttttt       60

atattgtagt tgttctattt taatcaaatg ttagcgtgat ttatattttt tttcgcctcg      120

acatcatctg cccagatgcg aagttaagtg cgcagaaagt aatatcatgc gtcaatcgta      180

tgtgaatgct ggtcgctata ctgctgtcga ttcgatacta acgccgccat ccagtgtcga      240


<210>  234
<211>  18
<212>  PRT
<213>  Saccharomyces cerevisiae

<400>  234

Met Gln Leu Leu Arg Cys Phe Ser Ile Phe Ser Val Ile Ala Ser Val
1               5                   10                  15


Leu Ala
```

```
<210>  235
<211>  274
<212>  PRT
<213>  Thermomyces lanuginosus

<400>  235

Glu Val Ser Gln Asp Leu Phe Asn Gln Phe Asn Leu Phe Ala Gln Tyr
1               5                   10                  15


Ser Ala Ala Ala Tyr Cys Gly Lys Asn Asn Asp Ala Pro Ala Gly Thr
            20                  25                  30


Asn Ile Thr Cys Thr Gly Asn Ala Cys Pro Glu Val Glu Lys Ala Asp
        35                  40                  45


Ala Thr Phe Leu Tyr Ser Phe Glu Asp Ser Gly Val Gly Asp Val Thr
    50                  55                  60


Gly Phe Leu Ala Leu Asp Asn Thr Asn Lys Leu Ile Val Leu Ser Phe
65                  70                  75                  80


Arg Gly Ser Arg Ser Ile Glu Asn Trp Ile Ala Asn Leu Asn Phe Trp
                85                  90                  95


Leu Lys Lys Ile Asn Asp Ile Cys Ser Gly Cys Arg Gly His Asp Gly
            100                 105                 110


Phe Thr Ser Ser Trp Arg Ser Val Ala Asp Thr Leu Arg Gln Lys Val
        115                 120                 125


Glu Asp Ala Val Arg Glu His Pro Asp Tyr Arg Val Val Phe Thr Gly
    130                 135                 140


His Ser Leu Gly Gly Ala Leu Ala Thr Val Ala Gly Ala Asp Leu Arg
145                 150                 155                 160


Gly Asn Gly Tyr Asp Ile Asp Val Phe Ser Tyr Gly Ala Pro Arg Val
                165                 170                 175
```

```
Gly Asn Arg Ala Phe Ala Glu Phe Leu Thr Val Gln Thr Gly Gly Thr
            180                 185                 190


Leu Tyr Arg Ile Thr His Thr Asn Asp Ile Val Pro Arg Leu Pro Pro
        195                 200                 205


Arg Glu Phe Gly Tyr Ser His Ser Ser Pro Glu Tyr Trp Ile Lys Ser
    210                 215                 220


Gly Thr Leu Val Pro Val Thr Arg Asn Asp Ile Val Lys Ile Glu Gly
225                 230                 235                 240


Ile Asp Ala Thr Gly Gly Asn Asn Gln Pro Asn Ile Pro Asp Ile Pro
                245                 250                 255


Ala His Leu Trp Tyr Phe Gln Ala Thr Asp Ala Cys Asn Ala Gly Gly
            260                 265                 270


Phe Ser



<210>  236
<211>  277
<212>  PRT
<213>  Thermomyces lanuginosus

<400>  236

Ala Pro Ala Pro Val Leu Arg Arg Asp Val Ser Ser Ser Val Leu Ser
1               5                   10                  15


Glu Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ser
            20                  25                  30


Asn Ile Gly Ser Pro Gly Thr Lys Leu Thr Cys Ser Val Gly Asn Cys
        35                  40                  45


Pro Arg Val Glu Ala Ala Asp Thr Glu Thr Leu Ile Glu Phe Asn Glu
    50                  55                  60


Ser Ser Ser Phe Gly Asp Val Thr Gly Tyr Ile Ala Val Asp Arg Thr
```

```
65                  70                  75                  80


Asn Ser Leu Leu Val Leu Ala Phe Arg Gly Ser Ser Thr Val Ser Asn
                85                  90                  95


Trp Glu Ala Asp Leu Asp Phe Pro Leu Thr Asp Ala Ser Ser Leu Cys
            100                 105                 110


Ser Gly Cys Glu Ile His Ser Gly Phe Trp Ala Ala Trp Gln Thr Val
        115                 120                 125


Gln Ala Ser Ile Thr Ser Thr Leu Glu Ser Ala Ile Ala Ser Tyr Pro
    130                 135                 140


Gly Tyr Thr Leu Val Phe Thr Gly His Ser Tyr Gly Ala Ala Leu Ala
145                 150                 155                 160


Ala Ile Ala Ala Thr Thr Leu Arg Asn Ala Gly Tyr Thr Ile Gln Leu
                165                 170                 175


Tyr Asp Tyr Gly Gln Pro Arg Leu Gly Asn Leu Ala Leu Ala Gln Tyr
            180                 185                 190


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


Asp Ile Val Pro Lys Leu Pro Pro Glu Leu Phe Gly Tyr His His Phe
    210                 215                 220


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


Ser Asp Val Gln Val Val Thr Gly Ile Asp Ser Thr Ala Gly Asn Asp
                245                 250                 255


Gly Thr Leu Leu Asp Ser Thr Ser Ala His Asp Trp Tyr Ile Val Tyr
            260                 265                 270


Ile Asp Gly Cys Asp
```

```
        275


<210>  237
<211>  594
<212>  PRT
<213>  Penicillium emersonii

<400>  237

Ser Ala Pro Tyr Asp Lys Arg Asp Leu Ala Gln Glu Ile Trp Asp Asp
1               5                   10                  15


Ile Lys Asn Ala Val Asp Cys Ala Gly Cys Gln Val Val Leu Thr Ala
            20                  25                  30


Leu Lys Gly Val Ala Asp Leu Gly Thr Thr Ala Leu Val Asp Val Leu
        35                  40                  45


Thr Glu Val Cys Asn Ile Ser Gly Lys Glu Asp Ser Asp Val Cys Ser
    50                  55                  60


Gly Ile Ile Ser Arg Glu Gly Pro Val Leu Asp Tyr Val Leu Gln His
65                  70                  75                  80


Leu Asp Ile Gly Ser His Thr Ser Gln Val Ile Cys Ala Ser Ala Phe
                85                  90                  95


Gly Leu Cys Gln Tyr Pro Glu Val Arg Pro Tyr Asn Leu Thr Phe Pro
            100                 105                 110


Lys Pro Lys Pro Asn Thr Thr Arg Pro Glu Pro Ser Gly Glu Ser Pro
        115                 120                 125


Ile Gln Val Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu
    130                 135                 140


Thr Gly Ser Asn Tyr Asn Cys Thr Lys Pro Ile Cys Cys Arg Pro Tyr
145                 150                 155                 160


Thr Ala Glu Asp Ala Pro Gly Asn Thr Thr Thr Pro Cys Gly Pro Tyr
                165                 170                 175
```

```
Gly Asn Thr Lys Cys Asp Ala Pro Leu Ser Leu Glu Glu Ser Met Phe
            180                 185                 190


Ala Ala Ile Lys Ala Leu Asn Pro Gln Pro Ala Phe Ser Ile Tyr Thr
        195                 200                 205


Gly Asp Val Val Ala His Asp Ile Trp Leu Val Asp Gln Asn Glu Val
    210                 215                 220


Ile Glu Asp Leu Asn Ala Thr Tyr Asp Arg Met Ala Gly Leu Gly Leu
225                 230                 235                 240


Val Tyr Ala Ala Ile Gly Asn His Asp Thr Ala Pro Val Asn Asp Leu
                245                 250                 255


Pro Thr Ser Asn Ile Pro Ser Glu Tyr Ser Ala Asn Trp Thr Tyr Glu
            260                 265                 270


Ala Leu Ser Tyr Asp Phe Thr Met Leu Thr Gln Ser Ala Ser Ala Gln
        275                 280                 285


Thr Ala Ala Asn Tyr Gly Ser Tyr Ser Ala Ile Tyr Pro Gly Ser Tyr
    290                 295                 300


Gly Thr Asp Leu Arg Val Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Val
305                 310                 315                 320


Asp Asn Phe Trp Ala Tyr Gln Asp Pro Met Glu Phe Asp Pro Asp Gly
                325                 330                 335


Gln Leu Ala Trp Leu Ile Asn Glu Leu Gln Glu Ala Glu Thr Ala Gly
            340                 345                 350


Gln Arg Val Trp Ile Ile Ala His Val Pro Thr Gly Thr Ser Asp His
        355                 360                 365


Phe His Asp Tyr Ser His Tyr Phe Asp Gln Ile Val Gln Arg Tyr Glu
    370                 375                 380
```

```
Ala Thr Ile Ala Ala Leu Phe Tyr Gly His Thr His Ile Asp Gln Phe
385                 390                 395                 400


Gln Ile Ser Tyr Ser Asn Tyr Ser Asn Arg Ala Phe Asp Thr Ala Thr
                405                 410                 415


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


Thr Phe Arg Val Tyr Asp Val Asp Pro Lys Thr Phe Ala Val Leu Asp
        435                 440                 445


Phe Thr Asn Tyr Ile Ala Asn Ile Ser Asp Pro Ala Phe Gln Ser Gly
    450                 455                 460


Pro Ser Trp Gln Lys Tyr Tyr Ser Ala Lys Glu Thr Tyr Gly Ser Leu
465                 470                 475                 480


Leu Ser Pro Pro Val Thr Asp Pro Thr Ala Glu Leu Thr Pro Ala Phe
                485                 490                 495


Trp His Asn Val Thr Val Ala Phe Glu Gln Asp Asn Ala Thr Phe Gln
            500                 505                 510


Glu Tyr Trp Ala Arg Gln Thr Arg Gly Tyr Asp Val Ser Ser Cys Thr
        515                 520                 525


Gly Ser Cys Ile Thr Gln Ala Ile Cys Gly Leu Arg Ala Gly Asp Ala
    530                 535                 540


Gln Tyr Asn Cys Val Thr Pro Thr Pro Gly Phe Asn Phe Ala Lys Arg
545                 550                 555                 560


Asp Thr Ser Asn Pro Lys Gln Ala Leu Ser His Val Glu Lys Cys Glu
                565                 570                 575


Gly Ser Gly Leu Leu Gly Leu Leu Arg Arg Met Val Ala Asp Ser Lys
            580                 585                 590
```

```
Ser Ser




<210>  238
<211>  259
<212>  PRT
<213>  Bacillus thuringiensis

<400>  238

His Glu Asn Asp Gly Gly Ser Lys Ile Lys Ile Ile His Arg Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


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


Asp Arg Val Ala Gln Leu Asn Glu Trp Arg Thr Glu Leu Glu Asn Gly
    50                  55                  60


Ile Tyr Ala Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Asn Gly Lys Thr Tyr Ile Pro Phe
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


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


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160
```

```
Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Val Ala Lys Gln Asp Tyr Ser Gly Ile Val Asn Asp Asn
        195                 200                 205


Thr Lys Asp Trp Phe Val Lys Ala Ala Val Ser Gln Glu Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Lys Arg Leu Met Asp
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Gly Asp Arg



<210>  239
<211>  297
<212>  PRT
<213>  Pseudomonas sp.

<400>  239

Gln Glu Ser Pro Ala Phe Ile Asp Pro Ala Ser Trp Asn Thr Pro Phe
1               5                   10                  15


Asn Gly Ile Ala Gln Val Ala Cys His Asn Cys Tyr Glu Lys Gln Tyr
            20                  25                  30


Ala Asn Thr Phe Ser Ser Val Leu Asp Ser Val Arg Thr Leu Glu Leu
        35                  40                  45


Asp Phe Trp Asp Gln Arg Asp Ala Val Ser Gly Gly Ser Pro His His
    50                  55                  60
```

```
Trp Phe Val Arg His Asn Pro Gly Thr Leu Phe Gln Ser Gly Asn Asp
65                  70                  75                  80


Asn Asn Cys Thr Gly Asp Gly Thr Gly Lys Asn Asp Leu Glu Ala Cys
                85                  90                  95


Leu Asn Asp Val Lys Asn Trp Ser Asp Lys His Pro Gly His Phe Pro
            100                 105                 110


Ile Thr Leu Ile Leu Asp Lys Lys Gln Gly Trp Ser Lys Glu Ser Ser
        115                 120                 125


Gly Arg Thr Pro Lys Asp Phe Asp Glu Leu Val Ala Arg Val Phe Gln
    130                 135                 140


Gly Lys Leu Phe Thr Pro Gln Asp Leu Ala Thr His Ile Gly Ser Gly
145                 150                 155                 160


Ala Gly Ala Leu Gln Gly Asn Leu Lys Gly Lys Ser Trp Pro Thr Ala
                165                 170                 175


Asn Asp Leu Gln Gly Lys Val Leu Leu Val Leu Asn His Ser Glu Asn
            180                 185                 190


Gln Lys Leu Ser Gln Tyr Ala Glu Ala Arg Thr Ser Lys Ala Lys Val
        195                 200                 205


Phe Ile Ser Pro Val Thr Asn Gly Gln Asn Asp Ile Ser Gly Lys Val
    210                 215                 220


Ser Gly Met Ser Ser Gln Ser Ser Gly Tyr Val Ala Met Asn Asn Met
225                 230                 235                 240


Gly Lys Gly Asp Lys Ser Trp Ala Lys Gln Ala Phe Ala Tyr Ser His
                245                 250                 255


Ile Gly Arg Val Trp Gly Asp Asp Glu Val Ser Phe Ala Gln His Ile
            260                 265                 270
```

```
Asn Gln Lys Ile Asn Leu Ser Ala Tyr Tyr Arg Phe Ala Ala Gln Ser
        275                 280                 285


Ala Gly Gly Tyr Arg Ile Arg Pro Phe
    290                 295


<210>  240
<211>  625
<212>  PRT
<213>  Kionochaeta sp.

<400>  240

Ala Val Asn Pro Ala Asp Val Leu Ser Val Val Glu Lys Arg Val Asp
1               5                   10                  15


Pro Ala Ser Gly Leu Glu Val Arg Ser Ile Trp Asp Thr Ile Trp Asn
            20                  25                  30


Asp Ile Lys Ser Ala Ala Asp Cys Thr Ala Cys Glu Ala Val Leu Thr
        35                  40                  45


Leu Leu Lys Gly Val Ala Ala Phe Gly Asp Asn Phe Phe Val Glu Val
    50                  55                  60


Leu Thr Glu Ile Cys Asp Leu Ser Gly Ala Glu Asp Asp Asp Val Cys
65                  70                  75                  80


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


Lys Met Ser Ile Gly Ser Lys Thr Ser Glu Leu Phe Cys Ile Thr Phe
            100                 105                 110


Leu Gly Leu Cys Ser Tyr Pro Ala Val Asp Ala Phe Thr Val Pro Phe
        115                 120                 125


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


Pro Ile Tyr Val Val His Tyr Ser Asp Ile His Ile Asp Pro Phe Tyr
```

```
145                 150                 155                 160

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

Tyr Thr Ser Ala Ser Ser Pro Gly Asn Asn Asn Ser Pro Ala Gly Pro
            180                 185                 190

Tyr Gly Asp His Asn Cys Asp Val Pro Ile Ser Leu Glu Asp Ser Met
        195                 200                 205

Tyr Ala Ala Ile Lys Lys Leu Val Pro Asp Ala Ala Phe Gly Ile Phe
    210                 215                 220

Thr Gly Asp Ile Val Asp His Ala Val Trp Asn Thr Ser Glu Ser Gln
225                 230                 235                 240

Asn Ile Ile Asp Met Asn Asp Ala Tyr Thr Arg Met Lys Asn Ser Gly
                245                 250                 255

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

Val Asn Ser Phe Pro Pro Pro Ala Ile Gly Asn Glu Ser Gln Trp Val
        275                 280                 285

Tyr Asp Thr Leu Ala Ser Asp Trp Ser Gln Trp Ile Gly Thr Ser Gly
    290                 295                 300

Ala Ser Ser Val Glu Ser Ile Gly Ala Tyr Ser Val Gln Tyr Gly Ser
305                 310                 315                 320

Thr Lys Leu Arg Val Ile Ser Leu Asn Thr Asn Met Tyr Tyr Ile Glu
                325                 330                 335

Asn Phe Tyr Leu Tyr Glu Pro Thr Met Glu Gln Asp Pro Ala Gly Gln
            340                 345                 350

Phe Ala Trp Leu Val Ser Glu Leu Ser Ala Ala Glu Ala Ala Gly Glu
```

```
        355                 360                 365

Arg Val Trp Ile Ile Gly His Met Pro Leu Gly Leu Ser Asp Ala Phe
    370                 375                 380

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

Thr Ile Ala Ala Met Phe Phe Gly His Thr His Glu Asp His Phe Gln
                405                 410                 415

Ile Ser Tyr Ser Asp Tyr Asn Ala Arg Thr Ala Ala Asn Ala Arg Ala
            420                 425                 430

Val Ser Tyr Ile Met Pro Ser Leu Thr Pro Thr Ser Gly His Pro Thr
        435                 440                 445

Phe Arg Val Tyr Thr Val Asp Pro Glu Thr Phe Gly Val Leu Asp Ala
    450                 455                 460

Thr Thr Tyr Tyr Ala Asp Met Ser Gln Pro Thr Tyr Gln Thr Ala Gly
465                 470                 475                 480

Pro Ala Trp Ser Val Tyr Tyr Ser Ala Lys Ala Ala Tyr Gly Gly Leu
                485                 490                 495

Val Asp Pro Pro Val Ala Ala Asp Asp Ala Ala Ala Glu Leu Thr Pro
            500                 505                 510

Ala Phe Trp His Asn Val Thr Ala Ala Leu Ala Ala Asp Pro Ala Ser
        515                 520                 525

Phe Asp Ala Tyr Tyr Ala Arg Lys Thr Arg Gly Trp Asp Val Ala Ala
    530                 535                 540

Cys Ala Gly Ala Cys Ala Ala Ala Glu Val Cys Ala Leu Arg Ala Ala
545                 550                 555                 560

Arg Ala Gln Asp Asn Cys Val Val Pro Thr Pro Gly Val His Phe Ser
```

```
                565                 570                 575

Lys Arg Ala Asp Glu Gly Thr Leu Ala His His Arg Asp Glu Cys Gly
            580                 585                 590

Val Ser Val Ala Arg Asn Ser Leu Ser Ser Leu Val Val Gln Arg Glu
        595                 600                 605

Ala Leu Glu His Leu Glu Gly Arg Leu Ser Glu Lys Arg Arg Met Ala
    610                 615                 620

Val
625


<210>  241
<211>  613
<212>  PRT
<213>  Mariannaea pinicola

<400>  241

Gln Glu Val Thr His Asp Leu Ala Gly Ile Lys Arg Ser Leu Glu Ser
1               5                   10                  15

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

Cys Ala Gly Cys Glu Ser Leu Val Leu Val Leu Lys Gly Leu Ala Ala
        35                  40                  45

Ile Ser Asp Gln Ala Phe Ile Asp Val Leu Gln Glu Ile Cys Lys Ile
    50                  55                  60

Ser Gly Ala Glu Asp Asp Asp Val Cys Asp Gly Ser Ile Gln Leu Glu
65                  70                  75                  80

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

Thr Ser Lys Glu Phe Cys Thr Thr Phe Leu Gly Leu Cys Ala Tyr Pro
            100                 105                 110
```

```
Ala Val Gln Gln Trp Ser Val Pro Phe Ser Ser Ser Lys Ser Ser Lys
        115                 120                 125


Thr Arg Pro Ser Ser Ser Gly Lys Asp Pro Ile Lys Val Val His Tyr
    130                 135                 140


Ser Asp Ile His Ile Asp Pro Leu Tyr Val Gly Gly Ser Asn Ser Asn
145                 150                 155                 160


Cys Thr Lys Pro Ile Cys Cys Arg Ser Tyr Thr Lys Ala Asp Gln Pro
                165                 170                 175


Gly Asn Asn Lys Tyr Pro Ala Gly Pro Asn Gly Asp His Asn Cys Asp
            180                 185                 190


Ser Pro Val Ser Leu Glu Lys Ser Met Tyr Asn Ala Ile Lys Glu Ile
        195                 200                 205


Val Pro Asp Ala Ala Phe Thr Ile Phe Thr Gly Asp Ile Val Asp His
    210                 215                 220


Ala Val Trp Asn Thr Ser Gln Ser Tyr Asn Thr Glu Gln Ile Thr Asn
225                 230                 235                 240


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


Gly Asn His Glu Ala His Pro Ala Asn Ala Phe Gln Pro Asn Ser Val
            260                 265                 270


Gly Asn Val Ser Gln Trp Val Tyr Asp Leu Leu Ser Gly Leu Trp Ser
        275                 280                 285


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


Tyr Ser Thr Lys Tyr Pro Gly Gly Asn Leu Arg Ile Ile Ser Leu Asn
305                 310                 315                 320
```

```
Thr Asn Met Tyr Tyr Arg Glu Asn Tyr Trp Leu Tyr Arg Lys Thr Met
                325                 330                 335

Ile Gln Asp Pro Ser Asn Gln Ile Ser Trp Leu Val Asn Glu Leu Glu
            340                 345                 350

Ala Ala Glu Thr Ala Gly Glu Arg Val Tyr Ile Ile Gly His Met Pro
        355                 360                 365

Leu Gly Asp Ser Asn Ser Phe His Asp Gln Ser Asn Tyr Leu Asp Gln
    370                 375                 380

Val Ile Asn Arg Tyr Ser Ala Thr Ile Ser Ala Met Phe Phe Gly His
385                 390                 395                 400

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

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

Pro Thr Ala Gly Met Pro Ala Phe Arg Val Tyr Asp Val Asp Pro Val
        435                 440                 445

Thr Phe Gly Ile Leu Asp Ser Thr Thr Tyr Ile Ala Asp Met Thr Asp
    450                 455                 460

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

Lys Glu Val Tyr Gly Ser Leu Leu Ser Pro Ala Val Thr Asp Ser Ser
                485                 490                 495

Ala Glu Leu Thr Ala Ala Phe Trp His Asn Val Thr Thr Leu Phe Glu
            500                 505                 510

Ala Asp Asn Thr Ala Phe Glu Ala Phe Leu Ser Arg Lys Ser Arg Gly
        515                 520                 525
```

```
Trp Lys Ser Glu Ser Cys Thr Gly Thr Cys Lys Ala Asn Glu Ile Cys
    530                 535                 540


Gln Leu Arg Ala Ala Arg Ser Glu Asn Asn Cys Tyr Thr Pro Ser Leu
545                 550                 555                 560


Gly Ile Ser Phe Asn Lys Arg Ser Leu Asn Pro Val Glu Glu Arg Asp
                565                 570                 575


Glu Cys Gly Ile Ser Val Thr Arg Ala Thr Val Ser Ala Met Gly Val
            580                 585                 590


Arg Lys Asp Val Leu Arg Leu Leu Lys Lys Arg Phe Ile Glu Lys Ala
        595                 600                 605


Gly Glu Val Arg Gly
    610


<210>  242
<211>  259
<212>  PRT
<213>  Fictibacillus macauensis

<400>  242

His Glu Asn Glu Gly Gly Asn Lys Val Arg Val Ile Gln Tyr Trp Ser
1               5                   10                  15


Ala Glu Asp Pro His His Glu Asp Thr Asn Thr His Leu Trp Ile Val
            20                  25                  30


Arg His Ala Met Glu Ile Met Ala Asn Asn Lys Asp Val Val Lys Pro
        35                  40                  45


Gly Glu Val Glu Gln Leu Lys Gln Trp Gln Ser Asp Leu Glu Gln Gly
    50                  55                  60


Ile Tyr Asp Ala Asp His Ala Asn Pro Tyr Tyr Asp Asn Ala Thr Phe
65                  70                  75                  80
```

```
Ala Ser His Phe Tyr Asp Pro Asp Thr Gly Lys Ser Tyr Ile Pro Leu
                85                  90                  95


Ala Ala His Ala Lys Thr Thr Ser Val Lys Tyr Phe Lys Arg Ala Gly
            100                 105                 110


Glu Ala Tyr Gln Lys Gly Asp His Lys Gln Ala Phe Tyr Asn Leu Gly
        115                 120                 125


Leu Ala Leu His Tyr Ile Gly Asp Leu Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Tyr Val Asp Ser Phe Lys Glu Asp Tyr Ala Val Lys Asp Gly Glu
                165                 170                 175


Gly Tyr Trp His Trp Lys Gly Thr Asn Pro Glu Asp Trp Leu His Gly
            180                 185                 190


Thr Ala Val Ala Ala Lys Lys Asp Tyr Pro Asp Ile Val Asn Asp Thr
        195                 200                 205


Thr Lys Ala Trp Phe Val Lys Ala Ala Val Ser Asn Ser Tyr Ala Ala
    210                 215                 220


Lys Trp Arg Ala Ala Val Val Pro Ala Thr Gly Lys Arg Leu Thr Glu
225                 230                 235                 240


Ala Gln Arg Ile Leu Ala Gly Tyr Met Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Val Asn Lys



<210>  243
<211>  250
<212>  DNA
```

```
<213>  Saccharomyces cerevisiae

<400>  243
acagaagacg ggagacacta gcacacaact ttaccaggca aggtatttga cgctagcatg       60

tgtccaattc agtgtcattt atgatttttt gtagtaggat ataaatatat acagcgctcc      120

aaatagtgcg gttgccccaa aaacaccacg gaacctcatc tgttctcgta ctttgttgtg      180

acaaagtagc tcactgcctt attatcacat tttcattatg caacgcttcg gaaaatacga      240

tgttgaaaat                                                             250


<210>  244
<211>  822
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  ARTIFICIAL SYNTHETIC DNA

<400>  244
gaggtttctc aggatctttt caatcagttc aatttgtttg ctcagtactc cgcagcagct       60

tactgtggca agaataacga tgccccagcc ggaaccaaca tcacgtgtac aggtaacgct      120

tgtcctgagg ttgaaaaggc agacgctacc ttcttataca gttttgaaga tagtggggtt      180

ggagacgtga ctggattcct ggcactagac aatacgaaca aattgattgt tttgtctttc      240

agaggctctc gttctatcga aaactggatt gcaaacctga acttttggtt gaagaagatt      300

aacgatatct gttctggttg tagaggacac gatggtttta catcttcttg gagatccgtg      360

gccgacacct tgagacaaaa ggttgaagat gccgttcgtg aacatccaga ttacagggtc      420

gtgtttacgg gtcatagttt aggtggtgct ttggccacag ttgctggtgc agaccttaga      480

ggtaatggtt acgatatcga tgtcttttcc tatggagcac caagggttgg taatagagct      540

ttcgctgagt tcttgacagt ccaaactggt gggaccttgt atagaatcac tcacaccaat      600

gatattgtgc ctagactacc cccaagagaa tttgggtatt ctcattcctc tcccgagtat      660

tggattaaga gtggaacatt agtacccgtt accaggaacg acattgtcaa gattgaaggg      720

attgacgcaa ctggtggcaa caatcaaccg aatatcccag atatcccagc acatctttgg      780

tactttcaag ctacagacgc ttgtaacgct ggtggattta gc                         822
```

```
<210>  245
<211>  831
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  ARTIFICIAL SYNTHETIC DNA

<400>  245
gctccagctc cagttcttag gagagatgta tcttcctctg tattgtctga gctggactta       60

ttcgctcagt actctgccgc tgcatattgc tcttccaata tcggttctcc gggtacgaag      120

cttacttgta gtgtcggtaa ttgtccccgt gttgaagctg ccgatacaga gacgttgata      180

gagtttaacg aatcatcttc ttttggtgat gtgactggct atatcgctgt ggataggacc      240

aattcactac tggtgttggc atttaggggc tcttccacag tgtcaaattg ggaagcagat      300

ctagattttc cattaacaga tgcttctagt ctgtgcagtg gctgtgaaat tcactctggt      360

ttttgggctg cctggcaaac cgtacaggca tccatcacta gcacattgga gtcagctatt      420

gcttcttacc ctggttatac tttggtcttc acaggtcatt catacggtgc cgctttggca      480

gcaatagcag caactacatt gagaaatgct ggttacacaa tccagttgta cgactatggc      540

cagccgaggt taggtaatct tgctctggcc cagtacatta cggcacaaac acagggtgcc      600

aactatcgtg ttactcatac cgatgacatc gtacccaaac taccccctga gttgtttggc      660

tatcaccact tctccccaga gtattggata acgtcaggcg ataatgttac agttacaact      720

agcgatgtgc aagtagtcac tggaattgac agtacagctg gaaatgatgg gactttgctt      780

gattctacaa gtgcccatga ttggtacatt gtctacattg atgggtgcga t               831


<210>  246
<211>  1782
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  ARTIFICIAL SYNTHETIC DNA

<400>  246
tctgctccgt atgacaaaag agacttggct caggagattt gggacgacat taagaatgcc       60

gttgactgcg ctggctgtca agttgttttg acagctttga aaggtgttgc cgatctgggc      120

acaacagctt tagttgatgt cttaactgag gtgtgcaata tctctggtaa ggaggattca      180
```

```
gatgtctgct ctggtatcat tagtagagag ggtcctgttc tagactacgt gcttcaacat      240
ctagacatcg ggtctcatac atcacaagtc atttgtgctt cagcatttgg tttatgccaa      300
tatcccgaag tgagacccta taacttgact tttcctaagc ccaaaccaaa cacaaccaga      360
cctgaacctt ccggtgaatc tccaattcaa gtagtgcact tctccgatac gcacgttgac      420
ttaagttacg agactggttc caattacaat tgcactaagc caatttgttg tagaccttac      480
actgccgaag atgcacctgg gaacactact actccatgtg gtccgtacgg taataccaag      540
tgtgatgccc cattatcctt ggaagagtct atgtttgctg ccatcaaagc cttaaaccct      600
caaccagcat tttctatcta cacaggagat gttgtagcac atgacatttg gttagttgat      660
caaaacgagg ttatcgaaga tttgaacgca acgtacgata gaatggctgg tctgggttta      720
gtctatgccg ctattggtaa tcatgataca gcaccggtta acgacctgcc gacgtcaaac      780
attccatccg agtattcagc aaattggact tatgaagctt tgtcttacga ctttacaatg      840
ttgactcaaa gcgccagtgc tcaaactgct gcaaactatg gttcctattc agccatttac      900
cctggatctt acggtacaga cctaagagtc atttcataca actctatctt ctattacgtt      960
gacaactttt gggcttatca agatccaatg gaatttgacc cagatggcca gctagcatgg     1020
ttgataaacg agttgcaaga agctgaaact gctggccaaa gagtctggat catagcacat     1080
gttcctacgg gtacttccga tcacttccat gactattctc actactttga ccaaatagtc     1140
caaagatatg aagccacgat tgctgccttg ttctatggtc atacccacat agaccagttt     1200
cagattagtt actcaaacta ttcaaacaga gcatttgata ccgcaactgc catcggctac     1260
attatgcctt ctttaacacc cactagcggt ccacctacct ttagagttta cgacgttgat     1320
ccaaagacgt tcgcagtgtt agatttcacc aattacattg ccaacatttc cgatcctgca     1380
tttcaatcag gtccatcatg gcagaaatac tattccgcca aggagaccta cggctcacta     1440
ttgtctccac ctgtaaccga ccctactgct gaattgacgc ctgcattctg gcataatgtc     1500
accgtggcat ttgagcaaga caacgcaaca tttcaagagt attgggctcg tcaaaccagg     1560
ggatacgatg tctcatcatg tacaggtagt tgcataaccc aagcaatatg cggattgcgt     1620
gctggcgacg cacaatacaa ttgtgttact cctactcccg gtttcaactt cgcaaagcgt     1680
gacactagta accccaaaca agccttgtca catgttgaga aatgtgaagg atccggtctt     1740
```

ctaggcttgt taaggcgtat ggttgcagac tctaaatctt ct 1782

<210> 247
<211> 777
<212> DNA
<213> Artificial Sequence

<220>
<223> ARTIFICIAL SYNTHETIC DNA

<400> 247
catgagaatg atgggggttc caagattaag atcatacata gatggtctgc cgaagataaa 60

cataaagaag ggttaactc tcacttatgg atagtcaaca gagcaatcga cattatgtca 120

agaaatacaa ctttagtgaa acaagacaga gtcgcccaac taaatgaatg gagaactgag 180

ctagaaaatg gcatttacgc tgcagattat gagaacccgt attacgataa ctccacgttc 240

gcttcccatt tctatgatcc agacaatggt aagacataca tcccctttgc aaagcaggca 300

aaagaaactg gtgccaaata cttcaagtta gctggggaat cctacaaaaa caaagatatg 360

aaacaagcct ttttctatct tggtctgtct ctgcattacc taggtgatgt caaccagcca 420

atgcatgcag ccaatttcac aaacttatct tatcctcaag gattccattc caagtatgag 480

aactttgttg atacgatcaa ggacaactac aaagtcacag atggaaacgg ttactggaat 540

tggaaaggga ccaacccgga agactggatt cacggtgctg ctgttgttgc caaacaagac 600

tattcaggaa tcgtaaatga caataccaaa gactggtttg taaaagcagc agtctctcaa 660

gaatatgcag acaaatggag agccgaggtt acacccatga cgggcaagag gttaatggat 720

gcccaacgtg tcactgctgg ttacatacaa ctatggtttg atacttatgg ggataga 777

<210> 248
<211> 891
<212> DNA
<213> Artificial Sequence

<220>
<223> ARTIFICAL SYNTHETIC DNA

<400> 248
caggaaagcc cagccttcat tgatccagct agctggaaca ctccgtttaa cggtatagca 60

caagtagcat gccacaattg ttatgagaag caatacgcaa acactttttc ttcagtatta 120

```
gactctgtta gaacattgga attggacttt tgggaccaaa gggatgctgt tagtggtggt      180

tctccgcatc actggtttgt cagacacaat ccagggactc tttttcaaag tggtaatgac      240

aacaattgca caggtgatgg tactggaaag aatgatttgg aagcctgtct gaatgatgtc      300

aagaattggt ccgataagca tccaggtcat tttcccatta cgcttattct agacaaaaag      360

caggggtggt caaaagaaag ttcagggagg actccaaaag acttcgatga acttgttgca      420

agagttttcc aaggtaaact attcactccc caagacttag caacccacat aggatcaggc      480

gctggcgcac tacagggcaa cttgaaagga aagtcatggc ctactgcaaa tgatttacaa      540

gggaaagtgt tgttagtctt gaatcatagt gaaaatcaga agttatccca gtatgctgag      600

gctagaacat ccaaggctaa agtgttcatt tcaccagtta caaacgggca aaacgacatt      660

tccggtaaag tgtctggtat gtcatcccaa agttccggtt atgttgcaat gaacaatatg      720

ggtaagggag ataagagttg ggcaaagcaa gcttttgcat actctcacat tgggagagtc      780

tggggtgatg acgaagtgtc atttgcccaa cacatcaatc aaaagatcaa tcttagtgcc      840

tactacagat ttgccgctca gtccgcaggt ggttaccgta tacgtccatt t               891


<210>  249
<211>  1875
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  ARTIFICIAL SYNTHETIC DNA

<400>  249
gcagtcaatc cagcagacgt tttgagtgtt gtggagaaaa gagtggatcc agcatccgga       60

cttgaagtac gttccatctg ggatactata tggaatgaca tcaaatctgc tgcagactgc      120

accgcatgtg aggccgtttt gactttactt aagggtgttg ctgctttcgg tgacaatttc      180

tttgttgaag tattgacaga aatctgcgat ttgtcaggag ccgaagatga tgatgtttgt      240

tctggggtgt tatcactaga aggaccaatc attgcaaacg acattaggaa aatgtcaatc      300

ggatccaaga cctccgagtt gttttgtata acttttctgg ggttatgttc ttatcctgca      360

gttgatgctt ttactgttcc atttccgacc gctaagtcag ctgctaccag accggtctcc      420

tcaggaaaag atccgatcta tgtcgtacac tattcagata ttcatattga tcctttctat      480
```

gtcgcaggga gcgcctcaaa ctgtactaag ccaatttgtt gtagagacta tacttcagct 540

tcttctcctg gcaacaacaa tagcccagca ggtccctacg gtgatcacaa ttgtgacgtt 600

ccaatctcat tagaagattc catgtacgct gccatcaaaa agctagttcc agatgctgca 660

ttcggtatct tcactggcga tatcgtggat cacgctgtat ggaatacttc tgaatcacag 720

aacatcatag acatgaacga tgcctatacc cgtatgaaga attctggtat gttacctacc 780

attttcgcca ctgcaggaaa tcatgaagcc tcaccagtga atagtttccc tccccctgct 840

atcggtaatg agtcacaatg ggtttatgat acactggcct cagattggtc tcagtggatt 900

ggaaccagtg gtgccagctc tgtcgaatcc ataggtgcct attctgtgca atacggttca 960

accaaattgc gtgtgatttc tttgaatacc aatatgtatt acattgagaa cttttaccta 1020

tatgaaccaa ccatggaaca agatccagcc ggacaattcg catggttagt ttcagaattg 1080

agcgcagctg aggctgcagg agaaagagtt tggatcattg gacatatgcc gttgggcctg 1140

tccgacgcct tccacgatcc ttccaactac tttgatcaga tcgtcaatag atatgaagct 1200

accatagccg ctatgttttt cggccacaca catgaggatc acttccagat ttcttactca 1260

gactataacg ccagaactgc cgcaaacgct agggctgttt cctacattat gccttccctt 1320

actcctacca gcggacatcc gactttccgt gtctacacgg ttgatccaga aacattcggc 1380

gtactagacg caacaaccta ctacgcagat atgagtcaac caacgtatca aactgctggg 1440

ccagcttggt ccgtctatta cagtgctaaa gcagcatatg gggtttggt cgatccacca 1500

gttgcagccg atgatgcagc cgcagagttg acaccagcct tttggcataa cgttactgca 1560

gcattagctg ccgatcccgc ttctttcgat gcctactatg ctagaaagac cagaggttgg 1620

gatgttgctg cctgcgcagg cgcttgtgct gctgctgaag tgtgcgcctt gagggctgcc 1680

cgtgcacaag acaattgtgt ggttccaact cctggtgtgc atttcagtaa gcgtgcagat 1740

gaaggcactt tagcccacca cagggatgaa tgcggtgtat ctgtagccag gaattcactt 1800

tcctctttgg ttgtacagag ggaagcatta gaacacttag aaggcaggct ttctgagaaa 1860

agaagaatgg cagtt 1875

<210> 250
<211> 1839

<212> DNA
<213> Artificial Sequence

<220>
<223> ARTIFICIAL SYNTHETIC DNA

<400> 250
caggaagtaa cacatgactt ggctggcatt aagagaagtt tggaatctag ggactgggtg 60

gaggacttat gggacaagtt cgaatcagat gcaacttgtg ctggatgtga aagtttagtt 120

ttagtcttga aaggcttagc cgcaatatca gaccaagcct tcatagacgt cttgcaagag 180

atatgcaaga tatctggagc cgaagatgat gatgtttgtg atgggagtat acagttagaa 240

ggcccagtta ttgcaagtgg cttgagatct atggcaattg gctctcgtac ttctaaagaa 300

ttctgtacaa cgttcttggg tttatgcgcc tacccagctg ttcaacaatg gagcgtgcct 360

ttttcctcct ccaaaagttc taaaaccaga ccaagctctt ctggtaagga tcctatcaag 420

gtagtgcact attcagatat tcatatcgac cctctatatg ttggtggatc aaattcaaat 480

tgtactaaac caatctgctg tcgttcatat actaaggcag accaacctgg caacaacaaa 540

tacccagctg gcccaaacgg tgatcacaat tgtgattcac ctgtgtctct agagaagagc 600

atgtataacg ccattaagga aattgtacca gatgctgctt ttaccatctt tactggagat 660

attgtagatc acgctgtatg gaacacctca caatcctata acaccgaaca aatcacaaat 720

gcatatggat tgatgtcaga caacttagga accatctatg gtacagcagg caatcacgag 780

gctcacccag ccaacgcatt ccaaccaaac tcagttggta atgtaagcca atgggtctac 840

gacttgttaa gtggactatg gtctcaatgg atttctactg aagcaaaggc agacagtgaa 900

aagttaggtg cttatagcac caaataccca ggcggaaacc ttaggattat ctcattgaac 960

acaaacatgt actatagaga aaactactgg ttatacagaa agactatgat tcaggaccct 1020

agcaaccaga tatcttggct agttaacgaa ttggaggcag cagaaactgc aggtgaacgt 1080

gtgtacatca ttggtcatat gcctttaggc gatagcaatt ctttccacga tcaatcaaac 1140

tacttggatc aagtgatcaa cagatactca gcaacaattt cagcaatgtt cttcggtcac 1200

actcacgatg atcaatttca gatttcatat tcaaattggt caaaccgtaa cttcagtaac 1260

gccttagtca cttcctacat tggacctagt ttaactccaa ctgctgggat gcctgccttt 1320

agagtttacg acgtggatcc agtgactttc ggcatcttag attccactac ctatatcgcc 1380 gatatgaccg atagtgcttt ccaaacaaca ggtccagtat ggaagaagta ttacagtgcc 1440

aaagaagtgt atggcagcct actaagccca gctgttacag atagtagtgc tgaattgaca 1500

gcagccttct ggcataatgt cactacctta ttcgaagcag acaatacggc ttttgaagca 1560

ttcttaagta ggaaatccag aggctggaag tctgaatcct gtacaggtac ttgcaaggca 1620

aatgagatct gccagttgag ggctgccaga tctgaaaaca attgttacac cccttctctt 1680

ggcatctcct ttaacaaaag atccttgaat ccagtggagg aaagagatga atgtgggatc 1740

tccgtaacca gagcaactgt ttctgcaatg ggggtcagaa aggatgtcct taggttgttg 1800

aagaaaaggt tcattgaaaa ggctggggaa gtcaggggc 1839

<210> 251
<211> 777
<212> DNA
<213> Artificial Sequence

<220>
<223> ARTIFICIAL SYNTHETIC DNA

<400> 251
catgagaatg aagggggtaa caaagttagg gtaatacagt attggtctgc cgaagatcca 60

catcatgaag acacaaacac tcacttatgg atagtccgtc atgcaatgga gattatggcc 120

aacaacaaag atgttgtgaa accaggcgaa gtcgagcaac taaaacaatg gcaatcagac 180

ctagaacaag gcatttacga tgcagatcat gccaacccgt attacgataa cgcaacgttc 240

gcttcccatt tctatgatcc agacactggt aagtcataca tccccttggc agcacacgca 300

aaaacaacca gcgtcaaata cttcaaaaga gctggggaag cataccaaaa gggtgatcat 360

aaacaagcct tttacaatct tggtctggct ctgcattaca taggtgatct aaaccagcca 420

atgcatgcag ccaatttcac aaacttatct tatcctcaag gattccattc caagtatgag 480

aactatgttg atagcttcaa ggaggattat gctgtcaaag atggagaggg ttactggcat 540

tggaaaggga ccaacccgga agactggttg cacggtacag ctgttgctgc caagaaagat 600

tatccagaca tcgtaaatga tacaaccaaa gcctggtttg taaaagcagc agtctcaaac 660

tcttatgcag ctaaatggag agctgccgtt gttcccgcaa cgggcaagag gttaacagaa 720

gcccaacgta tcttggctgg ttacatgcaa ctatggtttg atacttatgt gaacaaa 777

```
<210>  252
<211>  585
<212>  PRT
<213>  Aspergillus wentii

<400>  252

Asn Trp Ala Glu Ser Ile Trp Asp Asp Val Lys His Ala Val Asn Cys
1               5                   10                  15


Ala Gly Cys Glu Thr Val Leu Phe Ala Leu Lys Gly Val Ala Asp Leu
            20                  25                  30


Gly Glu His Ala Phe Gln Thr Val Leu Thr Asp Val Cys Asp Ile Ser
        35                  40                  45


Gly Thr Glu Asp Lys Asp Val Cys Ser Gly Leu Ile Ala Ala Glu Ser
    50                  55                  60


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


Ser Lys Val Leu Cys Ala Gln Leu Phe Gly Leu Cys Gln Phe Pro Ala
                85                  90                  95


Val Arg Pro Tyr Asn Leu Thr Phe Pro Ser Pro Lys Pro Thr Thr Ser
            100                 105                 110


Arg Pro Pro Pro Ser Gly Gln Ser Pro Ile Arg Val Ala His Ile Ser
        115                 120                 125


Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly Ser Asn Tyr Glu Cys
    130                 135                 140


Ser Lys Pro Ile Cys Cys Arg Val Tyr Thr Asp Glu Asp Ala Pro Gly
145                 150                 155                 160


Asn Thr Ser Phe Pro Cys Gly Pro Tyr Gly Asn Thr Asn Cys Asp Pro
                165                 170                 175
```

```
Pro Leu Arg Leu Glu Glu Ser Met Met Ala Ala Ile Lys Ser Leu Asn
            180                 185                 190


Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala His Asp Leu Trp
        195                 200                 205


Met Val Asp Lys Thr Glu Val Leu Asp Asp Phe Asn Ala Thr Tyr Ser
    210                 215                 220


Met Leu Asp Gln Leu Asp Leu Val Tyr Ala Ala Val Gly Asn His Asp
225                 230                 235                 240


Thr Thr Pro Val Asn Leu Phe Pro Ser Thr Gln Leu Pro Asp Lys Asp
                245                 250                 255


Asn Gln Trp Ala Tyr Asp Ala Leu Thr Ala Glu Trp Lys Ser Leu Thr
            260                 265                 270


Asn Ser Ser Ile Gln Thr Thr Glu Tyr Gly Ser Tyr Ser Ala Ile Tyr
        275                 280                 285


Glu Asn Leu Arg Ile Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Gln Asp
    290                 295                 300


Asn Phe Tyr Ala Tyr Thr Asp Pro Met Ala His Asp Pro Ser Asn Gln
305                 310                 315                 320


Leu Thr Trp Leu Ile Asp Gln Leu His Glu Ala Glu Ser Ala Asn Gln
                325                 330                 335


Arg Val Trp Leu Ile Ser His Ile Pro Thr Gly Gly Val Asp His Leu
            340                 345                 350


His Asp Tyr Ser His Tyr Ile Asp Glu Ile Val Gln Arg Tyr Glu Ala
        355                 360                 365


Thr Ile Ser Ala Leu Phe Phe Gly His Thr His Thr Asp Leu Phe Gln
    370                 375                 380
```

```
Ile Ala Tyr Ser Asp Tyr Lys Asn Arg Ala Trp Asp Thr Ala Ser Ala
385                 390                 395                 400


Ile Gly Tyr Val Ala Pro Ser Leu Thr Pro Thr Ser Gly Pro Pro Ala
                405                 410                 415


Phe Arg Ile Tyr Asp Ile Asp Pro Val Thr Phe Ala Val Leu Asp Tyr
            420                 425                 430


Thr Val Tyr Ile Ala Asn Ile Ser Asn Pro Ser Tyr Gln Ser Asn Pro
        435                 440                 445


Lys Trp Glu Lys Tyr Tyr Ser Ala Lys Glu Ala Tyr Gly Ser Leu Leu
    450                 455                 460


Ser Pro Pro Val Thr Asp Ser Ser Ser Glu Leu Thr Pro Ser Phe Trp
465                 470                 475                 480


His Asn Val Thr Ala Leu Met Glu Lys Asp Asp Ser Val Phe Gln Asp
                485                 490                 495


Trp Trp Ser Arg Thr Thr Arg Gly Tyr Asn Val Thr Thr Cys Thr Gly
            500                 505                 510


Asp Cys Ala Lys Lys Glu Ile Cys Ala Leu Arg Gly Ala Asp Ala Gln
        515                 520                 525


Tyr Asn Cys Val Thr Ala Thr Pro Gly Phe His Phe Asp Lys Arg Glu
    530                 535                 540


Glu Ser Glu Gln Lys Pro Arg Pro Glu Cys Glu Asp Gly Leu Gly Arg
545                 550                 555                 560


Val Leu Gly Asp Met Ile His Lys Lys Asp Phe Val Asp Leu Leu His
                565                 570                 575


Glu Arg Thr Ala Gln Tyr Gln His Arg
            580                 585
```

```
<210>  253
<211>  588
<212>  PRT
<213>  Penicillium cylindrosporum

<400>  253

Thr Tyr Asp Lys Arg Asp Leu Ala Gln Asp Leu Trp Asn Asp Ile Lys
1               5                   10                  15


Asn Ala Val Asp Cys Gly Gly Cys Gln Val Ile Leu Thr Ala Leu Lys
            20                  25                  30


Gly Leu Ser Asp Leu Gly Thr Thr Val Phe Val Asp Val Leu Thr Glu
        35                  40                  45


Val Cys Glu Ile Gly Lys Leu Glu Asp Ser Asp Val Cys Ser Gly Thr
    50                  55                  60


Ile Ser Arg Glu Gly Pro Val Leu Asp Tyr Ile Leu Gln His Leu Asp
65                  70                  75                  80


Ile Gly Ser His Thr Ser Gln Val Leu Cys Ala Ser Ala Phe Gly Leu
                85                  90                  95


Cys Gln Tyr Pro Ala Val Arg Pro Tyr Asn Leu Pro Phe Pro Ser Pro
            100                 105                 110


Lys Pro Asn Thr Thr Arg Pro Ala Pro Ser Gly Glu Leu Pro Ile Gln
        115                 120                 125


Val Val His Ile Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly
    130                 135                 140


Ser Ser Tyr Asn Cys Thr Lys Pro Ile Cys Cys Arg Pro Tyr Thr Ala
145                 150                 155                 160


Ala Asp Ala Pro Gly Asn Thr Thr Thr Pro Cys Gly Pro Tyr Gly Asn
                165                 170                 175
```

```
Thr Asn Cys Asp Ala Pro Ile Gly Leu Glu Glu Ser Met Phe Ala Ala
            180                 185                 190


Ile Lys Ala Leu Gln Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val
        195                 200                 205


Ala His Asp Leu Trp Leu Val Asp Gln Asn Glu Val Leu Gln Asp Phe
    210                 215                 220


Asn Ala Thr Phe Asn Arg Met Ala Glu Leu Gly Val Val Tyr Ala Ala
225                 230                 235                 240


Ile Gly Asn His Asp Thr Ala Pro Val Asn Asp Leu Pro Ala Ser Asn
                245                 250                 255


Ile Pro Ser Gln Tyr Ser Ala Asn Trp Thr Tyr Asp Ala Leu Ala Tyr
            260                 265                 270


Asp Phe Ser Thr Leu Thr Asn Ser Ala Ser Ala Gln Thr Ala Glu Asp
        275                 280                 285


Tyr Gly Ser Tyr Ser Ser Val Tyr Arg Gly Ser His Gly Thr Asp Leu
    290                 295                 300


Arg Val Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Val Asp Asn Phe Trp
305                 310                 315                 320


Val Tyr Gln Asp Pro Met Leu Tyr Asp Pro Asp Gly Gln Leu Ala Trp
                325                 330                 335


Leu Ile Ser Glu Leu Gln Glu Ala Glu Thr Gly Gly Gln Arg Val Trp
            340                 345                 350


Leu Ile Ala His Val Pro Ser Gly Ile Ser Asp His Phe His Asp Tyr
        355                 360                 365


Ser His Tyr Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr Ile Ala
    370                 375                 380
```

```
Ala Leu Phe Tyr Gly His Thr His Arg Asp Gln Phe Gln Ile Ser Tyr
385                 390                 395                 400


Ser Asp Tyr Thr Asn Arg Thr Trp Asn Thr Ala Thr Ala Met Gly Tyr
                405                 410                 415


Ile Thr Pro Ser Leu Thr Pro Thr Ser Gly Pro Pro Thr Tyr Arg Val
            420                 425                 430


Tyr Lys Val Asp Pro Lys Thr Phe Gly Val Leu Asp Phe Thr Asn Tyr
        435                 440                 445


Ile Ala Asn Ile Ser Asp Pro Ala Tyr Gln Ser Gly Pro Thr Trp Gln
    450                 455                 460


Lys Tyr Tyr Ser Ala Lys Glu Thr Tyr Gly Ser Leu Leu Ser Pro Pro
465                 470                 475                 480


Val Thr Asp Pro Thr Ala Glu Leu Thr Pro Ala Phe Trp His Asn Val
                485                 490                 495


Thr Val Leu Phe Glu Asn Asp Asn Ala Thr Phe Gln Gln Tyr Ile Ala
            500                 505                 510


Arg Gln Thr Arg Gly Trp Asp Pro Ser Ser Cys Thr Gly Ser Cys Ile
        515                 520                 525


Asp Gln Thr Ile Cys Gly Leu Arg Ala Gly Asp Ala Gln Tyr Asn Cys
    530                 535                 540


Val Thr Pro Thr Pro Gly Phe Asn Phe Ala Lys Arg Asp Ala Ser Thr
545                 550                 555                 560


Gly Gly Gln Pro Glu Thr His Val Glu Lys Cys Glu Gly Ser Gly Leu
                565                 570                 575


Leu Ala Leu Leu Gly Arg Met Val Ala Thr Lys Ser
            580                 585
```

```
<210>  254
<211>  588
<212>  PRT
<213>  Penicillium meridianum

<400>  254

Ser Ala Asp Ser Trp Ile Thr Ile Ile Trp Asp Asp Phe Lys Glu Ala
1               5                   10                  15


Val Asp Cys Ala Ser Cys Gln Ala Leu Leu Gly Gly Leu Lys Tyr Val
            20                  25                  30


Ala Gly Phe Gly Glu Ser Phe Met Glu Asp Val Leu Thr Gly Val Cys
        35                  40                  45


Asp Ile Ser Gly Ala Glu Asp Ser Asp Val Cys Ser Gly Ile Ile Ala
    50                  55                  60


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


Ser His Thr Ala Lys Thr Phe Cys Ser Asn Leu Val Gly Leu Cys Asp
                85                  90                  95


Tyr Pro Ala Val Arg Pro Tyr Asp Leu Ser Phe Pro Ser Pro Lys Pro
            100                 105                 110


Ser Ile Ser Arg Pro Pro Pro Ser Gly Lys Pro Pro Leu Lys Val Val
        115                 120                 125


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


Phe Asp Cys Thr Lys Pro Ile Cys Cys Arg Val Tyr Ser Glu Asp Asp
145                 150                 155                 160


Ala Pro Gly Asn Thr Ser Ser Pro Cys Gly Pro Trp Gly Asn Ala Lys
                165                 170                 175


Cys Asp Pro Pro His Gln Leu Gln Gln Ser Met Met Asp Ala Ile Ala
```

```
            180                 185                 190

Ser Leu Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala His
        195                 200                 205

Asp Val Trp Leu Val Asn Lys Thr Glu Val Leu Gln Asp Phe Asn Ala
    210                 215                 220

Thr Tyr Ser Thr Met Glu Ser Thr Leu Gly Leu Val Tyr Ala Ala Leu
225                 230                 235                 240

Gly Asn His Asp Thr Ala Pro Leu Asn Leu Phe Pro Ser Thr Asn Ile
                245                 250                 255

Pro Ser Ser Tyr Asn Pro Gln Trp Ala Tyr Asp Ala Leu Ser Thr Ser
            260                 265                 270

Trp Leu Thr Leu Thr Ser Asp Asn Pro Ala Ile Ser Thr Ala Lys Glu
        275                 280                 285

Tyr Gly Ser Tyr Ser Ala Arg His Lys Asp Thr Lys Leu Arg Ile Ile
    290                 295                 300

Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ser Tyr Glu
305                 310                 315                 320

Glu Pro Met Pro Phe Asp Pro Asp Gly Gln Leu Ser Trp Leu Ile Ser
                325                 330                 335

Glu Leu Ser Ala Ala Glu Ala Ala Ser Glu Arg Val Trp Leu Ile Ser
            340                 345                 350

His Ile Pro Ser Gly Asn Ser Asp His Phe Arg Asp His Ser His Tyr
        355                 360                 365

Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr Ile Ala Gly Leu Phe
    370                 375                 380

Phe Gly His Thr His Thr Asp Glu Phe Gln Val Ser Tyr Ser Asp Tyr
```

```
385                 390                 395                 400


Ala His Arg Ser Trp Asp Thr Ala Thr Ala Met Gly Tyr Val Ala Pro
                405                 410                 415


Ser Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Val Tyr Glu Ile
            420                 425                 430


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


Ile Ser Asp Ser Ser Glu Pro Lys Trp Met Pro Tyr Tyr Ser Ala Lys
    450                 455                 460


Lys Asp Tyr Gly Ser Arg Leu Asp Val Pro Val Gly Glu Asp Met Glu
465                 470                 475                 480


Leu Thr Pro Ala Phe Trp His Asn Val Thr Val Gly Met Glu Lys Asp
                485                 490                 495


Pro Ser Leu Phe Arg Asp Phe Trp Ala Arg Arg Thr Arg Gly Phe Glu
            500                 505                 510


Val Pro Gly Cys Glu Gly Asp Cys Val Ser Lys Glu Ile Cys Ala Leu
        515                 520                 525


Arg Gly Ala Asp Ala Gln Tyr Ser Cys Val Glu Ala Thr Pro Gly Phe
    530                 535                 540


Ser Phe Glu Lys Arg Gly Glu Arg Thr Val Leu Leu Glu Lys Arg Phe
545                 550                 555                 560


Gln Pro Glu Cys Asn His Ala Gly Met Ala Pro Leu Leu Ala Lys Ile
                565                 570                 575


Ala His Arg Ala Ser Leu Ala Arg Glu Met Glu Ala
            580                 585


<210>  255
```

```
<211>  590
<212>  PRT
<213>  Penicillium bialowiezense

<400>  255

Glu Val Leu Leu Glu Asn Ser Ile Ala Ser Leu Trp Asp Asp Phe Lys
1               5                   10                  15


Asn Ala Val Asp Cys Ala Ser Cys Gln Ala Leu Leu Gly Gly Leu Lys
            20                  25                  30


Leu Val Ser Gly Phe Gly Glu Asp Phe Met Ile Asp Val Leu Thr Gly
        35                  40                  45


Ile Cys Asp Ile Ser Lys Ala Glu Asp Ser Asp Val Cys Glu Gly Ile
    50                  55                  60


Ile Lys Lys Glu Gly Pro Ala Leu His Asp Ala Phe Gln Ala Leu His
65                  70                  75                  80


Ile Gly Ser Asn Ser Thr Gln Thr Met Cys Ala Ser Leu Ile Gly Leu
                85                  90                  95


Cys Gln Tyr Pro Glu Val Arg Ala His Ser Leu Ser Phe Pro Ser Pro
            100                 105                 110


Lys Pro Asn Lys Val Lys Pro Pro Pro Ser Gly Lys Pro Pro Ile Lys
        115                 120                 125


Val Val His Phe Ser Asp Thr His Val Asp Leu Tyr Tyr Glu Thr Gly
    130                 135                 140


Ser Ser Tyr Glu Cys Ser Lys Pro Ile Cys Cys Arg Val Phe Glu Asp
145                 150                 155                 160


Lys Tyr Ala Pro Gly Ile Thr Lys Thr Pro Cys Gly Pro Phe Gly Asn
                165                 170                 175


Pro Arg Cys Asp Pro Pro Leu Lys Leu Gln Glu Ser Met Asn Ala Ala
            180                 185                 190
```

```
Ile Ala Asp Ile Asn Pro Glu Phe Ser Ile Tyr Thr Gly Asp Val Val
        195                 200                 205

Ala His Asp Val Trp Leu Val Asn Gln Ala Glu Ala Leu Glu Ser Phe
    210                 215                 220

Asn Ser Thr Tyr Ser Gln Met Glu Lys Ser Leu Gly Met Val Tyr Ala
225                 230                 235                 240

Ala Ile Gly Asn His Asp Thr Ala Pro Leu Asn Leu Phe Pro Ser Ser
                245                 250                 255

Ile Val Pro Asp Gly Asp Asn Gln Trp Ala Tyr Asn Ala Leu Ala Glu
            260                 265                 270

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

Tyr Gly Ser Tyr Ser Ala Ile His Pro Asp Ser Asn Leu Arg Ile Ile
    290                 295                 300

Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Phe Asn Phe Tyr Met Tyr Gln
305                 310                 315                 320

Glu Pro Met Glu Lys Asp Pro Asn Gly Gln Phe Glu Trp Leu Ile Lys
                325                 330                 335

Glu Leu Gln Ala Ala Glu Asp Ala Gly Gln Arg Ala Trp Leu Ile Ser
            340                 345                 350

His Ile Pro Pro Gly Val Ala Asp His Phe His Asp Tyr Ser His Tyr
        355                 360                 365

Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr Ile Ala Gly Leu Phe
    370                 375                 380

Tyr Gly His Thr His Met Asp Glu Phe Gln Ile Ala Tyr Ser Asn Tyr
385                 390                 395                 400
```

```
Lys Asn Arg Asn His Glu Thr Ala Thr Ala Met Gly Tyr Ile Ala Pro
                405                 410                 415

Ala Met Thr Pro Thr Glu Gly Pro Pro Ser Phe Arg Val Tyr Glu Ile
            420                 425                 430

Asp Pro Glu Thr Phe Gly Val Leu Asp Tyr Thr Gln Tyr Ile Ala Asn
        435                 440                 445

Ile Ser Asp Pro Thr Tyr Gln Glu Lys Pro Gln Trp Leu Pro Tyr Tyr
    450                 455                 460

Ser Ala Lys Ala Asp Tyr Gly Ser Lys Leu Ser Pro Pro Val Thr Asp
465                 470                 475                 480

Pro Lys Ile Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val Ala
                485                 490                 495

Met Glu Asn Glu Pro Ser Ile Phe Gln Glu Phe Trp Ala Arg Arg Val
            500                 505                 510

Arg Gly Tyr Lys Val Thr Asp Cys Asn Gly Asp Cys Met Lys Thr Glu
        515                 520                 525

Ile Cys Ala Leu Arg Ala Ala Asp Ala Gln Phe Asn Cys Val Lys Pro
    530                 535                 540

Lys Pro Gly Phe Asn Phe Ser Lys Arg Asp Gly Lys Asp Thr Leu Ala
545                 550                 555                 560

Glu Gln Pro His His Cys Asp His Ala Gly Leu Ala Pro Leu Leu Gly
                565                 570                 575

Lys Ile Ala Tyr Arg Ala Arg Ile Ala Arg Glu Met Glu Ala
            580                 585                 590


<210>  256
<211>  590
```

```
<212>  PRT
<213>  Penicillium sclerotiorum

<400>  256

Ser Ala Asp Ser Trp Ile Ser Ser Ile Trp Asp Asp Phe Lys Glu Ala
1               5                   10                  15


Val Asp Cys Gly Ser Cys Gln Ala Leu Leu Gly Gly Leu Lys Val Val
            20                  25                  30


Ala Ala Phe Gly Glu Ser Phe Met Glu Asp Val Leu Ile Gly Val Cys
        35                  40                  45


Asp Ile Ser Gly Ala Glu Asp Ser Asp Val Cys Ala Gly Val Ile Ala
    50                  55                  60


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


Ser His Thr Ala Lys Thr Phe Cys Ala Thr Leu Val Gly Leu Cys Lys
                85                  90                  95


Tyr Pro Glu Val Arg Pro Tyr Asn Leu Thr Phe Pro Ser Pro Lys Pro
            100                 105                 110


Pro Thr Ser Arg Pro Pro Pro Ser Gly Lys Thr Pro Ile Lys Val Val
        115                 120                 125


His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly Ser Asn
    130                 135                 140


Tyr Asp Cys Ser Lys Pro Ile Cys Cys Arg Ala Tyr Thr Glu Asp Asp
145                 150                 155                 160


Ala Pro Gly Asn Thr Ser Ser Pro Cys Gly Pro Trp Gly Asn Thr Asn
                165                 170                 175


Cys Asp Pro Pro His Arg Leu Gln Lys Ser Met Asn Ala Ala Ile Ala
            180                 185                 190
```

```
Asp Leu Lys Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala His
        195                 200                 205


Asp Val Trp Leu Val Asn Lys Ser Glu Ala Leu Gln Asp Phe Asn Ala
    210                 215                 220


Thr Tyr Gly Ala Met Glu Asp Ser Leu Gly Arg Val Tyr Ala Ala Leu
225                 230                 235                 240


Gly Asn His Asp Ala Ala Pro Leu Asn Leu Phe Pro Ser Asn Gln Ile
                245                 250                 255


Pro Ser Glu Tyr Asn Pro Gln Trp Ala Tyr Asp Ala Leu Ala Ala Asp
            260                 265                 270


Trp Met Ala Leu Thr Asp Ile Pro Ser Val Glu Thr Ala Asn Glu His
        275                 280                 285


Gly Ser Tyr Ser Ala Ile His Pro Asp Ser Asn Leu Arg Ile Ile Ser
    290                 295                 300


Tyr Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ser Tyr Thr Glu
305                 310                 315                 320


Pro Met Glu Tyr Asp Pro Asn Gly Gln Leu Glu Trp Leu Ile Asn Glu
                325                 330                 335


Leu His Ala Ala Glu Thr Ala Asn Gln Arg Val Trp Leu Ile Ser His
            340                 345                 350


Ile Pro Ser Gly Asn Ser Asp His Phe His Asp His Ser His Tyr Phe
        355                 360                 365


Asp Glu Ile Ile Gln Arg Tyr Glu Ala Thr Ile Ala Gly Leu Phe Phe
    370                 375                 380


Gly His Thr His Thr Asp Glu Phe Gln Ile Ser Tyr Ser Asn Tyr Ser
385                 390                 395                 400
```

```
Asn Arg Asn Trp Asp Thr Ala Thr Ala Met Gly Tyr Val Ala Pro Ser
                405                 410                 415


Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Val Tyr Glu Ile Asp
            420                 425                 430


Pro Val Thr Phe Gly Val Leu Asp Phe Met Gln Tyr Ile Ala Asn Ile
        435                 440                 445


Ser Asp Pro Ser Tyr Gln Gln Lys Pro Glu Trp Val Pro Tyr Tyr Ser
    450                 455                 460


Ala Lys Ser Asp Tyr Gly Ser Arg Leu Ser Pro Pro Val Thr Asp Ala
465                 470                 475                 480


Asp Val Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val Leu Met
                485                 490                 495


Glu Glu Asp Ser Ser Val Phe Asp Glu Phe Trp Ala Arg Arg Thr Arg
            500                 505                 510


Gly Phe Gln Val Pro Ala Cys Thr Gly Asp Cys Val Ser Asn Glu Ile
        515                 520                 525


Cys Ala Leu Arg Gly Ala Asp Gly Gln Tyr Asn Cys Phe Ile Glu Lys
    530                 535                 540


Pro Gly Phe Ser Phe Glu Lys Arg Asp Gly Thr Val Asp Glu Val Ser
545                 550                 555                 560


Trp Lys Lys Arg Phe Gln Pro Glu Cys Asn His Ala Gly Met Ala Pro
                565                 570                 575


Leu Leu Ala Lys Ile Ala His Arg Ala Ser Leu Ala Arg Glu
            580                 585                 590


<210>  257
<211>  592
<212>  PRT
```

```
<213>  Rasamsonia byssochlamydoides

<400>  257

Ser Tyr Asn Lys Arg Gly Leu Ala Gln Glu Ile Trp Asp Asp Ile Val
1               5                   10                  15


Asn Ala Val Asp Cys Ser Gly Cys Gln Val Ile Leu Thr Ala Leu Gln
            20                  25                  30


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


Val Cys Asp Ile Ser Gly Lys Glu Asp Ser Asp Val Cys Ser Gly Ile
    50                  55                  60


Ile Ser Arg Glu Gly Pro Val Leu Asp Tyr Ile Leu Gln Asn Leu Asp
65                  70                  75                  80


Ile Gly Ser His Thr Ser Asp Val Ile Cys Ala Ser Ala Phe Gly Leu
                85                  90                  95


Cys Gln Tyr Pro Ala Val Arg Ser Tyr Asn Leu Thr Phe Pro Thr Pro
            100                 105                 110


Lys Pro Asp Thr Thr Arg Pro Ala Pro Ser Gly Glu Ser Pro Ile Gln
        115                 120                 125


Val Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly
    130                 135                 140


Ser Ser Tyr Asn Cys Thr Lys Pro Ile Cys Cys Arg Pro Tyr Thr Ala
145                 150                 155                 160


Ala Asp Ala Pro Gly Asn Thr Thr Thr Pro Cys Gly Pro Tyr Gly Asn
                165                 170                 175


Thr Asn Cys Asp Ala Pro Leu Ser Leu Glu Glu Ser Met Phe Asn Ala
            180                 185                 190
```

```
Ile Lys Ala Leu Ser Pro Gln Pro Ala Phe Ser Ile Tyr Thr Gly Asp
        195                 200                 205

Val Val Ala His Asp Ile Trp Leu Val Asp Gln Asn Glu Val Ile Gln
    210                 215                 220

Asp Leu Asn Thr Thr Tyr Asp Leu Met Ala Glu Leu Gly Leu Val Tyr
225                 230                 235                 240

Ala Ala Ile Gly Asn His Asp Thr Ala Pro Val Asn Asp Leu Pro Thr
                245                 250                 255

Thr Asn Ile Pro Ser Glu Tyr Ser Thr Asn Trp Thr Tyr Glu Ala Leu
            260                 265                 270

Ala Tyr Asp Phe Thr Met Leu Thr Ser Ser Ser Ser Ala Gln Thr Ala
        275                 280                 285

Ala Asn Tyr Gly Ser Tyr Ser Ser Ile Tyr Lys Gly Ser Tyr Gly Thr
    290                 295                 300

Asp Leu Arg Ile Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Ile Asp Asn
305                 310                 315                 320

Phe Trp Ala Tyr Gln Asp Pro Met Pro Tyr Asp Pro Asp Gly Gln Leu
                325                 330                 335

Ala Trp Leu Ile Asn Glu Leu Gln Glu Ala Glu Thr Ala Gly Gln Arg
            340                 345                 350

Val Trp Ile Ile Ala His Val Pro Thr Gly Thr Ser Asp His Phe His
        355                 360                 365

Asp Tyr Ser His Tyr Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr
    370                 375                 380

Ile Ala Ala Leu Phe Tyr Gly His Thr His Ile Asp Gln Phe Gln Ile
385                 390                 395                 400
```

```
Ser Tyr Ser Asp Tyr Ser Asn Gln Ala Trp Asp Thr Ala Thr Ala Ile
                405                 410                 415


Gly Tyr Ile Met Pro Ser Leu Thr Pro Thr Ser Gly Pro Pro Thr Phe
            420                 425                 430


Arg Val Tyr Asp Val Asp Pro Lys Thr Phe Ala Val Leu Asp Phe Thr
        435                 440                 445


Asn Tyr Ile Ala Asn Ile Ser Asp Pro Ala Tyr Gln Ser Gly Pro Thr
    450                 455                 460


Trp Gln Lys Tyr Tyr Ser Ala Lys Glu Thr Tyr Gly Ala Leu Leu Ser
465                 470                 475                 480


Pro Pro Leu Thr Asp Pro Thr Ala Glu Leu Thr Pro Ala Phe Trp His
                485                 490                 495


Asn Val Thr Val Ala Phe Glu Asn Asp Asn Ala Ala Phe Gln Glu Tyr
            500                 505                 510


Trp Ala Arg Gln Thr Arg Gly Trp Asp Val Ser Ser Cys Thr Gly Ser
        515                 520                 525


Cys Ile Thr Gln Ala Ile Cys Gly Leu Arg Ala Ala Asp Ala Gln Tyr
    530                 535                 540


Asn Cys Val Thr Pro Thr Pro Gly Phe Asn Phe Ala Lys Arg Asp Ala
545                 550                 555                 560


Ser Ser Ala Thr Gln Ala Met Ala His Val Glu Lys Cys Glu Gly Ser
                565                 570                 575


Gly Leu Leu Ala Leu Leu Gly Arg Met Val Ala Asp Lys Lys Ser Ala
            580                 585                 590


<210>  258
<211>  593
<212>  PRT
<213>  Rasamsonia eburnea
```

```
<400>  258

Thr Tyr Asp Lys Arg Gly Leu Ala Gln Asp Ile Trp Asn Asp Ile Lys
1               5                   10                  15


Asn Ala Val Asp Cys Ala Gly Cys Gln Gly Ile Leu Thr Ala Leu Lys
            20                  25                  30


Gly Leu Ser Tyr Leu Gly Thr Thr Ala Phe Val Asp Val Leu Thr Glu
        35                  40                  45


Val Cys Asp Ile Ser Gly Val Glu Asp Ser Asp Val Cys Ser Gly Ile
    50                  55                  60


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


Ile Gly Ser His Thr Ser Gln Val Ile Cys Ala Ser Val Phe Gly Leu
                85                  90                  95


Cys Gln Tyr Pro Ala Val Arg Ala Tyr Asn Leu Thr Phe Pro Ser Pro
            100                 105                 110


Lys Pro Asp Lys Thr Cys Pro Glu Pro Ser Gly Glu Ser Pro Val Gln
        115                 120                 125


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


Ser Asn Tyr Asn Cys Thr Lys Pro Ile Cys Cys Arg Ser Tyr Thr Ala
145                 150                 155                 160


Glu Asp Ala Pro Gly Asn Thr Thr Thr Pro Cys Gly Pro Tyr Gly Asn
                165                 170                 175


Pro Lys Cys Asp Ala Pro Met Ser Leu Glu Glu Ser Met Phe Ala Ala
            180                 185                 190


Ile Lys Ala Leu Ser Pro Gln Pro Ala Phe Ser Ile Tyr Thr Gly Asp
```

```
        195                 200                 205

Val Val Ala His Asp Ile Trp Leu Val Asp Gln Asn Glu Val Val Glu
    210                 215                 220

Asp Leu Asn Ala Thr Tyr Asp Arg Met Ala Gly Leu Gly Leu Val Tyr
225                 230                 235                 240

Ala Ala Ile Gly Asn His Asp Thr Ala Pro Val Asn Asn Leu Pro Thr
                245                 250                 255

Ser Asn Ile Pro Ser Gln Tyr Ser Ala Asn Trp Thr Tyr Glu Ala Leu
            260                 265                 270

Glu Tyr His Phe Ser Leu Leu Thr Lys Ser Ala Ser Ala Gln Thr Ala
        275                 280                 285

Glu Asn Tyr Gly Ser Tyr Ser Ser Val Tyr Arg Gly Arg Tyr Gly Thr
    290                 295                 300

Asp Leu Arg Val Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Ile Ala Asp
305                 310                 315                 320

Phe Trp Ala Tyr Gln Asp Pro Met Leu Tyr Asp Pro Asp Gly Gln Leu
                325                 330                 335

Ala Trp Leu Ile Asn Glu Leu Gln Glu Ala Glu Thr Ala Gly Gln Arg
            340                 345                 350

Val Trp Leu Ile Ala His Val Pro Ser Gly Thr Ala Asp His Phe His
        355                 360                 365

Asp Tyr Ser His Tyr Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr
    370                 375                 380

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

Ser Tyr Ser Asp Tyr Ser Asn Arg Ala Phe Asp Thr Ala Thr Ala Ile
```

```
                405                 410                 415

Gly Tyr Ile Met Pro Ser Met Thr Pro Thr Ser Gly Pro Pro Thr Phe
            420                 425                 430

Arg Val Tyr Asp Val Asp Pro Lys Thr Phe Ala Val Leu Asp Phe Thr
        435                 440                 445

Asn Tyr Ile Ala Asn Ile Ser Asp Pro Ala Tyr Gln Ser Gly Pro Thr
    450                 455                 460

Trp Gln Lys Tyr Tyr Ser Ala Lys Glu Ala Tyr Gly Ser Leu Leu Ser
465                 470                 475                 480

Pro Pro Val Thr Asp Ala Thr Ala Glu Leu Thr Pro Ala Phe Trp His
                485                 490                 495

Asn Val Thr Val Ala Phe Glu Asn Asp Asp Thr Ala Phe Gln Glu Tyr
            500                 505                 510

Trp Ala Arg Gln Thr Arg Gly Tyr Ala Val Ser Ser Cys Thr Gly Asp
        515                 520                 525

Cys Ile Thr Gln Ala Ile Cys Gly Leu Arg Ala Gly Glu Ser Gln His
    530                 535                 540

Asn Cys Val Thr Pro Thr Pro Gly Phe Asn Phe Ala Lys Arg Asp Val
545                 550                 555                 560

Ser Thr Asp Gly Gln Ala Leu Pro His Ile Glu Lys Cys Glu Gly Ser
                565                 570                 575

Gly Leu Met Ala Leu Leu Ala Lys Met Val Ala Ser Asn Arg Gln Ser
            580                 585                 590

Ser


<210>  259
```

```
<211>  593
<212>  PRT
<213>  Penicillium brefeldianum

<400>  259

Gly Ala Ile Glu Asn Trp Ala Ala Thr Ile Trp Glu Asp Phe Lys Glu
1               5                   10                  15


Ala Val Asp Cys Gly Ser Cys Gln Val Leu Leu Gly Gly Leu Lys Leu
            20                  25                  30


Val Ala Asp Phe Gly Glu Gly Phe Leu Gly Asp Val Leu Thr Gly Val
        35                  40                  45


Cys Asp Ile Ser Lys Ala Glu Asp Arg Asp Val Cys Ala Gly Val Val
    50                  55                  60


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


Gly Ser His Thr Ala Lys Thr Leu Cys Ser Ala Leu Val Gly Leu Cys
                85                  90                  95


Asp Phe Pro Asp Val Arg Pro Phe Asp Leu Thr Phe Pro Ser Pro Lys
            100                 105                 110


Pro Ala Thr Ser Arg Pro Pro Pro Ser Gly Lys Pro Pro Ile Lys Val
        115                 120                 125


Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly Ser
    130                 135                 140


Asn Tyr Asp Cys Ser Lys Pro Ile Cys Cys Arg Val Tyr Thr Asp Lys
145                 150                 155                 160


Asp Ala Pro Gly Thr Thr Asp Lys Pro Cys Gly Pro Trp Gly His Pro
                165                 170                 175


Lys Cys Asp Pro Pro His Gln Leu Gln Glu Ser Met Met Thr Ala Ile
            180                 185                 190
```

```
Ala Asn Leu Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala
        195                 200                 205

His Asp Val Trp Leu Val Asn Lys Asp Glu Val Leu Gln Asp Leu Asn
    210                 215                 220

Ala Thr Tyr Gly Ala Met Glu Asn His Leu Gly Leu Val Tyr Ala Ala
225                 230                 235                 240

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

Val Pro Ser Lys Tyr Asn Pro Gln Trp Ala Tyr Asp Ala Leu Thr Ala
            260                 265                 270

Asp Trp Met Thr Leu Thr Gly Leu Asp Ser Val Gln Asn Ala Asn Lys
        275                 280                 285

Tyr Gly Ser Tyr Ser Ala Val His Pro Asn Ser Lys Leu Arg Ile Ile
    290                 295                 300

Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ser Tyr Thr
305                 310                 315                 320

Glu Pro Met Glu Tyr Asp Pro Asn Gly Gln Leu Thr Trp Ile Ile Asn
                325                 330                 335

Glu Leu Gln Ala Ala Glu Thr Ala Gly Gln Arg Val Trp Leu Ile Ser
            340                 345                 350

His Ile Pro Ser Gly Asp Val Asp His Phe Arg Asp His Ser His Tyr
        355                 360                 365

Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr Ile Ala Gly Leu Phe
    370                 375                 380

Phe Gly His Thr His Thr Asp Glu Phe Gln Ile Ala Tyr Ser Asp Tyr
385                 390                 395                 400
```

```
Asn Asn Arg Asn Trp Asp Thr Ala Thr Ala Met Gly Tyr Val Ala Pro
                405                 410                 415

Ser Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Val Tyr Asp Ile
            420                 425                 430

Asp Pro Glu Thr Phe Gly Val Met Asp Tyr Thr Gln Tyr Ile Ala Asn
        435                 440                 445

Ile Ser Asp Pro Ser Phe Gln Thr Lys Gln Glu Trp Val Pro Tyr Tyr
    450                 455                 460

Thr Ala Lys Lys Asp Tyr Gly Ala Lys Leu Ser Pro Pro Pro Ala Pro
465                 470                 475                 480

Thr Gly Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val Ala Met
                485                 490                 495

Glu Lys Asp Ser Ser Val Phe Glu Ala Phe Trp Ala Arg Arg Thr Arg
            500                 505                 510

Gly Phe Ser Ile Pro Ala Cys Thr Gly Asp Cys Val Lys Asn Glu Ile
        515                 520                 525

Cys Ala Leu Arg Gly Ala Asp Ala Gln Tyr Ser Cys Val Lys Arg Thr
    530                 535                 540

Pro Gly Phe Ser Phe Ser Lys Arg Asp Glu Ile Glu Ser Asp Pro Leu
545                 550                 555                 560

Leu Ser Lys Arg Phe Gln Pro Glu Cys Asn His Ala Gly Met Ala Pro
                565                 570                 575

Leu Leu Ala Lys Ile Ala His Lys Ala Asn Val Ala Lys Trp Asn Gly
            580                 585                 590

Glu
```

```
<210>  260
<211>  593
<212>  PRT
<213>  Penicillium adametzii

<400>  260

Ser Val Asp Ser Trp Ile Thr Thr Ile Trp Asp Asp Phe Lys Glu Ala
1               5                   10                  15


Val Asp Cys Ala Ser Cys Gln Ala Leu Leu Gly Gly Leu Lys Leu Val
            20                  25                  30


Ala Val Phe Gly Glu Ser Phe Met Glu Asp Val Ile Thr Gly Val Cys
        35                  40                  45


Ser Ile Ser Gly Ala Glu Asp Ser Asp Val Cys Ala Gly Val Ile Ala
    50                  55                  60


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


Ser His Thr Ala Lys Thr Phe Cys Ala Ser Leu Val Gly Leu Cys Asp
                85                  90                  95


Tyr Pro Ala Val Arg Pro Tyr Ser Leu Thr Phe Pro Ser Pro Lys Pro
            100                 105                 110


Pro Thr Thr Arg Pro Pro Pro Ser Gly Lys Ser Pro Ile Lys Val Val
        115                 120                 125


His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly Ser Asn
    130                 135                 140


Tyr Asp Cys Ser Lys Pro Ile Cys Cys Arg Ala Tyr Thr Glu Asn Asp
145                 150                 155                 160


Ala Pro Gly Asn Thr Ser Ser Pro Cys Gly Pro Trp Gly Asn Ser Lys
                165                 170                 175
```

```
Cys Asp Pro Pro His Arg Leu Gln Glu Ser Met Asn Glu Ala Ile Ala
            180                 185                 190


Asp Leu Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala His
        195                 200                 205


Asp Val Trp Leu Val Asp Lys Ser Glu Ala Leu Gln Asp Phe Asn Ala
    210                 215                 220


Thr Phe Ser Ala Met Glu Thr Leu Gly Arg Val Tyr Ala Ala Leu Gly
225                 230                 235                 240


Asn His Asp Ala Ala Pro Leu Asn Leu Phe Pro Ser Asn Gln Ile Pro
                245                 250                 255


Ser Gln Tyr Asn Pro Gln Trp Ala Tyr Asp Thr Leu Ala Ser Asp Trp
            260                 265                 270


Met Gly Leu Thr Gly Ile Gln Ser Val Glu Thr Ala Asn Glu Tyr Gly
        275                 280                 285


Ser Tyr Ser Ala Ile His Pro Asn Ser Asn Leu Arg Ile Ile Ser Tyr
    290                 295                 300


Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ser Tyr Thr Glu Pro
305                 310                 315                 320


Met Glu Tyr Asp Pro Asn Ser Gln Leu Gln Trp Leu Ile Asn Glu Leu
                325                 330                 335


His Glu Ala Glu Leu Ala Asn Gln Arg Val Trp Leu Ile Ser His Ile
            340                 345                 350


Pro Ser Gly Asp Pro Asp His Phe His Asp His Ser His Tyr Phe Asp
        355                 360                 365


Gln Ile Val Gln Arg Tyr Asp Ala Thr Ile Ala Ala Leu Phe Phe Gly
    370                 375                 380
```

```
His Thr His Thr Asp Gln Phe Gln Ile Ser Tyr Ser Ser Tyr Gln Asn
385                 390                 395                 400


Arg Thr Trp Asp Lys Ala Thr Ala Met Gly Tyr Val Ala Pro Ser Met
                405                 410                 415


Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Val Tyr Glu Ile Asp Pro
            420                 425                 430


Val Thr Phe Gly Val Leu Asp Phe Thr Gln Tyr Ile Ala Asn Ile Ser
        435                 440                 445


Asp Pro Thr Gln Thr Lys Pro Lys Trp Val Pro Tyr Tyr Ser Ala Lys
    450                 455                 460


Lys Asp Tyr Gly Ser His Leu Asp Pro Pro Val Thr Asp Ala His Ala
465                 470                 475                 480


Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val Ser Met Glu Asn
                485                 490                 495


Asp Asn Ser Val Phe Gln Asp Phe Trp Ala Arg Arg Thr Arg Gly Phe
            500                 505                 510


Gln Val Pro Asp Cys Thr Gly Asp Cys Ser Ser Ser Glu Ile Cys Ala
        515                 520                 525


Leu Arg Gly Ala Asp Ala Gln Tyr Asn Cys Phe Val Glu Lys Pro Gly
    530                 535                 540


Phe Ser Phe Glu Lys Arg Asp Val Gln Glu Ser Asp Glu Glu Met Trp
545                 550                 555                 560


Lys Lys Arg Phe Gln Pro Glu Cys Asn His Ala Gly Met Ala Pro Leu
                565                 570                 575


Leu Ala Lys Ile Ala Tyr Arg Ala Ser Leu Glu Arg Glu Gln Lys Gly
            580                 585                 590
```

```
Lys




<210>  261
<211>  594
<212>  PRT
<213>  Rasamsonia brevistipitata

<400>  261

Thr Ser Leu Thr His Asp Lys Arg Asp Leu Ala Gln Glu Ile Trp Asn
1               5                   10                  15


Asp Ile Lys Asn Ala Ala Thr Cys Ala Gly Cys Gln Val Ile Leu Thr
            20                  25                  30


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


Leu Thr Glu Val Cys Asp Ile Ser Gly Leu Glu Asp Pro Asp Val Cys
    50                  55                  60


Ser Gly Ile Ile Ser Arg Glu Gly Pro Val Leu Asp Tyr Ile Leu Gln
65                  70                  75                  80


His Leu Asp Ile Gly Ser His Thr Ser Asp Val Leu Cys Ala Ser Ala
                85                  90                  95


Phe Gly Leu Cys Gln Tyr Pro Ala Val Arg Pro Tyr Asn Leu Thr Phe
            100                 105                 110


Pro Ser Pro Lys Pro Asp Thr Thr Arg Pro Ala Pro Ser Gly Glu Ser
        115                 120                 125


Pro Ile Gln Val Val His Ile Ser Asp Thr His Val Asp Leu Ser Tyr
    130                 135                 140


Glu Thr Gly Ser Ser Trp Asn Cys Thr Lys Pro Ile Cys Cys Arg Pro
145                 150                 155                 160
```

```
Tyr Thr Ala Glu Asp Ala Pro Gly Asn Thr Thr Thr Pro Cys Gly Pro
                165                 170                 175

Tyr Gly Asp Thr His Cys Asp Ala Pro Met Ser Leu Gln Glu Ser Met
            180                 185                 190

Ile Ala Ala Ile Gln Ala Leu Arg Pro Gln Pro Ala Phe Ser Ile Tyr
        195                 200                 205

Thr Gly Asp Val Val Ala His Asp Ile Trp Leu Val Asp Gln Asn Glu
    210                 215                 220

Val Ile Glu Asp Phe Asn Ala Thr Tyr Asn Arg Met Ala Glu Leu Gly
225                 230                 235                 240

Leu Val Tyr Ala Ala Ile Gly Asn His Asp Ser Ala Pro Val Asn Asp
                245                 250                 255

Leu Pro Ala Ser Asn Ile Pro Ser Gln Tyr Ser Val Asn Trp Thr Tyr
            260                 265                 270

Glu Ala Leu Ala Tyr Asp Phe Ser Met Leu Thr Gly Ser Ala Ser Ala
        275                 280                 285

Gln Glu Ala Glu Asn Tyr Gly Ser Tyr Ser Ser Ile Tyr Lys Gly Ser
    290                 295                 300

Asn Gly Thr Asp Leu Arg Val Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr
305                 310                 315                 320

Val Thr Asn Phe Trp Ala Phe Gln Asp Pro Met Pro Tyr Asp Pro Asp
                325                 330                 335

Gly Gln Leu Ala Trp Leu Ile Asn Glu Leu Gln Glu Ala Glu Thr Ala
            340                 345                 350

Gly Gln Arg Ala Trp Leu Ile Ala His Val Pro Thr Gly Thr Gly Asp
        355                 360                 365
```

```
His Phe His Asp Tyr Ser His Tyr Phe Asp Gln Ile Val Gln Arg Tyr
    370                 375                 380


Glu Ala Thr Ile Ala Ala Leu Phe Phe Gly His Thr His Gln Asp Glu
385                 390                 395                 400


Phe Gln Ile Ala Tyr Ser Asn Tyr Ser Asn Gln Asn Phe Asp Thr Ala
                405                 410                 415


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


Pro Ser Phe Arg Val Tyr Asp Ile Asp Pro Lys Thr Phe Gly Val Leu
        435                 440                 445


Asp Phe Thr Asn Tyr Ile Ala Asn Ile Ser Asp Pro Ala Tyr Gln Ser
    450                 455                 460


Gly Pro Thr Trp Gln Lys Tyr Tyr Ser Ala Lys Glu Ala Tyr Gly Thr
465                 470                 475                 480


Leu Leu Ser Pro Ala Val Thr Asp Pro Thr Ala Glu Leu Thr Pro Ala
                485                 490                 495


Phe Trp His Asn Leu Thr Val Val Phe Glu Asn Asp Asn Ala Thr Phe
            500                 505                 510


Gln Glu Tyr Trp Thr Arg Lys Thr Arg Gly His Ala Val Ser Asn Cys
        515                 520                 525


Thr Gly Ser Cys Ile Thr Gln Ser Ile Cys Gly Met Arg Ala Ala Asp
    530                 535                 540


Ala Gln Tyr Asn Cys Val Thr Pro Thr Pro Gly Leu Ser Phe Ala Lys
545                 550                 555                 560


Arg Asp Ala Glu Thr Ser Thr Pro Glu Pro His Ile Glu Pro Cys Glu
                565                 570                 575
```

```
Gly Ser Gly Leu Met Ser Leu Leu Gly Arg Met Val Ala Gln Gly Lys
            580                 585                 590


Ser Ser




<210>  262
<211>  594
<212>  PRT
<213>  Penicillium scabrosum

<400>  262

Glu Thr Thr Leu Glu Lys Ser Ile Ser Ser Ile Trp Glu Asp Phe Lys
1               5                   10                  15


Asn Ala Val Asp Cys Gly Ser Cys Gln Val Leu Leu Gly Gly Leu Lys
            20                  25                  30


Phe Val Ser Gly Phe Gly Glu Asn Phe Met Ile Asp Val Leu Thr Gly
        35                  40                  45


Leu Cys Asp Ile Ser Lys Ala Glu Asp Ser Asp Val Cys Glu Gly Ile
    50                  55                  60


Ile Lys Lys Glu Gly Pro Ala Leu His Asp Ala Phe Gln Ala Leu Lys
65                  70                  75                  80


Ile Gly Ser His Ser Thr Lys Thr Met Cys Ala Asn Leu Ile Gly Leu
                85                  90                  95


Cys Gln Tyr Pro Glu Val Arg Pro Asn Thr Leu Ser Phe Pro Ser Pro
            100                 105                 110


Lys Pro Lys Asp Val Arg Pro Thr Thr Ser Gly Lys Pro Pro Ile Lys
        115                 120                 125


Val Val His Phe Ser Asp Thr His Val Asp Leu Leu Tyr Glu Thr Gly
    130                 135                 140


Ser Asn Tyr Glu Cys Thr Lys Pro Ile Cys Cys Arg Val Phe Glu Asp
```

```
145                 150                 155                 160


Lys Asp Ala Pro Gly Ile Thr Lys Asn Pro Cys Gly Pro Phe Gly Asn
                165                 170                 175


Pro Lys Cys Asp Pro Pro Gln Ala Leu Gln Glu Ser Met Asn Ala Ala
            180                 185                 190


Ile Ala Glu Ile Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val
        195                 200                 205


Ser His Asp Val Trp Leu Val Asn Gln Glu Glu Ala Leu Glu Ser Phe
    210                 215                 220


Asn Ser Thr Tyr Ser Gln Ile Glu Lys Ser Leu Gly Met Val Tyr Ala
225                 230                 235                 240


Ala Ile Gly Asn His Asp Thr Ala Pro Leu Asn Leu Phe Pro Ser Lys
                245                 250                 255


Asn Gln Pro Asp Gly Asn Asn Gln Trp Ala Tyr Asp Ala Leu Ala Glu
            260                 265                 270


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


Tyr Gly Ser Tyr Ser Ala Ile His Pro Asn Ser Asn Leu Arg Ile Ile
    290                 295                 300


Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Phe Asn Phe Tyr Met Tyr Gln
305                 310                 315                 320


Glu Pro Ile Glu Lys Asp Pro Asn Gly Gln Phe Glu Trp Leu Ile Lys
                325                 330                 335


Glu Leu Gln Ala Ala Glu Asp Ala Gly Gln Arg Ala Trp Leu Ile Ser
            340                 345                 350


His Ile Pro Ser Gly Val Ala Asp His Phe His Asp His Ser Gln Tyr
```

```
        355                 360                 365

Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr Ile Ala Gly Met Phe
    370                 375                 380

Tyr Gly His Thr His Met Asp Glu Phe Gln Ile Ala Tyr Ser Asp Tyr
385                 390                 395                 400

Lys Asn Arg Asn Trp Glu Thr Ala Thr Ala Met Gly Tyr Ile Ala Pro
                405                 410                 415

Ala Met Thr Pro Thr Glu Gly Pro Pro Ser Phe Arg Val Tyr Glu Ile
            420                 425                 430

Asp Pro Asp Thr Phe Gly Val Leu Asp Phe Thr Gln Tyr Ile Ala Asn
        435                 440                 445

Ile Ser Asp Pro Ala Tyr Gln Lys Lys Pro Glu Trp Val Pro Tyr Tyr
    450                 455                 460

Ser Ala Lys Ala Asp Tyr Gly Ser Lys Leu Ser Pro Pro Val Thr Asp
465                 470                 475                 480

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

Met Glu Arg Asp Glu Ser Val Phe Gln Asp Phe Trp Ala Arg Arg Ser
            500                 505                 510

Arg Gly Tyr Asn Val Thr Ala Cys Thr Gly Asp Cys Met Lys Met Glu
        515                 520                 525

Leu Cys Thr Leu Arg Ala Ala Asp Ala Gln Tyr Asn Cys Val Lys Pro
    530                 535                 540

Lys Pro Gly Phe Asn Phe Ser Lys Arg Asp Gly Glu Leu Gly Gly Leu
545                 550                 555                 560

Leu Glu Gln Glu Ser His Ser Asn Cys Asp His Ala Gly Leu Ala Thr
```

```
                565                 570                 575


Leu Leu Gly Lys Ile Ala His Arg Ala Arg Val Ala Arg Lys Ile Glu
            580                 585                 590


Glu Ala




<210>  263
<211>  594
<212>  PRT
<213>  Penicillium manginii

<400>  263

Ser Ala Asp Asp Trp Ile Thr Thr Ile Trp Asp Asp Phe Lys Asn Ala
1               5                   10                  15


Val Asp Cys Phe Ser Cys Gln Ala Leu Leu Gly Gly Leu Lys Leu Val
            20                  25                  30


Ser Gly Leu Gly Glu Ser Phe Met Glu Asp Val Ile Thr Gly Val Cys
        35                  40                  45


Ser Ile Ser Gly Ala Glu Asp Asn Asp Val Cys Ala Gly Val Ile Ala
    50                  55                  60


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


Ser His Thr Ala Lys Thr Phe Cys Ala Thr Leu Thr Gly Leu Cys Glu
                85                  90                  95


Phe Pro Lys Val Arg Pro Tyr Asp Ile Ser Phe Pro Ser Pro Lys Pro
            100                 105                 110


Ser Thr Thr Arg Pro Pro Pro Ser Gly Glu Ala Pro Ile Lys Val Val
        115                 120                 125


His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Glu Gly Ser Asn
    130                 135                 140
```

```
Tyr Glu Cys Ser Lys Pro Ile Cys Cys Arg Ala Tyr Thr Glu Lys Asp
145                 150                 155                 160

Ala Pro Gly Asn Thr Thr Ser Pro Cys Gly Pro Trp Gly Asn Ser Lys
                165                 170                 175

Cys Asp Pro Pro His Arg Leu Gln Glu Ser Met Met Ser Ala Ile Ala
            180                 185                 190

Asp Ile Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala His
        195                 200                 205

Asp Val Trp Leu Val Asn Lys Thr Glu Val Leu Gln Asp Leu Asn Ala
    210                 215                 220

Thr Tyr Ser Ser Ile Glu Asn His Leu Gly Leu Val Tyr Ala Ala Leu
225                 230                 235                 240

Gly Asn His Asp Ala Ala Pro Leu Asn Leu Phe Pro Ser Asp Lys Ile
                245                 250                 255

Pro Ser Gln Tyr Asn Pro Gln Trp Ala Tyr Asp Ala Leu Ala Glu Asp
            260                 265                 270

Trp Leu Thr Leu Thr Gly Ile Pro Ser Val Gln Lys Ala Ser Glu Tyr
        275                 280                 285

Gly Ser Tyr Ser Ala Val His Pro Gly Ser Lys Leu Arg Ile Ile Ser
    290                 295                 300

Tyr Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ser Tyr Thr Glu
305                 310                 315                 320

Pro Met Glu Phe Asp Pro Asn Lys Gln Leu Asp Trp Leu Ile Ala Gln
                325                 330                 335

Leu Gln Glu Ala Glu Asp Ala Lys Gln Arg Val Trp Leu Ile Ser His
            340                 345                 350
```

```
Ile Pro Thr Gly Asn Ser Asp His Phe Arg Asp His Ser His Tyr Phe
        355                 360                 365

Asp Gln Ile Ile Gln Arg Tyr Asp Ala Thr Ile Ala Ala Leu Phe Phe
    370                 375                 380

Gly His Thr His Thr Asp Glu Phe Gln Ile Ser Tyr Ser Asn Tyr Lys
385                 390                 395                 400

Asn Arg Asn Trp Asp Thr Ala Thr Ala Met Gly Tyr Val Ala Pro Ser
                405                 410                 415

Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Val Tyr Glu Ile Asp
            420                 425                 430

Pro Val Thr Phe Gly Val Met Asp Phe Thr Gln Tyr Ile Ala Asn Ile
        435                 440                 445

Thr Asp Pro Ser Leu Gln Thr Glu Pro Glu Trp Lys Pro Tyr Tyr Ser
    450                 455                 460

Ala Lys Ala Asp Tyr Gly Ser Lys Leu Ser Pro Ala Ile Lys Asp Pro
465                 470                 475                 480

Gly Ile Glu Leu Thr Pro Gly Phe Trp His Asn Val Thr Val Ala Met
                485                 490                 495

Glu Lys Asp Ala Thr Val Phe Gln Asp Phe Trp Ser Arg Arg Thr Arg
            500                 505                 510

Gly Phe Asn Val Pro Gly Cys Thr Gly Asp Cys Ile Ser Asn Glu Ile
        515                 520                 525

Cys Ala Leu Arg Gly Ala Asp Ala Gln Tyr Ser Cys Tyr Lys Gln Ala
    530                 535                 540

Pro Gly Phe Ser Phe Glu Lys Arg Asp Gly Ser Gly Val Pro Tyr Leu
545                 550                 555                 560
```

```
Ser Glu Glu Ser Phe Gln Gln Pro Glu Cys Asn His Ala Gly Met Ala
                565                 570                 575


Pro Leu Phe Ala Lys Ile Ser His Arg Ala Lys Leu Ala Arg Glu Arg
            580                 585                 590


Gly Glu




<210>  264
<211>  594
<212>  PRT
<213>  Penicillium emersonii

<400>  264

Ser Ala Pro Tyr Asp Lys Arg Asp Leu Ala Gln Glu Ile Trp Asp Asp
1               5                   10                  15


Ile Lys Asn Ala Val Asp Cys Ala Gly Cys Gln Val Val Leu Thr Ala
            20                  25                  30


Leu Lys Gly Val Ala Asp Leu Gly Thr Thr Ala Leu Val Asp Val Leu
        35                  40                  45


Thr Glu Val Cys Asn Ile Ser Gly Lys Glu Asp Ser Asp Val Cys Ser
    50                  55                  60


Gly Ile Ile Ser Arg Glu Gly Pro Val Leu Asp Tyr Val Leu Gln His
65                  70                  75                  80


Leu Asp Ile Gly Ser His Thr Ser Gln Val Ile Cys Ala Ser Ala Phe
                85                  90                  95


Gly Leu Cys Gln Tyr Pro Glu Val Arg Pro Tyr Asn Leu Thr Phe Pro
            100                 105                 110


Lys Pro Lys Pro Asn Thr Thr Arg Pro Glu Pro Ser Gly Glu Ser Pro
        115                 120                 125
```

```
Ile Gln Val Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu
    130                 135                 140


Thr Gly Ser Asn Tyr Asn Cys Thr Lys Pro Ile Cys Cys Arg Pro Tyr
145                 150                 155                 160


Thr Ala Glu Asp Ala Pro Gly Asn Thr Thr Thr Pro Cys Gly Pro Tyr
                165                 170                 175


Gly Asn Thr Lys Cys Asp Ala Pro Leu Ser Leu Glu Glu Ser Met Phe
            180                 185                 190


Ala Ala Ile Lys Ala Leu Asn Pro Gln Pro Ala Phe Ser Ile Tyr Thr
        195                 200                 205


Gly Asp Val Val Ala His Asp Ile Trp Leu Val Asp Gln Asn Glu Val
    210                 215                 220


Ile Glu Asp Leu Asn Ala Thr Tyr Asp Arg Met Ala Gly Leu Gly Leu
225                 230                 235                 240


Val Tyr Ala Ala Ile Gly Asn His Asp Thr Ala Pro Val Asn Asp Leu
                245                 250                 255


Pro Thr Ser Asn Ile Pro Ser Glu Tyr Ser Ala Asn Trp Thr Tyr Glu
            260                 265                 270


Ala Leu Ser Tyr Asp Phe Thr Met Leu Thr Gln Ser Ala Ser Ala Gln
        275                 280                 285


Thr Ala Ala Asn Tyr Gly Ser Tyr Ser Ala Ile Tyr Pro Gly Ser Tyr
    290                 295                 300


Gly Thr Asp Leu Arg Val Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Val
305                 310                 315                 320


Asp Asn Phe Trp Ala Tyr Gln Asp Pro Met Glu Phe Asp Pro Asp Gly
                325                 330                 335
```

```
Gln Leu Ala Trp Leu Ile Asn Glu Leu Gln Glu Ala Glu Thr Ala Gly
            340                 345                 350


Gln Arg Val Trp Ile Ile Ala His Val Pro Thr Gly Thr Ser Asp His
        355                 360                 365


Phe His Asp Tyr Ser His Tyr Phe Asp Gln Ile Val Gln Arg Tyr Glu
    370                 375                 380


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


Gln Ile Ser Tyr Ser Asn Tyr Ser Asn Arg Ala Phe Asp Thr Ala Thr
                405                 410                 415


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


Thr Phe Arg Val Tyr Asp Val Asp Pro Lys Thr Phe Ala Val Leu Asp
        435                 440                 445


Phe Thr Asn Tyr Ile Ala Asn Ile Ser Asp Pro Ala Phe Gln Ser Gly
    450                 455                 460


Pro Ser Trp Gln Lys Tyr Tyr Ser Ala Lys Glu Thr Tyr Gly Ser Leu
465                 470                 475                 480


Leu Ser Pro Pro Val Thr Asp Pro Thr Ala Glu Leu Thr Pro Ala Phe
                485                 490                 495


Trp His Asn Val Thr Val Ala Phe Glu Gln Asp Asn Ala Thr Phe Gln
            500                 505                 510


Glu Tyr Trp Ala Arg Gln Thr Arg Gly Tyr Asp Val Ser Ser Cys Thr
        515                 520                 525


Gly Ser Cys Ile Thr Gln Ala Ile Cys Gly Leu Arg Ala Gly Asp Ala
    530                 535                 540
```

```
Gln Tyr Asn Cys Val Thr Pro Thr Pro Gly Phe Asn Phe Ala Lys Arg
545                 550                 555                 560


Asp Thr Ser Asn Pro Lys Gln Ala Leu Ser His Val Glu Lys Cys Glu
                565                 570                 575


Gly Ser Gly Leu Leu Gly Leu Leu Arg Arg Met Val Ala Asp Ser Lys
            580                 585                 590


Ser Ser



<210>  265
<211>  595
<212>  PRT
<213>  Rasamsonia argillacea

<400>  265

Gly Val Thr Tyr Asp Lys Arg Asp Leu Ala Gln Asp Ile Trp Asn Asp
1               5                   10                  15


Ile Lys Asn Ala Val Asp Cys Ala Gly Cys Gln Gly Ile Leu Thr Ala
            20                  25                  30


Leu Lys Gly Leu Ser Tyr Leu Gly Thr Thr Ala Phe Val Asp Val Leu
        35                  40                  45


Thr Glu Val Cys Asp Ile Ser Gly Met Glu Asp Ser Asp Val Cys Ser
    50                  55                  60


Gly Ile Ile Ser Ser Glu Gly Pro Val Leu Asp Tyr Ile Leu Lys Gln
65                  70                  75                  80


Leu Asp Ile Gly Ser His Thr Ser Gln Val Ile Cys Ala Ser Ala Phe
                85                  90                  95


Gly Leu Cys Gln Tyr Pro Ala Val Arg Ala Tyr Asn Leu Thr Phe Pro
            100                 105                 110
```

```
Ser Pro Lys Pro Asp Lys Thr Arg Pro Glu Pro Ser Gly Glu Ser Pro
        115                 120                 125


Met Gln Ile Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu
    130                 135                 140


Thr Gly Ser Asn Tyr Asn Cys Thr Lys Pro Ile Cys Cys Arg Pro Tyr
145                 150                 155                 160


Thr Ala Asp Asp Ala Pro Gly Asn Thr Thr Thr Pro Cys Gly Pro Tyr
                165                 170                 175


Gly Asn Thr Lys Cys Asp Ala Pro Met Thr Leu Glu Glu Ser Met Phe
            180                 185                 190


Ala Ala Ile Lys Ala Leu Ser Pro Gln Pro Ala Phe Ser Ile Tyr Thr
        195                 200                 205


Gly Asp Val Val Ala His Asp Ile Trp Leu Val Asp Gln Asn Glu Val
    210                 215                 220


Val Glu Asp Leu Asn Ala Thr Tyr Asp Arg Met Ala Gly Leu Gly Leu
225                 230                 235                 240


Val Tyr Ala Ala Ile Gly Asn His Asp Thr Ala Pro Val Asn Asp Leu
                245                 250                 255


Pro Thr Ser Asn Ile Pro Ser Gln Tyr Ser Ala Asn Trp Thr Tyr Glu
            260                 265                 270


Ala Leu Glu Tyr His Phe Ser Leu Leu Thr Asn Ser Ala Ser Ala Gln
        275                 280                 285


Thr Ala Glu Asn Tyr Gly Ser Tyr Ser Ser Val Tyr Pro Gly Lys Tyr
    290                 295                 300


Gly Thr Asp Leu Arg Val Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Val
305                 310                 315                 320
```

```
Asp Asn Phe Trp Ala Tyr Gln Asp Pro Met Leu Tyr Asp Pro Asp Gly
                325                 330                 335


Gln Leu Ala Trp Leu Ile Asn Glu Leu Gln Glu Ala Glu Thr Ala Gly
            340                 345                 350


Gln Arg Val Trp Leu Ile Ala His Val Pro Ser Gly Thr Ala Asp His
        355                 360                 365


Phe His Asp Tyr Ser His Tyr Phe Asp Gln Ile Val Gln Arg Tyr Glu
    370                 375                 380


Thr Thr Ile Ala Ala Leu Phe Tyr Gly His Thr His Met Asp Gln Phe
385                 390                 395                 400


Gln Ile Ser Tyr Ser Asp Tyr Ser Asn Arg Ala Phe Asp Thr Ala Thr
                405                 410                 415


Ala Ile Gly Tyr Ile Met Pro Ser Met Thr Pro Thr Ser Gly Pro Pro
            420                 425                 430


Thr Phe Arg Val Tyr Asp Val Asp Pro Lys Thr Phe Ala Val Leu Asp
        435                 440                 445


Phe Thr Asn Tyr Ile Ala Asn Ile Ser Asp Pro Ala Tyr Gln Ser Gly
    450                 455                 460


Pro Thr Trp Gln Lys Tyr Tyr Ser Ala Lys Glu Ala Tyr Gly Pro Leu
465                 470                 475                 480


Leu Ser Pro Pro Val Thr Asp Ala Thr Ala Glu Leu Thr Pro Ala Phe
                485                 490                 495


Trp His Asn Val Thr Val Ala Phe Glu Asn Asp Asp Thr Ala Phe Gln
            500                 505                 510


Glu Tyr Trp Ala Arg Gln Thr Arg Gly Tyr Ala Val Ser Asn Cys Thr
        515                 520                 525
```

```
Gly Asn Cys Val Thr Gln Ala Ile Cys Gly Leu Arg Ala Gly Glu Ser
    530                 535                 540


Gln Tyr Asn Cys Val Thr Pro Thr Pro Gly Phe Asn Phe Ala Lys Arg
545                 550                 555                 560


Asp Val Ser Ser Asp Gly Gln Ala Leu Pro His Ile Glu Lys Cys Glu
                565                 570                 575


Gly Ser Gly Leu Leu Ser Leu Leu Ala Lys Met Val Ala Ser Asn Gly
            580                 585                 590


Gln Ser Ser
        595


<210>  266
<211>  595
<212>  PRT
<213>  Penicillium parviverrucosum

<400>  266

His Ile Glu Ser Ala Asp Asn Trp Ile Thr Thr Ile Trp Asp Leu Ser
1               5                   10                  15


Lys Gln Ala Val Asp Cys Ala Gly Cys Gln Ala Leu Leu Gly Gly Leu
            20                  25                  30


Lys Leu Ala Ala Asp Leu Gly Glu Thr Phe Met Glu Asp Val Leu Ile
        35                  40                  45


Gly Val Cys Asn Ile Ala Gly Val Glu Asp His Asp Val Cys Ser Gly
    50                  55                  60


Ile Ile Gln Asn Glu Gly Pro Ala Val His Tyr Ser Leu Leu Asn Leu
65                  70                  75                  80


His Ile Gly Ser His Thr Ala Thr Thr Leu Cys Ala Ser Leu Phe Gly
                85                  90                  95


Leu Cys Gln Tyr Pro Ala Val Arg Pro Tyr Asn Leu Ser Phe Pro Val
```

```
            100                 105                 110


Pro Lys Pro Thr Lys Ser Arg Pro Glu Pro Ser Gly Gln Ser Pro Ile
        115                 120                 125


Arg Ile Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr
    130                 135                 140


Gly Ser Asn Tyr Asp Cys Ser Lys Pro Ile Cys Cys Arg Pro Tyr Thr
145                 150                 155                 160


Glu Glu Asp Ala Pro Gly Asn Thr Ser Thr Pro Cys Gly Pro Trp Gly
                165                 170                 175


Asn Pro Met Cys Asp Pro Pro Asn Arg Leu Gln Glu Ser Met Met Thr
            180                 185                 190


Ala Ile Ala Asp Leu Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val
        195                 200                 205


Pro Ala His Asp Ile Trp Ser Ala Thr Lys Ala Glu Ala Leu Arg Asp
    210                 215                 220


Phe Asn Ala Thr Tyr Gly Ser Met Glu Lys Arg Leu Gly Met Val Phe
225                 230                 235                 240


Ala Ala Leu Gly Asn His Asp Ala Ala Pro Leu Asn Leu Phe Pro Ser
                245                 250                 255


Asn Lys Ile Pro Ser Glu Tyr Ser Pro Gln Trp Ala Tyr Asp Ala Leu
            260                 265                 270


Ala Ala Asp Trp Leu Gly Leu Ser Ala Met Ala Ser Val His Ser Ala
        275                 280                 285


Ile His His Gly Ser Tyr Ser Ala Val His Ser Glu Asp Lys Leu Arg
    290                 295                 300


Val Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Asp Asn Phe Phe Met
```

```
305                 310                 315                 320

Tyr Glu Glu Pro Met Glu His Asp Pro Asn Gly Gln Phe Ala Trp Leu
                325                 330                 335

Ile Ser Glu Leu Gln Ser Ala Glu Ser Thr Ser Gln Arg Val Trp Leu
            340                 345                 350

Ile Ala His Ile Pro Ser Gly Asn Ala Asp His Phe Arg Asp Phe Ser
        355                 360                 365

His Tyr Phe Asp Glu Ile Val Gln Arg Tyr Asp Thr Thr Ile Ala Ala
    370                 375                 380

Leu Tyr Phe Gly His Thr His Thr Asp Thr Phe Gln Ile Ala Tyr Ser
385                 390                 395                 400

Asn Tyr Ser Asn Arg Ser Trp Asp Thr Ala Ser Ala Met Gly Tyr Val
                405                 410                 415

Ala Pro Ser Met Thr Pro Thr Ser Gly Ser Pro Ser Phe Arg Val Tyr
            420                 425                 430

Glu Val Asp Pro Val Thr Phe Gly Ile Ile Asp Phe Thr Gln Tyr Ile
        435                 440                 445

Ala Asn Ile Ser Asp Pro Ser Tyr Gln Ile Asn Pro Lys Trp Glu Pro
    450                 455                 460

Tyr Tyr Ser Ala Lys Lys Ala Tyr Gly Ser Lys Leu Ser Pro Pro Ala
465                 470                 475                 480

Gln Asp Pro Gly Ala Glu Met Thr Pro Ala Phe Trp His Asn Val Thr
                485                 490                 495

Ile Ala Met Glu Gln Asp Ala Ser Ile Phe Gln Ala Phe Trp Ala Arg
            500                 505                 510

Arg Thr Arg Gly Asn Lys Val Thr Ser Cys Thr Gly Asn Cys Met Ala
```

```
        515                 520                 525


Asn Glu Ile Cys Ala Leu Arg Gly Ala Asp Ala Gln Tyr Asn Cys Ala
    530                 535                 540


Thr Pro Thr Val Gly Phe Arg Phe Arg Lys Arg Asp Met Thr Ser Asp
545                 550                 555                 560


Leu Ser Leu Gln Lys Glu Glu Phe Arg Pro Glu Cys Asn His Ala Gly
                565                 570                 575


Met Gly Pro Leu Leu Ala Lys Ile Val His Gln Ala Ala Leu Glu Asn
            580                 585                 590


Glu Arg Gly
        595


<210>  267
<211>  595
<212>  PRT
<213>  Penicillium flavescens

<400>  267

His Ser Glu Ser Ala Glu Ser Trp Ile Ser Asp Ile Trp Asp His Phe
1               5                   10                  15


Lys Glu Ala Val Asp Cys Thr Ser Cys Gln Val Leu Leu Gly Ser Leu
            20                  25                  30


Lys Leu Val Ala Ala Phe Gly Asp Thr Phe Met Val Asp Val Leu Thr
        35                  40                  45


Gly Val Cys Ala Ile Ser Gly Ala Glu Asp His Asp Val Cys Ala Gly
    50                  55                  60


Val Ile Ala Gly Glu Gly Pro Ser Val Gln Tyr Ser Leu Lys Asn Leu
65                  70                  75                  80


Lys Ile Gly Ser His Thr Ala Lys Thr Phe Cys Ala Ser Leu Val Gly
                85                  90                  95
```

```
Leu Cys Gln Tyr Pro Lys Val Arg Glu Tyr Asp Leu Ala Phe Pro Ala
            100                 105                 110


Pro Lys Pro Pro Asn Gly Arg Pro Pro Pro Ser Gly Glu Pro Pro Ile
        115                 120                 125


Lys Val Val His Phe Ser Asp Thr His Val Asp Leu Ala Tyr Glu Pro
    130                 135                 140


Gly Ser Asn Tyr Ala Cys Ser Lys Pro Ile Cys Cys Arg Thr Tyr Lys
145                 150                 155                 160


Glu Asn Asp Ala Pro Gly Asn Thr Ser Ser Ala Cys Gly Pro Trp Gly
                165                 170                 175


Asn Pro Arg Cys Asp Ser Pro His Arg Leu Gln Glu Ser Met Asn Ala
            180                 185                 190


Ala Ile Ala Asp Leu Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val
        195                 200                 205


Val Ala His Asp Val Trp Leu Asp Asn Lys Phe Glu Val Leu Gln Asn
    210                 215                 220


Phe Asn Ala Thr Tyr Gly Ala Met Glu Thr Thr Leu Gly Gln Val Tyr
225                 230                 235                 240


Ala Ala Leu Gly Asn His Asp Thr Ala Pro Leu Asn Leu Phe Pro Ser
                245                 250                 255


Ser Lys Ile Pro Ser Ile Tyr Asn Pro Gln Trp Ala Tyr Asp Ala Leu
            260                 265                 270


Thr Glu Asn Trp Leu Ala Leu Thr Gly Ile Pro Ser Ile Glu Ser Ala
        275                 280                 285


Asp Gln Tyr Gly Ser Tyr Ser Val Leu His Pro Asp Ser Asn Leu Arg
    290                 295                 300
```

```
Ile Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ala
305                 310                 315                 320


Tyr Thr Glu Pro Met Glu Tyr Asp Pro Asn Ser Gln Leu Lys Trp Leu
                325                 330                 335


Ile Asn Glu Leu Gln Ala Ala Glu Lys Ala Ser Glu Arg Val Trp Leu
            340                 345                 350


Ile Ser His Ile Pro Ser Gly Asn Ser Asp His Phe His Asp His Ser
        355                 360                 365


His Tyr Phe Asp Gln Ile Ile Gln Arg Tyr Asp Ala Thr Ile Ala Ala
    370                 375                 380


Leu Phe Phe Gly His Thr His Leu Asp Glu Phe Gln Ile Ser Tyr Ser
385                 390                 395                 400


Asp Tyr Lys Ser Arg Thr Trp Asp Thr Ala Thr Ala Met Gly Tyr Ile
                405                 410                 415


Ala Pro Ser Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Val Tyr
            420                 425                 430


Asp Ile Asp Pro Val Thr Phe Gly Val Leu Asp Phe Thr Gln Tyr Ile
        435                 440                 445


Ala Asn Ile Asn Ala Pro Asp Gln Glu Ser Leu Glu Trp Val Pro Tyr
    450                 455                 460


His Ser Ala Lys Glu Ala Tyr Gly Ser Lys Leu Val Ser Pro Ile Thr
465                 470                 475                 480


Asp Pro Ser Ala Glu Leu Ser Pro Ala Phe Trp His Asn Val Thr Leu
                485                 490                 495


Ala Met Glu Asn Asp Ser Ala Ile Phe Gly Asp Phe Trp Ala Arg Arg
            500                 505                 510
```

```
Thr Arg Gly Tyr Gln Val Pro Ser Cys Thr Gly Asp Cys Ile Ser Gly
        515                 520                 525


Glu Ile Cys Thr Leu Arg Gly Ala Asp Ala Gln Tyr Asn Cys Phe Val
    530                 535                 540


Gln Lys Val Gly Phe Ser Phe Glu Lys Arg Asp His Gln Gly Asp Ser
545                 550                 555                 560


Thr Arg Glu Glu Arg Ile Leu Pro Glu Cys Asn His Ala Gly Met Ala
                565                 570                 575


Pro Leu Leu Ala Lys Ile Ala Arg Leu Ala Ala Ile Ala Arg Asp Met
            580                 585                 590


Glu Lys Arg
        595


<210>  268
<211>  596
<212>  PRT
<213>  Penicillium hispanicum

<400>  268

Glu Ser Ala Glu Ser Trp Val Ala Ser Ile Trp Asp Asp Phe Lys Val
1               5                   10                  15


Ala Val Asp Cys Ala Ser Cys Gln Ala Leu Leu Gly Gly Leu Lys Leu
            20                  25                  30


Val Ala Glu Phe Gly Glu Ser Phe Met Glu Asp Val Leu Ile Gly Val
        35                  40                  45


Cys Asp Val Ser Gly Val Glu Asp Ser Asp Val Cys Ala Gly Val Ile
    50                  55                  60


Ala Asn Glu Gly Pro Ala Val His Tyr Thr Leu Lys Asn Leu Glu Ile
65                  70                  75                  80
```

```
Gly Ser His Ala Ala Asn Thr Leu Cys Ala Ser Leu Val Gly Leu Cys
                85                  90                  95


Glu Tyr Pro Ala Val Arg Pro Tyr Asn Leu Ser Phe Pro Ser Leu Lys
            100                 105                 110


Pro Ala Thr Ser Arg Pro Pro Pro Ser Gly Lys Pro Ala Ile Lys Val
        115                 120                 125


Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly Ser
    130                 135                 140


Asn Phe Asp Cys Ser Lys Pro Ile Cys Cys Arg Val Tyr Thr Glu Glu
145                 150                 155                 160


Asp Ala Pro Gly Asn Thr Ser Ser Pro Cys Gly Pro Trp Gly Asn Pro
                165                 170                 175


Lys Cys Asp Pro Pro His Arg Leu Gln Glu Ser Met Val Glu Ala Ile
            180                 185                 190


Ala Val Leu Asp Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala
        195                 200                 205


His Asp Val Trp Leu Val Asn Lys Ser Glu Ala Leu Gln Asp Phe Asn
    210                 215                 220


Ala Thr Tyr Gly Ala Met Glu Asn Arg Phe Gly Pro Val Tyr Ala Ala
225                 230                 235                 240


Leu Gly Asn His Asp Thr Ala Pro Leu Asn Leu Phe Pro Ser Asn Lys
                245                 250                 255


Ile Ser Arg Glu Tyr Asn Pro Gln Trp Ala Tyr Asp Ala Leu Ala Ala
            260                 265                 270


Asp Trp Ala Ala Leu Thr Gly Ile Pro Ser Val Ala Ser Ala Arg Glu
        275                 280                 285
```

```
Tyr Gly Ser Tyr Ser Ala Ile His Pro Asn Ser Asn Leu Arg Ile Ile
    290                 295                 300


Ser Tyr Asn Ser Ile Phe Tyr Tyr Arg Phe Asn Phe Phe Ala Tyr Glu
305                 310                 315                 320


Glu Pro Met Glu Tyr Asp Pro Asp Ser Gln Leu Ala Trp Leu Ile Thr
                325                 330                 335


Glu Leu Asp Ala Ala Glu Thr Ala Gly Gln Arg Val Trp Leu Ile Ser
            340                 345                 350


His Ile Pro Ser Gly Lys Pro Asp His Phe Arg Asp His Ser His Tyr
        355                 360                 365


Phe Asp Gln Ile Val Gln Arg Tyr Asp Ala Thr Ile Ala Ala Leu Phe
    370                 375                 380


Phe Gly His Thr His Lys Asp Glu Phe Gln Ile Ser Tyr Ser Thr Tyr
385                 390                 395                 400


Thr Asn Arg Ala Trp Asp Thr Ala Thr Ala Met Gly Tyr Ile Ala Pro
                405                 410                 415


Ser Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Val Tyr Glu Ile
            420                 425                 430


Asp Pro Val Thr Phe Gly Val Met Asp Tyr Thr Gln Tyr Ile Ala Lys
        435                 440                 445


Ile Ser Asp Ser Ser Ala Gln Ile Asp Thr Thr Pro Glu Trp Val Pro
    450                 455                 460


Tyr Tyr Ser Ala Lys Ala Asp Tyr Gly Ala Lys Leu Ala Pro Pro Val
465                 470                 475                 480


Glu Gly Ala Gly Val Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr
                485                 490                 495
```

Val Ala Met Glu Ala Asp Ser Ser Leu Phe Gln Ala Phe Trp Gly Arg
            500   505   510

Arg Thr Arg Gly Tyr Asn Val Ser Ser Cys Thr Gly Glu Cys Met Ala
        515   520   525

Thr Glu Ile Cys Ala Leu Arg Gly Ala Asp Ala Gln Tyr Ser Cys Val
    530   535   540

Gly Ala Lys Pro Gly Leu Ser Phe Ser Lys Arg Gly Gly Lys Asp Val
545   550   555   560

Asp Val Leu Trp Gln Arg Arg Leu Gln Pro Glu Cys Asn His Ala Gly
                565   570   575

Met Ala Pro Leu Leu Gly Lys Ile Trp Thr Arg Ala Ala Leu Val Trp
            580   585   590

Arg Ser Glu Ala
        595

<210> 269
<211> 598
<212> PRT
<213> Penicillium simplicissimum

<400> 269

Gly Ala Thr Glu Asn Trp Ile Ser Thr Ile Trp Asn Asp Phe Lys Glu
1   5   10   15

Ala Val Asp Cys Gly Ser Cys Gln Val Leu Leu Gly Gly Leu Lys Leu
            20   25   30

Val Ala Asp Phe Gly Glu Gly Phe Met Glu Asp Val Leu Thr Gly Val
        35   40   45

Cys Asp Ile Ser Gly Ala Glu Asp Arg Asp Val Cys Ala Gly Val Ile
    50   55   60

```
Ala Ser Glu Val Pro Ala Leu His Tyr Ala Ile Lys Asn Met His Val
65                  70                  75                  80


Gly Ser His Thr Ala Lys Thr Leu Cys Ser Ala Leu Val Gly Leu Cys
                85                  90                  95


Asp Phe Pro Asp Val Arg Pro Phe Asp Leu Ala Phe Pro Ser Pro Lys
            100                 105                 110


Pro Ala Asn Ser Arg Pro Pro Pro Ser Gly Lys Pro Pro Ile Lys Val
        115                 120                 125


Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly Ser
    130                 135                 140


Asn Tyr Asp Cys Ser Lys Pro Ile Cys Cys Arg Val Tyr Thr Asp Ala
145                 150                 155                 160


Asp Ala Pro Gly Thr Thr Asp Lys Pro Cys Gly Pro Phe Gly Asn Thr
                165                 170                 175


Lys Cys Asp Pro Pro His Gln Leu Gln Glu Ser Met Met Thr Ala Ile
            180                 185                 190


Ala Glu Leu Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala
        195                 200                 205


His Asp Val Trp Leu Val Thr Lys Glu Glu Val Leu Gln Asp Leu Asn
    210                 215                 220


Ala Thr Tyr Gly Ala Met Glu Asn His Leu Gly Leu Val Tyr Ala Ala
225                 230                 235                 240


Leu Gly Asn His Asp Ala Ala Pro Leu Asn Leu Phe Pro Ser His Asn
                245                 250                 255


Val Pro Ser Lys Tyr Asn Pro Gln Trp Ala Tyr Asp Ala Leu Thr Ala
            260                 265                 270
```

```
Asp Trp Met Ala Leu Thr Gly Ile Glu Asn Val Gln Asn Ala Asn Glu
        275                 280                 285


Tyr Gly Ser Tyr Ser Ala Ile His Pro Asn Ser Lys Leu Arg Ile Ile
    290                 295                 300


Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ser Tyr Thr
305                 310                 315                 320


Glu Pro Met Glu Tyr Asp Pro Asn Gly Gln Leu Thr Trp Leu Thr Glu
                325                 330                 335


Glu Leu Gln Ala Ala Glu Asn Ala Gly Gln Arg Val Trp Leu Ile Ser
            340                 345                 350


His Ile Pro Ser Gly Asp Val Asp His Phe Arg Asp His Ser His Tyr
        355                 360                 365


Phe Asp Gln Ile Ile Gln Arg Tyr Glu Ala Thr Ile Ala Gly Leu Phe
    370                 375                 380


Phe Gly His Thr His Thr Asp Glu Phe Gln Val Ser Tyr Ser Asp Tyr
385                 390                 395                 400


Lys Asn Arg Asn Trp Asp Thr Ala Thr Ala Met Gly Tyr Val Ala Pro
                405                 410                 415


Ser Met Thr Pro Thr Ser Gly Ser Pro Ser Phe Arg Val Tyr Asp Ile
            420                 425                 430


Asp Pro Val Thr Phe Gly Val Leu Asp Phe Thr Gln Tyr Ile Ala Asn
        435                 440                 445


Ile Ser Asp Ala Ser Phe Gln Thr Lys Pro Thr Trp Ile Pro Tyr Tyr
    450                 455                 460


Thr Ala Lys Lys Asp Tyr Gly Ser Lys Leu Pro Thr Ile Pro Asp Asp
465                 470                 475                 480
```

```
Thr Ala Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val Ala Met
                485                 490                 495


Glu Lys Asp Ser Ala Val Phe Asp Glu Phe Trp Ala Arg Arg Thr Arg
            500                 505                 510


Gly Tyr Asn Val Pro Ala Cys Thr Gly Asp Cys Ala Lys Asn Glu Ile
        515                 520                 525


Cys Ala Leu Arg Gly Ala Asp Ala Gln Tyr Ser Cys Val Gln Arg Thr
    530                 535                 540


Pro Gly Phe Ser Phe Ser Lys Arg Asp Gly Val Asp Gly Glu Met Glu
545                 550                 555                 560


Glu Val Ala Pro Leu Leu Ser Lys Arg Phe Gln Pro Glu Cys Asn His
                565                 570                 575


Ala Gly Met Ala Pro Leu Leu Ala Lys Ile Ala His Asn Ala Asn Leu
            580                 585                 590


Ala Lys Met Asn Gly Glu
        595


<210>  270
<211>  599
<212>  PRT
<213>  Penicillium vasconiae

<400>  270

Gly Ala Val Glu Ser Trp Ile Ser Thr Ile Trp Asn Asp Phe Lys Glu
1               5                   10                  15


Ala Val Asp Cys Gly Ser Cys Gln Val Leu Leu Gly Gly Leu Lys Leu
            20                  25                  30


Val Ala Asp Phe Gly Glu Gly Phe Leu Glu Asp Val Leu Thr Gly Val
        35                  40                  45


Cys Asp Ile Ser Gly Ala Glu Asp Arg Asp Val Cys Ala Gly Val Ile
```

```
    50                  55                  60

Ala Ser Glu Val Pro Ala Leu His Tyr Ala Leu Lys Asn Met His Val
65                  70                  75                  80

Gly Ser His Thr Ala Lys Thr Leu Cys Ser Ala Leu Val Gly Leu Cys
                85                  90                  95

Asp Phe Pro Asp Val Arg Pro Phe Gly Leu Thr Phe Pro Ser Pro Lys
            100                 105                 110

Pro Ala Lys Ser Arg Pro Pro Pro Ser Gly Lys Ser Pro Ile Lys Val
        115                 120                 125

Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr Gly Ser
    130                 135                 140

Asn Tyr Asp Cys Ser Lys Pro Ile Cys Cys Arg Val Tyr Ser Asp Glu
145                 150                 155                 160

Asp Ala Pro Gly Lys Thr Asp Lys Pro Cys Gly Pro Phe Gly Asn Thr
                165                 170                 175

Lys Cys Asp Pro Pro His Gln Leu Gln Glu Ser Met Met Thr Ala Ile
            180                 185                 190

Ala Asp Leu Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Ala
        195                 200                 205

His Asp Val Trp Leu Val Asn Lys Asp Glu Val Leu Gln Asp Phe Asn
    210                 215                 220

Ser Thr Tyr Gly Ala Met Glu Asn His Leu Gly Leu Val Tyr Ala Ala
225                 230                 235                 240

Leu Gly Asn His Asp Ala Ala Pro Leu Asn Leu Phe Pro Ser Lys Asn
                245                 250                 255

Val Pro Ser Lys Tyr Asn Pro Gln Trp Ala Tyr Asp Thr Leu Thr Ala
```

```
            260                 265                 270

Asn Trp Met Thr Leu Thr Gly Ile Glu Ser Val Gln Asn Ala Asn Glu
        275                 280                 285

Tyr Gly Ser Tyr Ser Ala Ile His Pro Asn Ser Lys Leu Arg Ile Ile
    290                 295                 300

Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ser Tyr Thr
305                 310                 315                 320

Glu Pro Met Glu Tyr Asp Pro Asn Gly Gln Leu Thr Trp Leu Ile Ser
                325                 330                 335

Glu Leu Gln Ser Ala Glu Asn Ala Gly Gln Arg Val Trp Leu Ile Ser
            340                 345                 350

His Ile Pro Ser Gly Asn Val Asp His Phe Arg Asp His Ser His Tyr
        355                 360                 365

Phe Asp Gln Ile Ile Gln Arg Tyr Glu Ala Thr Ile Ala Gly Leu Phe
    370                 375                 380

Phe Gly His Thr His Thr Asp Glu Phe Gln Ile Ala Tyr Ser Asp Tyr
385                 390                 395                 400

Lys Asn Arg Asn Trp Asn Thr Ala Thr Ala Met Gly Tyr Val Ala Pro
                405                 410                 415

Ser Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Val Tyr Asp Ile
            420                 425                 430

Asp Pro Val Thr Phe Ala Val Ile Asp Phe Thr Gln Tyr Ile Ala Asn
        435                 440                 445

Ile Ser Asp Pro Thr Phe Gln Lys Lys Pro Asp Trp Val Pro Tyr Tyr
    450                 455                 460

Ser Ala Lys Lys Asp Tyr Gly Gly Lys Leu Ser Pro Arg Pro Ala Asp
```

```
465                 470                 475                 480


Thr Ala Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val Ala Met
                485                 490                 495


Glu Lys Asp Ser Ser Val Phe Asn Glu Phe Trp Ala Arg Arg Thr Arg
            500                 505                 510


Gly Tyr Asn Val Pro Ala Cys Thr Gly Asp Cys Val Lys Asn Glu Ile
        515                 520                 525


Cys Ala Leu Arg Gly Ala Asp Ala Gln Tyr Ser Cys Val Gln Arg Thr
    530                 535                 540


Pro Gly Phe Ser Phe Ser Lys Arg Asp Asp Glu Asn Val Asp Gly Asp
545                 550                 555                 560


Val Gly Asn Tyr Pro Leu Leu Ser Lys Arg Phe Gln Pro Glu Cys Asn
                565                 570                 575


His Ala Gly Met Ala Pro Leu Leu Ala Lys Ile Ala His Lys Ala Ser
            580                 585                 590


Leu Ala Lys Ala Asn Gly Glu
        595


<210>  271
<211>  600
<212>  PRT
<213>  Talaromyces columbinus

<400>  271

Tyr Asp Ser Ala Leu Val Asp His Asn Leu Val Ser Asp Ile Trp Glu
1               5                   10                  15


Asp Ile Lys Glu Ala Val Thr Cys Ala Gly Cys Gln Val Ile Leu Ala
            20                  25                  30


Ala Leu Lys Gly Val Ser Asp Leu Gly Thr Thr Ala Leu Val Asp Thr
        35                  40                  45
```

```
Leu Thr Gly Val Cys Lys Leu Ser Gly Ala Ala Asp Asp Asn Val Cys
    50                  55                  60


Glu Gly Ile Ile Ser Arg Glu Gly Ala Val Leu His Tyr Val Leu Ser
65                  70                  75                  80


Glu Leu Ser Leu Gly Ser Glu Thr Ser Asn Ala Leu Cys Ala Ser Ala
                85                  90                  95


Phe Gly Leu Cys Leu Tyr Pro Asp Val Arg Asn Tyr Thr Leu Asn Phe
            100                 105                 110


Pro Ser Ala Lys Pro Lys Asn Ile Thr Arg Pro Ala Pro Ser Gly Lys
        115                 120                 125


Pro Pro Ile Gln Val Ala His Phe Ser Asp Thr His Val Asp Leu Ser
    130                 135                 140


Tyr Glu Val Gly Ser Asn Trp Asn Cys Thr Lys Pro Ile Cys Cys Arg
145                 150                 155                 160


Ser Phe Glu Ala Ser Asp Ala Pro Gly Asn Thr Thr Thr Pro Cys Gly
                165                 170                 175


Pro Phe Gly Asn Thr Lys Cys Asp Thr Pro Leu Thr Leu Glu Glu Asn
            180                 185                 190


Met Leu Asp Ser Ile Lys Lys Ser Asp Pro Thr Pro Ala Phe Ser Ile
        195                 200                 205


Tyr Thr Gly Asp Val Val Ala His Asp Ile Trp Leu Val Asp Lys Asp
    210                 215                 220


Glu Val Leu Thr Asp Leu Asn Ala Thr Tyr Ser Leu Met Ala Glu Ile
225                 230                 235                 240


Gly Thr Val Tyr Ala Ala Ile Gly Asn His Asp Thr Ala Pro Leu Asn
                245                 250                 255
```

```
Asp Leu Pro Thr Thr Gln Val Pro Glu Ser Tyr Ser Ala Asn Trp Thr
            260                 265                 270


Tyr Gln Ala Leu Ala Thr Asn Phe Thr Thr Leu Thr Arg Asp Ser Ser
        275                 280                 285


Val Ile Ser Val Ala Lys Asn Tyr Gly Ser Tyr Ser Ser Val Phe Thr
    290                 295                 300


Gly Ser Tyr Gly Thr Asp Leu Lys Ile Ile Ser Tyr Asn Ser Met Phe
305                 310                 315                 320


Tyr Tyr Val Asp Asn Phe Tyr Ala Phe Leu Asp Pro Met Pro Tyr Asp
                325                 330                 335


Pro Asp Gly Gln Leu Ala Trp Leu Ile Asp Glu Leu Gln Ser Ala Glu
            340                 345                 350


Thr Ala Gly Gln Arg Val Trp Leu Ile Ala His Val Pro Thr Gly Ser
        355                 360                 365


Ser Asp His Phe His Asp Tyr Ser His Tyr Phe Asp Gln Ile Val Gln
    370                 375                 380


Arg Tyr Asp Ala Thr Ile Ala Ala Leu Phe Phe Gly His Thr His Thr
385                 390                 395                 400


Asp Gln Phe Gln Ile Ala Tyr Ser Asp Tyr Ala Asn Gln Asn Ala Asp
                405                 410                 415


Thr Ala Thr Ala Ile Gly Tyr Ile Met Pro Ser Leu Thr Pro Thr Ser
            420                 425                 430


Gly Pro Pro Ala Tyr Arg Ile Tyr Asp Ile Asp Pro Val Thr Phe Ser
        435                 440                 445


Val Leu Asp Tyr Thr Val Tyr Ile Thr Asn Ile Ser His Pro Asp Phe
    450                 455                 460
```

```
Gln Lys Gly Pro Lys Trp Glu Lys Tyr Tyr Ser Ala Lys Asp Thr Tyr
465                 470                 475                 480


Gly Ser Leu Leu Ser Pro Pro Val Thr Asp Pro Ser Ala Glu Met Thr
                485                 490                 495


Pro Ala Phe Trp His Asn Val Thr Ala Val Phe Glu Ser Asp Asp Val
            500                 505                 510


Ala Phe Gln Gly Tyr Trp Ala Arg Gln Thr Arg Gly Tyr Asp Val Ser
        515                 520                 525


Asp Cys Thr Asp Glu Ser Cys Lys Asn Gln Thr Ile Cys Ala Leu Arg
    530                 535                 540


Ala Ala Asp Ala Gln Tyr Asn Cys Val Val Pro Ser Ile Gly Phe Asn
545                 550                 555                 560


Phe Ala Lys Arg Asp Asp Thr Asp Gln Ala His Val Arg Ala Gln Lys
                565                 570                 575


Glu Lys Cys Asp Asp Thr Gly Leu Val Ser Leu Leu Gly Lys Ile Leu
            580                 585                 590


Ala Lys Ser Lys Glu Thr Thr Asn
        595                 600


<210>  272
<211>  600
<212>  PRT
<213>  Talaromyces variabilis

<400>  272

Ser Ser Ser Ala Leu Ile Asp Arg Asp Leu Ala Ser Glu Ile Trp Asp
1               5                   10                  15


Asp Ile Lys Glu Ala Ala Thr Cys Ala Gly Cys Gln Val Ile Leu Ala
            20                  25                  30
```

```
Ala Leu Lys Gly Val Ser Asp Leu Gly Thr Thr Ala Leu Ile Asp Thr
        35                  40                  45


Leu Thr Glu Val Cys Lys Ile Ser Gly Ala Glu Asp Asp Asp Val Cys
    50                  55                  60


Glu Gly Ile Ile Ser Arg Glu Gly Pro Val Leu His Tyr Ile Leu Ser
65                  70                  75                  80


Gln Leu Ser Leu Gly Ser Glu Thr Ser Asp Ala Leu Cys Thr Thr Ala
                85                  90                  95


Phe Gly Leu Cys Ala Tyr Pro Asp Val Arg Asn Tyr Thr Leu Thr Phe
            100                 105                 110


Pro Ser Ala Lys Pro Glu Asn Ser Thr Arg Pro Ser Ser Ser Gly Glu
        115                 120                 125


Ser Pro Ile Gln Val Val His Phe Ser Asp Thr His Val Asp Leu Ser
    130                 135                 140


Tyr Glu Thr Gly Ser Asn Trp Asn Cys Thr Lys Pro Ile Cys Cys Arg
145                 150                 155                 160


Ser Phe Asp Ser Ser Asp Ala Pro Gly Asn Thr Lys Thr Pro Cys Gly
                165                 170                 175


Pro Tyr Gly Asn Thr Lys Cys Asp Ala Pro Ile Ser Leu Glu Lys Ser
            180                 185                 190


Met Val Asp Ser Ile Lys Gly Leu Ser Pro Ala Pro Ala Phe Ser Ile
        195                 200                 205


Tyr Thr Gly Asp Val Val Ala His Asp Ile Trp Leu Val Asp Glu Asp
    210                 215                 220


Glu Val Leu Thr Asp Leu Ser Ser Thr Tyr Gly Leu Val Gln Asp Val
225                 230                 235                 240
```

```
Gly Thr Val Phe Ala Ala Ile Gly Asn His Asp Thr Ala Pro Val Asn
                245                 250                 255


Asp Leu Pro Thr Thr Gln Val Pro Ser Thr Tyr Ser Ala Asn Trp Thr
            260                 265                 270


Tyr Glu Ala Leu Ala Gly Asn Cys Thr Thr Leu Thr Gly Asp Ser Ser
        275                 280                 285


Val Met Ser Val Ala Glu Asn Tyr Gly Ser Tyr Ser Ser Val Phe Thr
    290                 295                 300


Gly Ser His Gly Thr Asp Leu Lys Val Ile Ser Tyr Asn Ser Ile Phe
305                 310                 315                 320


Tyr Tyr Ala Asp Asn Phe Tyr Ala Phe Leu Asp Pro Met Pro Tyr Asp
                325                 330                 335


Pro Asp Gly Gln Leu Ala Trp Leu Ile Asp Glu Leu Gln Ala Ser Glu
            340                 345                 350


Thr Ala Gly Gln Arg Val Trp Leu Ile Ala His Val Pro Thr Gly Ser
        355                 360                 365


Ser Asp His Phe His Asp Tyr Ser His Tyr Leu Asp Gln Ile Val Gln
    370                 375                 380


Arg Tyr Asp Ala Thr Ile Ala Ala Leu Phe Phe Gly His Thr His Thr
385                 390                 395                 400


Asp Gln Phe Gln Ile Ala Tyr Ser Asn Tyr Ser Asn Gln Asn Ala Asp
                405                 410                 415


Thr Ala Thr Ala Ile Gly Tyr Ile Ala Pro Ser Leu Thr Pro Thr Ser
            420                 425                 430


Gly Pro Pro Ala Tyr Arg Val Tyr Asp Ile Asp Pro Val Thr Phe Gly
        435                 440                 445
```

```
Val Leu Asp Phe Thr Val Tyr Ile Ala Asn Ile Ser Asp Pro Asp Tyr
    450                 455                 460


Gln Asn Gly Pro Thr Trp Ala Lys Tyr Tyr Ser Ala Lys Glu Thr Tyr
465                 470                 475                 480


Gly Ser Leu Leu Ser Pro Pro Val Thr Asp Ser Ser Ala Glu Leu Thr
                485                 490                 495


Pro Ala Phe Trp His Asn Val Thr Ala Val Phe Glu Thr Asp Asp Ala
            500                 505                 510


Ala Phe Gln Gly Tyr Trp Ala Arg Gln Thr Arg Gly Tyr Asp Val Ser
        515                 520                 525


Asn Cys Thr Asp Ser Ser Cys Lys Asn Gln Asn Ile Cys Ala Leu Arg
    530                 535                 540


Ala Ala Asp Ala Gln Tyr Asn Cys Val Val Pro Ser Ile Gly Phe Asn
545                 550                 555                 560


Phe Ala Lys Arg Asp Glu Thr Asp Gln Ala His Val Lys Ala Gln Lys
                565                 570                 575


Glu Lys Cys Asp Asp Ala Gly Leu Val Ser Leu Leu Gly Lys Ile Ile
            580                 585                 590


Ser Lys Ser Arg Asp Val Ser Asn
        595                 600


<210>  273
<211>  600
<212>  PRT
<213>  Talaromyces rugulosus

<400>  273

Ser Ser Ser Ala Leu Val Asp Arg Asp Leu Ala Ser Glu Ile Trp Asp
1               5                   10                  15
```

```
Asp Ile Lys Glu Ala Ala Thr Cys Thr Gly Cys Gln Val Ile Leu Ala
            20                  25                  30


Ala Leu Lys Gly Val Ser Asp Leu Gly Thr Thr Val Leu Val Asp Thr
        35                  40                  45


Leu Thr Glu Val Cys Lys Leu Ser Gly Ala Glu Asp Asp Asp Val Cys
    50                  55                  60


Glu Gly Ile Ile Ser Arg Glu Gly Pro Val Leu Gln Tyr Ile Leu Ser
65                  70                  75                  80


Gln Leu Ser Leu Gly Ser Glu Thr Ser Asp Ala Leu Cys Ala Ser Ala
                85                  90                  95


Phe Gly Leu Cys Ser Tyr Pro Asp Val Arg Ser Tyr Thr Leu Thr Phe
            100                 105                 110


Pro Ser Thr Lys Pro Glu Asn Ser Thr Arg Pro Ser Ser Ser Gly Gln
        115                 120                 125


Ala Pro Ile Gln Val Val His Phe Ser Asp Thr His Val Asp Leu Ser
    130                 135                 140


Tyr Glu Thr Gly Ser Asn Trp Asn Cys Thr Lys Pro Ile Cys Cys Arg
145                 150                 155                 160


Ser Phe Asp Ser Ser Asp Ala Pro Gly Asn Thr Ser Thr Pro Cys Gly
                165                 170                 175


Pro Tyr Gly Asn Thr Lys Cys Asp Ala Pro Leu Ser Leu Glu Glu Ser
            180                 185                 190


Met Phe Asp Ser Ile Lys Ser Leu Ser Pro Ala Pro Ala Phe Ser Ile
        195                 200                 205


Tyr Thr Gly Asp Val Val Ala His Asp Val Trp Ile Val Asp Lys Asp
    210                 215                 220
```

```
Glu Val Leu Thr Asp Leu Asn Ala Thr Tyr Ser Leu Met Ala Glu Val
225                 230                 235                 240


Gly Thr Val Tyr Ala Ala Ile Gly Asn His Asp Thr Ala Pro Leu Asn
                245                 250                 255


Asp Leu Pro Thr Ser Gln Val Pro Ser Thr Tyr Ser Ala Asn Trp Thr
            260                 265                 270


Tyr Gln Ala Leu Ala Thr Asn Phe Thr Thr Leu Ser Gly Asp Ser Ser
        275                 280                 285


Ile Met Ser Val Ala Glu Asn Tyr Gly Ser Tyr Ser Ser Val Phe Ala
    290                 295                 300


Gly Ser His Gly Thr Asp Leu Lys Val Ile Ser Tyr Asn Ser Ile Phe
305                 310                 315                 320


Tyr Tyr Val Asp Asn Phe Tyr Ala Phe Leu Asp Pro Met Pro Tyr Asp
                325                 330                 335


Pro Asp Gly Gln Leu Ala Trp Leu Ile Asp Glu Leu Gln Ala Ala Glu
            340                 345                 350


Ser Ala Gly Gln Arg Val Trp Leu Ile Ala His Val Pro Thr Gly Ser
        355                 360                 365


Ser Asp His Phe His Asp Tyr Ser His Tyr Phe Asp Gln Ile Val Gln
    370                 375                 380


Arg Tyr Asp Ala Thr Ile Ala Ala Leu Phe Phe Gly His Thr His Thr
385                 390                 395                 400


Asp Gln Phe Gln Ile Ala Tyr Ser Asp Tyr Ser Asn Gln Asn Ser Asp
                405                 410                 415


Thr Ala Thr Ala Ile Gly Tyr Ile Met Pro Ser Leu Thr Pro Thr Ser
            420                 425                 430
```

```
Gly Pro Pro Ala Tyr Arg Val Tyr Asp Ile Asp Pro Val Thr Phe Gly
        435                 440                 445


Val Leu Asp Phe Thr Val Tyr Ile Ala Asn Ile Ser Asp Pro Asp Tyr
    450                 455                 460


Gln Asn Gly Pro Thr Trp Ala Lys Tyr Tyr Ser Ala Lys Glu Thr Tyr
465                 470                 475                 480


Gly Thr Leu Leu Ser Pro Ala Val Thr Asp Ser Ser Ala Glu Leu Thr
                485                 490                 495


Pro Ala Phe Trp His Asn Val Thr Ala Val Phe Glu Thr Asp Asp Thr
            500                 505                 510


Ser Phe Gln Gly Tyr Trp Ala Arg Gln Thr Arg Gly Tyr Asp Val Ser
        515                 520                 525


Asn Cys Thr Asp Ser Ser Cys Lys Asn Gln Thr Ile Cys Ala Leu Arg
    530                 535                 540


Ala Ala Asp Ala Gln Tyr Asn Cys Val Val Pro Thr Ile Gly Phe Asn
545                 550                 555                 560


Phe Ala Lys Arg Asp Glu Thr Asp Gln Ala His Val Lys Ala Gln Lys
                565                 570                 575


Glu Lys Cys Asp Asp Thr Gly Leu Val Ser Leu Leu Gly Lys Ile Ile
            580                 585                 590


Ser Ser Ser Arg Asn Val Ser Ser
        595                 600


<210>  274
<211>  601
<212>  PRT
<213>  Hamigera terricola

<400>  274

Gln Met Gln Thr Ser Glu Arg Ser Trp Gly Ser Thr Ile Trp Lys Asp
```

```
1               5                   10                  15

Val Glu Glu Ala Val Asp Cys Ala Gly Cys Glu Val Ile Leu Gly Ala
            20                  25                  30

Leu Lys Leu Val Ala Asp Leu Gly Lys Gly Thr Leu Glu Thr Ala Met
        35                  40                  45

Ile Asp Val Cys Asp Leu Ser Gly Ala Glu Asp Ser Asp Val Cys Ser
    50                  55                  60

Gly Leu Ile Thr Ala Glu Ile Asp Ala Leu Tyr Tyr Ala Leu Asn Asn
65                  70                  75                  80

Val His Val Gly Ser His Thr Ser Lys Val Leu Cys Ala His Leu Phe
                85                  90                  95

Gly Leu Cys Ser Tyr Pro Asp Val Arg Ser Tyr His Leu Ile Phe Pro
            100                 105                 110

Ser Ser Lys Pro Ala Thr Ser Arg Pro Ser Pro Ser Gly Gln Lys Pro
        115                 120                 125

Ile Lys Val Ala His Ile Ser Asp Thr His Val Asp Leu Ser Tyr Glu
    130                 135                 140

Pro Gly Ser Asn Tyr Glu Cys Ser Lys Pro Ile Cys Cys Arg Ala Tyr
145                 150                 155                 160

Thr Lys Glu Asp Ser Pro Gly Asn Thr Pro His Pro Cys Gly Pro Tyr
                165                 170                 175

Gly Asn Thr Asn Cys Asp Ala Pro Tyr Arg Leu Glu Glu Ser Met Phe
            180                 185                 190

Ala Ala Ile Glu Ala Leu Asp Pro Ala Phe Ser Ile Tyr Thr Gly Asp
        195                 200                 205

Val Val Ala His Asp Ile Trp Leu Val Asn Glu Thr Glu Val Leu Asp
```

```
    210                 215                 220


Asp Leu Asp Ala Thr Tyr Ser Leu Met Lys Ser Leu Gly Leu Val Tyr
225                 230                 235                 240


Ala Ala Val Gly Asn His Asp Ala Ala Pro Val Asn Leu Phe Pro Ser
                245                 250                 255


Asn Arg Ile Pro Ser Thr Tyr Ser Pro Gln Trp Ala Tyr Asp Ala Leu
            260                 265                 270


Ala Glu Asp Trp Leu Ala Leu Thr Asn Asp Ser Ser Val Asp Ser Ala
        275                 280                 285


Arg Glu Tyr Gly Ser Tyr Ser Ala Val Tyr Pro Gly Ser Asn Leu Arg
    290                 295                 300


Ile Ile Ser Tyr Asn Ser Val Phe Tyr Tyr Lys Asp Asn Phe Trp Met
305                 310                 315                 320


Tyr Glu Asp Pro Met Glu Tyr Asp Pro Asn Gly Gln Leu Ala Trp Leu
                325                 330                 335


Ile Asn Glu Leu Gln Ala Ala Glu Ser Ala Gly Glu Arg Val Trp Leu
            340                 345                 350


Ile Ser His Ile Pro Ser Gly Asn Ser Asp His Leu Tyr Asp Tyr Ser
        355                 360                 365


His Tyr Phe Asp Ala Ile Val Gln Arg Tyr Glu Ala Thr Ile Ala Ala
    370                 375                 380


Leu Phe Phe Gly His Thr His Thr Asp Leu Phe Gln Ile Ala Tyr Ser
385                 390                 395                 400


Asp Tyr Asp Asn Arg Asn Trp Asp Thr Ala Thr Ala Ile Gly Tyr Ile
                405                 410                 415


Ala Pro Ser Met Thr Pro Thr Ser Gly Ser Pro Ala Phe Arg Ile Tyr
```

```
            420                 425                 430

Glu Val Asp Pro Val Thr Phe Gly Ile Leu Asp Tyr Thr Val Tyr Ile
        435                 440                 445

Ala Asn Ile Ser His Pro Ser Tyr Gln Thr Gln Pro Thr Trp Glu Lys
    450                 455                 460

Tyr Tyr Ser Ala Lys Glu Ala Tyr Gly Ser Leu Leu Thr Pro Pro Val
465                 470                 475                 480

Thr Asn Pro Ser Ile Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr
                485                 490                 495

Val Leu Met Glu Asp Asp Glu Ser Val Phe Lys Asp Phe Trp Ala Arg
            500                 505                 510

Thr Thr Arg Gly Phe Asn Val Ser Thr Cys Val Gly Ser Cys Met Thr
        515                 520                 525

Glu Glu Ile Cys Ala Leu Arg Ser Ala Asp Ala Lys Tyr Asn Cys Ala
    530                 535                 540

Thr Ala Lys Pro Gly Leu Asn Phe Leu Lys Arg Asp Asp Val Glu Ala
545                 550                 555                 560

Gln Ser Lys Pro Val Lys Pro Gln Cys Glu Asp Ser Gly Leu Ala Ala
                565                 570                 575

Val Leu Val Lys Met Met Glu Asn Thr Asp Asp Phe Ala Gly Leu Leu
            580                 585                 590

Lys Glu Lys Ala Leu Ala His Gly Lys
        595                 600


<210>  275
<211>  601
<212>  PRT
<213>  Penicillium piscarium
```

```
<400>  275

Arg Thr Glu Ala Ala Asp Ser Trp Ile Ser Asn Ile Trp Asn Glu Phe
1               5                   10                  15


Lys Glu Ala Val Asp Cys Gly Ser Cys Gln Val Leu Leu Gly Gly Leu
            20                  25                  30


Lys Leu Val Ala Asp Phe Gly Glu Gly Phe Leu Glu Asp Val Leu Thr
        35                  40                  45


Gly Val Cys Asp Val Ser Gly Ala Glu Asp Arg Asp Val Cys Ala Gly
    50                  55                  60


Val Ile Ala Asn Glu Val Pro Ala Leu His Tyr Ala Leu Lys Asn Met
65                  70                  75                  80


His Val Gly Ser His Thr Ala Lys Thr Leu Cys Ser Ala Leu Val Gly
                85                  90                  95


Leu Cys Asp Phe Pro Asn Val Arg Pro Phe Asp Leu Thr Phe Pro Ser
            100                 105                 110


Pro Lys Pro Ala Lys Ser Arg Pro Pro Pro Ser Gly Lys Pro Pro Ile
        115                 120                 125


Lys Val Val His Phe Ser Asp Thr His Val Asp Leu Ser Tyr Glu Thr
    130                 135                 140


Gly Ser Asn Tyr Asp Cys Ser Lys Pro Ile Cys Cys Arg Val Tyr Ser
145                 150                 155                 160


Asp Lys Asp Ala Pro Gly Lys Thr Asp Lys Pro Cys Gly Pro Phe Gly
                165                 170                 175


Asn Thr Lys Cys Asp Pro Pro Glu Arg Leu Gln Asp Ser Met Met Ala
            180                 185                 190


Ala Ile Ala Asp Leu Asn Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val
        195                 200                 205
```

```
Val Ala His Asp Val Trp Leu Val Asn Lys Asp Glu Val Leu Gln Asp
    210                 215                 220


Phe Asn Ser Thr Tyr Gly Ala Met Glu Asn His Leu Gly Leu Val Tyr
225                 230                 235                 240


Ala Ala Leu Gly Asn His Asp Ala Ala Pro Leu Asn Leu Phe Pro Ser
                245                 250                 255


Asn Asn Ile Pro Ser Lys Tyr Asn Pro Arg Trp Ala Tyr Glu Ala Leu
            260                 265                 270


Thr Ala Asn Trp Ile Thr Leu Thr Gly Ile Gln Ser Val Gln Asn Ala
        275                 280                 285


Asn Glu Tyr Gly Ser Tyr Ser Ala Ile His Pro Asn Ser Lys Leu Arg
    290                 295                 300


Ile Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Tyr Asn Phe Phe Ser
305                 310                 315                 320


Tyr Thr Glu Pro Met Glu Tyr Asp Pro Asn Gly Gln Leu Thr Trp Leu
                325                 330                 335


Ile Glu Glu Leu Gln Ala Ala Glu Asn Ala Gly Gln Arg Val Trp Leu
            340                 345                 350


Ile Ser His Ile Pro Ser Gly Asn Val Asp His Phe Arg Asp His Ser
        355                 360                 365


His Tyr Phe Asp Gln Ile Ile Gln Arg Tyr Glu Ala Thr Ile Ala Gly
    370                 375                 380


Leu Phe Phe Gly His Thr His Thr Asp Glu Phe Gln Ile Ser Tyr Ser
385                 390                 395                 400


Asp Tyr Lys Asn Arg Asn Trp Asp Thr Ala Thr Ala Met Gly Tyr Val
                405                 410                 415
```

```
Ala Pro Ser Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg Ile Tyr
            420                 425                 430


Asp Ile Asp Pro Glu Thr Phe Ala Val Met Asp Phe Thr Gln Tyr Ile
        435                 440                 445


Ala Asn Ile Ser Glu Ala Ser Phe Gln Thr Lys Pro Asn Trp Ile Pro
    450                 455                 460


Tyr Tyr Ser Ala Lys Lys Asp Tyr Gly Gly Arg Leu Thr Pro Pro Thr
465                 470                 475                 480


Pro Asn Thr Ala Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val
                485                 490                 495


Ala Met Glu Lys Asp Ser Ser Val Phe Asn Glu Phe Trp Ala Arg Arg
            500                 505                 510


Thr Arg Gly Tyr Ser Val Pro Ala Cys Thr Gly Asp Cys Val Lys Asn
        515                 520                 525


Glu Ile Cys Ala Leu Arg Gly Ala Asp Ala Gln Tyr Ser Cys Val Gln
    530                 535                 540


Arg Thr Pro Gly Phe Ser Phe Ser Lys Arg Asp Asp Gly Glu Val Glu
545                 550                 555                 560


Val Asp Leu Glu Asn Ala Pro Leu Leu Ser Lys Arg Phe Gln Pro Glu
                565                 570                 575


Cys Asn His Ala Gly Met Ala Pro Leu Leu Ala Lys Ile Ala His Lys
            580                 585                 590


Ala Ser Ile Ala Lys Met Asn Gly Glu
        595                 600


<210>  276
<211>  602
```

```
<212>  PRT
<213>  Talaromyces bacillisporus

<400>  276

Gly Gln Thr Pro Thr Ser Ser Leu Val Ala Arg Asp Leu Ala Ser Glu
1               5                   10                  15


Ile Trp Asn Asp Ile Lys Glu Ala Ala Thr Cys Ala Gly Cys Lys Val
            20                  25                  30


Ile Leu Ala Ala Leu Lys Gly Val Ala Asp Leu Gly Thr Thr Val Leu
        35                  40                  45


Ile Asp Val Leu Thr Glu Val Cys Lys Ile Ser Gly Glu Glu Asp Asp
    50                  55                  60


Asp Val Cys Glu Gly Ile Ile Ser Arg Glu Gly Pro Val Leu Glu Tyr
65                  70                  75                  80


Ile Leu Ser Gln Leu Ser Leu Ser Ser Glu Thr Ser Asp Val Leu Cys
                85                  90                  95


Ala Ser Ala Phe Gly Leu Cys Ser Tyr Pro Ala Val Arg Asp Tyr Thr
            100                 105                 110


Leu Thr Phe Pro Ser Pro Lys Pro Ala Asn Ile Thr Arg Pro Ser Pro
        115                 120                 125


Ser Gly Lys Ser Pro Ile Gln Val Val His Phe Ser Asp Thr His Val
    130                 135                 140


Asp Leu Ser Tyr Glu Thr Gly Ser Asn Trp Asn Cys Thr Lys Pro Ile
145                 150                 155                 160


Cys Cys Arg Ala Tyr Glu Ala Ser Asp Ala Pro Gly Asn Thr Thr Thr
                165                 170                 175


Pro Cys Gly Pro Tyr Gly Asn Thr Lys Cys Asp Ala Pro Leu Ser Leu
            180                 185                 190
```

```
Glu Gln Ser Met Ile Asp Ser Ile Lys Ala Leu Asp Pro Ala Pro Ala
        195                 200                 205


Phe Ser Ile Tyr Thr Gly Asp Val Val Ala His Asp Ile Trp Ile Val
    210                 215                 220


Asp Glu Asp Glu Val Leu Thr Asp Leu Asn Ala Ser Tyr Ser Leu Met
225                 230                 235                 240


Ala Glu Thr Gly Lys Val Phe Ala Ala Ile Gly Asn His Asp Ser Ala
                245                 250                 255


Pro Val Asn Asp Leu Pro Thr Thr Gln Val Pro Ser Lys Tyr Asn Ala
            260                 265                 270


Asn Trp Thr Tyr Gln Ala Leu Ala Asn Asn Phe Ser Thr Leu Thr Gly
        275                 280                 285


Asp Ser Ala Val Leu Ser Val Ala Glu Gln Tyr Gly Ser Tyr Ser Ser
    290                 295                 300


Val Phe Thr Gly Ser Tyr Gly Thr Asp Leu Lys Val Ile Ser Tyr Asn
305                 310                 315                 320


Ser Ile Phe Tyr Tyr Ile Asp Asn Phe Tyr Ala Phe Leu Asp Pro Met
                325                 330                 335


Pro Tyr Asp Pro Asp Gly Gln Leu Ala Trp Leu Ile Glu Glu Leu Gln
            340                 345                 350


Ala Ser Glu Thr Ala Gly Gln Arg Val Trp Leu Ile Ala His Val Pro
        355                 360                 365


Thr Ser Ser Ser Asp His Phe His Asp Tyr Ser His Tyr Phe Asp Gln
    370                 375                 380


Ile Val Gln Arg Tyr Glu Ala Thr Ile Ala Ala Leu Phe Phe Gly His
385                 390                 395                 400
```

```
Thr His Thr Asp Gln Phe Gln Ile Ser Tyr Ser Asn Tyr Ser Asn Gln
                405                 410                 415

Asn Ala Asp Thr Ala Ser Ala Ile Gly Tyr Ile Met Pro Ser Leu Thr
            420                 425                 430

Pro Thr Ser Gly Pro Pro Ala Tyr Arg Val Tyr Asp Ile Asp Pro Val
        435                 440                 445

Thr Phe Gly Val Leu Asp Phe Thr Val Tyr Ile Ser Asn Ile Ser Asp
    450                 455                 460

Pro Ala Phe Gln Asn Gly Pro Thr Trp Ser Lys Tyr Tyr Ser Ala Lys
465                 470                 475                 480

Glu Thr Tyr Gly Ser Leu Leu Ser Pro Pro Val Thr Asp Ser Thr Ala
                485                 490                 495

Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Ala Val Phe Glu Thr
            500                 505                 510

Asp Asp Asp Ala Phe Gln Gly Tyr Trp Ala Arg Gln Thr Arg Gly Tyr
        515                 520                 525

Asp Val Ser Asn Cys Thr Asp Thr Cys Lys Asn Gln Thr Ile Cys Gly
    530                 535                 540

Ile Arg Gly Ala Asp Ala Gln Tyr Asn Cys Val Val Pro Lys Ile Gly
545                 550                 555                 560

Phe Asn Phe Ala Lys Arg Asp Glu Thr Asp Gln Ala His Val Lys Thr
                565                 570                 575

Gln Lys Glu Lys Cys Asp Asp Ala Gly Leu Ala Ser Leu Phe Gly Arg
            580                 585                 590

Met Val Ala Asn Ser Lys Asn Ala Ser Asn
        595                 600
```

<210> 277
<211> 604
<212> PRT
<213> Galactomyces candidus

<400> 277

Ala Pro Pro Thr Thr Lys Arg Ser Leu Ala Ser Asp Ile Trp Asp Asp
1 5 10 15

Ile Val Asp Ala Val Asp Cys Gly Ala Cys Asp Thr Ile Leu Glu Ala
20 25 30

Leu Lys Gly Leu Ala Asp Leu Gly Asn Thr Val Phe Val Asp Val Leu
35 40 45

Thr Asp Val Cys Asp Ile Ser Gly Ala Glu Asp Ser Asp Val Cys Ser
50 55 60

Gly Thr Ile Ser Glu Glu Gly Pro Ile Leu Arg Thr Ile Ile Lys Gly
65 70 75 80

Leu Ser Val Gly Ser Ala Thr Ser Asp Leu Phe Cys Gly Thr Leu Leu
85 90 95

Gly Leu Cys Gln Asn Pro Ala Ile Ala Ser Trp Ser Val Pro Phe Pro
100 105 110

Lys Pro Lys Pro Asn Thr Val Arg Pro Pro Pro Ser Gly Gln Ser Pro
115 120 125

Ile Ser Val Ala His Ile Ser Asp Val His Val Asp Leu Ser Tyr Thr
130 135 140

Thr Gly Ala Asn Tyr Asp Cys Ser Lys Pro Ile Cys Cys Arg Pro Tyr
145 150 155 160

Thr Ser Asp Asp Ala Pro Gly Asn Thr Asp Tyr Pro Ala Gly Pro Tyr
165 170 175

```
Gly Asn Thr Asn Cys Asp Ala Pro Leu Asp Leu Glu Ser Ser Ala Met
            180                 185                 190


Ala Ala Ile Lys Lys Leu Asn Pro Ala Phe Ser Ile Phe Thr Gly Asp
        195                 200                 205


Val Ala Ala His Asp Val Trp Leu Val Asn Gln Ala Glu Val Glu Leu
    210                 215                 220


Asp Leu Asn Thr Thr Tyr Asn Thr Gln Phe Thr Thr Leu Gly Thr Val
225                 230                 235                 240


Phe Pro Ala Leu Gly Asn His Asp Val Ala Pro Val Asn Gly Phe Ala
                245                 250                 255


Pro Ser Gly Val Ser Ser Asn Pro Asn Ile Gln Trp Ala Tyr Asp Thr
            260                 265                 270


Asn Ala Glu Asp Trp Thr Lys Trp Ile Gly Ser Thr Ala Ala Asn Ala
        275                 280                 285


Glu Glu Ser Phe Gly Ala Tyr Ser Ile Val His Gly Asn Leu Arg Val
    290                 295                 300


Ile Ser Phe Asn Ser Ile Phe Tyr Tyr Arg Leu Asn Phe Tyr Met Tyr
305                 310                 315                 320


Gln Asp Pro Leu Gln Arg Asp Pro Ser Ser Gln Phe Ser Trp Leu Val
                325                 330                 335


Asn Gln Leu Gln Ala Ala Glu Asp Ala Gly Gln Arg Ala Trp Leu Ile
            340                 345                 350


Ser His Val Pro Ser Gly Ser Gly Asp Tyr Phe Pro Gln Tyr Ser Asn
        355                 360                 365


Tyr Phe Asn Gln Ile Val Asn Arg Tyr Glu Ala Thr Ile Ala Ala Leu
    370                 375                 380
```

```
Phe Tyr Gly His Thr His Val Asp Gln Phe Glu Ile Ser Tyr Ser Asp
385                 390                 395                 400


Tyr Ser Asn Gln Asn Ser Asn Thr Ala Val Ala Met Ser Tyr Ile Thr
                405                 410                 415


Pro Ser Leu Thr Pro Thr Ser Gly Ser Pro Ser Phe Arg Ile Tyr Ser
            420                 425                 430


Ile Asp Pro Val Thr Tyr Gly Val Leu Asp Tyr Thr Asn Tyr Ile Ala
        435                 440                 445


Asn Ile Ser Ser Pro Thr Tyr Gln Asn Gly Pro Gln Trp Val Glu Tyr
    450                 455                 460


Tyr Ser Ala Lys Ala Ala Tyr Gly Pro Tyr Val Ser Pro Pro Leu Thr
465                 470                 475                 480


Ser Ala Ala Ala Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val
                485                 490                 495


Ala Phe Gln Asn Asn Asn Asp Leu Phe Gln Glu Tyr Ile Ser Arg Lys
            500                 505                 510


Ser Arg Gly Phe Asp Val Ser Ser Cys Thr Gly Ser Cys Gln Thr Asp
        515                 520                 525


Glu Ile Cys Gln Leu Arg Ala Ala Glu Ser Gln Tyr Asn Cys Val Thr
    530                 535                 540


Ile Ser Pro Gly Ile Asn Phe Asn Lys Arg Asp Gln Gln Ser Asn Leu
545                 550                 555                 560


Gly Ala Gln Glu Lys His Arg Asp Gly Cys Glu Gly Ser Pro Ile Arg
                565                 570                 575


Asp Ile Phe Ala Thr Leu Met Gln Asp Arg Arg Gly Leu Val Ser Ala
            580                 585                 590
```

```
Ile Asn Glu Gly Ile Ala Lys Arg Ser Ile Arg Ala
        595                 600


<210>  278
<211>  607
<212>  PRT
<213>  Penicillium megasporum

<400>  278

Asn Ile Ile Glu Ser Trp Ala Ser Glu Ile Trp Asp Asp Ile Lys Asn
1               5                   10                  15


Ala Val Asp Cys Ala Gly Cys Glu Thr Ile Ile Gly Ala Leu Lys Val
            20                  25                  30


Val Ala Asp Leu Gly Lys Gly Thr Leu Asn Gly Thr Leu Ile Asp Val
        35                  40                  45


Cys Asp Leu Ser Gly Val Glu Asp Pro Asp Val Cys Thr Gly Leu Ile
    50                  55                  60


Ser Ser Glu Ile Asp Ala Leu Tyr Tyr Ser Leu Lys Asn Met Ala Val
65                  70                  75                  80


Asp Ser His Thr Ser Lys Val Leu Cys Ala Gly Leu Phe Ser Leu Cys
                85                  90                  95


Pro Phe Pro Ala Ala Arg Pro Tyr Asn Leu Ser Phe Pro Thr Pro Lys
            100                 105                 110


Pro Ala Thr Ser Arg Pro Ala Pro Ser Gly Gln Gln Pro Ile Lys Val
        115                 120                 125


Ala His Ile Ser Asp Thr His Val Asp Leu Asp Tyr Glu Ala Gly Ser
    130                 135                 140


Asn Tyr Gln Cys Ser Lys Pro Ile Cys Cys Arg Pro Tyr Thr Ala Glu
145                 150                 155                 160


Asp Ala Pro Gly Asn Thr Ser His Pro Cys Gly Pro Trp Gly Asn Thr
```

```
                165                 170                 175

Lys Cys Asp Pro Pro Phe Arg Leu Glu Glu Ser Met Val Ala Ala Val
            180                 185                 190

Asn Ala Leu Asn Pro Ser Phe Ser Ile Tyr Thr Gly Asp Val Val Ala
        195                 200                 205

His Asp Ile Trp Leu Val Asn Glu Ser Glu Val Leu Thr Asp Leu Asn
    210                 215                 220

Ala Thr Tyr Ser Leu Phe Gln Asn Leu Asn Ser Leu Val Tyr Ala Ala
225                 230                 235                 240

Val Gly Asn His Asp Val Ala Pro Val Asn Leu Phe Pro Ser Asn Lys
                245                 250                 255

Ile Asp Ser Ala Tyr Asn Pro Gln Trp Ala Tyr Asp Ala Leu Thr Ala
            260                 265                 270

Asp Trp Leu Ala Leu Thr Asn Gly Asp Ser Ser Val Ala Ser Ala Lys
        275                 280                 285

Ala Asp Gly Ser Tyr Ser Ala Ile Tyr Pro Gly Thr Asn Leu Arg Ile
    290                 295                 300

Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Lys Asp Asn Phe Trp Met Tyr
305                 310                 315                 320

Ser Asp Pro Met Glu Tyr Asp Pro Asn Gly Gln Phe Ala Trp Leu Ile
                325                 330                 335

Asp Glu Leu Gln Ala Ala Glu Thr Ala Gly Gln Arg Val Trp Leu Ile
            340                 345                 350

Ser His Ile Pro Ser Gly Asn Ser Asp His Leu Tyr Asp Tyr Ser His
        355                 360                 365

Tyr Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr Ile Ala Ala Leu
```

```
    370                 375                 380


Phe Phe Gly His Thr His Thr Asp Leu Phe Gln Val Ala Tyr Ser Asp
385                 390                 395                 400


Tyr Gly Asn Arg Asn Ser Asp Thr Ala Ser Ala Ile Gly Tyr Val Thr
                405                 410                 415


Pro Ser Met Thr Pro Thr Ser Gly Pro Pro Ala Phe Arg Ile Tyr Glu
            420                 425                 430


Ile Asp Pro Val Thr Phe Gly Val Leu Asp Tyr Thr Val Tyr Ile Ala
        435                 440                 445


Asn Ile Ser Asp Pro Ala Tyr Gln Thr Gly Pro Ser Trp Gln Lys Tyr
    450                 455                 460


Tyr Ser Ala Lys Glu Val Tyr Gly Ser Leu Leu Ser Pro Pro Leu Thr
465                 470                 475                 480


Asp Pro Ala Ala Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Val
                485                 490                 495


Leu Met Glu Glu Asp Asp Ser Val Phe Gln Asp Trp Trp Ala Arg Thr
            500                 505                 510


Thr Arg Gly Phe Asn Val Ser Thr Cys Thr Gly Ser Cys Ala Thr Asn
        515                 520                 525


Glu Ile Cys Ala Leu Arg Gly Ala Asp Ala Gln Tyr Asn Cys Val Thr
    530                 535                 540


Ala Ser Pro Gly Ile Gln Phe Ala Lys Arg Gly Gly Ala Val Asp Phe
545                 550                 555                 560


Asp Pro Asn Ala Gln Pro Val Ala Lys Pro His Cys Asp Glu Gly Ser
                565                 570                 575


Gly Leu Ala Pro Val Leu Val Lys Met Met Arg Asn Thr Asp Asp Phe
```

```
            580                 585                 590


Ala Gly Leu Leu Lys Glu Arg Ala Ala Leu Gln Asp Ser Gln Gln
        595                 600                 605



<210>  279
<211>  610
<212>  PRT
<213>  Penicillium jensenii

<400>  279

Glu Thr Ser Lys Ala Ser Thr Glu Ser Phe Ile Ser Ser Ile Trp Asp
1               5                   10                  15


Asp Phe Lys Gln Ala Val Asp Cys Gly Ser Cys Gln Ala Leu Leu Gly
            20                  25                  30


Gly Leu Lys Leu Val Ser Gly Phe Gly Glu Gly Phe Met Ile Asp Val
        35                  40                  45


Phe Ile Gly Leu Cys Asn Leu Ser Gly Val Glu Asp Pro Asp Val Cys
    50                  55                  60


Arg Gly Ile Ile Glu Lys Glu Gly Pro Ala Leu His Asp Ala Phe Gln
65                  70                  75                  80


Asn Leu His Ile Gly Ser His Ala Thr Arg Thr Met Cys Ala Ser Leu
                85                  90                  95


Ile Gly Leu Cys Gln Tyr Pro Glu Val Arg Pro His Thr Leu Gln Phe
            100                 105                 110


Pro Ser Ser Lys Pro Asp Thr Thr Arg Pro Pro Pro Ser Gly Lys Ser
        115                 120                 125


Pro Ile Lys Val Val His Phe Ser Asp Thr His Val Asp Leu Phe Tyr
    130                 135                 140


Glu Thr Gly Ala Ser Tyr Glu Cys Ser Lys Pro Ile Cys Cys Arg Val
145                 150                 155                 160
```

```
Tyr Glu Asp Lys Asp Ala Pro Gly Ile Thr Lys Thr Pro Cys Gly Pro
                165                 170                 175


Phe Gly Asn Thr Lys Cys Asp Pro Pro His Ile Leu Gln Glu Ser Met
            180                 185                 190


Asn Ala Ala Ile Ala Lys Ile Asp Pro Asp Phe Ser Ile Tyr Thr Gly
        195                 200                 205


Asp Val Val Ala His Asp Ile Trp Leu Val Gly Gln Asp Glu Ala Leu
    210                 215                 220


Gln Val Phe Asn Asp Thr Tyr Gly Gln Met Glu Lys Asp Leu Gly Met
225                 230                 235                 240


Val Tyr Ala Ala Ile Gly Asn His Asp Thr Ala Pro Val Asn Leu Phe
                245                 250                 255


Pro Pro Asn Asp Ile Lys Gly Lys Asp Ser Ala Gln Phe Ala Tyr Asn
            260                 265                 270


Ala Leu Ala Glu Asp Trp Tyr Ala Leu Thr Gly Ile Pro Ser Val Lys
        275                 280                 285


Ser Ala Asp Glu Phe Gly Ser Tyr Ser Ala Ile His Pro Asn Ser Asn
    290                 295                 300


Leu Arg Ile Ile Ser Tyr Asn Ser Ile Phe Tyr Tyr Asn Phe Asn Phe
305                 310                 315                 320


Tyr Met Tyr Gln Asp Pro Met Glu Lys Asp Pro Asn Gly Gln Phe Glu
                325                 330                 335


Trp Leu Ile Lys Glu Leu Gln Ala Ala Glu Asp Ala Gly Gln Arg Ala
            340                 345                 350


Trp Leu Ile Ser His Ile Pro Ser Gly Val Thr Asp His Phe Arg Asp
        355                 360                 365
```

```
Tyr Ser Gln Tyr Phe Asp Gln Ile Val Gln Arg Tyr Glu Ala Thr Ile
    370                 375                 380


Ala Gly Leu Phe Tyr Gly His Thr His Met Asp Glu Phe Gln Ile Ala
385                 390                 395                 400


Tyr Ser Asp Tyr Asn Asn Arg Lys Trp Asp Thr Ala Thr Ala Met Gly
                405                 410                 415


Tyr Ile Ala Pro Ser Met Thr Pro Thr Ser Gly Pro Pro Ser Phe Arg
            420                 425                 430


Val Tyr Glu Ile Asp Pro Val Thr Tyr Gly Val Leu Asp Phe Thr Gln
        435                 440                 445


Tyr Ile Ala Asn Ile Ser Asp Pro Ser Tyr Gln Thr Lys Pro Glu Trp
    450                 455                 460


Val Pro Tyr Tyr Ser Ala Lys Ala Ala Tyr Gly Ser Lys Leu Ser Pro
465                 470                 475                 480


Pro Leu Thr Asp Ser Thr Ala Glu Leu Thr Pro Ala Phe Trp His Asn
                485                 490                 495


Val Thr Val Thr Met Glu Lys Asp Pro Ser Ile Phe Gln Asp Phe Trp
            500                 505                 510


Ala Arg Arg Asn Arg Gly Trp Asn Ile Ala Ala Cys Thr Gly Asp Cys
        515                 520                 525


Met Lys Lys Glu Leu Cys Thr Leu Arg Ala Ala Asp Ala Gln His Asn
    530                 535                 540


Cys His Glu Pro Thr Pro Gly Leu Asn Ile Ser Ile Asn Lys Arg Asp
545                 550                 555                 560


Gln Gly Ser Gly Asp Val Pro Leu Glu Gly Glu Lys Val Ser Gly Pro
                565                 570                 575
```

```
Glu Cys Asp His Ala Gly Met Ala Thr Leu Leu Gly Lys Ile Ala Tyr
            580                 585                 590


Arg Ala Arg Leu Val Arg Glu Ala Glu Glu Arg Asp Pro Val Arg Ala
        595                 600                 605


Glu Ala
    610


<210>  280
<211>  610
<212>  PRT
<213>  Aspergillus stramenius

<400>  280

Glu Asn Trp Val Asn Thr Ile Trp Asp Glu Ile Lys Glu Thr Ile Ser
1               5                   10                  15


Cys Ala Gly Cys Glu Gly Leu Leu Gly Thr Leu Lys Leu Val Ala Gly
            20                  25                  30


Leu Gly Pro Asp Val Leu Thr Asn Val Leu Thr Asp Val Cys Lys Leu
        35                  40                  45


Ala Lys Val Glu Asp Pro Asp Val Cys Ala Gly Ile Ile Glu Ala Glu
    50                  55                  60


Gly Pro Ala Ala Tyr Tyr Val Leu Lys Gln Leu Lys Val Gly Ser His
65                  70                  75                  80


Thr Ser Lys Ser Phe Cys Ser Gln Met Val Gly Leu Cys Asp Tyr Pro
                85                  90                  95


Glu Val Arg Pro Tyr Asn Ile Ser Phe Pro Ile Pro Lys Pro Ser Thr
            100                 105                 110


His Arg Pro Pro Pro Ser Gly Gln Pro Pro Ile Arg Val Ala His Ile
        115                 120                 125
```

```
Ser Asp Thr His Val Asp Arg Ala Tyr Glu Thr Gly Ala Asn Tyr Glu
    130                 135                 140


Cys Ser Lys Pro Ile Cys Cys Arg Val Tyr Thr Glu Asp Asp Ala Pro
145                 150                 155                 160


Gly Lys Thr Ser Phe Pro Cys Gly Pro Tyr Gly His Pro Lys Cys Asp
                165                 170                 175


Pro Pro Leu Arg Leu Glu Glu Ser Met Met Ala Ala Ile Ala Ala Met
            180                 185                 190


Asp Pro Ala Phe Ser Ile Tyr Thr Gly Asp Val Val Pro His Asp Val
        195                 200                 205


Trp Ser Val Asn Arg Thr Glu Val Leu His Asp Leu Asn Ala Thr Tyr
    210                 215                 220


Ser Leu Leu Asp Arg Leu Gly Leu Val Tyr Ala Ala Leu Gly Asn His
225                 230                 235                 240


Asp Thr Ala Pro Val Asn Leu Phe Pro Ser Glu Arg Ile Pro Val Ser
                245                 250                 255


His Asn Pro Gln Trp Ala Tyr Asp Ala Leu Ala Glu Asp Trp Thr Asn
            260                 265                 270


Leu Val Asp Gly Pro Leu Ser Ala Pro Val Val His Ala Thr Asp Gln
        275                 280                 285


Phe Gly Ser Tyr Ser Ala Leu His Pro Gly Gly Lys Leu Arg Ile Ile
    290                 295                 300


Ser Tyr Asn Ser Val Phe Tyr Tyr Thr Tyr Asn Phe Tyr Ala Tyr Gln
305                 310                 315                 320


Glu Pro Met Glu Tyr Asp Pro Asn Gly Gln Leu Ala Trp Leu Val Ala
                325                 330                 335
```

```
Glu Leu Gln Ala Ala Glu Thr Ala Gly Gln Arg Val Trp Leu Ile Ala
            340                 345                 350


His Ile Pro Thr Gly Ala Ala Asp Thr Leu Arg Asp Tyr Ser His Tyr
        355                 360                 365


Leu Asp Gln Ile Ile Gln Arg Tyr Asp Ala Thr Ile Ala Ala Leu Phe
    370                 375                 380


Phe Gly His Thr His Thr Asp Leu Phe Gln Val Ser Tyr Ala Asn Pro
385                 390                 395                 400


Ala His Pro Ser Ala Asp Ser Ala Ser Ala Val Gly Tyr Ile Thr Pro
                405                 410                 415


Ser Leu Thr Pro Thr Ser Gly Pro Pro Ala Phe Arg Ile Tyr Asp Ile
            420                 425                 430


Asp Pro Val Thr Phe Ala Val Leu Asp Tyr Thr Val Tyr Thr Ala Asn
        435                 440                 445


Ile Ser Thr Gly Ala Thr Pro Lys Trp Asn Lys Tyr Tyr Ser Ala Lys
    450                 455                 460


Gln Thr Tyr Gly Ser Leu Leu Thr Pro Pro Leu Thr Asp Pro Thr Ala
465                 470                 475                 480


Glu Leu Thr Pro Ala Phe Trp His Asn Val Thr Ala Leu Met Glu Thr
                485                 490                 495


Asp Asn Thr Val Phe Gln Ala Trp Trp Ala Arg Thr Thr Arg Gly Phe
            500                 505                 510


Asn Val Pro Glu Cys Asn Ala Gln Cys Ala Arg Asp Gln Ile Cys Ser
        515                 520                 525


Leu Arg Ala Ala Asp Ala Gln Tyr Gly Cys Val Arg Gly Thr Leu Ser
    530                 535                 540
```

```
Ile Thr Lys Arg Ala Gly Asp Gly Asp Gly Leu Asp Leu Gly Gly Ala
545                 550                 555                 560


Gly Ala Gly Gly Pro Pro Gly Arg Arg Arg His Val Gln Ser Ala Arg
                565                 570                 575


Pro Gln Cys Glu Glu Ala Gly Leu Ala Arg Val Leu Ala Ala Val Ile
            580                 585                 590


Arg Glu Thr Asp Asp Leu Gln Gly Leu Leu Leu Gln Arg Ala Gln Leu
        595                 600                 605


Tyr Ile
    610


<210>  281
<211>  258
<212>  PRT
<213>  Bacillus pseudomycoides

<400>  281

His Thr Asn Asp Cys Gly Asn Glu Ala Pro Ile Leu Arg Trp Ser Ala
1               5                   10                  15


Glu Asp Arg His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val Asn
            20                  25                  30


Arg Ala Ile Asp Ile Met Ser Arg Asn Asn Thr Ile Val Lys Pro Asn
        35                  40                  45


Glu Thr Ala Leu Leu Asn Glu Trp Arg Asn Glu Leu Glu Asn Gly Ile
    50                  55                  60


Tyr Ser Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe Ala
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gln Lys Thr Tyr Ile Pro Leu Ala
                85                  90                  95
```

```
Lys Gln Ala Lys Glu Thr Gly Ser Lys Tyr Phe Lys Leu Ala Gly Glu
            100                 105                 110


Ala Tyr Gln Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly Leu
        115                 120                 125


Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala Asn
    130                 135                 140


Phe Thr Asn Leu Ser Tyr Pro Met Gly Phe His Ser Lys Tyr Glu Asn
145                 150                 155                 160


Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Ala Asp Gly Asn Gly
                165                 170                 175


Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Glu Trp Ile His Gly Ala
            180                 185                 190


Ala Ala Ala Ala Lys Gln Asp Tyr Pro Gly Ile Val Asn Asp Ser Thr
        195                 200                 205


Lys Ser Gly Phe Val Lys Ala Ala Thr Ser Gln Glu Tyr Ala Asn Lys
    210                 215                 220


Trp Arg Ala Glu Val Thr Pro Ala Thr Gly Lys Arg Leu Thr Glu Ala
225                 230                 235                 240


Gln Arg Val Thr Ala Gly Tyr Ile His Leu Trp Phe Asp Thr Tyr Val
                245                 250                 255


Asn Arg




<210>  282
<211>  259
<212>  PRT
<213>  Bacillus mycoides

<400>  282

Gln Glu Asn Asp Gly Gly Asn Arg Val Asn Ile Ile Gln Tyr Trp Ser
```

```
1               5                   10                  15

Ala Glu Asp Lys His Thr Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30

Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Met Thr Leu Val Lys Gln
        35                  40                  45

Asp Gln Val Ala Leu Leu Asn Glu Trp Arg Thr Asp Leu Glu Asn Gly
    50                  55                  60

Ile Tyr Ser Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80

Ala Ser His Phe Tyr Asp Pro Asp Asp Gly Ser Thr Tyr Ile Pro Phe
                85                  90                  95

Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110

Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125

Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140

Asn Phe Thr Asn Ile Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160

Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Asn
                165                 170                 175

Gly Tyr Trp Asn Trp Lys Gly Ala Asn Pro Glu Asp Trp Ile His Gly
            180                 185                 190

Ala Ala Val Ala Ala Lys Gln Asp Phe Pro Gly Ile Val Asn Ser Asn
        195                 200                 205

Thr Lys Ser Trp Phe Val Lys Ala Ala Val Ser Gln Ser Tyr Ala Asp
```

```
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Lys Arg Leu Ile Glu
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Val Asn Arg




<210>  283
<211>  259
<212>  PRT
<213>  Bacillus thuringiensis

<400>  283

His Glu Lys Thr Glu Gly His Asn Val Asn Ile Ile Gln Tyr Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Ser Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Thr Arg Val Lys Gln
        35                  40                  45


Asp Gln Val Val Leu Leu Asn Glu Trp Arg Thr Asp Val Glu Asn Gly
    50                  55                  60


Ile Tyr Ser Ala Asp His Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Asp Gly Ser Thr Tyr Ile Pro Phe
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125
```

```
Val Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Met Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Ile His Pro Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Ala Ala Lys Gln Asp Phe Ser Gly Ile Val Asn Arg Asn
        195                 200                 205


Thr Lys Ser Trp Phe Val Gln Ala Ala Val Ser Gln Ser Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Lys Arg Leu Ile Glu
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Gly Asn Arg



<210>  284
<211>  262
<212>  PRT
<213>  Listeria innocua

<400>  284

Cys Cys Asp Glu Tyr Leu Gln Ala Pro Ala Ala Pro His Asp Ile Asp
1               5                   10                  15


Ser Lys Leu Pro His Lys Leu Ser Trp Ser Ala Asp Asn Pro Thr Asn
            20                  25                  30
```

```
Thr Asp Val Asn Thr His Tyr Trp Leu Phe Lys Gln Ala Glu Lys Ile
        35                  40                  45


Leu Ala Lys Asp Val Asn His Ile Arg Ala Asn Leu Met Asn Glu Leu
    50                  55                  60


Lys Asn Phe Asp Lys Gln Ile Ala Gln Gly Ile Tyr Asp Ala Asp His
65                  70                  75                  80


Lys Asn Pro Tyr Tyr Asp Thr Ser Thr Phe Leu Ser His Phe Tyr Asn
                85                  90                  95


Pro Asp Arg Asp Asn Thr Tyr Leu Pro Gly Phe Ala Asn Ala Lys Ile
            100                 105                 110


Thr Gly Ala Lys Tyr Phe Asn Gln Ser Val Ala Asp Tyr Arg Glu Gly
        115                 120                 125


Lys Phe Asp Thr Ala Phe Tyr Lys Leu Gly Leu Ala Ile His Tyr Tyr
    130                 135                 140


Thr Asp Ile Ser Gln Pro Met His Ala Asn Asn Phe Thr Ala Ile Ser
145                 150                 155                 160


Tyr Pro Pro Gly Tyr His Cys Ala Tyr Glu Asn Tyr Val Asp Thr Ile
                165                 170                 175


Lys His Asn Tyr Gln Ala Thr Glu Asp Met Val Val Lys Arg Phe Cys
            180                 185                 190


Ser Asp Asp Val Lys Val Trp Leu Tyr Glu Asn Ala Lys Arg Ala Lys
        195                 200                 205


Ala Asp Tyr Pro Lys Ile Val Asn Ala Lys Thr Lys Lys Ser Tyr Leu
    210                 215                 220


Val Gly Asn Ser Lys Trp Lys Lys Asp Thr Val Glu Pro Thr Gly Ala
225                 230                 235                 240
```

```
Arg Leu Arg Asp Ser Gln Gln Thr Leu Ala Gly Phe Leu Glu Phe Trp
                245                 250                 255


Ser Lys Lys Thr Asn Glu
            260


<210>  285
<211>  275
<212>  PRT
<213>  Aspergillus egyptiacus

<400>  285

Ala Pro Ala Pro Leu Thr Arg Arg Asp Val Ser Ser Glu Val Leu Glu
1               5                   10                  15


Gln Leu Thr Leu Phe Ala Glu Tyr Ser Ala Ala Ser Tyr Cys Pro Ser
            20                  25                  30


Asn Leu Asp Ser Pro Gly Thr Lys Leu Thr Cys Ser Thr Gly Asn Cys
        35                  40                  45


Pro Thr Val Glu Ala Ala Asp Thr Glu Thr Leu Ala Glu Phe Tyr His
    50                  55                  60


Ala Asp Glu Tyr Gly Asp Val Ala Gly Tyr Leu Ala Val Asp Thr Thr
65                  70                  75                  80


Asn Gln Leu Leu Val Val Ala Phe Arg Gly Ser Arg Ala Leu Asp Thr
                85                  90                  95


Trp Ile Ala Asn Leu Asn Phe Gly Lys Asp Ser Val Asp Asp Leu Cys
            100                 105                 110


Ser Gly Cys Glu Val His Gly Gly Phe Trp Gln Ser Trp Gln Val Val
        115                 120                 125


Ala Asp Ser Val Ala Ser Gly Val Glu Ser Ala Leu Gln Thr Tyr Pro
    130                 135                 140
```

```
Asp Tyr Thr Ile Val Phe Thr Gly His Ser Phe Gly Gly Ala Val Ala
145                 150                 155                 160


Thr Leu Gly Ala Val Glu Leu Arg Asn Ala Gly Tyr Asp Ile Glu Leu
                165                 170                 175


Tyr Pro Tyr Gly Ala Pro Arg Val Gly Asn Glu Ala Leu Ala Gln Tyr
            180                 185                 190


Ile Thr Asp Gln Gly Ser Asn Tyr Arg Val Thr His Thr Asn Asp Ile
        195                 200                 205


Val Pro Arg Leu Pro Pro Met Ser Phe Gly Phe Ser His Ser Ser Pro
    210                 215                 220


Glu Tyr Trp Ile Thr Ser Asp Asp Glu Val Thr Pro Thr Thr Ala Asp
225                 230                 235                 240


Val Glu Val Ile Glu Gly Val Gly Ser Thr Glu Gly Asn Ala Gly Glu
                245                 250                 255


Phe Pro Gln Ser Thr Ala Ala His Ser His Tyr Ile Ile Asp Ile Ser
            260                 265                 270


Ala Cys Glu
        275


<210>  286
<211>  276
<212>  PRT
<213>  Aspergillus tamarii

<400>  286

Thr Pro Ala Pro Leu Arg Arg Asp Val Ser Ser Ser Leu Leu Asn Asn
1               5                   10                  15


Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Glu Asn
            20                  25                  30


Leu Asn Ser Thr Gly Thr Lys Leu Thr Cys Ser Val Gly Asn Cys Pro
```

```
        35                  40                  45

Leu Val Glu Leu Ala Ser Thr Asn Thr Leu Asp Glu Phe Asp Glu Ser
    50                  55                  60

Ser Ser Tyr Gly Asn Pro Ala Gly Tyr Leu Ala Ala Asp Glu Thr Asn
65                  70                  75                  80

Lys Leu Leu Val Leu Ser Phe Arg Gly Ser Ser Asp Leu Ala Asn Trp
                85                  90                  95

Val Ala Asn Leu Asn Phe Gly Leu Glu Asp Ala Ser Asp Leu Cys Ser
            100                 105                 110

Gly Cys Glu Val His Ser Gly Phe Trp Lys Ala Trp Ser Glu Ile Ala
        115                 120                 125

Asp Thr Ile Thr Ser Lys Val Glu Ser Ala Leu Ser Asp His Ser Asp
    130                 135                 140

Tyr Ser Leu Val Leu Thr Gly His Ser Tyr Gly Ala Ala Leu Ala Ala
145                 150                 155                 160

Leu Ala Ala Thr Ala Leu Arg Asn Ala Gly His Ser Val Gln Leu Tyr
                165                 170                 175

Asn Tyr Gly Gln Pro Arg Leu Gly Asn Glu Ala Leu Ala Thr Tyr Ile
            180                 185                 190

Thr Asp Gln Asn Lys Gly Ala Asn Tyr Arg Val Thr His Thr Asn Asp
        195                 200                 205

Ile Val Pro Lys Leu Pro Pro Thr Leu Leu Gly Tyr His His Phe Ser
    210                 215                 220

Pro Glu Tyr Tyr Ile Ser Ser Ala Asp Glu Ala Thr Val Thr Thr Ala
225                 230                 235                 240

Asp Val Thr Glu Val Thr Gly Ile Asp Ala Thr Gly Gly Asn Asp Gly
```

```
                245                 250                 255


Thr Asp Gly Thr Ser Ile Asp Ala His Arg Trp Tyr Phe Ile Tyr Ile
            260                 265                 270


Ser Gln Cys Ser
        275


<210>  287
<211>  277
<212>  PRT
<213>  Aspergillus niger

<400>  287

Ala Pro Ala Pro Met Gln Arg Arg Asp Ile Ser Ser Thr Val Leu Asp
1               5                   10                  15


Asn Ile Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ser
            20                  25                  30


Asn Ile Glu Ser Thr Gly Thr Thr Leu Thr Cys Asp Val Gly Asn Cys
        35                  40                  45


Pro Leu Val Glu Ala Ala Gly Ala Thr Thr Ile Asp Glu Phe Asp Asp
    50                  55                  60


Thr Ser Ser Tyr Gly Asp Pro Thr Gly Phe Ile Ala Val Asp Pro Thr
65                  70                  75                  80


Asn Glu Leu Ile Val Leu Ser Phe Arg Gly Ser Ser Asp Leu Ser Asn
                85                  90                  95


Trp Ile Ala Asp Leu Asp Phe Gly Leu Thr Ser Val Ser Ser Ile Cys
            100                 105                 110


Asp Gly Cys Glu Met His Lys Gly Phe Tyr Glu Ala Trp Glu Val Ile
        115                 120                 125


Ala Asp Thr Ile Thr Ser Lys Val Glu Ala Ala Val Ser Ser Tyr Pro
    130                 135                 140
```

```
Asp Tyr Thr Leu Val Phe Thr Gly His Ser Tyr Gly Ala Ala Leu Ala
145                 150                 155                 160


Ala Val Ala Ala Thr Val Leu Arg Asn Ala Gly Tyr Thr Leu Asp Leu
                165                 170                 175


Tyr Asn Phe Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala Asp Tyr
            180                 185                 190


Ile Thr Gly Gln Asn Met Gly Ser Asn Tyr Arg Val Thr His Thr Asp
        195                 200                 205


Asp Ile Val Pro Lys Leu Pro Pro Glu Leu Leu Gly Tyr His His Phe
    210                 215                 220


Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Asp Val Thr Val Thr Thr
225                 230                 235                 240


Ser Asp Val Thr Glu Val Val Gly Val Asp Ser Thr Ala Gly Asn Asp
                245                 250                 255


Gly Thr Leu Leu Asp Ser Thr Thr Ala His Arg Trp Tyr Thr Ile Tyr
            260                 265                 270


Ile Ser Glu Cys Ser
        275


<210>  288
<211>  349
<212>  PRT
<213>  Bacillus luciferensis

<400>  288

Ile Thr Ser Phe Phe Gly Asn Tyr Gln Lys Ala Phe Ala Trp Ser Asp
1               5                   10                  15


Glu Asp Val His Asn Gln Asp His Ser Thr His His Phe Ile Val Asn
            20                  25                  30
```

```
Gly Ser Val Lys Leu Ile Ala Asp Asn Ala Asn Pro Ala Ile Asn Lys
        35                  40                  45

Pro Thr Thr Leu Leu Asn Gln Phe Arg Asp Arg Trp Glu Gln Gly Leu
    50                  55                  60

Tyr Asp Ala Asp His Ile Asn Pro Phe Tyr Asp Thr Gly Thr Phe Met
65                  70                  75                  80

Ser His Phe Tyr Asp Pro Asp Thr Gln Thr Asn Tyr Thr Gly Ala Ser
                85                  90                  95

Tyr Pro Thr Ala Arg Gln Ser Gly Ala Lys Tyr Phe Asn Leu Ala Ser
            100                 105                 110

Asp Tyr Tyr Lys Lys Gly Asp Phe Asn Asn Ala Phe Tyr Tyr Leu Gly
        115                 120                 125

Val Ser Leu His Tyr Phe Thr Asp Val Thr Gln Pro Leu His Ala Ser
    130                 135                 140

Asn Ile Ser Asn Leu Asp His His Ala Pro Gly Tyr His Ser Lys Phe
145                 150                 155                 160

Glu Thr Tyr Ala Glu Ser Ile Gln Asn Glu Met Thr Val Pro Asp Ser
                165                 170                 175

Gly Leu Tyr Asn Trp Ile Gly Ser Thr Asp Pro Glu Ala Trp Ile His
            180                 185                 190

Gln Ala Ala Val Gln Ala Lys Ser Val Leu Pro Gln Val Trp Asn Asp
        195                 200                 205

Thr Ile Ile Asn Trp Phe Trp Gln Ala Ala Tyr Ser Asn Tyr Tyr Ser
    210                 215                 220

Ala Met Trp Lys Asn Glu Val Lys Asn Pro Thr Leu Val Gln Leu Asn
225                 230                 235                 240
```

```
Gln Ala Glu Arg Glu Thr Ala Gly Phe Ile Asp Met Phe Phe Arg Val
                245                 250                 255


Asn Gly Val Glu Met Pro Val Thr Val Tyr Lys Glu Asn Ala Phe Gly
            260                 265                 270


Gly Val Ser Glu Leu Leu Gly Ser Gly Asn Tyr Asp Tyr Asp Gln Leu
        275                 280                 285


Val Lys Gly Ile Gly Asn Asp Thr Ile Ser Ser Ile His Ile Ala Pro
    290                 295                 300


Gly Tyr Gln Val Thr Leu Phe Ser Asp Ala Asn Tyr Lys Gly Ala Ser
305                 310                 315                 320


Ile Val Leu Thr Asn Asp Val His Asp Leu Gly Asn Phe Ser His Gln
                325                 330                 335


Val Ser Ser Ile Lys Ile Ala Lys Ile Ser Ala Leu Lys
            340                 345


<210>  289
<211>  258
<212>  PRT
<213>  Bacillus mycoides

<400>  289

Gln Thr Asn Asn Ser Glu Asn Pro Thr Pro Val Leu Arg Trp Ser Ala
1               5                   10                  15


Glu Asp Lys His Asn Glu Gly Val Ser Thr His Leu Trp Ile Val Asn
            20                  25                  30


Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Ala Ile Val Lys Pro Asn
        35                  40                  45


Glu Thr Ala Leu Leu Asn Glu Trp Arg Thr Asp Leu Glu Asn Gly Ile
    50                  55                  60
```

```
Tyr Ser Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Gly Thr Tyr Ala
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gly Gly Thr Tyr Ile Pro Phe Ala
                85                  90                  95


Lys Gln Ala Lys Glu Thr Gly Thr Lys Tyr Phe Lys Leu Ala Gly Glu
            100                 105                 110


Ala Tyr Gln Asn Gln Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly Leu
        115                 120                 125


Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala Asn
    130                 135                 140


Phe Thr Asn Leu Ser Tyr Pro Met Gly Phe His Ser Lys Tyr Glu Asn
145                 150                 155                 160


Phe Val Asp Thr Val Lys Asp Asn Tyr Ile Val Ser Asp Ser Asn Gly
                165                 170                 175


Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Asp Trp Ile Gln Gly Ser
            180                 185                 190


Ala Val Ala Ala Lys Gln Asp Tyr Pro Gly Ile Val Asn Asp Thr Thr
        195                 200                 205


Lys Asp Trp Phe Val Lys Ala Ala Val Ser Gln Glu Tyr Ala Asp Lys
    210                 215                 220


Trp Arg Ala Glu Val Thr Pro Val Thr Gly Lys Arg Leu Met Glu Ala
225                 230                 235                 240


Gln Arg Val Thr Ala Gly Tyr Ile His Leu Trp Phe Asp Thr Tyr Val
                245                 250                 255


Asn Arg
```

```
<210>  290
<211>  259
<212>  PRT
<213>  Bacillus mycoides

<400>  290

His Glu Asn Glu Gly Gly Asn Lys Val Arg Val Ile Gln Tyr Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Ala Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Thr Val Val Lys Gln
        35                  40                  45


Asp Gln Val Ala Leu Leu Asn Glu Trp Arg Thr Glu Leu Glu Asn Gly
    50                  55                  60


Ile Tyr Ala Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Thr Gly Lys Thr Tyr Ile Pro Phe
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ala Tyr Gln Lys Gln Glu Ile Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asn Asn Tyr Lys Val Ala Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Val Asn Pro Glu Asp Trp Ile His Gly
```

```
            180                 185                 190

Ala Ala Val Ala Ala Lys Gln Asp Tyr Ala Gly Ile Val Asn Gly Thr
        195                 200                 205

Thr Lys Asp Trp Phe Val Arg Ala Ala Val Ser Gln Glu Tyr Ala Asp
    210                 215                 220

Lys Trp Arg Ala Glu Val Thr Leu Thr Thr Gly Lys Arg Leu Val Glu
225                 230                 235                 240

Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255

Val Asn Arg



<210>  291
<211>  259
<212>  PRT
<213>  Bacillus sp.

<400>  291

His Glu Asn Asp Gly Gly His Gly Val Gly Val Ile Pro Arg Trp Ser
1               5                   10                  15

Ala Glu Asp Arg His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30

Asn Arg Gly Ile Asp Ile Met Ser His Asn Thr Thr Val Val Lys Gln
        35                  40                  45

Asp Glu Val Ala Leu Leu Asn Glu Trp Arg Thr Asp Leu Glu Asn Gly
    50                  55                  60

Ile Tyr Ser Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80

Ala Ser His Phe Tyr Asp Pro Asp Asn Gly Thr Thr Tyr Ile Pro Phe
                85                  90                  95
```

Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100   105   110

Glu Ser Tyr Gln Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115   120   125

Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130   135   140

Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145   150   155   160

Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Asn Asp Gly Asn
                165   170   175

Gly Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Asp Trp Ile His Ala
            180   185   190

Ser Ala Val Ala Ala Lys Gln Asp Phe Pro Ser Ile Val Asn Asp Asn
        195   200   205

Thr Lys Asp Trp Phe Val Lys Ala Ala Val Ser Gln Asp Tyr Ala Asn
    210   215   220

Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Lys Arg Leu Met Glu
225   230   235   240

Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245   250   255

Val Asn Arg

<210> 292
<211> 263
<212> PRT
<213> Bacillus drentensis

<400> 292

```
Ala Arg Val Asn His Asp Ser Ser Tyr Asp Ser Gly Ile Ile Ile Ser
1               5                   10                  15


Pro Tyr Trp Ser Ala Glu Glu Met His Thr Glu Gly Lys Asn Thr His
            20                  25                  30


Leu Trp Ile Val Asn Arg Ala Ile Asp Ile Met Ala Arg Asp Asn Thr
        35                  40                  45


Val Val Lys Glu Asn Glu Val Ala Leu Leu Asn Glu Trp Arg Thr Asp
    50                  55                  60


Leu Glu Asp Gly Ile Tyr Thr Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp
65                  70                  75                  80


Asn Gly Thr Phe Ala Ser His Phe Tyr Asp Pro Asp Thr Asp Asp Thr
                85                  90                  95


Tyr Ile Pro Phe Ala Lys Asn Ala Lys Val Thr Gly Val Lys Tyr Phe
            100                 105                 110


Lys Leu Ala Gly Glu Ala Tyr Gln Gln Gln Ala Met Asn Gln Ala Phe
        115                 120                 125


Phe Tyr Leu Gly Leu Ser Leu His Tyr Phe Gly Asp Ile Asn Gln Pro
    130                 135                 140


Met His Ala Ser Asn Phe Thr Asn Ile Ser His Pro Phe Gly Phe His
145                 150                 155                 160


Ser Lys Tyr Glu Asn Phe Val Asp Thr Ile Lys Ala Pro Tyr Ser Val
                165                 170                 175


Thr Asp Gly Asn Gly Tyr Trp Asn Phe Ala Gly Glu Thr Pro Glu Glu
            180                 185                 190


Trp Leu His Thr Ala Ala Val Ala Ala Lys Gln Asp Ala Pro Gly Ile
        195                 200                 205
```

Val Asn Glu Thr Thr Ile Ser Trp Phe Leu Gln Ala Ala Phe Ser Gln
    210   215   220

Glu Tyr Ala Asp Met Trp Arg Ala Glu Val Thr Pro Glu Thr Gly Ala
225   230   235   240

Arg Leu Ile Glu Ala Gln Arg Ala Met Ala Gly Tyr Ile His Leu Trp
                245   250   255

Phe Asp Thr Tyr Val Asn Leu
            260

<210> 293
<211> 275
<212> PRT
<213> Aspergillus turcosus

<400> 293

Ala Pro Ala Gly Leu Ala Glu Arg Asp Val Ser Ala Ser Val Leu Gln
1   5   10   15

Glu Leu Ser Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Thr Asn
            20   25   30

Asn Ile Asn Ser Thr Gly Thr Lys Leu Thr Cys Ser Ala Gly Asn Cys
        35   40   45

Pro Leu Val Glu Ala Ala Asn Thr Lys Thr Leu Ala Glu Phe Tyr Asp
    50   55   60

Ser Asp Ser Phe Gly Asp Thr Ala Gly Phe Leu Val Ala Asp Thr Thr
65   70   75   80

Asn Lys Leu Leu Val Val Ser Phe Arg Gly Ser Arg Thr Leu Asp Asn
                85   90   95

Trp Ile Ala Asn Leu Asp Phe Val Leu Asp Ser Ile Ser Asp Ile Cys
            100   105   110

```
Ser Gly Cys Ala Ala His Gly Gly Phe Trp Lys Ser Trp Glu Val Val
        115                 120                 125


Ala Asn Ser Leu Thr Thr Glu Leu Asn Ser Ala Val Asn Thr Tyr Pro
    130                 135                 140


Gly Tyr Thr Ile Val Phe Thr Gly His Ser Leu Gly Ala Ala Leu Ala
145                 150                 155                 160


Thr Leu Gly Ala Thr Thr Leu Arg Lys Ala Gly Ile Pro Val Gln Leu
                165                 170                 175


Tyr Asn Tyr Gly Ser Pro Arg Val Gly Asn Lys Ala Leu Ala Thr Tyr
            180                 185                 190


Ile Thr Ala Gln Gly Pro Asn Tyr Arg Val Thr His Thr Asn Asp Ile
        195                 200                 205


Val Pro Arg Leu Pro Pro Gln Ser Phe Gly Phe Ser His Leu Ser Pro
    210                 215                 220


Glu Tyr Trp Ile Thr Ser Gly Asp Asn Val Pro Val Thr Thr Ser Asp
225                 230                 235                 240


Ile Thr Val Ile Gln Gly Ile Asp Ser Asn Ala Gly Asn Ser Gly Glu
                245                 250                 255


Asp Ile Thr Ser Ile Glu Ala His Asn Trp Tyr Ile Gly Asn Ile Asp
            260                 265                 270


Ala Cys Pro
        275


<210>  294
<211>  276
<212>  PRT
<213>  Talaromyces subinflatus

<400>  294

Val Leu Ser Pro Ile Gly Arg Arg Thr Val Thr Thr Thr Gln Leu Asp
```

```
1               5                   10                  15


Asp Met Asn Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ala
            20                  25                  30


Asn Leu Asn Ser Thr Gly Ser Ala Leu Ala Cys Asn Val Gly Asn Cys
        35                  40                  45


Pro Leu Val Glu Gly Ala Asp Thr Thr Ile Leu Tyr Asp Phe Asp Glu
    50                  55                  60


Ser Ala Gly Phe Gly Asp Ala Thr Gly Tyr Ile Ala Val Asp Glu Thr
65                  70                  75                  80


His Lys Ser Ile Ile Leu Ala Phe Arg Gly Ser Ser Asp Leu Asp Asn
                85                  90                  95


Trp Ile Ala Asp Leu Asp Ile Pro Leu Val Ala Ser Ser Ile Cys Leu
            100                 105                 110


Gly Cys Glu Val His Gln Gly Phe Trp Asp Thr Trp Gln Thr Val Ala
        115                 120                 125


Ser Asp Val Thr Ser Gln Val Glu Tyr Ala Leu Ser Ala Tyr Ala Gly
    130                 135                 140


Tyr Thr Phe Val Val Thr Gly His Ser Met Gly Ala Ala Leu Ala Ala
145                 150                 155                 160


Ile Ala Ala Thr Val Phe Arg Asp Ser Gly Tyr Thr Val Glu Leu Tyr
                165                 170                 175


Asn Tyr Gly Gln Pro Arg Ile Gly Asn Leu Ile Leu Ala Tyr Tyr Ile
            180                 185                 190


Thr Asn Gln Asn His Gly Ser Asn Tyr Arg Val Thr His Thr Asp Asp
        195                 200                 205


Ile Val Pro Lys Leu Pro Pro Glu Leu Leu Gly Tyr Asp His Phe Ser
```

```
    210                 215                 220


Pro Glu Tyr Trp Ile Thr Ser Gly Asp Asn Val Thr Val Thr Asp Ser
225                 230                 235                 240


Asp Ile Asp Val Ile Val Gly Ile Asp Ser Ala Asp Gly Asn Asp Gly
                245                 250                 255


Thr Ile Asp Asp Ser Val Glu Ala His His Trp Tyr Phe Val Tyr Ile
            260                 265                 270


Ser Glu Cys Ser
        275


<210>  295
<211>  277
<212>  PRT
<213>  Aspergillus tubingensis

<400>  295

Ala Pro Ala Pro Met Gln Arg Arg Asp Ile Ser Ser Thr Val Leu Asp
1               5                   10                  15


Asn Ile Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ser
            20                  25                  30


Asn Ile Glu Ser Thr Gly Thr Thr Leu Thr Cys Asp Val Gly Asn Cys
        35                  40                  45


Pro Leu Val Glu Ala Ala Gly Ala Thr Thr Ile Asp Glu Phe Asp Asp
    50                  55                  60


Ser Ser Ser Tyr Gly Asp Pro Thr Gly Phe Ile Ala Val Asp Pro Thr
65                  70                  75                  80


Asn Glu Leu Ile Val Leu Ala Leu Arg Gly Ser Ser Asp Ile Ser Asn
                85                  90                  95


Trp Ile Ala Asp Leu Asp Phe Gly Leu Thr Ser Val Ser Asp Ile Cys
            100                 105                 110
```

```
Asp Gly Cys Glu Met His Lys Gly Phe Tyr Glu Ala Trp Glu Val Ile
        115                 120                 125


Ala Asp Thr Ile Thr Ser Lys Val Glu Ala Ala Val Ser Ser Tyr Pro
    130                 135                 140


Asp Tyr Ser Ile Val Phe Thr Gly His Ser Tyr Gly Ala Ala Leu Ala
145                 150                 155                 160


Ala Ile Ala Ala Thr Val Leu Arg Asn Ala Gly Tyr Thr Leu Asp Leu
                165                 170                 175


Tyr Asn Phe Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala Asp Tyr
            180                 185                 190


Ile Thr Asp Gln Asn Met Gly Ser Asn Tyr Arg Val Thr His Thr Asp
        195                 200                 205


Asp Ile Val Pro Lys Leu Pro Pro Lys Leu Leu Gly Tyr His His Phe
    210                 215                 220


Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Asp Val Thr Val Thr Thr
225                 230                 235                 240


Ser Asp Val Thr Glu Val Val Gly Val Asp Ser Thr Asp Gly Asn Asp
                245                 250                 255


Gly Thr Leu Leu Asp Ser Thr Thr Ala His Arg Trp Tyr Thr Ile Tyr
            260                 265                 270


Ile Ser Glu Cys Ser
        275


<210>  296
<211>  350
<212>  PRT
<213>  Bacillus acidiceler

<400>  296
```

```
Ile Thr Ser Leu Phe Ser Asn Asp Gln Lys Ala Phe Ala Trp Ser Asp
1               5                   10                  15


Glu Asp Val His Asn Gln Asp His Ser Thr His His Phe Ile Val Asn
            20                  25                  30


Gly Ser Val Lys Leu Ile Ala Asp Asn Thr Asn Pro Ala Ile Asn Lys
        35                  40                  45


Pro Thr Thr Leu Leu Asn Gln Phe Arg Asp Arg Trp Glu Gln Gly Leu
    50                  55                  60


Tyr Asp Ala Asp His Ile Asn Pro Phe Tyr Asp Thr Gly Thr Phe Met
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gln Thr Asn Tyr Thr Gly Val Ser
                85                  90                  95


Tyr Pro Thr Ala Arg Gln Ser Gly Gly Lys Tyr Phe Asn Leu Ala Ser
            100                 105                 110


Asp Tyr Tyr Lys Lys Gly Asp Phe Tyr Asn Ala Phe Tyr Tyr Leu Gly
        115                 120                 125


Val Ser Leu His Tyr Phe Thr Asp Val Thr Gln Pro Leu His Ala Ser
    130                 135                 140


Asn Ile Ser Asn Leu Asp His Asn Ala Pro Gly Tyr His Ser Lys Phe
145                 150                 155                 160


Glu Asn Tyr Ala Glu Ser Ile Gln Asn Gln Met Ala Ile Pro Asp Ser
                165                 170                 175


Gly Leu Tyr Asn Trp Ile Ser Ser Thr Asp Pro Glu Ala Trp Ile His
            180                 185                 190


Gln Ala Ala Val Gln Ala Lys Ser Val Leu Pro Gln Val Trp Asn Asp
        195                 200                 205
```

Thr Ile Ile Asn Phe Phe Trp Gln Ala Ala Tyr Ser Asn Tyr Tyr Ser
    210   215   220

Ser Met Trp Lys Asn Glu Val Lys Asn Pro Thr Leu Val Gln Leu Asn
225   230   235   240

Gln Ala Glu Arg Glu Thr Ala Gly Phe Ile Asp Met Phe Phe Arg Val
                245   250   255

Asn Gly Val Glu Met Pro Val Lys Val Tyr Lys Glu Asn Ala Phe Gly
            260   265   270

Gly Ala Ser Glu Ile Leu Gly Leu Gly Asn Tyr Asp Tyr Asp Gln Phe
        275   280   285

Val Lys Gly Ile Gly Asn Asp Thr Ile Ser Ser Ile His Ile Ala Pro
    290   295   300

Gly Tyr Gln Val Thr Leu Phe Ser Asp Ala Asn Tyr Lys Gly Thr Ser
305   310   315   320

Thr Val Leu Thr Gly Asp Val Asn Asp Leu Gly Asn Phe Asn His Gln
                325   330   335

Val Ser Ser Leu Lys Ile Val Lys Ile Ser Ala Ile Ser Lys
            340   345   350

<210> 297
<211> 259
<212> PRT
<213> Lysinibacillus xylanilyticus

<400> 297

His Glu Asn Cys Tyr Gln Asp Pro Pro Ile Pro Leu Lys Trp Ser Ala
1   5   10   15

Glu Ser Ile His Asn Glu Gly Val Ser Ser His Leu Trp Ile Val Asn
            20   25   30

```
Arg Ala Ile Asp Ile Met Ser Gln Asn Thr Thr Ile Val Lys Gln His
        35                  40                  45


Glu Thr Asp Leu Leu Asn Glu Trp Arg Thr Asp Leu Glu Glu Gly Ile
    50                  55                  60


Tyr Ser Ala Asp Tyr Gln Asn Pro Tyr Tyr Asp Asn Ser Thr Phe Ala
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Ser Gly Lys Thr Tyr Ile Pro Phe Ala
                85                  90                  95


Lys Gln Ala Lys Gln Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly Glu
            100                 105                 110


Ala Tyr Gln Asn Lys Asp Leu Lys Asn Ala Phe Phe Tyr Leu Gly Leu
        115                 120                 125


Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala Asn
    130                 135                 140


Phe Thr Asn Ile Ser His Pro Phe Gly Phe His Ser Lys Tyr Glu Asn
145                 150                 155                 160


Phe Val Asp Thr Val Lys Asp Asn Tyr Arg Val Thr Asp Gly Asn Gly
                165                 170                 175


Tyr Trp Asn Trp Lys Ser Ala Asn Pro Glu Glu Trp Val His Ala Ser
            180                 185                 190


Ala Val Ala Ala Lys Ala Asp Phe Leu Leu Ile Val Asn Asp Asn Thr
        195                 200                 205


Glu Ser Gly Phe Leu Lys Ala Ala Val Ser Gln Asp Ser Ala Asp Lys
    210                 215                 220


Trp Arg Ala Glu Val Thr Pro Val Thr Gly Lys Arg Leu Met Glu Ala
225                 230                 235                 240
```

```
Gln Arg Ile Thr Ala Gly Tyr Ile His Leu Trp Phe Asp Thr Tyr Val
                245                 250                 255


Asn Asn Lys




<210>  298
<211>  259
<212>  PRT
<213>  Bacillus toyonensis

<400>  298

His Glu Asn Glu Asp Val Asn Tyr Asn Ala Pro Ile Leu Arg Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ser Ile Asp Met Met Ser Arg Asn Thr Thr Ile Val Lys Lys
        35                  40                  45


Asn Gln Val Ala Leu Leu Asn Glu Trp Arg Thr Glu Leu Glu Asn Gly
    50                  55                  60


Ile Tyr Asn Ala Asp His Glu Asn Pro Tyr Phe Asp Asn Phe Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Glu Thr Gly Ser Thr Tyr Ile Pro Leu
                85                  90                  95


Val Ser Thr Gln Ala Lys Glu Ala Gly Ser Lys Tyr Phe Lys Leu Ala
            100                 105                 110


Gly Glu Ser Tyr Lys Lys Asn Asp Met Lys Gln Ala Phe Phe Tyr Leu
        115                 120                 125


Gly Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala
    130                 135                 140


Ala Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr
```

```
145                 150                 155                 160


Glu Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Asn Asp Gly
                165                 170                 175


Asn Gly Tyr Trp Asn Trp Lys Gly Ser Asn Pro Gly Asp Trp Ile His
            180                 185                 190


Gly Ala Ala Val Ala Ala Lys Lys Asp Tyr Thr Gly Ile Val Asn Asp
        195                 200                 205


Thr Thr Lys Asp Trp Phe Val Lys Ala Ala Ile Ser Ser Glu Tyr Ala
    210                 215                 220


Asp Lys Trp Arg Ala Glu Val Thr Pro Ala Thr Gly Lys Arg Leu Met
225                 230                 235                 240


Glu Ala Gln Arg Ile Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr
                245                 250                 255


Tyr Ala Asn



<210>  299
<211>  259
<212>  PRT
<213>  Bacillus wiedmannii

<400>  299

His Glu Asn Asp Gly Gly Ser Lys Ile Lys Ile Val His Arg Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Thr Leu Val Lys Gln
        35                  40                  45


Asp Arg Val Thr Gln Leu Asn Glu Trp Arg Thr Glu Leu Glu Asn Gly
    50                  55                  60
```

```
Ile Tyr Ala Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Asn Gly Lys Thr Tyr Ile Pro Leu
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Glu Trp Ile His Gly
            180                 185                 190


Ala Ala Val Val Ala Lys Gln Asp Tyr Ser Gly Ile Val Asn Asp Asn
        195                 200                 205


Thr Lys Asp Trp Phe Val Lys Ala Ala Val Ser Gln Glu Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Lys Arg Leu Met Asp
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Gly Asp Arg
```

```
<210>  300
<211>  268
<212>  PRT
<213>  Listeria seeligeri

<400>  300

Cys Gly Asp Glu Ser Ile Lys Asp Gln Ile Ala Pro His Ala Ile Gln
1               5                   10                  15


Asn Lys Leu Pro Ser Lys Leu Gly Trp Ser Ala Glu His Pro Ser Lys
            20                  25                  30


Asp Glu Ile Asn Thr His Leu Trp Leu Phe Asn Gln Ala Glu Lys Ile
        35                  40                  45


Leu Ala Lys Asp Val Thr Gly Ala Gln Leu Asp Leu Val Arg Glu Leu
    50                  55                  60


Lys Asn Tyr Asn Lys Glu Ile Ala Gln Gly Ile Phe Asp Ala Asp His
65                  70                  75                  80


Lys Asn Pro Tyr Tyr Asp Lys Asn Thr Phe Leu Ser His Phe Tyr Asn
                85                  90                  95


Pro Lys Thr His Lys Thr Tyr Ile Pro Gly Phe Pro Asn Ala Lys Asp
            100                 105                 110


Thr Gly Thr Lys Tyr Phe Asn Ile Ser Val Glu Glu Tyr Gln Asp Gly
        115                 120                 125


Asn Phe Glu Lys Ala Phe Tyr Asn Leu Gly Leu Ala Ile His Tyr Tyr
    130                 135                 140


Thr Asp Val Ser Gln Pro Met His Ala Asn Asn Phe Thr Ala Leu Ser
145                 150                 155                 160


His Pro Val Gly Tyr His Cys Ala Tyr Glu Asn Tyr Val Asp Thr Phe
                165                 170                 175
```

```
Lys Gln Ile Phe Gln Ala Ser Ala Glu Ser Glu Ala Lys Trp Phe Cys
            180                 185                 190


Thr Asp Asp Ile Ser Glu Trp Tyr His Glu Asn Ala Lys Arg Ala Gln
        195                 200                 205


Ala Asp Tyr Pro Lys Ile Val Asn Ala Ile Ile Lys Lys Ser Tyr Ile
    210                 215                 220


Gln Gly Leu Ser Asp Ser Gln Lys Asp Arg Thr Trp Lys Lys Ala Val
225                 230                 235                 240


Arg Ala Ala Thr Gly Lys Arg Leu Arg Asp Ser Gln Glu Thr Leu Ala
                245                 250                 255


Gly Phe Leu Glu Phe Trp Tyr Ala Lys Thr Asn Glu
            260                 265


<210>  301
<211>  275
<212>  PRT
<213>  Penicillium swiecickii

<400>  301

Ala Pro Ser Arg Pro Val Pro Arg Asp Val Ser Thr Ser Val Leu Ser
1               5                   10                  15


Gln Leu Ser Leu Phe Ala Glu Tyr Ser Ala Ala Ser Tyr Cys Ser Asn
            20                  25                  30


Asn Ile Asn Ser Thr Gly Asn Ala Leu Ser Cys Glu Ala Gly Asn Cys
        35                  40                  45


Pro Ser Val Gln Ser Ala Asp Thr Thr Thr Leu Trp Glu Phe Asp Arg
    50                  55                  60


Thr Cys Ser Tyr Gly Asn Val Ala Gly Phe Leu Ala Val Asp Lys Thr
65                  70                  75                  80
```

```
Asn Lys Leu Leu Val Val Ser Phe Arg Gly Ser Arg Ser Ile Ser Asn
                85                  90                  95


Trp Ile Ala Asn Ile Asn Phe Gly Leu Thr Asp Ala Pro Ser Leu Cys
            100                 105                 110


Ser Gly Cys Glu Ala His Ser Gly Phe Leu Glu Ser Trp Glu Thr Val
        115                 120                 125


Ala Asp Asp Leu Thr Thr Asn Ile Lys Ser Ala Gln Ser Thr Tyr Ser
    130                 135                 140


Gly Tyr Thr Leu Val Leu Thr Gly His Ser Phe Gly Gly Ala Val Ala
145                 150                 155                 160


Ala Leu Gly Gly Thr Ala Leu Arg Asn Gly Gly Ser Thr Leu Asn Val
                165                 170                 175


Tyr Thr Tyr Gly Gln Pro Arg Val Gly Asn Gly Ala Leu Ala Ser Tyr
            180                 185                 190


Ile Thr Asn Gln Gly Ser Leu Trp Arg Val Thr His Thr Asp Asp Ile
        195                 200                 205


Val Pro Lys Leu Pro Pro Ser Ser Phe Gly Phe Ser His Pro Ser Pro
    210                 215                 220


Glu Tyr Trp Ile Thr Ser Glu Asn Glu Val Thr Val Thr Ser Ser Asp
225                 230                 235                 240


Val Glu Val Ile Glu Gly Val Gly Ser Lys Ser Gly Asn Ala Gly Thr
                245                 250                 255


Leu Asn Pro Asp Val Glu Ala His Asn Trp Tyr Leu Gly Tyr Ile Asp
            260                 265                 270


Gly Cys Gln
        275
```

```
<210>  302
<211>  276
<212>  PRT
<213>  Talaromyces boninensis

<400>  302

Val Pro Thr Pro Val Thr Arg Arg Thr Val Ser Thr Ala Leu Leu Asp
1               5                   10                  15


Thr Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Pro Ala
            20                  25                  30


Asn Phe Asn Ser Ser Ser Thr Ser Leu Ala Cys Ser Ala Gly Asn Cys
        35                  40                  45


Pro Thr Val Gln Ala Ala Asp Thr Thr Ile Leu Tyr Ser Phe Asp Lys
    50                  55                  60


Ser Ala Ser Phe Gly Asp Ala Thr Gly Tyr Val Ala Val Asp Asn Thr
65                  70                  75                  80


Asn Gln Leu Ile Val Ile Ala Phe Arg Gly Ser Ser Asp Leu Ser Asn
                85                  90                  95


Trp Ile Ala Asn Leu Asp Val Pro Phe Thr Asp Ala Gly Asn Ile Cys
            100                 105                 110


Ser Gly Cys Glu Val His Ser Gly Phe Tyr Asp Thr Trp Gln Thr Val
        115                 120                 125


Ala Ser Asp Ile Thr Ala Thr Val Asp Ser Ala Leu Ser Thr Tyr Pro
    130                 135                 140


Gly Tyr Thr Val Val Ala Thr Gly His Ser Leu Gly Gly Ala Leu Ala
145                 150                 155                 160


Ala Ile Gly Ala Thr Val Leu Arg Ser Ser Gly Gln Val Val Gln Leu
                165                 170                 175


Tyr Asp Tyr Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala Asp Phe
```

```
            180                 185                 190


Ile Thr Ser Glu Thr Ala Gly Ser Asn Tyr Arg Val Thr His Ser Asp
        195                 200                 205


Asp Ile Val Pro Lys Leu Pro Pro Glu Phe Leu Gly Tyr Ala His Phe
    210                 215                 220


Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asp Asn Val Ala Val Thr Asp
225                 230                 235                 240


Ala Asp Ile Val Glu Val Ile Gly Val Asp Ser Thr Ala Gly Asn Asp
                245                 250                 255


Gly Thr Phe Gly Asp Ser Ile Asn Ala His Leu Trp Tyr Phe Glu Ala
            260                 265                 270


Ile Ser Ala Cys
        275


<210>  303
<211>  277
<212>  PRT
<213>  Hamigera striata

<400>  303

Ala Pro Ala Pro Ile Leu Arg Arg Asp Val Ser Ala Ser Val Leu Asn
1               5                   10                  15


Glu Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ser
            20                  25                  30


Asn Ile Gly Ser Thr Gly Asn Lys Leu Met Cys Asn Val Gly Asn Cys
        35                  40                  45


Pro Arg Val Glu Ala Ser Asp Thr Val Thr Ile Asp Glu Phe Asn Glu
    50                  55                  60


Ser Ala Ser Tyr Gly Asp Val Ala Gly Tyr Ile Ala Val Asp Asn Thr
65                  70                  75                  80
```

```
Asn Gln Leu Leu Val Leu Ser Phe Arg Gly Ser Ser Ser Leu Ser Asn
                85                  90                  95


Trp Ile Ala Asn Ile Asp Val Asp Leu Thr Asp Ala Ser Ser Leu Cys
            100                 105                 110


Ser Gly Cys Glu Val His Ser Gly Phe Trp Ser Ala Trp Gln Thr Val
        115                 120                 125


Gln Gly Thr Ile Thr Ser Lys Leu Glu Ser Ala Arg Ala Ser Tyr Pro
    130                 135                 140


Gly Tyr Thr Leu Val Phe Thr Gly His Ser Tyr Gly Ala Ala Leu Ala
145                 150                 155                 160


Gly Leu Ala Ala Thr Thr Leu Arg Asp Ala Gly Trp Thr Ile Gln Leu
                165                 170                 175


Tyr Asn Tyr Gly Gln Pro Arg Leu Gly Asn Leu Ala Leu Ala Gln Tyr
            180                 185                 190


Ile Thr Ser Gln Thr Gln Gly Ser Asn Tyr Arg Val Thr His Thr Asp
        195                 200                 205


Asp Ile Val Pro Lys Leu Pro Pro Glu Phe Leu Gly Tyr Asp His Tyr
    210                 215                 220


Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asp Asn Val Thr Val Thr Thr
225                 230                 235                 240


Ser Asp Val Gln Val Ile Glu Gly Ile Asp Ser Val Ala Gly Asn Asp
                245                 250                 255


Gly Thr Ser Asp Asp Ser Thr Glu Ala His Gln Trp Tyr Phe Ile Tyr
            260                 265                 270


Ile Ser Glu Cys Ser
        275
```

```
<210>  304
<211>  351
<212>  PRT
<213>  Bacillus sp.

<400>  304

Ile Thr Ser Leu Phe Gly Ser Phe Gln Lys Ala Phe Ala Trp Ser Cys
1               5                   10                  15


Asp Asp Pro His Asn Gln Asp Gln Ser Thr His Leu Phe Ile Val Asn
            20                  25                  30


Asn Gly Val Lys Leu Ile Ser Gly Asn Ala Asp Pro Ala Ile Asn Lys
        35                  40                  45


Pro Ser Thr Leu Leu Glu Gln Phe Arg Asp Arg Trp Glu Gln Gly Leu
    50                  55                  60


Tyr Asp Ala Asp His Ile Asn Pro Phe Tyr Asp Thr Ser Thr Phe Met
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gln Thr Asn Tyr Ala Gly Arg Ser
                85                  90                  95


Tyr Pro Thr Ala Arg Gln Ser Gly Ala Lys Tyr Phe Asn Leu Ala Ser
            100                 105                 110


Asp Tyr Tyr Lys Asn Gly Asp Phe Tyr Asn Ala Phe Tyr Tyr Leu Gly
        115                 120                 125


Val Ser Leu His Tyr Phe Thr Asp Ala Thr Met Pro Leu His Ala Ser
    130                 135                 140


Asn Ile Ser Asn Leu Asp His Gln Ala Pro Gly Tyr His Ser Lys Leu
145                 150                 155                 160


Glu Ser Tyr Ser Glu Ser Ile Gln Asp Gln Val Thr Val Pro Asp Ser
                165                 170                 175
```

```
Gly Leu Phe Asn Trp Val Ser Ser Thr Asp Pro Glu Leu Trp Ile His
            180                 185                 190


Gln Ala Ala Val Gln Ala Lys Ser Val Leu Pro Gln Val Trp Asn Asp
        195                 200                 205


Ser Ile Ile Ser Trp Phe Trp Gln Ala Ala Tyr Ser Asn Tyr Tyr Ser
    210                 215                 220


Asp Met Trp Lys Ser Ala Val Lys Ala Pro Ile Leu Asn Gln Leu Asn
225                 230                 235                 240


Gln Ala Glu Arg Glu Thr Ala Gly Phe Ile Asp Met Phe Phe Arg Leu
                245                 250                 255


Asn Gly Val Glu Met Pro Val Thr Val Tyr Ser Glu Thr Ala Phe Gly
            260                 265                 270


Gly Ala Ser Glu Leu Leu Gly Ser Gly Asn Tyr Asp Tyr Asp Gln Leu
        275                 280                 285


Val Lys Gly Ile Gly Asn Asp Ala Ile Ser Ser Ile His Ile Ala Pro
    290                 295                 300


Gly Tyr Gln Val Thr Leu Phe Ala Asp Ser Asn Tyr Ser Gly Ala Ser
305                 310                 315                 320


Lys Val Leu Thr Ala Asp Ala Ser Asp Leu Asp Asn Phe Asn Lys Thr
                325                 330                 335


Ile Ser Ser Leu Lys Ile Glu Lys Ile Gln Pro Val Asn Val His
            340                 345                 350


<210>  305
<211>  259
<212>  PRT
<213>  Bacillus thuringiensis

<400>  305
```

```
His Glu Asn Ala Gly Gly Gln Arg Val Gly Val Ile Pro Arg Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Thr Ile Val Lys Gln
        35                  40                  45


Asp Gln Val Ala Leu Leu Asn Glu Trp Arg Thr Asp Leu Glu Asn Gly
    50                  55                  60


Ile Tyr Ser Ala Asp Phe Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Ser Glu Lys Thr Tyr Ile Pro Leu
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Gln Asn Asn Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Thr
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Val Ala Lys Gln Asp Tyr Ser Gly Ile Val Asn Asn Asn
        195                 200                 205
```

```
Thr Lys Glu Trp Phe Val Lys Ala Ala Val Ser Gln Glu Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Lys Arg Leu Ile Asp
225                 230                 235                 240


Ala Gln Arg Ile Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Val Asn Arg




<210>  306
<211>  259
<212>  PRT
<213>  Bacillus mycoides

<400>  306

His Glu Asn Cys His Gln Asp Pro Pro Ile Ala Leu Lys Trp Ser Ala
1               5                   10                  15


Glu Ser Ile His Asn Glu Gly Val Ser Ser His Leu Trp Ile Val Asn
            20                  25                  30


Lys Ala Ile Asp Ile Met Ser Gln Asn Thr Thr Val Val Lys Gln Asn
        35                  40                  45


Glu Thr Ala Leu Leu Asn Glu Trp Arg Thr Asp Leu Glu Lys Gly Ile
    50                  55                  60


Tyr Ser Ala Asp Tyr Gln Asn Pro Tyr Tyr Asp Asn Ser Thr Phe Ala
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Ser Gly Lys Thr Tyr Ile Pro Phe Ala
                85                  90                  95


Lys Gln Ala Lys Gln Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly Glu
            100                 105                 110


Ala Tyr Gln Asn Lys Asp Met Lys Asn Ala Phe Phe Tyr Leu Gly Leu
```

```
        115                 120                 125

Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala Asn
    130                 135                 140

Phe Thr Asn Ile Ser His Pro Phe Gly Phe His Ser Lys Tyr Glu Asn
145                 150                 155                 160

Phe Val Asp Thr Val Lys Asp Asn Tyr Arg Val Thr Asp Gly Asn Gly
                165                 170                 175

Tyr Trp Asn Trp Gln Ser Thr Asn Pro Glu Asp Trp Val His Ala Ser
            180                 185                 190

Ala Ser Ala Ala Lys Ala Asp Phe Pro Ser Ile Val Asn Asp Asn Thr
        195                 200                 205

Lys Asn Trp Phe Leu Lys Ala Ala Val Ser Gln Asp Ser Ala Asp Lys
    210                 215                 220

Trp Arg Ala Glu Val Thr Pro Val Thr Gly Lys Arg Leu Ile Glu Ala
225                 230                 235                 240

Gln Arg Ile Thr Ala Gly Tyr Ile His Leu Trp Phe Asp Thr Tyr Val
                245                 250                 255

Asn Asn Lys



<210>  307
<211>  259
<212>  PRT
<213>  Fictibacillus macauensis

<400>  307

His Glu Asn Glu Gly Gly Asn Lys Val Arg Val Ile Gln Tyr Trp Ser
1               5                   10                  15

Ala Glu Asp Pro His His Glu Asp Thr Asn Thr His Leu Trp Ile Val
            20                  25                  30
```

```
Arg His Ala Met Glu Ile Met Ala Asn Asn Lys Asp Val Val Lys Pro
        35                  40                  45


Gly Glu Val Glu Gln Leu Lys Gln Trp Gln Ser Asp Leu Glu Gln Gly
    50                  55                  60


Ile Tyr Asp Ala Asp His Ala Asn Pro Tyr Tyr Asp Asn Ala Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Thr Gly Lys Ser Tyr Ile Pro Leu
                85                  90                  95


Ala Ala His Ala Lys Thr Thr Ser Val Lys Tyr Phe Lys Arg Ala Gly
            100                 105                 110


Glu Ala Tyr Gln Lys Gly Asp His Lys Gln Ala Phe Tyr Asn Leu Gly
        115                 120                 125


Leu Ala Leu His Tyr Ile Gly Asp Leu Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Tyr Val Asp Ser Phe Lys Glu Asp Tyr Ala Val Lys Asp Gly Glu
                165                 170                 175


Gly Tyr Trp His Trp Lys Gly Thr Asn Pro Glu Asp Trp Leu His Gly
            180                 185                 190


Thr Ala Val Ala Ala Lys Lys Asp Tyr Pro Asp Ile Val Asn Asp Thr
        195                 200                 205


Thr Lys Ala Trp Phe Val Lys Ala Ala Val Ser Asn Ser Tyr Ala Ala
    210                 215                 220


Lys Trp Arg Ala Ala Val Val Pro Ala Thr Gly Lys Arg Leu Thr Glu
225                 230                 235                 240
```

```
Ala Gln Arg Ile Leu Ala Gly Tyr Met Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Val Asn Lys




<210>  308
<211>  268
<212>  PRT
<213>  Listeria seeligeri

<400>  308

Cys Gly Asp Glu Ser Val Lys Asp Gln Ile Ala Pro His Asp Ile Gln
1               5                   10                  15


Asn Lys Leu Pro Ser Lys Leu Gly Trp Ser Ala Glu His Pro Ser Lys
            20                  25                  30


Asn Glu Ile Asn Thr His Leu Trp Leu Phe Asn Gln Ala Glu Lys Ile
        35                  40                  45


Leu Ala Lys Asp Val Thr Gly Ala Gln Leu Asp Leu Val Arg Glu Leu
    50                  55                  60


Lys Asn Tyr Asn Lys Glu Ile Ala Gln Gly Ile Phe Asp Ala Asp His
65                  70                  75                  80


Lys Asn Pro Tyr Tyr Asp Lys Asn Thr Phe Leu Ser His Phe Tyr Asn
                85                  90                  95


Pro Lys Thr His Lys Thr Tyr Ile Ala Gly Phe Pro Asn Ala Lys Asp
            100                 105                 110


Thr Gly Thr Lys Tyr Phe Asn Ile Ser Ile Glu Glu Tyr Gln Asp Gly
        115                 120                 125


Asn Phe Glu Lys Ala Phe Tyr Asn Leu Gly Leu Ala Ile His Tyr Tyr
    130                 135                 140
```

```
Thr Asp Ile Ser Gln Pro Met His Ala Asn Asn Phe Thr Ala Leu Ser
145                 150                 155                 160


His Pro Val Gly Tyr His Cys Ala Tyr Glu Asn Tyr Val Asp Thr Phe
                165                 170                 175


Lys Gln Ile Phe Gln Ala Ser Ala Glu Ser Glu Ala Lys Trp Phe Cys
            180                 185                 190


Thr Asp Asp Val Ser Glu Trp Phe His Glu Asn Ala Lys Arg Ala Gln
        195                 200                 205


Ala Asp Tyr Pro Lys Ile Val Asn Thr Ile Ile Lys Lys Ser Tyr Ile
    210                 215                 220


Gln Gly Leu Ser Asp Ser Gln Lys Asp Arg Thr Trp Lys Lys Ala Val
225                 230                 235                 240


Arg Ala Ala Thr Gly Lys Arg Leu Arg Asp Ser Gln Glu Thr Leu Ala
                245                 250                 255


Gly Leu Leu Glu Phe Trp Tyr Thr Lys Thr Asn Glu
            260                 265


<210>  309
<211>  275
<212>  PRT
<213>  Penicillium donkii

<400>  309

Ala Pro Ala Arg Pro Val Pro Arg Asp Ile Ser Ser Ser Leu Leu Asp
1               5                   10                  15


Glu Leu Thr Leu Phe Ala Glu Tyr Ala Ala Ala Ser Tyr Cys Ser Asn
            20                  25                  30


Asn Ile Asp Ser Thr Gly Asp Ala Val Thr Cys Ser Gly Asp Tyr Cys
        35                  40                  45
```

```
Pro Leu Val Gln Ser Ala Gly Ala Lys Thr Leu Tyr Glu Phe Asn Asp
    50                  55                  60


Ser Thr Glu Trp Gly Asp Val Ala Gly Phe Leu Ala Val Asp Thr Thr
65                  70                  75                  80


Asn Lys Leu Ile Val Leu Ser Phe Arg Gly Ser Arg Ser Ile Ser Thr
                85                  90                  95


Trp Ile Ala Asn Leu Asp Phe Gly Leu Thr Asp Thr Ser Ser Leu Cys
            100                 105                 110


Asp Asp Cys Glu Ala His Ser Gly Phe Trp Lys Ser Trp Glu Thr Val
        115                 120                 125


Ala Asp Asp Met Thr Ala Gln Ile Glu Ser Ala Gln Ser Ser Tyr Pro
    130                 135                 140


Ser Tyr Thr Leu Val Leu Thr Gly His Ser Phe Gly Ala Ala Val Ala
145                 150                 155                 160


Ala Leu Gly Ala Thr Ala Leu Arg Asn Ala Gly Tyr Thr Leu Asp Leu
                165                 170                 175


Tyr Thr Tyr Gly Gln Pro Arg Val Gly Asn Glu Ala Leu Ala Thr Tyr
            180                 185                 190


Met Thr Ser Gln Gly Ser Leu Trp Arg Val Thr His Glu Asp Asp Ile
        195                 200                 205


Val Pro Lys Leu Pro Pro Met Ser Trp Gly Phe Ser His Ala Ser Pro
    210                 215                 220


Glu Tyr Trp Val Thr Ser Asp Ser Asp Val Thr Val Thr Thr Ser Asp
225                 230                 235                 240


Val Glu Glu Val Val Gly Val Asp Ser Thr Ala Gly Asn Ala Gly Thr
                245                 250                 255
```

```
Ser Gly Glu Ser Ile Ser Ala His Asn Trp Tyr Phe Val Glu Ile Asp
            260                 265                 270


Gly Cys Asp
        275


<210>  310
<211>  276
<212>  PRT
<213>  Hamigera paravellanea

<400>  310

Ala Pro Ala Ala Val Arg Arg Asp Val Ser Ala Gly Val Leu Ala Asn
1               5                   10                  15


Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Asp Ser Asn
            20                  25                  30


Leu Asn Ser Asp Gly Thr Lys Leu Thr Cys Gln Ala Gly Asn Cys Pro
        35                  40                  45


Leu Val Glu Ala Ala Asp Thr Glu Thr Leu Asp Glu Phe Asp Met Thr
    50                  55                  60


Ala Thr Tyr Gly Asn Val Ala Gly Tyr Ile Ala Val Asp Arg Thr Asn
65                  70                  75                  80


Arg Leu Leu Val Leu Ala Phe Arg Gly Ser Ala Ser Ile Ser Asn Trp
                85                  90                  95


Ile Ala Asn Leu Asn Leu Gly Leu Thr Asp Ala Ser Ala Leu Cys Ala
            100                 105                 110


Gly Cys Arg Val His Ser Gly Phe Trp Glu Ala Trp Gln Thr Ala Glu
        115                 120                 125


Ala Thr Met Ser Asp Ile Ile Ala Ser Ala Ala Gln Thr Tyr Pro Gly
    130                 135                 140


Tyr Thr Leu Val Ala Thr Gly His Ser Tyr Gly Ala Ala Leu Ala Ala
```

```
145                 150                 155                 160


Ile Ala Ala Thr Lys Phe Arg Asn Glu Gly Tyr Ala Val Glu Leu Tyr
                165                 170                 175


Asp Tyr Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala Gln Tyr Ile
            180                 185                 190


Thr Asn Gln Ser Ser Gly Gly Asn Phe Arg Val Thr His Thr Asn Asp
        195                 200                 205


Ile Val Pro Lys Leu Pro Pro Asp Trp Leu Gly Tyr Ser His Phe Gly
    210                 215                 220


Pro Glu Tyr Trp Ile Thr Ser Gly Asp Gly Ile Pro Val Thr Thr Ala
225                 230                 235                 240


Asp Val Glu Val Ile Ser Gly Val Asp Ala Thr Gly Gly Asn Asp Gly
                245                 250                 255


Ala Glu Gly Thr Ser Val Asp Ala His Arg Trp Tyr Phe Val Tyr Ile
            260                 265                 270


Ser Gln Cys Glu
        275


<210>  311
<211>  277
<212>  PRT
<213>  Talaromyces lecycettanus

<400>  311

Ala Pro Ala Pro Val Leu Arg Arg Asp Val Ser Ser Ser Val Leu Ser
1               5                   10                  15


Glu Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ser
            20                  25                  30


Asn Ile Gly Ser Pro Gly Thr Lys Leu Thr Cys Ser Val Gly Asn Cys
        35                  40                  45
```

```
Pro Arg Val Glu Ala Ala Asp Thr Glu Thr Leu Ile Glu Phe Asn Glu
    50                  55                  60


Ser Ser Ser Phe Gly Asp Val Thr Gly Tyr Ile Ala Val Asp Arg Thr
65                  70                  75                  80


Asn Ser Leu Leu Val Leu Ala Phe Arg Gly Ser Ser Thr Val Ser Asn
                85                  90                  95


Trp Glu Ala Asp Leu Asp Phe Pro Leu Thr Asp Ala Ser Ser Leu Cys
            100                 105                 110


Ser Gly Cys Glu Ile His Ser Gly Phe Trp Ala Ala Trp Gln Thr Val
        115                 120                 125


Gln Ala Ser Ile Thr Ser Thr Leu Glu Ser Ala Ile Ala Ser Tyr Pro
    130                 135                 140


Gly Tyr Thr Leu Val Phe Thr Gly His Ser Tyr Gly Ala Ala Leu Ala
145                 150                 155                 160


Ala Ile Ala Ala Thr Thr Leu Arg Asn Ala Gly Tyr Thr Ile Gln Leu
                165                 170                 175


Tyr Asp Tyr Gly Gln Pro Arg Leu Gly Asn Leu Ala Leu Ala Gln Tyr
            180                 185                 190


Ile Thr Ala Gln Thr Gln Gly Ala Asn Tyr Arg Val Thr His Thr Asp
        195                 200                 205


Asp Ile Val Pro Lys Leu Pro Pro Glu Leu Phe Gly Tyr His His Phe
    210                 215                 220


Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asp Asn Val Thr Val Thr Thr
225                 230                 235                 240


Ser Asp Val Gln Val Val Thr Gly Ile Asp Ser Thr Ala Gly Asn Asp
                245                 250                 255
```

```
Gly Thr Leu Leu Asp Ser Thr Ser Ala His Asp Trp Tyr Ile Val Tyr
            260                 265                 270


Ile Asp Gly Cys Asp
        275



<210>  312
<211>  449
<212>  PRT
<213>  Paenibacillus sp.

<400>  312

Ile Thr Ser Ile Phe Gly Asn Ser Gln Asp Ala Tyr Ala Trp Ser Ala
1               5                   10                  15


Asp Asp Pro His Ser Gln Asp Phe Ser Thr His Leu Phe Ile Val Asn
            20                  25                  30


Gly Gly Val Lys Leu Ile Ser Gly Asn Val Asp Ser Ala Ile Asn Lys
        35                  40                  45


Ser Ser Thr Leu Leu Glu Gln Phe Arg Gly Arg Trp Glu Gln Gly Leu
    50                  55                  60


Tyr Asp Ala Asp His Leu Asn Pro Phe Tyr Asp Ser Ser Thr Phe Met
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gln Thr Asn Tyr Ala Gly Leu Ser
                85                  90                  95


Tyr Pro Thr Ala Arg Gln Ser Gly Ser Lys Tyr Phe Lys Val Ala Ser
            100                 105                 110


Asn Tyr Tyr Lys Asn Gly Asp Phe Ser Asn Ala Phe Tyr Tyr Leu Gly
        115                 120                 125


Val Ser Leu His Tyr Phe Thr Asp Ser Thr Met Pro Leu His Ala Ser
    130                 135                 140
```

```
Asp Ile Ser Asn Leu Asp His Arg Ala Pro Gly Tyr His Ala Lys Leu
145                 150                 155                 160


Glu Glu Tyr Ala Thr Ser Ile Gln Asn Gln Ile Asn Val Pro Asp Ser
                165                 170                 175


Gly Leu Phe Asn Trp Ile Ser Ser Thr Asp Pro Glu Leu Trp Ile His
            180                 185                 190


Gln Ala Ala Val Gln Ala Lys Ser Val Met Pro Glu Val Phe Asn Asp
        195                 200                 205


Thr Ile Thr Asp Trp Phe Trp Lys Ala Ala Phe Ser Tyr Tyr Tyr Ser
    210                 215                 220


Asp Met Trp Lys Ser Ala Val Lys Ile Pro Ile Leu Asn Gln Leu Asn
225                 230                 235                 240


Gln Ala Glu Arg Glu Thr Ala Gly Tyr Ile Asp Leu Phe Phe Arg Leu
                245                 250                 255


Asn Gly Val Asp Met Pro Val Ala Val Tyr Lys Gly Thr Ala Phe Gly
            260                 265                 270


Gly Ala Leu Gln Leu Leu Gly Phe Gly Asn Tyr Asp Tyr Asp Gln Leu
        275                 280                 285


Val Lys Gly Ile Gly Asn Asp Thr Val Ser Ser Ile Arg Ile Ala Pro
    290                 295                 300


Gly Tyr Gln Val Thr Leu Phe Ala Asp Ser Asn Tyr Ser Gly Val Ser
305                 310                 315                 320


Lys Val Leu Thr Ala Asp Ala Ser Asp Leu Gly Asn Phe Asn Lys Thr
                325                 330                 335


Thr Ser Ser Leu Lys Ile Glu Lys Ile Gln Pro Val Thr Val Tyr Thr
            340                 345                 350
```

```
Asp Ala Ser Phe Ser Gly Ser Ser Gln Ser Phe Ser Val Gly Asn His
        355                 360                 365


Asp Tyr Asn Glu Ile Val Asn Arg Lys Leu Asn Asp Thr Ile Ser Ser
    370                 375                 380


Ile Arg Ile Ala Pro Gly Tyr Gln Val Thr Leu Phe Arg Asp Ser Asn
385                 390                 395                 400


Tyr Ser Gly Val Ser Thr Val Val Thr Gly Asp Val Tyr Gly Leu Ser
                405                 410                 415


Asn Leu Asn Asp Gln Thr Ser Ser Leu Lys Val Glu Val Ile Pro Thr
            420                 425                 430


Asn Pro Ala Pro Ser Gln Thr Lys Gln Ser Ile Phe Ser Asn Pro Leu
        435                 440                 445


Asn



<210>  313
<211>  259
<212>  PRT
<213>  Bacillus toyonensis

<400>  313

His Glu Asn Asp Gly Gly Gln Arg Val Gly Val Ile Pro Arg Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Met Asp Ile Met Ser Arg Asn Thr Thr Leu Val Lys Gln
        35                  40                  45


Asp Arg Val Ala Leu Leu Asn Glu Trp Arg Thr Glu Leu Glu Asn Gly
    50                  55                  60
```

```
Ile Tyr Ala Ala Asp Tyr Glu Asn Leu Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Asn Gly Lys Thr Tyr Ile Pro Tyr
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Leu Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Val Ala Lys Gln Asp Tyr Ala Gly Ile Val Asn Asp Asn
        195                 200                 205


Thr Lys Asp Trp Phe Val Arg Ala Ala Val Ser Gln Glu Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Val Glu Val Thr Pro Met Thr Gly Lys Arg Leu Met Asp
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Gly Asn Arg
```

```
<210>  314
<211>  259
<212>  PRT
<213>  Bacillus thuringiensis

<400>  314

Asp Glu His Thr Thr Asn Asn Lys Ile Asp Ile Phe Gln Pro Trp Ser
1               5                   10                  15


Asn Glu Glu Asn His Lys Glu Gly Lys Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Gly Ala Ile Asp Ile Met Ser Arg Asn Thr Thr Ile Val Lys Gln
        35                  40                  45


Glu Asn Leu Ala Leu Leu Gln Gln Trp Arg Thr His Leu Glu Asn Gly
    50                  55                  60


Leu Tyr Val Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Ser Gly Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asn Pro Asp Thr Asp Ser Thr Tyr Leu Pro Phe
                85                  90                  95


Ala Lys His Ala Lys Glu Thr Gly Ala Thr Tyr Phe Thr Leu Ala Gly
            100                 105                 110


Glu Ala Tyr Gln His Lys Asn Ile Gln Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Val Ser Leu His Tyr Leu Gly Asp Ile Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Phe Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


His Phe Val Asp Thr Ile Lys Gln Asn Tyr Glu Ile Met Asp Gly Glu
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Arg Asp Pro Glu Asp Trp Ile His Gln
```

```
            180                 185                 190

Ala Ala Val Ala Ala Asn Gln Asp Phe Ser Asp Ile Val Asn Ser Asp
        195                 200                 205

Thr Lys Asn Trp Phe Val Lys Ala Ala Val Ser Gln Thr Tyr Ala Asp
    210                 215                 220

Arg Trp Arg Ala Ala Val Thr Pro Ile Thr Gly Lys Arg Leu Ile Glu
225                 230                 235                 240

Ala Gln Arg Ile Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255

Ile His Gln



<210>  315
<211>  259
<212>  PRT
<213>  Bacillus thuringiensis

<400>  315

His Glu Asn Asp Gly Gly Ser Lys Ile Lys Ile Ile His Arg Trp Ser
1               5                   10                  15

Ala Glu Asp Lys His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30

Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Thr Leu Val Lys Gln
        35                  40                  45

Asp Arg Val Ala Gln Leu Asn Glu Trp Arg Thr Glu Leu Glu Asn Gly
    50                  55                  60

Ile Tyr Ala Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80

Ala Ser His Phe Tyr Asp Pro Asp Asn Gly Lys Thr Tyr Ile Pro Phe
                85                  90                  95
```

```
Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Val Ala Lys Gln Asp Tyr Ser Gly Ile Val Asn Asp Asn
        195                 200                 205


Thr Lys Asp Trp Phe Val Lys Ala Ala Val Ser Gln Glu Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Lys Arg Leu Met Asp
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Gly Asp Arg



<210>  316
<211>  269
<212>  PRT
<213>  Talaromyces rugulosus

<400>  316
```

```
Asp Val Thr Thr Ala Val Leu Asp Asp Leu Thr Leu Phe Ser Gln Tyr
1               5                   10                  15


Ser Ala Ala Ala Tyr Cys Ser Thr Asn Leu Asn Ser Thr Gly Val Ala
            20                  25                  30


Val Thr Cys Ser Val Gly Asn Cys Pro Leu Val Glu Ala Ala Asp Thr
        35                  40                  45


Gln Ile Leu Tyr Asp Phe Asp Glu Ser Cys Lys Phe Gly Asp Ala Ser
    50                  55                  60


Gly Phe Ile Ala Val Asp Asn Thr Asn Asn Leu Ile Val Leu Ser Phe
65                  70                  75                  80


Arg Gly Ser His Asp Leu Ser Asn Trp Ile Ala Asn Leu Asp Phe Phe
                85                  90                  95


Leu Val Glu Thr Ala Ser Ile Cys Glu Gly Cys Tyr Met His Gly Gly
            100                 105                 110


Phe Trp Glu Thr Trp Gln Thr Val Ala Ala Asn Val Thr Glu Gln Leu
        115                 120                 125


Glu Ala Ala Ile Thr Ala Asn Pro Gly Tyr Thr Leu Val Met Thr Gly
    130                 135                 140


His Ser Leu Gly Ala Ala Leu Ala Ala Ile Val Ala Thr Glu Phe Arg
145                 150                 155                 160


Asn Glu Gly Ile Asp Val Glu Met Tyr Asn Tyr Gly Gln Pro Arg Leu
                165                 170                 175


Gly Asn Leu Ala Leu Ala Gln Tyr Met Thr Asn Gln Thr Gln Thr Ser
            180                 185                 190


Asn Tyr Arg Val Thr His Ser Asp Asp Ile Val Pro Lys Leu Pro Pro
        195                 200                 205
```

```
Arg Val Leu Asp Phe Asp His Tyr Ser Pro Glu Tyr Trp Ile Thr Ser
    210                 215                 220


Ala Asn Asn Val Ser Val Ser Asp Ala Asp Val Val Gln Val Val Gly
225                 230                 235                 240


Ile Asp Ser Thr Asp Gly Asn Asp Gly Thr Ile Leu Asp Asp Ile Glu
                245                 250                 255


Ala His Arg Trp Tyr Leu Gly Tyr Ile Ser Glu Cys Ser
            260                 265


<210>  317
<211>  275
<212>  PRT
<213>  Penicillium sp.

<400>  317

Ala Pro Ala Arg Pro Val Pro Arg Asp Val Ser Ser Ala Thr Leu Ser
1               5                   10                  15


Glu Leu Thr Leu Phe Ala Glu Tyr Ala Ala Ala Ala Tyr Cys Ser Asn
            20                  25                  30


Asn Ile Asp Ser Thr Gly Asp Ala Leu Ser Cys Ser Gly Gly Tyr Cys
        35                  40                  45


Pro Glu Val Gln Ser Ala Gly Ala Thr Thr Leu Tyr Glu Phe Glu Asp
    50                  55                  60


Ser Thr Asp Phe Gly Asp Val Thr Gly Phe Phe Ala Val Asp Asn Thr
65                  70                  75                  80


Asn Lys Leu Leu Val Leu Ser Phe Arg Gly Ser Ser Ser Ile Ser Asn
                85                  90                  95


Trp Ile Ala Asn Leu Asp Phe Gly Leu Thr Asp Ala Ser Ser Leu Cys
            100                 105                 110
```

```
Ser Gly Cys Glu Ala His Ser Gly Phe Tyr Lys Ser Trp Gly Val Val
        115                 120                 125


Ala Asp Thr Leu Thr Ala Gln Val Ala Ser Ala Val Ser Thr Tyr Pro
    130                 135                 140


Ser Tyr Thr Leu Val Val Thr Gly His Ser Leu Gly Gly Ala Leu Ala
145                 150                 155                 160


Ala Leu Gly Gly Thr Ala Leu Arg Asn Ala Gly Tyr Thr Leu Asp Ile
                165                 170                 175


Tyr Thr Tyr Gly Gln Pro Arg Val Gly Asn Thr Ala Leu Ala Asp Tyr
            180                 185                 190


Met Thr Asn Gln Gly Ser Leu Trp Arg Val Thr His Ser Asn Asp Ile
        195                 200                 205


Val Pro Lys Leu Pro Pro Ala Ser Trp Gly Phe Thr His Ala Ser Pro
    210                 215                 220


Glu Tyr Trp Ile Thr Ser Gly Asn Asp Val Thr Val Thr Thr Ser Asp
225                 230                 235                 240


Val Thr Glu Val Thr Gly Val Gly Ser Ser Asp Gly Asn Ala Gly Ser
                245                 250                 255


Ser Gly Asp Ser Val Ser Ala His Asn Trp Tyr Ile Val Asp Ile Asp
            260                 265                 270


Gly Cys Ser
        275


<210>  318
<211>  276
<212>  PRT
<213>  Hamigera avellanea

<400>  318

Ala Pro Ala Pro Val Arg Arg Asp Val Ser Ala Gly Val Leu Ala Asn
```

```
1               5                   10                  15


Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Asp Ser Asn
            20                  25                  30


Leu Asn Ser Asp Gly Thr Lys Leu Thr Cys Ala Ala Gly Asn Cys Pro
        35                  40                  45


Leu Val Glu Ala Ala Asp Thr Glu Thr Leu Asp Glu Phe Asp Met Thr
    50                  55                  60


Ala Thr Tyr Gly Asn Val Ala Gly Tyr Ile Ala Val Asp Arg Thr Asn
65                  70                  75                  80


Arg Leu Leu Val Leu Ala Phe Arg Gly Ser Ala Ser Ile Ser Asn Trp
                85                  90                  95


Ile Ala Asn Leu Asn Leu Gly Leu Thr Asp Ala Ser Ala Leu Cys Ala
            100                 105                 110


Gly Cys Glu Val His Ser Gly Phe Trp Glu Ala Trp Gln Thr Ala Glu
        115                 120                 125


Ala Thr Ile Ser Asp Ile Ile Ala Ser Ala Ala Gln Thr Tyr Pro Gly
    130                 135                 140


Tyr Thr Leu Val Val Thr Gly His Ser Tyr Gly Ala Ala Leu Ala Ala
145                 150                 155                 160


Ile Ala Ala Thr Arg Phe Arg Asn Glu Gly Tyr Ala Val Glu Leu Tyr
                165                 170                 175


Asp Tyr Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala Gln Tyr Ile
            180                 185                 190


Thr Asn Gln Ser Gly Gly Gly Asn Phe Arg Val Thr His Thr Asn Asp
        195                 200                 205


Ile Val Pro Lys Leu Pro Pro Asp Trp Leu Gly Tyr Ser His Phe Gly
```

```
    210                 215                 220


Pro Glu Tyr Trp Ile Thr Ser Gly Asp Gly Val Pro Val Thr Thr Ala
225                 230                 235                 240


Asp Val Glu Val Ile Ser Gly Val Asp Ala Thr Gly Gly Asn Asp Gly
                245                 250                 255


Ala Glu Gly Thr Ser Val Asp Ala His Arg Trp Tyr Phe Val Tyr Ile
            260                 265                 270


Ser Gln Cys Glu
        275


<210>  319
<211>  278
<212>  PRT
<213>  Penicillium spikei

<400>  319

Ala Pro Thr Arg Leu Leu Ile Pro Arg Asp Ile Ser Ser Asp Val Leu
1               5                   10                  15


Ala Glu Leu Thr Leu Phe Ala Glu Tyr Ser Ala Ala Ala Tyr Cys Ser
            20                  25                  30


Ala Asn Ile Asp Ser Ala Ser Ala Gly Ser Ala Leu Thr Cys Glu Ser
        35                  40                  45


Gly Asn Cys Pro Glu Val Gln Ser Ala Asp Thr Ser Thr Leu Tyr Glu
    50                  55                  60


Phe Asp Glu Thr Thr Asp Tyr Gly Asp Val Ala Gly Phe Phe Ala Val
65                  70                  75                  80


Asp Lys Thr Asn Glu Leu Leu Val Leu Ser Phe Arg Gly Ser Arg Thr
                85                  90                  95


Ile Ser Asn Trp Val Ala Asn Leu Asp Phe Asp Leu Thr Asp Ala Ser
            100                 105                 110
```

```
Ser Leu Cys Ser Asp Cys Glu Ala His Ser Gly Phe Trp Lys Ser Trp
        115                 120                 125


Glu Thr Val Ala Asp Glu Leu Thr Thr Gln Ile Glu Ser Ala Gln Asn
    130                 135                 140


Ser Tyr Pro Asp Tyr Gln Leu Val Leu Thr Gly His Ser Leu Gly Ala
145                 150                 155                 160


Ala Leu Ala Ala Leu Ala Gly Thr Ala Leu Arg Asn Ala Gly Tyr Thr
                165                 170                 175


Leu Asp Leu Tyr Thr Phe Gly Gln Pro Arg Val Gly Asn Leu Ala Leu
            180                 185                 190


Ala Asp Tyr Met Thr Asp Gln Gly Ser Leu Trp Arg Val Thr His Thr
        195                 200                 205


Asp Asp Ile Val Pro Arg Val Pro Pro Glu Ser Phe Gly Tyr Ala His
    210                 215                 220


Ala Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Asp Val Thr Val Thr
225                 230                 235                 240


Thr Ser Asp Val Glu Glu Ile Val Gly Val Asn Ser Ser Ala Gly Asn
                245                 250                 255


Ala Gly Glu Ala Asp Leu Ser Ile Asp Ala His Asn Trp Tyr Ile Val
            260                 265                 270


Tyr Ile Asp Glu Cys Glu
        275


<210>  320
<211>  480
<212>  PRT
<213>  Paenibacillus alginolyticus

<400>  320
```

```
Ile Thr Ser Val Phe Gly Asn Tyr Gln Asn Ala Tyr Ala Trp Ser Ala
1               5                   10                  15


Asp Asp Val His Asn Gln Asp Tyr Ser Thr His Leu Phe Ile Val Asn
            20                  25                  30


Gly Gly Val Lys Leu Ile Ser Gly Asn Ala Asp Ser Ala Ile Asn Lys
        35                  40                  45


Ser Ser Thr Leu Leu Glu Gln Phe Arg Asp Arg Trp Glu Gln Gly Leu
    50                  55                  60


Tyr Asp Ala Asp His Leu Asn Pro Phe Tyr Asp Ser Ser Thr Phe Met
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gln Thr Asn Tyr Ala Gly Leu Ser
                85                  90                  95


Tyr Pro Thr Ala Arg Gln Ser Gly Ser Lys Tyr Phe Lys Val Ala Ser
            100                 105                 110


Asp Tyr Tyr Lys Asn Gly Asp Phe Ser Asn Ala Phe Tyr Tyr Leu Gly
        115                 120                 125


Ile Ser Leu His Tyr Phe Thr Asp Ser Thr Met Pro Leu His Ala Ser
    130                 135                 140


Asp Ile Ser Asn Leu Asp His Arg Ala Pro Gly Tyr His Ala Lys Leu
145                 150                 155                 160


Glu Glu Tyr Thr Thr Ser Ile Gln Asn Gln Ile Thr Val Pro Asp Ser
                165                 170                 175


Gly Leu Phe Asn Trp Ile Ser Ser Thr Asp Pro Glu Leu Trp Ile His
            180                 185                 190


Gln Ala Ala Val Gln Ala Lys Ser Val Met Pro Gln Val Phe Asn Asp
        195                 200                 205
```

```
Ser Ile Thr Asp Trp Phe Trp Lys Ala Ala Val Ser Tyr Tyr Tyr Ser
    210                 215                 220


Asp Met Trp Lys Asn Thr Val Lys Thr Gln Ile Leu Asn Gln Leu Asn
225                 230                 235                 240


Gln Ala Glu Arg Glu Thr Ala Gly Tyr Ile Asp Leu Phe Phe Arg Leu
                245                 250                 255


Asn Gly Val Asp Met Pro Val Thr Val Tyr Asn Gly Thr Ala Phe Gly
            260                 265                 270


Gly Ala Ser Gln Leu Leu Gly Phe Gly Asn Tyr Asp Tyr Asn Gln Leu
        275                 280                 285


Val Lys Gly Ile Gly Asn Asp Thr Ile Ser Ser Ile Arg Ile Ala Pro
    290                 295                 300


Gly Tyr Gln Val Thr Leu Phe Ala Asp Ser Asn Tyr Ser Gly Val Ser
305                 310                 315                 320


Thr Val Val Thr Gly Asn Val Tyr Gly Leu Ser Asn Leu Asn Asp Gln
                325                 330                 335


Thr Ser Ser Leu Lys Val Gly Val Ile Pro Thr Asn Pro Ala Pro Ser
            340                 345                 350


Pro Thr Ile Gln Ala Glu Ser Phe Ser Gly Ser Gln Gly Ile Leu Thr
        355                 360                 365


His Ser Ala Gly Ser Gly Thr Val Val Gly Asn Ile Asn Ser Gly Ser
    370                 375                 380


Trp Leu Ser Tyr Asp Asn Val Asp Phe Gly Thr Gly Lys Thr Lys Phe
385                 390                 395                 400


Val Ala Ser Val Gly Met Asp Pro Ala Phe Ala Ala Ile Gly Lys Gln
                405                 410                 415
```

```
Leu Glu Leu Arg Leu Asp Ser Pro Thr Gly Thr Leu Ile Gly Thr Phe
            420                 425                 430


Thr Ile Ser Ser Ser Gly Gly Trp Asp Ala Tyr Thr Thr Gln Asn Cys
        435                 440                 445


Tyr Val Thr Ser Ala Ser Gly Thr His Lys Leu Tyr Ile Ile Thr Lys
    450                 455                 460


Gly Asn Gly Ser Gly Phe Gly Asn Ile Asp Trp Phe Thr Phe Ser Ser
465                 470                 475                 480


<210>  321
<211>  259
<212>  PRT
<213>  Bacillus mycoides

<400>  321

His Glu Asn Asp Gly Gly Ser Arg Ile Asn Ile Val His Arg Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Lys Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Met Asp Ile Met Ser Arg Asn Thr Thr Leu Val Lys Gln
        35                  40                  45


Asp Gln Val Ala Leu Leu Asn Glu Trp Arg Thr Glu Leu Glu Asn Gly
    50                  55                  60


Ile Tyr Ala Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Asn Gly Lys Thr Tyr Ile Pro Phe
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110
```

```
Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Ala Ala Lys Gln Asp Tyr Ser Gly Ile Val Asn Asp Asn
        195                 200                 205


Thr Lys Asp Trp Phe Val Lys Ala Ala Val Ser Gln Glu Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Thr Arg Leu Met Asp
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Gly Asn Arg



<210>  322
<211>  259
<212>  PRT
<213>  Bacillus bingmayongensis

<400>  322

His Glu Asn Glu Gly Gly Asn Lys Ile Arg Val Ile Gln Tyr Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Ala Glu Gly Val Asn Ser His Leu Trp Ile Val
```

```
            20                  25                  30


Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Thr Ile Val Lys Gln
        35                  40                  45


Asp Glu Val Ala Leu Leu Asn Glu Trp Arg Thr Glu Leu Glu Asn Gly
    50                  55                  60


Ile Tyr Ala Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Ser Gly Lys Thr Tyr Ile Pro Phe
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Gln Lys Gln Glu Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Val Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Ala Ile Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Thr Asn Pro Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Ala Ala Lys Gln Glu Tyr Ala Gly Ile Val Asn Asp Thr
        195                 200                 205


Thr Lys Asp Trp Phe Val Trp Ala Ala Val Ser Gln Glu Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Ala Thr Gly Lys Arg Leu Val Glu
```

```
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Gly Asn Arg




<210>  323
<211>  260
<212>  PRT
<213>  Bacillus mycoides

<400>  323

His Glu Asn Ser His Gln Asn Gly Ile Ser Phe Gly His Lys Trp Ser
1               5                   10                  15


Ala Glu Ala Ile His Asp Glu Gly Val Ser Thr His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ser Ile Glu Val Met Ala Gln Asn Lys Thr Val Val Gln Pro
        35                  40                  45


Asn Glu Ile Ser Leu Leu Asn Glu Trp Arg Ala Asp Leu Glu Lys Gly
    50                  55                  60


Ile Tyr Ser Ala Asp Tyr Asp Asn Pro Tyr Phe Asp Asn Gly Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Thr Gly Gly Thr Tyr Leu Pro Leu
                85                  90                  95


Ala Lys His Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ala Tyr Gln Asn Asn Asp Leu Lys Asn Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140
```

```
Asn Phe Thr Asn Val Ser Leu Pro Val Ala Leu His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Val Lys Asp Asn Tyr Lys Val Lys Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Ser Val Asn Pro Glu Asp Trp Val His Ala
            180                 185                 190


Ser Ala Val Gly Ala Lys Ala Asp Phe Pro Leu Ile Val Asn Asp Lys
        195                 200                 205


Thr Lys Lys Trp Phe Leu Asp Ala Ala Ile Ser Gln Asp Ala Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Val Thr Gly Lys Arg Leu Met Glu
225                 230                 235                 240


Ala Gln Arg Ile Thr Ala Gly Tyr Ile His Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Val Asn Tyr Lys
            260


<210>  324
<211>  269
<212>  PRT
<213>  Brevibacillus sp.

<400>  324

Lys Lys Glu Tyr Lys Val Lys Tyr His Gly Lys Thr Ile Thr Ser Pro
1               5                   10                  15


Tyr Lys Ile Asp Pro Arg Trp Ser Glu Glu Ser Pro His Glu Glu Gly
            20                  25                  30


His Ala Thr His Leu Trp Ile Val Asn Arg Ala Ile Asp Ile Leu Ser
        35                  40                  45
```

```
Arg Thr Ser Asn Lys Asp Val Asn Ser Lys Glu Thr Glu Met Leu Asn
    50                  55                  60


Ala Trp Arg Ser Ser Trp Glu Gln Gly Leu Tyr Asp Ala Asp His Thr
65                  70                  75                  80


Asn Pro Tyr Tyr Asn Phe Gly Thr Phe Ala Ser His Phe Tyr Asp Pro
                85                  90                  95


Asp Thr Lys Ser Asn Trp Leu Asp Thr Ser Gly Thr Ala Leu Thr Glu
            100                 105                 110


Gly Ser Arg Tyr Phe Ala Leu Ala Gly Lys Tyr Tyr Gln Asn Gly Asp
        115                 120                 125


Lys Glu Lys Ala Phe Tyr Tyr Leu Gly Leu Ser Leu His Tyr Leu Thr
    130                 135                 140


Asp Val Thr Gln Pro Met His Ala Ala Asn Phe Thr Trp Leu Asn Trp
145                 150                 155                 160


Pro Thr Ser Phe His Gly Lys Phe Glu Asp Tyr Thr Asp Asp Ile Gln
                165                 170                 175


Gly Asn Tyr Ala Val Thr Asp Gly Glu Gly Tyr Trp Asp Phe Gln Asp
            180                 185                 190


Ser Asn Pro Glu His Trp Ile His Gln Ala Ala Val Asp Ala Lys Ala
        195                 200                 205


Glu Phe Pro Asn Ile His Thr Ser Asp Ile Thr Lys Trp Phe Leu Ala
    210                 215                 220


Ala Ala Val Ser Asp Tyr Tyr Ser Asp Lys Trp His Lys Ala Val Gln
225                 230                 235                 240


Pro Thr Ile Glu His Arg Leu Thr Glu Ala Gln Arg Ile Thr Ala Gly
                245                 250                 255
```

```
Tyr Leu His Leu Trp Phe Lys Thr Tyr Val Asp Asn Gln
            260                 265


<210>  325
<211>  275
<212>  PRT
<213>  Penicilliumvasconiae

<400>  325

Ala Pro Ala Arg Pro Val Pro Arg Asp Val Ser Ser Ala Thr Leu Ser
1               5                   10                  15


Glu Leu Thr Leu Phe Ser Gln Tyr Ala Ala Ala Ala Tyr Cys Thr Asn
            20                  25                  30


Asn Val Asn Ser Ala Gly Asp Ala Val Ser Cys Ser Gly Gly Tyr Cys
        35                  40                  45


Pro Glu Val Gln Ser Ala Gly Ala Thr Thr Leu Tyr Glu Phe Asp Asp
    50                  55                  60


Ser Thr Asp Phe Gly Asp Val Ala Gly Phe Phe Ala Val Asp Ala Thr
65                  70                  75                  80


Asn Lys Leu Leu Val Leu Ser Phe Arg Gly Ser Arg Thr Ile Ser Asn
                85                  90                  95


Trp Ile Ala Asn Leu Asp Phe Gly Gln Thr Asp Ala Ser Ser Leu Cys
            100                 105                 110


Ser Gly Cys Glu Ala His Ser Gly Phe Phe Lys Ala Trp Glu Ala Val
        115                 120                 125


Ala Asp Thr Leu Thr Ala Gln Ile Ala Ser Ala Val Ala Thr Tyr Pro
    130                 135                 140


Ser Tyr Thr Leu Val Leu Thr Gly His Ser Phe Gly Gly Ala Val Ala
145                 150                 155                 160
```

```
Ala Leu Gly Gly Thr Ala Leu Arg Asn Ala Gly Tyr Thr Leu Asp Leu
                165                 170                 175


Tyr Thr Tyr Gly Gln Pro Arg Val Gly Asn Thr Ala Leu Ala Asp Tyr
            180                 185                 190


Met Thr Asn Gln Gly Ser Leu Trp Arg Val Thr His Ser Asp Asp Ile
        195                 200                 205


Val Pro Lys Leu Pro Pro Thr Ser Trp Gly Phe Thr His Ala Ser Pro
    210                 215                 220


Glu Tyr Trp Ile Thr Ser Gly Asp Asp Val Thr Val Thr Thr Ser Asp
225                 230                 235                 240


Val Thr Glu Val Thr Gly Val Gly Ser Ser Gly Gly Asn Ala Gly Thr
                245                 250                 255


Ser Gly Asp Ser Val Ser Ala His Asn Trp Tyr Ile Val Asp Ile Asp
            260                 265                 270


Gly Cys Gln
        275


<210>  326
<211>  277
<212>  PRT
<213>  Talaromyces diversus

<400>  326

Ala Ile Asp Pro Leu Asn Arg Arg Thr Ile Ser Glu Ser Leu Leu Asp
1               5                   10                  15


Glu Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ala
            20                  25                  30


Asn Leu Asp Ser Thr Gly Ser Ala Leu Ala Cys Asp Val Gly Asn Cys
        35                  40                  45


Pro Leu Val Glu Ala Ala Ser Thr Thr Ile Leu Tyr Asp Phe Asp Glu
```

50 55 60

Thr Asn Asp Phe Gly Asp Ala Thr Gly Tyr Ile Ala Val Asp Thr Thr
65 70 75 80

Asn Glu Tyr Ile Ile Leu Ser Phe Arg Gly Thr Asp Asp Leu Glu Asn
85 90 95

Trp Ile Ala Asn Leu Asp Phe Pro Leu Ile Asp Ala Ser Asp Ile Cys
100 105 110

Ser Gly Cys Glu Ile His Glu Gly Trp Trp Asp Ser Trp Glu Thr Val
115 120 125

Ala Ser Asp Ile Thr Ala Gln Ile Glu Ser Ala Val Ser Thr Tyr Pro
130 135 140

Asp Tyr Thr Leu Val Ala Thr Gly His Ser Leu Gly Ala Ala Leu Ala
145 150 155 160

Ala Ile Ala Ala Thr Val Leu Arg Leu Asp Gly Tyr Thr Val Gln Leu
165 170 175

Tyr Asn Tyr Gly Glu Pro Arg Ile Gly Asn Leu Ala Leu Ala Asp Tyr
180 185 190

Ile Thr Thr Glu Thr Met Gly Ser Asn Tyr Arg Val Thr His Thr Asp
195 200 205

Asp Ile Val Pro Lys Leu Pro Pro Glu Leu Leu Gly Tyr Asp His Phe
210 215 220

Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asp Asp Val Thr Val Leu Asp
225 230 235 240

Thr Asp Val Thr Glu Val Val Gly Val Asp Ser Thr Ala Gly Asn Asp
245 250 255

Gly Thr Leu Leu Asp Ser Ile Asp Ala His Arg Trp Tyr Phe Val Tyr

```
            260                 265                 270


Ile Ser Glu Cys Ser
        275



<210>  327
<211>  280
<212>  PRT
<213>  Aspergillus wentii

<400>  327

Ala Pro Ser Pro Val Arg Arg Asp Val Asp Ser Ser Val Leu Asn Asn
1               5                   10                  15


Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ser Tyr Cys Leu Glu Asn
            20                  25                  30


Leu Asn Ser Ser Asn Thr Lys Leu Glu Cys Ser Val Gly Asn Cys Pro
        35                  40                  45


Leu Val Glu Ala Ala Ser Thr Val Thr Leu Asp Glu Phe Asp Glu Ser
    50                  55                  60


Ser Ser Phe Gly Asp Val Thr Gly Phe Ile Ala Ala Asp Glu Thr Asn
65                  70                  75                  80


Lys Leu Leu Val Leu Ser Phe Arg Gly Ser Ser Asp Ile Ala Asn Trp
                85                  90                  95


Ile Ala Asp Leu Asp Phe Gly Leu Thr Asp Gly Ser Asp Leu Cys Ser
            100                 105                 110


Gly Cys Lys Val His Ser Gly Phe Trp Glu Ala Trp Gly Thr Val Ser
        115                 120                 125


Asp Asn Ile Thr Ser Ile Ile Glu Ser Ala Thr Ala Lys Tyr Pro Asn
    130                 135                 140


Tyr Glu Leu Ala Phe Thr Gly His Ser Tyr Gly Ala Ala Leu Ala Ala
145                 150                 155                 160
```

```
Val Ala Ala Val Val Phe Arg Asn Ser Gly Tyr Thr Val Gln Leu Tyr
                165                 170                 175


Asn Tyr Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala Asp Tyr Ile
            180                 185                 190


Thr Asn Val Thr Asp Lys Gly Asp Asn Tyr Arg Val Thr His Thr Asp
        195                 200                 205


Asp Ile Val Pro Lys Leu Pro Pro Lys Leu Leu Gly Tyr His His Ala
    210                 215                 220


Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Asn Val Thr Val Thr Thr
225                 230                 235                 240


Ala Asp Val Asp Val Val Thr Gly Val Asp Ser Thr Asp Gly Asn Asp
                245                 250                 255


Gly Thr Thr Ala Asp Ser Arg Thr Ala His Arg Trp Tyr Phe Gly Tyr
            260                 265                 270


Ile Ser Glu Cys Ser Thr Leu Tyr
        275                 280


<210>  328
<211>  480
<212>  PRT
<213>  Bacillus acidiceler

<400>  328

Ile Thr Ser Leu Phe Gly Asn Tyr Gln Arg Ala Phe Ala Trp Ser Asp
1               5                   10                  15


Glu Asp Val His Asn Gln Asp His Ser Thr His His Phe Ile Val Asn
            20                  25                  30


Gly Gly Val Lys Leu Ile Ala Asp Asn Thr Asp Pro Ala Ile Asn Lys
        35                  40                  45
```

```
Pro Thr Thr Leu Leu Asn Gln Phe Arg Asp Arg Trp Glu Gln Gly Leu
    50                  55                  60


Tyr Asp Ala Asp His Ile Asn Pro Phe Tyr Asp Thr Gly Thr Phe Met
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gln Thr Asn Tyr Ser Gly Leu Ser
                85                  90                  95


Tyr Pro Thr Ala Arg Gln Ser Gly Gly Lys Tyr Phe Asn Leu Ala Ser
            100                 105                 110


Asp Tyr Tyr Lys Lys Gly Asp Phe Asn Asn Ala Phe Tyr Tyr Leu Gly
        115                 120                 125


Val Ser Leu His Tyr Phe Thr Asp Val Thr Gln Pro Leu His Ala Ser
    130                 135                 140


Asn Ile Ser Asn Leu Asp His Asn Ala Pro Gly Tyr His Ser Lys Tyr
145                 150                 155                 160


Glu Thr Tyr Ala Glu Ser Ile Gln Ser Gln Ile Ile Val Pro Asp Ser
                165                 170                 175


Gly Leu Tyr Asn Trp Thr Asp Ser Thr Asp Pro Glu Ala Trp Ile His
            180                 185                 190


Lys Ala Ala Ile Gln Ala Lys Ser Val Leu Pro Leu Val Trp Asn Asp
        195                 200                 205


Thr Ile Ile Asn Trp Phe Trp Gln Ala Ala Tyr Ser Asn Tyr Tyr Ser
    210                 215                 220


Ala Met Trp Lys Asn Glu Val Lys Asn Pro Thr Leu Ala Gln Leu Asn
225                 230                 235                 240


Gln Ala Glu Arg Glu Thr Ala Gly Phe Ile Asp Met Phe Phe Arg Leu
                245                 250                 255
```

```
Asn Gly Val Glu Met Pro Val Thr Val Tyr Asn Glu Asn Ala Phe Gly
            260                 265                 270


Gly Ala Ser Glu Leu Leu Gly Ser Gly Asn Tyr Asp Tyr Asp Gln Leu
        275                 280                 285


Ile Lys Cys Ile Gly Asn Asp Thr Ile Ser Ser Ile His Ile Ala Pro
    290                 295                 300


Gly Tyr Gln Val Thr Leu Phe Ala Asp Ala Asn Tyr Lys Gly Ala Ser
305                 310                 315                 320


Ile Val Leu Thr Gly Asp Val Asn Asp Leu Gly Asn Phe Asn His Gln
                325                 330                 335


Val Ser Ser Leu Lys Ile Glu Lys Ile Ser Thr Asn Pro Ala Ser Ser
            340                 345                 350


Pro Thr Ile Gln Ala Glu Ser Phe Ile Ser Ser Lys Gly Ile Leu Thr
        355                 360                 365


His Asn Val Gly Ser Gly Thr Val Val Gly Asn Ile Asn Ser Gly Ser
    370                 375                 380


Trp Ile Gly Tyr Asp Asn Val Asp Phe Gly Thr Gly Lys Thr Lys Phe
385                 390                 395                 400


Ile Ala Arg Val Gly Met Asp Pro Ser Tyr Ala Ile Phe Asp Lys Gln
                405                 410                 415


Leu Glu Leu Arg Leu Asp Ser Pro Thr Gly Thr Ile Ile Gly Thr Phe
            420                 425                 430


Thr Ile Asn Asn Thr Gly Gly Trp Asp Thr Tyr Ala Thr Gln Thr Ser
        435                 440                 445


Ile Leu Ser Gly Ala Thr Gly Thr His Lys Leu Tyr Ile Val Ser Lys
    450                 455                 460
```

```
Gly Ser Gly Asp Gly Phe Gly Asn Ile Asp Trp Ile Thr Phe Ser Pro
465                 470                 475                 480


<210>  329
<211>  259
<212>  PRT
<213>  Bacillus luti

<400>  329

His Glu Lys Asn Glu Gly Asn Val Pro Ile Ile Thr Gln Tyr Trp Ser
1               5                   10                  15


Ala Glu Asp Thr His Ser Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Thr Leu Val Arg Gln
        35                  40                  45


Asp Glu Val Ala Leu Leu Asn Ala Trp Arg Thr Asp Leu Glu Lys Gly
    50                  55                  60


Ile Tyr Ala Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Phe
65                  70                  75                  80


Thr Ser His Phe Tyr Asp Pro Asp Thr Gly Lys Thr Tyr Val Gly Leu
                85                  90                  95


Ala Lys Gln Ala Lys Glu Thr Gly Asn Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160
```

```
Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Met Asn Pro Glu Glu Trp Ile His Gly
            180                 185                 190


Ala Ala Val Ala Ala Lys Gln Asp Tyr Ser Gly Ile Val Asn Ser Asn
        195                 200                 205


Thr Lys Ser Trp Phe Val Lys Ala Ala Val Ser Gln Ser Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Thr Thr Gly Lys Arg Leu Met Glu
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Gly Asn Arg



<210>  330
<211>  259
<212>  PRT
<213>  Bacillus pseudomycoides

<400>  330

His Thr Asn Asp Cys Gly Asn Glu Ala Pro Val Leu Lys Trp Ser Ala
1               5                   10                  15


Glu Asp Lys His Asn Glu Gly Arg Asn Ser His Leu Trp Ile Val Asn
            20                  25                  30


Arg Ala Ile Asp Ile Met Ser Arg Asp Lys Thr Val Val Lys Pro Asn
        35                  40                  45


Glu Thr Ala Leu Leu Asn Glu Trp Arg Asp Asp Leu Glu Asn Gly Ile
    50                  55                  60


Tyr Ser Ala Asp Tyr Glu Asn Pro Tyr Phe Asp Asn Gly Thr Phe Ala
```

```
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gln Lys Ser Tyr Ile Pro Phe Ala
                85                  90                  95


Lys His Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly Glu
            100                 105                 110


Ala Tyr Gln Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly Leu
        115                 120                 125


Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala Asn
    130                 135                 140


Phe Thr Asn Ile Ser Thr Glu Ala Pro Ile Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Ala Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Thr Asn Ser Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Ala Ser Lys Gln Asp Tyr Ser Ser Ile Val Asn Asp Thr
        195                 200                 205


Thr Thr Ser Trp Phe Leu Lys Ala Ala Thr Ser Gln Glu Tyr Ala Asn
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Thr Ser Gly Lys Arg Leu Ile Glu
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile His Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Val Asn Arg


<210>  331
```

```
<211>  260
<212>  PRT
<213>  Bacillus mycoides

<400>  331

His Glu Asn Asp Gly Gln Phe Asp Pro Pro Ile Ala Gln Arg Trp Ser
1               5                   10                  15


Ala Glu Ser Ile His Asn Glu Gly Val Ser Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Ile Asp Ile Met Ser Gln Asn Thr Thr Val Val Lys Gln
        35                  40                  45


Asn Glu Thr Ala Leu Leu Asn Glu Trp Arg Thr Asn Leu Glu Glu Gly
    50                  55                  60


Ile Tyr Ser Ala Asp Tyr Lys Asn Pro Tyr Tyr Asp His Ser Thr Phe
65                  70                  75                  80


Ala Ser His Phe Tyr Asp Pro Asp Ser Gly Lys Thr Tyr Ile Pro Phe
                85                  90                  95


Ala Lys Gln Ala Lys Gln Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ala Tyr Gln Asn Lys Asp Met Lys Asn Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Leu Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Ile Ser His Pro Phe Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Val Lys Asp Asn Tyr Arg Val Thr Asp Gly Asp
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Ser Ala Asn Pro Glu Glu Trp Val His Ala
            180                 185                 190
```

```
Ser Ala Ser Ala Ala Lys Ala Asp Phe Pro Ser Ile Val Asn Asp Asn
        195                 200                 205


Thr Lys Asn Trp Phe Leu Lys Ala Thr Val Ser Gln Asp Ser Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Val Thr Gly Lys Arg Leu Met Glu
225                 230                 235                 240


Ala Gln Arg Ile Thr Ala Gly Tyr Ile His Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Val Asn Asn Lys
            260


<210>  332
<211>  272
<212>  PRT
<213>  Penicillium cinnamopurpureum

<400>  332

Val Pro Leu Arg Arg Asp Val Ser Ser Asp Asp Leu Lys Gln Leu Thr
1               5                   10                  15


Leu Phe Ala Glu Tyr Ala Ser Ala Ser Tyr Cys Thr Asn Asn Ile Asn
            20                  25                  30


Ser Thr Gly Asp Ala Leu Ser Cys Ala Glu Gly Asn Cys Pro Ala Val
        35                  40                  45


Gln Ser Ala Thr Thr Lys Thr Leu Tyr Glu Phe Asn Asp Ser Thr Glu
    50                  55                  60


Phe Gly Asp Val Ala Gly Phe Leu Ala Ala Asp Glu Thr Asn Glu Leu
65                  70                  75                  80


Leu Val Leu Ser Phe Arg Gly Ser Arg Thr Ile Ser Thr Trp Val Ala
                85                  90                  95
```

```
Asn Leu Asp Phe Gly Leu Thr Asp Thr Ser Asp Leu Cys Ser Gly Cys
            100                 105                 110


Glu Ala His Gly Gly Phe Trp Lys Ser Trp Gln Thr Val Thr Asp Asp
        115                 120                 125


Ile Thr Ser Lys Ile Asp Ala Gly Leu Lys Ser His Pro Gly Tyr Thr
    130                 135                 140


Val Val Leu Thr Gly His Ser Phe Gly Ala Ala Met Ala Thr Leu Gly
145                 150                 155                 160


Gly Thr Ala Leu Arg Asn Ala Gly Tyr Lys Ile Lys Leu Tyr Thr Tyr
                165                 170                 175


Gly Glu Pro Arg Val Gly Asn Glu Ala Leu Ala Lys Tyr Ile Thr Lys
            180                 185                 190


Gln Gly Asp Leu Tyr Arg Val Thr His Ala Asp Asp Val Val Pro Lys
        195                 200                 205


Val Pro Pro Ala Ser Phe Gly Phe Ser His Ala Ser Pro Glu Tyr Trp
    210                 215                 220


Ile Thr Ser Gly Asn Asn Lys Thr Val Ser Thr Ser Asp Ile Lys Val
225                 230                 235                 240


Ile Gln Gly Val Gly Ser Lys Asp Gly Asn Ala Gly Thr Ile Asn Pro
                245                 250                 255


Asp Ile Glu Ala His Asn Trp Tyr Ile Val His Ile Asp Gly Cys Gln
            260                 265                 270
```

<210> 333
<211> 275
<212> PRT
<213> Talaromyces verruculosus

<400> 333

```
Glu Pro Ile Tyr Arg Arg Lys Ile Ala Thr Ser Leu Leu Asp Ser Leu
1               5                   10                  15


Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ala Asn Leu
            20                  25                  30


Asp Thr Thr Gly Thr Ala Leu Ala Cys Asn Val Gly Asn Cys Pro Ala
        35                  40                  45


Val Glu Ala Ala Asp Thr Thr Ile Leu Tyr Ser Phe Asp Ser Ser Ser
    50                  55                  60


Ser Phe Gly Asp Ala Thr Gly Tyr Ile Ala Val Asp Glu Ser His Gly
65                  70                  75                  80


Tyr Ile Ile Leu Ser Phe Arg Gly Thr Ser Asn Leu Glu Asn Phe Ile
                85                  90                  95


Ala Thr Leu Asp Met Gln Leu Ile Asp Ala Ser Ser Ile Cys Ser Gly
            100                 105                 110


Cys Lys Val His Lys Gly Phe Trp Asn Thr Trp Glu Thr Val Ala Ser
        115                 120                 125


Asp Val Thr Ser Gln Ile Lys Ala Ala Leu Ser Ala Tyr Pro Asp Tyr
    130                 135                 140


Thr Leu Val Ala Thr Gly His Ser Leu Gly Ala Ala Leu Ala Ala Ile
145                 150                 155                 160


Ala Ala Thr Val Phe Arg Ala Ser Gly Tyr Thr Val Gln Leu Tyr Asn
                165                 170                 175


Tyr Gly Glu Pro Arg Ile Gly Asn Leu Ala Leu Ala Asp Phe Ile Thr
            180                 185                 190


Ser Glu Thr Ser Gly Thr Asn Tyr Arg Val Thr His Ser Asn Asp Ile
        195                 200                 205
```

```
Ile Pro Lys Leu Pro Pro Gly Leu Leu Gly Tyr His His Phe Ser Pro
    210                 215                 220


Glu Tyr Trp Ile Thr Ser Lys Asp Asn Val Thr Val Thr Asp Ser Asp
225                 230                 235                 240


Val Val Glu Ile Lys Gly Val Asp Ser Thr Asp Gly Asn Asp Gly Thr
                245                 250                 255


Ala Gly Ala Ser Ile Glu Ala His Thr Trp Tyr Phe Val Tyr Ile Ser
            260                 265                 270


Glu Cys Leu
        275


<210>  334
<211>  277
<212>  PRT
<213>  Talaromyces cellulolyticus

<400>  334

Ala Pro Lys Pro Ile His Arg Arg Thr Ile Pro Thr Ser Leu Leu Asp
1               5                   10                  15


Asn Leu Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Ala
            20                  25                  30


Asn Leu Glu Thr Thr Gly Thr Ala Leu Ala Cys Asn Val Gly Asn Cys
        35                  40                  45


Pro Ala Val Glu Ala Ala Asp Thr Ile Ile Leu Tyr Ser Phe Asp Ser
    50                  55                  60


Ser Ser Ser Phe Gly Asp Ala Thr Gly Tyr Val Ala Val Asp Glu Ser
65                  70                  75                  80


Asn Glu Tyr Ile Ile Leu Ser Phe Arg Gly Ser Ser Asn Leu Glu Asn
                85                  90                  95


Trp Ile Ala Asn Leu Asp Ile Pro Leu Ile Asp Ala Ser Ser Ile Cys
```

```
            100                 105                 110


Ser Gly Cys Thr Val His Glu Gly Phe Trp Asp Thr Trp Glu Thr Val
        115                 120                 125


Ala Ser Asp Val Thr Ser Gln Ile Glu Ser Ala Leu Ser Thr Tyr Pro
    130                 135                 140


Asn Tyr Thr Leu Val Ala Thr Gly His Ser Leu Gly Gly Ala Leu Ala
145                 150                 155                 160


Ala Ile Ala Ala Thr Val Phe Arg Ala Ser Gly Tyr Thr Val Gln Leu
                165                 170                 175


Tyr Asn Tyr Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala Asp Phe
            180                 185                 190


Ile Thr Ser Glu Thr Ser Gly Thr Asn Tyr Arg Val Thr His Ser Asp
        195                 200                 205


Asp Ile Val Pro Lys Leu Pro Pro Glu Leu Leu Gly Tyr His His Phe
    210                 215                 220


Ser Pro Glu Tyr Trp Ile Thr Ser Asn Asp Asn Val Thr Val Thr Asp
225                 230                 235                 240


Ser Asp Val Val Glu Ile Gln Gly Val Asp Ser Thr Ala Gly Asn Asp
                245                 250                 255


Gly Thr Ser Gly Asp Ser Ile Asp Ala His Ser Trp Tyr Phe Val Ser
            260                 265                 270


Ile Ser Glu Cys Ser
        275


<210>  335
<211>  280
<212>  PRT
<213>  Penicillium megasporum
```

```
<400>  335

Gly Pro Val Ser Val Leu Arg Arg Asp Glu Asp Val Ser Ala Ser Val
1               5                   10                  15


Leu Ser Glu Leu Asp Phe Phe Ser Gln Tyr Ser Ala Ala Ala Tyr Cys
            20                  25                  30


Ser Thr Asn Ile Asn Ser Ala Gly Thr Lys Leu Thr Cys Ser Glu Gly
        35                  40                  45


Ile Cys Pro Leu Val Glu Asn Ala Asp Thr Glu Thr Leu Asp Glu Phe
    50                  55                  60


Asp Glu Ser Ala Ser Tyr Gly Asp Val Ala Gly Phe Ile Ala Val Asp
65                  70                  75                  80


Arg Thr Asn Glu Leu Leu Val Leu Ser Phe Arg Gly Ser Ala Ser Phe
                85                  90                  95


Ser Asn Trp Leu Ala Asn Ile Asp Leu Phe Leu Asp Asp Ala Ser Ser
            100                 105                 110


Val Cys Ser Gly Cys Glu Val His Ser Gly Phe Trp Asp Ala Trp Gln
        115                 120                 125


Thr Val Glu Gly Gln Ile Thr Thr Ala Leu Gly Ser Ala Met Glu Thr
    130                 135                 140


Tyr Pro Gly Tyr Thr Leu Val Phe Thr Gly His Ser Tyr Gly Ala Ala
145                 150                 155                 160


Leu Ala Ala Ile Ala Ala Thr Ile Phe Arg Asn Ser Gly Tyr Thr Val
                165                 170                 175


Glu Leu Tyr Asn Tyr Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala
            180                 185                 190


Glu Tyr Ile Thr Asn Gln Asn Lys Gly Gly Asn Tyr Arg Val Thr His
        195                 200                 205
```

```
Thr Asp Asp Ile Val Pro Lys Val Pro Pro Lys Ile Thr Gly Tyr His
    210                 215                 220


His Ala Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Asn Val Thr Val
225                 230                 235                 240


Thr Thr Ser Asp Val Gln Leu Ile Thr Gly Val Asp Ser Thr Ser Gly
                245                 250                 255


Asn Asp Gly Thr Ser Asp Asp Ser Val Glu Ala His Arg Trp Tyr Phe
            260                 265                 270


Val His Ile Ser Met Cys Thr Ile
        275                 280


<210>  336
<211>  259
<212>  PRT
<213>  Bacillus toyonensis

<400>  336

His Glu Lys Thr Glu Gly His Asn Val Asn Ile Ile Gln Tyr Trp Ser
1               5                   10                  15


Ala Glu Asp Lys His Ser Glu Gly Val Asn Ser His Leu Trp Ile Val
            20                  25                  30


Asn Arg Ala Ile Asp Ile Met Ser Arg Asn Thr Lys Leu Val Lys Gln
        35                  40                  45


Asp Gln Ile Ile Leu Leu Asn Glu Trp Arg Thr Asp Leu Glu Asn Gly
    50                  55                  60


Ile Tyr Ser Ala Asp His Glu Asn Pro Tyr Tyr Asp Asn Ser Thr Leu
65                  70                  75                  80


Val Ser His Phe Tyr Asp Pro Asp Asp Gly Ser Thr Tyr Ile Pro Phe
                85                  90                  95
```

```
Ala Lys Gln Ala Lys Glu Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly
            100                 105                 110


Glu Ser Tyr Lys Asn Lys Asp Met Lys Gln Ala Phe Phe Tyr Leu Gly
        115                 120                 125


Val Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala
    130                 135                 140


Asn Phe Thr Asn Leu Ser Tyr Pro Gln Gly Phe His Ser Lys Tyr Glu
145                 150                 155                 160


Asn Phe Val Asp Thr Ile Lys Asp Asn Tyr Lys Val Thr Asp Gly Asn
                165                 170                 175


Gly Tyr Trp Asn Trp Lys Gly Ile His Pro Glu Asp Trp Ile His Gly
            180                 185                 190


Ala Ala Val Gly Ala Lys Gln Asp Phe Ser Gly Ile Val Asn Ser Asn
        195                 200                 205


Thr Lys Ser Trp Phe Val Lys Ala Ala Val Ser Gln Ser Tyr Ala Asp
    210                 215                 220


Lys Trp Arg Ala Glu Val Thr Pro Met Thr Gly Lys Arg Leu Ile Glu
225                 230                 235                 240


Ala Gln Arg Val Thr Ala Gly Tyr Ile Gln Leu Trp Phe Asp Thr Tyr
                245                 250                 255


Val Asn Arg



<210>  337
<211>  259
<212>  PRT
<213>  Bacillus sp.

<400>  337
```

```
His Glu Asp Thr His Gln Asp Pro Pro Ile Ala Leu Lys Trp Ser Ala
1               5                   10                  15


Glu Ser Val His Asn Glu Gly Val Ser Ser His Leu Trp Ile Val Asn
            20                  25                  30


Arg Ala Ile Asp Ile Met Ser Gln Asn Thr Thr Val Val Lys Gln Asn
        35                  40                  45


Glu Thr Ala Leu Leu Asn Asp Trp Arg Thr Asn Leu Glu Glu Gly Ile
    50                  55                  60


Tyr Ser Ala Asp Tyr Lys Asn Pro Tyr Tyr Asp Asn Ser Thr Phe Ala
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Ser Glu Lys Thr Tyr Ile Pro Phe Ala
                85                  90                  95


Lys Gln Ala Lys Gln Thr Gly Ala Lys Tyr Phe Lys Leu Ala Gly Glu
            100                 105                 110


Ala Tyr Gln Asn Lys Asp Met Lys Asn Ala Phe Phe Tyr Leu Gly Leu
        115                 120                 125


Ser Leu His Tyr Leu Gly Asp Val Asn Gln Pro Met His Ala Ala Asn
    130                 135                 140


Phe Thr Asn Ile Ser His Pro Phe Gly Phe His Ser Lys Tyr Glu Asn
145                 150                 155                 160


Phe Val Asp Thr Val Lys Asp Asn Tyr Arg Val Thr Asp Gly Asn Gly
                165                 170                 175


Tyr Trp Asn Trp Lys Ser Ala Asn Pro Glu Glu Trp Val His Glu Ser
            180                 185                 190


Ala Ala Ala Ala Lys Ala Asp Phe Pro Ser Ile Val Asn Asp Asn Thr
        195                 200                 205
```

```
Lys Ser Trp Phe Leu Lys Ala Ala Val Ser Gln Asp Ser Ala Asp Lys
    210                 215                 220


Trp Arg Ala Glu Val Thr Pro Val Thr Gly Lys Arg Leu Ile Glu Ala
225                 230                 235                 240


Gln Arg Ile Thr Ala Gly Tyr Ile His Leu Trp Phe Asp Thr Tyr Val
                245                 250                 255


Asn Asn Lys




<210>  338
<211>  262
<212>  PRT
<213>  Bacillus manliponensis

<400>  338

His Gly Asn His Asp Ala Ser Asn Asp Ser Gly Ile Ser Ile Ser Pro
1               5                   10                  15


Arg Trp Ser Ala Glu Glu Met His Ala Glu Gly Lys Asn Ser His Leu
            20                  25                  30


Trp Ile Val Asn Arg Ala Ile Asp Ile Met Ala Arg Asp Thr Thr Val
        35                  40                  45


Val Lys Glu Asn Glu Val Ala Leu Leu Asn Glu Trp Arg Thr Asp Leu
    50                  55                  60


Glu Asp Gly Ile Tyr Thr Ala Asp Tyr Glu Asn Pro Tyr Tyr Asp Asn
65                  70                  75                  80


Ser Thr Phe Ala Ser His Phe Tyr Asp Pro Asp Thr Asp Asp Thr Tyr
                85                  90                  95


Ile Pro Phe Ala Lys Asn Ala Lys Val Thr Gly Ala Lys Tyr Phe Lys
            100                 105                 110


Leu Ala Gly Glu Ala Tyr Glu Gln Gln Asp Met Gln Gln Ala Phe Phe
```

```
        115                 120                 125


Tyr Leu Gly Leu Ser Leu His Tyr Phe Gly Asp Ile Asn Gln Pro Met
    130                 135                 140


His Ala Ser Asn Phe Thr Asn Ile Ser His Pro Phe Gly Phe His Ser
145                 150                 155                 160


Lys Tyr Glu Asn Phe Val Asp Thr Ile Lys Ala Pro Tyr Ala Val Thr
                165                 170                 175


Asp Ser Lys Gly Tyr Trp Asn Phe Ala Gly Gly Thr Pro Glu Glu Trp
            180                 185                 190


Leu His Thr Ala Ala Val Ala Ala Lys Lys Asp Ala Pro Gly Ile Val
        195                 200                 205


Asn Glu Thr Thr Lys Ser Trp Phe Leu Lys Ala Ser Val Ser Gln Glu
    210                 215                 220


Tyr Ala Asn Met Trp Arg Ala Glu Val Thr Pro Glu Thr Gly Ala Arg
225                 230                 235                 240


Leu Met Glu Ala Gln Arg Ala Met Ala Gly Tyr Ile His Leu Trp Phe
                245                 250                 255


Asp Thr Tyr Val Asn Arg
            260


<210>  339
<211>  274
<212>  PRT
<213>  Penicillium simplicissimum

<400>  339

Ala Pro Ala Arg Ser Val Pro Arg Asp Val Ser Ala Ser Val Leu Glu
1               5                   10                  15


Gln Phe Thr Leu Tyr Ala Gln Trp Ala Ala Ala Ala Tyr Cys Ser Asn
            20                  25                  30
```

```
Asn Leu Asp Ser Thr Gly Asp Ala Ile Thr Cys Ala Gly Gly Tyr Cys
        35                  40                  45


Pro Glu Val Glu Ser Ser Thr Thr Ile Ser Leu Ser Glu Phe Asn Asp
    50                  55                  60


Thr Asn Asp Phe Gly Asp Thr Ala Gly Phe Val Ala Val Asp Lys Thr
65                  70                  75                  80


Asn Lys Gln Ile Val Val Ala Phe Arg Gly Ser Lys Ser Ile Ser Asn
                85                  90                  95


Trp Ile Ala Asp Leu Asp Phe Gly Leu Thr Asp Ala Ser Asn Leu Cys
            100                 105                 110


Ser Gly Cys Glu Ala His Thr Gly Phe Leu Glu Ala Trp Glu Thr Val
        115                 120                 125


Ala Asp Ser Ile Thr Ser Gln Ile Gly Ala Ala Met Lys Thr Tyr Ser
    130                 135                 140


Gly Tyr Thr Leu Val Val Thr Gly His Ser Leu Gly Gly Ala Ile Ala
145                 150                 155                 160


Ala Ile Gly Ala Thr Val Leu Arg Asn Ala Gly Tyr Thr Leu Asp Leu
                165                 170                 175


Tyr Thr Phe Gly Gln Pro Arg Val Gly Asn Leu Ala Leu Ala Thr Phe
            180                 185                 190


Leu Thr Lys Gln Gly Asn Asn Arg Met Thr His Leu Asn Asp Ile Val
        195                 200                 205


Pro Arg Leu Pro Pro Thr Ser Phe Gly Phe Ser His Ser Ser Pro Glu
    210                 215                 220


Tyr Trp Ile Thr Ser Ala Asp Asp Val Thr Val Thr Thr Ser Asp Ile
225                 230                 235                 240
```

```
Glu Val Ile Glu Gly Ile Asp Ser Thr Ala Gly Asn Ala Gly Glu Leu
                245                 250                 255


Ile Glu Ser Val Ala Ala His Ala Trp Tyr Ile Ile Asp Ile Asp Gly
            260                 265                 270


Cys Glu




<210>  340
<211>  276
<212>  PRT
<213>  Penicillium arenicola

<400>  340

Ala Pro Phe Gln Leu Trp Ser Arg Ala Val Thr Pro Ser Val Leu Ser
1               5                   10                  15


Lys Leu Asp Leu Tyr Gly Gln Tyr Ala Ile Ala Ala Tyr Cys Asp Asp
            20                  25                  30


Asn Ile Ala Ser Ala Gly Thr Glu Val Thr Cys Ser Ala Gly Asn Cys
        35                  40                  45


Pro Leu Val Gln Ala Ala Thr Thr Asn Thr Leu Ser Glu Phe Asn Glu
    50                  55                  60


Ser Asn Glu Phe Gly Asp Val Ala Gly Phe Phe Ala Val Asp Thr Thr
65                  70                  75                  80


Asn Gln Ala Leu Val Leu Ser Phe Arg Gly Ser His Thr Ile Asp Asn
                85                  90                  95


Trp Ile Ala Asn Leu Asp Phe Gly Leu Thr Ser Val Ser Thr Leu Cys
            100                 105                 110


Ser Gly Cys Lys Ala His Thr Gly Phe Trp Lys Ala Trp Asn Thr Val
        115                 120                 125
```

```
Ala Ser Asp Ile Ala Ala Ala Val Asp Ala Ala Gln Asp Thr Tyr Pro
    130                 135                 140


Ser Tyr Pro Ile Ile Phe Thr Gly His Ser Tyr Gly Ala Ala Leu Ala
145                 150                 155                 160


Ala Leu Ala Ala Thr Thr Met Arg Asn Ala Gly Tyr Ser Ile Glu Leu
                165                 170                 175


Tyr Thr Tyr Gly Gln Pro Arg Ile Gly Asn Thr Ala Leu Ala Thr Tyr
            180                 185                 190


Ile Thr Asn Gln Asn Lys Gly Gly Asn Tyr Arg Val Thr His Thr Asn
        195                 200                 205


Asp Ile Val Pro Arg Leu Val Pro Arg Leu Leu Gly Tyr Ser His Phe
    210                 215                 220


Ser Pro Glu Tyr Trp Ile Thr Ser Gly Asn Asn Val Thr Val Thr Ala
225                 230                 235                 240


Ser Asp Ile Thr Leu Val Thr Gly Ile Asp Ser Asn Gly Gly Asn Ala
                245                 250                 255


Gly Glu Leu Leu Gln Ser Val Glu Pro His Tyr Trp Tyr Phe Val Glu
            260                 265                 270


Val Glu Asp Cys
        275


<210>  341
<211>  277
<212>  PRT
<213>  Aspergillus aculeatus

<400>  341

Ala Pro Ala Pro Ile Glu Arg Arg Ser Val Ser Thr Thr Leu Leu Asp
1               5                   10                  15
```

```
Gln Met Asp Leu Phe Ala Gln Tyr Ser Ala Ala Ala Tyr Cys Ser Thr
            20                  25                  30


Asn Ile Asp Ser Ala Ser Thr Ala Leu Ser Cys Ser Ala Asp Asn Cys
        35                  40                  45


Pro Leu Val Val Ala Ala Ala Pro Thr Val Leu Asp Glu Phe Asn Glu
    50                  55                  60


Thr Ala Glu Phe Gly Asp Thr Ala Gly Phe Val Ala Val Asp Ser Thr
65                  70                  75                  80


Asn Lys Ala Ile Val Val Ala Phe Arg Gly Ser Ser Asp Leu Ser Asn
                85                  90                  95


Trp Ile Ala Asn Ile Asp Phe Gly Leu Thr Asp Ala Ser Ser Ile Cys
            100                 105                 110


Thr Gly Cys Glu Ile His Ser Gly Phe Trp Lys Ala Trp Glu Thr Val
        115                 120                 125


Ala Ser Thr Ile Ala Ser Lys Val Glu Ala Ala Val Thr Thr Tyr Ser
    130                 135                 140


Asp Tyr Asp Val Val Phe Thr Gly His Ser Leu Gly Ala Ala Leu Ala
145                 150                 155                 160


Ala Ile Gly Ala Thr Val Leu Arg Asn Asp Gly Tyr Thr Val Asp Leu
                165                 170                 175


Tyr Asn Phe Gly Gln Pro Arg Ile Gly Asn Leu Ala Leu Ala Asp Tyr
            180                 185                 190


Ile Thr Asp Gln Asn Lys Gly Ser Asn Tyr Arg Val Thr His Thr Asp
        195                 200                 205


Asp Ile Val Pro Lys Val Pro Pro Glu Leu Leu Gly Tyr His His Phe
    210                 215                 220
```

```
Ser Pro Glu Tyr Trp Ile Thr Ser Asp Asn Asp Val Thr Val Thr Thr
225                 230                 235                 240


Ser Asp Ile Thr Glu Val Thr Gly Val Asp Ser Thr Ala Gly Asn Asp
                245                 250                 255


Gly Thr Leu Leu Asp Ser Val Ser Ala His Lys Phe Tyr Phe Glu Tyr
            260                 265                 270


Ile Ser Ala Cys Asp
        275


<210>  342
<211>  349
<212>  PRT
<213>  Bacillus acidiceler

<400>  342

Ile Thr Ser Phe Phe Gly Asn Tyr Gln Lys Ala Phe Ala Trp Ser Asp
1               5                   10                  15


Glu Asp Val His Asn Gln Asp His Ser Thr His His Phe Ile Val Asn
            20                  25                  30


Gly Ser Val Lys Leu Ile Ala Asp Asn Thr Asn Pro Ala Ile Asn Lys
        35                  40                  45


Pro Thr Thr Leu Leu Asn Gln Phe Arg Asp Arg Trp Glu Gln Gly Leu
    50                  55                  60


Tyr Asp Ala Asp His Ile Asn Pro Phe Tyr Asp Thr Gly Thr Phe Met
65                  70                  75                  80


Ser His Phe Tyr Asp Pro Asp Thr Gln Thr Asn Tyr Thr Gly Ala Ser
                85                  90                  95


Tyr Pro Thr Ala Arg Gln Ser Gly Ala Lys Tyr Phe Asn Leu Ala Ser
            100                 105                 110


Asp Tyr Tyr Lys Lys Gly Asp Phe Asn Asn Ala Phe Tyr Tyr Leu Gly
```

```
        115                 120                 125


Val Ser Leu His Tyr Phe Thr Asp Val Thr Gln Pro Leu His Ala Ser
    130                 135                 140


Asn Ile Ser Asn Leu Asp His His Ala Pro Gly Tyr His Ser Lys Tyr
145                 150                 155                 160


Glu Thr Tyr Ala Glu Ser Ile Gln Asn Glu Met Thr Met Pro Asp Ser
                165                 170                 175


Gly Leu Tyr Asn Trp Ile Ala Ser Thr Asp Pro Glu Ala Trp Ile His
            180                 185                 190


Gln Ala Ala Val Gln Ala Lys Ser Val Leu Pro Gln Val Trp Asn Asp
        195                 200                 205


Thr Ile Ile Asn Tyr Phe Trp Gln Ala Ala Tyr Ser Asn Tyr Tyr Ser
    210                 215                 220


Ala Met Trp Lys Ser Glu Val Lys Asn Pro Thr Leu Asp Gln Leu Asn
225                 230                 235                 240


Gln Ala Glu Arg Glu Thr Ala Gly Phe Ile Asp Met Phe Phe Arg Val
                245                 250                 255


Asn Gly Val Glu Met Pro Val Thr Val Tyr Lys Glu Asn Ala Phe Ser
            260                 265                 270


Gly Ala Ser Glu Leu Leu Gly Ser Gly Asn Tyr Asp Tyr Asp Gln Leu
        275                 280                 285


Val Lys Gly Ile Gly Asn Asp Thr Ile Ser Ser Ile His Ile Ala Pro
    290                 295                 300


Gly Tyr Gln Val Thr Leu Phe Ser Asp Ala Asn Tyr Lys Gly Ala Ser
305                 310                 315                 320


Thr Val Leu Thr Asn Asp Val His Asp Leu Gly Asn Phe Ser His Gln
```

```
                325                 330                 335

Val Ser Ser Ile Lys Val Ala Lys Ile Ser Ala Leu Lys
            340                 345
```

<210> 343
<211> 1815
<212> DNA
<213> Aspergillus wentii

<400> 343

```
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctaac        60

tgggcagaaa gtatctggga cgatgtaaaa catgccgtga attgcgctgg ttgtgaaaca       120

gttttgtttg ctctaaaagg tgtggcagat ctgggtgagc atgcatttca aacggtctta       180

accgatgtgt gtgacattag cgggacggaa gacaaagacg tttgttctgg tttgatcgca       240

gctgaatcac ctgctttgta ctacaacatc aagaatttgg gtgtcaaatc tcatacatct       300

aaagttttgt gtgcccaact gtttggttta tgccaatttc cagcagttag gccttacaac       360

ttgacctttc cttcccctaa accaactact tctaggcctc ctccctctgg gcaatcaccc       420

atcagagttg ctcacatctc cgatactcac gttgatttgt catatgagac tggtagcaac       480

tatgaatgta gtaaacctat ctgttgtaga gtgtacacag acgaggatgc tccaggaaat       540

acgtcatttc cctgtgggcc atacggaaac acaaactgtg acccaccttt gaggctggag       600

gaaagtatga tggcagctat caaatcccta aatcccgctt tttcaatcta cactggggat       660

gtcgtcgctc atgacttgtg gatggtcgac aaaactgaag tattggatga cttcaatgcc       720

acttattcaa tgttggatca attggatcta gtttatgctg ctgtggggaa ccatgacact       780

acccctgtta atctatttcc atctacacaa ttgccagata aggataatca atgggcatat       840

gatgctttaa ctgcagaatg gaaatccctt accaattctt caatccaaac tacggagtat       900

ggctcatata gcgccatata cgaaaacctg aggatcataa gctacaacag catcttctac       960

tatcaagaca acttctacgc atacacagac ccgatggcac atgatccttc aaatcagtta      1020

acatggttga tagatcaact gcacgaagct gaatctgcaa atcaaagggt ttggttgata      1080

agtcacattc caactggcgg tgtggatcat ttgcacgatt acagtcatta catagatgaa      1140

atagtccaac gttacgaagc aactatctcc gctttgttct ttggtcacac acatacagac      1200
```

ttgtttcaaa tcgcttacag cgactacaaa aacagagctt gggacacagc ctccgccatt 1260

ggttacgtag ctcccagttt aactccaact tctggcccac cagcttttag gatctacgat 1320

attgatcctg ttacctttgc cgtccttgac tatacggtct atatcgcaaa catatcaaac 1380

ccctcatacc aaagcaatcc gaaatgggag aagtactatt cagccaagga ggcctatggt 1440

agtttgttga gtcctccagt caccgattca tcttctgagt tgacgccttc tttctggcat 1500

aatgtgacag cattgatgga aaaggacgac tcagttttcc aagactggtg gtcccgtacg 1560

accagaggtt acaatgtcac aacatgcact ggggattgcg ccaaaaagga gatatgtgct 1620

ttgagaggtg cagatgctca gtacaattgt gtgacggcta cacctgggtt tcattttgac 1680

aaaagagagg agtccgaaca aaaacccaga cctgaatgcg aggatggctt gggcagagtg 1740

ttaggtgata tgatccacaa gaaagatttt gtggatttgt tgcatgaaag aaccgcacaa 1800

taccaacata gataa 1815

<210> 344
<211> 1824
<212> DNA
<213> Penicillium cylindrosporum

<400> 344
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctaca 60

tacgataaga gagatcttgc ccaagacttg tggaatgaca tcaagaatgc tgttgattgt 120

ggtggctgcc aagtgattct tactgcattg aaagggttat cagacttggg gacaacagtt 180

ttcgtggacg ttttgacaga ggtttgtgaa attggtaagt tagaagattc agatgtttgc 240

tctggtacta tttctagaga aggtccagtt ttggattaca ttttgcaaca tctagacata 300

gggtctcata caagtcaagt attgtgtgct agtgcatttg ggttgtgcca ataccctgca 360

gtaagaccct acaatctacc tttcccctcc ccgaaaccaa acaccactag accagctccg 420

tccggtgaac tgccaattca agtagttcac atttcagaca ctcatgtaga tctttcatac 480

gagactggat ccagctacaa ttgcacgaaa ccaatttgtt gtcgtcctta taccgctgcc 540

gatgcacctg gaaataccac aaccccatgt ggtccttacg gcaataccaa ctgtgatgct 600

cccattggac tagaagagtc aatgtttgct gccattaagg ctctacagcc tgctttctcc 660

```
atctataccg gtgatgttgt cgcacatgac ttatggttag tggatcaaaa tgaagtttta      720

caagacttta acgctacctt caatcgtatg gccgaacttg gtgtcgtcta tgctgcaatt      780

ggtaatcatg acactgctcc agtgaatgat ttacctgcat ccaacattcc ttcacagtat      840

agcgcaaact ggacctatga tgcacttgct tatgacttct ctaccttaac aaactctgca      900

agtgctcaga cggcagaaga ttacgggagc tacagcagtg tctatagagg aagtcacggc      960

acagacttac gtgtgatatc ctataactcc atcttttact atgtagacaa cttttgggta     1020

taccaggatc caatgttgta cgatccagac ggtcaattag catggttgat ttctgaacta     1080

caagaggcag aaactggggg tcagcgtgtt tggttgattg ctcatgtccc aagcggcatt     1140

tccgatcact ttcatgacta ttctcattac ttcgatcaaa tagtacaaag atacgaagcc     1200

acgattgcag ctctgttcta tggtcacaca cacagagacc aatttcagat ttcatacagt     1260

gactatacaa atagaacctg gaatactgct acagccatgg gctacataac accatccttg     1320

acgcccacct ctggtccgcc tacatacagg gtgtacaaag tcgacccaaa gacattcggt     1380

gtgttggatt tcaccaacta catagccaac atcagtgatc cagcctatca aagtggacca     1440

acctggcaga agtactatag tgccaaggaa acttacggat ctttactgtc ccctcctgta     1500

acagatccga cggcagaatt gacacctgct tttggcaca acgtcactgt tctatttgag      1560

aatgataacg ccacgtttca gcagtacata gccaggcaaa caagaggttg ggatccttct     1620

tcttgtacag gaagttgcat tgatcaaacg atttgtggtt tgagagctgg cgacgcacag     1680

tacaattgcg ttacccctac tcccggtttc aatttcgcta agagagatgc ttctactggc     1740

ggtcaaccag aaacgcatgt tgaaaagtgt gaaggctccg gtctgttggc tttgttggga     1800

agaatggtcg caactaaatc ataa                                            1824
```

```
<210>  345
<211>  1824
<212>  DNA
<213>  Penicillium meridianum

<400>  345
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttca       60

gccgatagtt ggattaccat catatgggat gacttcaaag aagctgttga ttgtgcatca      120

tgtcaggcac tactgggtgg cttgaagtat gttgccggtt ttggagaaag ctttatggaa      180
```

gacgtgttga caggggtatg cgacatttct ggtgctgagg attcagatgt atgttctggc 240

atcattgcaa atgaaggtcc agctgtctac tattctttga agaacttaga actagggagt 300

cacactgcta aaaccttttg ttccaatttg gtcggattat gcgattaccc agcagtaaga 360

ccatatgatt tgtctttccc tagtcccaag ccgtcaattt cccgtcctcc accaagcggg 420

aagcctccac tgaaagttgt tcacttttcc gatactcacg ttgacttatc atacgaacct 480

ggctctagtt ttgactgtac aaagccgatt tgttgtagag tttactcaga agacgatgcc 540

ccaggcaata cctcatcccc atgcggtcct tggggaaacg ccaaatgcga tccacctcat 600

cagttgcaac aatctatgat ggatgcaatc gcctctctga atccagcctt ttctatctat 660

actggtgacg ttgttgctca cgatgtttgg ttagtcaata agactgaagt attgcaagat 720

ttcaatgcaa cctattctac tatggagagc acgttaggct tggtctacgc tgctctaggt 780

aatcatgata ccgctccatt gaacttgttt ccttcaacca acattccaag ttcatacaat 840

ccgcaatggg cctacgatgc tttatccaca tcttggttga ctcttacatc agacaatcct 900

gccatttcca cggcaaaaga atacgggagc tacagcgcca gacataaaga caccaagcta 960

agaatcattt cctacaattc cattttctac tacaaataca actttttcag ctatgaagaa 1020

ccgatgccat ttgacccaga cggtcaactt tcatggttga tatccgagtt gtctgctgca 1080

gaagccgcat ctgaacgtgt ttggttgatt tcccatattc caagtggaaa tagcgaccat 1140

ttcagagacc attcacacta ctttgatcaa atagttcaaa ggtatgaagc taccattgct 1200

gggttgttct ttgggcatac tcataccgat gagtttcagg tttcttactc agattacgcc 1260

catagatctt gggataccgc tactgctatg ggatacgtag caccatcaat gactcctact 1320

tctggtcccc catcattcag agtatacgaa atcgatccag tcacctttgg ggtcctggat 1380

ttcactcaat acattgcaga catatccgac tcctccgaac caaagtggat gccctactat 1440

tccgccaaga aagattatgg cagccgtcta gatgtgcctg ttggagagga tatggagtta 1500

acacctgcct tctggcataa cgtaaccgtt ggtatggaga aggacccatc tttgtttagg 1560

gacttttggg ctcgtagaac gagaggtttc gaggtaccag gttgtgaagg tgattgtgtt 1620

tctaaagaga tatgcgcctt gagaggagcc gatgcacagt attcatgtgt ggaggcaaca 1680

ccaggtttct ctttcgaaaa gaggggtgag agaaccgttc tgttagagaa aagattccag 1740 ccagaatgta atcacgctgg tatggcacca ttgcttgcca aaatcgctca tagagcttca 1800

ttggctaggg aaatggaagc ataa 1824

<210> 346
<211> 1830
<212> DNA
<213> Penicillium bialowiezense

<400> 346
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgaa 60

gttcttcttg aaaactctat tgcttcctta tgggatgact ttaagaatgc tgtggactgt 120

gcctcttgcc aagcattgtt aggtggctta aagttggtgt caggatttgg ggaggacttt 180

atgattgacg ttttgactgg tatttgcgac atttccaaag cagaagactc agatgtttgt 240

gaaggcatca tcaagaaaga aggtcctgct ttgcatgatg cattccaagc cttgcatatt 300

ggctcaaatt ctacacaaac catgtgtgcc tctttgattg gattatgtca atatccagaa 360

gttagggcac acagtctaag ctttccaagt cccaaaccca ataaggtgaa gcctccaccg 420

tctggtaaac ctcccatcaa agttgtgcac ttttccgata cgcatgtcga cttgtactat 480

gagacaggta gcagctatga atgttccaaa ccgatttgtt gcagagtgtt tgaggataag 540

tatgcaccag gcattacaaa aacaccgtgc ggtcccttcg gtaatccaag gtgtgaccct 600

ccattgaagt tacaagagag tatgaacgct gcaatcgcag atatcaatcc agaattctcc 660

atctataccg gagatgttgt agctcatgac gtttggttag ttaatcaagc agaagcacta 720

gaatccttca atagcacgta ctcccagatg gagaagtctt tgggaatggt ttatgcagca 780

attggtaatc acgatactgc acccttgaat ttgtttcctt catccatagt gccagatggc 840

gacaatcaat gggcctacaa tgccctggct gagtattggt tgactttgac ctctatcagc 900

tccgtacaat ctgccgacga gtacggctca tattcagcaa tccacccaga tagtaatctt 960

aggatcattt cttacaactc cattttctat tacaagttca acttctatat gtaccaagaa 1020

cctatggaga aagatcccaa tggtcaattt gagtggttga tcaaagagtt gcaggcagct 1080

gaagacgctg ggcagagagc ctggttgatt tcccacattc cgcctggtgt cgcagaccat 1140

tttcatgact attctcacta ctttgatcaa attgttcaaa ggtatgaggc cacaatagct 1200 gggttgttct atggccatac gcatatggat gaattccaaa ttgcctactc caactacaag 1260

aataggaatc atgaaactgc aaccgcaatg ggctacatag ctcctgctat gacccccact 1320

gaagggcctc ctagtttccg tgtatatgaa atcgatccgg aaacgtttgg ggttttagac 1380

tatacacagt atatcgcaaa catctcagat cccacttatc aggaaaaacc ccagtggtta 1440

ccctattaca gcgccaaggc agactacggt tccaagttat cacctcctgt aacagacccg 1500

aagattgagt taaccccagc tttttggcac aacgttactg tcgcaatgga aaatgagccg 1560

agcattttcc aagaattctg ggcaagaaga gttagaggct ataaggttac agattgtaat 1620

ggcgactgta tgaaaacgga gatatgtgct ttaagagccg cagatgcaca gtttaactgt 1680

gtcaagccca agccaggctt taactttagc aaaagagatg gtaaggacac tttggctgaa 1740

cagccacatc attgtgatca tgccggatta gctcccttat tgggcaagat tgcttacagg 1800

gctagaatag caagagagat ggaagcttaa 1830

<210> 347
<211> 1830
<212> DNA
<213> Penicillium sclerotiorum

<400> 347
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttct 60

gcagactcct ggatctcttc tatttgggat gacttcaaag aagcagtaga ttgcggcagt 120

tgccaagcct tgttaggtgg tctgaaagta gtcgctgcct ttggagaaag cttcatggaa 180

gacgtattga ttggtgtttg tgatatctca ggtgcagaag attcagacgt ttgtgctggt 240

gttattgcaa atgaaggtcc agctgtccac tattcattga caaacctaga gattggttca 300

cacacagcaa aaacattttg cgcaacactg gttggcttgt gcaagtatcc agaagttaga 360

ccatacaatt tgaccttccc gtcaccaaaa cccccaactt ctcgtccgcc tccatctggg 420

aaaactccca tcaaagtcgt tcatttctca gatacacatg tggatctatc ctatgaaaca 480

ggctccaatt acgactgttc taaacctatt tgctgtagag cctatacgga agacgatgca 540

cctggcaata cctcttcacc atgtggtccc tggggcaaca caaattgtga cccacctcac 600

agacttcaga aatcaatgaa cgctgccatt gcagacttga aaccggcttt ttccatctat 660

actggtgacg tagttgctca tgatgtatgg ttggtcaaca aatctgaagc attgcaagac 720 ttcaatgcta cttatggtgc catggaggat tccctaggta gagtctatgc tgctttagga 780

aatcatgatg ccgctccctt gaacttgttt ccatcaaatc aaatacctag cgaatacaac 840

ccccaatggg catacgatgc tcttgccgca gactggatgg ccttgacaga cattcccagc 900

gtagaaacag ccaacgagca cgggtcctat tcagctatac acccagacag taacttacgt 960

atcatatcct ataactccat cttttactac aaatacaact tcttttcata cacggaacca 1020

atggaatacg atccaaacgg tcaattagaa tggttgatca atgaactaca tgccgcagaa 1080

actgccaatc agcgtgtttg gttgatttct catataccaa gcggcaatag tgatcacttt 1140

catgatcatt ctcattactt cgatgagatc attcaaagat acgaagccac gattgcaggt 1200

ctgttctttg gtcacacaca cacagacgaa tttcagattt catactccaa ctattcaaat 1260

agaaactggg atactgctac agccatggga tatgtagcac caagtatgac gcccacctct 1320

ggtccgcctt cattcagggt gtacgaaata gacccagtga cattcggtgt gttggatttc 1380

atgcagtaca tagccaacat ctccgatcca tcctatcaac agaagccaga gtgggttccc 1440

tactattccg ccaagagtga ttacggatct aggctgagtc ctcctgtaac agatgccgac 1500

gtagaattga cacctgcttt ttggcacaac gtcactgttt tgatggagga agattccagc 1560

gtgtttgacg agttttgggc caggagaaca agaggttttc aagtaccagc ttgtacagga 1620

gactgcgttt caaatgagat ttgtgctttg agaggtgccg acggacagta caattgcttc 1680

atagaaaaac ccggtttctc tttcgaaaag agagatggta ctgtcgacga agtttcttgg 1740

aagaaaagat ttcaaccaga atgcaaccat gccggtatgg ctcccttatt ggctaagata 1800

gctcatagag catcactggc aagagaataa 1830

<210> 348
<211> 1836
<212> DNA
<213> Rasamsonia byssochlamydoides

<400> 348
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttcc 60

tacaacaaaa gaggattagc tcaagagatt tgggatgata tcgtcaacgc cgttgactgt 120

tcaggttgtc aggtcatttt gactgcctta caaggtgctg ccgagttagg gacaagcgct 180 tttgttgata ttcttacaga agtatgtgac attagtggta aagaagattc agatgtttgt 240

tcaggcatca tttccagaga aggtccagtc ctggattaca ttttgcaaaa cttagatatt 300

ggatctcaca catccgacgt catatgtgca tccgcatttg gtttatgtca ataccctgca 360

gtcaggagct acaatttgac ctttccaact ccgaagccag atactacgag accagctcct 420

tctggcgaat ctccgattca agtagtacac ttttccgaca ctcatgtaga cctatcatac 480

gagactggtt catcctataa ctgtacaaag ccaatctgtt gcagacctta taccgctgcc 540

gatgcaccag gaaacaccac taccccttgt ggaccatacg gtaacaccaa ttgcgatgct 600

cctctgagtt tggaggaaag tatgttcaat gccatcaaag ctctatctcc acaacctgca 660

ttttccatct atacaggcga tgttgtagct catgacatat ggttagtcga tcaaaatgaa 720

gtgatccagg atttgaatac tacctatgat ttgatggctg aattaggatt ggtttatgcc 780

gctattggaa atcatgatac tgctcctgtt aatgatctgc caacaaccaa cattccatca 840

gagtattcta cgaactggac ctatgaagcc ttggcatacg atttcacgat gttaacaagc 900

agcagctctg cccagacagc tgcaaactac ggatcctaca gttcaatcta caaaggttct 960

tacggcacag atcttaggat cataagctac aattcaatct tctactacat agataacttt 1020

tgggcctatc aagatcctat gccctatgat ccagacggtc agttagcttg gttgattaac 1080

gagttgcagg aagctgaaac agcaggtcag agggtatgga ttatcgcaca tgtccctact 1140

ggtacctccg atcatttcca tgactatagt cattacttcg atcaaattgt gcaaagatat 1200

gaggctacga tagccgcttt gttctatggt cacacccata ttgatcaatt tcagatttct 1260

tattcagatt actccaatca agcatgggat accgctacgg ccatcggcta tatcatgcct 1320

agtttgacgc ctacttctgg cccaccgaca ttcagagtgt atgatgtgga tccaaaaaca 1380

ttcgcagtgc ttgactttac caactatatc gccaatatca gtgatcctgc ttatcagtct 1440

gggcctactt ggcagaaata ctactccgca aaggaaacat atggtgcctt attgagccct 1500

cctttgacag atcccactgc cgaattgaca cctgcctttt ggcacaacgt gactgtggct 1560

tttgaaaacg ataatgctgc ttttcaagaa tactgggcta gacaaacacg tgggtgggat 1620

gtaagctcat gtactggttc atgtatcacc caagcaattt gtggcttgag ggcagccgac 1680

gctcagtata actgtgtgac accaactcca ggcttcaact ttgctaaacg tgatgcttct 1740 tccgctactc aggcaatggc ccatgttgag aaatgtgaag gttccggatt gttggccttg 1800

ttagggagga tggttgcaga caagaaatcc gcttaa 1836

<210> 349
<211> 1839
<212> DNA
<213> Rasamsonia eburnea

<400> 349
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctact 60

tatgacaaaa gaggtttggc tcaagacatt tggaacgaca taaagaatgc cgttgattgt 120

gctgggtgtc aaggcatttt gacagcattg aaggggctgt catacttagg gactactgct 180

tttgttgacg tcttaacaga agtatgtgac atttcaggtg tagaagattc agatgtttgt 240

tctggcatca tttcttcaga aggaccggca ctggtctaca ttcttaaaca tttggatatt 300

ggcagtcata cgtctcaggt catatgtgca tcagtttttg gtttgtgcca atatcccgca 360

gtgagagctt acaacttgac ttttccgagc cctaaaccag acaaaacttg tcctgaacct 420

tctggtgagt ctccagtaca aatcgtacac ttctcagata cacacgcaga tcttagctat 480

gaaacaggat caaactacaa ttgcacaaag ccaatatgtt gcagatccta taccgctgaa 540

gatgcaccag gcaataccac aactccttgt ggcccatacg gaaatcccaa atgtgatgct 600

cccatgagct tagaggagtc aatgttcgct gccattaagg ctttgtctcc tcaaccagct 660

ttttccatat acactggtga tgttgttgct catgacatat ggttagttga tcaaaacgag 720

gtggtagagg atcttaacgc tacttacgat agaatggcag gattgggttt ggtgtatgct 780

gcaataggta atcatgatac agctcctgta aacaatctac ccacctccaa catacccctca 840

caatacagcg caaactggac ttacgaagca cttgaatacc acttctcctt attgacgaag 900

agcgcctccg cacaaacagc agagaactac ggatcctatt ccagcgtcta tagaggaagg 960

tatggtaccg acttaagggt gatatcctat aacagcatct tttactatat cgcagatttc 1020

tgggcttatc aagaccccat gttgtatgac ccagacggtc aattggcctg gttgatcaat 1080

gagttacaag aagcagaaac agctggccaa agggtttggt tgattgcaca tgttccaagt 1140

ggaactgcag accattttca tgactattcc cactactttg atcagatagt tcaaaggtat 1200

gaggcaacca ttgctgcctt gttttacggc catactcata ttgatcagtt tcagatttca 1260

```
tactccgact attcaaatag ggctttcgat acggctaccg ctattgggta cataatgcct     1320

agcatgactc ctacctcagg gcctccgact ttcagagtat acgatgtaga tcctaagacc     1380

ttcgccgttt tagactttac aaactacatt gccaacattt cagatccagc ctaccagagt     1440

ggtccgacat ggcaaaagta ctatagtgca aaagaagcct acggttctct gttaagtcca     1500

ccagtaacgg acgccactgc tgagttaacc ccagcattct ggcacaatgt gactgttgca     1560

ttcgaaaatg atgatactgc ttttcaagag tattgggcta gacagacgag aggttatgcc     1620

gtttcatctt gtacaggtga ctgcataaca caagctatct gtggactaag agccggtgag     1680

tctcagcata actgtgttac tccaactcca ggcttcaact ttgccaaaag agatgtctct     1740

acagacggac aagccttgcc acatattgag aaatgtgaag gatctggctt aatggcactg     1800

ctagccaaaa tggtcgcctc aaacagacaa agttcataa                            1839


<210>  350
<211>  1839
<212>  DNA
<213>  Penicillium brefeldianum

<400>  350
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctggt       60

gctattgaga attgggctgc tactatatgg gaagacttca aggaggctgt ggattgtggt      120

tcttgccaag tactattagg tggcttgaaa ctggtggccg atttcggtga gggctttttg      180

ggtgatgtct taacaggagt atgtgatatc tctaaagctg aagatagaga tgtttgtgct      240

ggtgttgtcg cttctgaagt tcctgcccta cactatgcct taaagaatat gaaagtaggt      300

agtcatacag ccaaaacctt gtgctccgca ttagttggtt tgtgtgactt tccagacgtc      360

cgtccatttg accttacttt tccaagcccg aagccagcta cgtctcgtcc acctccaagt      420

ggtaaacctc ccatcaaagt agtgcatttc agtgatacac atgtggactt aagctacgaa      480

actggttcca attacgattg tagtaaaccg atttgctgta gggtatacac agacaaagat      540

gctcctggga ccacagacaa gccatgtggt ccctggggac acccaaagtg tgatcctccg      600

caccaactgc aagagagtat gatgacggct attgcaaact tgaatccagc attttccatc      660

tatactggag acgttgttgc acatgatgtt tggttggtaa acaaagatga agttctgcag      720
```

gacttaaacg ctacctacgg tgctatggaa aatcatttag gattggttta tgccgctttg 780

ggaaatcatg atgctgctcc cttgaactta ttcccatcca acaaggtacc atcaaagtac 840

aatccccagt gggcctatga tgccttgaca gccgattgga tgacattaac agggctggac 900

agcgtgcaga atgccaataa gtacggatcc tacagtgctg tgcacccaaa ttctaagcta 960

aggattatct catacaacag catcttctat tacaagtaca atttctttag ttatactgag 1020

ccaatggaat acgaccccaa tggtcaattg acttggatca tcaatgagtt gcaagccgct 1080

gagacagctg gtcaaagggt ttggttgatt tcccatatcc cttcaggaga tgttgatcac 1140

ttcagagatc actcacacta tttcgatcag atcgtacaaa gatacgaagc tactatagct 1200

gggttattct ttggtcacac acataccgac gaatttcaaa ttgcttactc agactacaat 1260

aacaggaatt gggatacagc aactgcaatg gggtacgtcg ctccaagcat gacacccaca 1320

agcggtccac ctagttttcg tgtctacgat atcgatcctg agacttttgg tgtaatggac 1380

tacacccagt atatcgccaa tatctccgat cccagttttc aaactaaaca ggagtgggtc 1440

ccatactaca ctgcaaagaa ggattacgga gctaagctga gccctccacc ggcacctact 1500

ggtgaactta ctcccgcttt ttggcataac gttacagtgg ccatggaaaa ggattcttcc 1560

gtgttcgaag ctttttgggc tagaaggact agaggttttt ccattccggc ttgtacaggg 1620

gattgtgtca agaatgaaat ctgcgcacta agaggtgccg atgcacaata cagttgtgtc 1680

aaaaggactc cgggattttc ttttagtaag agagatgaaa ttgagtcaga tccactattg 1740

tctaagaggt ttcagccaga atgtaatcat gctggtatgg caccattgtt agccaaaatc 1800

gcacataaag caaacgtcgc taagtggaat ggagaataa 1839

<210> 351
<211> 1839
<212> DNA
<213> Penicillium adametzii

<400> 351
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttct 60

gttgattcct ggattactac aatttgggat gatttcaagg aagccgttga ctgtgcatct 120

tgtcaggctt tactaggtgg gttaaagttg gtggccgtgt ttggggaaag ctttatggaa 180

gatgttatca caggtgtatg ttccattagt ggtgctgaag attcagatgt ttgtgctggt 240 gttattgcaa atgaaggtcc agcagtgtac cactctttgt caaacttgaa gattggatct 300

cacacagcaa agactttctg tgcatcctta gtaggtttat gtgattaccc tgcagtcagg 360

ccgtattcat tgacctttcc atctccgaag cctccaacta cgcgtcctcc accttctggc 420

aaatctccga tcaaagtagt acacttttcc gacactcatg tagacctatc atacgagact 480

ggttccaact atgactgttc aaagccaatc tgttgcagag catataccga aaacgatgca 540

ccaggaaaca cctctagtcc ttgtggacca tggggtaact ccaaatgcga tccacctcac 600

aggttgcagg aaagtatgaa tgaagccatt gcagatctaa atccagcttt ctccatctat 660

acaggtgatg tggttgctca tgatgtttgg ctagttgata agtcagaagc tttgcaggac 720

ttcaatgcca ctttcagtgc tatggaaaca ttgggtagag tctatgctgc tctgggtaat 780

catgatgcag ctccattgaa cttgtttcct agcaatcaaa tcccctcaca gtataaccca 840

caatgggcct atgacacatt agcctcagat tggatgggct tgacaggaat acagagcgtg 900

gagacggcca atgaatatgg aagttactcc gcaatccatc ccaactccaa tttgaggatc 960

atttcttaca attccatatt ctactacaaa tacaacttct tttcctatac cgaaccaatg 1020

gaatatgatc caaacagtca attgcaatgg ttgatcaatg aattgcacga agccgagttg 1080

gccaatcaaa gagtctggtt aatcagtcat ataccaagcg gagatccaga tcattttcac 1140

gatcattccc actactttga tcagattgtg cagagatatg atgccacaat tgctgcctta 1200

ttctttggcc atactcacac agatcagttc cagatttctt attctagtta tcagaataga 1260

acatgggata aagctacagc aatgggatat gttgctccct ctatgacgcc tacaagtgga 1320

ccgccttctt tcagggttta cgaaatcgat ccggttacat tcggtgtatt ggatttcacc 1380

cagtacattg caaacatttc agaccctact cagaccaaac ctaaatgggt gccgtactac 1440

tctgccaaga aagattacgg atcacactta gatcctccgg tgacagatgc ccatgcagag 1500

ttaacaccag ccttctggca taacgtaacc gtttccatgg agaacgataa ctctgttttc 1560

caggactttt gggctagaag aacaaggggt tttcaagttc cagactgcac tggtgattgc 1620

tcatcatctg agatttgtgc cctaagagga gcagatgccc aatacaactg cttcgttgag 1680

aaacctggtt tctcttttga gaaaagggac gttcaagaat cagacgaaga aatgtggaag 1740

aaacgtttcc aaccggaatg taatcatgca ggtatggcac ctttgttggc caagatagcc 1800 tacagagctt ctctagagag agaacaaaaa ggaaaataa 1839

<210> 352
<211> 1842
<212> DNA
<213> Rasamsonia brevistipitata

<400> 352
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctact 60

agtttaacac atgacaaaag ggatttggcc caggaaatct ggaacgacat caagaatgcc 120

gctacatgcg ctgggtgtca agttatcttg acggctctga aaggggtttc agatttgggt 180

acctccattt tcgtagatgt tcttactgaa gtttgtgaca tttctggttt agaagatcca 240

gatgtttgtt caggcataat cagtcgtgaa ggtcctgtct tagactacat attgcagcat 300

ttagacattg gctctcatac atcagatgtc ttatgtgcta gtgcattcgg cctatgccaa 360

tatccagccg ttagaccata caacttaact tttccgtctc caaaaccaga taccactaga 420

ccggctccaa gtggtgagtc acctatccaa gtagtacaca tatcagacac gcatgttgac 480

ttatcttacg aaacaggctc aagctggaac tgtaccaaac ctatttgctg tagaccatac 540

actgccgaag acgcaccagg aaataccact accccttgtg gcccatatgg tgacacccat 600

tgcgatgcac ccatgtctct gcaagaatct atgattgctg ctatacaagc tttgagacca 660

caacccgctt tttccatcta tactggagat gtagtcgctc atgacatttg gctggtggat 720

cagaatgagg tcattgaaga cttcaatgct acatacaata gaatggccga attgggatta 780

gtatatgctg ctataggtaa tcatgactct gcacccgtca atgatttacc cgcttcaaac 840

atcccatccc agtatagcgt taactggact tacgaggcat tagcatacga cttcagcatg 900

cttacaggtt cagcatccgc acaggaagcc gaaaactacg gatcatatag ttccatctat 960

aagggtagta acgggacaga tttacgtgtg atttcttaca attccatctt ttactatgtt 1020

accaatttct gggcttttca agacccaatg ccttatgatc cggatgggca gttggcctgg 1080

ttgattaacg aattacagga ggcagaaact gccggacaaa gggcatggtt gatagcacat 1140

gtccctacag gtacaggcga tcacttccat gactatagcc actactttga ccaaatcgta 1200

cagagatatg aggcaacaat tgccgcattg ttctttggtc acactcatca agatgaattc 1260 caaatagctt attccaatta ctcaaaccag aactttgata cggcaacagc catagggtac 1320

attatgccct cattgacacc gactagcggt cctccctctt ttagagtata cgacatcgac 1380

ccaaaaacct ttggtgtgct agatttcacc aactacattg caaacatcag cgatccagcc 1440

taccaaagtg ggcctacatg gcagaaatac tacagcgcaa aagaggcata cggtacttta 1500

ctttctcccg ctgttacaga tcccacagca gagttgacgc cagccttttg gcacaactta 1560

actgttgttt ttgaaaatga taatgctaca tttcaagagt actggacaag aaagactaga 1620

ggtcatgcag tttccaactg tacaggttct tgcattaccc aatccatctg tggcatgagg 1680

gctgccgatg ctcagtataa ctgcgttact ccaactccgg gtttgtcttt cgctaaacgt 1740

gatgcagaga cttcaactcc agaaccacat atagaaccat gtgaaggatc agggttgatg 1800

tctttgctag gcagaatggt tgctcaaggt aaatcttcat aa 1842

<210> 353
<211> 1842
<212> DNA
<213> Penicillium scabrosum

<400> 353
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgaa 60

acaacattag agaaatctat atcatctatc tgggaagact ttaagaatgc agttgattgc 120

ggttcatgcc aagtgttgtt aggtgggctg aagtttgtgt cagggtttgg tgagaacttt 180

atgattgatg tcttaacagg tctttgtgac atttcaaaag ctgaagattc agatgtttgt 240

gaaggcatca tcaaaaagga gggaccggct ttgcatgacg catttcaagc attgaagata 300

ggaagccatt ccactaagac aatgtgtgcc aatttgattg gcttatgcca gtacccggaa 360

gttaggccca atactttgag cttcccttca ccaaagccaa aagatgtaag acctactact 420

agcggtaaac ctcctatcaa agtcgtgcat ttcagtgaca cacatgtgga cttgttgtat 480

gaaactgggt ccaattacga atgcactaag cctatatgtt gcagagtgtt tgaagataag 540

gatgccccag gcataaccaa gaatccctgt ggaccttttg gcaatccaaa atgcgaccca 600

ccgcaagcac ttcaagaaag catgaatgct gcaattgctg agatcaatcc agctttttcc 660

atatacactg gtgatgttgt ttcacatgat gtatggttag ttaatcaaga ggaggcctta 720

gagtctttca actctactta ctcacaaatt gaaaagtctt taggtatggt ttatgcagca 780 attggtaatc atgatactgc acctctgaat ctattcccct ccaagaatca gccagatggc 840

aacaatcagt gggcttacga tgcacttgct gaggactggt tagcaatcac ggggatcccg 900

tccgtacaat cagcagacga atacggatcc tattccgcca tacatccaaa ctccaatttg 960

aggatcatat cctacaattc cattttctac tacaaattca atttctatat gtaccaagaa 1020

ccaatagaga aggatccaaa tggccaattc gaatggttga tcaaagagct tcaagccgca 1080

gaagatgcag gacaacgtgc atggttgatt agccatattc ctagtggtgt tgcagatcat 1140

ttccacgatc attcacagta tttcgaccaa atagttcaga gatatgaagc aacaatcgca 1200

ggcatgtttt acggtcatac ccacatggat gaatttcaaa tagcttattc agattacaag 1260

aatagaaatt gggaaactgc aactgccatg ggctacattg cccctgcaat gacaccgaca 1320

gaaggacccc caagcttccg tgtttacgaa atagacccag atacttttgg cgtccttgac 1380

tttacacagt acattgccaa catttccgac ccagcatatc aaaagaagcc ggaatgggtg 1440

ccctattaca gcgcaaaagc agattatgga agcaagttat ctccgcctgt cacagatcct 1500

aaggtggagt tgtctcctgc attctggcat aacgtgacgg ttagcatgga aagggacgaa 1560

tctgtttttc aagacttttg ggctagaaga tcaagaggct acaatgtaac agcctgtaca 1620

ggtgattgta tgaagatgga actatgtact cttagagcag cagacgccca atacaattgc 1680

gttaagccta aaccaggttt caacttttct aaaagagacg gtgaattggg aggtttgctt 1740

gaacaagagt ctcattcaaa ttgtgatcat gcaggattgg ctaccttgtt agggaagatt 1800

gctcataggg ccagagtcgc taggaagatt gaagaagcat aa 1842

<210> 354
<211> 1842
<212> DNA
<213> Penicillium manginii

<400> 354
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttct 60

gcagatgatt ggattactac aatttgggac gacttcaaga atgccgttga ttgttttagc 120

tgtcaagcat tgctgggagg attgaagctg gtgtcagggt taggggaatc ctttatggaa 180

gacgtcatta caggtgtatg ttccatttca ggtgctgaag ataatgatgt ttgtgctggt 240 gtcattgcaa atgaaggacc ggcagtgtac tattcattga agaatttgaa attgggcagt 300

catacggcta agactttctg tgcaacattg actggtttgt gcgaattccc caaggtgaga 360

ccatacgaca tttcttttcc gagccctaaa ccaagcacta ctagacctcc accttctggt 420

gaggctccca tcaaagtggt acacttctca gatacacacg tcgatcttag ctatgaagaa 480

ggatcaaact atgaatgctc aaagccaata tgttgcagag catataccga aaaagatgca 540

ccaggcaata ccacatctcc ttgtggccca tggggaaatt ccaaatgtga tccaccccat 600

cgtttacagg agtcaatgat gtctgctatt gcagatatca atcctgcatt ttccatctat 660

acaggcgatg ttgtagctca tgatgtctgg ttagtcaaca aaactgaagt gctgcaggat 720

cttaatgcta cctattctag tattgaaaat catctaggtt tagtttacgc tgctttagga 780

aatcatgatg ctgcaccctt gaatctgttt ccttccgaca agattccttc ccagtataac 840

ccgcaatggg cttatgacgc tctagccgaa gactggttga cattaacggg gatcccgagc 900

gtgcaaaaag ctagtgagta cggcagttac tcagccgtgc atcctggtag taagttaaga 960

atcattagtt acaactccat cttttactac aagtataact tttctctta taccgaacca 1020

atggaattcg accccaacaa acagttggac tggttgattg cccaactgca ggaagccgaa 1080

gatgctaagc aaagagtgtg gttgatatct cacataccta caggaaattc agaccacttt 1140

agggaccatt cacattactt tgaccagatc atacaacgtt atgatgctac cattgccgca 1200

ttgttctttg ggcatacaca caccgatgaa tttcagattt cctattccaa ctataagaac 1260

agaaattggg atacagctac cgctatgggc tacgttgctc cgagtatgac gcctacgagt 1320

ggtcctccct cattcagggt gtatgagatt gatcccgtta catttggagt gatggacttc 1380

actcaataca ttgcaaacat aacagacccc tctttacaaa ctgagccgga gtggaaaccg 1440

tactatagtg ccaaggcaga ctatggtagt aagctgtcac cagccattaa ggatccagga 1500

atcgagctta ctccaggatt ttggcataat gtgacggtgg ctatggaaaa agatgccaca 1560

gtttttcaag acttttggag tagaagaaca agaggattca acgttcctgg atgcactgga 1620

gattgtattt caaacgagat atgtgctttg aggggtgcag acgcccagta ttcctgttac 1680

aaacaggcac caggtttttc cttcgagaaa agagatgggt ctggtgttcc ctatttgtcc 1740

gaagaaagct ttcaacaacc agaatgtaat catgcaggta tggcaccctt attcgccaag 1800

```
atttctcaca gggctaagtt ggctagagaa agaggtgaat aa                        1842


<210>  355
<211>  1842
<212>  DNA
<213>  Penicillium emersonii

<400>  355
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttct       60

gctccgtatg acaaaagaga cttggctcag gagatttggg acgacattaa gaatgccgtt      120

gactgcgctg gctgtcaagt tgttttgaca gctttgaaag gtgttgccga tctgggcaca      180

acagctttag ttgatgtctt aactgaggtg tgcaatatct ctggtaagga ggattcagat      240

gtctgctctg gtatcattag tagagagggt cctgttctag actacgtgct tcaacatcta      300

gacatcgggt ctcatacatc acaagtcatt tgtgcttcag catttggttt atgccaatat      360

cccgaagtga gaccctataa cttgactttt cctaagccca aaccaaacac aaccagacct      420

gaaccttccg gtgaatctcc aattcaagta gtgcacttct ccgatacgca cgttgactta      480

agttacgaga ctggttccaa ttacaattgc actaagccaa tttgttgtag accttacact      540

gccgaagatg cacctgggaa cactactact ccatgtggtc cgtacggtaa taccaagtgt      600

gatgccccat tatccttgga agagtctatg tttgctgcca tcaaagcctt aaaccctcaa      660

ccagcatttt ctatctacac aggagatgtt gtagcacatg acatttggtt agttgatcaa      720

aacgaggtta tcgaagattt gaacgcaacg tacgatagaa tggctggtct gggtttagtc      780

tatgccgcta ttggtaatca tgatacagca ccggttaacg acctgccgac gtcaaacatt      840

ccatccgagt attcagcaaa ttggacttat gaagctttgt cttacgactt tacaatgttg      900

actcaaagcg ccagtgctca aactgctgca aactatggtt cctattcagc catttaccct      960

ggatcttacg gtacagacct aagagtcatt tcatacaact ctatcttcta ttacgttgac     1020

aacttttggg cttatcaaga tccaatggaa tttgacccag atggccagct agcatggttg     1080

ataaacgagt tgcaagaagc tgaaactgct ggccaaagag tctggatcat agcacatgtt     1140

cctacgggta cttccgatca cttccatgac tattctcact actttgacca aatagtccaa     1200

agatatgaag ccacgattgc tgccttgttc tatggtcata cccacataga ccagtttcag     1260

attagttact caaactattc aaacagagca tttgataccg caactgccat cggctacatt     1320
```

atgccttctt taacacccac tagcggtcca cctaccttta gagtttacga cgttgatcca 1380

aagacgttcg cagtgttaga tttcaccaat tacattgcca acatttccga tcctgcattt 1440

caatcaggtc catcatggca gaaatactat tccgccaagg agacctacgg ctcactattg 1500

tctccacctg taaccgaccc tactgctgaa ttgacgcctg cattctggca taatgtcacc 1560

gtggcatttg agcaagacaa cgcaacattt caagagtatt gggctcgtca aaccagggga 1620

tacgatgtct catcatgtac aggtagttgc ataacccaag caatatgcgg attgcgtgct 1680

ggcgacgcac aatacaattg tgttactcct actcccggtt tcaacttcgc aaagcgtgac 1740

actagtaacc ccaaacaagc cttgtcacat gttgagaaat gtgaaggatc cggtcttcta 1800

ggcttgttaa ggcgtatggt tgcagactct aaatcttctt aa 1842

<210> 356
<211> 1845
<212> DNA
<213> Rasamsonia argillacea

<400> 356
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctggt 60

gtcacctacg ataagcgtga tttagcacaa gacatatgga acgacataaa gaatgctgta 120

gattgtgctg gttgtcaagg tatcttgacc gctctaaaag gtctttcata tcttggcact 180

acggcctttg ttgatgtttt gaccgaagtc tgtgacatct ccggaatgga ggactcagac 240

gtttgttccg gcatcataag cagcgaaggc ccagtgcttg actatatcct gaagcaatta 300

gatatcgggt ctcatacttc tcaagtgatc tgcgcctcag cttttggtct gtgccagtat 360

cctgctgttc gtgcttacaa ccttacattt ccttcaccaa agccagataa gactcgtcct 420

gaaccgagtg gagaatcacc aatgcaaatt gttcacttta gcgatacaca tgtggactta 480

tcatatgaaa caggtagcaa ctacaattgc actaagccta tttgctgcag accgtatacg 540

gcagacgatg cacctggtaa caccactact ccatgtggac cctacggaaa tacaaaatgt 600

gacgcaccta tgaccttaga ggaatcaatg ttcgcagcca tcaaagcact ttcacctcaa 660

cccgctttca gcatctatac cggtgatgta gtagcccacg acatatggtt agtagaccaa 720

aacgaagtcg ttgaagactt gaatgcaaca tacgatagaa tggcaggttt gggcttggtt 780 tacgctgcca ttggcaacca cgatactgct cccgttaatg atcttcctac ttccaacatt 840

ccctctcagt attcagcaaa ttggacgtat gaagccttag aataccattt ctctttgtta 900

acaaactcag cctctgccca aactgccgag aactatggtt cttactcatc cgtctatcct 960

ggcaagtatg gcacggattt gagagtgatt tcatacaatt ccatattcta ctatgtcgac 1020

aacttctggg catatcaaga tccgatgttg tacgatccag acggccaact ggcctggttg 1080

atcaatgaat tacaagaggc cgaaactgct ggtcaaagag tctggttgat agctcatgtt 1140

ccgagtggga ctgccgacca tttccacgat tactcccact actttgacca aattgttcag 1200

aggtatgaaa ccacgattgc tgccttgttt tacggtcata cccatatgga tcaatttcag 1260

atttcttatt cagactattc caatagggct tttgatacag caaccgctat aggttacatt 1320

atgccttcca tgacgcctac atctggtccg cctacattca gagtttatga tgttgaccca 1380

aaaacattcg ctgtcttgga cttcaccaac tacatagcca acattagtga tcccgcatac 1440

cagagtggtc caacctggca aaagtactat agtgcaaaag aagcttatgg tccacttctg 1500

tctcctccag tcacagacgc tactgcagag ttaactccag cattttggca taatgttacc 1560

gtggctttcg aaaatgacga tacggctttc caagagtact gggctagaca gacgaggggt 1620

tacgcagttt caaattgcac cggtaattgc gttacccagg ctatctgtgg cctgagggca 1680

ggtgaaagtc aatacaattg tgtcactcca acaccaggct tcaactttgc aaaaagagat 1740

gtctcttcag atggtcaagc acttccccac atagagaagt gtgaaggttc tggcctacta 1800

tccttattgg ccaaaatggt agcctcaaac ggtcagtcaa gttaa 1845

<210> 357
<211> 1845
<212> DNA
<213> Penicillium parviverrucosum

<400> 357
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat 60

attgaatcag cagacaattg gatcaccaca atctgggact tgtcaaaaca agccgtagat 120

tgcgctgggt gtcaagctct gttagggggt ctgaaactgg ctgcagattt gggtgagacc 180

tttatggaag atgttcttat tggtgtttgc aacattgctg gtgttgaaga tcatgatgtt 240

tgttcaggca taatccaaaa cgaaggtcct gccgtacact attcattgct taacttacac 300 attggctctc atacagcaac aactttatgt gcttccttat tcggcctatg ccaatatcca 360

gccgttagac catacaactt atcatttccg gttccaaaac ctactaagtc tagaccggaa 420

ccatccggtc agtcacctat cagaatagta cacttctcag acacgcatgt tgacttatct 480

tacgaaacag gctcaaacta tgactgttcc aaacctattt gctgtagacc atacacggag 540

gaagacgcac caggaaatac ctctacccct tgtggcccat ggggtaaccc catgtgtgat 600

ccacccaata gactgcaaga atctatgatg actgctatag cagatttgaa tccagcattc 660

tccatctata ctggtgatgt cccagcacac gacatttggt ctgccacgaa ggcagaggct 720

cttagggact ttaacgctac ttatggatcc atggaaaaac gtttgggtat ggtatttgct 780

gctttgggaa atcatgatgc cgctcctctt aacttgtttc cttccaacaa aatcccgtct 840

gagtattcac cgcaatgggc ctatgacgcc ctagcagcag actggctggg gctgagtgca 900

atggcttccg tgcactccgc aatccatcac gggtcctatt ctgcagtcca ttctgaggat 960

aaactacgtg tcatttcata caactccatt ttctattaca aagataactt ctttatgtac 1020

gaggagccaa tggaacacga tccgaatggt caattcgctt ggttgattag tgaattgcaa 1080

tccgcagaaa gcacctcaca aagagtgtgg ttgatagcac atattccttc cggtaacgca 1140

gatcacttta gggatttcag ccactacttt gacgaaattg ttcagagata cgataccact 1200

attgctgcct tatacttcgg acatactcat acagacactt ttcaaattgc atactccaac 1260

tattcaaata gatcctggga caccgcctct gctatgggat atgtggcacc gtccatgaca 1320

cccactagcg gaagcccaag ctttagggtg tatgaagttg atcccgtcac cttcggcatt 1380

atcgacttta cccagtatat cgccaacatt tcagatccca gctaccagat taaccctaaa 1440

tgggagccct attactcagc taagaaggcc tatggtagca aactatctcc acctgcccag 1500

gacccaggtg cagaaatgac acctgccttc tggcataacg ttactatagc catggaacaa 1560

gatgcttcca tattccaagc tttttgggca cgtcgtacta gaggaaacaa agtaacttct 1620

tgtactggca actgtatggc aaatgagatt tgcgcactta ggggtgccga tgcacaatac 1680

aattgtgcta ctcccaccgt tggttttaga ttcagaaaaa gagatatgac tagtgactta 1740

agcttgcaaa aagaagagtt tagacctgaa tgtaatcatg caggaatggg tccattgttg 1800

gcaaagattg tccatcaagc agctttggaa aatgaacgtg ggtaa 1845

<210> 358
<211> 1845
<212> DNA
<213> Penicillium flavescens

<400> 358
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat 60

agtgaatccg ctgagagctg gattagtgac atatgggacc acttcaaaga agctgttgat 120

tgtacttctt gtcaagtttt acttggttcc ttaaagttag tagccgcatt tggcgacact 180

ttcatggtag atgtattgac tggcgtatgt gctatcagtg gcgcagaaga ccacgatgtg 240

tgtgctggcg ttattgcagg ggagggtcct tctgtgcagt attcactgaa gaacttgaag 300

attggcagcc atactgctaa aactttctgc gccagtttag ttggtttgtg ccagtaccca 360

aaggttagag agtatgacct ggccttccct gcaccaaaac cgccaaatgg aagaccgcct 420

cctagcggag aacctcccat caaagtagtt catttctcag acacacatgt agacttggca 480

tatgaaccag gttcaaacta tgcatgtagc aaacccatat gttgcaggac ttacaaagag 540

aatgacgctc ctggcaatac cagttctgct tgtggtcctt ggggcaatcc tagatgtgat 600

agccctcata gactacaaga gtctatgaat gccgcaatcg cagacttaaa cccagcattt 660

tccatttaca ctggcgatgt ggttgctcat gatgtgtggc tagacaacaa gtttgaagtt 720

ctacaaaact tcaatgcaac atatggagct atggaaacta ccctaggtca agtctatgct 780

gccttaggca atcacgatac ggcacctctt aacttgtttc caagttccaa gattccatca 840

atctataacc cacaatgggc ttatgacgct ttgaccgaga attggttagc attgaccgga 900

ataccttcaa tcgaaagcgc agaccagtac ggatcttatt ctgtcttaca cccagattcc 960

aatttgagaa tcatctccta caattccatc ttttactaca aatacaactt ctttgcctac 1020

accgaaccta tggaatatga tccgaattct cagttgaaat ggttgataaa cgagttgcaa 1080

gctgctgaaa aagctagtga gagagtttgg ttgatttcac acataccttc cggtaactca 1140

gaccacttcc acgaccactc tcactacttc gaccagatca tccaaaggta tgatgctacc 1200

atagctgctc tattctttgg tcatactcat ctggatgaat tccaaatctc ctattcagac 1260

tacaaatcta gaacttggga cactgccact gctatgggtt acatcgctcc ttcaatgaca 1320

```
cctaccagtg gtccgccttc atttagagtg tacgatatag atccagttac ttttggcgtt     1380

ttagatttca ctcagtacat agccaacatc aatgcaccag atcaagaaag tcttgagtgg     1440

gtgccttatc atagtgctaa agaagcttat ggcagtaaac tagtttctcc aattaccgac     1500

ccatcagctg aattgagccc agctttctgg cataatgtta cattagctat ggaaaatgac     1560

agcgctatct tcggagactt ttgggctagg agaaccaggg gttatcaagt gccgagttgt     1620

accggagatt gtattagtgg cgagatttgc acacttaggg gtgccgacgc ccagtacaac     1680

tgtttcgtcc aaaaggttgg tttctctttt gaaaagagag atcatcaagg agattctact     1740

agggaagaaa ggatcttacc tgagtgcaac catgctggca tggctccatt gcttgcaaag     1800

attgcaagat tagctgctat agccagagac atggagaaaa ggtaa                     1845


<210>  359
<211>  1848
<212>  DNA
<213>  Penicillium hispanicum

<400>  359
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgaa       60

tcagctgaat catgggtggc atccatctgg gacgacttca aagttgccgt agattgcgct      120

agctgtcaag ctctgttagg gggtctgaaa ctggttgctg aatttggtga gtcctttatg      180

gaagatgttc ttattggtgt ttgtgatgta tctggtgttg aagattcaga tgtttgtgct      240

ggtgtcatcg caaacgaagg tcctgccgta cactatacat tgaagaactt agagattggc      300

tctcatgcag caaatacttt atgtgcttcc ttagtcggcc tatgcgaata tccagccgtt      360

agaccataca acttatcatt tccgtctttg aaacctgcta cctctagacc tccaccatcc      420

ggtaagcctg caatcaaagt agtacacttc tcagacacgc atgttgactt atcttacgaa      480

acaggctcaa actttgactg ttccaaacct atttgctgta gagtttacac ggaggaagac      540

gcaccaggaa atacctcttc cccttgtggc ccatggggta accccaaatg cgatccaccc      600

catagactgc aagaatctat ggttgaagct atagcagttt tggatccagc attctccatc      660

tatactggtg atgtcgttgc acacgatgtt tggttggtga acaagtccga ggctcttcag      720

gactttaacg ctacttatgg agcaatggaa aatcgttttg gtcctgtata tgctgctttg      780

ggaaatcatg atacggctcc tcttaacttg tttccttcca acaaaatcag cagagagtac      840
```

aatccgcaat gggcctatga cgccctagca gcagactggg ctgccttgac cggaattcca 900

tccgtggcat ccgcaaggga atacgggtcc tattctgcaa tacatccaaa ctcaaatcta 960

aggatcattt catacaactc cattttctat tacaggttta acttctttgc ttacgaggag 1020

ccaatggaat acgatccgga ttctcaactg gcttggttga ttaccgaatt ggatgcagca 1080

gaaacggcag gtcaaagagt gtggttgata tcccatattc cttccggtaa gccagatcac 1140

tttagggatc acagccacta ctttgaccaa attgttcaga gatacgatgc cactattgct 1200

gccttattct tcggacatac tcataaagac gaatttcaga tttcctactc cacatataca 1260

aatagagcat gggacaccgc cactgctatg ggctatatcg caccgtccat gacacccact 1320

agcggaccgc caagctttag ggtgtatgaa attgatcccg tcaccttcgg tgtaatggac 1380

tatacccagt atatcgccaa gatttcagat agttctgccc aaattgacac aactcctgag 1440

tgggtaccct actattccgc caaggcagat tacggtgcca agttagctcc accggtcgaa 1500

ggtgcaggag tcgagttaac tccagccttt tggcataatg tcacggtagc tatggaagca 1560

gattcatcct tgtttcaagc tttttggggg agaagaacac gtggctacaa tgtttcatct 1620

tgcaccggag aatgtatggc cactgagata tgcgccttga ggggtgcaga tgcccagtat 1680

tcttgtgttg gcgctaaacc aggtctgtct tttctaaga gaggtggcaa ggatgtggat 1740

gttttgtggc aaagaagact acaaccagaa tgtaatcatg ctggcatggc tccactactt 1800

ggtaagattt ggacaagagc tgctttagtt tggcgttcag aagcttaa 1848

<210> 360
<211> 1854
<212> DNA
<213> Penicillium simplicissimum

<400> 360
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctggt 60

gctaccgaga actggattag tactatatgg aatgacttca aagaagctgt ggattgtggt 120

agctgccagg ttctgttagg gggtttgaaa ttggttgccg attttggaga aggctttatg 180

gaagatgtct taactggtgt ttgtgacatt tctggtgcag aagatagaga tgtctgcgca 240

ggggttattg caagtgaagt accagcattg cactacgcaa tcaaaaacat gcatgtaggt 300 tcacatactg ctaaaacctt atgcagtgca ctggttggtc tatgcgattt tccagacgtg 360

aggccatttg acttggcttt tccttctcct aaaccagcca attctagacc tccccccttcc 420

ggcaaacctc ctatcaaggt tgtgcacttt tcagatacac atgtggactt aagttatgag 480

actggctcaa actatgactg tagtaaacct atttgttgca gggtttacac agatgcagat 540

gccccaggaa ccacagacaa accatgtggt ccctttggga ataccaagtg tgatccgcca 600

catcaactac aagaatctat gatgactgct attgctgaac ttaatccagc attttccatt 660

tacactggag acgttgttgc tcatgacgtg tggttagtga ctaaggagga agttctacaa 720

gatttgaatg caacttatgg tgccatggaa aatcatttag gtttggttta tgctgcatta 780

gggaatcacg atgccgcacc cttaaacttg tttcccagcc ataacgttcc aagcaaatac 840

aacccacagt gggcatatga tgccttgact gccgactgga tggctttaac cggcatagaa 900

aatgtgcaaa acgccaatga atatggatcc tattctgcca ttcatccaaa ctccaagtta 960

cgtatcattt cttacaattc catcttttac tacaagtaca atttcttctc ttatactgag 1020

ccaatggaat atgatccgaa tgggcagttg acctggttga ctgaagaatt acaggcagca 1080

gaaaatgccg gacaaagggt atggttgata tcccatatac cttcaggtga tgtcgatcac 1140

ttcagagatc atagccacta ctttgaccaa atcatacaga gatatgaggc aacaattgcc 1200

ggattgttct ttggtcacac tcatacagat gaattccaag tatcttattc cgattacaaa 1260

aacaggaact gggatacggc aacagccatg ggtacgttg caccctcaat gacaccgact 1320

agcggttccc cctcttttag agtatacgac atcgacccag taacctttgg tgtgctagat 1380

ttcacccagt acattgcaaa catcagcgat gctagcttcc aaacaaagcc tacatggata 1440

ccatactaca cggccaaaaa ggattacggt tcaaagcttc cgaccattcc agatgatacc 1500

gctgaactta ctccggcttt ctggcataac gtgacagttg ctatggaaaa agattccgct 1560

gtttttgatg aattctgggc tagaagaacg agaggctaca atgtaccagc ctgcacagga 1620

gattgtgcca aaaacgaaat ctgcgctctt agaggcgcag acgcacagta ttcttgcgtg 1680

caaagaactc cagggttttc tttttccaaa agagacggag tagacggtga aatggaagaa 1740

gttgctcctc tattgtctaa aagatttcag cctgaatgta atcatgccgg tatggctccc 1800

ttgttagcca agatagctca caacgccaat ttggctaaga tgaatggcga ataa 1854

<210> 361
<211> 1857
<212> DNA
<213> Penicillium vasconiae

<400> 361
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctggc 60

gcagtcgagt cttggatttc aactatttgg aatgatttca aagaggcagt agattgcggg 120

agctgtcagg tactgttggg tggtttgaaa cttgtagcag attttggaga aggctttttg 180

gaagatgtct taactggtgt ttgtgacatt agtggtgctg aagataggga cgtctgcgct 240

ggtgtaatcg caagtgaagt accagcccta cattacgctt tgaaaaacat gcatgtaggt 300

tcacatactg caaaaaccct ttgtagcgct ttggtcggct tgtgtgattt cccggatgtt 360

agaccgtttg gtttgacatt tccttctcca aagccagcta aatcacgtcc tcctccctct 420

ggaaaaagcc ccattaaggt ggttcacttt agtgatacgc atgtagactt aagctatgag 480

acaggatcaa actatgactg ttcaaaacct atctgctgtc gtgtctatag tgatgaggat 540

gcacctggta agacagataa accgtgcggt ccgtttggca acacaaaatg cgatccacca 600

caccaattgc aagaaagtat gatgacagct atagccgatt tgaatccagc tttttccatc 660

tataccggtg atgttgttgc ccacgacgta tggttggtca acaaagatga agtattgcaa 720

gatttcaatt caacttacgg tgctatggaa aatcatttgg gtttagttta cgcagccttg 780

ggaaaccacg atgctgcacc cttgaatctt ttcccatcca agaatgtgcc aagtaagtat 840

aacccgcaat gggcatacga cacgttgacg gccaattgga tgacccttac cggcatagag 900

tcagtgcaga atgcaaatga atacggttct tactcagcaa tacacccaaa ttcaaagctt 960

aggatcatat cttacaattc tatcttctac tacaaataca acttcttttc atacactgag 1020

cctatggaat acgatccgaa cggtcagtta acttggttga tatcagagct acaaagtgct 1080

gagaatgctg gacaaagagt ttggttgatt agtcacattc catcaggcaa tgtggaccac 1140

tttagagacc attctcatta ctttgaccaa atcattcaac gttatgaagc taccatagct 1200

ggtttgtttt tcggtcatac tcatacagac gaatttcaaa tagcatatag tgattacaag 1260

aacagaaatt ggaatacagc cacagccatg ggttacgtcg ctccgagtat gactccgact 1320

agtggcccac catcttttcg tgtctacgac attgatcccg ttactttcgc agttatcgac 1380 tttacacagt atatcgccaa catatcagac cctacttttc agaagaaacc agattgggtc 1440

ccgtactatt ctgccaaaaa ggattatgga ggcaagcttt ctccaaggcc tgccgataca 1500

gccgagttga ctccggcttt ttggcacaac gttacagttg ctatggaaaa ggattcttca 1560

gtctttaacg agttttgggc acgtagaaca agaggctaca atgtgcctgc atgtactggt 1620

gactgtgtca agaacgagat ttgcgctcta agaggggcag atgctcaata ctcctgtgtt 1680

caaagaacgc caggttttag tttttctaag agggatgacg aaaatgttga tggagatgtt 1740

ggaaactatc ccttgttatc aaagaggttt caaccagaat gcaatcatgc tggtatggct 1800

ccattgttag ctaagatcgc tcataaagct tccttggcta aggcaaatgg tgaataa 1857

<210> 362
<211> 1860
<212> DNA
<213> Talaromyces columbinus

<400> 362
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttac 60

gactctgcct tggtagatca taacttagta tccgatatct gggaagatat caaggaggct 120

gtgacatgcg ctggttgtca agttatctta gctgccttga aaggtgtctc agatttgggt 180

actacagctt tggttgatac tttgacaggt gtttgtaaac taagcggagc cgcagatgat 240

aacgtatgtg aaggcattat ctccagggag ggtgcagttc tacattatgt attgtcagaa 300

ttgtccttag gaagtgaaac gtcaaatgca ctttgtgctt ctgccttcgg attatgtctg 360

tatccagatg taagaaacta tactctgaac tttccttcag ccaaacctaa gaacataaca 420

cgtcctgctc cgagcggtaa acctcctatt caggtagctc actttagcga tacccatgtc 480

gatctatcat acgaagtagg ttccaactgg aattgcacaa aacctatttg ctgtaggtcc 540

tttgaggctt cagatgctcc cggtaacaca actacccctt gtgggccatt tggtaacact 600

aaatgtgaca caccattgac attggaagag aatatgttag attccattaa gaaatcagac 660

ccaactccag ctttcagcat ctatacgggt gacgtcgttg ctcacgacat ttggttagtc 720

gataaagatg aggttttgac agacttgaat gctacttatt ccttaatggc cgaaataggc 780

accgtatatg cagccattgg taaccacgat accgctccac tgaatgatct tccaaccacg 840 caagtacctg agagctacag cgccaactgg acatatcaag ccctagcaac aaactttacc 900

acgttaacaa gagattcctc agttatctca gtagcaaaga actatggtag ctactcttct 960

gtctttaccg gttcttacgg tacagactta aagatcattt cctataactc tatgttctac 1020

tatgtggata acttctatgc ctttttggat cctatgccat acgacccaga tggtcagtta 1080

gcttggttga ttgatgaact acaatccgca gaaacagctg gccaacgtgt gtggttgatt 1140

gcccatgttc caaccggtag ctccgaccat tttcacgact atagtcacta ctttgatcaa 1200

attgtccaaa gatatgatgc aaccatagca gccttgttct ttggacatac gcacaccgat 1260

caattccaaa tagcctacag cgattatgca aaccaaaacg cagacactgc cactgcaatc 1320

ggctacatta tgcccagtct taccccaaca agtggtccac ccgcatatag gatctatgat 1380

attgatcccg tgacgttctc tgtgctagat tacacggtct acataaccaa catatctcac 1440

ccagatttcc aaaagggtcc aaagtgggag aagtactatt ccgcaaagga tacatacggg 1500

agcttgctgt ctccacctgt gacagatcca tctgctgaaa tgacaccagc tttttggcat 1560

aacgtgactg cagtattcga atcagatgat gtagctttcc agggatactg ggctaggcaa 1620

accaggggct acgatgtctc agactgtacg gatgaatctt gtaagaacca aactatttgt 1680

gccttgagag ctgcagatgc tcagtacaat tgcgttgttc catctatagg ctttaacttc 1740

gctaaaagag atgatacgga ccaagctcat gtcagggctc aaaaagagaa atgtgatgat 1800

acaggtcttg tgtccttatt gggtaagatt ttggcaaaat caaaagaaac tacaaactaa 1860

<210> 363
<211> 1860
<212> DNA
<213> Talaromyces variabilis

<400> 363
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttcc 60

agctctgcct tgatagatag agacttagca tccgaaatct gggatgatat caaggaggct 120

gccacatgcg ctggttgtca agttatctta gctgccttga aaggtgtctc agatttgggt 180

actacagctt tgattgatac tttgacagaa gtttgcaaga taagcggagc cgaagatgat 240

gacgtatgtg aaggcattat ctccagggag ggtcctgttc tacactacat tttgtcacaa 300

ttgtccttag gaagtgaaac gtcagatgca ctttgtacta ctgccttcgg attatgtgcc 360 tatccagatg taagaaacta tactttgact tttccttcag ccaaacctga gaattccaca 420

cgtccttcaa gcagcggtga atcacctatt caggtagtac actttagcga tacccatgtc 480

gatctatcat acgaaacagg ttccaactgg aattgcacaa aacctatttg ctgtaggtcc 540

tttgactcat cagatgctcc cggtaacaca aagacccctt gtgggccata tggtaacact 600

aaatgtgacg caccaatttc attggaaaag tctatggtag attccattaa gggtttaagt 660

ccagctccag ctttcagcat ctatacgggt gacgtcgttg ctcacgacat ttggttagtc 720

gatgaagatg aggttttgac agacttatct tctacttatg gtttagtaca ggatgtcggc 780

accgtatttg cagccattgg taaccacgat accgctccag tgaatgatct tccaaccacg 840

caagtaccta gcacgtacag cgccaactgg acatatgaag ccctagcagg aaactgtacc 900

acgttaacag gtgattcctc agttatgtca gtagcagaga actatggtag ctactcttct 960

gtctttaccg gttctcacgg tacagactta aaggtgattt cctataactc tatcttctac 1020

tatgccgata acttctatgc ctttttggat cctatgccat acgacccaga tggtcagtta 1080

gcttggttga ttgatgaact acaagcatcc gaaacagctg gccaacgtgt gtggttgatt 1140

gcccatgttc caaccggtag ctccgaccat tttcacgact atagtcacta tttggatcaa 1200

attgtccaaa gatatgatgc aaccatagca gccttgttct ttggacatac gcacaccgat 1260

caattccaaa tagcctacag caactattcc aaccaaaacg cagacactgc cactgcaatc 1320

ggctacattg cacccagtct taccccaaca agtggtccac ccgcatatag ggtgtatgat 1380

attgatcccg tgacgttcgg tgtgctagac tttacggtct acatagccaa cataagcgac 1440

ccagattacc aaaacggtcc aacatgggcc aagtactatt ccgcaaagga aacatacggg 1500

agcttgctgt ctccacctgt gacagattca tctgctgagt taacaccagc tttttggcat 1560

aacgtgactg cagtattcga aacagatgat gcagctttcc agggatactg ggctaggcaa 1620

accaggggct acgatgtctc aaactgtacg gattcatctt gtaagaacca gaacatttgt 1680

gccttgagag ctgcagatgc tcagtacaat tgcgttgttc catctatagg ctttaacttc 1740

gctaaaagag atgaaacgga ccaagctcat gtcaaggctc aaaaagagaa atgtgatgat 1800

gcaggtcttg tgtccttatt gggtaagatc attagtaaat caagagacgt ttcaaactaa 1860

<210> 364
<211> 1860
<212> DNA
<213> Talaromyces rugulosus

<400> 364
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttct   60

tccagtgcat tggtcgacag agatctagca agtgagatat gggatgacat caaagaagct   120

gctacttgta ctggatgtca agtgattctt gctgccttga aaggcgtatc agaccttggt   180

acgaccgtat tggtagatac tcttacagaa gtttgcaagc ttagtggagc cgaggatgac   240

gatgtatgcg aaggcataat cagcagagag ggtccggtct tgcaatacat cctttcacag   300

ttatccctgg gttctgaaac ttcagacgcc ctgtgcgcat cagcttttgg gctttgctca   360

tacccagatg tgagaagcta caccttgaca tttccatcta cgaaacctga gaatagcaca   420

aggccgagta gttcaggaca agctcctatt caagtcgttc acttttcaga tacccatgta   480

gatttgtctt atgaaacggg tagtaattgg aattgcacaa aaccgatctg ttgcagatcc   540

tttgactcta gtgacgctcc aggcaatact tcaactcctt gtggccctta tggaaataca   600

aagtgtgatg cacctttaag cttggaagag tccatgttcg attccataaa gtcattatct   660

cccgctccag ccttctcaat ctatactgga gatgtggtcg cacatgatgt ttggatagtt   720

gacaaagatg aagtcttaac agacttgaat gccacttatt ccttgatggc tgaggttggt   780

acggtatacg ctgccatagg gaatcacgac accgctccct taaacgattt gccaacttca   840

caggttcctt ctacatattc agcaaactgg acttaccaag ctttagctac caatttcaca   900

acactatcag gcgatagctc tatcatgtcc gtagctgaga attacggttc ctactcatcc   960

gtttttgctg gctcccatgg tacagacttg aaagtgatta gttacaactc cattttctac   1020

tacgtcgaca acttctatgc attcttagat cctatgccat acgacccaga cggccaatta   1080

gcttggttga tagatgagct gcaagctgct gaatctgctg gccagagagt ctggttgatt   1140

gcccacgtgc cgaccgggtc tagcgaccat ttccacgact actctcacta ctttgatcag   1200

atagttcaaa ggtacgatgc tactattgca gccttgtttt tcggtcacac acatacagat   1260

caatttcaaa tagcttattc cgattactca aatcagaata gtgacactgc aacagcaatt   1320

ggatacatca tgccgtcatt aactccaacg agtggacctc cagcttatag agtttacgat   1380 attgatccgg ttacctttgg cgtgttagac tttacagtct acattgcaaa catctccgac 1440

ccggattatc aaaacggtcc aacctgggct aagtactata gtgctaaaga aacttacggg 1500

accttattga gtccagccgt tacagactct agtgctgagt taacaccagc tttttggcac 1560

aacgttaccg cagtattcga aacggatgat acttccttcc aaggttattg ggccaggcaa 1620

accaggggtt atgatgtgtc caattgtacc gattcctcct gtaagaacca gacgatctgc 1680

gcactaaggg ctgccgatgc tcagtacaat tgtgtcgtac ctactattgg cttcaacttt 1740

gccaaaagag atgaaacaga tcaggcacac gtaaaggccc aaaaagagaa atgcgacgat 1800

actggtttgg tatccttgtt agggaaaatc atttcctcaa gtcgtaatgt ttcctcttaa 1860

<210> 365
<211> 1860
<212> DNA
<213> Hamigera terricola

<400> 365
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcaa 60

atgcaaacat ctgaacgttc atggggatct acgatatgga aagacgtgga ggaagccgta 120

gactgtgctg gttgtgaagt catcttagga gccttgaaac ttgttgcaga tttaggtaaa 180

ggtactttag aaactgctat gattgatgtt tgtgatctgt ctggggctga agatagtgat 240

gtatgttcag gtttgataac agccgaaata gatgccttgt actatgcctt gaacaatgtc 300

catgtcggct cccacacatc aaaggtgttg tgtgctcacc tgtttggttt gtgctcttat 360

ccagatgtta ggtcttatca cttgatcttt cctagttcaa aacccgctac atcccgtcct 420

tcaccgagcg gtcaaaaacc cattaaggta gctcacatta gcgataccca tgtcgatcta 480

tcatacgaac ctggttccaa ctacgaatgc tccaaaccta tttgctgtag ggcatatacc 540

aaagaagatt ctcccggtaa cacaccccac ccttgtgggc catatggtaa cacaaattgt 600

gacgcaccat atagattgga agagtctatg tttgctgcta ttgaagcttt agacccagct 660

ttttctatct acacgggaga cgttgtcgca catgacatat ggttggttaa tgaaactgaa 720

gttctggatg atttagatgc aacttattcc ttaatgaaat ccctgggtct agtctacgca 780

gctgtaggca atcatgatgc cgctcccgtt aatctgtttc ctagtaatcg tatcccttca 840

acatactctc cgcagtgggc ctatgatgct ctagccgaag actggcttgc tcttacgaat 900

```
gattcttccg tcgattctgc cagagaatac gggtcatatt cagccgtgta tccaggatca      960

aacttgagaa tcatttccta caatagtgtg ttctactata aggataactt ttggatgtac     1020

gaagacccca tggagtatga tccaaacgga caactggcat ggttgattaa cgaattacaa     1080

gcagctgaat ccgcaggtga aagggtatgg ttaatctctc acatcccttc aggtaactca     1140

gatcatctat atgactatag tcactatttc gatgctatcg tgcaaagata tgaagctacc     1200

attgctgcct tattcttcgg acatactcat acagatctat ttcagatcgc ctattcagac     1260

tatgataaca ggaactggga tacagccact gccatagggt atatcgctcc tagtatgaca     1320

ccaacaagtg gcagtcccgc ttttaggatc tatgaggtcg atcccgtgac ttttggtatt     1380

cttgactaca cagtttacat agccaatatc tcccatcctt catatcaaac gcagcctact     1440

tgggaaaagt actattccgc caaggaggct tatggatcct tgttaactcc accggtgaca     1500

aacccatcta tagagttaac tccagctttt tggcataacg ttactgtctt aatggaggac     1560

gatgaatcag tgttcaaaga cttttgggct cgtaccacaa ggggctttaa cgtttccacc     1620

tgcgtcggta gttgtatgac tgaggagatt tgtgctctta ggtctgcaga tgctaagtac     1680

aattgtgcaa ctgctaagcc tggtctgaac tttttgaaaa gagatgatgt cgaagctcaa     1740

tcaaaacctg tgaagccaca atgtgaagac tctggattgg ctgcagtttt ggtcaaaatg     1800

atggagaata cagatgattt cgctggtttg ttgaaagaaa aggctttagc acatggctaa     1860


<210>  366
<211>  1860
<212>  DNA
<213>  Penicillium piscarium

<400>  366
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctaga       60

accgaagcag cagacagctg gatttccaac atatggaacg agttcaaaga agctgttgat      120

tgtggttctt gtcaagtttt acttggtggc ttaaagttag tagccgattt tggcgagggt      180

ttccttgaag atgtattgac tggcgtatgt gatgtgtctg gcgcagaaga cagggatgtg      240

tgtgctggcg ttattgcaaa cgaggtacct gctctgcact atgcactgaa gaacatgcat      300

gtaggcagcc atactgctaa aactctgtgc agcgccttag ttggtttgtg cgacttccca      360
```

aacgttagac cgtttgactt gaccttccct tcaccaaaac cggctaaaag tagaccgcct 420

cctagcggaa aacctcccat caaagtagtt catttctcag acacacatgt agacttgtca 480

tatgaaactg gttcaaacta tgattgtagc aaacccatat gttgcagggt ttactcagac 540

aaagacgctc ctggcaaaac cgacaaacca tgtggtcctt tcggcaatac aaaatgtgat 600

ccgcctgaaa gactacaaga ctctatgatg gctgcaatcg cagacttaaa cccagcattt 660

tccatttaca ctggcgatgt ggttgctcat gatgtgtggc tagtcaacaa agatgaagtt 720

ctacaagact tcaatagtac atatggagct atggaaaatc acctaggttt ggtctatgct 780

gccttaggca atcacgatgc cgcacctctt aacttgtttc catccaacaa cattccatca 840

aagtataacc caagatgggc ttatgaggct ttgaccgcaa attggattac cttgaccgga 900

atacaatcag tccaaaacgc aaacgagtac ggatcttatt ctgcaattca cccaaattcc 960

aaattgagaa tcatctccta caattccatc ttttactaca aatacaactt cttttcctac 1020

accgaaccta tggaatatga tccgaatggt cagttaactt ggcttataga ggagttgcaa 1080

gctgctgaaa atgctggcca gagagtttgg ttgatttcac acatacctag tggtaacgtt 1140

gaccacttcc gtgaccactc tcactacttc gaccagatca tccaaaggta tgaagctacc 1200

atagctggtc tattctttgg tcatactcat acggatgaat tccaaatcag ttattcagac 1260

tacaagaata gaaattggga cactgccact gctatgggtt acgtggctcc ttcaatgaca 1320

cctacctccg gtccgccttc atttagaatc tacgatatag atccagaaac ttttgccgtt 1380

atggatttca ctcagtacat agccaacatt tctgaagctt cttttcaaac caagccaaac 1440

tggataccct attactctgc taagaaagat tatggcggta ggttgactcc accaaccccg 1500

aatacagctg aattgacgcc agctttctgg cataatgtta cagtagctat ggaaaaagac 1560

agctctgtct tcaatgagtt ttgggctagg agaaccaggg gttattctgt tccagcctgt 1620

accggagatt gtgtaaagaa cgagatttgc gctcttaggg gtgccgacgc ccagtacagt 1680

tgtgtccaaa gaacgccagg tttctctttt tcaaagagag atgatggtga agttgaagtt 1740

gacttggaaa atgctccttt actttccaag agattccagc cagaatgtaa tcacgcagga 1800

atggcaccct tgttagccaa aatcgctcac aaagcctcaa tagccaaaat gaacggttaa 1860

<210> 367

<211> 1866
<212> DNA
<213> Talaromyces bacillisporus

<400> 367
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctggt 60

caaactccaa cgtcatcact agttgccaga gatttggcca gcgagatttg gaatgacatc 120

aaagaagctg ctacctgtgc tggatgtaaa gttatcttgg ctgccttgaa aggtgttgca 180

gatttgggta ctacagtttt gattgatgtc ttgacagagg tttgcaaaat ctcaggagaa 240

gaagatgacg atgtatgcga aggcatcata agtagagaag gtccagtttt ggagtacata 300

cttagtcagt tatcactatc ctctgaaact agcgacgtct tatgtgcctc tgcttttgga 360

ttgtgctctt atccggctgt tagagattac acattgacct ttcctagtcc caagccagcc 420

aacattacta gaccttctcc gtcaggtaag tcaccgattc aggtagtcca tttctcagac 480

actcatgttg atctgtccta tgagacaggt agtaattgga attgcaccaa acccatttgt 540

tgtcgtgcct atgaggcttc cgacgctcca gggaatacta ctaccccatg tggtccttac 600

ggtaatacaa aatgtgacgc tccattatct ttggaacaat ctatgatcga ttccatcaaa 660

gccctggacc ctgccccagc cttctccatt tacacaggtg atgtagtcgc tcatgatatc 720

tggattgtag atgaagatga agtcttaaca gacttaaacg ctagttactc cttaatggca 780

gagacaggta aggtgtttgc cgctattggg aatcatgact ctgctccggt aaatgatctg 840

ccgacgacgc aggtgccttc caaatacaac gcaaactgga cctatcaggc cttagccaat 900

aacttctcaa ctcttacagg agacagcgca gtcttaagcg tggctgaaca atatggctct 960

tattcctcag tctttacagg ctcctatggt acagacttga aggtcatttc ttacaatagc 1020

atcttttact acattgataa cttctatgcc ttcttagatc caatgcctta tgatccagat 1080

ggtcaactag cttggttgat tgaagaactt caagccagcg aaacagctgg gcaaagagtt 1140

tggttaatcg cacacgttcc aacgtcatca tccgaccatt ttcatgacta ttcccactac 1200

tttgatcaaa tcgtacaaag atatgaagct accattgctg ccttgttctt tgggcataca 1260

cacacagacc aatttcaaat ctcatacagt aactatagca atcaaaacgc agatactgca 1320

tccgcaatcg gctacattat gccatctctt accccaacct ccggtcctcc agcttaccgt 1380

gtgtacgata tcgatccagt aacgtttgga gtcttagatt tcacggtgta cattagcaac 1440 atatcagatc ctgccttcca gaatggtcct acatggtcaa agtactacag cgctaaggaa 1500

acttacggga gtttgttatc tccaccagta acagattcta cagctgaact tacgccagca 1560

ttttggcata atgttactgc agttttcgag acagatgatg atgcctttca aggctactgg 1620

gctaggcaaa ccagagggta tgatgtttca aactgcacag atacttgtaa gaatcaaact 1680

atatgtggta tcaggggtgc cgatgctcag tacaattgtg ttgtccccaa gattggcttc 1740

aatttcgcaa aaagagatga aaccgatcaa gctcatgtca aaactcaaaa agaaaagtgc 1800

gatgatgctg gtctagcttc tctatttggt agaatggttg caaactcaaa gaatgcctcc 1860

aattaa 1866

<210> 368
<211> 1872
<212> DNA
<213> Galactomyces candidus

<400> 368
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgcc 60

ccacctacca ctaagagatc cttggccagc gacatttggg atgacattgt tgatgctgtt 120

gactgtggtg catgtgatac tatcttggaa gccttgaaag gtttggcaga tttgggtaat 180

acagtttttg ttgatgtctt gacagacgtt tgtgatatct caggagctga agatagtgat 240

gtatgctctg gcactatatc cgaagaaggt cccattttga ggaccataat caaggggtta 300

tcagtcggct ctgctactag cgacttgttt tgtgggactt tgttgggatt gtgccaaaat 360

ccggctattg catcatggtc agtccccttt cctaaaccca agccaaacac ggttcgtcca 420

cctccaagcg gtcaaagtcc aatctctgtc gcacacataa gtgatgtgca tgtagatcta 480

agctacacta ccggagccaa ctatgactgt tccaagccaa tctgttgtag accgtacact 540

agcgatgatg cccctggtaa cacagattat cctgctggtc catacggaaa tacaaattgt 600

gatgccccat tggatttgga atcatccgct atggcagcca tcaagaaact gaatccggca 660

ttctctatct tcactggtga cgtagctgct catgacgttt ggttggtgaa tcaagcagaa 720

gtagaattgg acttgaatac aacatacaat acacagttca caactttagg cacagttttt 780

ccggctcttg gtaatcacga tgttgcccca gtgaacggat ttgcaccgtc tggggtgagc 840 agtaatccca acatacagtg ggcatacgac acaaacgccg aagattggac aaagtggatt 900

ggctcaacag cagccaatgc tgaagagagc tttggtgcat atagtattgt tcacggcaac 960

ttaagagtca tctccttcaa ttccattttc tactatagac tgaatttcta catgtaccaa 1020

gatccactac aaagagaccc ttcatcccaa ttctcctggc tagtaaatca actacaagct 1080

gcagaagatg ctggtcagag agcctggttg atatcacacg taccatctgg ctcaggggat 1140

tactttccac agtattcaaa ctacttcaat caaattgtta acagatatga agctacaatc 1200

gcagcattgt tttacggtca cactcacgtc gaccaatttg agatatcata ctccgactac 1260

tcaaaccaga atagcaacac ggctgtggct atgtcctaca ttactcctag tttgaccccc 1320

acttcaggct ctccaagttt cagaatctac tctattgatc cagtgacgta cggagttctg 1380

gactatacaa actacatagc caacatttcc agcccgacat atcagaatgg accacaatgg 1440

gtggagtact attctgcaaa agccgcttat ggtccgtacg ttagcccacc attgacgtcc 1500

gctgctgctg agttaacacc tgctttttgg cataatgtga cggttgcatt tcagaacaac 1560

aatgacttgt ttcaggagta catatcaaga aagtctaggg gcttcgacgt tagttcttgc 1620

actgggtcat gtcaaacaga cgagatttgt caattgcgtg ctgctgaatc ccagtataac 1680

tgtgtaacga tttcaccagg catcaacttt aacaagagag atcaacaatc aaacctaggt 1740

gctcaagaaa agcatgggga tggttgtgaa ggttctccta ttcgtgacat ctttgctact 1800

ttgatgcaag acagaagagg tctagtttca gccattaacg aagggatcgc taagagatct 1860

attagagcct aa 1872

<210> 369
<211> 1881
<212> DNA
<213> Penicillium megasporum

<400> 369
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctaat 60

atcatagaat cttgggcctc agagatatgg gatgacataa agaatgcagt cgattgtgct 120

ggttgtgaaa ccatcattgg tgccttgaag gtagtcgcag atcttggtaa aggcaccttg 180

aacggcacat tgatagatgt ttgcgatcta tcaggggtgg aggatccaga cgtctgtacc 240

ggcttaatct cttcagaaat cgacgcattg tattactcct tgaaaaacat ggcagtagat 300 tcacacacgt ctaaagtttt gtgtgctggc ctgttctcat tatgtccatt tccagccgct 360

aggccctata acttgagctt ccccacacct aaaccagcta cgtcaagacc tgctccgagt 420

ggacagcaac ccatcaaagt agctcacatt tcagacactc acgttgattt agactatgaa 480

gctggttcca actatcagtg tagtaaaccg atttgctgta gaccgtacac tgccgaagac 540

gctcccggta atacctctca cccttgtggt ccatggggaa acaccaaatg tgatccacct 600

ttcagattag aagaatcaat ggttgcagcc gtgaatgcct tgaatccttc cttttccatt 660

tacactgggg acgtcgttgc ccatgacata tggctggtca acgaatctga agtattgaca 720

gacttgaacg ctacttactc cttgtttcaa aacttgaatt ccctagttta tgccgctgtt 780

gggaatcacg atgtcgcacc ggtaaacctt ttcccatcca ataagataga ttctgcctat 840

aacccacaat gggcttatga tgctttgaca gcagactggt tggcattaac caatggcgat 900

agtagtgtag cctctgccaa agccgacggc tcatattctg ccatctatcc tggaacaaac 960

ttgaggatta tctcctacaa tagtatcttc tattacaaag ataacttctg gatgtacagc 1020

gaccctatgg aatatgatcc aaacggtcaa ttcgcttggt tgatcgatga gcttcaagca 1080

gctgaaactg caggtcagcg tgtttggttg atttctcata tccccagtgg aaatagtgat 1140

cacctatacg actacagcca ttacttcgat cagatcgtgc agagatacga agctactatc 1200

gcagctttgt tcttcggtca tactcataca gacttgtttc aggtagccta ttcagattat 1260

ggtaatagaa attcagatac cgcttccgct attggatatg tcaccccaag tatgacccct 1320

acctctggcc caccggcatt taggatttac gaaatagacc cagttacttt tggtgtcttg 1380

gactatacgg tttacattgc aaacatttca gatcctgctt atcaaacagg tccctcctgg 1440

cagaagtact attccgctaa agaagtttat ggctccttgc tatctccacc attgaccgac 1500

ccagcagctg aattgacgcc agctttctgg cataatgtta cagtattgat ggaagaagac 1560

gactctgtct tccaagactg gtgggctagg actaccaggg gcttcaatgt gagcacctgt 1620

accggatctt gtgctacgaa cgagatttgc gctcttaggg gtgccgacgc ccagtacaac 1680

tgtgtcaccg ctagcccagg tatccaattt gctaagagag gaggtgctgt agattttgat 1740

cccaatgcac aaccagtagc aaagccccac tgtgacgagg gttctggttt agcccctgtc 1800

ttggtcaaaa tgatgagaaa tacggatgac tttgccggtc tactgaaaga acgtgctgca 1860 ttgcaagatt ctcaacagta a 1881

<210> 370
<211> 1890
<212> DNA
<213> Penicillium jensenii

<400> 370
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgaa 60

acctccaagg ctagtacgga atcattcata tcctccatat gggatgattt caaacaagct 120

gttgattgtg gttcctgtca agccttgctt ggtggcttga aacttgtatc aggcttcggt 180

gagggcttta tgatagatgt tttcattgga ttatgcaacc tttccggagt cgaggatccc 240

gatgtatgca gaggcataat cgagaaagag ggtccagcct tgcatgacgc cttccagaac 300

ttacacatcg gttctcatgc tactcgtacc atgtgcgcat cattgattgg gctttgccaa 360

tacccagaag tgagaccgca caccctacaa tttccatcta gcaaaccaga tactacgagg 420

cctccgcctt ccggtaaatc acccatcaaa gttgtccatt tctcagatac acacgttgac 480

ttgttctatg aaactggggc ttcctatgag tgtagtaagc caatctgctg tcgtgtttac 540

gaagacaaag atgcaccagg cataactaaa acaccatgtg gcccttttgg taatactaaa 600

tgcgatcctc ctcacattct gcaagaaagt atgaatgccg ctattgcaaa gattgatcca 660

gactttagca tctacactgg cgatgttgta gcacacgaca tatggttggt tggacaagat 720

gaggctctac aagtcttcaa tgatacatat ggccaaatgg agaaggattt gggcatggtt 780

tacgctgcca ttggcaacca cgatactgct cccgtcaact tattccctcc aaatgacatt 840

aagggtaagg attcagctca atttgcctac aatgccttag ctgaagattg gtatgcctta 900

acaggaatac cctctgtgaa atctgccgac gaatttggtt cttactcagc aatacatcca 960

aattcaaatc ttaggatcat ttcctacaat tcaatcttct attacaactt caatttctac 1020

atgtaccaag atcctatgga aaaggatcca aacggtcaat tcgagtggtt gatcaaagaa 1080

ttgcaagctg cagaagatgc cggtcaaaga gcttggttaa tcagtcatat accatccggt 1140

gtgaccgacc acttccgtga ttacagtcaa tacttcgacc agattgtcca aagatatgag 1200

gcaactattg caggcttgtt ctatggtcat acgcatatgg acgaattcca aattgcttat 1260 tcagactaca acaatagaaa gtgggacact gctacagcta tgggctacat agctccctca 1320

atgaccccca caagcggtcc tccatctttc agagtctacg aaattgatcc agttacctat 1380

ggtgtactgg atttcactca gtacattgcc aacatatcag atccatccta ccagaccaag 1440

ccggaatggg ttccctacta ttccgctaaa gcagcatatg gatccaaatt gtctccaccg 1500

ttgacagatt ccactgccga attgacccca gcattttggc ataatgttac tgttactatg 1560

gagaaagacc cttccatctt tcaggatttc tgggcaagga gaaatagagg gtggaacatt 1620

gcagcatgta ctggtgactg catgaaaaag gaactttgca ctcttcgtgc tgccgacgca 1680

caacacaact gtcacgaacc aaccccaggc ttaaacatat ccatcaataa gagagatcaa 1740

ggctctggtg atgttccttt agagggcgag aaagtgagtg gtccagaatg tgaccacgca 1800

ggtatggcta ccttgttagg aaagattgcc tatagggcaa ggctggttag agaggctgaa 1860

gaaagagatc cagtcagggc tgaagcataa 1890

<210> 371
<211> 1890
<212> DNA
<213> Aspergillus stramenius

<400> 371
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgaa 60

aactgggtca ataccatctg ggatgagata aaggaaacca tctcttgtgc aggttgtgaa 120

ggtttgttgg gtaccttgaa acttgttgcc ggtctaggac cagacgtctt aaccaacgtt 180

ttgaccgatg tttgcaaatt ggccaaagtc gaagaccccg acgtctgtgc tggcattatc 240

gaagctgagg gtcctgcagc ctactatgtc ttgaagcagt tgaaagtggg gtcccataca 300

tcaaagagct tttgttctca aatggtgggc ctgtgcgatt atccagaagt gcgtccctat 360

aacatttcat tcccaatccc gaagccttca acacatagac ctccacctag tggtcagcct 420

cctatcaggg tagctcacat ttcagatact catgtcgatc gtgcttatga aaccggtgcc 480

aactatgaat gttctaagcc aatatgttgc agagtctaca cagaggacga tgccccaggc 540

aaaacctctt ttccttgtgg cccttatggt catccaaaat gcgaccctcc tttaagatta 600

gaggaaagta tgatggctgc cattgcagct atggatccgg cttttagtat ctatacaggt 660

gacgttgtgc cgcacgatgt gtggtctgta aatcgtaccg aggtcttgca tgatctaaat 720 gcaacttact ctttgttaga tagattaggt cttgtttatg ccgcattggg taaccatgat 780

acggctcccg ttaacctatt ccctagtgag aggattcctg tttcccataa tccacaatgg 840

gcctatgatg ctttagctga agattggaca aatcttgtag atggaccact atctgcccct 900

gtagtccatg ccacagacca attcggctcc tattctgctt tgcaccctgg cggaaaacta 960

aggatcattt cctacaactc tgtattctac tatacgtaca atttctacgc ctatcaggag 1020

cctatggaat atgatccaaa cgggcaattg gcatggttgg tggccgaact gcaggctgca 1080

gaaacagctg gacaaagggt gtggttgatt gctcatattc ccaccggagc agcagatact 1140

ctgagggact actcccacta tctggaccaa atcatccaga ggtatgacgc tactattgcc 1200

gcattgtttt tcggccatac tcatacagat ctgtttcaag tctcatacgc aaatccagca 1260

catccatctg cagattcagc ctctgccgtt ggctacatta ccccctcttt aacacccaca 1320

agtggtcccc cagcctttag gatctatgac atagaccctg ttacatttgc tgttcttgac 1380

tatacagtgt ataccgcaaa catctcaaca ggtgcaactc caaaatggaa caagtactac 1440

agcgcaaaac aaacctatgg tagtttgttg acccctccat tgacagatcc aactgccgag 1500

ttgacaccag cattttggca taatgtcact gcattgatgg aaacagacaa tactgttttc 1560

caggcttggt gggcaaggac tacgagaggc tttaacgtcc cagaatgtaa cgcccagtgt 1620

gcaagggatc agatttgctc cttaagagcc gcagacgccc aatacgggtg cgtgaggggc 1680

acactaagta ttacgaaaag agccggtgat ggtgacggtt tagatttggg aggtgctggt 1740

gccggtggtc ctccaggaag acgtaggcac gtacagtccg ctagaccaca atgcgaagaa 1800

gctggtttgg caagagtttt agccgctgtg attagggaaa cagacgattt gcagggctta 1860

ttgttgcaaa gagcacagtt gtacatataa 1890

<210> 372
<211> 834
<212> DNA
<213> Bacillus pseudomycoides

<400> 372
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat 60

accaacgact gtggcaacga agctcctata ctaaggtgga gtgctgaaga cagacataaa 120 gaaggtgtca attcccactt atggattgtc aatagggcaa ttgacattat gagtaggaat 180

aacaccattg ttaagccaaa tgagacagca ttactgaacg agtggagaaa cgagttagag 240

aatggtatct attcagcaga ctacgaaaac ccatactacg acaatagcac gttcgcatca 300

catttctacg atccagatac tcaaaagacc tacatccctt tagctaaaca ggccaaggaa 360

acaggttcaa agtatttcaa gcttgcaggt gaagcttatc agaacaaaga tatgaagcaa 420

gcattcttct acttaggatt atctttacat tatcttggtg acgttaatca acccatgcat 480

gctgccaact ttacaaactt gtcctatccg atgggctttc atagcaagta tgagaatttc 540

gttgacacca taaaggataa ctacaaagtt gcagatggaa acggctattg gaattggaaa 600

gggacaaatc ctgaagaatg gattcatggt gccgcagccg ctgctaaaca ggattaccca 660

ggcattgtga acgactcaac caaatctgga tttgtgaagg cagcaacttc acaagaatat 720

gccaataagt ggagagcaga agttacacca gccactggta agaggttgac tgaggctcaa 780

cgtgtaaccg ctggctacat ccatctatgg ttcgatacat atgtcaacag ataa 834

<210> 373
<211> 837
<212> DNA
<213> Bacillus mycoides

<400> 373
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcag 60

gagaatgacg gaggtaatag agtgaacatc attcagtatt ggagtgctga ggacaagcac 120

accgaaggtg tcaactctca cttatggatc gtcaatagag caatagacat tatgtccagg 180

aatatgacct tggtaaagca agatcaagtg gcactgttaa acgagtggag aacagatctt 240

gaaaacggca tctattcagc agattatgag aatccgtatt acgataacag cacttttgcc 300

tctcacttct atgatccaga cgacggttct acctatatcc catttgccaa acaagcaaag 360

gaaactgggg ctaagtactt taagcttgct ggagaatctt acaagaataa ggatatgaag 420

caagccttct tctatcttgg cctatcttta cattatctgg gtgatgtaaa ccaacctatg 480

catgcagcca actttaccaa catatcttat ccccaaggct tccactccaa atacgagaac 540

tttgttgata ccatcaagga caattacaaa gttacagatg gtaatggcta ttggaactgg 600

aaaggcgcaa atcctgaaga ttggatacat ggcgctgctg tcgcagccaa gcaagatttt 660

```
cctggtattg tcaatagcaa cacaaagtct tggttcgtca aggctgctgt ttcccaatca      720

tatgcagata agtggagagc agaagtaacc ccaatgaccg gaaaaaggtt gattgaagca      780

caaagagtta cagcaggata catacagtta tggttcgata cctatgtgaa cagataa         837


<210>  374
<211>  837
<212>  DNA
<213>  Bacillus thuringiensis

<400>  374
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac       60

gagaaaaccg aaggtcataa tgtgaacatc attcagtatt ggtccgctga ggacaagcac      120

tccgaaggtg tcaactctca cttatggatc gtcaatagag caatagacat tatgagtaga      180

aatactacca gagtaaagca agatcaagtg gtcctgttaa acgagtggag aacagatgtg      240

gaaaacggca tctattcagc agatcatgag aatccgtatt acgataacag cacttttgcc      300

tctcacttct atgatccaga cgacggttct acctatatcc catttgccaa acaagcaaag      360

gaaactgggg ctaagtactt taagcttgct ggagaatctt acaagaataa ggatatgaag      420

caagccttct tctatcttgg cgtctcttta cattatctgg gtgatgtaaa ccaacctatg      480

catgcagcca actttacaaa tctatcttat ccccaaggct tccactccaa atacgagaac      540

tttgttgata ccatcaagga caattacaaa gttatggatg gtaatggcta ttggaactgg      600

aaaggcattc atcctgaaga ttggatacat ggcgctgctg tcgcagccaa gcaagacttt      660

tcaggtattg ttaatcgtaa cacaaagtct tggttcgtcc aggctgctgt tagtcaatca      720

tatgcagata agtggagagc agaagtaacc ccaatgaccg gaaaaaggtt gattgaagca      780

caaagagtta cagcaggata catacagtta tggttcgata cctatgggaa cagataa         837


<210>  375
<211>  846
<212>  DNA
<213>  Listeria innocua

<400>  375
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttgt       60

tgtgacgagt atttgcaggc tccagccgct ccccacgaca tcgacagtaa actacctcat      120
```

```
aagttatcat ggtctgcaga taaccctaca aatacagatg tcaatactca ctattggttg      180

ttcaaacaag ccgagaagat acttgccaaa gatgttaatc acataagggc caatttgatg      240

aatgagttaa agaatttcga taagcaaata gcccaaggta tctatgatgc agatcacaaa      300

aacccctact atgatacttc cacatttctg tctcactttt acaacccaga cagagacaat      360

acataccttc caggatttgc aaacgccaag ataactggtg ccaaatactt caatcaatcc      420

gtcgcagact atagagaagg gaagtttgat acagcattct acaaactagg tttagctatt      480

cattactata cagacatttc ccagcctatg catgccaaca actttactgc tatatcctac      540

cctccagggt atcattgtgc atatgaaaac tatgttgaca ccattaagca caactatcaa      600

gctacggaag acatggttgt taagaggttc tgctcagatg atgtaaaagt ttggttgtac      660

gagaatgcaa aaagagcaaa ggccgattat ccaaagattg ttaatgctaa gaccaagaaa      720

tcctacttag tcggtaacag taaatggaag aaagatacag tagaaccaac tggagcaagg      780

ctgagagatt cacagcagac acttgcaggg ttcttggaat tctggagcaa gaaaaccaat      840

gaataa                                                                846


<210>  376
<211>  885
<212>  DNA
<213>  Aspergillus egyptiacus

<400>  376
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct       60

cctgcacctt taactagaag ggatgtttct agtgaagtat tagaacagtt aacgctattc      120

gcagagtact ctgctgcttc ttactgccct tccaatttgg attcaccagg aacgaaattg      180

acttgctcaa cagggaattg tcccactgta gaagctgcag ataccgagac tttggcagaa      240

ttctatcatg ccgatgaata tggagacgtt gccggttact tggcagtcga cactacaaat      300

caactattag tagtcgcttt tcgtggaagc cgtgctttgg acacctggat tgccaatttg      360

aactttggta aagattccgt cgatgatcta tgttcaggtt gtgaagtcca tggtggcttt      420

tggcagtcct ggcaagtcgt agcagattct gttgcaagtg gagtcgaaag cgctttgcaa      480

acatatccag actatactat agtctttacc ggtcattcat ttggtggggc agtggccact      540
```

ttaggcgcag tcgagttaag aaatgctggt tatgatattg agctatatcc ttatggagca 600

cctagggttg gtaatgaagc attagctcaa tacataacag atcaaggatc aaactatcgt 660

gtcacacata caaatgatat tgtacctaga ttacctccta tgagctttgg atttagtcac 720

tccagtcctg agtactggat tacctccgac gacgaagtca caccaaccac agcagatgtt 780

gaggtaatcg aaggtgttgg ttctacagag ggtaacgctg gtgaatttcc tcagagtaca 840

gcagcccatt ctcactacat cattgacatt tcagcctgtg aataa 885

<210> 377
<211> 888
<212> DNA
<213> Aspergillus tamarii

<400> 377
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctact 60

cccgcacctt tgaggcgtga tgtatccagt agtctactaa acaacttaga cttgtttgct 120

cagtattctg ctgcagctta ttgctctgag aatttgaatt caaccggtac aaagcttact 180

tgctccgtag gtaattgtcc acttgtagaa ttagcctcca ccaacacact tgacgaattc 240

gatgaatcct cttcatacgg gaaccctgca ggttaccttg ctgcagacga gaccaacaag 300

ttacttgtgt tgtcttttag aggtagctcc gaccttgcaa attgggttgc caacttgaat 360

ttcggtttag aggatgccag cgacctatgt tcaggttgtg aggttcatag tggtttctgg 420

aaggcctgga gtgaaatagc agatacaatt acatccaaag tggaatcagc actttcagat 480

cattcagact attctctggt cttaactggg cattcctacg gtgctgcctt agccgctctt 540

gctgccactg cactaagaaa cgcaggtcat tcagttcaac tttacaacta tggacaacct 600

cgtttaggaa atgaagctct ggctacatac atcacagacc agaacaaagg tgccaactat 660

cgtgttacgc acaccaatga cattgttccc aagttacccc ctacattgtt aggataccat 720

cactttagtc cagaatacta catttcatca gccgatgaag ccacagttac taccgcagat 780

gtgacagagg ttaccggaat cgatgcaact ggcggtaatg atggcacaga tggtacttca 840

atcgatgcac atagatggta ctttatctac atttcccaat gtagttaa 888

<210> 378
<211> 891

```
<212>  DNA
<213>  Aspergillus niger

<400>  378
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgca        60

ccagctccta tgcaaagaag ggacataagt tctacagtac ttgacaacat agaccttttt       120

gctcagtatt ccgcagcagc ttattgttca tccaacatag agtctacggg taccacattg       180

acgtgtgatg tgggtaattg tccattggtt gaagccgctg gtgcaactac cattgatgag       240

tttgatgata ccagttctta cggtgaccca acaggattca ttgcagttga tcctacaaat       300

gagttgattg tgttaagctt cagaggttcc tccgacttgt caaattggat cgcagattta       360

gatttcggct tgactagtgt ttcatcaatt tgtgacggtt gtgagatgca caagggcttc       420

tatgaggctt gggaagttat tgcagacaca ataactagca aagttgaagc agctgtttcc       480

tcatatccag actatacctt agtctttact ggtcacagtt atggcgctgc tcttgcagcc       540

gtggcagcta cagtattgag aaatgctggg tacacactag acttatacaa cttcggtcaa       600

ccaaggattg gcaacttagc actagcagac tacataacag gccaaaacat gggatccaac       660

tatagagtta cacatacaga tgatatagtc ccgaagcttc cacccgagtt acttggttat       720

caccactttt cccctgagta ctggatcaca tcaggcaatg atgttactgt gacaacctca       780

gatgttactg aagttgtggg tgtggattca actgctggca acgacggtac cctgttagat       840

tcaacaactg ctcatagatg gtacaccatt tacatttccg agtgtagtta a               891


<210>  379
<211>  1107
<212>  DNA
<213>  Bacillus luciferensis

<400>  379
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctatt        60

acctccttct ttggcaacta tcaaaaggca ttcgcatgga gtgatgaaga cgttcataat       120

caagatcatt ctacacatca tttcattgtc aatggctcag taaagttgat agccgacaat       180

gccaacccag ccatcaacaa acccacaaca ttactgaacc agttcagaga caggtgggag       240

caaggtcttt atgatgcaga ccacattaac ccattctacg atacagggac gttcatgtca       300

catttctacg atccagatac tcaaacgaac tacaccggtg cttcttatcc gaccgccaga       360
```

```
caatctggtg ccaaatactt caacctagca tcagactatt acaagaaagg agatttcaac      420

aacgccttct actacttagg tgtttcattg cattacttta cggatgtaac acagccatta      480

catgcttcca acattagcaa cttagatcac catgcacctg gttaccactc taagtttgag      540

acttacgctg aaagtattca gaacgaaatg acagttccag acagtggctt atacaattgg      600

atcggatcca cagacccaga ggcttggatc caccaagccg ctgttcaagc caaatccgtt      660

cttccacagg tgtggaatga caccatcatc aattggttct ggcaagctgc ttattccaat      720

tactattccg ctatgtggaa gaatgaagtt aagaatccaa ccctagttca acttaatcaa      780

gccgaacgtg aaaccgcagg gttcatagac atgttcttta gagtcaacgg tgttgaaatg      840

cccgttacag tctacaaaga aaatgccttt ggtggcgtat ctgaattact aggtagtggc      900

aattacgatt acgatcagtt ggtgaagggc ataggtaatg atacaattag ttccattcac      960

attgctccag gctaccaagt tacattgttt tcagacgcca attacaaagg cgctagtatc     1020

gtcttgacaa atgatgttca tgacttaggt aacttttctc accaggtaag ctccatcaag     1080

attgccaaga tatctgcact gaaataa                                         1107


<210>  380
<211>  834
<212>  DNA
<213>  Bacillus mycoides

<400>  380
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcaa       60

acgaacaact ctgaaaaccc aactcctgtg ctaagatggt ccgctgagga caaacacaac      120

gagggggtca gtacacacct atggatcgtc aatagggcta ttgacataat gtcaagaaat      180

acagctattg ttaagccaaa tgaaactgca ttacttaacg agtggaggac cgatttggaa      240

aatggcatat actctgcaga ttatgaaaat ccttactatg acaatggcac atacgcctct      300

catttctatg atccagatac tggtggaacc tacattcctt ttgccaaaca agccaaagaa      360

acaggaacca aatactttaa gttggcagga gaggcttacc aaaatcaaga tatgaagcaa      420

gctttctttt acctgggttt gtccctacac tacttaggtg atgtgaatca acctatgcat      480

gcagccaatt tcaccaactt atcataccct atgggtttcc attccaagta cgagaatttc      540
```

gtagatacag ttaaagacaa ctacatagtt agcgattcaa atggatattg gaactggaaa 600

ggcacaaatc ccgaagattg gattcaaggg agtgccgtcg ctgctaagca agactaccct 660

ggtatagtaa atgatactac taaggactgg ttcgttaaag cagcagtctc tcaagaatac 720

gcagacaaat ggagggcaga agttacacct gtaaccggta agaggttaat ggaagcacaa 780

agagtaacag ctggttacat acacctgtgg tttgatacct acgtaaacag ataa 834

<210> 381
<211> 837
<212> DNA
<213> Bacillus mycoides

<400> 381
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac 60

gagaatgaag gaggcaacaa agtgagggta attcagtatt ggagtgctga ggacaagcac 120

gcagaaggtg tcaactctca cttatggatc gtcaatagag caatagacat tatgtccaga 180

aatactaccg ttgtaaagca agatcaagtg gcactgttaa acgagtggag aactgaactt 240

gaaaacggca tctatgcagc agattatgag aatccgtatt acgataacag cacttttgcc 300

tctcacttct atgatccaga caccggtaaa acctatatcc catttgccaa acaagcaaag 360

gaaactgggg ctaagtactt taagcttgct ggagaagctt accaaaaaca ggagattaag 420

caagccttct tctatcttgg cctatcttta cattatctgg gtgatgtaaa ccaacctatg 480

catgcagcca actttacaaa tctatcttat ccccaaggct tccactccaa atacgagaac 540

tttgttgata ccatcaagaa caattacaaa gttgcagatg gtaatggcta ttggaactgg 600

aaaggcgtaa atcctgaaga ttggatacat ggcgctgctg tcgcagccaa gcaagattat 660

gctggtattg ttaatgggac cacaaaggat tggttcgtca gggctgctgt ttcccaagaa 720

tatgcagata agtggagagc agaagtaacc ttgacgaccg gaaaaagatt agttgaagca 780

caaagagtta cagcaggata catacagtta tggttcgata cctatgtgaa cagataa 837

<210> 382
<211> 837
<212> DNA
<213> Bacillus sp.

<400> 382

atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac 60

gagaatgacg gaggtcatgg tgtgggcgta attcccagat ggtccgctga ggacaggcac 120

aaggaaggtg tcaactctca cttatggatc gtcaatagag gcatagacat tatgagtcac 180

aatactaccg ttgtaaagca agatgaagtg gcactgttaa acgagtggag aacagatctt 240

gaaaacggca tctattcagc agattatgag aatccgtatt acgataacag cacttttgcc 300

tctcacttct atgatccaga caacggtact acctatatcc catttgccaa acaagcaaag 360

gaaactgggg ctaagtactt taagcttgct ggagaatctt accagaataa ggatatgaag 420

caagccttct tctatcttgg cctatcttta cattatctgg gtgatgtaaa ccaacctatg 480

catgcagcca actttacaaa tctatcttat ccccaaggct tccactccaa atacgagaac 540

tttgttgata ccatcaagga caattacaaa gttaatgatg gtaatggcta ttggaactgg 600

aaaggcacaa atcctgaaga ttggatacac gcctctgctg tcgcagccaa gcaagatttt 660

ccttctattg ttaatgacaa cacaaaggat tggttcgtca aggctgctgt tagtcaagat 720

tatgcaaaca agtggagagc agaagtaacc ccaatgaccg gaaaaaggtt aatggaagca 780

caaagagtta cagcaggata catacagtta tggttcgata cctatgtgaa cagataa 837

<210> 383
<211> 849
<212> DNA
<213> Bacillus drentensis

<400> 383
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgcc 60

agggtaaatc acgatagtag ttatgacagc ggcatcatca tatcacctta ctggagcgct 120

gaagagatgc atacagaggg caagaatact catttgtgga ttgtcaatag agcaattgac 180

attatggcac gtgataacac cgttgttaaa gaaaacgaag tcgccttatt gaatgaatgg 240

agaacggatc tggaagacgg catatacact gcagactatg aaaatcccta ctatgacaac 300

ggtacttttg ctagtcactt ttacgatcca gataccgacg atacgtatat cccatttgca 360

aagaatgcaa aagttacagg tgtaaagtac tttaagttag ctggggaagc ttaccagcag 420

caagcaatga atcaggcctt cttttaccta ggcttgtctc tacactactt tggtgacatc 480

aatcaaccca tgcacgcatc caactttacc aacatttcac atccattcgg cttccactct 540 aagtatgaga actttgttga taccatcaaa gcaccatata gtgtaacaga tggtaatggg 600

tattggaact ttgctggcga aactccggaa gaatggttac atactgctgc tgtggcagca 660

aagcaagatg cacctggcat tgttaatgaa acaacaattt catggttctt acaagcagca 720

tttagtcaag agtacgcaga tatgtggaga gctgaagtaa ctccagaaac aggagccagg 780

ttgattgagg cacaaagggc aatggctggc tacatacatc tgtggtttga cacatatgtc 840

aacttataa 849

<210> 384
<211> 885
<212> DNA
<213> Aspergillus turcosus

<400> 384
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct 60

cccgcaggat tggcagagag agatgtcagt gcaagtgtcc ttcaagaact atctttgttt 120

gctcagtatt ctgcagctgc ttactgtacc aataacatca attccacagg aaccaagttg 180

acgtgctcag ctggaaattg tcccttagtc gaagctgcca acacaaaaac ccttgctgag 240

ttctatgact cagatagttt cggggatacc gctgggttct tggtagccga cactaccaac 300

aaacttctgg ttgtttcttt tagagggtcc cgtaccttag acaattggat cgccaactta 360

gattttgttc tggatagcat ctccgacatt tgttcaggtt gcgctgcaca cggtgggttc 420

tggaagagtt gggaagtagt agcaaattct ttaaccactg agttgaattc agccgtcaat 480

acttatccag gttatacgat tgtctttacg ggtcacagtt taggtgccgc tctggctacg 540

ttaggcgcta caaccttgag gaaggctggt attccagtac agttgtacaa ttacggtagt 600

ccgagagtag gtaacaaagc cttggcaacc tacataacgg ctcaaggacc caattacaga 660

gtgactcaca cgaacgatat cgttccaaga cttccacccc agagttttgg ttttagtcat 720

ctatctcctg agtattggat tacatcaggt gacaatgttc ccgtcactac ttccgacatt 780

acggtaatcc aaggcataga ctcaaatgct ggcaatagtg gtgaggacat tacttctatt 840

gaggctcaca attggtacat tggtaacatt gatgcctgtc cataa 885

<210> 385

```
<211>  888
<212>  DNA
<213>  Talaromyces subinflatus

<400>  385
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgtc       60

ttatcaccaa ttggaagaag aactgtcact acaacacaat tagatgacat gaacttattc      120

gcccagtatt ctgctgccgc atactgttca gccaacttga attcaacggg tagcgctctt      180

gcatgtaacg ttggtaactg tcctttggtt gaaggtgcag acactaccat cttatacgat      240

tttgacgaat ctgcaggatt cggtgacgct accggctaca tagccgttga tgaaactcac      300

aaatccatca ttttggcctt tcgtgggtct tcagacctag acaattggat tgcagacttg      360

gatatacctc tagtcgcttc tagtatttgt ttaggttgtg aagttcatca gggtttctgg      420

gacacctggc agacagttgc atcagatgtc accagtcaag ttgagtatgc tttaagtgct      480

tatgcaggtt atacctttgt tgtcacaggt cattctatgg gtgcagccct tgctgctatc      540

gcagccacgg tctttagaga ttctggttat actgtggagt tatacaacta tggccaaccc      600

agaattggta acttgatttt ggcttactac ataacaaatc aaaatcacgg tagcaactat      660

agagttacac atacagatga tattgttcct aaactaccgc ctgaattact tggctacgac      720

catttctccc cagaatactg gatcacgtca ggcgataatg tcacagtaac agattccgat      780

atcgatgtta ttgttggtat tgactctgcc gatggtaatg atggcaccat cgatgacagc      840

gtagaagctc atcattggta ctttgtttac atttctgaat gttcctaa                   888


<210>  386
<211>  891
<212>  DNA
<213>  Aspergillus tubingensis

<400>  386
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgca       60

ccagctccta tgcaaagaag ggacataagt tctacagtac ttgacaacat agaccttttt      120

gctcagtatt ccgcagcagc ttattgttca tccaacatag agtctacggg taccacattg      180

acgtgtgatg tgggtaattg tccattggtt gaagccgctg gtgcaactac cattgatgag      240

tttgatgata gtagttctta cggtgaccca acaggattca ttgcagttga tcctacaaat      300
```

```
gagttgattg tgttagccct gagaggttcc tccgacattt caaattggat cgcagattta      360

gatttcggct tgactagtgt ttcagacatt tgtgacggtt gtgagatgca caagggcttc      420

tatgaggctt gggaagttat tgcagacaca ataactagca aagttgaagc agctgtttcc      480

tcatatccag actattccat tgtctttact ggtcacagtt atggcgctgc tcttgcagcc      540

atcgcagcta cagtattgag aaatgctggg tacacactag acttatacaa cttcggtcaa      600

ccaaggattg gcaacttagc actagcagac tacataacag accaaaacat gggatccaac      660

tatagagtta cacatacaga tgatatagtc ccgaagcttc cacccaagtt acttggttat      720

caccactttt cccctgagta ctggatcaca tcaggcaatg atgttactgt gacaacctca      780

gatgttactg aagttgtggg tgtggattca acagatggca acgacggtac cctgttagat      840

tcaacaactg ctcatagatg gtacaccatt tacatttccg agtgtagtta a               891


<210>  387
<211>  1110
<212>  DNA
<213>  Bacillus acidiceler

<400>  387
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctatc       60

acatccttgt tttcaaacga tcagaaggct tttgcctggt ccgacgaaga tgtacataat      120

caagatcata gcacccatca cttcatagtc aacggctctg tcaaattgat tgcagacaat      180

acaaaccctg ccatcaacaa acctactacg ttgttgaatc agtttagaga tagatgggaa      240

caaggcttat acgacgcaga tcatatcaac cctttctatg acaccggtac tttcatgagc      300

cacttttacg atccagacac acaaaccaat tacacaggcg tttcatatcc aactgctcgt      360

caaagcggtg gcaagtattt caaccttgca tccgactact acaagaaagg tgacttctac      420

aatgccttct attacttggg cgtgtcacta cactacttta cagatgtgac ccaaccttta      480

catgcctcca acatttcaaa cctggaccat aacgctcccg gataccactc taagtttgag      540

aactatgcag agtctattca gaatcagatg gccattccag attccggttt gtacaactgg      600

attagtagca ccgatcctga ggcctggata caccaagccg ctgtacaagc taaatctgtt      660

ctgccacagg tttggaatga caccatcatc aactttttct ggcaggctgc atattccaac      720

tattacagtt ccatgtggaa gaatgaagta aagaatccaa ctttagttca attgaatcaa      780
```

```
gccgagaggg agactgctgg tttcattgat atgttctttc gtgtcaatgg cgtagagatg      840

cccgtgaaag tgtacaaaga gaatgctttt ggtggtgcct cagagatttt gggtctaggc      900

aactatgatt atgaccaatt cgtaaaagga ataggaaatg atactatatc ttcaattcat      960

attgccccag gctaccaagt caccttattc tccgacgcca actacaaagg cactagcacc     1020

gttttgactg gggatgtaaa cgacttgggc aactttaacc atcaagttag tagtcttaag     1080

attgtcaaga tatccgcaat atcaaaataa                                      1110


<210>  388
<211>  837
<212>  DNA
<213>  Lysinibacillus xylanilyticus

<400>  388
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac       60

gagaattgct accaagatcc tcccatacct ttgaagtgga gtgccgaaag tatccacaac      120

gagggcgtat cctcccatct gtggattgtc aatagagcta tagacataat gtctcagaat      180

actactatcg ttaaacaaca tgaaacagac ctactgaatg agtggagaac agatttggag      240

gaaggcatct attctgcaga ttatcaaaac ccatactatg acaattccac gtttgctagt      300

cacttctatg atccagattc cggcaaaacc tacattccct ttgctaagca agctaaacaa      360

accggtgcca aatacttcaa actagccggt gaagcttatc agaacaaaga cttgaaaaac      420

gcattcttct atttgggcct aagtttgcac tatttggggg atgttaatca acctatgcat      480

gctgccaact ttaccaacat atcccatcca ttcggtttcc actccaagta tgagaacttt      540

gtagatactg tcaaggataa ctatcgtgtt acagatggaa atggttactg gaattggaaa      600

tctgccaatc cagaagaatg ggtgcatgcc agtgctgttg ccgcaaaggc cgacttcttg      660

ttgattgtta atgataacac cgaaagtggt tttctaaaag ccgctgtttc tcaagattca      720

gcagataagt ggagagctga agtaacacct gttacgggaa aaagattgat ggaagctcaa      780

agaattactg caggatacat ccacttatgg ttcgacacat acgtaaacaa caaataa         837


<210>  389
<211>  837
<212>  DNA
```

```
<213>  Bacillus toyonensis

<400>  389
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac       60

gagaatgaag acgtcaacta taacgcacct attcttagat ggagtgctga ggacaagcac      120

aaggaaggtg tcaactctca cttatggatc gtcaatagaa gtatagatat gatgtccaga      180

aatactacca ttgtaaagaa gaatcaagtg gcactgttaa acgagtggag aactgaactt      240

gaaaacggca tctacaatgc agatcatgag aatccgtatt tcgataactt cacttttgcc      300

tctcacttct atgatccaga aaccggttct acctatatcc cattagtgtc tactcaagca      360

aaggaagccg gttccaagta tttcaagttg gcaggtgaat cctacaaaaa gaatgatatg      420

aaacaggcct tcttttacct aggcttgtca ttgcattact tgggtgatgt caaccagcca      480

atgcatgctg ccaactttac aaacttgtct tacccacagg gcttccactc taagtatgag      540

aactttgttg acaccataaa ggataactac aaagtaaatg atggtaacgg ttattggaat      600

tggaagggtt caaatccagg tgactggatc cacggtgctg ccgttgctgc caagaaagac      660

tatactggta ttgttaacga cacaaccaaa gattggttcg tcaaagctgc tatatcatca      720

gaatatgcag acaaatggag agcagaagtc actccggcaa caggtaaaag attgatggaa      780

gcacaaagaa taacagcagg gtacatacaa ctttggtttg acacatacgc caattaa         837


<210>  390
<211>  837
<212>  DNA
<213>  Bacillus wiedmannii

<400>  390
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac       60

gagaatgacg gaggttccaa aatcaagatt gttcacagat ggagtgctga ggacaagcac      120

aaggaaggtg tcaactctca cttatggatc gtcaatagag caatagacat tatgtccaga      180

aatactacct tggtaaagca agatagagtg acccagttaa acgagtggag aactgaactt      240

gaaaacggca tctatgcagc agattatgag aatccgtatt acgataacag cacttttgcc      300

tctcacttct atgatccaga caacggtaaa acctatatcc cattagccaa acaagcaaag      360

gaaactgggg ctaagtactt taagcttgct ggagaatctt acaagaataa ggatatgaag      420
```

caagccttct tctatcttgg cctatcttta cattatctgg gtgatgtaaa ccaacctatg 480

catgcagcca actttacaaa tctatcttat ccccaaggct tccactccaa atacgagaac 540

tttgttgata ccatcaagga caattacaaa gttacagatg gtaatggcta ttggaactgg 600

aaaggcacaa atcctgaaga atggatacat ggcgctgctg tcgtcgccaa gcaagactat 660

tcaggtattg ttaatgacaa cacaaaggat tggttcgtca aggctgctgt ttcccaagaa 720

tatgcagata agtggagagc agaagtaacc ccaatgaccg gaaaaaggtt aatggatgca 780

caaagagtta cagcaggata catacagtta tggttcgata cctatgggga cagataa 837

<210> 391
<211> 864
<212> DNA
<213> Listeria seeligeri

<400> 391
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttgt 60

ggcgacgagt ccattaagga ccaaatcgct ccacacgcta ttcaaaacaa gttaccatct 120

aagttgggtt ggagtgctga acatccatcc aaagacgaga tcaataccca cttgtggttg 180

tttaaccaag cagagaagat cttagctaaa gatgtgactg gggctcagtt agatctggtt 240

agagagttga agaactacaa caaagaaatc gctcaaggca ttttcgatgc agaccacaag 300

aatccttact atgacaaaaa cacttttcta agtcatttct acaatcctaa aacacacaaa 360

acttacatac cagggtttcc aaacgcaaag gatacaggta ctaagtactt caacatatcc 420

gtcgaagaat accaagatgg caatttcgaa aaagctttct ataacctagg cctagctatc 480

cactactata cagatgtcag tcaacctatg cacgccaaca actttacagc tctatcacat 540

cctgttggtt accattgtgc atatgaaaac tatgtggaca cctttaagca aatcttccaa 600

gcttcagctg aatctgaagc taagtggttt tgcacagatg acataagtga atggtatcac 660

gaaaatgcta aaagggcaca agcagattat cctaagattg tgaacgccat catcaagaaa 720

tcctacatac aaggtctatc agacagccaa aaagatagga cctggaagaa agccgtcaga 780

gctgcaacag ggaagagact tagagatagt caagaaactt tagccggatt cttagagttt 840

tggtatgcta agacaaacga ataa 864

```
<210>  392
<211>  885
<212>  DNA
<213>  Penicillium swiecickii

<400>  392
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct       60

cctagtagac ctgttccaag ggatgtttct acctctgtct tatctcagtt aagtctattc      120

gcagagtact ctgctgcttc ttactgctcc aacaacatca attcaactgg aaacgctctg      180

tcttgcgaag cagggaattg tccctctgta caatctgcag atactaccac tttgtgggaa      240

ttcgatagaa cgtgttctta tggaaacgtt gccggtttct tggcagtcga caaaaccaac      300

aaactattag tagtctcttt tcgtggaagc cgttctatta gtaactggat tgccaacatt      360

aactttggtt taacagatgc accatctcta tgttcaggtt gtgaagcaca ttctggcttt      420

ctagagtcct gggaaaccgt agcagatgac ttaactacca acatcaaaag cgctcaatca      480

acatattctg gctatactct agttttgacc ggtcattcat ttggtggggc agttgccgct      540

ttaggcggaa ccgccttaag aaatggtggt tctactttga acgtctatac ctatggacag      600

cctagggttg gtaatggagc attagcttca tacataacaa atcaaggatc actatggcgt      660

gtcacacata cagatgatat tgtacccaag ttacctcctt ccagctttgg atttagtcac      720

cctagtcctg agtactggat tacctccgag aacgaagtca cagttacctc atccgatgtt      780

gaggtaatcg aaggtgttgg ttctaaaagc ggtaacgctg gtaccttaaa ccccgacgta      840

gaggcccaca attggtattt gggctacatt gatgggtgtc aataa                      885


<210>  393
<211>  888
<212>  DNA
<213>  Talaromyces boninensis

<400>  393
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgtc       60

cctacaccag ttacaagaag aactgtctct acagcattgt tagatacgct agacttattc      120

gcccagtatt ctgctgccgc atactgtcct gccaacttca attcaagctc tacgtctctt      180

gcatgtagcg ctggtaactg tcctactgtt caagctgcag acactaccat cttatactca      240

tttgacaaat ctgcaagttt cggtgacgct accggttatg tcgccgttga caatacaaac      300
```

```
cagttgatag ttattgcctt tcgtgggtct tcagacctat ccaattggat tgcaaacttg      360

gatgtacctt tcaccgatgc tggcaacatt tgttcaggat gcgaagttca ctctggcttc      420

tacgacactt ggcaaactgt agcttcagac atcacagcaa ctgtggattc tgcattatca      480

acttaccctg gttacactgt tgtcgctact ggacattcac tgggaggtgc cttggctgcc      540

ataggtgcca cagtcttaag atcttctggt caagtggtcc aactatatga ttacggacag      600

ccaagaattg gcaacttagc tttagcagac ttcattacaa gtgaaaccgc tgggtccaac      660

tatagagtaa ctcatagtga tgatattgtc cctaagctgc ctcctgaatt cctaggatac      720

gcacacttct ctccagagta ttggatcaca tccggtgata acgtagcagt tacagacgca      780

gacattgttg aagttattgg tgtggatagc actgcaggta atgacggcac gtttggcgac      840

tccatcaatg cacatttgtg gtactttgag gctattagtg cttgctaa                  888


<210>  394
<211>  891
<212>  DNA
<213>  Hamigera striata

<400>  394
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct       60

cccgcaccta ttctacgtag agatgtcagt gcaagtgtcc ttaatgaact agatttgttt      120

gctcagtatt ctgcagctgc ttactgttcc tcaaacatag gttccacagg aaacaagttg      180

atgtgcaatg ttggaaattg tcccagagtc gaagcctccg acacagtaac catcgatgag      240

ttcaatgagt ctgcaagtta cggggatgtc gctgggtaca ttgcagtgga caacacaaat      300

caacttctgg ttttgtcttt tagagggtcc agctccttat caaattggat cgccaacatt      360

gatgttgatt tgacagacgc ctccagttta tgttcaggtt gcgaagtaca ctctgggttc      420

tggagcgcat ggcaaacagt acaaggaact attacctcta agttagaatc agccagagca      480

tcatatccag gttatacgtt ggtctttacg ggtcacagtt atggtgccgc tctggctggc      540

ttagccgcta caaccttgag ggacgctggt tggactatac agttgtacaa ttacggtcaa      600

ccgagattag gtaacttagc cttggcacag tacataacgt ctcaaacaca gggttccaat      660

tacagagtga cgcacacaga cgatattgta cctaagcttc ctcctgagtt cttaggatat      720
```

```
gaccattact ctccagagta ttggataaca tccggtgata acgtcactgt taccacttca      780

gacgtacagg ttatcgaagg gattgactcc gtcgctggaa atgacggaac ttcagatgat      840

tccactgaag ctcatcaatg gtatttcatc tatatcagtg aatgttcata a               891


<210>  395
<211>  1113
<212>  DNA
<213>  Bacillus sp.

<400>  395
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctatt       60

acatccttat tcggaagctt ccaaaaagcc ttcgcctggt catgtgatga tccacataat      120

caagaccagt caacccactt attcatagtc aacaatggtg tcaagttgat ttcaggaaac      180

gcagatcctg ccataaacaa accgtccaca ttgttggaac agtttagaga tagatgggaa      240

caaggactgt atgatgcaga ccacataaac cctttctacg atactagtac attcatgtca      300

cacttctatg acccagatac tcaaaccaat tacgctggta gatcttatcc aacggctcgt      360

caatcaggtg ctaagtactt caatctagcc tccgactact acaagaatgg agacttttac      420

aatgctttct attaccttgg tgtctcatta cactacttta ccgacgcaac aatgccactt      480

catgcatcca atatcagcaa cttagaccat caggcaccag ggtatcattc taagttggaa      540

tcatactctg aaagcattca ggaccaggtt acagtccccg attctggact attcaattgg      600

gtgagttcta cagacccgga actatggatt caccaagcag ctgttcaagc taaaagcgtt      660

cttccacagg tttggaatga ctccatcatt tcctggttct ggcaagctgc atactcaaac      720

tattactcag atatgtggaa atccgcagtt aaagctccca ttttgaatca gttaaaccag      780

gcagagagag aaactgcagg cttcatagac atgttcttca gactaaatgg ggtcgagatg      840

ccagtgacag tttactcaga aactgctttt gggggagctt ctgaattgct aggctcaggc      900

aactatgact atgaccaatt ggtaaaagga ataggaaatg atgctatttc atctattcac      960

attgctcccg gttaccaggt aacgcttttc gccgattcca attactcagg tgcctctaaa     1020

gttttgacag cagatgcctc agatttggat aacttcaaca aaaccataag ttccttaaag     1080

attgaaaaga tacaacctgt aaacgttcac taa                                 1113
```

<210> 396
<211> 837
<212> DNA
<213> Bacillus thuringiensis

<400> 396
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac   60

gagaatgcag gaggtcaaag agtgggcgta attcccagat ggagtgctga ggacaagcac   120

aaggaaggtg tcaactctca cttatggatc gtcaatagag caatagacat tatgtccaga   180

aatactacca ttgtaaagca agatcaagtg gcactgttaa acgagtggag aacagatctt   240

gaaaacggca tctattcagc agattttgag aatccgtatt acgataacag cacttttgcc   300

tctcacttct atgatccaga cagtgagaaa acctatatcc cattagccaa acaagcaaag   360

gaaactgggg ctaagtactt taagcttgct ggagaatctt accagaataa cgatatgaag   420

caagccttct tctatcttgg cctatcttta cattatctgg gtgatgtaaa ccaacctatg   480

catgcagcca actttacaaa tctatcttat ccccaaggct tccactccaa atacgagaac   540

tttgttgata ccatcaagga caattacaaa gttacagatg gtactggcta ttggaactgg   600

aaaggcacaa atcctgaaga ttggatacat ggcgctgctg tcgtcgccaa gcaagactat   660

tcaggtattg tcaataacaa cacaaaggaa tggttcgtca aggctgctgt ttcccaagaa   720

tatgcagata agtggagagc agaagtaacc ccaatgaccg gaaaaaggtt gattgatgca   780

caaagaatta cagcaggata catacagtta tggttcgata cctatgtgaa cagataa   837

<210> 397
<211> 837
<212> DNA
<213> Bacillus mycoides

<400> 397
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac   60

gagaattgtc accaagatcc tcccatagca ttgaagtggt ctgccgaatc catccacaac   120

gagggcgtaa gtagtcatct gtggattgtc aacaaagcta tagacataat gtctcagaat   180

actactgtcg ttaaacaaaa tgaaacagcc ctactgaatg agtggagaac agatttggag   240

aagggcatct attctgcaga ttatcaaaac ccatactatg acaatagtac gtttgcttcc   300

cacttctatg atccagatag tggcaaaacc tacattccct ttgctaagca agctaaacaa   360 accggtgcca aatacttcaa actagccggt gaagcttatc agaacaaaga catgaaaaac 420

gcattcttct atttgggcct atccttgcac tatttggggg atgttaatca acctatgcat 480

gctgccaact ttaccaacat aagtcatcca ttcggtttcc acagtaagta tgagaacttt 540

gtagatactg tcaaggataa ctatcgtgtt acagatggaa atggttactg gaattggcaa 600

tctaccaatc cagaagattg ggtgcatgcc tccgcttctg ccgcaaaggc cgattttcct 660

tcaattgtta atgataacac caaaaactgg tttctaaaag ccgctgtttc tcaagattca 720

gcagataagt ggagagctga agtaacacct gttacgggaa aaagattgat agaagctcaa 780

agaattactg caggatacat ccacttatgg ttcgacacat acgtaaacaa caaataa 837

<210> 398
<211> 837
<212> DNA
<213> Fictibacillus macauensis

<400> 398
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat 60

gagaatgaag gggtaacaa agttagggta atacagtatt ggtctgccga agatccacat 120

catgaagaca caaacactca cttatggata gtccgtcatg caatggagat tatggccaac 180

aacaaagatg ttgtgaaacc aggcgaagtc gagcaactaa aacaatggca atcagaccta 240

gaacaaggca tttacgatgc agatcatgcc aacccgtatt acgataacgc aacgttcgct 300

tcccatttct atgatccaga cactggtaag tcatacatcc ccttggcagc acacgcaaaa 360

acaaccagcg tcaaatactt caaaagagct ggggaagcat accaaaaggg tgatcataaa 420

caagcctttt acaatcttgg tctggctctg cattacatag gtgatctaaa ccagccaatg 480

catgcagcca atttcacaaa cttatcttat cctcaaggat tccattccaa gtatgagaac 540

tatgttgata gcttcaagga ggattatgct gtcaaagatg gagagggtta ctggcattgg 600

aaagggacca acccggaaga ctggttgcac ggtacagctg ttgctgccaa gaaagattat 660

ccagacatcg taaatgatac aaccaaagcc tggtttgtaa aagcagcagt ctcaaactct 720

tatgcagcta aatggagagc tgccgttgtt cccgcaacgg gcaagaggtt aacagaagcc 780

caacgtatct tggctggtta catgcaacta tggtttgata cttatgtgaa caaataa 837

```
<210>  399
<211>  864
<212>  DNA
<213>  Listeria seeligeri

<400>  399
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagcttgt       60

ggcgacgaga gtgtaaagga ccaaatcgct ccacacgata ttcaaaacaa gttaccatct      120

aagttgggtt ggtccgctga acatccatcc aaaaacgaga tcaataccca cttgtggttg      180

tttaaccaag cagagaagat cttagctaaa gatgtgactg gggctcagtt agatctggtt      240

agagagttga agaactacaa caaagaaatc gctcaaggca ttttcgatgc agaccacaag      300

aatccttact atgacaaaaa cacttttcta tcccatttct acaatcctaa aacacacaaa      360

acttacatag ctgggtttcc aaacgcaaag gatacaggta ctaagtactt caacataagt      420

atagaagaat accaagatgg caatttcgaa aaagctttct ataacctagg cctagctatc      480

cactactata cagacatatc ccaacctatg cacgccaaca actttacagc tctatcacat      540

cctgttggtt accattgtgc atatgaaaac tatgtggaca cctttaagca aatcttccaa      600

gcttcagctg aatctgaagc taagtggttt tgcacagatg acgtctccga atggtttcac      660

gaaaatgcta aaagggcaca agcagattat cctaagattg tgaacaccat catcaagaaa      720

tcctacatac aaggtctatc agacagccaa aaagatagga cctggaagaa agccgtcaga      780

gctgcaacag ggaagagact tagagattcc caagaaactt tagccggact tttagagttt      840

tggtatacaa agacaaacga ataa                                             864


<210>  400
<211>  885
<212>  DNA
<213>  Penicillium donkii

<400>  400
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct       60

cctgcaagac ctgttccaag ggacatttct tcctccttgt tagatgagtt aacgctattc      120

gcagagtacg ctgctgcttc ttactgctcc aacaacattg attcaactgg agacgctgtg      180

acttgctcag gagactattg tcccttggta caatctgctg gtgcaaagac tttgtatgaa      240
```

ttcaatgata gcactgaatg gggagacgtt gccggtttct tggcagtcga cactaccaac 300

aaattgattg tactatcttt tcgtggaagc cgttctattt ccacctggat tgccaatttg 360

gactttggtt taacagatac ctcttctcta tgtgatgatt gtgaagcaca ttctggcttt 420

tggaagagtt gggaaaccgt agcagatgat atgactgccc aaatagaaag cgctcaatca 480

agttatccat cctatactct agttttgacc ggtcattcat ttggtgccgc agttgccgct 540

ttaggcgcaa ccgccttaag aaatgctggt tatactttgg acttgtatac ctatggacag 600

cctagggttg gtaatgaagc attagctact tacatgacat ctcaaggatc actatggcgt 660

gtcacacatg aagatgatat tgtacccaag ttacctccta tgagctgggg attttcccac 720

gcatcccctg agtactgggt taccagtgac agcgatgtca cagttaccac aagtgatgtt 780

gaggaagtgg ttggtgttga ttctacagcc ggtaacgctg gtacttcagg cgagtccatt 840

tctgcccaca attggtactt tgttgaaatt gatgggtgtg attaa 885

<210> 401
<211> 888
<212> DNA
<213> Hamigera paravellanea

<400> 401
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct 60

cccgcagcag ttaggcgtga tgtaagtgca ggagtcctag ccaacttaga cttgtttgct 120

cagtattctg ctgcagctta ttgcgattcc aatttgaatt cagacggtac aaagcttact 180

tgccaggctg gtaattgtcc acttgtagaa gctgccgaca ccgaaacact tgacgaattc 240

gatatgaccg ctacatacgg gaacgtagca ggttacatcg ctgtagaccg taccaataga 300

ttacttgtgt tggcttttag aggtagcgcc agcatctcaa attggattgc caacttgaac 360

ttaggtttaa cggatgcctc tgccctatgt gcaggttgtc gtgttcattc cggtttctgg 420

gaagcctggc aaacagcaga agctacaatg tcagacatta tcgcttcagc agcccaaaca 480

tatccaggtt atactctggt tgcaactggg catagttacg gtgctgcctt agccgctatc 540

gctgctacca aattcagaaa cgagggttat gctgttgaac tttacgatta tggacaacct 600

cgtataggaa atctagctct ggctcaatac atcacaaacc aatcttctgg tggcaacttt 660

cgtgttacgc acaccaatga cattgttccc aagttacccc cagattggtt aggatactct 720 cactttggac cagaatactg gattacatca ggcgatggta tccctgttac taccgcagat 780

gtggaagtga ttagtggagt ggatgcaact ggcggtaatg atggcgcaga aggtacttca 840

gtggatgcac atagatggta ctttgtgtac attagtcaat gtgaataa 888

<210> 402
<211> 891
<212> DNA
<213> Talaromyces lecycettanus

<400> 402
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct 60

ccagctccag ttcttaggag agatgtatct tcctctgtat tgtctgagct ggacttattc 120

gctcagtact ctgccgctgc atattgctct tccaatatcg gttctccggg tacgaagctt 180

acttgtagtg tcggtaattg tccccgtgtt gaagctgccg atacagagac gttgatagag 240

tttaacgaat catcttcttt tggtgatgtg actggctata tcgctgtgga taggaccaat 300

tcactactgg tgttggcatt taggggctct tccacagtgt caaattggga agcagatcta 360

gattttccat taacagatgc ttctagtctg tgcagtggct gtgaaattca ctctggtttt 420

tgggctgcct ggcaaaccgt acaggcatcc atcactagca cattggagtc agctattgct 480

tcttaccctg gttatacttt ggtcttcaca ggtcattcat acggtgccgc tttggcagca 540

atagcagcaa ctacattgag aaatgctggt tacacaatcc agttgtacga ctatggccag 600

ccgaggttag gtaatcttgc tctggcccag tacattacgg cacaaacaca gggtgccaac 660

tatcgtgtta ctcataccga tgacatcgta cccaaactac cccctgagtt gtttggctat 720

caccacttct ccccagagta ttggataacg tcaggcgata atgttacagt tacaactagc 780

gatgtgcaag tagtcactgg aattgacagt acagctggaa atgatgggac tttgcttgat 840

tctacaagtg cccatgattg gtacattgtc tacattgatg ggtgcgatta a 891

<210> 403
<211> 1407
<212> DNA
<213> Paenibacillus sp.

<400> 403
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctatt 60

acttctatct ttggcaatag ccaagacgct tacgcatggt cagcagacga cccacattct 120

caggactttt ccacacactt gttcattgta aatggaggcg tcaaattgat ttctggtaat 180

gttgatagcg ccataaacaa atcttctacc ttgttggaac agtttcgtgg aagatgggaa 240

cagggccttt acgatgccga tcatcttaat cccttctatg atagctcaac ctttatgtca 300

cacttctatg atccagatac ccaaacgaac tatgcaggat tatcataccc aacagctaga 360

caatctggtt ccaaatactt caaagtcgcc tcaaactact acaagaatgg tgatttctca 420

aacgccttct actatctggg agtaagtctt cactacttta cagactcaac tatgcctcta 480

cacgcatcag acattagtaa cctagatcat agagccccag gctaccacgc caaattggaa 540

gaatatgcca catccataca aaatcagatc aatgttccgg atagcggctt attcaattgg 600

atttccagta cagatcctga actatggatt catcaggctg ctgtacaagc caaatctgtg 660

atgccagaag tcttcaatga cacgattacc gattggtttt ggaaagccgc tttttcctat 720

tactattccg atatgtggaa atccgctgtc aaaatcccta tactaaatca gcttaatcaa 780

gcagaaagag aaacagccgg ttacattgac ttgttcttta ggttaaacgg tgtggatatg 840

ccggttgccg tgtacaaagg gactgcattt ggtggggcac tacaacttct gggtttcggc 900

aactatgatt acgaccaact tgttaaaggt ataggtaatg atacagttag ttcaattagg 960

atagcaccgg gttaccaagt aactttgttc gcagattcca attactcagg agttagcaag 1020

gtgttaacgg cagacgcttc agatttgggt aacttcaata agacaacatc ttccttgaag 1080

attgagaaga ttcaaccagt tactgtctat acagatgctt catttagtgg gagtagccaa 1140

tcattttccg taggaaatca tgattacaac gaaatcgtta acagaaagtt gaatgatact 1200

atttcttcta taagaatagc ccctgggtat caagtcacct tgtttagaga cagcaactat 1260

tctggggttt ctactgtagt taccggtgat gtgtatggtt tatcaaactt aaacgaccaa 1320

acaagtagcc taaaagtgga ggttattcca acaaatccgg caccatccca aacgaaacag 1380

tccatctttt ccaatccctt gaattaa 1407

<210> 404
<211> 837
<212> DNA
<213> Bacillus toyonensis

<400> 404
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac   60

gagaatgacg gaggtcaaag agtgggcgta attcccagat ggtccgctga ggacaagcac   120

aaggaaggtg tcaactctca cttatggatc gtcaatagag caatggacat tatgagtaga   180

aatactacct tggtaaagca agatagagtg gcactgttaa acgagtggag aactgaactt   240

gaaaacggca tctatgcagc agattatgag aatctgtatt acgataacag cacttttgcc   300

tctcacttct atgatccaga caacggtaaa acctatatcc catatgccaa acaagcaaag   360

gaaactgggg ctaagtactt taagcttgct ggagaatctt acaagaataa ggatatgaag   420

caagccttct tctatcttgg cctatcttta cattatctgg gtgatgtaaa ccaacctatg   480

catgcagcca actttacaaa tctatcttat cttcaaggct tccactccaa atacgagaac   540

tttgttgata ccatcaagga caattacaaa gttacagatg gtaatggcta ttggaactgg   600

aaaggcacaa atcctgaaga ttggatacat ggcgctgctg tcgtcgccaa gcaagattat   660

gctggtattg ttaatgacaa cacaaaggat tggttcgtca gggctgctgt tagtcaagaa   720

tatgcagata agtggagagt agaagtaacc ccaatgaccg gaaaaaggtt aatggatgca   780

caaagagtta cagcaggata catacagtta tggttcgata cctatgggaa cagataa   837

<210> 405
<211> 837
<212> DNA
<213> Bacillus thuringiensis

<400> 405
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgat   60

gagcacacca caaacaacaa gattgacata ttccaacctt ggtcaaatga agaaaatcat   120

aaagaaggca agaattcaca tctttggatc gtaaacggag caatcgacat aatgagtaga   180

aacaccacaa ttgtaaaaca agagaatcta gctctgcttc agcaatggag gacccatctt   240

gaaaatggct tgtatgtcgc cgactatgag aatccgtact atgatagcgg gacctttgca   300

tcacacttct acaatccaga tacagacagt acgtacttac catttgctaa gcacgccaaa   360

gaaactggtg ccacttactt caccctagca ggtgaagctt accaacataa gaatatccaa   420

caagccttct tctacttagg tgtttcattg cattacttgg gggacatcaa tcagccaatg   480

```
catgctgcca actttacgaa cttatcttac ccattcggat ttcactccaa atacgaacac      540

tttgtcgata ccatcaaaca gaactatgag attatggatg gcgagggata ttggaattgg      600

aagggaaggg atcctgaaga ctggatacac caggcagccg ttgctgcaaa ccaagacttt      660

agtgatatcg tgaactcaga caccaagaat tggttcgtca aggcagctgt ttcacaaact      720

tacgcagata gatggagagc tgctgtaaca cccattactg gcaagagatt gatcgaagct      780

cagagaatca ctgccggata cattcaactt tggtttgata catacataca tcaataa         837


<210>  406
<211>  837
<212>  DNA
<213>  Bacillus thuringiensis

<400>  406
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat       60

gagaatgatg ggggttccaa gattaagatc atacatagat ggtctgccga agataaacat      120

aaagaagggg ttaactctca cttatggata gtcaacagag caatcgacat tatgtcaaga      180

aatacaactt tagtgaaaca agacagagtc gcccaactaa atgaatggag aactgagcta      240

gaaaatggca tttacgctgc agattatgag aacccgtatt acgataactc cacgttcgct      300

tcccatttct atgatccaga caatggtaag acatacatcc cctttgcaaa gcaggcaaaa      360

gaaactggtg ccaaatactt caagttagct ggggaatcct acaaaaacaa agatatgaaa      420

caagcctttt tctatcttgg tctgtctctg cattacctag gtgatgtcaa ccagccaatg      480

catgcagcca atttcacaaa cttatcttat cctcaaggat tccattccaa gtatgagaac      540

tttgttgata cgatcaagga caactacaaa gtcacagatg gaaacggtta ctggaattgg      600

aaagggacca acccggaaga ctggattcac ggtgctgctg ttgttgccaa acaagactat      660

tcaggaatcg taaatgacaa taccaaagac tggtttgtaa aagcagcagt ctctcaagaa      720

tatgcagaca aatggagagc cgaggttaca cccatgacgg gcaagaggtt aatggatgcc      780

caacgtgtca ctgctggtta catacaacta tggtttgata cttatgggga tagataa         837


<210>  407
<211>  867
<212>  DNA
```

```
<213>  Talaromyces rugulosus

<400>  407
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgac        60

gtcaccacag cagtcttgga cgacttaacc ttgttttcac agtattcagc tgctgcatat       120

tgttctacca acttgaattc tacaggtgtg gcagtgacat gcagtgttgg taattgtccc       180

ctagtcgaag cagcagatac acaaatactg tatgactttg acgaatcctg caagtttggc       240

gatgcatctg gcttcattgc agtggacaat accaataact tgattgtgtt gtcttttagg       300

ggatctcacg atctttcaaa ttggatcgca aacttagatt tcttcttagt cgaaactgcc       360

tcaatctgcg aaggttgcta catgcatggt ggtttttggg aaacttggca aacagtcgct       420

gcaaacgtta cagaacaatt agaagctgct atcactgcaa accctggata taccttagtt       480

atgactggtc acagtctagg agctgccttg gctgcaatag ttgctaccga gtttaggaat       540

gaaggcattg atgtagaaat gtacaattac ggccaaccaa ggctaggcaa cttagcttta       600

gctcagtata tgacaaacca gacacagact tcaaactaca gggttactca ttccgatgat       660

attgttccta agcttccacc tagagtacta gatttcgacc actattctcc tgagtattgg       720

ataacttcag ccaataacgt gtcagtatca gacgcagatg tcgtacaggt cgttggtata       780

gatagcacgg atggcaatga tggcaccatc ttagatgaca tagaggctca tagatggtac       840

ttagggtata tctctgaatg ttcataa                                           867


<210>  408
<211>  885
<212>  DNA
<213>  Penicillium sp.

<400>  408
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct        60

cctgcaagac ctgttccaag ggatgtttct agtgctacat tatctgagtt aacgctattc       120

gcagagtacg ctgctgctgc ttactgctcc aacaacattg attcaactgg agacgctctg       180

tcttgctcag gagggtattg tcccgaagta caatctgctg gtgcaaccac tttgtatgaa       240

ttcgaagata gcacagattt tggagacgtt acgggtttct ttgcagtcga caataccaac       300

aaactattag tactatcttt tcgtggaagc agctctatta gtaactggat tgccaatttg       360
```

gactttggtt taacagatgc atcttctcta tgttcaggtt gtgaagcaca ttctggcttt 420

tacaagtcct ggggtgtcgt agcagatact ttaactgccc aagtcgctag cgctgtttca 480

acatatccaa gttatactct agttgttacc ggtcattcat tgggtggggc attagccgct 540

ttaggcggaa ccgccttaag aaatgctggt tatactttgg acatctatac ctatggacag 600

cctagggttg gtaataccgc attagcagat tacatgacaa atcaaggatc actatggcgt 660

gtcacacatt caaatgatat tgtacccaag ttacctcctg caagctgggg atttacccac 720

gcaagtcctg agtactggat tacctccggg aacgatgtca cagttaccac atccgatgtt 780

accgaagtga ctggtgttgg ttcttcagac ggtaacgctg gttcatcagg cgacagtgta 840

agtgcccaca attggtacat tgttgatatt gatgggtgtt cttaa 885

<210> 409
<211> 888
<212> DNA
<213> Hamigera avellanea

<400> 409
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct 60

cccgcacctg ttaggcgtga tgtaagtgca ggagtcctag ccaacttaga cttgtttgct 120

cagtattctg ctgcagctta ttgcgattcc aatttgaatt cagacggtac aaagcttact 180

tgtgccgctg gtaattgtcc acttgtagaa gctgccgaca ccgaaacact tgacgaattc 240

gatatgaccg ctacatacgg gaacgtagca ggttacatcg ctgtagaccg taccaataga 300

ttacttgtgt tggcttttag aggtagcgcc agcatctcaa attggattgc caacttgaac 360

ttaggtttaa cggatgcctc tgccctatgt gcaggttgtg aggttcattc cggtttctgg 420

gaagcctggc aaacagcaga agctacaatt tcagacatta tcgcttcagc agcccaaaca 480

tatccaggtt atactctggt tgtaactggg catagttacg gtgctgcctt agccgctatc 540

gctgccacta gattcagaaa cgagggttat gctgttgaac tttacgatta tggacaacct 600

cgtataggaa atctagctct ggctcaatac atcacaaacc aatctggagg tggcaacttt 660

cgtgttacgc acaccaatga cattgttccc aagttacccc cagattggtt aggatactct 720

cactttggac cagaatactg gattacatca ggcgatggtg tgcctgttac taccgcagat 780

gtggaagtga ttagtggagt ggatgcaact ggcggtaatg atggcgcaga aggtacttca 840 gtggatgcac atagatggta ctttgtgtac attagtcaat gtgaataa 888

<210> 410
<211> 894
<212> DNA
<213> Penicillium spikei

<400> 410
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct 60

cctactagat tgcttattcc tagggacata tcaagtgacg tgttagccga gttgactttg 120

tttgccgaat actctgcagc tgcatattgt tcagccaata tcgatagtgc atctgccggt 180

tctgccttga catgtgaatc tggtaactgc ccagaagtac aaagtgcaga tacgtctacc 240

ttatacgaat ttgacgaaac cacagattac ggcgatgtag ctggtttctt tgctgtcgac 300

aaaacgaatg agctgttggt tcttagtttc agaggttcta gaacgatttc aaattgggtc 360

gccaatttgg attttgactt aacagatgca tcttctcttt gtagtgactg cgaagctcac 420

tcaggttttt ggaaatcctg ggaaacagtt gccgatgagt taacaacaca aatagaatct 480

gcacagaata gttatccaga ttatcaactg gtattgaccg gtcatagtct aggtgccgca 540

ttggcagctt tggctggtac tgccctaaga aacgctggat acacccttga tttgtatacc 600

tttggtcaac caagggtcgg caacttagca ttagcagatt acatgacaga tcaaggatca 660

ttatggagag ttactcatac agacgacata gtaccaaggg tccctcccga aagcttcggt 720

tatgcacatg ccagccctga gtattggatc acatccggta atgacgtaac cgttactaca 780

tcagatgttg aggaaatcgt tggtgtcaat tccagtgccg gtaatgccgg agaagcagat 840

ttgtcaatag atgctcacaa ttggtacatt gtctacattg atgaatgtga ataa 894

<210> 411
<211> 1500
<212> DNA
<213> Paenibacillus alginolyticus

<400> 411
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctatt 60

acctccgtct ttggcaacta tcaaaacgca tacgcatgga gtgcagatga cgttcataat 120

caagactatt ctacacactt attcattgtc aatggcggag taaagttgat aagtggcaat 180 gccgactcag ccatcaacaa aagttcaaca ttactggagc agttcagaga caggtgggag 240

caaggtcttt atgatgcaga ccacttaaac ccattctacg attcaagcac gttcatgtca 300

catttctacg atccagatac tcaaacgaac tatgccggtt tatcttatcc gaccgccaga 360

caatctggta gcaaatactt caaggtcgca tcagactatt acaagaatgg agatttctcc 420

aacgccttct actacttagg tatttcattg cattacttta cggattcaac aatgccatta 480

catgcttcag acattagcaa cttagatcac agagcacctg gttaccacgc taagttggag 540

gaatacacta caagtattca gaaccagatt acagttccag acagtggctt gttcaattgg 600

atctcctcca cagacccaga gttgtggatc caccaagccg ctgttcaagc caaatccgtt 660

atgccacagg tgttcaatga ctctattaca gattggttct ggaaggctgc tgtatcctat 720

tactattccg atatgtggaa gaatacagtt aagactcaaa tcctaaatca acttaatcaa 780

gccgaacgtg aaaccgcagg gtacatagac ttgttcttta gacttaacgg tgttgatatg 840

cccgttacag tctacaatgg tactgccttt ggtggcgcat ctcaattact aggtttcggc 900

aattacgatt acaatcagtt ggtgaagggc ataggtaatg atacaattag ttccattagg 960

attgctccag gctaccaagt tacacttttt gcagactcca attactctgg cgttagtacg 1020

gtcgtcacag gaaatgttta cgggttatca aacttgaatg accagacaag cagtttgaaa 1080

gttggtgtta taccaaccaa cccagctcca tctccaacaa tccaggcaga atctttctct 1140

gggtcccagg ggatcttgac tcacagtgca gggagtggga ccgttgtcgg caacattaac 1200

agtggttctt ggctttctta tgataatgta gactttggta ccggtaagac caagtttgta 1260

gcttctgttg gaatggatcc cgctttcgct gctataggta agcagttgga gttaaggtta 1320

gacagtccca cagggacctt gattggtacg tttacaatat cttcatctgg tggttgggat 1380

gcttatacga ctcagaattg ctacgtaaca tctgcatctg gtactcataa gctttacatc 1440

atcacaaaag gtaacggttc tggatttggt aacatagatt ggtttacttt ttctagttaa 1500

<210> 412
<211> 837
<212> DNA
<213> Bacillus mycoides

<400> 412

```
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat        60

gagaacgacg gtggcagcag gattaacata gtccataggt ggtctgcaga agataaacat       120

aaagaaggtg tcaattcaca tctttggatc gtaaacagag caatggacat aatgagtaga       180

aacaccacat tggtaaaaca agaccaagtc gctctgctta acgaatggag gaccgaactt       240

gaaaatggca tctatgcagc cgactatgag aatccgtact atgataacag cacctttgca       300

tcacacttct atgatccaga taatgggaag acgtacattc catttgctaa gcaggccaaa       360

gaaactggtg ccaaatactt caagctagca ggtgaatctt acaagaataa ggatatgaag       420

caagccttct tctacttagg tttgtcattg cattacttgg gggatgtaaa tcagccaatg       480

catgctgcca actttacgaa cttatcttac ccacagggat ttcactccaa atacgaaaac       540

tttgtcgata ccatcaaaga caactacaaa gttacagatg gcaacggata ttggaattgg       600

aagggaacaa atcctgaaga ctggatacat ggcgcagccg ttgctgcaaa gcaagactat       660

agtggtatcg tgaacgataa cactaaagat tggttcgtca aggcagctgt ttcacaagaa       720

tacgcagaca aatggagagc tgaagtaaca cccatgactg gcacaagatt gatggatgct       780

cagagagtga ctgccggata cattcaactt tggtttgata catacggaaa tagataa          837


<210>  413
<211>  837
<212>  DNA
<213>  Bacillus bingmayongensis

<400>  413
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac        60

gagaatgaag gaggcaacaa aatcagggta attcagtatt ggtccgctga ggacaagcac       120

gcagaaggtg tcaactctca cttatggatc gtcaatagag caatagacat tatgagtaga       180

aatactacca ttgtaaagca agatgaagtg gcactgttaa acgagtggag aactgaactt       240

gaaaacggca tctatgcagc agattatgag aatccgtatt acgataacag cacttttgcc       300

tctcacttct atgatccaga ctccggtaaa acctatatcc catttgccaa acaagcaaag       360

gaaactgggg ctaagtactt taagcttgct ggagaatctt accaaaaaca ggaaatgaag       420

caagccttct tctatcttgg cctatcttta cattatctgg gtgatgtaaa ccaacctatg       480

catgtagcca actttacaaa tctatcttat ccccaaggct tccactccaa atacgagaac       540
```

```
tttgttgata ccatcaagga caattacaaa gctattgatg gtaatggcta ttggaactgg      600

aaaggcacaa atcctgaaga ttggatacat ggcgctgctg tcgcagccaa gcaagaatat      660

gctggtattg ttaatgacac cacaaaggat tggttcgtct gggctgctgt tagtcaagaa      720

tatgcagata agtggagagc agaagtaacc ccagctaccg gaaaaagatt agttgaagca      780

caaagagtta cagcaggata catacagtta tggttcgata cctatgggaa cagataa         837


<210>  414
<211>  840
<212>  DNA
<213>  Bacillus mycoides

<400>  414
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat       60

gagaacagtc atcagaacgg aatttccttt ggacataagt ggtctgcaga agctattcat      120

gatgaaggtg ttagtactca tctttggatc gtaaacagat caatcgaagt aatggcccaa      180

aacaagacag ttgtacaacc aaacgagata tcactgctta acgaatggag agccgatctt      240

gaaaaaggca tctatagtgc cgactatgac aatccgtact ttgataacgg gacctttgca      300

tcacacttct atgatccaga tactggtggc acgtacttac cattggctaa gcacgccaaa      360

gaaactggtg ccaaatactt caagctagca ggtgaagctt accagaataa cgatctgaag      420

aacgccttct tctacttagg tttgtcattg cattacttgg gggatgtaaa tcagccaatg      480

catgctgcca actttacgaa tgtatctctg ccagtcgcat tacactccaa atacgaaaac      540

tttgtcgata cagtcaaaga caactacaaa gttaaagatg gcaacggata ttggaattgg      600

aagagtgtaa atcctgaaga ctgggtacac gcctcagccg ttggtgcaaa ggcagatttt      660

cccttgatcg tgaacgataa gaccaagaaa tggttccttg acgcagctat ttcacaagat      720

gcagcagaca aatggagagc tgaagtaaca cccgttactg gcaagagatt gatggaagct      780

cagagaatca ctgccggata cattcacctt tggtttgata catacgtcaa ctacaaataa      840


<210>  415
<211>  867
<212>  DNA
<213>  Brevibacillus sp.
```

```
<400>  415
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctaag       60

aaggagtata aggtcaaata ccatggtaag actattacaa gtccctacaa gattgatcca      120

agatggagtg aagaatcccc acatgaagag ggccacgcaa cccacttgtg gattgttaac      180

agggcaattg acatcttatc aagaacaagc aataaggatg tgaattccaa ggaaactgag      240

atgttgaatg cttggagatc cagttgggaa caaggtcttt atgatgccga tcatacaaac      300

ccctattaca atttcggtac attcgcctct cacttctatg atccagatac caaatcaaac      360

tggctggaca cttctggcac cgcattgaca gaaggtagca ggtactttgc actagcaggc      420

aaatactatc aaaatggtga taaggaaaaa gccttttact acctaggatt gagtttacac      480

tatttgacag acgtcacaca accaatgcat gctgccaact ttacttggtt gaattggcca      540

actagttttc atggcaagtt tgaggattac accgatgata tccaaggcaa ctatgctgta      600

acagatggtg aaggttactg ggatttccaa gatagtaacc ccgaacattg gatacatcaa      660

gctgctgtcg acgcaaaagc agaatttccc aatatccaca catcagacat aactaaatgg      720

tttttggctg cagcagtcag cgactactat agtgacaaat ggcataaggc cgttcaacct      780

acaatcgagc ataggttaac tgaggcacaa agaattaccg caggctactt acatttgtgg      840

tttaagactt acgttgataa tcaataa                                          867


<210>  416
<211>  885
<212>  DNA
<213>  Penicilliumvasconiae

<400>  416
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct       60

cccgcaaggc cagtcccgag agatgtcagt agtgcaaccc tttctgaatt gactttgttt      120

tcacaatatg ctgcagctgc ttactgtacc aataacgtca attccgcagg agacgccgtt      180

agctgctcag gtggatattg tcccgaagtc caatctgctg gcgcaacaac cctttatgag      240

tttgatgact ctacagattt cggggatgtc gctgggttct ttgcagtgga cgcaaccaac      300

aaacttctgg ttttgtcttt tagagggtcc cgtaccattt caaattggat cgccaactta      360

gattttggtc agacagacgc ctccagttta tgttcaggtt gcgaagcaca ctctgggttc      420
```

```
ttcaaggcat gggaagcagt agcagatact ttaaccgctc agattgcatc agccgttgca      480

acttatccat catatacgtt ggtattgacg ggtcacagtt ttggtggcgc tgtggctgcc      540

ttaggcggta cagcattgag gaacgctggt tatactttag acttgtatac atacggtcaa      600

ccgagagtag gtaacacagc cttggcagac tacatgacga atcaaggatc cttatggaga      660

gtgactcaca gcgacgatat cgttcccaag cttccaccca ccagttgggg ttttacccat      720

gcatctcctg agtattggat tacatcaggt gacgatgtta ccgtcactac ttccgatgtt      780

acggaagtga ctggcgtcgg gtcaagtggt ggcaatgcag gtaccagtgg tgattctgtt      840

tccgctcaca attggtacat tgttgacatt gatggctgtc aataa                      885


<210>  417
<211>  891
<212>  DNA
<213>  Talaromyces diversus

<400>  417
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct       60

atcgaccctt tgaaccgtag aacaataagt gaaagtctac ttgatgaact agatttgttt      120

gctcagtatt ctgcagctgc ttactgttcc gcaaacttag attccacagg atccgccttg      180

gcctgcgatg ttggaaattg tcccttagtc gaagctgcct ccacaacaat cctttatgac      240

tttgatgaga caaatgattt cggggatgca actgggtaca ttgcagtgga caccacaaat      300

gaatacatca ttttgtcttt tagagggacc gacgacttag agaattggat cgccaactta      360

gattttccat tgattgacgc ctccgacatt tgttcaggtt gcgaaataca cgaagggtgg      420

tgggacagtt gggaaacagt agcttcagac attaccgctc agattgaatc agccgtttca      480

acttatccag actatacgtt ggtagctacg ggtcacagtt taggtgccgc tctggctgcc      540

attgccgcta cagtcttgag gctagatggt tatactgtac agttgtacaa ttacggtgaa      600

ccgagaatag gtaacttagc cttggcagac tacataacga ctgaaacaat gggttccaat      660

tacagagtga cgcacacaga cgatattgta cctaagcttc ctcctgagtt gttaggatat      720

gaccatttct ctccagagta ttggataaca tccggtgatg acgtcactgt tcttgataca      780

gacgtaaccg aagtcgtcgg ggtagactcc accgctggaa atgacggaac tttgttggat      840

tccattgatg ctcatagatg gtatttcgtc tatatcagtg aatgttcata a               891
```

<210> 418
<211> 900
<212> DNA
<213> Aspergillus wentii

<400> 418
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct 60

cccagtcctg ttaggcgtga tgtagacagt agtgtcctaa acaacttaga cttgtttgct 120

cagtattctg ctgcatcata ttgcttggag aatttgaatt catccaatac aaagcttgaa 180

tgctccgtag gtaattgtcc acttgtagaa gctgcctcca ccgtcacact tgacgaattc 240

gatgaatcct cttcattcgg ggacgtaacc ggtttcatcg ctgcagacga gaccaacaag 300

ttacttgtgt tgtcttttag aggtagctcc gacatcgcaa attggattgc cgaccttgat 360

ttcggtttaa cggatgggag cgacctatgt tcaggttgta aggttcatag tggtttctgg 420

gaagcctggg gaacagtatc agacaacatt acatccatta tcgaatcagc aaccgccaag 480

tatcccaact atgaactggc ttttactggg cattcctacg gtgctgcctt agccgctgtg 540

gctgccgttg tattcagaaa ctccggttat acagttcaac tttacaacta tggacaacct 600

cgtataggaa atctagctct ggcagattac atcacaaacg ttacagataa gggtgacaat 660

tacagagtga cgcacacaga cgatattgta cctaagcttc ctcccaagtt gttaggatat 720

caccatgcat ctccagagta ttggataaca tccggcaata acgtcactgt taccactgca 780

gacgtagacg ttgtcacagg ggtagactcc accgatggaa atgacggaac tactgcagat 840

tccagaacag ctcatagatg gtatttcggc tatatcagtg aatgttcaac cttgtactaa 900

<210> 419
<211> 1500
<212> DNA
<213> Bacillus acidiceler

<400> 419
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctata 60

accagcttgt tcggcaatta ccaaagagct tttgcttggt cagatgaaga tgttcacaac 120

caagatcatt caacccatca cttcattgta aatggaggag tcaaattgat tgcagacaat 180

acagacccag ccatcaataa gcccacaacg cttctgaacc agtttagaga cagatgggag 240 caaggtttgt acgatgcaga tcacatcaat cccttttacg atactggtac cttcatgtcc 300

catttctatg atcccgatac acaaacaaac tattccggac tatcctatcc aacagctaga 360

cagtcaggtg gcaagtactt caacttagct agcgattact acaaaaaggg tgactttaac 420

aacgcctttt actatctagg ggtttctctt cactacttta cagacgttac tcagccgttg 480

catgcttcca atatcagcaa tctagatcat aatgctccag gctatcattc caaatacgaa 540

acctacgctg aatctataca atcacaaatc attgtcccag attccggctt gtacaactgg 600

acagatagta cggatcccga agcctggata cataaagcag ccattcaggc aaaaagcgtt 660

ctgcccttgg tttggaatga taccatcatc aactggtttt ggcaggctgc ctattccaac 720

tattactccg caatgtggaa gaatgaagtc aagaatccaa ctctagctca acttaaccaa 780

gccgaacgtg aaacagctgg tttcattgat atgtttttca ggttgaatgg ggtggagatg 840

ccggtaacgg tctacaatga aaatgccttt ggtggagcaa gtgaactttt gggttctggc 900

aactatgatt atgatcaatt gattaagtgt attggtaatg atacgataag ctctattcat 960

atcgcacctg gttatcaagt caccttattc gcagacgcaa actacaaagg tgcttcaatt 1020

gttttgacag gagacgtcaa cgatttgggc aacttcaatc atcaggtgag ttcattgaag 1080

attgagaaga tatctaccaa tccagcctct tctcctacaa tccaagcaga gtctttcata 1140

agcagtaaag gcatcttgac tcataatgtt gggtcaggta ccgttgtggg taacataaac 1200

tcaggctcat ggattggata tgataacgtc gatttcggaa ctggaaaaac caaattcata 1260

gctagggttg gtatggaccc ctcttacgcc atattcgata aacagttgga attgaggttg 1320

gattctccta caggtaccat cattggaacc tttaccatca acaatactgg aggttgggac 1380

acatatgcta ctcagacgag catactttct ggcgcaactg gtacccacaa attgtacata 1440

gtttcaaaag ggtctggtga tggatttggc aacattgatt ggataacatt ctctccttaa 1500

<210> 420
<211> 837
<212> DNA
<213> Bacillus luti

<400> 420
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac 60

gagaaaaacg aaggtaatgt acccatcatt actcagtatt ggagtgctga ggacacccac 120

agtgaaggtg tcaactctca cttatggatc gtcaatagag caatagacat tatgtccaga 180

aatactacct tggtaaggca agatgaagtg gcactgttaa acgcctggag aacagatctt 240

gaaaagggca tctatgcagc agattatgag aatccgtatt acgataacag cacttttacc 300

tctcacttct atgatccaga caccggtaaa acatatgtcg gtttagccaa acaagcaaag 360

gaaactggga ataagtactt taagcttgct ggagaatctt acaagaataa ggatatgaag 420

caagccttct tctatcttgg cctatcttta cattatctgg gtgatgtaaa ccaacctatg 480

catgcagcca actttacaaa tctatcttat ccccaaggct tccactccaa atacgagaac 540

tttgttgata ccatcaagga caattacaaa gttacagatg gtaatggcta ttggaactgg 600

aaaggcatga atcctgaaga atggatacat ggcgctgctg tcgcagccaa gcaagactat 660

tcaggtattg tcaatagcaa cacaaagtct tggttcgtca aggctgctgt ttcccaatca 720

tatgcagata agtggagagc agaagtaacc ccaacgaccg gaaaaaggtt aatggaagca 780

caaagagtta cagcaggata catacagtta tggttcgata cctatgggaa cagataa 837

<210> 421
<211> 837
<212> DNA
<213> Bacillus pseudomycoides

<400> 421
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat 60

accaacgact gtggcaacga agctcctgta ctaaagtggt ccgctgaaga caaacataat 120

gaaggtagaa atagtcactt atggattgtc aatagggcaa ttgacattat gtccagggat 180

aagaccgtag ttaagccaaa tgagacagca ttactgaacg agtggagaga cgacttagag 240

aatggtatct attcagcaga ctacgaaaac ccatacttcg ataatgggac gttcgcatca 300

catttctacg atccagatac tcaaaagtcc tacatccctt ttgctaaaca cgccaaggaa 360

acaggtgcta agtatttcaa gcttgcaggt gaagcttatc agaacaaaga tatgaagcaa 420

gcattcttct acttaggatt atctttacat tatcttggtg acgttaatca acccatgcat 480

gctgccaact ttacaaacat tagtactgag gctcccatct ttcactccaa atacgaaaac 540

tttgtcgata ccatcaaaga caactacaaa gttgcagatg gcaacggata ttggaattgg 600

```
aagggaacaa atagtgaaga ctggatacat ggcgcagccg ttgctagtaa gcaagactat      660

tcctctatcg tgaacgatac cactactagt tggttcctta aggcagctac atcacaagaa      720

tacgcaaaca aatggagagc tgaagtaaca cccacttctg gcaagagatt gatcgaagct      780

cagagagtga ctgccggata cattcacctt tggtttgata catacgtcaa tagataa         837


<210>  422
<211>  840
<212>  DNA
<213>  Bacillus mycoides

<400>  422
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat       60

gaaaacgatg gtcaattcga ccctccaatc gctcagaggt ggagtgccga gagcatccac      120

aatgaaggcg ttagctcaca tctttggatt gtaaacagag caattgacat aatgtctcaa      180

aacactacag tagttaaaca aaacgagacg gcacttctta atgaatggag aaccaaccta      240

gaagaaggca tctattcagc agactataag aatccctatt acgaccattc tacctttgca      300

tctcacttct atgaccccga ttctggaaaa acctacattc cgtttgctaa acaagcaaaa      360

cagactggtg ccaaatactt caaactagct ggtgaagctt atcagaacaa agacatgaag      420

aacgcctttt tctacctagg tttatctttg cactatttgg gagatgtcaa ccaaccaatg      480

catgctgcca atttcaccaa cattagtcat cctttcggct tccattccaa gtatgagaac      540

tttgtcgaca cagtcaaaga caactataga gtaacagatg gcgatggtta ctggaattgg      600

aaatctgcaa atccagagga atgggtccat gctagtgcaa gtgccgcaaa agcagatttt      660

ccatctattg tgaacgataa caccaaaaac tggttcttga aagctaccgt atcacaagat      720

tccgcagaca aatggagagc agaggttacg cctgtaactg gtaaaaggtt aatggaagct      780

caaaggataa ctgctggcta cattcaccta tggttcgata cgtacgtcaa taacaaataa      840


<210>  423
<211>  876
<212>  DNA
<213>  Penicillium cinnamopurpureum

<400>  423
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgtt       60
```

```
ccgttaagaa gggatgtttc atccgatgat ttgaaacaat tgactttgtt cgctgaatac      120

gctagtgcat cctactgcac aaacaacatc aattctactg gcgacgcatt gtcatgtgca      180

gaaggtaatt gcccagccgt tcagtcagca acgactaaaa ccttgtatga gttcaatgat      240

agtaccgaat ttggagatgt cgctggtttc ttggctgcag acgaaacaaa cgaacttttg      300

gtactatcct ttaggggttc taggacaatt tccacttggg tggcaaacct ggattttggc      360

ttgaccgata catcagatct gtgttctgga tgcgaagcac atggtggatt ttggaaatca      420

tggcagactg ttaccgatga cataacctcc aaaatcgatg ctggtttgaa aagtcaccct      480

ggatatacgg ttgtcttaac aggtcattcc tttggtgcag ctatggccac attgggaggt      540

acagccttac gtaacgctgg ttacaagatc aagttgtata catatggtga accaagagtg      600

ggcaatgagg ctttagcaaa gtacattact aaacaaggtg atttgtatag ggtcacacat      660

gcagatgatg tcgttccgaa ggttccacca gcatcatttg gattttctca tgcatcacct      720

gagtattgga ttacctccgg aaacaataag accgtttcta ccagtgacat caaagtcatt      780

caaggcgtag gatcaaaaga cggaaacgct ggtaccatca atccagacat tgaggctcac      840

aattggtaca tcgtgcatat agacggatgt caataa                                876


<210>  424
<211>  885
<212>  DNA
<213>  Talaromyces verruculosus

<400>  424
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgaa       60

cccatctata gaaggaagat agctacttct cttttggata gtttggactt attcgcacag      120

tattctgccg ctgcttattg ttccgcaaac ttggatacta caggtactgc actggcttgc      180

aatgtgggta actgcccagc tgtggaagca gcagatacta ccatattgta ttcttttgat      240

tcctcatcaa gctttggtga tgcaaccggt tacattgccg ttgatgaatc ccatggctac      300

atcatcttat cattcagagg tacgtcaaac ctggagaatt tcatcgcaac tttagatatg      360

cagttgattg atgcaagttc catttgtagt ggttgtaaag ttcataaggg tttttggaat      420

acctgggaaa ccgttgcctc agatgtaact tcacaaatca aggcagctct gtctgcttat      480
```

ccagactata ccttagttgc aactggtcac tcattgggag ctgctctggc agccatcgct 540

gctaccgtct tccgtgcatc tggatatact gttcaattgt acaactatgg cgaacctagg 600

ataggcaatt tggctctagc agacttcatt acaagtgaaa cttcaggaac aaactatcgt 660

gtcacacatt caaatgacat catacccaag ttacctcctg gactgttagg atatcaccac 720

ttttcccctg agtactggat taccagtaag gacaatgtca cagttaccga tagtgatgtt 780

gtggaaatca aaggtgttga ttctacagac ggtaacgatg gtactgctgg tgcctccatt 840

gaggcccata cttggtactt tgtctacatt tcagagtgtt tgtaa 885

<210> 425
<211> 891
<212> DNA
<213> Talaromyces cellulolyticus

<400> 425
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgca 60

ccaaaaccta ttcatagaag gactatacct acttccttac ttgacaactt agaccttttt 120

gctcagtata gtgcagcagc ttattgttca gccaacttag agactacggg taccgcacta 180

gcctgtaatg tgggtaattg tccagctgtt gaagccgcag ataccattat cttgtatagc 240

tttgattcat cctcctcttt cggtgacgct acaggatacg ttgcagttga tgaatcaaat 300

gagtacatta tcttaagctt cagaggtagt agtaacttgg agaattggat cgccaactta 360

gatatacctt tgattgatgc ttcatcaatt tgttccggtt gtaccgttca cgagggcttc 420

tgggacacat gggaaactgt tgcaagtgat gtcactagcc aaattgaatc cgctttgagt 480

acatatccca actatacctt agttgcaact ggtcactcct taggcggtgc tcttgcagcc 540

atcgcagcta cagtctttag agcttctggg tacacagtcc agttatacaa ctacggtcaa 600

ccaaggattg gcaacttagc actagcagac ttcataacaa gtgaaacgtc cggaaccaac 660

tatagagtta cacattcaga tgatatagtc ccgaagcttc cacccgagtt acttggttat 720

caccacttta gtcctgagta ctggatcaca tcaaacgata atgttactgt gacagactca 780

gatgttgttg aaattcaggg tgtggattca actgctggca acgacggtac cagcggagat 840

tcaattgatg ctcattcttg gtactttgtt tccattagtg agtgttccta a 891

<210> 426
<211> 900
<212> DNA
<213> Penicillium megasporum

<400> 426
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctggt 60

cccgtttcag tattgagaag agacgaggac gtatccgcct ctgttttgtc tgagctagac 120

ttcttttctc agtattcagc agccgcttac tgttccacaa acatcaattc tgccggtacc 180

aaattgactt gtagtgaggg tatttgtcca cttgttgaaa acgcagatac agaaaccttg 240

gacgaattcg atgaaagtgc ctcttacggt gatgtcgctg gtttcattgc tgtggatcgt 300

acgaatgaac ttctagtctt gtcatttaga gggtctgcta gtttcagtaa ctggttggcc 360

aacattgact tattcctaga tgatgcctct tccgtctgca gtggttgcga agttcattct 420

ggtttctggg atgcatggca gactgttgaa ggacagatta ccacagctct aggttctgcc 480

atggaaacat atccagggta tacgcttgtc tttaccggac acagctatgg tgcagctttg 540

gctgctattg ccgcaaccat ctttagaaac agtggctata ctgttgagtt gtacaactat 600

ggacaaccta gaattggaaa tctagctctg gcagagtaca ttacaaatca gaacaaaggt 660

ggtaactata gggtgacaca tacagacgac atagtcccta aggtcccacc aaagataacg 720

gggtatcacc atgcttcccc tgagtattgg atcacatccg gcaacaatgt tactgttacg 780

actagcgatg tacagttgat aactggcgta gacagcacat ctggtaatga tggtacatca 840

gatgactctg ttgaagctca caggtggtac tttgtacaca tttctatgtg cacaatataa 900

<210> 427
<211> 837
<212> DNA
<213> Bacillus toyonensis

<400> 427
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac 60

gagaaaaccg aaggtcataa tgtgaacatc attcagtatt ggagtgctga ggacaagcac 120

agtgaaggtg tcaactctca cttatggatc gtcaatagag caatagacat tatgtccaga 180

aatactaagt tggtaaagca agatcaaatc atactgttaa acgagtggag aacagatctt 240

gaaaacggca tctattcagc agatcatgag aatccgtatt acgataacag cactttggtg 300 tctcacttct atgatccaga cgacggttct acctatatcc catttgccaa acaagcaaag 360

gaaactgggg ctaagtactt taagcttgct ggagaatctt acaagaataa ggatatgaag 420

caagccttct tctatcttgg cgtctcttta cattatctgg gtgatgtaaa ccaacctatg 480

catgcagcca actttacaaa tctatcttat ccccaaggct tccactccaa atacgagaac 540

tttgttgata ccatcaagga caattacaaa gttacagatg gtaatggcta ttggaactgg 600

aaaggcattc atcctgaaga ttggatacat ggcgctgctg tcggagccaa gcaagacttt 660

tcaggtattg tcaatagcaa cacaaagtct tggttcgtca aggctgctgt ttcccaatca 720

tatgcagata agtggagagc agaagtaacc ccaatgaccg gaaaaaggtt gattgaagca 780

caaagagtta cagcaggata catacagtta tggttcgata cctatgtgaa cagataa 837

<210> 428
<211> 837
<212> DNA
<213> Bacillus sp.

<400> 428
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcac 60

gaggataccc accaagatcc tcccatagca ttgaagtgga gtgccgaaag tgtgcacaac 120

gagggcgtat cctcccatct gtggattgtc aatagagcta tagacataat gtctcagaat 180

actactgtcg ttaaacaaaa tgaaacagcc ctactgaatg actggagaac caatttggag 240

gaaggcatct attctgcaga ctacaaaaac ccatactatg acaattccac gtttgctagt 300

cacttctatg atccagattc cgagaaaacc tacattccct ttgctaagca agctaaacaa 360

accggtgcca aatacttcaa actagccggt gaagcttatc agaacaaaga catgaaaaac 420

gcattcttct atttgggcct aagtttgcac tatttggggg atgttaatca acctatgcat 480

gctgccaact ttaccaacat atcccatcca ttcggtttcc actccaagta tgagaacttt 540

gtagatactg tcaaggataa ctatcgtgtt acagatggaa atggttactg gaattggaaa 600

tctgccaatc cagaagaatg ggtgcatgag agtgctgctg ccgcaaaggc cgattttcct 660

tcaattgtta atgataacac caaaagttgg tttctaaaag ccgctgtttc tcaagattca 720

gcagataagt ggagagctga agtaacacct gttacgggaa aaagattgat agaagctcaa 780 agaattactg caggatacat ccacttatgg ttcgacacat acgtaaacaa caaataa 837

<210> 429
<211> 846
<212> DNA
<213> Bacillus manliponensis

<400> 429
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctcat 60

ggcaaccacg atgcaagcaa tgattccgga ataagtatat ccccaagatg gtctgctgaa 120

gaaatgcatg ctgaaggcaa aaactctcac ttatggatag taaacagagc aatcgacatt 180

atggccagag atacaactgt tgtgaaagaa aatgaggtgg ccttgttaaa cgagtggagg 240

acagatcttg aagatggaat ctacacagca gattacgaga atccttacta cgacaattca 300

acattcgcct ctcacttcta tgatccggac acggacgata cctacattcc gttcgccaaa 360

aacgctaaag tgactggtgc caagtacttc aagttagctg ggaagcata cgaacagcaa 420

gatatgcaac aagccttctt ctacttaggt ttatccttgc actactttgg agacatcaat 480

caaccaatgc atgctagcaa ctttacaaac atttcccatc cattcggctt tcactctaag 540

tatgagaact ttgtcgatac catcaaagct ccatatgcag tcaccgattc aaaaggttac 600

tggaactttg caggaggtac gccagaagag tggttacaca ctgctgcagt ggctgccaaa 660

aaggatgctc caggcattgt gaatgaaaca acaaagtcct ggttcttgaa agcaagtgtt 720

tcccaagaat atgccaatat gtggagagct gaggttactc ccgaaactgg tgccagattg 780

atggaagccc aaagggcaat ggcaggatac atccacttat ggttcgatac ttatgttaat 840

cgttaa 846

<210> 430
<211> 882
<212> DNA
<213> Penicillium simplicissimum

<400> 430
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgcc 60

ccagctagat ccgtacctag agatgtatct gcttctgtct tggaacagtt taccttatac 120

gcacagtggg ctgccgctgc ttattgttcc aacaacttgg attctacagg tgatgcaatc 180

```
acttgcgctg gcggttactg cccagaagtg gaatcatcta ctactattag tctttctgag      240

ttcaatgaca caaatgactt tggtgatacc gcaggtttcg ttgccgttga taagaccaat      300

aagcaaattg tcgttgcttt cagaggtagc aaaagcatct caaattggat cgcagattta      360

gattttgggt tgacagatgc aagtaacttg tgtagtggtt gtgaagctca taccggtttt      420

cttgaagcat gggaaaccgt tgccgattct attacttcac aaatcggagc agctatgaaa      480

acttatagtg gttatacctt agttgtcact ggtcactcat tgggaggtgc tatcgcagcc      540

atcggtgcta ccgtccttcg taatgctgga tatactttgg atttgtacac ctttggccaa      600

cctagggtcg gcaatttggc tctagcaacc ttcttaacaa agcaaggcaa caatagaatg      660

actcacctaa atgatattgt accaagatta cctccaacta gttttggatt ctcacattca      720

tctcccgaat actggatcac ctctgcagac gatgtgacgg taaccacatc agacattgaa      780

gttattgagg gaatcgattc aacagctggt aatgccggtg agttgattga atcagttgct      840

gcccatgcat ggtacatcat tgatattgat ggatgtgaat aa                         882


<210>  431
<211>  888
<212>  DNA
<213>  Penicillium arenicola

<400>  431
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgca       60

ccttttcaat tgtggtctag agctgtcact ccttccgtct tatcaaagct agacttatac      120

ggccaatatg ctattgccgc atactgtgat gacaacattg cttcagccgg tacggaagtg      180

acatgtagcg ctggtaactg tcctttggtt caagctgcaa ccacaaatac attaagtgag      240

tttaacgaat caaatgaatt cggtgacgtt gctggctttt tcgccgttga tacaacaaac      300

caagctctag ttttgagctt tcgtgggtct catacgatcg acaattggat tgcaaacttg      360

gattttggat tgacctctgt ttccacttta tgttcaggat gcaaagctca cactggcttc      420

tggaaggctt ggaatactgt agcttcagac atcgcagcag ctgtggatgc tgcacaagat      480

acttaccctt cttaccccat tatctttact ggacattcat acggagctgc cttggctgcc      540

ctagctgcca caactatgag aaatgctggt tatagcatag aattgtatac atacggacag      600

ccaagaattg gaaatacagc tttagcaacc tacattacaa atcaaaacaa aggtggcaac      660
```

tatagagtaa ctcatacaaa tgatattgtc cctaggctgg tacctagact tctaggatac 720

tcacacttct ctccagagta ttggatcaca agtggcaata acgtaacagt tactgcctcc 780

gacattactt tagttactgg tatcgatagc aatggtggta atgcaggcga gttactacag 840

tccgttgaac ctcactattg gtactttgtg gaagttgaag attgctaa 888

<210> 432
<211> 891
<212> DNA
<213> Aspergillus aculeatus

<400> 432
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctgct 60

cccgcaccta ttgagcgtag atcagtctcc acaacactac ttgatcaaat ggatttgttt 120

gctcagtatt ctgcagctgc ttactgtagt acaaacatag atagtgcatc aaccgccttg 180

agctgctcag cagacaattg tcccttagtc gttgctgctg cccctacagt ccttgatgag 240

ttcaatgaga ctgcagaatt cggggatacc gctgggttcg ttgcagtgga cagtaccaac 300

aaagccatcg ttgttgcttt tagagggagt agcgacttat caaattggat cgccaacatt 360

gattttggtt tgacagacgc cagttccatt tgtacaggtt gcgaaataca ctctgggttc 420

tggaaggcat gggaaacagt agcttcaact attgcctcta aggttgaagc agccgttaca 480

acttattcag attatgacgt tgtctttacg ggtcactcct taggtgccgc tctggctgcc 540

attggcgcta cagtcttgag gaacgatggt tatactgtag acttgtacaa ctttggtcaa 600

ccgagaatag gtaacttagc cttggcagac tacataacgg atcagaataa gggttccaat 660

tacagagtga cgcacacaga cgatattgta cctaaggtcc ctcctgagtt gttaggatat 720

caccatttct ctccagagta ttggataaca agtgataatg acgtcactgt taccacttca 780

gacattaccg aagtcacagg ggtagacagt accgctggaa atgacggaac tttgttggat 840

agtgtttccg ctcacaagtt ctatttcgag tatatctccg cttgtgatta a 891

<210> 433
<211> 1107
<212> DNA
<213> Bacillus acidiceler

<400> 433
atgagatttc cttcaatttt tactacagtt ttattcgcag catcctccgc attagctatt 60

acttccttct ttggcaacta tcagaaagcc ttcgcttgga gtgatgagga cgtacataat 120

caagatcatt ctactcacca cttcatagtt aatggctccg tcaaattgat tgcagacaat 180

acaaatcctg ccatcaacaa acctacaacc ttgctgaacc agtttagaga tagatgggaa 240

caaggcttat acgatgcaga ccacatcaat cccttctacg acacagggac ctttatgagt 300

catttctacg atcccgatac tcagaccaac tatactggcg caagttatcc aacagctaga 360

caaagcggtg ccaagtactt caatctagcc agtgattact acaagaaagg tgacttcaac 420

aatgcctttt actatttggg cgttagtctt cattacttta cagatgttac tcagccttta 480

catgcatcaa acatttccaa tttggatcac cacgctcccg gttaccacag caagtatgaa 540

acttacgctg aatcaatcca aaatgagatg acgatgcccg attccggatt gtacaattgg 600

atagcctcaa cagaccccga agcatggatc catcaagccg ctgtgcaagc aaaatctgtt 660

ttgccacagg tttggaatga cactatcatt aactactttt ggcaagctgc ctattccaat 720

tactactctg ccatgtggaa atctgaagtc aagaatccta ctttggatca attgaatcaa 780

gctgaacgtg agaccgcagg cttcattgac atgttctttc gtgttaacgg agtagaaatg 840

ccggtcaccg tgtataagga aaatgccttt tcaggtgctt ctgagttatt gggttctggt 900

aactacgatt atgatcaact tgttaagggt attggaaatg atacaatatc ttccattcat 960

attgctccag gctatcaggt gactctattc tcagacgcca actacaaagg tgctagtact 1020

gtgcttacaa atgatgtgca cgatctaggc aacttttctc atcaggtttc ttccataaag 1080

gtcgccaaaa tctcagcact taagtaa 1107

<210> 434
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Artificial DNA Primer

<400> 434
tcttttcgcg ccctggaaag g 21

```
<210>  435
<211>  49
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial DNA Primer

<400>  435
tgttttatat ttgttgtaaa aagtagataa ttacttcctt gatgatctg                   49


<210>  436
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial DNA Primer

<400>  436
gtgacaacaa cagcctgttc tc                                                22


<210>  437
<211>  21
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial DNA Primer

<400>  437
agctaatgcg gaggatgctg c                                                 21


<210>  438
<211>  22
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Artificial DNA Primer

<400>  438
acagaagacg ggagacacta gc                                                22


<210>  439
<211>  18
<212>  DNA
<213>  Artificial Sequence
```

```
<220>
<223>  Artificial DNA Primer

<400>  439
ggggtcgcaa cttttccc                                                    18
```