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(54) COMPOSITIONS, SYSTEMS AND METHODS FOR PRODUCTION OF VALUE-ADDED CHEMICALS

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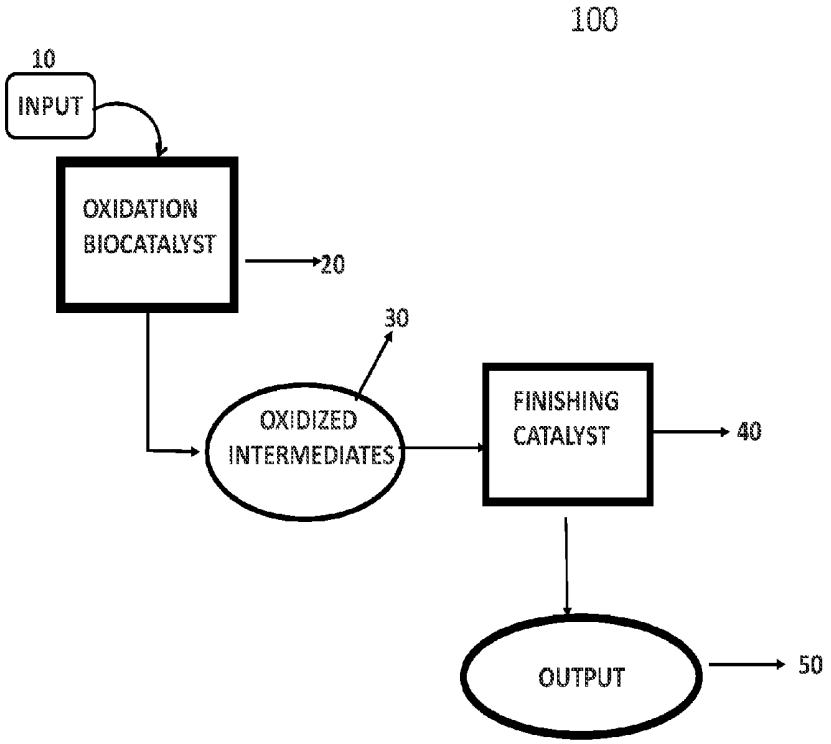
(57) **ABSTRACT**

A system for the production of high value chemicals includes (a) an input selected from the group consisting of ethylene glycol, glycerol, ethanol methanol or a combination thereof. In addition, the system includes (b) an oxidation biocatalyst including an alcohol oxidase, a copper radical oxidase, a glycerol oxidase, an alditol oxidase or a combination thereof. Further, the system includes (c) an oxidized intermediate. The system also includes (d) a finishing catalyst including a supported metal catalyst, a carboligating catalyst, an amine oxidase, a glyoxalase, an acid catalyst, a base catalyst, an isomerization catalyst or a combination thereof. Still further, the system includes (e) an output.

Specification includes a Sequence Listing.



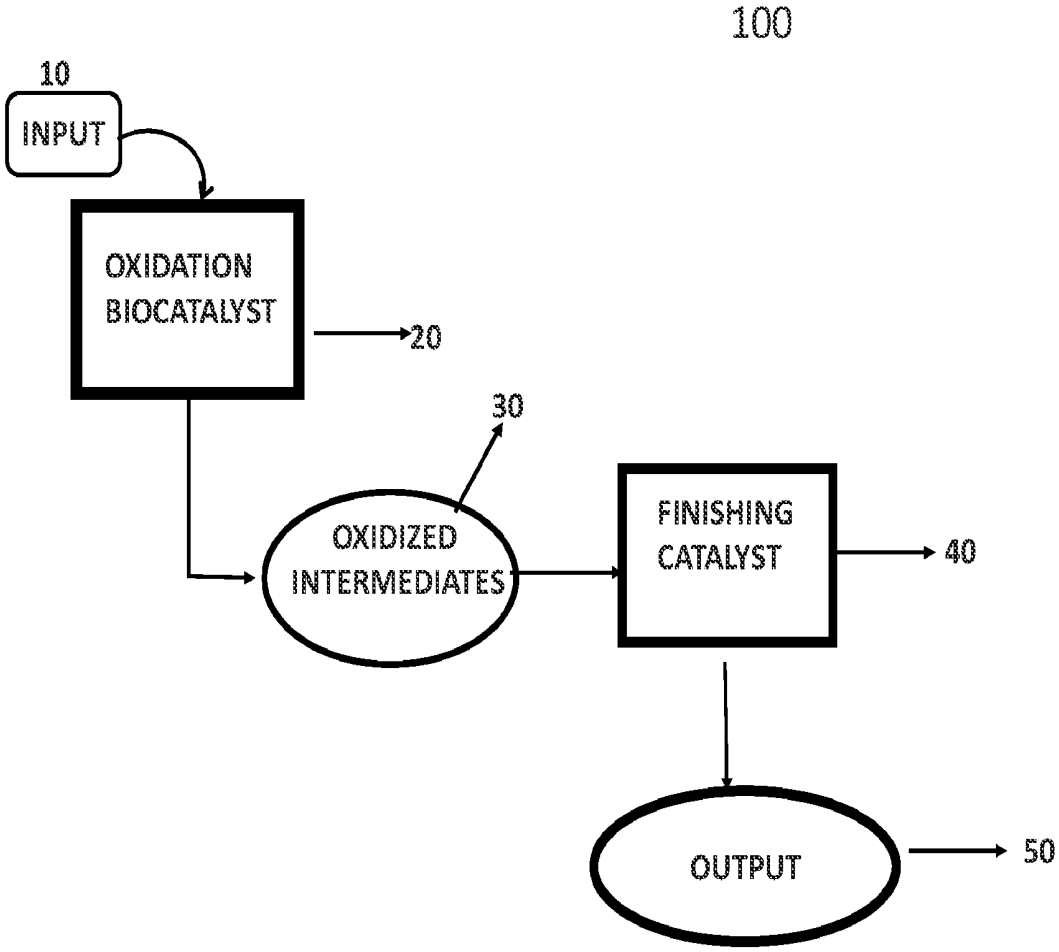

100
10
INPUT
OXIDATION BIOCATALYST
20
30
OXIDIZED INTERMEDIATES
FINISHING CATALYST
40
OUTPUT
50

FIGURE 1

COMPOSITIONS, SYSTEMS AND METHODS FOR PRODUCTION OF VALUE-ADDED CHEMICALS

CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] The present application is a 35 U.S.C. § 371 U.S. National Stage Entry application of PCT/US2021/012351 filed Jan. 6, 2021 and entitled "Compositions, Systems, and Methods for Production of Value-Added Chemicals," which claims priority to U.S. Provisional Patent Application No. 62/989,460 filed Mar. 13, 2020 and entitled "COMPOSITIONS AND METHODS FOR ACETALDEHYDE PRODUCTION FROM ETHANOL"; U.S. Provisional Patent Application No. 63/037,440 filed Jun. 10, 2020 and entitled "COMPOSITIONS AND METHODS FOR GYCOLIC ACID PRODUCTION"; U.S. Provisional Patent Application No. 63/060,721 filed Aug. 4, 2020 and entitled "COMPOSITIONS AND METHODS FOR DIHYDROXYACETONE PRODUCTION FROM GLYCEROL"; U.S. Provisional Patent Application No. 63/071,753 filed Aug. 28, 2020 and entitled "COMPOSITIONS AND METHODS FOR ETHANOLAMINE PRODUCTION FROM ETHYLENE GLYCOL"; U.S. Provisional Patent Application No. 63/090,784 filed Oct. 13, 2020 and entitled "COMPOSITIONS AND METHODS FOR PRODUCTION OF GLYCEROL FROM ETHYLENE GLYCOL"; U.S. Provisional Patent Application No. 62/969,475 filed Feb. 3, 2020 and entitled "IN VITRO ENZYMATIC FORMALDEHYDE PRODUCTION FROM METHANOL"; and U.S. Provisional Patent Application No. 62/957,678 filed Jan. 6, 2020 and entitled "IN VITRO LACTATE PRODUCTION FROM GLYCEROL"; each of which is incorporated by reference herein in its entirety for all purposes.

STATEMENT REGARDING FEDERALLY SPONSORED RESEARCH OR DEVELOPMENT

[0002] Not applicable.

TECHNICAL FIELD

[0003] The present disclosure relates generally to compositions, systems and methods for the production of value-added chemicals. More particularly, the present disclosure relates to chemoenzymatic systens and methods for the conversion of alcohols and polyols to higher value chemicals.

BACKGROUND

[0004] Oxidation is a key reaction in organic synthesis and plays a significant role in the production of value-added chemicals. For example, mono- and polyalcohols (e.g., ethanol, and glycerol) are important platform molecules for industrial manufacturing of a large number of value-added products, including but not limited to aldehydes, ketones, ethers, and molecular hydrogen. Another essential and important step in the synthesis of many valuable products including polymers and pharmaceuticals is the oxidation of amines. Challenges in the production of these valuable products include the use of reagents and conditions that are harsh, costly, and environmentally unfriendly. Further, the reactions typically result in a mixture of products and impurities that require substantial processing to obtain the compound(s) of interest at an acceptable percentage purity. Thus, an ongoing need exists for systems, methods and compositions that produce high purity, value-added chemicals via oxidation.

SUMMARY

[0005] A system for the production of high value chemicals, comprising (a) an input selected from the group consisting of ethylene glycol, glycerol, ethanol methanol and a combination thereof; (b) an oxidation biocatalyst comprising an alcohol oxidase, a copper radical oxidase, a glycerol oxidase, an alditol oxidase or a combination thereof; (c) an oxidized intermediate; (d) a finishing catalyst comprising a supported metal catalyst, a carboligating catalyst, an amine oxidase, a glyoxalase, an acid catalyst, a base catalyst, an isomerization catalyst or a combination thereof; and (e) an output.

[0006] A method for the production of high value chemicals, comprising (a) contacting an input selected from the group consisting of ethylene glycol, glycerol, ethanol methanol and a combination thereof with an oxidation biocatalyst comprising an alcohol oxidase, a copper radical oxidase, a glycerol oxidase, an alditol oxidase or a combination thereof to form an oxidized intermediate; (b) contacting the oxidized intermediate with a finishing catalyst comprising a supported metal catalyst, a carboligating catalyst, an amine oxidase, a glyoxalase, an acid catalyst, a base catalyst, an isomerization catalyst or a combination thereof to form an output.

BRIEF DESCRIPTION OF DRAWINGS

[0007] For a detailed description of the aspects of the disclosed processes and systems, reference will now be made to the accompanying drawings in which:

[0008] FIG. **1** is a schematic depiction of a High Value Chemical Output System, termed "HVCOS", of the present disclosure.

DETAILED DESCRIPTION

[0009] The instant application contains a Sequence Listing which has been submitted electronically in ASCII format and is incorporated herein by reference in its entirety for all purposes. Said ASCII copy, created on Dec. 26, 2020 is named HVC_ST25.txt and is 591,000 bytes in size.

[0010] Disclosed herein are aspects of systems, methods and compositions for the conversion of alcohols, polyols, and amines to higher value chemicals (HVC). Also disclosed herein are aspects of processes for the conversion of alcohols, polyols, and amines to an oxidized intermediate which is subsequently converted to an output that may be further processed or used as a final product.

[0011] In one or more aspects, the compositions and methods disclosed herein result in a final product that is an HVC and may utilized without further processing. Alternatively, the compositions and methods disclosed herein result in a final product that is additionally processed to generate an HVC. For purposes of simplicity and further explanation, a final product of the methods and compositions disclosed herein, whether or not subjected to additional processing, is termed an "HVC."

[0012] In an aspect, the production of an HVC is carried out according to a configuration having a first input to a first catalyst system, hereinafter referred to as the "oxidation biocatalyst," to produce an intermediate. The intermediate

may be subsequently used as an input (i.e., a second input) to a second catalyst system, hereinafter referred to as a "finishing catalyst," to produce an output. In some aspects, the first input, the intermediate (i.e., second input), the output, or a combination thereof comprises a mixture of molecules or compounds.

[0013] In an aspect, the oxidation biocatalyst comprises a biocatalyst, which when contacted with the first input, under suitable conditions, oxidizes the first input to form one or more oxidized intermediates. The one or more oxidized intermediates, as produced or following processing, may be contacted with the finishing catalyst, under conditions suitable for the formation of an output. In one or more aspects, the output is a final product that may be used as produced or may be further processed to achieve some user and/or process goal.

[0014] It is contemplated that the oxidation biocatalyst, the finishing catalyst, or both may comprise one or more catalytic species, one or more cofactors, or both as desired to obtain some user and/or process desired characteristics such as reaction rate, catalyst stability, and the like. Configurations of the type disclosed herein are referred to as "high value chemical output systems" and are designated "HVCOS."

[0015] It is contemplated that the systems, compositions, and methods disclosed herein may be utilized or readily adapted to the production of any number of HVCs. Consequently, while particular inputs, oxidation biocatalysts, oxidized intermediates, finishing catalysts, and outputs are described herein, it should be appreciated that these are exemplary and nonlimiting.

[0016] A schematic depiction of an aspect of a HVCOS **100** of the present disclosure is shown in FIG. **1**. Referring to FIG. **1**, a method of the present disclosure comprises introduction of a first input **10** to an oxidation biocatalyst **20**. Herein, introduction of the first input **10** to the oxidation biocatalyst **20** involves contacting of the first input **10** with the oxidation biocatalyst **20** under conditions suitable for the formation of an oxidized intermediate **30**. Such conditions will be described in more detail below. In an aspect, the first input **10** comprises ethylene glycol, glycerol, ethanol, methanol, or a combination thereof. In an aspect, the oxidation biocatalyst **20** comprises an alcohol oxidase, a copper radical oxidase, a glycerol oxidase, an alditol oxidase, or a combination thereof.

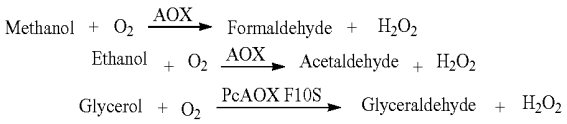
[0017] It is to be understood that while the oxidation biocatalyst may be specifically described in terms of the input being oxidized (e.g. oxidizes ethylene glycol, termed an ethylene glycol oxidase), the oxidation biocatalyst may catalyze oxidation of a range of substrates and/or a range of reactions in addition to those presently disclosed.

[0018] As depicted in FIG. **1**, the oxidized intermediate **30** may be introduced as an input to the finishing catalyst **40**. Herein introduction of the oxidized intermediate **30** to the finishing catalyst **40** involves contacting of the oxidized intermediate **30** with the finishing catalyst **40** under conditions suitable for the formation of an output **50**. Such conditions will be described in more detail later herein. In an aspect, the finishing catalyst **40** comprises a supported metal catalyst, a carboligating catalyst, an amine oxidase, a glyoxalase, an acid catalyst, a base catalyst, an isomerization catalyst or a combination thereof. In some aspects, the oxidized intermediate **30** and output **50** are the same. In such aspects, the oxidized intermediate **30** is not contacted with a finishing catalyst **40**.

[0019] In an aspect of the present disclosure, the output **50** is characterized by a percentage purity of from about 60% to about 95%, alternatively greater than about 70%, alternatively greater than about 80%, alternatively greater than about 90%, alternatively greater than about 95% or alternatively greater than about 99%. Herein, the percentage purity has its standard definition and is calculated by dividing the mass of the product of interest by the total mass of the product, and then multiplying this number by 100.

[0020] In an aspect, the oxidation biocatalyst is an alcohol oxidase (AOX, E.C. 1.1.3.13) or alcohol oxidase homolog. AOX is a ubiquitous flavin-dependent enzyme that oxidizes lower primary alcohols to aldehydes using oxygen as an oxidizing agent. An example is depicted in Reaction Scheme 1.

Reaction Scheme 1



[0021] AOX may be sourced from methylotrophic yeast of the species *Kloeckera, Torulopsis, Candida, Pichia*, Hansenia spora, and Metschnikowia. In an alternative aspect, the AOX is sourced from methanol-utilizing bacteria such as *Methylococcus capsulatus*, thermophilic soil fungi such as *Thermoascus aurantiacus*, and brown rot fungus such as *Gloeophyllum trabeum*. Alternatively, the AOX may be sourced from the white-rot basidiomycete *Phanerochaete chrysosporium*.

[0022] Methylotrophic yeasts are widely employed in fermentative processes for protein production and chemical synthesis. In many cases, these yeasts are used to generate proteins heterologously under control of the methanol-inducible AOX1 promoter. The endogenous AOX1 gene can be retained (Mut^+ strains), deleted (Muts), or deleted along with that of the minor alcohol oxidase AOX2 (Mut^-). Generally, higher protein titers are achieved in strains capable of utilizing methanol as a carbon source, while AOX genes may be deleted to improve protein titers in non-methanol induced processes.

[0023] In an aspect, the AOX is sourced from Mut^+ cells generated as a byproduct of methylotrophic yeast fermentation. Cell density in these processes can reach a final level of from about 350 g/L to about 450 g/L wet cells. When grown in methanol, AOX can comprise 30% of soluble cellular protein, 20% of cell-free extracts, and 80% of cell volume. Alternatively, AOX sequences used in this process may be sourced from organisms other than methylotrophic yeasts.

[0024] In an aspect, the oxidation biocatalyst is an inherently stable form of an AOX from thermophilic organisms such as *Candida methanosorbosa* (T_{opt}=45° C.), *Ogataea thermomethanolica* (T_{opt}=50° C.), or *Phanerochaete chrysosporium* (T_{opt}=50° C.). Potential sources of AOX suitable for use in the present disclosure are given in Table 1.

TABLE 1

Organism	
Achatina achatina	*Achatina fulica*
Arion ater	*Aspergillus ochraceus*
Aspergillus nidulans	*Aspergillus terreus*
Basidiomycota	*Byssochlamys spectabilis*
Candida boidinii	*Candida cariosilignicola*
Candida guilliermondii	*Candida methanolovescens*
Candida methanosorbosa	*Candida sonorensis*
Candida sithepensis	*Candida* sp. (in:
Candida succiphila	*Candida tropicalis*
Comamonas sp.	*Hansenula polymorpha*
Gloeophyllum trabeum	*Helix aspersa*
Kuraishia capsulata	*Lachnellula arida*
Lachnellula cervina	*Lachnellula occidentalis*
Lachnellula subtilissima	*Lachnellula suecica*
Lachnellula willkommii	*Methylococcus capsulatus*
Methylophilus methylotrophus	*Ochrobactrum* sp.
Ogataea glucozyma	*Ogataea henricii*
Ogataea methanolica	*Ogataea minuta*
Ogataea naganishii	*Ogataea philodendri*
Ogataea pignaliae	*Ogataea pini*
Ogataea siamensis	*Ogataea trehalophila*
Passalora fulva	*Penicillium chrysogenum*
Penicillium purpurascens	*Phanerochaete*
Pichia pastoris	*Komagataella pastoris* IFP
Phlebiopsis gigantea	*Pichia putida*
Thermoascus aurantiacus	*Poria contigua* CCA41016.1
Radulodon casearius	*Trametes cinnabarina*

[0025] An AOX for use in the present disclosure may be utilized in the oxidation of ethylene glycol and in such instances is termed an ethylene glycol oxidase or EgOX.

[0026] In an aspect, the oxidation biocatalyst is a member of the copper radical oxidase family. For example, and without limitation, a copper radical oxidase suitable for use in the present disclosure is galactose oxidase (GAO, EC 1.1.3.9). GAO is one of the most extensively studied alcohol oxidases with respect to both mechanistic investigations and practical applications. Other members in the copper radical oxidase family may be suitable employed in the present disclosure. GAO is a copper-dependent alcohol oxidase that oxidizes galactose residues either as monosaccharides or glycoconjugates that contain galactose at the nonreducing end. GAO is a novel metallo-radical complex comprising a protein radical coordinated to a copper ion in the active site. The unusually stable protein radical is formed from the redox-active side chain of a cross-linked tyrosine residue (Tyr-Cys).

[0027] In an aspect, the GAO is a mutated GAO isolated from *Fusarium graminearum* GAO (FgGAO) or a native GAO homolog from *Colletotrichum spinosum* (CsAlcOX), both of which are capable of oxidizing ethylene glycol. The FgGAO sequence containing the M1 mutations and R330K, Q406T, and W290F, and the C383S mutation and the mutations Y405F Q406E was able to oxidize 50 mM ethylene glycol with a specific activity of about 18 U mL^{-1} bacterial lysate and 3.9 U mg^{-1} with purified protein. This mutant has been designated FgGAO-Mut1. The FgGAO-M-RQW-S mutant (M1 mutations plus R330K, Q406T, W290F, C383S) was also found to be active on ethylene glycol. CsAlcOX exhibited a specific activity for the oxidation of 50 mM ethylene glycol of about 0.6 U mL^{-1}. The FgGAO-M-RQW-S, FgGAO-Mut1, CsAlcOX may have any of SEQ ID NO.:1 to SEQ ID NO.:5. In an alternative aspect, the GAO has any of SEQ ID NO: 6

[0028] In an aspect, the oxidation biocatalyst is a glycerol oxidase (GlyOx). GlyOx (E.C. 1.1.3.64) catalyzes the oxidation of glycerol with the concomitant consumption of oxygen to form glyceraldehyde and hydrogen peroxide according to the following reaction:

$$CH_2OHCHOHCH_2OH+O_2 \rightarrow CHOCHOHCH_2OH+H_2O_2$$

[0029] The reaction proceeds in the absence of exogeneous cofactors. Natural glycerol oxidases containing copper-heme cofactors have been sourced from *Botrytis allii, Aspergillus japonicus* (AT 001 and AT 008), *Aspergillus oryzae* AT 105, *Aspergillus parasiticus* AT 462, *Aspergillus flavus* AT 853, *Aspergillus tamarii* AT 857, *Aspergillus itaconicus* AT 923, *Aspergillus usamii* AT 989, *Neurospora crassa* AT 003, *Neurospora sitophila* AT 045, *Neurospora tetrasperma* AT 053, and *Penicffium* sp. UT 1750.

[0030] In an aspect, the oxidation biocatalyst is an alditol oxidase (AldO, E.C. 1.1.3.41). AldO is a soluble monomeric flavoprotein with subunits of 45.1 kDa, each containing a covalently bound FAD cofactor. AldOs are FAD-bound polyol oxidases which are members of the vanillyl-alcohol oxidase (VAO) family that catalyze the regioselective terminal oxidation of sugars including xylitol, sorbitol, L-threitol, D-mannitol, and smaller sugars. When fed a glycerol substrate, the AldO from *Streptomyces coelicolor* A3 can catalyze conversion of the sugar to glyceraldehyde. The enzyme performs a second oxidation event to transform glyceraldehyde into D-(R)-glyceric acid as depicted in Reaction Scheme 2.

Reaction Scheme 2

$$\text{Glycerol} + \frac{1}{2} O_2 \xrightarrow{\text{AldO}} \text{Glyceraldehyde} + H_2O_2$$

$$\text{Glyceraldehyde} + \frac{1}{2} O_2 \xrightarrow{\text{AldO}} \text{Glyceric Acid} + H_2O_2$$

[0031] In an aspect, an AldO suitable for use in the present disclosure is a wild type enzyme, a functional fragment thereof or a functional variant thereof. In an aspect, the AldO is a mutant having one or more mutations selected from the group consisting of the mutation of residues R322, E290, and K375.

[0032] In an aspect, the finishing catalyst comprises a metal oxidation catalyst. In such aspects the metal oxidation catalyst is a supported transition-metal oxidation catalyst, alternatively a nanoparticle supported transition-metal oxidation catalyst. Hereinafter, these are collectively designated "TMC." In an aspect, the support comprises carbon, silica, alumina, titania (TiO_2), zirconia (ZrO_2), a zeolite, or any combination thereof, which contains less than about 1.0 weight percent (wt. %), alternatively less than about 0.1 wt. %, or alternatively less than about 0.01 wt. % SiO_2 binders based on the total weight of the support.

[0033] Suitable support materials are predominantly mesoporous or macroporous, and substantially free from micropores. For example, the support may comprise less than about 20% micropores. In an aspect, the support is a porous nanoparticle support. As used herein, the term "micropore" refers to pores with diameter<2 nm, as measured by nitrogen adsorption and mercury porosimetry methods and as defined by IUPAC. As used herein, the term "mesopore" refers to pores with diameter from ca. 2 nm to ca. 50 nm, as measured by nitrogen adsorption and mercury

porosimetry methods and as defined by IUPAC. As used herein, the term "macropore" refers to pores with diameters larger than 50 nm, as measured by nitrogen adsorption and mercury porosimetry methods and as defined by IUPAC.

[0034] In an aspect, the support comprises a mesoporous carbon extrudate having a mean pore diameter ranging from about 10 nm to about 100 nm and a surface area greater than about 20 m^2 g^{-1} but less than about 300 m^2 g^{-1}. Supports suitable for use in the present disclosure may have any suitable shape. For example, the support may be shaped into 0.8-3 mm trilobes, quadralobes, or pellet extrudates. Such shaped supports enable the used of fixed trickle bed reactors to perform the final oxidation step under continuous flow.

[0035] In one or more aspects, the metal comprises a Group 8 metal (e.g., Re, Os, Ir, Pt, Ru, Rh, Pd, Ag), a 3d transition metal, an early transition metal, or combinations thereof. In an aspect, the TMC comprises gold, Au.

[0036] In an aspect, the TMC comprise platinum and gold and are heterogeneous, solid-phase TMCs. In such aspects, suitable catalyst supports include, without limitation, carbon, surface treated aluminas (such as passivated aluminas or coated aluminas), silicas, titanias, zirconias, zeolites, montmorillonites, and modifications, mixtures or combinations thereof. The catalyst support may be treated so as to promote the preferential deposition of platinum and gold on the outer surface of the support so as to create a shell type TMC. The platinum and gold-containing compounds that function as a TMC may be produced by any suitable methodology. For example, the platinum and gold-containing TMCs may be produced using deposition procedures such as incipient wetness, ion-exchange and deposition-precipitation.

[0037] In other aspects, the finishing catalyst is a TMC comprising metal phases that are monometallic or multimetallic combinations of Cu, Ag, Au, Ni, Pd, Pt, or Ir. The activity, selectivity, and stability of the active phases can be modulated with dopants of early 3d, 4d, and 5d transition metals, or heavy post transition metals such as Sn, Sb, and Bi. In some aspects, metals (e.g., Group 1 metals) are intercalated into the metal lattice to modulate catalyst properties. In an aspect, salt precursors of the active phases are deposited onto a support of the type disclosed herein using any suitable methodology. For example, deposition of the active phases may be carried out using techniques such as incipient wetness impregnation, bulk adsorption impregnation, or deposition precipitation.

[0038] In an aspect, the deposited salt precursor of the active phase is then converted to the active phase via Liquid Phase Reduction (LPR) with a suitable salt (e.g., formate salt) at temperatures of less than about 100° C. or via Gas Phase Reduction (GPR) at temperatures ranging from about 200° C. to about 500° C. or alternatively from about 200° C. to about 450° C. In an aspect, the finishing catalyst comprises gold, platinum or a combination thereof and calcination in air at temperatures of equal to or greater than about 150° C. is performed.

[0039] In an aspect, the amount of active phase loaded onto a support of the type disclosed herein is less than about 2.0 weight percent (wt. %), alternatively less than about 1.5 wt. % or alternatively less than about 1.0 wt. % based on the total weight of the TMC finishing catalyst. In an aspect, the amount of active phase loaded onto a support of the type disclosed herein is equal to or less than about 0.5 wt. % based on the total weight of the TMC finishing catalyst. In an aspect, the radial distribution of the active phase across the support is anisotropic where the active phase is substantially concentrated in a <500 μm annulus near the surface of the extrudate support in a "core-shell" configuration. A TMC finishing catalyst of the type disclosed herein may be characterized by a productivity for the conversion of aldehyde functionalities to carboxylic acids of equal to or greater than about 0.05 mol acid g^{-1} active metal h^{-1} or equal to or greater than about 0.1 mol acid g^{-1} active metal h^{-1} at selectivities from about 70% to about 90%, alternatively equal to or greater than about 70%, alternatively equal to or greater than about 80%, alternatively equal to or greater than about 85%, or alternatively equal to or greater than about 90%. In such aspects, the TMC finishing catalyst exhibits conversions of from about 60% to about 95%, alternatively equal to or greater than about 70%, alternatively equal to or greater than about 80%, or alternatively equal to or greater than about 90%. Such TMC finishing catalysts may display a steady state leaching amount of from about 1 ppb to about 100 ppb, alternatively less than about 100 ppb or alternatively less than about 90 ppb. In an aspect, a TMC finishing catalyst of the type disclosed herein may be utilized in a temperature range of from about 40° C. to about 120° C., alternatively form about 40° C. to about 110° C. or alternatively from about 50° C. to about 100° C. at pressures ranging from about 10 bar to about 100 bar, alternatively from about 20 bar to about 100 bar or alternatively from about 20 bar to about 90 bar.

[0040] In some aspects, the finishing catalyst is an isomerization catalyst. Any isomerization catalyst compatible with the other components of the HVCOS may be utilized. In some aspects, the isomerization catalyst comprises a zeolite.

[0041] In an aspect, the finishing catalyst comprises a carboligating catalyst. In such aspects, the carboligating catalyst comprises pyruvate decarboxylase (PDC) from prokaryote microorganisms, eukaryotic microorganisms or yeast, formolase, the E1 component of α-ketoglutarate dehydrogenase complex from SucA, the branched-chain alpha-keto acid decarboxylase, KdcA protein, of *Lactococcus lactis*, which decarboxylates a variety of branched and linear ketoacid substrates, B1 (thiamine) cofactor, or combinations thereof.

[0042] In an aspect, the carboligating catalyst is a pyruvate decarboxylase (PDC). Pyruvate decarboxylase (E.C. 4.1.1.1, also known as 2-oxo-acid decarboxylase, alpha-ketoacid decarboxylase, and pyruvic decarboxylase) is a homotetrameric enzyme that catalyzes the decarboxylation of pyruvic acid to produce acetaldehyde using magnesium and a thiamine pyrophosphate (TPP) cofactor. The enzyme is found in the cytoplasm of prokaryotes, and in the cytoplasm and mitochondria of eukaryotes. In yeast, this enzyme is a key player in the fermentation process that produces ethanol. A homolog of the yeast PDC is also present in filamentous fungi, e.g., *Aspergillus* spp., but less is known about its exact reaction mechanism.

[0043] Once regarded as irreversible due to CO_2 evolution in the biologically-relevant reaction, decarboxylase reactions have proved reversible. In an aspect, a PDC suitable for use in the present disclosure may be sourced from microbes with high specific activity on pyruvate including those sourced from *Acetobacter pasteurianus* PDC, *Zymobacter palmae* PDC (ZpPDC), *Zymomonas mobilis* PDC (ZmPDC), *Saccharomyces cerevisiae* PDC, or other sources mentioned herein.

[0044] In an aspect, the carboligating catalyst is a formolase. Formolase (FLS) is a computationally-designed enzyme derived from benzaldehyde lyase (BAL). Formolase contains the mutations mutant A28I, W89R, L90T, R188H, A394G, G419N, and A480W.

[0045] In an aspect, the carboligating catalyst is a KdcA from *Lactococcus lactis*. The natural substrate of KdcA decarboxylation is 3-methyl-2-oxobutanoic acid or α-ketoisovaleric acid to generate 2-methylbutanal. This enzyme has demonstrated the ability to carboligate carbon dioxide and 4-methylthio-2-oxobutanoate (MTOB) to produce L-methionine. The enzyme has also been shown to decarboxylate pyruvate with a specific activity of 3.67 U mg^{-1}. As such, it appears that KdcA is a promiscuous enzyme that can accept a wide range of branched and non-branched substrates for both decarboxylation and carboligation.

[0046] In an aspect, the carboligating catalyst comprises an immobilized vitamin B1 (or thiamine). For example, the carboligating catalyst can comprise thiamine immobilized to nanoparticles such as silica or maghemite-silica beads. In such aspects, a resonance-stabilized conjugate base of the thiazolium ion, thiamine, and the resonance stabilized carbanion (C) that it forms, are intermediats formed during the reaction. In an aspect, the carboligating catalyst may have any of SEQ ID NO:72 through SEQ ID NO: 86 or SEQ ID NO: 113.

[0047] In an aspect, the finishing catalyst is an amine oxidase (AMO, 1.4.3). AMOs can be grouped as either type I enzymes which contain a copper and topaquinone (TPQ or 2,4,5-trihydrophenylalanine quinone) in the active site or as type II enzymes which contain one FAD per subunit. AMOs suitable for use as a biocatalyst in the present disclosure include, without limitation, 1) monoamine oxidases (MAOs, EC 1.4.3.4), 2) primary-amine oxidases or amine oxidase (copper containing) (CAOs, EC 1.4.3.21), and 3) ethanolamine (EA) oxidases (EAOs, EC 1.4.3.8). In an aspect, an AMO suitable for use in the present disclosure has any of SEQ ID NO: 87 through SEQ ID NO:90.

[0048] In an aspect, the finishing catalyst is a monoamine oxidase (MAO). MAOs are mitochondrial outer-membrane type II AMOs that natively catalyze the reversible oxidative deamination of neurotransmitters and biogenic amines. MAOs act on primary amines, but to a lesser extent on secondary and tertiary amines. Unlike CAOs, MAOs cannot oxidize methylamine. In an aspect, an MAO suitable for use in the present disclosure is sourced from the bunch-flowered daffodil (*Narcissus tazetta*) that was found to use EA as a substrate with a K_m of 2.0×10^{-3} M and 50% the activity on the proposed native substrate n-propylamine.

[0049] In an aspect, the finishing catalyst is a copper-containing primary amine oxidase or copper-containing amine oxidase (CAO). CAOs are type I AMOs that reversibly oxidize primary monoamines but have little or no activity towards diamines. In the native forward reaction, catalysis proceeds via a Ping Pong Bi Bi reaction mechanism consisting of an oxidative half where molecular oxygen is reduced to hydrogen peroxide and a reductive half where a primary amine is oxidized to an aldehyde. In one or more aspects, this reaction is reversible in the presence of ammonia, hydrogen peroxide, and an aldehyde. Examples of CAOs that may be suitable for use in the present disclosure include without limitation MdAO2 enzyme from apple (*Malus domestica*), which demonstrates a specific activity of 0.0239 U mg^{-1} on EA; *Rhodococcus opacus* A01 and A02 which were shown to have activity on EA with A01 exhibiting a k_{cat} of 3.3 s^{-1} and K_m of 2.05 mM; and a secreted CAO from Sycephalastrum *racemosum* strain M0945, SrAOX (GenBank AB828595), was demonstrated to have a high specific activity of 7.01 U mg^{-1} on EA. SrAOX is not only expressible in *E. coli*, but can also be purified in functional form from this host, showing that TPQ and copper incorporation is achievable without further intervention. The affinity of SrAOX for EA is much higher than that of the *Arthrobacter* sp. EAO described below (K_m of mM compared with 15 mM).

[0050] In an aspect, the finishing catalyst is an ethanolamine oxidase (EAO). EAO is a homodimeric type I AMO similar to CAOs with a subunit mass of approximately 70 kDa. In an aspect, an EAO suitable for use in the present disclosure is sourced from *Arthrobacter* sp. (ArEAO) that was found to have a specific activity on ethanolamine of 9 U mg^{-1}. ArEAO can be heterologously expressed in *E. coli*.

[0051] In an aspect, the finishing catalyst is a glyoxalase. The major system for reactive α-carbonyl species (e.g., methylglyoxal (MG) and glyoxal (GO) detoxification in both prokaryotes and eukaryotes involves two enzymes, glyoxalase I (GLO1, EC 4.4.1.5) and glyoxalase II (GLO2, EC 3,1.2.6). GLO1 converts MG into S-D-lactoylglutathione (SLG) with glutathione (GSH) as a catalytic cofactor, and then GLO2 hydrolyzes SLG to D-lactate and GSH. Most recently, a GSH-independent glyoxalase system was identified in *Escherichia coli, Caenorhabditis eiegans*, mice and humans. In this system, glyoxalase III (GLY III) converts MG directly into D-lactate in a single step, with no cofactors. The enzyme instead relies on a conserved catalytic glu/asp-cys-tyr/his triad in its active site with the cysteine playing the pivotal role in catalysis. The in vitro activity of glyoxalase III is typically higher than the glyoxalase I/II system that generates D-lactate using a glutathione cofactor. In an aspect, the GLY III is sourced as the product of *E. coli* gene hchA, also known as Hsp31.

[0052] In an aspect, a GLYIII suitable for use in the present disclosure has any of SEQ ID NO: 91 through SEQ ID NO:112.

[0053] In an aspect, the finishing catalyst is a small molecule chemical catalyst such as an acid or base. Examples of acids or bases suitable for use as a finishing catalyst include without limitation hydrochloric acid, sulfuric acid, formic acid, sodium hydroxide and urea.

[0054] In an aspect, the biocatalysts suitable for use as an HVCOS of the type disclosed herein may further include one or more purified cofactors. Herein, a cofactor refers to non-protein chemical compound that modulates the biological activity of the biocatalyst. Many enzymes require cofactors to function properly. Nonlimiting examples of purified enzyme cofactors suitable for use in the present disclosure include thiamine pyrophosphate, NAD+, NADP+, pyridoxal phosphate, methyl cobalamin, cobalamine, biotin, Coenzyme A, tetrahydrofolic acid, menaquinone, ascorbic acid, flavin mononucleotide, flavin adenine dinucleotide, and Coenzyme F420. Such cofactors may be included in the biocatalyst preparation and/or be added at various points during the reaction. In some aspects, cofactors included with the biocatalyst preparation may be readily regenerated with oxygen and/or may remain stable throughout the lifetime of the enzyme(s).

[0055] As will be understood by one of ordinary skill in the art with the benefit of the present disclosure, reactions of

the type disclosed herein (e.g., biocatalyst oxidation of ethylene glycol) may result in the production of byproducts (e.g., hydrogen peroxide) that can detrimentally impact other components of the reaction mixture. For example, hydrogen peroxide may degrade the biocatalyst resulting in a loss of catalytic activity. In such aspects, mitigation of the detrimental effects of hydrogen peroxide may be carried out such as by the introduction of a catalase (E.C. 1.11.1.61), the use of a hydrogen peroxide-resistant biocatalyst, or combinations thereof.

[0056] In an aspect, a biocatalyst of the type disclosed herein is a wild type enzyme, a functional fragment thereof, or a functional variant thereof. As used herein, "fragment" is meant to include any amino acid sequence shorter than the full-length biocatalyst (e.g., AOX), but where the fragment maintains a catalytic activity sufficient to meet some user or process goal. Fragments may include a single contiguous sequence identical to a portion of the biocatalyst sequence. Alternatively, the fragment may have or include several different shorter segments where each segment is identical in amino acid sequence to a different portion of the amino acid sequence of the biocatalyst but linked via amino acids differing in sequence from the biocatalyst. Herein, a "functional variant" of the biocatalyst refers to a polypeptide which has at one or more positions of an amino acid insertion, deletion, or substitution, either conservative or non-conservative, and wherein each of these types of changes may occur alone, or in combination with one or more of the others, one or more times in a given sequence but retains catalytic activity.

[0057] In the alternative or in combination with the aforementioned mutations, the biocatalyst may be mutated to improve the catalytic activity. Mutations may be carried out in order to enhance the protein or a homolog activity, increase the protein stability in the presence of glycolaldehyde and/or hydrogen peroxide, and increase protein yield.

[0058] Herein, reference has been made to "sources" of biocatalysts. It is to be understood this refers to the biomolecule as expressed by the named organism. It is contemplated the biocatalyst may be obtained from the organism or a version of said biocatalyst (wildtype or recombinant) provided as a suitable construct to an appropriate expression system.

[0059] In an aspect, any biocatalyst of the type disclosed herein may be cloned into an appropriate expression vector and used to transform cells of an expression system such as *E. coli, Saccharomyces* sp., *Pichia* sp., *Aspergillus* sp., *Trichoderma* sp., or *Myceliophthora* sp. A "vector" is a replicon, such as plasmid, phage, viral construct or cosmid, to which another DNA segment may be attached. Vectors are used to transduce and express a DNA segment in cells. As used herein, the terms "vector" and "construct" may include replicons such as plasmids, phage, viral constructs, cosmids, Bacterial Artificial Chromosomes (BACs), Yeast Artificial Chromosomes (YACs) Human Artificial Chromosomes (HACs) and the like into which one or more gene expression cassettes may be or are ligated. Herein, a cell has been "transformed" by an exogenous or heterologous nucleic acid or vector when such nucleic acid has been introduced inside the cell, for example, as a complex with transfection reagents or packaged in viral particles. The transforming DNA may or may not be integrated (covalently linked) into the genome of the cell.

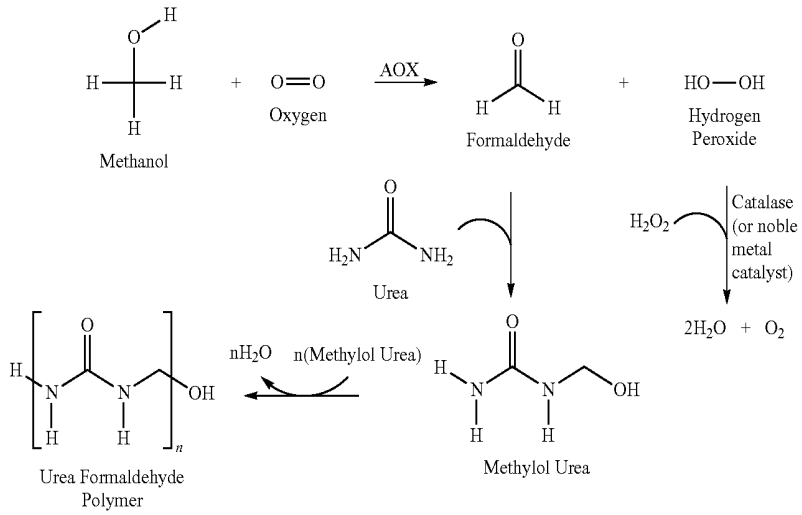
[0060] In an aspect, the gene of a biocatalyst disclosed herein is provided as a recombinant sequence in a vector where the sequence is operatively linked to one or more control or regulatory sequences. "Operatively linked" expression control sequences refers to a linkage in which the expression control sequence is contiguous with the gene of interest to control the gene of interest, as well as expression control sequences that act in trans or at a distance to control the gene of interest.

[0061] The term "expression control sequence" or "regulatory sequences" are used interchangeably and are used herein refer to polynucleotide sequences, which are necessary to affect the expression of coding sequences to which they are operatively linked. Expression control sequences are sequences that control the transcription, post-transcriptional events, and translation of nucleic acid sequences. Expression control sequences include appropriate transcription initiation, termination, promoter, and enhancer sequences; efficient RNA processing signals such as splicing and polyadenylation signals; sequences that stabilize cytoplasmic mRNA; sequences that enhance translation efficiency (e.g., ribosome binding sites); sequences that enhance protein stability; and when desired, sequences that enhance protein secretion. The nature of such control sequences differs depending upon the host organism; in prokaryotes, such control sequences generally include promoter, ribosomal binding site, and transcription termination sequence. The term "control sequences" is intended to include, at a minimum, all components whose presence is essential for expression, and can also include additional components whose presence is advantageous, for example, leader sequences and fusion partner sequences.

[0062] The term "recombinant host cell" ("expression host cell", "expression host system", "expression system" or simply "host cell"), as used herein, is intended to refer to a cell into which a recombinant vector has been introduced. It should be understood that such terms are intended to refer not only to the particular subject cell but to the progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term "host cell" as used herein. A recombinant host cell may be an isolated cell or cell line grown in culture or may be a cell which resides in a living tissue or organism.

[0063] In an aspect, an HVCOS is used in the production of formaldehyde. In such aspects, the input comprises methanol, the oxidation biocatalyst comprises an AOX, the oxidized intermediate comprises formaldehyde, the finishing catalyst comprises urea, and the output comprises a urea formaldehyde polymer. In such aspects, the oxidation biocatalyst, AOX is utilized in a bubble column reactor where oxygen is introduced under pressure to increase availability to the enzyme. The oxidation biocatalyst generates formaldehyde and hydrogen peroxide. The peroxide can be catalytically disproportionated into water and oxygen (e.g., using a catalase) to preserve enzyme function or hydrogen peroxide may be recovered as a coproduct. This is depicted in Reaction Scheme 3.

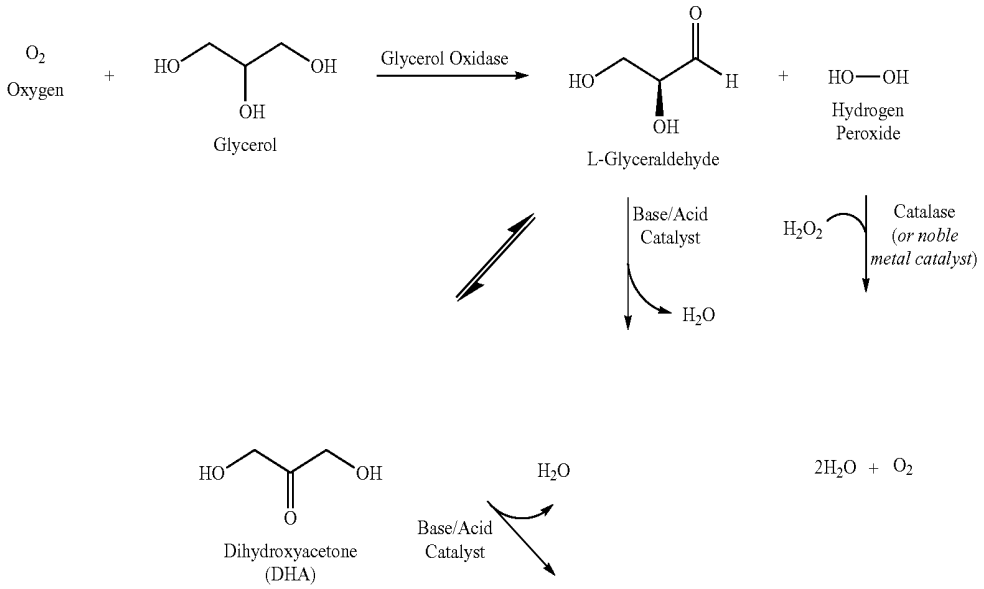
Reaction Scheme 3



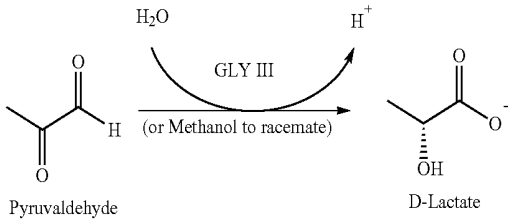
[0064] Because formaldehyde is a known crosslinker, it may be necessary to maintain low formaldehyde concentrations as it is generated through subsequent chemical reactions to protect the AOX, further enrichment and purification trains are not shown. It has been noted that AOX activity is negatively affected by aldehydes in two ways: 1) competitive inhibition by the aldehyde product with rapid equilibrium and 2) covalent interaction between the aldehyde and the enzyme. Short urea formaldehyde polymers precipitate from solution as a white solid until the condensation products reach a length at which the product remains soluble at room temperature. Upon further polymerization, the viscosity of the solution increases until an insoluble gel is irreversibly formed. These properties facilitate recovery of formaldehyde products from the reactor. The remaining solution containing a lower amount of formaldehyde and unreacted methanol can be recycled to the enzyme reactor. Other chemicals that may be useful for stabilizing produced formaldehyde include melamine, hydrazine hydrate, methylcellulose, guanamines, and bismelamines.

[0065] In an aspect, an HVCOS is used in the production of lactate. In such aspects, the input comprises glycerol, the oxidation biocatalyst comprises a GlyOX, the oxidized intermediate is L-glyceraldehyde, the finishing catalyst is an acid/base catalyst and the outputs are dihydroxyacetone, pyruvaldehyde (also known as methylglyoxal, or MG) and D-lactate. The reaction is depicted in Reaction Scheme 4.

Reaction Scheme 4



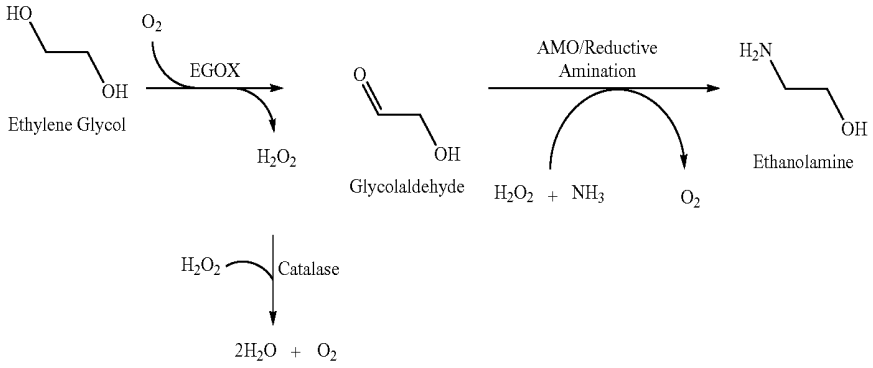
-continued



[0066] Referring to Reaction Scheme 4, GlyOX oxidizes glycerol to glyceraldehyde, generating hydrogen peroxide upon reduction of molecular oxygen. Hydrogen peroxide can be degraded with enzyme or retained. Glyceraldehyde, which exists in equilibrium with dihydroxyacetone, can be further dehydrated to methylglyoxal in the presence of an acid or base catalyst. Stereoselective conversion of MG to D-lactic acid then occurs in the presence of GLYIII. Generation of the lactic acid racemate may occur by treatment of the L-glyceraldehyde with enough base or acid to bypass the MG intermediate or by treating MG with methanol.

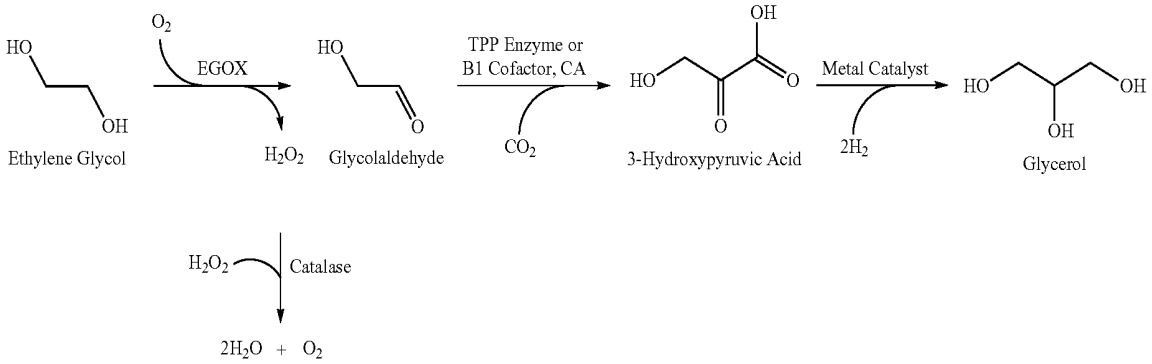
[0067] In an aspect, an HVCOS is used in the production of ethanolamine. In such aspects, the input comprises ethylene glycol, the oxidation biocatalyst comprises a CRO, a GAO, an AOX, a GlyOx or combinations thereof; the oxidized intermediate comprises a glycolaldehyde; the finishing catalyst comprises an AMO and the output comprises ethanolamine. The process is generally depicted in Reaction Scheme 5.

Reaction Scheme 5



[0068] In an aspect, an HVCOS is used in the production of glycerol. In such aspects, the input comprises ethylene glycol, the oxidation biocatalyst comprises an EgOX, the oxidized intermediate comprises a glycolaldehyde; the finishing catalyst comprises a carboligating catalyst, a TMC or both; and the output comprises glycerol. The reaction is generally depicted in Reaction Scheme 6.

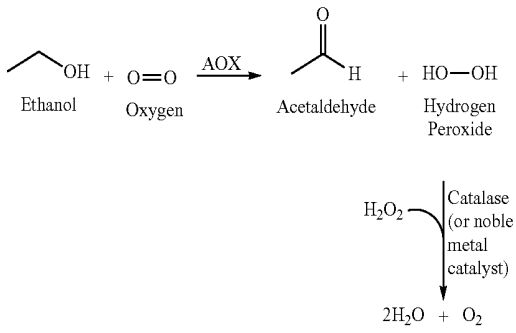
Reaction Scheme 5



[0069] Referring to Reaction Scheme 6, the HVCOS production comprises conversion of ethylene glycol to glycolaldehyde. In an aspect, EgOx catalyzes the conversion of ethylene glycol to form the intermediate, glycolaldehyde, using molecular oxygen and generating hydrogen peroxide. Glycolaldehyde and carbon dioxide in the presence of the finishing catalyst, a carboligation catalyst is converted to 3-hydroxypyruvic acid that is subsequently reduced by a TMC to glycerol.

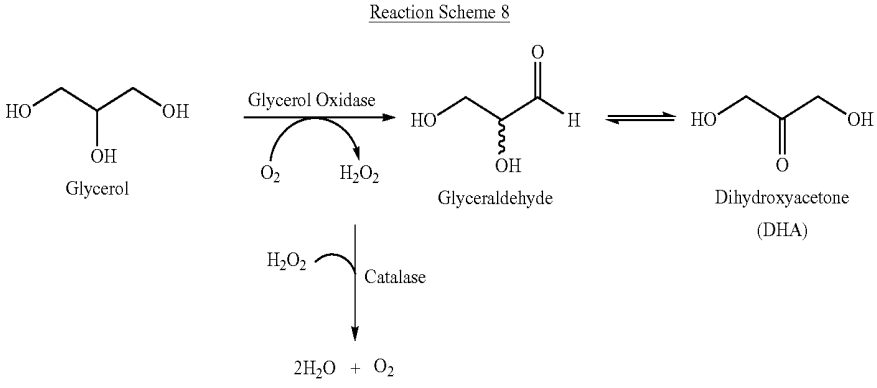
[0070] In an aspect, an HVCOS is used in the production of acetaldehyde. In such aspects, the input comprises ethanol; the oxidation biocatalyst comprises AOX and the output is acetaldehyde. The reaction is generally depicted in Reaction Scheme 6. In this aspect, AOX may be added either as a purified protein, or by the addition of whole cell *Pichia Pastoris* with AOX expressed.

Reaction Scheme 7



[0071] In an aspect, an HVCOS is used in the production of dihydroxyacetone (DHA). In such aspects, the input comprises glycerol; the oxidation biocatalyst comprises an AOX, a AldO, a CRO, a GlyOX or combinations thereof; the intermediate comprises glyceraldehyde the finishing catalyst comprise an isomerization catalyst and the output comprises DHA. This is depicted in Reaction Scheme 8.

Reaction Scheme 8



Examples

[0072] The subject matter having been generally described, the following examples are given as particular aspects of the disclosure and are included to demonstrate the practice and advantages thereof, as well as aspects and features of the presently disclosed subject matter. It should be appreciated by those of skill in the art that the techniques disclosed in the examples that follow represent techniques discovered by the inventors to function well in the practice of the present subject matter, and thus can be considered to constitute preferred modes for its practice. However, those of skill in the art should, in light of the present disclosure, appreciate that many changes can be made in the specific aspects which are disclosed and still obtain a like or similar result without departing from the scope of the instant disclosure. It is understood that the examples are given by way of illustration and are not intended to limit the specification of the claims to follow in any manner.

[0073] A mutated *Fusarium graminearum* GAO (FgGAO) and a native GAO homolog from *Colletotrichum spinosum* (CsAlcOX) has both been shown to be capable of oxidizing ethylene glycol. The FgGAO sequence containing the M1 mutations and R330K, Q406T, and W290F, as well as the C383S mutation was able to oxidize ethylene glycol with a specific activity of about 18 U mL^{-1} bacterial lysate and 3.9 U mg^{-1} with purified protein as while CsAlcOX exhibited a specific activity for the oxidation of ethylene glycol of about 0.6 U mL^{-1}. Studies are underway to elucidate mutations in the FgGAO M-RQW-S scaffold to enhanced stability and activity.

Example Protocol for Enzyme Testing

Colorimetric Microtiter Plate Screening

[0074] Mutants of biocatalysts may be screened using a microtiter plate-base colorimetric assay that monitors the production of hydrogen peroxide. For example, the reagents o-dianisidine and 2,2'-azino-bis(3-ethylbenzothiazoline-6-sulphonic acid) (ABTS) may be used in conjunction with horseradish peroxidase to elicit a color change in the presence of hydrogen peroxide. Enzymes or combination of enzymes are diluted to total stock concentration of 1 mg/mL and then diluted further into a roughly 200 μL volume containing glucose substrate, the reporter molecule, buffer, and horseradish peroxidase. The dilution factor is chosen such that the change in color falls within the range of 0.01-0.06 absorbance units per minute as measured with a plate-based spectrophotometer. This rate of change can be used along with the dilution factor and extinction coefficient of the reporter molecule to calculate the specific activity of the enzyme(s) or plotted to select mutants with high activity for further characterization.

Parr Bomb Scale Testing

[0075] Once suitable enzymes have been identified through the screening process, a pressurized Parr bomb system will be used to mimic the reactor conditions at scale in order to assess the efficacy of converting an input (e.g., ethylene glycol) to a HVC (e.g., ethanolamine) using the disclosed processes. In a final volume of about 50 mL, biocatalysts at amounts ranging from about 0.001 percent weight by volume (w/v %) to about 1 w/v % will be combined with approximately 20 w/v % input (e.g., ethylene glycol) and a suitable buffer at an initial pH in the range of from about 4 to about 7. Catalase may be added to provide a ratio of from about 1:1 to 1:20 biocatalyst to catalase ratio to prevent accumulation of hydrogen peroxide. The mixture will be loaded into the Parr bomb containing a stir bar. To improve mass transfer of oxygen into the solution, the vessel will be sparged with oxygen two times, then pressurized to 100 psig. The reactor will be held at constant temperature, typically about 20° C. but within the range of from about 10° C. to about 80° C. and the mixture allowed to react until the reaction is complete. During the reaction, the vessel may be depressurized to adjust the pH and obtain samples to assess conversion and product profile. Testing methods may include monitoring pH decrease as acids are produced, a colorimetric o-dianisidine assay to monitor formation of hydrogen peroxide, and HPLC for the detection of glycolaldehyde and EA.

[0076] Reactions of the type disclosed herein are carried out in a reactor system. Such reactor systems may utilize multiple reactors, but it could be a single continuous stirred tank slurry reactor (CSTR) or comprise a plurality of reactors (e.g., fixed bed reactors) of various sizes with or without interstage cooling and interstage caustic injection. Similarly, the enzymatic reactor could be a sparged bubble column or an air lift column or a falling film high pressure oxidation vessel. In an aspect, the inputs and oxidation biocatalyst are dosed into a bubble column reactor sparged with air to improve oxygen mass transfer. Typical operating ranges for the Enzyme Reactor is 20-60° C. at pressures between 1 and 15 bar. pH can be controlled by the addition of strong acids, bases, or buffers. Enzyme reactor effluent may be sent to a tangential flow filter (TFF) to preserve enzymes in the enzyme reactor as recycled retentate, with permeate flowing further down the process.

Additional Disclosure

[0077] The following are non-limiting, specific aspects in accordance with the present disclosure:

[0078] A first aspect which is a system for the production of high value chemicals, comprising (a) an input selected from the group consisting of ethylene glycol, glycerol, ethanol methanol or a combination thereof; (b) an oxidation biocatalyst comprising an alcohol oxidase, a copper radical oxidase, a glycerol oxidase, an alditol oxidase or a combination thereof; (c) an oxidized intermediate; (d) a finishing catalyst comprising a supported metal catalyst, a carboligating catalyst, an amine oxidase, a glyoxalase, an acid catalyst, a base catalyst, an isomerization catalyst or a combination thereof; and (e) an output.

[0079] A second aspect which is the system of the first aspect wherein the alcohol oxidase has any of SEQ ID NO: 1 to SEQ ID NO: 71.

[0080] A third aspect which is the system of any of the first through second aspects wherein the carboligating catalyst has any of SEQ ID NO: 72 to SEQ ID NO: 86.

[0081] A fourth aspect which is the system of any of the first through third aspects wherein the carboligating catalyst has SEQ ID NO: 113.

[0082] A fifth aspect which is the system of any of the first through fourth aspects wherein the amine oxidase has any of SEQ ID NO: 87 to SEQ ID NO: 90.

[0083] A sixth aspect which is the system of any of the first through fifth aspects wherein the glyoxalase has any of SEQ ID NO: 91 to SEQ ID NO: 112.

[0084] A seventh aspect which is the system of any of the first through sixth aspects wherein the supported metal catalyst comprises a nanoparticle support.

[0085] An eighth aspect which is the system of any of the first through seventh aspects wherein the support of the supported metal catalyst comprises the support comprises carbon, silica, surface treated alumina, titania (TiO_2), zirconia (ZrO_2), a zeolite, montmorillonites, or a combination thereof.

[0086] A ninth aspect which is the system of any of the first through eighth aspects wherein the supported metal catalyst comprises a Group 8 metal, a 3d transition metal, an early transition metal, or combinations thereof.

[0087] A tenth aspect which is the system of any of the first through ninth aspects wherein the supported metal catalyst comprises gold, platinum or a combination thereof.

[0088] An eleventh aspect which is the system of any of the first through tenth aspects wherein the carboligating catalyst comprises pyruvate decarboxylase, formolase, the E1 component of α-ketoglutarate dehydrogenase complex from SucA, the KdcA gene product of *Lactococcus lactis*, a cofactor, or a combination thereof.

[0089] A twelfth aspect which is the system of any of the first through eleventh aspects wherein (i) the input comprises methanol; (ii) the oxidation biocatalyst comprises an alcohol oxidase; (iii) the intermediate comprises formaldehyde; (iv) the finishing catalyst comprises urea; and (v) the output comprises a urea formaldehyde polymer.

[0090] A thirteenth aspect which is the system of any of the first through twelfth aspects further comprising a catalase.

[0091] A fourteenth aspect which is the system of any of the first through thirteenth aspects wherein (i) the input comprises glycerol; (ii) the oxidation biocatalyst comprises a glycerol oxidase; (iii) the oxidized intermediate comprises L-glyceraldehyde; (iv) the finishing catalyst comprises an acid catalyst; and (v) the output comprises D-lactate.

[0092] A fifteenth aspect which is the system of any of the first through fourteenth aspects wherein (i) the input comprises ethylene glycol; (ii) the oxidation biocatalyst comprises a copper radical oxidase, a galactose oxidase, an alcohol oxidase, a glycerol oxidase or a combination thereof; (iii) the oxidized intermediate comprises a glycolaldehyde; (iv) the finishing catalyst comprises an amine monooxidase; and (v) the output comprises ethanolamine.

[0093] A sixteenth aspect which is the system of any of the first through fourteenth aspects wherein (i) the input comprises ethylene glycol; (ii) the oxidation biocatalyst comprises an ethylene glycol oxidase; (iii) the oxidized intermediate comprises a glycolaldehyde; (iv) the finishing catalyst comprises a carboligating catalyst, a supported metal catalyst or a combination thereof; and (v) the output comprises glycerol.

[0094] A seventeenth aspect which is the system of any of the first through fourteenth aspects wherein (i) the input comprises ethanol; (ii) the oxidation biocatalyst comprises an alcohol oxidase; (iii) the oxidized intermediate and (iv) the output comprises an acetaldehyde.

[0095] An eighteenth aspect which is the system of the seventeenth aspect further comprising a catalase.

[0096] A nineteenth aspect which is the system of any of the first through fourteenth aspects wherein (i) the input comprises glycerol; (ii) the oxidation biocatalyst comprises an alcohol oxidase, an alditol oxidase, a copper-radical oxidase, a glycerol oxidase or a combination thereof; (iii) the oxidized intermediate comprises glyceraldehyde; (iv) the finishing catalyst comprises an isomerization catalyst; and (v) the output comprises dihydroxyacetone.

[0097] A twentieth aspect which is the system of any of the first through nineteenth aspects wherein the output has a percentage purity of from about 60% to about 95%.

[0098] A twenty-first aspect which is a method for the production of high value chemicals, comprising:(a) contacting an input selected from the group consisting of ethylene glycol, glycerol, ethanol methanol or a combination thereof with an oxidation biocatalyst comprising an alcohol oxidase, a copper radical oxidase, a glycerol oxidase, an alditol oxidase or a combination thereof to form an oxidized intermediate; (b) contacting the oxidized intermediate with a finishing catalyst comprising a supported metal catalyst, a carboligating catalyst, an amine oxidase, a glyoxalase, an acid catalyst, a base catalyst, an isomerization catalyst or a combination thereof to form an outpyt.

[0099] A twenty-second aspect which is the method of the twenty-first aspect wherein the alcohol oxidase has any of SEQ ID NO: 1 to SEQ ID NO: 71.

[0100] A twenty-third aspect which is the method of any of the twenty-first through twenty-second aspects wherein the carboligating catalyst has any of SEQ ID NO: 72 to SEQ ID NO: 86.

[0101] A twenty-fourth aspect which is the method of any of the twenty-first through twenty-third aspects wherein the carboligating catalyst has SEQ ID NO: 113.

[0102] A twenty-fifth aspect which is the method of any of the twenty-first through twenty-fourth aspects wherein the amine oxidase has any of SEQ ID NO: 87 to SEQ ID NO: 90.

[0103] A twenty-sixth aspect which the method of any of the twenty-first through twenty-fifth aspects wherein the glyoxalase has any of SEQ ID NO: 91 to SEQ ID NO: 112.

[0104] A twenty-seventh aspect which is the method of any of the twenty-first through twenty-sixth aspects wherein the supported metal catalyst comprises a nanoparticle support.

[0105] A twenty-eighth aspect which is the method of any of the twenty-first through twenty-seventh aspects the carboligating catalyst comprises pyruvate decarboxylase, formolase, the E1 component of α-ketoglutarate dehydrogenase complex from SucA, the KdcA gene product of *Lactococcus lactis*, a cofactor, or a combination thereof.

[0106] A twenty-ninth aspect which is the method of any of the twenty-first through twenty-eight aspects wherein the output has a percentage purity of from about 60% to about 95%.

[0107] The subject matter having been shown and described, modifications thereof can be made by one skilled in the art without departing from the spirit and teachings of the subject matter. The aspects described herein are exemplary only and are not intended to be limiting. Many variations and modifications of the subject matter disclosed herein are possible and are within the scope of the disclosed subject matter. Where numerical ranges or limitations are expressly stated, such express ranges or limitations should be understood to include iterative ranges or limitations of like magnitude falling within the expressly stated ranges or limitations (e.g., from about 1 to about 10 includes, 2, 3, 4, etc.; greater than 0.10 includes 0.11, 0.12, 0.13, etc.). Use of the term "optionally" with respect to any element of a claim

is intended to mean that the subject element is required, or alternatively, is not required. Both alternatives are intended to be within the scope of the claim. Use of broader terms such as comprises, includes, having, etc. should be understood to provide support for narrower terms such as consisting of, consisting essentially of, comprised substantially of, etc.

[0108] Accordingly, the scope of protection is not limited by the description set out above but is only limited by the claims which follow, that scope including all equivalents of the subject matter of the claims. Each and every claim is incorporated into the specification as an aspect of the present disclosure. Thus, the claims are a further description and are an addition to the aspects of the present invention. The discussion of a reference herein is not an admission that it is prior art to the presently disclosed subject matter, especially any reference that may have a publication date after the priority date of this application. The disclosures of all patents, patent applications, and publications cited herein are hereby incorporated by reference, to the extent that they provide exemplary, procedural or other details supplementary to those set forth herein.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 113

<210> SEQ ID NO 1
<211> LENGTH: 657
<212> TYPE: PRT
<213> ORGANISM: Fusarium graminearum

<400> SEQUENCE: 1

```
Met Gly His His His His His His Ser Ser Gly His Ile Glu Gly Arg
1               5                  10                  15

His Met Ala Ser Ala Pro Ile Gly Ser Ala Ile Pro Arg Asn Asn Trp
            20                  25                  30

Ala Val Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala
        35                  40                  45

Ile Asp Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn
    50                  55                  60

Gly Asp Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr
65                  70                  75                  80

Gln Asn Val Asn Gly Leu Ser Val Leu Pro Arg Gln Asp Gly Asn Gln
                85                  90                  95

Asn Gly Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr
            100                 105                 110

Asn Trp Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr
        115                 120                 125

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

Val Ala Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu
145                 150                 155                 160

Ile Asn Val Phe Gln Ala Ser Ser Tyr Thr Ala Pro Gln Pro Gly Leu
                165                 170                 175

Gly Arg Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala
            180                 185                 190

Ala Ile Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg
        195                 200                 205

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

Trp Asp Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr
225                 230                 235                 240

Lys His Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln
                245                 250                 255

Ile Val Val Thr Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp
            260                 265                 270
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Ser Ser Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg
        275                 280                 285

Gly Tyr Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile
    290                 295                 300

Gly Gly Ser Phe Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr
305                 310                 315                 320

Ser Pro Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn
                325                 330                 335

Pro Met Leu Thr Ala Asp Lys Gln Gly Leu Tyr Lys Ser Asp Asn His
            340                 345                 350

Ala Trp Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro
        355                 360                 365

Ser Thr Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys
    370                 375                 380

Ser Ala Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met
385                 390                 395                 400

Ser Gly Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr
                405                 410                 415

Phe Gly Gly Ser Pro Asp Tyr Thr Asp Ser Asp Ala Thr Thr Asn Ala
            420                 425                 430

His Ile Ile Thr Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe
        435                 440                 445

Ala Ser Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val
    450                 455                 460

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

Pro Phe Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro
                485                 490                 495

Glu Gln Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala
            500                 505                 510

Tyr His Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly
        515                 520                 525

Gly Gly Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln
    530                 535                 540

Ile Phe Thr Pro Asn Tyr Leu Tyr Asp Ser Asn Gly Asn Leu Ala Thr
545                 550                 555                 560

Arg Pro Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly
                565                 570                 575

Arg Ile Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile
            580                 585                 590

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

Pro Leu Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val
    610                 615                 620

Pro Ser Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val
625                 630                 635                 640

Met Asn Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr
                645                 650                 655

Gln
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<210> SEQ ID NO 2

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<211> LENGTH: 639
<212> TYPE: PRT
<213> ORGANISM: Fusarium graminearum

<400> SEQUENCE: 2

```
Ala Ser Ala Pro Ile Gly Ser Ala Ile Pro Arg Asn Asn Trp Ala Val
1               5                  10                  15

Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
            20                  25                  30

Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
        35                  40                  45

Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
    50                  55                  60

Val Asn Gly Leu Ser Val Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
65                  70                  75                  80

Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
                85                  90                  95

Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
            100                 105                 110

Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
        115                 120                 125

Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
    130                 135                 140

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

Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile
                165                 170                 175

Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
            180                 185                 190

Ala Phe Glu Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
        195                 200                 205

Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
    210                 215                 220

Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
225                 230                 235                 240

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

Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
            260                 265                 270

Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
        275                 280                 285

Ser Phe Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
    290                 295                 300

Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
305                 310                 315                 320

Leu Thr Ala Asp Lys Gln Gly Leu Tyr Lys Ser Asp Asn His Ala Trp
                325                 330                 335

Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
            340                 345                 350

Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
        355                 360                 365

Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Ser Gly
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    370                 375                 380

Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
385                 390                 395                 400

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

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

Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
        435                 440                 445

Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
    450                 455                 460

Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
465                 470                 475                 480

Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Ala Tyr His
                485                 490                 495

Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
            500                 505                 510

Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
        515                 520                 525

Thr Pro Asn Tyr Leu Tyr Asp Ser Asn Gly Asn Leu Ala Thr Arg Pro
    530                 535                 540

Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
545                 550                 555                 560

Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
                565                 570                 575

Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
            580                 585                 590

Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
        595                 600                 605

Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
    610                 615                 620

Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
625                 630                 635


<210> SEQ ID NO 3
<211> LENGTH: 496
<212> TYPE: PRT
<213> ORGANISM: Colletotrichum spinosum

<400> SEQUENCE: 3

Met Gly Gln Gly Val Gly Gln Trp Gly Pro Leu Val Lys Phe Pro Ile
1               5                   10                  15

Val Pro Val Ala Val Ala Leu Ile Pro Glu Ser Gly Asn Met Leu Val
            20                  25                  30

Trp Ser Ser Gly Trp Pro Asn Arg Trp Thr Asn Ala Gly Asn Gly Lys
        35                  40                  45

Thr Phe Thr Ser Leu Tyr Asp Val Ser Thr Gly Lys Ala Gly Asp Ala
    50                  55                  60

Ile Val Gln Asn Thr Gln His Asp Met Phe Cys Pro Gly Thr Ser Leu
65                  70                  75                  80

Asp Val Glu Gly Arg Ile Ile Val Thr Gly Gly Ser Ser Ala Ala Lys
                85                  90                  95
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Thr Ser Val Leu Asp Phe Arg Lys Gly Glu Ser Ser Ser Trp Ala Pro
            100                 105                 110

Leu Ser Asn Met Gln Ile Ser Arg Gly Tyr Gln Ser Ser Cys Thr Thr
        115                 120                 125

Ser Glu Gly Lys Ile Phe Val Ile Gly Gly Ser Phe Ser Gly Ala Gly
    130                 135                 140

Thr Arg Asn Gly Glu Ile Tyr Asp Thr Ala Ser Asn Lys Trp Thr Lys
145                 150                 155                 160

Leu Ala Gly Cys Pro Val Lys Pro Leu Val Met Gln Arg Gly Leu Phe
                165                 170                 175

Gln Asp Ser His Thr Trp Leu Trp Ser Trp Lys Asn Gly Ser Val Leu
            180                 185                 190

Gln Ala Gly Pro Ala Lys Gln Met Asn Trp Tyr Asp Thr Lys Gly Thr
        195                 200                 205

Gly Ala Asn Thr Pro Ala Gly Leu Arg Gly Ala Asp Asp Asp Ala Met
    210                 215                 220

Cys Gly Val Ser Val Met Phe Asp Ala Val Ala Gly Lys Ile Phe Thr
225                 230                 235                 240

Tyr Gly Gly Gly Lys Ala Tyr Thr Gly Tyr Ala Ala Ser Ser Asn Ala
                245                 250                 255

His Ile Leu Thr Leu Gly Glu Pro Gly Gln Gln Val Gln Val Gln Lys
            260                 265                 270

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

Pro Asp Gly Arg Ile Trp Val Val Gly Gly Met Arg Gln Met Gln Leu
    290                 295                 300

Phe Ser Asp Asn Thr Pro Gln Leu Thr Pro Glu Leu Phe Asp Pro Ala
305                 310                 315                 320

Thr Gly Lys Phe Thr Pro Thr Ala Pro His Ala Ile Pro Arg Asn Tyr
                325                 330                 335

His Ser Thr Ala Leu Leu Met Ala Asp Ala Thr Val Trp Ser Gly Gly
            340                 345                 350

Gly Gly Leu Cys Gly Ala Asn Cys Lys Glu Asn Lys Phe Asp Gly Gln
        355                 360                 365

Phe Trp Ser Pro Pro Tyr Leu Phe Glu Ala Asp Gly Lys Thr Pro Ala
    370                 375                 380

Gln Arg Pro Val Ile Asp Ser Leu Ser Asp Lys Thr Val Arg Ala Gly
385                 390                 395                 400

Ala Pro Leu Val Val Thr Met Lys Asp Glu Gly Lys Tyr Thr Phe Ser
                405                 410                 415

Met Leu Arg Val Ser Ala Thr Thr His Thr Val Asn Thr Asp Gln Arg
            420                 425                 430

Arg Ile Pro Leu Asp Gly Gln Asp Gly Gly Asp Gly Lys Ser Phe Thr
        435                 440                 445

Val Asn Met Pro Gly Asp Tyr Gly Val Val Ile Pro Gly Tyr Tyr Met
    450                 455                 460

Met Phe Ala Met Asn Glu Ala Gly Val Pro Cys Val Ala Lys Phe Phe
465                 470                 475                 480

Lys Val Ala Leu Gly Gln Thr Gly Leu Glu His His His His His His
                485                 490                 495
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<210> SEQ ID NO 4
<211> LENGTH: 483
<212> TYPE: PRT
<213> ORGANISM: Colletotrichum spinosum

<400> SEQUENCE: 4

Gly Gln Gly Val Gly Gln Trp Gly Pro Leu Val Lys Phe Pro Ile Val
1 5 10 15

Pro Val Ala Val Ala Leu Ile Pro Glu Ser Gly Asn Met Leu Val Trp
20 25 30

Ser Ser Gly Trp Pro Asn Arg Trp Thr Asn Ala Gly Asn Gly Lys Thr
35 40 45

Phe Thr Ser Leu Tyr Asp Val Ser Thr Gly Lys Ala Gly Asp Ala Ile
50 55 60

Val Gln Asn Thr Gln His Asp Met Phe Cys Pro Gly Thr Ser Leu Asp
65 70 75 80

Val Glu Gly Arg Ile Ile Val Thr Gly Gly Ser Ser Ala Ala Lys Thr
85 90 95

Ser Val Leu Asp Phe Arg Lys Gly Glu Ser Ser Ser Trp Ala Pro Leu
100 105 110

Ser Asn Met Gln Ile Ser Arg Gly Tyr Gln Ser Ser Cys Thr Thr Ser
115 120 125

Glu Gly Lys Ile Phe Val Ile Gly Gly Ser Phe Ser Gly Ala Gly Thr
130 135 140

Arg Asn Gly Glu Ile Tyr Asp Thr Ala Ser Asn Lys Trp Thr Lys Leu
145 150 155 160

Ala Gly Cys Pro Val Lys Pro Leu Val Met Gln Arg Gly Leu Phe Gln
165 170 175

Asp Ser His Thr Trp Leu Trp Ser Trp Lys Asn Gly Ser Val Leu Gln
180 185 190

Ala Gly Pro Ala Lys Gln Met Asn Trp Tyr Asp Thr Lys Gly Thr Gly
195 200 205

Ala Asn Thr Pro Ala Gly Leu Arg Gly Ala Asp Asp Asp Ala Met Cys
210 215 220

Gly Val Ser Val Met Phe Asp Ala Val Ala Gly Lys Ile Phe Thr Tyr
225 230 235 240

Gly Gly Gly Lys Ala Tyr Thr Gly Tyr Ala Ala Ser Ser Asn Ala His
245 250 255

Ile Leu Thr Leu Gly Glu Pro Gly Gln Gln Val Gln Val Gln Lys Leu
260 265 270

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

Asp Gly Arg Ile Trp Val Val Gly Gly Met Arg Gln Met Gln Leu Phe
290 295 300

Ser Asp Asn Thr Pro Gln Leu Thr Pro Glu Leu Phe Asp Pro Ala Thr
305 310 315 320

Gly Lys Phe Thr Pro Thr Ala Pro His Ala Ile Pro Arg Asn Tyr His
325 330 335

Ser Thr Ala Leu Leu Met Ala Asp Ala Thr Val Trp Ser Gly Gly Gly
340 345 350

Gly Leu Cys Gly Ala Asn Cys Lys Glu Asn Lys Phe Asp Gly Gln Phe
355 360 365

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Trp Ser Pro Pro Tyr Leu Phe Glu Ala Asp Gly Lys Thr Pro Ala Gln
    370                 375                 380

Arg Pro Val Ile Asp Ser Leu Ser Asp Lys Thr Val Arg Ala Gly Ala
385                 390                 395                 400

Pro Leu Val Val Thr Met Lys Asp Glu Gly Lys Tyr Thr Phe Ser Met
                405                 410                 415

Leu Arg Val Ser Ala Thr Thr His Thr Val Asn Thr Asp Gln Arg Arg
            420                 425                 430

Ile Pro Leu Asp Gly Gln Asp Gly Gly Asp Gly Lys Ser Phe Thr Val
        435                 440                 445

Asn Met Pro Gly Asp Tyr Gly Val Val Ile Pro Gly Tyr Tyr Met Met
    450                 455                 460

Phe Ala Met Asn Glu Ala Gly Val Pro Cys Val Ala Lys Phe Phe Lys
465                 470                 475                 480

Val Ala Leu


<210> SEQ ID NO 5
<211> LENGTH: 728
<212> TYPE: PRT
<213> ORGANISM: Hypomyces rosellus

<400> SEQUENCE: 5

Met Ala Asp Gln Gln Thr Val Leu Ser Val Ser Val Pro Gly Tyr Ile
1               5                   10                  15

Arg Leu Glu Asp Ile Ser Tyr Ser Ser Ser Ala Ser Lys Thr Phe Ile
            20                  25                  30

Ile Leu Ser Ser His Ser Leu Leu Ile Ile Ile Ser Leu Tyr Val Asn
        35                  40                  45

Met Lys His Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala
    50                  55                  60

Val Ala Val Thr Val Pro His Lys Ala Val Gly Thr Gly Ile Pro Glu
65                  70                  75                  80

Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser
                85                  90                  95

Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser
            100                 105                 110

Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe Trp
        115                 120                 125

His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr
    130                 135                 140

Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu
145                 150                 155                 160

Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu Val
                165                 170                 175

Tyr Leu Ser Ser Asp Gly Thr Asn Trp Gly Ser Pro Val Ala Ser Gly
            180                 185                 190

Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg
        195                 200                 205

Pro Ala Arg Tyr Val Arg Leu Val Ala Ile Thr Glu Ala Asn Gly Gln
    210                 215                 220

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser Tyr
225                 230                 235                 240
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Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp Leu
                245                 250                 255

Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg Val
            260                 265                 270

Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
        275                 280                 285

Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser Thr Gly Ile Val Ser
    290                 295                 300

Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
305                 310                 315                 320

Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala
                325                 330                 335

Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
            340                 345                 350

Pro Asp Met Gln Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Met Ser
        355                 360                 365

Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Val Phe
    370                 375                 380

Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr Ser
385                 390                 395                 400

Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln Gly
                405                 410                 415

Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys Gly
            420                 425                 430

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
        435                 440                 445

Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg
    450                 455                 460

Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
465                 470                 475                 480

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp
                485                 490                 495

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro Gly
            500                 505                 510

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

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

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe
545                 550                 555                 560

Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn
                565                 570                 575

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
            580                 585                 590

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr
        595                 600                 605

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn
    610                 615                 620

Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr
625                 630                 635                 640

Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser Ser
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                645                 650                 655

Ile Ser Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val
            660                 665                 670

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly
        675                 680                 685

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu Pro
    690                 695                 700

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val
705                 710                 715                 720

Ala Ser Thr Ile Arg Val Thr Gln
                725


<210> SEQ ID NO 6
<211> LENGTH: 680
<212> TYPE: PRT
<213> ORGANISM: Fusarium graminearum

<400> SEQUENCE: 6

Met Lys His Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala
1               5                   10                  15

Val Ala Val Thr Val Pro His Lys Ala Val Gly Thr Gly Ile Pro Glu
            20                  25                  30

Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser
        35                  40                  45

Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser
    50                  55                  60

Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe Trp
65                  70                  75                  80

His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr
                85                  90                  95

Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu
            100                 105                 110

Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu Val
        115                 120                 125

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

Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Ile Thr Glu Ala Asn Gly Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser Tyr
            180                 185                 190

Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp Leu
        195                 200                 205

Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg Val
    210                 215                 220

Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser Thr Gly Ile Val Ser
                245                 250                 255

Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270
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```
Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Val Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg
                405                 410                 415

Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro Gly
    450                 455                 460

Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr
                485                 490                 495

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe
            500                 505                 510

Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn
                565                 570                 575

Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr
            580                 585                 590

Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser Ser
        595                 600                 605

Ile Ser Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly
625                 630                 635                 640

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu Pro
                645                 650                 655

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val
            660                 665                 670

Ala Ser Thr Ile Arg Val Thr Gln
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675 680

<210> SEQ ID NO 7
<211> LENGTH: 685
<212> TYPE: PRT
<213> ORGANISM: Purpureocillium lilacinum

<400> SEQUENCE: 7

Met Lys Leu Leu Gly Thr Val Ala Ala Leu Ala Leu Cys Asp Ala Ala
1 5 10 15

Ser His Thr Tyr Ala Val Ala Val Lys Pro Arg Pro His Thr Ala Met
20 25 30

Pro Asn Leu Ala Ala Arg Gly Thr Glu Met Ser Leu Met Ala Ala Lys
35 40 45

Pro Ile Gly Asn Ala Ile Asn Arg Ala Gly Trp Lys Val Thr Cys Asp
50 55 60

Gly Glu Glu Gln Gly Asn Glu Cys Ala Lys Ala Ile Asp Gly Asp Asn
65 70 75 80

Asn Thr Met Trp His Thr Ala Trp Gln Asn Asp Asn Pro Pro Pro Pro
85 90 95

His Thr Ile Thr Val Asp Met Gly Ser Ala Gln Thr Ile Asn Gly Ile
100 105 110

Ser Val Leu Pro Arg Gln Asp Gly Ser Glu His Gly Trp Ile Ala Arg
115 120 125

His Asp Val Leu Val Ser Asn Asp Gly Gln Thr Trp Gly Asp Pro Val
130 135 140

Ala Thr Gly Thr Trp Tyr Thr Asp Ala Thr Ala Lys Tyr Ala Asn Phe
145 150 155 160

Glu Pro Arg Ser Ala Arg Tyr Val Arg Leu Val Ala Arg Ser Glu Ala
165 170 175

Gln Gly Arg Pro Trp Thr Ser Ile Ala Glu Leu Asn Val Tyr Arg Ala
180 185 190

Asp Gly Pro Pro Val Pro Lys Asn Gly Ile Gly Lys Trp Gly Leu Thr
195 200 205

Leu Asp Phe Pro Val Val Pro Val Ala Gly Val Val Asp Pro Leu Thr
210 215 220

Gly Lys Val Val Val Trp Ser Ala Tyr Glu Asn Asp Gln Tyr Glu Gly
225 230 235 240

Ser Pro Gly Gly Trp Thr Leu Thr Ser Thr Trp Asp Pro Ala Thr Gly
245 250 255

Glu Val Thr Glu Arg Asn Val Thr Asn Ile Gly His Asp Met Phe Cys
260 265 270

Pro Gly Val Ser Leu Asp Ala Ser Gly Arg Val Val Val Thr Gly Gly
275 280 285

Ser Asn Ala Gln Lys Thr Ser Phe Tyr Asp Ala Ala Thr Glu Ala Trp
290 295 300

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

Thr Cys Ser Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly
325 330 335

Gly Gln Phe Glu Lys Asn Gly Glu Val Trp Asp Pro Lys Thr Asn Ser
340 345 350

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Trp Arg Ala Leu Pro Gly Ala Ala Val Lys Pro Met Leu Thr Lys Asp
        355                 360                 365

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

Arg Asn Gly Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp
385                 390                 395                 400

Tyr Tyr Thr Ala Gly Asp Gly Arg Val Arg Ser Ala Gly Gln Arg Arg
                405                 410                 415

Ala Pro Arg Gly Ala Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met
            420                 425                 430

Phe Asp Ala Thr Ala Gly Lys Ile Leu Thr Val Gly Gly Ala Pro His
        435                 440                 445

Tyr Glu Asp Ala Asp Ala Thr Thr Asn Ala His Val Leu Thr Leu Gly
    450                 455                 460

Asp Ala Gly Ala Ala Pro Lys Val Val Phe Ala Gly Asn Gly Met Ala
465                 470                 475                 480

His Pro Arg Ile Phe Ala Asn Ala Val Val Leu Pro Asp Gly Thr Val
                485                 490                 495

Phe Val Thr Gly Gly Gln Gln His Ala Glu Leu Phe Lys Asp Thr Thr
            500                 505                 510

Pro Gln Leu Thr Pro Glu Leu Tyr Asp Pro Ala Leu Gly Ala Phe Val
        515                 520                 525

Glu Gln Ala Pro Asn Ser Val Val Arg Val Tyr His Ser Met Ala Leu
    530                 535                 540

Leu Leu Pro Asp Ala Thr Val Leu Ser Gly Gly Gly Gly Leu Cys Gly
545                 550                 555                 560

Gly Ala Cys Asp Thr Asn His Phe Asp Ala Gln Val Phe Ser Pro Arg
                565                 570                 575

Tyr Leu Phe Asp Gly Glu Gly Gln Pro Ala Ala Arg Pro Lys Ile Arg
            580                 585                 590

Ala Val Ala Ser Lys Glu Val His Ala Gly Asp Ala Ile Lys Val Thr
        595                 600                 605

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

Thr His Ser Val Asn Thr Asp Gln Arg Arg Val Pro Leu Thr Leu Arg
625                 630                 635                 640

Gln Asp Gly Gly Ser Tyr Ala Tyr Ser Ala Asp Leu Pro Arg Asp Leu
                645                 650                 655

Gly Val Leu Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Asp Lys
            660                 665                 670

Gly Val Pro Ser Val Ala Ala Thr Val Lys Val Leu Leu
        675                 680                 685


<210> SEQ ID NO 8
<211> LENGTH: 680
<212> TYPE: PRT
<213> ORGANISM: Fusarium graminearum PH-1

<400> SEQUENCE: 8

Met Lys His Phe Leu Ser Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala
1               5                   10                  15

Val Ala Val Thr Val Pro His Lys Ser Gly Gly Thr Gly Ser Pro Glu
            20                  25                  30
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Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser
        35                  40                  45

Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser
    50                  55                  60

Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe Trp
65                  70                  75                  80

His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr
                85                  90                  95

Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu
            100                 105                 110

Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu Val
        115                 120                 125

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

Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Gly Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser Tyr
            180                 185                 190

Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp Leu
        195                 200                 205

Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg Val
    210                 215                 220

Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser Thr Gly Ile Val Ser
                245                 250                 255

Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Val Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg
                405                 410                 415

Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430
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Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro Gly
    450                 455                 460

Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr
                485                 490                 495

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe
            500                 505                 510

Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn
                565                 570                 575

Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr
            580                 585                 590

Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile Ser Thr Asp Ser Ser
        595                 600                 605

Ile Thr Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly
625                 630                 635                 640

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu Pro
                645                 650                 655

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val
            660                 665                 670

Ala Ser Thr Ile Arg Val Thr Gln
        675                 680


<210> SEQ ID NO 9
<211> LENGTH: 680
<212> TYPE: PRT
<213> ORGANISM: Fusarium pseudograminearum CS3096

<400> SEQUENCE: 9

Met Lys His Phe Leu Ser Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala
1               5                   10                  15

Val Ala Val Thr Val Pro His Lys Val Ala Gly Thr Gly Asn Pro Glu
            20                  25                  30

Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser
        35                  40                  45

Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser
    50                  55                  60

Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Ser Lys Asp Thr Phe Trp
65                  70                  75                  80

His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr
                85                  90                  95

Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu
            100                 105                 110
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Pro Arg Gln Asp Gly Ser Gln Asn Gly Trp Ile Gly Arg His Glu Val
        115                 120                 125

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

Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Gly Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser Tyr
            180                 185                 190

Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp Leu
        195                 200                 205

Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg Val
    210                 215                 220

Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Ser Trp Asp Pro Ser Ser Gly Val Val Ser
                245                 250                 255

Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Val Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Arg Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg
                405                 410                 415

Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro Gly
    450                 455                 460

Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr
                485                 490                 495

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe
            500                 505                 510
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Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn
                565                 570                 575

Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Ala
            580                 585                 590

Gln Ser Val Lys Val Gly Gly Arg Ile Thr Met Ser Thr Asp Ser Ser
        595                 600                 605

Ile Thr Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly
625                 630                 635                 640

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu Pro
                645                 650                 655

Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser Val
            660                 665                 670

Ala Ser Thr Ile Arg Val Thr Gln
        675                 680


<210> SEQ ID NO 10
<211> LENGTH: 639
<212> TYPE: PRT
<213> ORGANISM: Hypomyces rosellus

<400> SEQUENCE: 10

Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
1               5                   10                  15

Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
            20                  25                  30

Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
        35                  40                  45

Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
    50                  55                  60

Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
65                  70                  75                  80

Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
                85                  90                  95

Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
            100                 105                 110

Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
        115                 120                 125

Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
    130                 135                 140

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

Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile
                165                 170                 175

Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
            180                 185                 190
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Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
        195                 200                 205

Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
    210                 215                 220

Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
225                 230                 235                 240

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

Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
            260                 265                 270

Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
        275                 280                 285

Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
    290                 295                 300

Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
305                 310                 315                 320

Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
                325                 330                 335

Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
            340                 345                 350

Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
        355                 360                 365

Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly
    370                 375                 380

Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
385                 390                 395                 400

Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
                405                 410                 415

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

Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
        435                 440                 445

Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
    450                 455                 460

Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
465                 470                 475                 480

Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Val Tyr His
                485                 490                 495

Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
            500                 505                 510

Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
        515                 520                 525

Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro
    530                 535                 540

Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
545                 550                 555                 560

Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
                565                 570                 575

Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
            580                 585                 590
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Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
        595                 600                 605

Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
    610                 615                 620

Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
625                 630                 635


<210> SEQ ID NO 11
<211> LENGTH: 680
<212> TYPE: PRT
<213> ORGANISM: Fusarium sporotrichioides

<400> SEQUENCE: 11

Met Lys His Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala
1               5                   10                  15

Val Ala Ile Thr Asn Pro His Lys Thr Ala Gly His Asp His Pro Glu
            20                  25                  30

Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser
        35                  40                  45

Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser
    50                  55                  60

Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Gln Asp Thr Phe Trp
65                  70                  75                  80

His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr
                85                  90                  95

Thr Ile Asp Met Lys Ser Thr Gln Asn Val Asn Gly Leu Ser Met Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Arg Asn Gly Trp Ile Gly Arg His Glu Val
        115                 120                 125

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

Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Ser Gly Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Gln Ala Ser Ser Tyr
            180                 185                 190

Thr Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp Leu
        195                 200                 205

Pro Ile Val Pro Ala Ala Ala Ala Val Glu Pro Thr Ser Gly Arg Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Ser Trp Asp Pro Ser Ser Gly Ile Val Ser
                245                 250                 255

Asp Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

Pro Asp Met Gln Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Met Ser
305                 310                 315                 320
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Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln Gly
        355                 360                 365

Val Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg
                405                 410                 415

Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Arg Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Ala Asn Ala His Ile Ile Thr Leu Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Asn Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr
                485                 490                 495

Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Phe
            500                 505                 510

Thr Pro Glu Val Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asp
                565                 570                 575

Gly Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr
            580                 585                 590

Gln Ser Val Lys Val Gly Gly Arg Val Thr Ile Ser Thr Asp Ser Ser
        595                 600                 605

Ile Val Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn Gly Gly
625                 630                 635                 640

Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu Pro
                645                 650                 655

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val
            660                 665                 670

Ala Ala Thr Ile Arg Val Thr Gln
        675                 680
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<210> SEQ ID NO 12
<211> LENGTH: 682
<212> TYPE: PRT
<213> ORGANISM: Fusarium longipes

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<400> SEQUENCE: 12

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Met Lys Gln Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala
1               5                  10                  15

Val Ala Ile Asn Pro His Gly His His Asn Asn Lys Gly Thr Gly Asp
            20                  25                  30

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

Gly Ser Ala Ile Ala Arg Glu Asn Trp Val Val Thr Cys Asp Ser Ala
    50                  55                  60

Gln Pro Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asp Thr Asn Thr
65                  70                  75                  80

Phe Trp His Thr Phe Tyr Gly Asn Asn Gly Asp Pro Lys Pro Pro His
                85                  90                  95

Thr Tyr Thr Ile Asp Met Gly Ser Asn Arg Asn Val Asn Gly Leu Ser
            100                 105                 110

Val Leu Pro Arg Gln Asp Gly Asn Arg Asn Gly Trp Ile Gly Arg His
        115                 120                 125

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

Tyr Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu
145                 150                 155                 160

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

Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Tyr Gln Ala Gly
            180                 185                 190

Ser Tyr Thr Ala Pro Gln Ala Gly Leu Gly Arg Trp Gly Pro Thr Ile
        195                 200                 205

Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly
    210                 215                 220

Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser
225                 230                 235                 240

Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser Ser Gly Ile
                245                 250                 255

Val Ser Asp Arg Thr Val Thr Val Thr Asn His Asp Met Phe Cys Pro
            260                 265                 270

Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn
        275                 280                 285

Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile
    290                 295                 300

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

Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly
                325                 330                 335

Ile Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp
            340                 345                 350

Thr Ser Leu Pro Gly Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys
        355                 360                 365

Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys
    370                 375                 380

Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr
385                 390                 395                 400
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Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Arg Arg Gln Ser
                405                 410                 415

Asn Arg Gly Leu Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr
            420                 425                 430

Asp Ala Val Ala Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr
        435                 440                 445

Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu
    450                 455                 460

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

Pro Arg Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe
                485                 490                 495

Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro
            500                 505                 510

Gln Leu Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys
        515                 520                 525

Gln Asn Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu
    530                 535                 540

Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp
545                 550                 555                 560

Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu
                565                 570                 575

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

Ser Ala Gln Ser Val Arg Val Gly Gly Arg Ile Thr Ile Ser Thr Asp
        595                 600                 605

Ser Ser Ile Arg Arg Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His
    610                 615                 620

Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr Asn Asn
625                 630                 635                 640

Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala
                645                 650                 655

Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro
            660                 665                 670

Ser Val Ala Thr Thr Leu Arg Val Thr Arg
        675                 680


<210> SEQ ID NO 13
<211> LENGTH: 679
<212> TYPE: PRT
<213> ORGANISM: Fusarium sambucinum

<400> SEQUENCE: 13

Met Tyr Leu Leu Ser Leu Ala Leu Cys Phe Ser Ser Ile Asn Ala Val
1               5                   10                  15

Ala Ile Asn Asn Pro His Lys Ala Ser Gly Ala Glu Lys Pro Glu Gly
            20                  25                  30

Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser Ala
        35                  40                  45

Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Pro Gly
    50                  55                  60

Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Arg Asp Thr Phe Trp His
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65 70 75 80

Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr Asn
85 90 95

Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu Pro
100 105 110

Arg Gln Asp Gly Ser Gln Asn Gly Trp Ile Gly Arg His Glu Val Tyr
115 120 125

Leu Ser Ser Asp Gly Lys Thr Trp Gly Ser Pro Val Ala Thr Gly Ser
130 135 140

Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg Pro
145 150 155 160

Ala Arg Tyr Val Arg Leu Val Ala Leu Ala Glu Ala Asn Gly Gln Pro
165 170 175

Trp Thr Ser Ile Ala Glu Ile Asn Val Tyr Gln Ala Ser Ser Tyr Thr
180 185 190

Ala Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Ile Asp Leu Pro
195 200 205

Ile Val Pro Ala Ala Ala Ala Ile Glu Pro Thr Ser Gly Arg Val Leu
210 215 220

Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly Gly
225 230 235 240

Val Thr Leu Thr Ser Ser Trp Asp Pro Ser Ser Gly Ile Val Ser Asp
245 250 255

Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile Ser
260 265 270

Met Asp Gly Asn Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala Lys
275 280 285

Lys Thr Ser Leu Tyr Asp Ser Pro Ser Asp Ser Trp Val Pro Gly Pro
290 295 300

Asp Met Gln Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Met Ser Asp
305 310 315 320

Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe Glu
325 330 335

Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser Lys Thr Trp Thr Ser Leu
340 345 350

Pro Asn Ala Lys Val Asn Pro Met Leu Thr Ala Asp Lys Gln Gly Leu
355 360 365

Tyr Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Lys Gly Ser
370 375 380

Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr Ser
385 390 395 400

Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg Gly
405 410 415

Val Ala Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala Val
420 425 430

Gln Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp Ser
435 440 445

Asp Ala Thr Thr Asn Ala His Ile Ile Thr Leu Gly Glu Pro Gly Ser
450 455 460

Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Phe Ala Arg Thr
465 470 475 480

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Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr Gly
                485                 490                 495

Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Val Leu Thr
            500                 505                 510

Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr Phe Tyr Lys Gln Asn Pro
        515                 520                 525

Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro Asp
    530                 535                 540

Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr Thr
545                 550                 555                 560

Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asp Ser
                565                 570                 575

Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Arg Thr Ser Thr Gln
            580                 585                 590

Ser Val Lys Val Gly Gly Arg Val Thr Ile Ser Thr Asp Tyr Ser Ile
        595                 600                 605

Arg Lys Ala Ser Leu Ile Arg Tyr Gly Thr Ala Thr His Thr Val Asn
    610                 615                 620

Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Met Asn Asn Gly Gly Asn
625                 630                 635                 640

Ser Tyr Ser Phe Gln Val Pro Ser Asp Thr Gly Ile Ala Leu Pro Gly
                645                 650                 655

Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser Val Ala
            660                 665                 670

Ser Thr Ile Arg Val Thr Gln
        675


<210> SEQ ID NO 14
<211> LENGTH: 639
<212> TYPE: PRT
<213> ORGANISM: Fusarium sp.

<400> SEQUENCE: 14

Ala Ser Ala Pro Ile Gly Ser Ala Ile Ser Arg Asn Asn Trp Ala Val
1               5                   10                  15

Thr Cys Asp Ser Ala Gln Ser Gly Asn Glu Cys Asn Lys Ala Ile Asp
            20                  25                  30

Gly Asn Lys Asp Thr Phe Trp His Thr Phe Tyr Gly Ala Asn Gly Asp
        35                  40                  45

Pro Lys Pro Pro His Thr Tyr Thr Ile Asp Met Lys Thr Thr Gln Asn
    50                  55                  60

Val Asn Gly Leu Ser Met Leu Pro Arg Gln Asp Gly Asn Gln Asn Gly
65                  70                  75                  80

Trp Ile Gly Arg His Glu Val Tyr Leu Ser Ser Asp Gly Thr Asn Trp
                85                  90                  95

Gly Ser Pro Val Ala Ser Gly Ser Trp Phe Ala Asp Ser Thr Thr Lys
            100                 105                 110

Tyr Ser Asn Phe Glu Thr Arg Pro Ala Arg Tyr Val Arg Leu Val Ala
        115                 120                 125

Ile Thr Glu Ala Asn Gly Gln Pro Trp Thr Ser Ile Ala Glu Ile Asn
    130                 135                 140

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

Trp Gly Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile
                165                 170                 175

Glu Pro Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp
            180                 185                 190

Ala Phe Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp
        195                 200                 205

Pro Ser Thr Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His
    210                 215                 220

Asp Met Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val
225                 230                 235                 240

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

Ser Asp Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr
            260                 265                 270

Gln Ser Ser Ala Thr Met Ser Asp Gly Arg Val Phe Thr Ile Gly Gly
        275                 280                 285

Ser Trp Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro
    290                 295                 300

Ser Ser Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met
305                 310                 315                 320

Leu Thr Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp
                325                 330                 335

Leu Phe Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr
            340                 345                 350

Ala Met Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala
        355                 360                 365

Gly Lys Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Ser Gly
    370                 375                 380

Asn Ala Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly
385                 390                 395                 400

Gly Ser Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile
                405                 410                 415

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

Asn Gly Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro
        435                 440                 445

Asp Gly Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe
    450                 455                 460

Glu Asp Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln
465                 470                 475                 480

Asp Thr Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Val Tyr His
                485                 490                 495

Ser Ile Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly
            500                 505                 510

Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe
        515                 520                 525

Thr Pro Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro
    530                 535                 540

Lys Ile Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile
545                 550                 555                 560
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Thr Ile Ser Thr Asp Ser Ser Ile Ser Lys Ala Ser Leu Ile Arg Tyr
                565                 570                 575

Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu
            580                 585                 590

Thr Leu Thr Asn Asn Gly Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser
        595                 600                 605

Asp Ser Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn
    610                 615                 620

Ser Ala Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
625                 630                 635


<210> SEQ ID NO 15
<211> LENGTH: 679
<212> TYPE: PRT
<213> ORGANISM: Fusarium avenaceum

<400> SEQUENCE: 15

Met Lys Ser Leu Leu Thr Leu Ala Leu Cys Phe Ser Ser Val Leu Ala
1               5                   10                  15

Val Ala Ile Thr Gln Pro His Lys Ala Thr Gln Ala Lys Thr His Glu
            20                  25                  30

Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser
        35                  40                  45

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

Gly Asn Glu Cys Ser Lys Ala Ile Asp Gly Asn Arg Asp Thr Phe Trp
65                  70                  75                  80

His Thr Thr Trp Gly Ser Ser Asp Pro Lys Pro Pro His Thr Tyr Thr
                85                  90                  95

Ile Asp Met Lys Ser Thr Gln Asn Val Asn Gly Ile Ser Met Leu Pro
            100                 105                 110

Arg Gln Asp Gly Ser Pro Asn Gly Trp Ile Gly Arg His Asn Val Phe
        115                 120                 125

Leu Ser Thr Asp Gly Lys Asn Trp Gly Ser Ala Val Ala Thr Gly Thr
    130                 135                 140

Trp Tyr Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg Pro
145                 150                 155                 160

Val Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asn Gln Pro
                165                 170                 175

Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Asp Ser Tyr Thr
            180                 185                 190

Lys Pro Gln Thr Gly Ile Gly Ser Trp Gly Pro Thr Leu Asp Phe Pro
        195                 200                 205

Ile Val Pro Val Ala Ala Ala Ile Glu Pro Thr Ser Gly Lys Val Leu
    210                 215                 220

Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly Gly
225                 230                 235                 240

Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Asn Val Ile Ser Gln
                245                 250                 255

Arg Thr Val Thr Ile Thr Lys His Asp Met Phe Cys Pro Gly Ile Ser
            260                 265                 270

Leu Asp Gly Thr Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala Gln
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        275                 280                 285

Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Asp Trp Thr Pro Gly Pro
    290                 295                 300

Asn Met Gln Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Leu Ser Asn
305                 310                 315                 320

Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ser Phe Glu
                325                 330                 335

Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser Leu
            340                 345                 350

Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Lys Gln Gly Ile
        355                 360                 365

Tyr Arg Ala Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly Ser
    370                 375                 380

Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Phe Thr Ser
385                 390                 395                 400

Gly Lys Gly Asp Val Lys Pro Ala Gly Lys Arg Gln Ser Asp Arg Gly
                405                 410                 415

Ile Ala Pro Asp Ala Met Cys Gly Asn Ser Val Met Tyr Asp Ala Val
            420                 425                 430

Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Asp Tyr Gln Asp Ala
        435                 440                 445

Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Asp Glu Pro Gly Lys
    450                 455                 460

Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Ala Arg Thr
465                 470                 475                 480

Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Val Phe Ile Thr Gly
                485                 490                 495

Gly Gln Gln His Gly Val Pro Phe Ala Asp Thr Thr Pro Gln Leu Thr
            500                 505                 510

Pro Glu Leu Tyr Val Pro Asp Ala Asp Thr Phe Tyr Lys Gln Gln Pro
        515                 520                 525

Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro Asp
    530                 535                 540

Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr Thr
545                 550                 555                 560

Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asn Asn
                565                 570                 575

Asp Gly Thr Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Thr Lys
            580                 585                 590

Ser Val Lys Val Gly Gly Lys Val Thr Val Ser Thr Asn Gly Thr Ile
        595                 600                 605

Lys Gln Ala Ser Leu Val Arg Tyr Ser Thr Ala Thr His Thr Val Asn
    610                 615                 620

Thr Asp Gln Arg Arg Val Pro Leu Ser Leu Thr Asn Thr Gly Gly Asn
625                 630                 635                 640

Ser Tyr Ser Phe Gln Leu Pro Asn Asp Ser Gly Ile Val Leu Pro Gly
                645                 650                 655

Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val Ala
            660                 665                 670

Ser Thr Leu Phe Val Thr Gln
        675
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<210> SEQ ID NO 16
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium subglutinans

<400> SEQUENCE: 16

Met Lys Ser Phe Trp Thr Leu Ala Phe Tyr Leu Gly Asn Ala Asn Ala
1 5 10 15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
20 25 30

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

Asn Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Gln Gly Asp
50 55 60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asn Thr Phe Trp His Thr
65 70 75 80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
100 105 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
115 120 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asn Ala Val Ala Thr Gly
130 135 140

Thr Trp Phe Ala Asp Ile Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145 150 155 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
165 170 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Asn Ala Ala Ser Tyr
180 185 190

Thr Ser Pro Gln Pro Gly Leu Gly Leu Trp Gly Pro Thr Leu Asp Phe
195 200 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
210 215 220

Leu Val Trp Ser Ser Tyr Lys Asn Asp Ala Phe Gly Gly Ser Pro Gly
225 230 235 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
245 250 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
260 265 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
275 280 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
290 295 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Thr Phe
325 330 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
340 345 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly

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        355                 360                 365

Ile Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Lys Gly Asn Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Ser
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Asn Val Ser Ala
            580                 585                 590

Lys Ser Ala Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Ile Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 17
<211> LENGTH: 669
<212> TYPE: PRT
<213> ORGANISM: Fusarium culmorum

<400> SEQUENCE: 17

Met Lys His Leu Leu Ser Leu Ala Leu Cys Phe Thr Ser Ile Asn Ala
1               5                   10                  15

Val Ala Val Thr Ile Pro His Lys Ser Ala Gly Thr Gly Ser Pro Glu
            20                  25                  30
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Gly Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Ser
        35                  40                  45

Ala Ile Ser Arg Asn Asn Trp Ala Val Thr Cys Asp Ser Ala Gln Ser
    50                  55                  60

Gly Asn Glu Cys Asn Lys Ala Ile Asp Gly Asn Lys Asp Thr Phe Trp
65                  70                  75                  80

His Thr Phe Tyr Gly Ala Asn Gly Asp Pro Lys Pro Pro His Thr Tyr
                85                  90                  95

Thr Ile Asp Met Lys Thr Thr Gln Asn Val Asn Gly Leu Ser Met Leu
            100                 105                 110

Pro Arg Gln Asp Gly Asn Gln Asn Gly Trp Ile Gly Arg His Glu Val
        115                 120                 125

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

Ser Trp Phe Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Gly Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Pro Gly Leu Gly Arg Trp Gly
            180                 185                 190

Pro Thr Ile Asp Leu Pro Ile Val Pro Ala Ala Ala Ala Ile Glu Pro
        195                 200                 205

Thr Ser Gly Arg Val Leu Met Trp Ser Ser Tyr Arg Asn Asp Ala Phe
    210                 215                 220

Gly Gly Ser Pro Gly Gly Ile Thr Leu Thr Ser Ser Trp Asp Pro Ser
225                 230                 235                 240

Ser Gly Ile Val Ser Asp Arg Thr Val Thr Val Thr Lys His Asp Met
                245                 250                 255

Phe Cys Pro Gly Ile Ser Met Asp Gly Asn Gly Gln Ile Val Val Thr
            260                 265                 270

Gly Gly Asn Asp Ala Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp
        275                 280                 285

Ser Trp Ile Pro Gly Pro Asp Met Gln Val Ala Arg Gly Tyr Gln Ser
    290                 295                 300

Ser Ala Thr Thr Ser Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp
305                 310                 315                 320

Ser Gly Gly Val Phe Glu Lys Asn Gly Glu Val Tyr Ser Pro Ser Ser
                325                 330                 335

Lys Thr Trp Thr Ser Leu Pro Asn Ala Lys Val Asn Pro Met Leu Thr
            340                 345                 350

Ala Asp Lys Gln Gly Leu Tyr Arg Ser Asp Asn His Ala Trp Leu Phe
        355                 360                 365

Gly Trp Lys Lys Gly Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met
    370                 375                 380

Asn Trp Tyr Tyr Thr Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys
385                 390                 395                 400

Arg Gln Ser Asn Arg Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala
                405                 410                 415

Val Met Tyr Asp Ala Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser
            420                 425                 430

Pro Asp Tyr Gln Asp Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr
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        435                 440                 445

Leu Gly Glu Pro Gly Thr Ser Pro Asn Thr Val Phe Ala Ser Asn Gly
    450                 455                 460

Leu Tyr Phe Ala Arg Thr Phe His Thr Ser Val Val Leu Pro Asp Gly
465                 470                 475                 480

Ser Thr Phe Ile Thr Gly Gly Gln Arg Arg Gly Ile Pro Phe Glu Asp
                485                 490                 495

Ser Thr Pro Val Phe Thr Pro Glu Ile Tyr Val Pro Glu Gln Asp Thr
            500                 505                 510

Phe Tyr Lys Gln Asn Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile
        515                 520                 525

Ser Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu
    530                 535                 540

Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro
545                 550                 555                 560

Asn Tyr Leu Tyr Asn Ser Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile
                565                 570                 575

Thr Arg Thr Ser Thr Gln Ser Val Lys Val Gly Gly Arg Ile Thr Ile
            580                 585                 590

Ser Thr Asp Ser Ser Ser Thr Lys Ala Ser Leu Ile Arg Tyr Gly Thr
        595                 600                 605

Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu
    610                 615                 620

Thr Asn Asn Gly Gly Asn Ile Tyr Ser Phe Gln Val Pro Ser Asp Ser
625                 630                 635                 640

Gly Val Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala
                645                 650                 655

Gly Val Pro Ser Val Ala Ser Thr Ile Arg Val Thr Gln
            660                 665


<210> SEQ ID NO 18
<211> LENGTH: 680
<212> TYPE: PRT
<213> ORGANISM: Fusarium sp. FIESC_12

<400> SEQUENCE: 18

Met Arg His Leu Leu Thr Leu Ala Leu Cys Phe Thr Ser Ile Asn Ala
1               5                   10                  15

Val Ala Ile Thr Lys Ser His Lys Ser Ala Gly Thr Gly Glu Pro Glu
            20                  25                  30

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

Thr Ile Ser Arg Asp Lys Trp Ser Val Thr Cys Asp Ser Phe His Asp
    50                  55                  60

Gly Glu Gly Cys Asp Lys Ala Ile Asp Gly Asp Arg Asn Thr Phe Trp
65                  70                  75                  80

His Ser Gln Trp Gly Asn Gly Asn Asp Pro Lys Pro Pro His Thr Tyr
                85                  90                  95

Thr Ile Asp Met Gly Ser Thr Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Ser Asn Gly Trp Ile Gly Arg His Glu Val
        115                 120                 125
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Phe Leu Ser Ser Asp Gly Ser Asn Trp Gly Ser Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Tyr Ala Asp Ser Thr Thr Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Ile Val Ala Leu Thr Glu Ala Lys Gly Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Asp Ser Tyr
            180                 185                 190

Ser Ala Pro Gln Ala Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Ala Ala Ala Tyr Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Val Val Phe Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Ile Thr Leu Thr Ser Thr Trp Asp Pro Ala Ser Asn Val Ile Ser
                245                 250                 255

Glu Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Thr Gly Gln Ile Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

Lys Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asp Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Ile Tyr Asn Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Lys Val Asn Pro Met Leu Thr Ala Asp Arg Gln Gly
        355                 360                 365

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

Thr Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Asn Arg
                405                 410                 415

Gly Val Ala Thr Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Gln Gly Lys Ile Leu Thr Phe Gly Gly Ala Lys Asp Tyr Gln Asp
        435                 440                 445

Thr Asp Ala Thr Thr Asp Ala His Ile Ile Thr Leu Gly Glu Pro Gly
    450                 455                 460

Thr Thr Pro Asn Thr Val Tyr Ala Ser Asn Gly Leu Trp Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Ser Thr Phe Ile Thr
                485                 490                 495

Gly Gly Gln Val Arg Gly Ile Pro Phe Glu Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Gly Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Val Ser Leu Leu Leu Pro
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    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn Tyr Leu Tyr Asp
                565                 570                 575

Asn Asn Gly Asn Leu Ala Thr Arg Pro Lys Ile Thr Asn Thr Ser Thr
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Arg Val Thr Ile Thr Thr Asp Gly Ser
        595                 600                 605

Ile Gln Lys Ala Ser Leu Val Arg Tyr Gly Thr Ala Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Ser Ser Ser Gly Arg
625                 630                 635                 640

Asn Ser Tyr Ser Phe Thr Val Pro Asn Asp Ser Gly Val Ala Leu Pro
                645                 650                 655

Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser Val
            660                 665                 670

Ser Thr Thr Ile Arg Ile Thr Gln
        675                 680


<210> SEQ ID NO 19
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. cubense

<400> SEQUENCE: 19

Met Lys Ser Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205
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Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Arg Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Asn Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
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    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 20
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum Fo47

<400> SEQUENCE: 20

Met Lys Ser Phe Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Val Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285
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Gln Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Arg Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680
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<210> SEQ ID NO 21
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium sp. FOSC 3-a

<400> SEQUENCE: 21

Met Lys Ser Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Val Ser Ala
1 5 10 15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
20 25 30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
50 55 60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65 70 75 80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
100 105 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
115 120 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
130 135 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145 150 155 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
165 170 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
180 185 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
195 200 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
210 215 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225 230 235 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
245 250 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
260 265 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
275 280 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
325 330 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
340 345 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
355 360 365

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Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Arg Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Pro Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Ile Thr Gln
        675                 680


<210> SEQ ID NO 22
<211> LENGTH: 666
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 22

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

Ser Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Thr Ala
            20                  25                  30

Ile Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly
        35                  40                  45
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Asp Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His
    50                  55                  60

Thr Ala Trp Ala Ala Gly Gly Thr Asn Asp Pro Lys Pro Pro His Thr
65                  70                  75                  80

Ile Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val
                85                  90                  95

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

Val Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr
        115                 120                 125

Gly Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr
    130                 135                 140

Arg Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp
145                 150                 155                 160

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

Tyr Ala Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp
            180                 185                 190

Phe Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys
        195                 200                 205

Val Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro
    210                 215                 220

Gly Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile
225                 230                 235                 240

Ser Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly
                245                 250                 255

Ile Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp
            260                 265                 270

Ala Gln Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro
        275                 280                 285

Gly Pro Asp Met Lys Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Leu
    290                 295                 300

Ser Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile
305                 310                 315                 320

Phe Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr
                325                 330                 335

Ser Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln
            340                 345                 350

Gly Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys
        355                 360                 365

Gly Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr
    370                 375                 380

Thr Ser Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Arg Ser Ser
385                 390                 395                 400

Arg Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp
                405                 410                 415

Ala Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln
            420                 425                 430

Asp Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro
        435                 440                 445
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Gly Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro
    450                 455                 460

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

Thr Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln
                485                 490                 495

Leu Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln
            500                 505                 510

Gln Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu
        515                 520                 525

Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys
    530                 535                 540

Asp Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr
545                 550                 555                 560

Asp Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser
                565                 570                 575

Ala Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr
            580                 585                 590

Ser Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr
        595                 600                 605

Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly
    610                 615                 620

Thr Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala
625                 630                 635                 640

Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro
                645                 650                 655

Ser Val Ala Ser Thr Leu Leu Val Thr Gln
            660                 665


<210> SEQ ID NO 23
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. radicis-lycopersici 26381

<400> SEQUENCE: 23

Met Lys Ser Phe Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Val Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140
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Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Arg Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540
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Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 24
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. lycopersici 4287

<400> SEQUENCE: 24

Met Lys Pro Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Pro Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220
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Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Arg Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620
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Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 25
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. cubense race 1

<400> SEQUENCE: 25

Met Lys Ser Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

Gln Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300
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Pro Asp Met Lys Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Leu Ser
305                 310                 315                 320

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Thr Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 26
<211> LENGTH: 681
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<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 26

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

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
20 25 30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
50 55 60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65 70 75 80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
100 105 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
115 120 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
130 135 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145 150 155 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
165 170 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
180 185 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
195 200 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
210 215 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225 230 235 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
245 250 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
260 265 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
275 280 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
325 330 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
340 345 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
355 360 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
370 375 380

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Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Thr Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 27
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. raphani 54005

<400> SEQUENCE: 27

Met Lys Ser Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
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    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Thr Gly Asn Gly Gly Val Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460
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Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 28
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. pisi HDV247

<400> SEQUENCE: 28

Met Lys Ser Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Leu Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
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    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Thr Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540
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Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 29
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium nygamai

<400> SEQUENCE: 29

Met Lys Ser Phe Trp Thr Leu Ala Phe Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ser Glu Thr Pro Ala Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Gln Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
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    210                 215                 220

Leu Val Trp Ser Ser Tyr Lys Asn Asp Glu Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Asn Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Arg Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Ile Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Gly Gly Lys Gly Asp Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Val Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Gly Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Ile Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620
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Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Ile Thr Gln
        675                 680


<210> SEQ ID NO 30
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. cubense race 4

<400> SEQUENCE: 30

Met Lys Ser Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Lys Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Thr Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Arg Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680
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<210> SEQ ID NO 31

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<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. vasinfectum 25433

<400> SEQUENCE: 31

Met Lys Ser Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1 5 10 15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
20 25 30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
50 55 60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65 70 75 80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
100 105 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
115 120 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
130 135 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145 150 155 160

Pro Ala Arg Tyr Val Arg Leu Val Thr Val Thr Glu Ala Asn Asp Gln
165 170 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Ile Phe Lys Ala Ala Ser Tyr
180 185 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
195 200 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
210 215 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225 230 235 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
245 250 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
260 265 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
275 280 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
325 330 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
340 345 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
355 360 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly

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    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Thr Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Arg Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 32
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium mangiferae

<400> SEQUENCE: 32

Met Lys Ser Phe Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Thr Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Thr Ala Ile
        35                  40                  45
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Asn Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Ala Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asn Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
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    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asp Ile Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Ala Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Val Val Thr Gln
        675                 680


<210> SEQ ID NO 33
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 33

Met Lys Pro Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125
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Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Thr Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285

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

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Thr Gly Asn Gly Asp Val Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
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    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 34
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium verticillioides 7600

<400> SEQUENCE: 34

Met Lys Ser Phe Trp Thr Leu Ala Phe Tyr Leu Gly Gly Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ser Glu Thr Pro Ala Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asn His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asn Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Ala Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205
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Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Lys Asn Asp Glu Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Asn Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Ser
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Ser Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asn Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Asn Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Val Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Gly Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asp Ser Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
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    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 35
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum Fo5176

<400> SEQUENCE: 35

Met Lys Ser Leu Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Arg Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asp Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asp Ala
        275                 280                 285
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Gln Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Thr Gly Asn Gly Gly Val Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Ser Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe Leu Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Thr Ala Asp Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Arg Thr Gly Thr
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680
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<210> SEQ ID NO 36
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium verticillioides

<400> SEQUENCE: 36

Met Lys Ser Phe Trp Thr Leu Ala Phe Tyr Leu Gly Gly Ala Ser Ala
1 5 10 15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ser Glu Thr Pro Ala Gly Ser
20 25 30

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

Asn Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
50 55 60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asn Thr Phe Trp His Thr
65 70 75 80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
100 105 110

Pro Arg Gln Asp Gly Ser Asn His Gly Trp Ile Gly Arg His Asn Val
115 120 125

Phe Leu Ser Thr Asn Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
130 135 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145 150 155 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
165 170 175

Ala Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
180 185 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
195 200 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
210 215 220

Leu Val Trp Ser Ser Tyr Lys Asn Asp Glu Phe Gly Gly Ser Pro Gly
225 230 235 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
245 250 255

Gln Arg Thr Val Thr Asn Thr Lys His Asp Met Phe Cys Pro Gly Ile
260 265 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
275 280 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
290 295 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Ser
325 330 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
340 345 350

Leu Ser Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
355 360 365

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Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asn Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Val Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Gly Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asp Ser Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 37
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium proliferatum

<400> SEQUENCE: 37

Met Lys Ser Phe Trp Thr Phe Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Thr Ala Ile
        35                  40                  45
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Ser Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Ile Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Glu Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445
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Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 38
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium verticillioides

<400> SEQUENCE: 38

Met Lys Ser Phe Trp Thr Leu Ala Phe Tyr Leu Gly Gly Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ala Lys Ser Glu Thr Pro Ala Gly Ser
            20                  25                  30

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

Asn Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asn His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125
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Phe Leu Ser Thr Asn Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Ala Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Lys Asn Asp Glu Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Asn Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Ser
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Ser Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Asn Gly Asn Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525
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Pro Asn Ser Ile Val Arg Val Tyr His Ser Val Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Gly Cys Thr
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Asn Gly Lys Leu Ala Thr Arg Pro Lys Ile Ile Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asp Ser Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 39
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium proliferatum

<400> SEQUENCE: 39

Met Lys Ser Phe Trp Thr Phe Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Ser Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205
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Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Ile Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Glu Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605
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Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 40
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium proliferatum ET1

<400> SEQUENCE: 40

Met Lys Ser Phe Trp Thr Phe Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Ser Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285
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Glu Lys Thr Ser Leu Tyr Asp Ser Ser Arg Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680
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<210> SEQ ID NO 41
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium proliferatum

<400> SEQUENCE: 41

Met Lys Ser Leu Trp Thr Phe Ala Phe Tyr Leu Gly Ser Ala Ser Ala
1 5 10 15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
20 25 30

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

Asn Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
50 55 60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asn Thr Phe Trp His Thr
65 70 75 80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
100 105 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
115 120 125

Leu Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
130 135 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145 150 155 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
165 170 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
180 185 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
195 200 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
210 215 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225 230 235 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
245 250 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
260 265 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
275 280 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
290 295 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
325 330 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
340 345 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
355 360 365

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Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Pro Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Val Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 42
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium fujikuroi

<400> SEQUENCE: 42

Met Lys Ser Phe Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Ser Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Ser Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445
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Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 43
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium fujikuroi IMI 58289

<400> SEQUENCE: 43

Met Lys Ser Phe Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Ser Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Arg Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
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        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Ser Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Glu Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525
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Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 44
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium fujikuroi

<400> SEQUENCE: 44

Met Lys Ser Phe Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Ser Arg Asp Lys Trp Lys Leu Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Ile Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
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        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Ser Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605
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Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 45
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium proliferatum

<400> SEQUENCE: 45

Met Lys Ser Phe Trp Thr Phe Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

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

Ser Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Ala Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asn Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
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        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Val Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680
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<210> SEQ ID NO 46
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium fujikuroi
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (55)..(55)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 46

Met Lys Ser Phe Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1 5 10 15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
20 25 30

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

Ser Arg Asp Lys Trp Lys Xaa Thr Cys Asp Ser Gln His Glu Gly Asp
50 55 60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65 70 75 80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
100 105 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
115 120 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
130 135 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145 150 155 160

Pro Ala Arg Tyr Ile Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
165 170 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
180 185 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
195 200 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
210 215 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225 230 235 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
245 250 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
260 265 270

Ser Met Asp Gly Ser Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
275 280 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
290 295 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Ile Phe
325 330 335

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Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Asn Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 47
<211> LENGTH: 684
<212> TYPE: PRT
<213> ORGANISM: Fusarium euwallaceae

<400> SEQUENCE: 47

Met Arg Ser Pro Ile Leu Thr Leu Cys Leu Ala Gly Leu Phe Trp Asp
1               5                   10                  15
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Glu Ala Met Ala Ile Val Ile Pro Ala Gln Asn Ser Thr Lys Val Lys
            20                  25                  30

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

Ala Ile Asn Arg Asn Asn Trp Lys Val Thr Cys Asp Ser Asp Asn Pro
    50                  55                  60

Asp Ser Asp Asn Ala Cys Gln Lys Ala Ile Asp Gly Asp Val Asn Ser
65                  70                  75                  80

Phe Trp His Thr Ala Trp Phe Glu Asp Thr Ser Lys Asp Pro Gly Leu
                85                  90                  95

Pro His Thr Ile Thr Val Asp Met Lys Thr Val Gln Asn Val Asn Gly
            100                 105                 110

Ile Ser Ala Leu Pro Arg Gln Asp Gly Thr Thr His Gly Trp Ile Ala
        115                 120                 125

Arg His Asp Ile Phe Leu Ser Thr Asp Gly Lys Thr Trp Gly Ser Pro
    130                 135                 140

Val Ala Thr Gly Thr Trp Tyr Ala Asp Gly Thr Glu Lys Phe Ser Asn
145                 150                 155                 160

Phe Glu Thr Lys Arg Ala Arg Tyr Val Arg Ile Val Ala Ile Thr Glu
                165                 170                 175

Ala Tyr Asp Gly Pro Trp Thr Ser Ile Ala Glu Phe Asn Val Tyr Lys
            180                 185                 190

Ala Ala Thr Tyr Thr Ala Pro Lys Thr Gly Ile Gly Met Trp Gly Pro
        195                 200                 205

Thr Leu Asp Phe Pro Ile Val Pro Val Ala Gly Ala Val Asp Pro Gly
    210                 215                 220

Thr Gly Lys Val Leu Val Trp Ser Ser Tyr Tyr His Asp Thr Met Asn
225                 230                 235                 240

Gly Ser Pro Gly Gly Met Thr Leu Thr Ser Leu Trp Asp Pro Glu Thr
                245                 250                 255

Gly Ile Ile Thr Gln Arg Glu Val Phe Glu Thr Asn His Asp Met Phe
            260                 265                 270

Cys Pro Gly Ile Ser Met Asp Gly Thr Gly Gln Ile Val Val Thr Gly
        275                 280                 285

Gly Asn Asn Ala Ala Arg Thr Ser Thr Trp Asp Pro Val Lys Asn Gln
    290                 295                 300

Trp Val Ser Ala Pro Asp Met Lys Ile Pro Arg Gly Tyr Gln Ser Ser
305                 310                 315                 320

Ala Thr Thr Ser Asn Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Gly
                325                 330                 335

Gly Asp Arg Thr Phe Lys Pro Gly Glu Ile Phe Asp Pro Ser Ser Arg
            340                 345                 350

Lys Trp Thr Leu Leu Gln Asn Ala Lys Val Glu Pro Met Leu Thr Ala
        355                 360                 365

Asp Ala Gln Gly Ile Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly
    370                 375                 380

Trp Lys Gly Glu Thr Ile Phe Gln Ala Gly Pro Ser Ser Ala Met Asn
385                 390                 395                 400

Trp Tyr Tyr Thr Gln Gly Lys Gly Thr Val Lys Pro Ala Gly Lys Arg
                405                 410                 415
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Gln Ser Ser Arg Gly Val Asp Pro Asp Ser Met Cys Gly Asn Ala Val
            420                 425                 430

Met Phe Asp Ala Val Lys Gly Lys Ile Val Thr Phe Gly Gly Thr Pro
        435                 440                 445

Asn Tyr Gln Asp Ser Tyr Ala Thr Thr Asn Ala His Ile Ile Thr Ile
    450                 455                 460

Gly Ala Pro Gly Thr Gln Ala Ser Val Ala Phe Ala Ser Asn Gly Met
465                 470                 475                 480

Tyr Tyr Pro Arg Val Phe His Thr Ser Val Leu Leu Pro Asp Gly Thr
                485                 490                 495

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

Thr Pro Gln Leu Thr Pro Glu Met Tyr Ile Pro Asp Ser Asp Thr Phe
        515                 520                 525

Ile Lys Gln Gln Pro Asn Ser Ile Val Arg Thr Tyr His Ser Met Ser
    530                 535                 540

Ile Leu Leu Pro Asp Ala Arg Val Phe Asn Gly Gly Gly Gly Leu Cys
545                 550                 555                 560

Gly Asp Cys Ser Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Asn
                565                 570                 575

Tyr Leu Leu Thr Lys Asp Gly Lys Pro Ala Thr Arg Pro Lys Ile Val
            580                 585                 590

Ser Val Ser Ala Thr Thr Ile Lys Val Gly Gly Ser Ile Thr Val Thr
        595                 600                 605

Thr Gly Gly Val Val Asn Thr Ala Ser Leu Ile Arg Tyr Gly Thr Ala
    610                 615                 620

Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr
625                 630                 635                 640

Gly Ala Gly Lys Asn Lys Tyr Thr Phe Lys Val Pro Gly Asp Ser Gly
                645                 650                 655

Ile Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly
            660                 665                 670

Val Pro Ser Val Ala Ser Thr Ile Lys Val Thr Thr
        675                 680


<210> SEQ ID NO 48
<211> LENGTH: 684
<212> TYPE: PRT
<213> ORGANISM: Fusarium ambrosium

<400> SEQUENCE: 48

Met Arg Ser Pro Ile Leu Thr Leu Cys Leu Ala Ile Phe Phe Trp Asp
1               5                   10                  15

Glu Ala Met Ala Ile Val Ile Pro Ala Gln Asn Ser Thr Lys Val Lys
            20                  25                  30

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

Ala Ile Asn Arg Asn Asn Trp Lys Val Thr Cys Asp Ser Asp Asn Pro
    50                  55                  60

Asp Ser Asp Asn Ala Cys Gln Lys Ala Ile Asp Gly Asp Val Asn Ser
65                  70                  75                  80

Phe Trp His Thr Ala Trp Phe Glu Asp Thr Ser Lys Asp Pro Gly Leu
                85                  90                  95
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Pro His Thr Leu Thr Val Asp Met Lys Thr Val Gln Asn Val Asn Gly
           100                 105                 110

Ile Ser Ala Leu Pro Arg Gln Asp Gly Thr Thr His Gly Trp Ile Ala
        115                 120                 125

Arg His Asp Ile Phe Leu Ser Arg Asp Gly Lys Ala Trp Gly Ser Pro
    130                 135                 140

Val Ala Thr Gly Thr Trp Tyr Ala Asp Gly Thr Glu Lys Phe Ser Asn
145                 150                 155                 160

Phe Glu Thr Lys Arg Ala Arg Tyr Val Arg Ile Val Ala Thr Thr Glu
                165                 170                 175

Ala Tyr Asp Gly Pro Trp Thr Ser Ile Ala Glu Phe Asn Val Tyr Lys
           180                 185                 190

Ala Ala Thr Tyr Thr Ala Pro Lys Thr Gly Ile Gly Met Trp Gly Pro
        195                 200                 205

Thr Leu Asp Phe Pro Ile Val Pro Val Ala Gly Ala Val Asp Pro Gly
    210                 215                 220

Thr Gly Lys Val Leu Val Trp Ser Ser Tyr Tyr His Asp Thr Met Asn
225                 230                 235                 240

Gly Ser Pro Gly Gly Met Thr Leu Thr Ser Leu Trp Asp Pro Glu Thr
                245                 250                 255

Gly Ile Ile Thr Gln Arg Glu Val Phe Glu Thr Asn His Asp Met Phe
           260                 265                 270

Cys Pro Gly Ile Ser Met Asp Gly Thr Gly Gln Ile Val Val Thr Gly
        275                 280                 285

Gly Asn Asn Ala Ala Arg Thr Ser Thr Trp Asp Pro Val Lys Asn Gln
    290                 295                 300

Trp Val Ser Ala Pro Asp Met Lys Ile Pro Arg Gly Tyr Gln Ser Ser
305                 310                 315                 320

Ala Thr Thr Ser Asn Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Gly
                325                 330                 335

Gly Asp Arg Thr Phe Lys Pro Gly Glu Ile Phe Asp Pro Ser Ser Arg
           340                 345                 350

Lys Trp Thr Leu Leu Ser Asn Ala Lys Val Glu Pro Met Leu Thr Ala
        355                 360                 365

Asp Ala Gln Gly Ile Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly
    370                 375                 380

Trp Lys Gly Glu Thr Ile Phe Gln Ala Gly Pro Ser Ser Ala Met Asn
385                 390                 395                 400

Trp Tyr Tyr Thr Gln Gly Lys Gly Thr Val Lys Pro Ala Gly Lys Arg
                405                 410                 415

Gln Ser Ser Arg Gly Val Asp Pro Asp Ser Met Cys Gly Asn Ala Val
           420                 425                 430

Met Phe Asp Ala Val Lys Gly Lys Ile Val Thr Phe Gly Gly Thr Pro
        435                 440                 445

Asn Tyr Gln Asp Ser Tyr Ala Thr Thr Asn Ala His Ile Ile Thr Ile
    450                 455                 460

Gly Ala Pro Gly Thr Gln Ala Ser Val Ala Phe Ala Ser Asn Gly Met
465                 470                 475                 480

Tyr Tyr Pro Arg Val Phe His Thr Ser Val Leu Leu Pro Asp Gly Thr
                485                 490                 495
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```
Val Phe Ile Thr Gly Gly Gln Glu Tyr Ala Ile Pro Phe Glu Asp Ser
            500                 505                 510

Thr Pro Gln Leu Thr Pro Glu Met Tyr Ile Pro Asp Ser Asp Thr Phe
        515                 520                 525

Ile Lys Gln Gln Pro Asn Ser Ile Val Arg Thr Tyr His Ser Met Ser
    530                 535                 540

Ile Leu Leu Pro Asp Ala Arg Val Phe Asn Gly Gly Gly Gly Leu Cys
545                 550                 555                 560

Gly Asp Cys Ser Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Ser
                565                 570                 575

Tyr Leu Leu Asn Lys Asp Gly Lys Pro Ala Thr Arg Pro Lys Ile Val
            580                 585                 590

Ser Val Ser Ala Thr Thr Ile Lys Val Gly Gly Ser Ile Thr Val Thr
        595                 600                 605

Thr Gly Gly Val Val Asn Thr Ala Ser Leu Ile Arg Tyr Gly Thr Ala
    610                 615                 620

Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr
625                 630                 635                 640

Gly Ala Gly Lys Asn Lys Tyr Thr Phe Lys Val Pro Gly Asp Ser Gly
                645                 650                 655

Ile Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly
            660                 665                 670

Val Pro Ser Val Ala Ser Thr Ile Lys Val Thr Thr
        675                 680


<210> SEQ ID NO 49
<211> LENGTH: 684
<212> TYPE: PRT
<213> ORGANISM: Fusarium sp. AF-3

<400> SEQUENCE: 49

Met Trp Ser Pro Ile Leu Thr Leu Cys Leu Ala Gly Ile Phe Trp Asp
1               5                   10                  15

Glu Ala Met Ala Ile Val Ile Pro Ala Gln Asn Ser Thr Lys Val Lys
            20                  25                  30

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

Ala Ile Asn Arg Asn Asn Trp Lys Val Thr Cys Asp Ser Asp Asn Pro
    50                  55                  60

Asp Ser Asp Asn Ala Cys Gln Lys Ala Ile Asp Gly Asp Val Asn Ser
65                  70                  75                  80

Phe Trp His Thr Ala Trp Phe Glu Asp Thr Ser Lys Asp Pro Gly Leu
                85                  90                  95

Pro His Thr Leu Thr Val Asp Met Lys Thr Val Gln Asn Val Asn Gly
            100                 105                 110

Ile Ser Ala Leu Pro Arg Gln Asp Gly Thr Thr His Gly Trp Ile Ala
        115                 120                 125

Arg His Asp Ile Phe Leu Ser Thr Asp Gly Lys Thr Trp Gly Ser Pro
    130                 135                 140

Val Ala Thr Gly Thr Trp Tyr Ala Asp Gly Thr Glu Lys Phe Ser Asn
145                 150                 155                 160

Phe Glu Thr Lys Arg Ala Arg Tyr Val Arg Ile Val Ala Thr Thr Glu
                165                 170                 175
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Ala Tyr Asp Gly Pro Trp Thr Ser Ile Ala Glu Phe Asn Val Tyr Lys
            180                 185                 190

Ala Ala Thr Tyr Thr Ala Pro Lys Thr Gly Ile Gly Met Trp Gly Pro
        195                 200                 205

Thr Leu Asp Phe Pro Ile Val Pro Val Ala Gly Ala Val Asp Pro Gly
    210                 215                 220

Thr Gly Lys Val Leu Val Trp Ser Ser Tyr Tyr His Asp Thr Met Asn
225                 230                 235                 240

Gly Ser Pro Gly Gly Met Thr Leu Thr Ser Leu Trp Asp Pro Glu Thr
                245                 250                 255

Gly Ile Ile Thr Gln Arg Glu Val Phe Glu Thr Asn His Asp Met Phe
            260                 265                 270

Cys Pro Gly Ile Ser Met Asp Gly Thr Gly Gln Ile Val Val Thr Gly
        275                 280                 285

Gly Asn Asn Ala Ala Arg Thr Ser Thr Trp Asp Pro Val Lys Asn Gln
    290                 295                 300

Trp Val Ser Ala Pro Asp Met Lys Ile Pro Arg Gly Tyr Gln Ser Ser
305                 310                 315                 320

Ala Thr Thr Ser Asn Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Gly
                325                 330                 335

Gly Asp Arg Ala Phe Lys Pro Gly Glu Ile Phe Asp Pro Ser Ser Arg
            340                 345                 350

Lys Trp Thr Leu Leu Ser Asn Ala Lys Val Glu Pro Met Leu Thr Ala
        355                 360                 365

Asp Ala Gln Gly Ile Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly
    370                 375                 380

Trp Lys Gly Glu Thr Ile Phe Gln Ala Gly Pro Ser Ser Ala Met Asn
385                 390                 395                 400

Trp Tyr Tyr Thr Gln Gly Lys Gly Thr Val Lys Pro Ala Gly Lys Arg
                405                 410                 415

Gln Ser Ser Arg Gly Val Asp Pro Asp Ser Met Cys Gly Asn Ala Val
            420                 425                 430

Met Phe Asp Ala Val Lys Gly Lys Ile Val Thr Phe Gly Gly Thr Pro
        435                 440                 445

Asn Tyr Gln Asp Ser Tyr Ala Thr Thr Asn Ala His Ile Ile Thr Ile
    450                 455                 460

Gly Ala Pro Gly Thr Gln Ala Ser Val Ala Phe Ala Ser Asn Gly Met
465                 470                 475                 480

Tyr Tyr Pro Arg Val Phe His Thr Ser Val Leu Leu Pro Asp Gly Thr
                485                 490                 495

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

Thr Pro Gln Leu Thr Pro Glu Met Tyr Ile Pro Asp Ser Asp Thr Phe
        515                 520                 525

Ile Lys Gln Gln Pro Asn Ser Ile Val Arg Thr Tyr His Ser Met Ser
    530                 535                 540

Ile Leu Leu Pro Asp Ala Arg Val Phe Asn Gly Gly Gly Gly Leu Cys
545                 550                 555                 560

Gly Asp Cys Ser Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Ser
                565                 570                 575
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Tyr Leu Leu Thr Lys Asp Gly Lys Pro Ala Thr Arg Pro Lys Ile Val
            580                 585                 590

Ser Val Ser Ala Thr Thr Ile Lys Val Gly Gly Ser Ile Thr Val Thr
        595                 600                 605

Thr Gly Gly Val Val Asn Thr Ala Ser Leu Ile Arg Tyr Gly Thr Ala
    610                 615                 620

Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr
625                 630                 635                 640

Gly Ala Gly Lys Asn Lys Tyr Thr Phe Lys Val Pro Gly Asp Ser Gly
                645                 650                 655

Ile Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly
            660                 665                 670

Val Pro Ser Val Ala Ser Thr Ile Lys Val Thr Thr
        675                 680


<210> SEQ ID NO 50
<211> LENGTH: 684
<212> TYPE: PRT
<213> ORGANISM: Fusarium kuroshium

<400> SEQUENCE: 50

Met Trp Ser Pro Ile Leu Thr Leu Cys Leu Ala Gly Leu Phe Trp Asp
1               5                   10                  15

Glu Ala Met Ala Ile Val Ile Pro Ala Gln Asn Ser Thr Lys Val Lys
            20                  25                  30

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

Ala Ile Asn Arg Asn Asn Trp Lys Val Thr Cys Asp Ser Asp Asn Pro
    50                  55                  60

Asp Ser Asp Asn Ala Cys Gln Lys Ala Ile Asp Gly Asp Val Asn Ser
65                  70                  75                  80

Phe Trp His Thr Ala Trp Phe Glu Asp Thr Ser Lys Asp Pro Gly Leu
                85                  90                  95

Pro His Thr Leu Thr Val Asp Met Lys Thr Val Gln Asn Val Asn Gly
            100                 105                 110

Ile Ser Ala Leu Pro Arg Gln Asp Gly Ile Thr His Gly Trp Ile Ala
        115                 120                 125

Arg His Asp Ile Phe Leu Ser Thr Asp Gly Lys Thr Trp Gly Ser Pro
    130                 135                 140

Val Ala Thr Gly Thr Trp Tyr Ala Asp Gly Thr Glu Lys Phe Ser Asn
145                 150                 155                 160

Phe Glu Thr Lys Arg Ala Arg Tyr Val Arg Ile Val Ala Thr Thr Glu
                165                 170                 175

Ala Tyr Asp Gly Pro Trp Thr Ser Ile Ala Glu Phe Asn Val Tyr Lys
            180                 185                 190

Ala Ala Thr Tyr Thr Ala Pro Lys Thr Gly Ile Gly Met Trp Gly Pro
        195                 200                 205

Thr Leu Asp Phe Pro Ile Val Pro Val Ala Gly Ala Val Asp Pro Gly
    210                 215                 220

Thr Gly Lys Val Leu Val Trp Ser Ser Tyr Tyr His Asp Thr Met Asn
225                 230                 235                 240

Gly Ser Pro Gly Gly Met Thr Leu Thr Ser Leu Trp Asp Pro Glu Thr
                245                 250                 255
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Gly Ile Ile Thr Gln Arg Glu Val Phe Glu Thr Asn His Asp Met Phe
            260                 265                 270

Cys Pro Gly Ile Ser Met Asp Gly Thr Gly Gln Ile Val Val Thr Gly
        275                 280                 285

Gly Asn Asn Ala Ala Arg Thr Ser Thr Trp Asp Pro Val Lys Asn Gln
    290                 295                 300

Trp Val Ser Ala Pro Asp Met Lys Ile Pro Arg Gly Tyr Gln Ser Ser
305                 310                 315                 320

Ala Thr Thr Ser Asn Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Gly
                325                 330                 335

Gly Asp Arg Thr Phe Lys Pro Gly Glu Ile Phe Asp Pro Ser Ser Arg
            340                 345                 350

Lys Trp Thr Leu Leu Gln Asn Ala Lys Val Glu Pro Met Leu Thr Ala
        355                 360                 365

Asp Ala Gln Gly Ile Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly
    370                 375                 380

Trp Lys Gly Glu Thr Ile Phe Gln Ala Gly Pro Ser Ser Ala Met Asn
385                 390                 395                 400

Trp Tyr Tyr Thr Gln Gly Lys Gly Thr Val Lys Pro Ala Gly Lys Arg
                405                 410                 415

Gln Ser Ser Arg Gly Val Asp Pro Asp Ser Met Cys Gly Asn Ala Val
            420                 425                 430

Met Phe Asp Ala Val Lys Gly Lys Ile Val Thr Phe Gly Gly Thr Pro
        435                 440                 445

Asn Tyr Gln Asp Ser Tyr Ala Thr Thr Asn Ala His Ile Ile Thr Ile
    450                 455                 460

Gly Ala Pro Gly Thr Gln Ala Ser Val Ala Phe Ala Ser Asn Gly Met
465                 470                 475                 480

Tyr Tyr Pro Arg Val Phe His Thr Ser Val Leu Leu Pro Asp Gly Thr
                485                 490                 495

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

Thr Pro Gln Leu Thr Pro Glu Met Tyr Ile Pro Asp Ser Asp Thr Phe
        515                 520                 525

Ile Lys Gln Gln Pro Asn Ser Ile Val Arg Thr Tyr His Ser Met Ser
    530                 535                 540

Ile Leu Leu Pro Asp Ala Arg Val Phe Asn Gly Gly Gly Gly Leu Cys
545                 550                 555                 560

Gly Asp Cys Ser Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Ser
                565                 570                 575

Tyr Leu Leu Thr Lys Asp Gly Lys Pro Ala Thr Arg Pro Lys Ile Val
            580                 585                 590

Ser Val Ser Ala Thr Thr Ile Lys Val Gly Gly Ser Ile Thr Val Thr
        595                 600                 605

Thr Gly Gly Val Val Asn Thr Ala Ser Leu Ile Arg Tyr Gly Thr Ala
    610                 615                 620

Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr
625                 630                 635                 640

Gly Ala Gly Lys Asn Lys Tyr Thr Phe Lys Val Pro Gly Asp Ser Gly
                645                 650                 655
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Ile Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly
            660                 665                 670

Val Pro Ser Val Ala Ser Thr Ile Lys Val Thr Thr
        675                 680


<210> SEQ ID NO 51
<211> LENGTH: 684
<212> TYPE: PRT
<213> ORGANISM: Fusarium sp. AF-6

<400> SEQUENCE: 51

Met Arg Ser Ser Ile Leu Thr Phe Cys Leu Ala Gly Leu Phe Trp Asp
1               5                   10                  15

Glu Ala Met Ala Ile Val Ile Pro Thr Gln Asn Ser Thr Lys Val Lys
            20                  25                  30

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

Ala Ile Asn Arg Ser Asn Trp Lys Val Thr Cys Asp Ser Asp Asn Pro
    50                  55                  60

Asp Ser Asp Asn Ala Cys Gln Lys Ala Ile Asp Gly Asp Val Asn Ser
65                  70                  75                  80

Phe Trp His Thr Ala Trp Phe Glu Asp Thr Ser Lys Asp Pro Gly Leu
                85                  90                  95

Pro His Thr Leu Thr Val Asp Met Lys Thr Val Gln Asn Val Asn Gly
            100                 105                 110

Ile Ser Ala Leu Pro Arg Gln Asp Gly Ile Thr His Gly Trp Ile Ala
        115                 120                 125

Arg His Asp Ile Phe Leu Ser Thr Asp Gly Lys Thr Trp Gly Thr Pro
    130                 135                 140

Val Ala Thr Gly Thr Trp Tyr Ala Asp Gly Thr Glu Lys Phe Ser Asn
145                 150                 155                 160

Phe Glu Thr Lys Arg Ala Arg Tyr Val Arg Ile Ala Ala Val Thr Glu
                165                 170                 175

Ala Tyr Asp Gly Pro Trp Thr Ser Ile Ala Glu Phe Asn Val Tyr Lys
            180                 185                 190

Ala Ala Thr Tyr Thr Ala Pro Lys Ser Gly Ile Gly Met Trp Gly Pro
        195                 200                 205

Thr Leu Asp Phe Pro Ile Val Pro Val Ala Gly Ala Val Asp Pro Gly
    210                 215                 220

Thr Gly Lys Val Leu Val Trp Ser Ser Tyr Tyr His Asp Thr Met Asn
225                 230                 235                 240

Gly Ser Pro Gly Gly Met Thr Leu Thr Ser Leu Trp Asp Pro Glu Thr
                245                 250                 255

Gly Ile Ile Thr Gln Arg Glu Val Phe Glu Thr Asn His Asp Met Phe
            260                 265                 270

Cys Pro Gly Ile Ser Met Asp Gly Thr Gly Gln Ile Val Val Thr Gly
        275                 280                 285

Gly Asn Asn Ala Ala Arg Thr Ser Thr Trp Asp Pro Val Lys Asn Gln
    290                 295                 300

Trp Val Ser Ala Pro Asp Met Lys Ile Pro Arg Gly Tyr Gln Ser Ser
305                 310                 315                 320

Ala Thr Thr Ser Asn Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Gly
                325                 330                 335
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Gly Asp Arg Ala Phe Lys Pro Gly Glu Ile Phe Asp Pro Ser Ser Arg
            340                 345                 350

Lys Trp Thr Leu Leu Gln Asn Ala Lys Val Glu Pro Met Leu Thr Ala
        355                 360                 365

Asp Ala Gln Gly Ile Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly
    370                 375                 380

Trp Lys Gly Glu Thr Ile Phe Gln Ala Gly Pro Ser Ser Ala Met Asn
385                 390                 395                 400

Trp Tyr Tyr Thr Gln Gly Lys Gly Thr Val Lys Pro Ala Gly Lys Arg
                405                 410                 415

Gln Ser Ser Arg Gly Val Asp Pro Asp Ser Met Cys Gly Asn Ala Val
            420                 425                 430

Met Phe Asp Ala Val Lys Gly Lys Ile Val Thr Phe Gly Gly Thr Pro
        435                 440                 445

Asn Tyr Gln Asp Ser Tyr Ala Thr Thr Asn Ala His Ile Ile Thr Ile
    450                 455                 460

Gly Ala Pro Gly Thr Gln Ala Ser Val Ala Phe Ala Ser Asn Gly Met
465                 470                 475                 480

Tyr Tyr Pro Arg Val Phe His Thr Ser Val Leu Leu Pro Asp Gly Thr
                485                 490                 495

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

Thr Pro Gln Leu Thr Pro Glu Met Tyr Ile Pro Asp Ser Asp Thr Phe
        515                 520                 525

Ile Lys Gln Gln Pro Asn Ser Ile Val Arg Thr Tyr His Ser Met Ser
    530                 535                 540

Ile Leu Leu Pro Asp Ala Arg Val Phe Asn Gly Gly Gly Gly Leu Cys
545                 550                 555                 560

Gly Asp Cys Ser Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Ser
                565                 570                 575

Tyr Leu Leu Thr Lys Asp Gly Lys Pro Ala Thr Arg Pro Lys Ile Val
            580                 585                 590

Ser Val Ser Ala Thr Thr Ile Lys Val Gly Gly Ser Ile Thr Val Thr
        595                 600                 605

Thr Gly Gly Val Val Asn Thr Ala Ser Leu Ile Arg Tyr Gly Thr Ala
    610                 615                 620

Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Thr
625                 630                 635                 640

Gly Ala Gly Lys Asn Lys Tyr Thr Phe Lys Val Pro Gly Asp Ser Gly
                645                 650                 655

Ile Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly
            660                 665                 670

Val Pro Ser Val Ala Ser Thr Ile Lys Val Thr Thr
        675                 680


<210> SEQ ID NO 52
<211> LENGTH: 684
<212> TYPE: PRT
<213> ORGANISM: Fusarium sp. AF-8

<400> SEQUENCE: 52

Met Trp Ser Pro Ile Leu Thr Leu Cys Leu Thr Gly Leu Phe Trp Asp
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1               5                   10                  15

Glu Ala Met Ala Ile Val Val Pro Ala Gln Asn Ser Thr Lys Val Lys
            20                  25                  30

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

Ala Ile Asn Arg Asn Asn Trp Lys Val Thr Cys Asp Ser Asp Asn Pro
    50                  55                  60

Asp Ser Asp Asn Ala Cys Gln Lys Ala Ile Asp Gly Asp Val Asn Ser
65                  70                  75                  80

Phe Trp His Thr Ala Trp Phe Glu Asp Thr Ser Lys Asp Pro Gly Leu
                85                  90                  95

Pro His Thr Leu Thr Val Asp Met Lys Thr Val Lys Asn Val Asn Gly
            100                 105                 110

Ile Ser Ala Leu Pro Arg Gln Asp Gly Thr Thr His Gly Trp Ile Ala
        115                 120                 125

Arg His Asp Ile Phe Leu Ser Thr Asp Gly Lys Thr Trp Gly Ser Pro
    130                 135                 140

Val Ala Thr Gly Thr Trp Tyr Ala Asp Gly Thr Glu Lys Phe Ser Asn
145                 150                 155                 160

Phe Glu Thr Lys Arg Ala Arg Tyr Val Arg Ile Val Ala Ile Thr Glu
                165                 170                 175

Ala Tyr Asp Gly Pro Trp Thr Ser Ile Ala Glu Phe Asn Val Tyr Lys
            180                 185                 190

Ala Ala Thr Tyr Thr Ala Pro Lys Thr Gly Ile Gly Met Trp Gly Pro
        195                 200                 205

Thr Leu Asp Phe Pro Ile Val Pro Val Ala Gly Ala Val Asp Pro Gly
    210                 215                 220

Thr Gly Lys Val Leu Val Trp Ser Ser Tyr Tyr His Asp Thr Met Asn
225                 230                 235                 240

Gly Ser Pro Gly Gly Met Thr Leu Thr Ser Leu Trp Asp Pro Glu Thr
                245                 250                 255

Gly Ile Ile Thr Gln Arg Glu Val Phe Glu Thr Asn His Asp Met Phe
            260                 265                 270

Cys Pro Gly Ile Ser Met Asp Gly Thr Gly Gln Ile Val Val Thr Gly
        275                 280                 285

Gly Asn Asn Ala Ala Arg Thr Ser Thr Trp Asp Pro Val Lys Asn Gln
    290                 295                 300

Trp Val Ser Ala Pro Asp Met Lys Ile Pro Arg Gly Tyr Gln Ser Ser
305                 310                 315                 320

Ala Thr Thr Ser Asn Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Gly
                325                 330                 335

Gly Asp Arg Ala Phe Lys Pro Gly Glu Ile Phe Asp Pro Lys Ser Arg
            340                 345                 350

Lys Trp Thr Leu Leu Pro Asn Ala Lys Val Glu Pro Met Leu Thr Ala
        355                 360                 365

Asp Ala Gln Gly Ile Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly
    370                 375                 380

Trp Lys Gly Glu Thr Val Phe Gln Ala Gly Pro Ser Ser Ala Met Asn
385                 390                 395                 400

Trp Tyr Tyr Thr Gln Gly Lys Gly Thr Val Lys Pro Ala Gly Lys Arg
                405                 410                 415
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Gln Ser Ser Arg Gly Val Asp Pro Asp Ser Met Cys Gly Asn Ala Val
            420                 425                 430

Met Phe Asp Ala Ala Lys Gly Lys Ile Val Thr Phe Gly Gly Thr Pro
        435                 440                 445

Asn Tyr Gln Asp Ser Tyr Ala Thr Thr Asn Ala His Ile Ile Thr Ile
    450                 455                 460

Gly Ala Pro Gly Thr Gln Ala Ser Val Ala Phe Val Ser Asp Gly Met
465                 470                 475                 480

Tyr Tyr Pro Arg Val Phe His Thr Ser Val Leu Leu Pro Asp Gly Thr
                485                 490                 495

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

Thr Pro Gln Leu Thr Pro Glu Leu Tyr Ile Pro Asp Ser Asp Thr Phe
        515                 520                 525

Ile Lys Gln Gln Pro Asn Ser Ile Val Arg Thr Tyr His Ser Met Ser
    530                 535                 540

Ile Leu Leu Gln Asp Ala Arg Val Phe Asn Gly Gly Gly Gly Leu Cys
545                 550                 555                 560

Gly Asp Cys Ser Thr Asn His Phe Asp Ala Gln Ile Phe Thr Pro Ser
                565                 570                 575

Tyr Leu Leu Thr Lys Asp Gly Lys Pro Ala Ala Arg Pro Lys Ile Val
            580                 585                 590

Ser Val Ser Ala Thr Thr Ile Lys Val Gly Gly Ser Ile Thr Val Thr
        595                 600                 605

Thr Gly Gly Val Val Asn Thr Ala Ser Leu Ile Arg Tyr Gly Thr Ala
    610                 615                 620

Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Thr Leu Ala
625                 630                 635                 640

Ser Ala Gly Lys Asn Lys Tyr Thr Phe Lys Val Pro Gly Asp Ser Gly
                645                 650                 655

Ile Ala Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Ser Ala Gly
            660                 665                 670

Val Pro Ser Val Ala Thr Thr Ile Lys Val Thr Thr
        675                 680


<210> SEQ ID NO 53
<211> LENGTH: 681
<212> TYPE: PRT
<213> ORGANISM: Fusarium fujikuroi
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (330)..(330)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid
<220> FEATURE:
<221> NAME/KEY: misc_feature
<222> LOCATION: (332)..(332)
<223> OTHER INFORMATION: Xaa can be any naturally occurring amino acid

<400> SEQUENCE: 53

Met Lys Ser Phe Trp Thr Leu Ala Leu Tyr Leu Gly Ser Ala Ser Ala
1               5                   10                  15

Val Ala Ile Ser Gln Pro Ala Ser Lys Ala Glu Thr Pro Glu Gly Ser
            20                  25                  30

Leu Gln Phe Leu Ser Leu Arg Ala Ser Ala Pro Ile Gly Thr Ala Ile
        35                  40                  45
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Ser Arg Asp Lys Trp Lys Val Thr Cys Asp Ser Gln His Glu Gly Asp
    50                  55                  60

Glu Cys Ser Lys Ala Ile Asp Gly Asp Ser Asn Thr Phe Trp His Thr
65                  70                  75                  80

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

Thr Ile Asp Met Gly Ser Ser Gln Asn Val Asn Gly Leu Ser Val Leu
            100                 105                 110

Pro Arg Gln Asp Gly Ser Asp His Gly Trp Ile Gly Arg His Asn Val
        115                 120                 125

Phe Leu Ser Thr Asp Gly Lys Asn Trp Gly Asp Ala Val Ala Thr Gly
    130                 135                 140

Thr Trp Phe Ala Asp Asn Thr Glu Lys Tyr Ser Asn Phe Glu Thr Arg
145                 150                 155                 160

Pro Ala Arg Tyr Val Arg Leu Val Ala Val Thr Glu Ala Asn Asp Gln
                165                 170                 175

Pro Trp Thr Ser Ile Ala Glu Ile Asn Val Phe Lys Ala Ala Ser Tyr
            180                 185                 190

Thr Ser Pro Gln Pro Gly Leu Gly Arg Trp Gly Pro Thr Leu Asp Phe
        195                 200                 205

Pro Ile Val Pro Val Ala Ala Ala Val Glu Pro Thr Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Arg Asn Asp Ala Phe Gly Gly Ser Pro Gly
225                 230                 235                 240

Gly Val Thr Leu Thr Ser Thr Trp Asp Pro Ser Thr Gly Val Ile Ser
                245                 250                 255

Gln Arg Thr Val Thr Val Thr Lys His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Met Asp Gly Asp Gly Gln Val Val Val Thr Gly Gly Asn Asn Ala
        275                 280                 285

Glu Lys Thr Ser Leu Tyr Asp Ser Ser Ser Asp Ser Trp Ile Pro Gly
    290                 295                 300

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

Asn Gly Arg Val Phe Thr Ile Gly Gly Xaa Trp Xaa Gly Gly Ile Phe
                325                 330                 335

Glu Lys Asn Gly Glu Val Tyr Asp Pro Ser Ser Lys Thr Trp Thr Ser
            340                 345                 350

Leu Pro Gly Ala Leu Val Lys Pro Met Leu Thr Ala Asp Gln Gln Gly
        355                 360                 365

Leu Tyr Arg Ser Asp Asn His Gly Trp Leu Phe Gly Trp Lys Lys Gly
    370                 375                 380

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Tyr Thr
385                 390                 395                 400

Ser Gly Ser Gly Ala Thr Lys Ser Ala Gly Lys Arg Gln Ser Ser Arg
                405                 410                 415

Gly Thr Asp Pro Asp Ala Met Cys Gly Asn Ala Val Met Tyr Asp Ala
            420                 425                 430

Val Lys Gly Lys Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp
        435                 440                 445
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Ser Asp Ala Thr Thr Asn Ala His Ile Ile Thr Ile Gly Glu Pro Gly
    450                 455                 460

Ser Thr Pro Lys Thr Val Phe Ala Ser Asn Gly Leu Tyr Tyr Pro Arg
465                 470                 475                 480

Thr Phe His Thr Ser Val Ile Leu Pro Asp Gly Asn Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Gln Arg Gly Ile Pro Phe Ala Asp Ser Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Val Pro Asn Asp Asp Thr Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro
    530                 535                 540

Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Asp Cys Asp
545                 550                 555                 560

Thr Asn His Phe Asp Ala Gln Ile Tyr Thr Pro Asn Asn Leu Tyr Asp
                565                 570                 575

Ser Ser Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Lys Val Ser Ala
            580                 585                 590

Lys Ser Val Lys Val Gly Gly Lys Ile Thr Ile Ser Thr Asn Thr Ser
        595                 600                 605

Ile Lys Gln Ala Ser Leu Ile Arg Tyr Gly Thr Ser Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Ser Leu Arg Ser Thr Gly Ser
625                 630                 635                 640

Gly Ser Ser Tyr Ser Phe Gln Val Pro Ser Asp Ser Gly Ile Ala Leu
                645                 650                 655

Pro Gly Tyr Trp Met Leu Phe Val Ile Asn Ser Ala Gly Val Pro Ser
            660                 665                 670

Val Ala Ser Thr Leu Leu Val Thr Gln
        675                 680


<210> SEQ ID NO 54
<211> LENGTH: 674
<212> TYPE: PRT
<213> ORGANISM: Pochonia chlamydosporia 170

<400> SEQUENCE: 54

Met Lys Phe Thr Ala Glu Thr Val Leu Leu Ala Thr Leu Phe Ala Gly
1               5                   10                  15

His Val Ala Ala Leu Val Pro Arg Lys Ile Lys Leu Lys Gln His Tyr
            20                  25                  30

Arg Glu Asn Ser Thr Phe Ala Lys Leu Trp Ala Ala Ala Pro Ile Gly
        35                  40                  45

Asn Glu Ile Asn Arg Ala Gly Trp Lys Val Thr Cys Asp Ser Phe Glu
    50                  55                  60

Pro Gly Asn Glu Cys Gly Lys Ala Ile Asp Gly Asn Asn Asn Ser Phe
65                  70                  75                  80

Trp His Thr Lys Tyr Asp Gly Ser Asn Leu Pro His Gln Ile Val Val
                85                  90                  95

Asp Phe Gly Thr Val Lys Asn Val Asn Gly Ile Ser Ala Leu Pro Arg
            100                 105                 110

Gln Asp Asp Asn Asp His Gly Phe Ile Ala Gln His Asp Val Ser Val
        115                 120                 125
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Ser Thr Asp Gly Lys Thr Trp Glu Ser Val Ala Gly Gly Asn Trp Tyr
    130                 135                 140

Gly Gly Asp Lys Thr Leu Lys Phe Ala Asn Phe Glu Thr Arg Ser Ile
145                 150                 155                 160

Arg Tyr Val Arg Leu Lys Ala Thr Ser Glu Val Asn Gly Asn Pro Trp
                165                 170                 175

Thr Ser Leu Ala Glu Ile Lys Ala Tyr Glu Ala Lys Ala Gly Pro Thr
            180                 185                 190

Ala Tyr Asn Gln Asn Gly Lys Trp Gly Pro Thr Ile Asn Phe Pro Thr
        195                 200                 205

Val Pro Val Ala Ala Thr Val Asp Pro Asn Ser Gly Lys Val Ile Val
    210                 215                 220

Trp Ser Ser Tyr Thr Tyr Asp Asn Tyr Leu Gly Ser Ser Gln Asp Arg
225                 230                 235                 240

Val Phe Thr Ser Ile Trp Asp Pro Lys Thr Gly Ile Val Thr Pro Lys
                245                 250                 255

Leu Val Asp Asn Thr Asp His Asp Met Phe Cys Pro Gly Ile Ser Ile
            260                 265                 270

Asp Gly Thr Gly Lys Met Val Val Thr Gly Gly Asn Ser Ala Gln Lys
        275                 280                 285

Thr Thr Leu Tyr Asp Phe Ala Ser Gln Thr Trp Ile Pro Gly Pro Asp
    290                 295                 300

Met Asn Leu Pro Arg Gly Tyr Gln Ala Ser Ala Thr Leu Ser Asp Gly
305                 310                 315                 320

Arg Val Phe Thr Ile Gly Gly Cys Trp Ser Gly Gly Trp Phe Glu Lys
                325                 330                 335

Asn Gly Glu Val Tyr Asp Pro Lys Ala Lys Thr Trp Lys Asn Leu Ser
            340                 345                 350

Gly Ala Leu Val Lys Pro Met Leu Thr Asn Asp Ala Gln Gly Ile Tyr
        355                 360                 365

Arg Ala Asp Asn His Gly Trp Phe Phe Gly Trp Lys Ser Gly Ser Val
    370                 375                 380

Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Ser Thr Thr Gly
385                 390                 395                 400

Asn Gly Gly Val Thr Pro Ala Gly Gln Arg Lys Ser Asp Arg Gly Val
                405                 410                 415

Asp Gly Asp Ser Met Asn Gly Asn Ala Val Met Tyr Asp Ala Thr Gln
            420                 425                 430

Gly Lys Ile Leu Thr Phe Gly Gly Ala Pro Ser Tyr Gln Asp Ser Asp
        435                 440                 445

Ala Thr Ala His Ala His Leu Ile Thr Ile Gly Asn Pro Gly Thr Gln
    450                 455                 460

Ala Lys Val Gln Phe Ala Ser Asn Gly Leu Trp Ser Ala Arg Ser Phe
465                 470                 475                 480

His Thr Ser Val Val Leu Pro Asp Gly Asn Val Phe Ile Thr Gly Gly
                485                 490                 495

Gln Ser Tyr Ala Val Pro Phe Ser Asp Asp Thr Pro Gln Leu Thr Pro
            500                 505                 510

Glu Leu Tyr Lys Pro Ala Asp Asp Ser Phe Tyr Gln Gln Gln Pro Asn
        515                 520                 525
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Ser Ile Ile Arg Val Tyr His Ser Ile Ser Leu Leu Leu Pro Asp Gly
    530                 535                 540

Arg Val Leu Asn Ala Gly Gly Gly Leu Cys Gly Asp Cys Asn Thr Asn
545                 550                 555                 560

His Phe Asp Gly Gln Ile Phe Thr Pro Gln Tyr Leu Leu Thr Ser Thr
                565                 570                 575

Gly Gln Pro Ala Thr Arg Pro Val Ile Lys Ser Ala Thr Leu Ser Gly
            580                 585                 590

Arg Lys Ile Thr Ile Ser Thr Asp Ser Ala Val Ser Thr Ala Ser Leu
        595                 600                 605

Ile Arg Phe Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg
    610                 615                 620

Ile Pro Leu Thr Leu Thr Lys Thr Gly Thr Asn Met Tyr Thr Ala Asn
625                 630                 635                 640

Ala Pro Thr Asp Ser Gly Ile Leu Leu Pro Gly Tyr Tyr Met Leu Phe
                645                 650                 655

Val Met Asn Ala Asn Gly Val Pro Ser Val Ser Lys Thr Leu Ser Phe
            660                 665                 670

Leu Val


<210> SEQ ID NO 55
<211> LENGTH: 1067
<212> TYPE: PRT
<213> ORGANISM: Pochonia chlamydosporia 170

<400> SEQUENCE: 55

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

Ala Asp Ala Ile Ala Ile Pro Glu Phe Val Ser Pro Lys Val Gly Tyr
            20                  25                  30

Ser Thr Ser Leu Asn His Gly Glu Lys Lys Ala Glu Ser Gly Ser Asp
        35                  40                  45

Ala Asn Ser Ser Pro Arg Val Phe Gly Ala Tyr Gly Pro Lys Ser Lys
    50                  55                  60

Leu Val Gly Leu Pro Pro Val Arg Arg Ser Asp Lys Thr Glu Glu Ser
65                  70                  75                  80

Tyr Gly Ser Asp Asp Gly Val Asp Asp Asp Asp Gln Asp Asp Ser Gly
                85                  90                  95

Asp Asn Thr Ala Asp Pro Pro Glu Asp Ser Pro Asp Ser Asp Asp Pro
            100                 105                 110

Glu Leu Ile Tyr Pro Glu Pro Met Met Ala Pro Ala Tyr Val His Thr
        115                 120                 125

Gly Val Leu Pro Val Asp Lys Pro Glu Glu Ala Pro Lys Ser Lys Ser
    130                 135                 140

Ser Lys Val Asp Thr Lys Ser Lys Ser Lys Ser Gly Ser Lys Pro Asp
145                 150                 155                 160

Asp Thr Val His Thr Ala Lys His Gly Gly Tyr Asp Asp Ser Glu Ser
                165                 170                 175

Gly Ser Ser Gly Lys Lys Lys Gln Lys Gly Lys Asp Lys Asn Lys Gly
            180                 185                 190

Asn Asp Asp Asn Pro Gly Lys His Ser Gly Asp Asp Asp Ala Ser Lys
        195                 200                 205
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Ser Arg Thr Lys Ser Glu Asp Ser Lys Pro Thr Ser Lys Ser Thr Thr
    210                 215                 220

Ser Asn Thr Ser Thr Ser Gly Thr Ala Pro Leu Pro Thr Ser Val Asn
225                 230                 235                 240

Thr Arg Pro Thr Thr Gly Arg His Ser Gly Asp Asp Asp Lys Lys
                245                 250                 255

Ser Arg Ser Lys Thr Glu Asp Ser Pro Arg Ser Gly Ser Pro Lys Pro
            260                 265                 270

Thr Ser Thr Ser Asp Ala Ser Ser Lys Gly Ser Gly Lys Gly Lys Gly
        275                 280                 285

Lys Gly Asn Asp Gly Ser Gly Lys His Ser Gly Asp Asp Asp Ala Thr
    290                 295                 300

Lys Thr Ser Ser Lys Lys Gly Ser Lys Asp Asp Ser Ala Lys Ala Asp
305                 310                 315                 320

Asp Ser Lys Ser Ala Lys Pro Ala Phe Lys Lys Ser Ser Ser Thr Pro
                325                 330                 335

Arg His Pro Arg Gly Ile Thr Ala Thr His Gln Ser Gly Ser Thr Phe
            340                 345                 350

Asp Pro Asn Ser Ala Lys Gly Gly Gly Lys Asn Gly Pro Gly Phe Phe
        355                 360                 365

Lys Pro Phe Glu Pro Pro Lys Leu Asn Asn Gly Tyr Ile Gln Ala Val
    370                 375                 380

Pro Pro Gln Ala Ser Gln Lys Asn Ser Lys Ser Ser Pro Lys Val Lys
385                 390                 395                 400

Pro Lys Pro Arg Leu Asn Gly Lys Val Ser Gly Pro Phe Ser Ser Leu
                405                 410                 415

Arg Lys Arg Glu Gln Leu Leu Ser Leu Arg Ala Ala Ala Pro Leu Glu
            420                 425                 430

Ser Val Thr Ile Asp Arg Ser Lys Trp Lys Ala Thr Cys Asp Ser Val
        435                 440                 445

His Glu Gly Asp Glu Cys Gln Asn Ala Ile Asp Gly Asn Gly Asp Thr
    450                 455                 460

Ile Trp His Thr Gln Trp Glu Gly Thr Glu Pro Ala Pro Pro His Met
465                 470                 475                 480

Ile Thr Val Asp Met Lys Lys Val Tyr Asn Val Asn Gly Ile Ser Met
                485                 490                 495

Leu Pro Arg Gln Asp Gly Ser Gln Asn Gly Tyr Ile Ala Gln His Gln
            500                 505                 510

Val Phe Leu Ser Lys Asp Asn His Asn Trp Gly Ser Pro Val Ala Tyr
        515                 520                 525

Gly Thr Trp Tyr Ser Asp Tyr Thr Thr Lys Tyr Ala Asn Phe Asp Thr
    530                 535                 540

Gln Pro Ala Arg Tyr Val Arg Leu Val Ala Ile Thr Glu Ala Asn Gly
545                 550                 555                 560

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

Tyr Thr Ala Pro Gln Pro Ser Ser Leu Gly Ala Trp Gly Pro Thr Val
            580                 585                 590

Asn Phe Pro Val Ile Pro Val Ala Gly Thr Val Asp Pro Lys Thr Gly
        595                 600                 605

Lys Val Leu Ile Trp Ser Ser Trp Ala Arg Asp Thr Met Asp Gly Gly
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    610                 615                 620

Pro Gly Gly Leu Thr Leu Thr Ser Met Trp Asp Pro Ala Thr Gly Leu
625                 630                 635                 640

Val Ala Glu Arg Asp Val Thr Glu Thr Asn His Asp Met Phe Cys Pro
                645                 650                 655

Gly Ile Ser Leu Asp Gly Asn Gly Gln Leu Val Val Thr Gly Gly Asn
            660                 665                 670

Asn Ala Glu Arg Thr Ser Leu Phe Asp Pro Val Lys Gln Ala Trp Ile
        675                 680                 685

Pro Gly Pro Asp Met Lys Val Ala Arg Gly Tyr His Ala Ser Ala Thr
    690                 695                 700

Thr Ser Thr Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly
705                 710                 715                 720

Glu Tyr Phe Lys Asn Gly Glu Val Tyr Asp Pro Lys Lys Lys Thr Trp
                725                 730                 735

Thr Leu Leu Asn Lys Ala Asp Val Gln Lys Met Leu Thr Ala Asp Thr
            740                 745                 750

Gln Gly Leu Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys
        755                 760                 765

Lys Gly Thr Val Phe Gln Ala Gly Pro Ser Gln Ala Met Asn Trp Tyr
    770                 775                 780

Tyr Thr Asp Gly Lys Asp Gly Asn Val Lys Thr Ala Gly Lys Arg Gln
785                 790                 795                 800

Ser Asp Arg Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Ile Met
                805                 810                 815

Phe Asp Ala Val Lys Gly Lys Ile Leu Thr Asn Gly Gly Thr Pro Asn
            820                 825                 830

Tyr Gln Asp Ser Asp Ala Thr Ala Asp Ala His Ile Ile Thr Ile Asn
        835                 840                 845

Asn Pro Gly Asn Lys Ala Asp Val Ser Tyr Ala Ser Glu Gly Leu Tyr
    850                 855                 860

His Ala Arg Val Phe His Ser Ser Val Val Leu Pro Asn Gly Asn Val
865                 870                 875                 880

Phe Ile Thr Gly Gly Gln Glu Tyr Ala Ile Pro Phe Ala Asp Ser Met
                885                 890                 895

Pro Val Leu Glu Pro Glu Met Tyr Leu Pro Asp Glu Asp Arg Phe Val
            900                 905                 910

Leu Met Lys Pro Asn Asn Ile Val Arg Thr Tyr His Ser Ile Ala Leu
        915                 920                 925

Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly
    930                 935                 940

Gly Cys Asp Thr Asn His Phe Asp Ala Gln Leu Tyr Thr Pro Pro Tyr
945                 950                 955                 960

Leu Tyr Asp Ser Lys Gly Arg Leu Ala Thr Arg Pro Lys Ile Ala Ser
                965                 970                 975

Val Ser Val Ser Thr Val Lys Val Gly Gly Thr Val Thr Val Gln Thr
            980                 985                 990

Ser Gly Ala Val Val Arg Ala Ser  Leu Val Arg Tyr Gly  Thr Ala Thr
        995                 1000                1005

His Thr  Val Asn Ser Asp Gln  Arg Arg Val Pro Leu  Thr Leu Ser
    1010                1015                1020
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Asn Ala  Gly Lys Asn Ser Tyr  Ser Phe Gln Val Pro  Ser Asp Pro
    1025                1030                1035

Gly Val  Ala Leu Pro Gly Tyr  Trp Met Leu Phe Val  Met Asp Lys
    1040                1045                1050

Asn Gly  Val Pro Ser Val Ala  Ser Thr Ile Lys Val  Thr Gly
    1055                1060                1065


<210> SEQ ID NO 56
<211> LENGTH: 1067
<212> TYPE: PRT
<213> ORGANISM: Fusarium graminearum

<400> SEQUENCE: 56

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

Ala Asp Ala Ile Ala Ile Pro Glu Phe Val Ser Pro Lys Val Gly Tyr
            20                  25                  30

Ser Thr Ser Leu Asn His Gly Glu Lys Lys Ala Glu Ser Gly Ser Asp
        35                  40                  45

Ala Asn Ser Ser Pro Arg Val Phe Gly Ala Tyr Gly Pro Lys Ser Lys
    50                  55                  60

Leu Val Gly Leu Pro Pro Val Arg Arg Ser Asp Lys Thr Glu Glu Ser
65                  70                  75                  80

Tyr Gly Ser Asp Asp Gly Val Asp Asp Asp Asp Gln Asp Asp Ser Gly
                85                  90                  95

Asp Asn Thr Ala Asp Pro Pro Glu Asp Ser Pro Asp Ser Asp Asp Pro
            100                 105                 110

Glu Leu Ile Tyr Pro Glu Pro Met Met Ala Pro Ala Tyr Val His Thr
        115                 120                 125

Gly Val Leu Pro Val Asp Lys Pro Glu Glu Ala Pro Lys Ser Lys Ser
    130                 135                 140

Ser Lys Val Asp Thr Lys Ser Lys Ser Lys Ser Gly Ser Lys Pro Asp
145                 150                 155                 160

Asp Thr Val His Thr Ala Lys His Gly Gly Tyr Asp Asp Ser Glu Ser
                165                 170                 175

Gly Ser Ser Gly Lys Lys Lys Gln Lys Gly Lys Asp Lys Asn Lys Gly
            180                 185                 190

Asn Asp Asp Asn Pro Gly Lys His Ser Gly Asp Asp Asp Ala Ser Lys
        195                 200                 205

Ser Arg Thr Lys Ser Glu Asp Ser Lys Pro Thr Ser Lys Ser Thr Thr
    210                 215                 220

Ser Asn Thr Ser Thr Ser Gly Thr Ala Pro Leu Pro Thr Ser Val Asn
225                 230                 235                 240

Thr Arg Pro Thr Thr Gly Arg His Ser Gly Asp Asp Asp Asp Lys Lys
                245                 250                 255

Ser Arg Ser Lys Thr Glu Asp Ser Pro Arg Ser Gly Ser Pro Lys Pro
            260                 265                 270

Thr Ser Thr Ser Asp Ala Ser Ser Lys Gly Ser Gly Lys Gly Lys Gly
        275                 280                 285

Lys Gly Asn Asp Gly Ser Gly Lys His Ser Gly Asp Asp Asp Ala Thr
    290                 295                 300

Lys Thr Ser Ser Lys Lys Gly Ser Lys Asp Asp Ser Ala Lys Ala Asp
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305                 310                 315                 320

Asp Ser Lys Ser Ala Lys Pro Ala Phe Lys Lys Ser Ser Ser Thr Pro
                325                 330                 335

Arg His Pro Arg Gly Ile Thr Ala Thr His Gln Ser Gly Ser Thr Phe
            340                 345                 350

Asp Pro Asn Ser Ala Lys Gly Gly Gly Lys Asn Gly Pro Gly Phe Phe
        355                 360                 365

Lys Pro Phe Glu Pro Pro Lys Leu Asn Asn Gly Tyr Ile Gln Ala Val
    370                 375                 380

Pro Pro Gln Ala Ser Gln Lys Asn Ser Lys Ser Ser Pro Lys Val Lys
385                 390                 395                 400

Pro Lys Pro Arg Leu Asn Gly Lys Val Ser Gly Pro Phe Ser Ser Leu
                405                 410                 415

Arg Lys Arg Glu Gln Leu Leu Ser Leu Arg Ala Ala Ala Pro Leu Glu
            420                 425                 430

Ser Val Thr Ile Asp Arg Ser Lys Trp Lys Ala Thr Cys Asp Ser Val
        435                 440                 445

His Glu Gly Asp Glu Cys Gln Asn Ala Ile Asp Gly Asn Gly Asp Thr
    450                 455                 460

Ile Trp His Thr Gln Trp Glu Gly Thr Glu Pro Ala Pro Pro His Met
465                 470                 475                 480

Ile Thr Val Asp Met Lys Lys Val Tyr Asn Val Asn Gly Ile Ser Met
                485                 490                 495

Leu Pro Arg Gln Asp Gly Ser Gln Asn Gly Tyr Ile Ala Gln His Gln
            500                 505                 510

Val Phe Leu Ser Lys Asp Asn His Asn Trp Gly Ser Pro Val Ala Tyr
        515                 520                 525

Gly Thr Trp Tyr Ser Asp Tyr Thr Thr Lys Tyr Ala Asn Phe Asp Thr
    530                 535                 540

Gln Pro Ala Arg Tyr Val Arg Leu Val Ala Ile Thr Glu Ala Asn Gly
545                 550                 555                 560

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

Tyr Thr Ala Pro Gln Pro Ser Ser Leu Gly Ala Trp Gly Pro Thr Val
            580                 585                 590

Asn Phe Pro Val Ile Pro Val Ala Gly Thr Val Asp Pro Lys Thr Gly
        595                 600                 605

Lys Val Leu Ile Trp Ser Ser Trp Ala Arg Asp Thr Met Asp Gly Gly
    610                 615                 620

Pro Gly Gly Leu Thr Leu Thr Ser Met Trp Asp Pro Ala Thr Gly Leu
625                 630                 635                 640

Val Ala Glu Arg Asp Val Thr Glu Thr Asn His Asp Met Phe Cys Pro
                645                 650                 655

Gly Ile Ser Leu Asp Gly Asn Gly Gln Leu Val Val Thr Gly Gly Asn
            660                 665                 670

Asn Ala Glu Arg Thr Ser Leu Phe Asp Pro Val Lys Gln Ala Trp Ile
        675                 680                 685

Pro Gly Pro Asp Met Lys Val Ala Arg Gly Tyr His Ala Ser Ala Thr
    690                 695                 700

Thr Ser Thr Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly
705                 710                 715                 720
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Glu Tyr Phe Lys Asn Gly Glu Val Tyr Asp Pro Lys Lys Lys Thr Trp
                725                 730                 735

Thr Leu Leu Asn Lys Ala Asp Val Gln Lys Met Leu Thr Ala Asp Thr
            740                 745                 750

Gln Gly Leu Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys
        755                 760                 765

Lys Gly Thr Val Phe Gln Ala Gly Pro Ser Gln Ala Met Asn Trp Tyr
    770                 775                 780

Tyr Thr Asp Gly Lys Asp Gly Asn Val Lys Thr Ala Gly Lys Arg Gln
785                 790                 795                 800

Ser Asp Arg Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Ile Met
                805                 810                 815

Phe Asp Ala Val Lys Gly Lys Ile Leu Thr Asn Gly Gly Thr Pro Asn
            820                 825                 830

Tyr Gln Asp Ser Asp Ala Thr Ala Asp Ala His Ile Ile Thr Ile Asn
        835                 840                 845

Asn Pro Gly Asn Lys Ala Asp Val Ser Tyr Ala Ser Glu Gly Leu Tyr
    850                 855                 860

His Ala Arg Val Phe His Ser Ser Val Val Leu Pro Asn Gly Asn Val
865                 870                 875                 880

Phe Ile Thr Gly Gly Gln Glu Tyr Ala Ile Pro Phe Ala Asp Ser Met
                885                 890                 895

Pro Val Leu Glu Pro Glu Met Tyr Leu Pro Asp Glu Asp Arg Phe Val
            900                 905                 910

Leu Met Lys Pro Asn Asn Ile Val Arg Thr Tyr His Ser Ile Ala Leu
        915                 920                 925

Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly
    930                 935                 940

Gly Cys Asp Thr Asn His Phe Asp Ala Gln Leu Tyr Thr Pro Pro Tyr
945                 950                 955                 960

Leu Tyr Asp Ser Lys Gly Arg Leu Ala Thr Arg Pro Lys Ile Ala Ser
                965                 970                 975

Val Ser Val Ser Thr Val Lys Val Gly Gly Thr Val Thr Val Gln Thr
            980                 985                 990

Ser Gly Ala Val Val Arg Ala Ser  Leu Val Arg Tyr Gly  Thr Ala Thr
        995                 1000                1005

His Thr  Val Asn Ser Asp Gln  Arg Arg Val Pro Leu  Thr Leu Ser
    1010                1015                1020

Asn Ala  Gly Lys Asn Ser Tyr  Ser Phe Gln Val Pro  Ser Asp Pro
    1025                1030                1035

Gly Val  Ala Leu Pro Gly Tyr  Trp Met Leu Phe Val  Met Asp Lys
    1040                1045                1050

Asn Gly  Val Pro Ser Val Ala  Ser Thr Ile Lys Val  Thr Gly
    1055                1060                1065


<210> SEQ ID NO 57
<211> LENGTH: 1071
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 57

Met Lys Val Val Tyr Ala Leu Thr Leu Cys Leu Gly Ile Ala Asp Ala
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1               5                   10                  15

Val Val Leu Pro Val Phe Ser Ala Pro Lys Gly Gly Tyr Ala Leu Pro
            20                  25                  30

Arg Pro Asp Ser Asp Asp Thr Thr Asp Ser Ser Lys Thr Ala Ala Gly
        35                  40                  45

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

Pro Lys Thr Gly Phe Pro Ala Ser Ala Leu Ser Arg Arg Val Ala Arg
65                  70                  75                  80

Ile Glu Gln Thr Tyr Gly Ser Asp Asp Glu Ser Thr Asp Asp Ser Asp
                85                  90                  95

Asp Thr Pro Thr Asp Pro Ser Asp Ala Thr Pro Ser Ser Pro Pro Asp
            100                 105                 110

Asp Thr Pro Ser Asp Ser Ser Asp Asp Ile Asp Glu Val Val Tyr Ala
        115                 120                 125

Glu Pro Phe Met Gln Pro Thr Tyr Val Arg Phe Gly Pro Ala Pro Val
    130                 135                 140

Asp Lys Pro Glu Val Ala Pro Lys Ala Lys Ser Asn Ser Lys Asp Thr
145                 150                 155                 160

Ala Ser Val Ala Lys His Gly Gly Asp Asp Asp Ser Ser Ser Gly Gly
                165                 170                 175

His Lys Gln Lys Gly Lys Asp Lys Asn Lys Gly Lys Asp Asp Ala Thr
            180                 185                 190

Lys Ser Arg Lys Lys Pro Glu Asp Ser Pro Lys Thr Ser Ser Asn Ser
        195                 200                 205

Ala Thr Asp Ser Val Ser Val Thr Ala Thr Ser Thr Ala Ala Pro Thr
    210                 215                 220

Ser Thr Ala Ala Pro Thr Ser Pro Pro Lys Gly Asp Asp Lys Gly Lys
225                 230                 235                 240

Ser Lys Gly Lys Gly Lys Gly Lys Gly Lys Asp Gly Gly Gly Arg His
                245                 250                 255

Asn Gly Asp Asp Asp Ala Ala Lys Ser Arg Thr Lys Val Glu Asp Ser
            260                 265                 270

Thr Lys Thr Tyr Ser Asp Asp Ser Gly Lys Gly Lys Gly Lys Gly Lys
        275                 280                 285

Gly Asp Gly Lys Gly Arg His Asp Gly Gly Val Asp Ala Thr Lys Ser
    290                 295                 300

Arg Ala Lys Ala Glu Asp Ser Glu Thr Asn Ser Lys Lys Ser Ser Lys
305                 310                 315                 320

Lys Gly Ser Lys Asp Asp Ser Lys Ser Lys Pro Ser Lys Lys Ser Phe
                325                 330                 335

Ile Thr His Gln Ser Gly Lys Thr Phe Asp Ala Asp Ser Thr Lys Gly
            340                 345                 350

Gly Gly Lys Asn Gly Pro Gly Tyr Asn Pro Ser Phe Asp Val Pro Lys
        355                 360                 365

Leu Asn Lys Gly Tyr Ile Gln Ala Ile Pro Pro Lys Ala Ser Thr Ile
    370                 375                 380

Asn Asn Lys Phe Ser Ser Arg Val Lys Pro Arg Pro Gln Leu Asn Thr
385                 390                 395                 400

Glu Lys Val Arg Pro Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser
                405                 410                 415
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```
Leu Leu Lys Arg Asp Glu Ser Lys Asn Ile Leu Ser Leu Arg Ala Ala
            420                 425                 430

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

Cys Asp Ser Val His Glu Gly Asp Asp Cys Lys Asn Ala Ile Asp Gly
    450                 455                 460

Asn Gly Asp Thr Met Trp His Thr Gln Trp Glu Gly Ser Glu Pro Ala
465                 470                 475                 480

Pro Pro His Ser Ile Thr Val Asp Met Lys Lys Ser Tyr Asn Val Asn
                485                 490                 495

Gly Ile Ser Met Leu Pro Arg Gln Asp Gly Ser Gln Asn Gly Tyr Ile
            500                 505                 510

Ala Gln His Gln Ile Phe Leu Ser Lys Asp Gly Lys Thr Trp Gly Ser
        515                 520                 525

Pro Val Ala Tyr Gly Asn Trp Tyr Ser Asp Trp Thr Val Lys Tyr Ala
    530                 535                 540

Asn Phe Asp Thr Gln Pro Ala Arg Phe Val Lys Leu Val Ala Leu Thr
545                 550                 555                 560

Glu Ala Asn Gly Asn Pro Trp Thr Ser Ile Ala Glu Leu Asn Val Phe
                565                 570                 575

Gln Ala Asn Asp Tyr Val Pro Pro Gln Ala Ser Gln Gly Ala Trp Gly
            580                 585                 590

Pro Thr Ile Asn Phe Pro Ile Ile Pro Val Ala Gly Thr Val Asp Pro
        595                 600                 605

Asn Thr Gly Lys Val Leu Val Trp Ser Ser Trp Ala Arg Asp Thr Met
    610                 615                 620

Ser Gly Gly Pro Gly Gly Leu Thr Leu Thr Ser Thr Trp Asp Pro Ala
625                 630                 635                 640

Thr Gly Gln Val Ala Glu Arg Gln Val Thr Glu Thr Asn His Asp Met
                645                 650                 655

Phe Cys Pro Gly Ile Ser Leu Asp Gly Asn Gly Gln Leu Val Val Thr
            660                 665                 670

Gly Gly Asn Asn Ala Glu Arg Thr Ser Leu Phe Asp Pro Val Lys Gln
        675                 680                 685

Ala Trp Val Ser Gly Pro Asn Met Lys Val Ala Arg Gly Tyr Gln Ser
    690                 695                 700

Ser Ala Thr Thr Ser Thr Gly Lys Val Phe Thr Ile Gly Gly Ser Trp
705                 710                 715                 720

Ser Gly Gly Glu Ser Phe Lys Asn Gly Glu Val Tyr Asp Pro Lys Lys
                725                 730                 735

Lys Thr Trp Thr Leu Leu Asn Lys Ala Asp Val Gln Lys Met Leu Thr
            740                 745                 750

Asn Asp Ala Gln Gly Leu Phe Arg Ser Asp Asn His Ala Trp Leu Phe
        755                 760                 765

Gly Trp Lys Ser Gly Thr Val Phe Gln Ala Gly Pro Ser Lys Asn Met
    770                 775                 780

Asn Trp Tyr Tyr Thr Glu Lys Lys Asn Gly Asp Val Lys Thr Ala Gly
785                 790                 795                 800

Gln Arg Ala Ser Asp Arg Gly Val Ala Pro Asp Ala Met Cys Gly Asn
                805                 810                 815
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```
Ala Ile Met Phe Asp Ala Val Lys Gly Lys Ile Leu Thr His Gly Gly
            820                 825                 830

Thr Pro Asn Tyr Gln Asp Ser Asp Ala Thr Thr Asp Ala His Ile Ile
        835                 840                 845

Thr Val Gly Asn Pro Gly Ala Asn Val Ser Val Ala Tyr Ala Ser Glu
    850                 855                 860

Gly Leu Phe Phe Pro Arg Val Phe His Ser Ser Val Val Leu Pro Asn
865                 870                 875                 880

Gly Asn Val Phe Ile Thr Gly Gly Gln Gln Tyr Ala Val Pro Phe Glu
                885                 890                 895

Asp Ser Thr Pro Gln Leu Gln Pro Glu Met Tyr Tyr Pro Asp Arg Asp
            900                 905                 910

Gly Phe Glu Leu Met Lys Pro Asn Asn Ile Val Arg Thr Tyr His Ser
        915                 920                 925

Ile Ala Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly
    930                 935                 940

Leu Cys Gly Gly Cys Asp Thr Asn His Phe Asp Ala Gln Leu Tyr Thr
945                 950                 955                 960

Pro Pro Tyr Leu Tyr Asp Ser Lys Gly Lys Leu Ala Thr Arg Pro Lys
                965                 970                 975

Ile Thr Ser Val Ser Val Ser Thr Ile Lys Val Gly Gly Thr Val Thr
            980                 985                 990

Val Gln Thr Gly Gly Ala Ile Val  Gln Ala Ser Leu Val  Arg Tyr Gly
        995                 1000                1005

Thr Ala  Thr His Thr Val Asn  Ser Asp Gln Arg Arg  Ile Pro Leu
    1010                1015                1020

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

Ser Asp  Pro Gly Val Ala Leu  Pro Gly Tyr Trp Met  Leu Phe Val
    1040                1045                1050

Met Asp  Lys Asn Gly Val Pro  Ser Val Ala Ser Thr  Ile Lys Val
    1055                1060                1065

Thr Gly  Ser
    1070


<210> SEQ ID NO 58
<211> LENGTH: 947
<212> TYPE: PRT
<213> ORGANISM: Fusarium graminearum PH-1

<400> SEQUENCE: 58

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

Glu Glu Ala Pro Lys Ser Lys Ser Ser Lys Val Asp Thr Lys Ser Lys
            20                  25                  30

Ser Lys Ser Gly Ser Lys Pro Asp Asp Thr Val His Thr Ala Lys His
        35                  40                  45

Gly Gly Asp Asp Asp Ser Glu Ser Gly Ser Ser Gly Lys Lys Lys Gln
    50                  55                  60

Lys Gly Lys Asp Lys Asn Lys Gly Asn Gly Asp Asn Pro Gly Lys His
65                  70                  75                  80

Ser Gly Asp Asp Asp Ala Ser Lys Ser Arg Thr Lys Ser Glu Asp Ser
                85                  90                  95
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Lys Pro Thr Ser Lys Leu Thr Thr Ser Asn Thr Ser Thr Ser Gly Thr
            100                 105                 110

Ala Pro Leu Pro Thr Ser Val Asn Thr Arg Pro Thr Thr Gly Arg His
        115                 120                 125

Ser Gly Asp Asp Asp Asp Lys Lys Ser Arg Ser Lys Thr Glu Asp Ser
    130                 135                 140

Pro Arg Ser Gly Ser Pro Lys Pro Thr Ser Thr Ser Asp Ala Ser Ser
145                 150                 155                 160

Lys Gly Ser Gly Lys Gly Lys Gly Lys Gly Asn Asp Gly Ser Gly Lys
                165                 170                 175

His Ser Gly Asp Asp Asp Ala Thr Lys Thr Ser Ser Lys Lys Gly Ser
            180                 185                 190

Lys Asp Asp Ser Ala Lys Ala Asp Asp Ser Lys Ser Ala Lys Ser Ala
        195                 200                 205

Phe Lys Lys Ser Ser Ser Thr Pro Arg His Pro Arg Gly Ile Thr Ala
    210                 215                 220

Thr His Gln Ser Gly Ser Thr Phe Asp Pro Asn Ser Ala Lys Gly Gly
225                 230                 235                 240

Gly Lys Asn Gly Pro Gly Phe Phe Lys Pro Phe Glu Pro Pro Lys Leu
                245                 250                 255

Asn Asn Gly Tyr Ile Gln Ala Val Pro Pro Gln Ala Ser Gln Lys Asn
            260                 265                 270

Ser Lys Ser Ser Pro Lys Val Lys Pro Lys Pro Arg Leu Asn Gly Lys
        275                 280                 285

Val Ser Gly Pro Phe Ser Ser Leu Arg Lys Arg Glu Gln Leu Leu Ser
    290                 295                 300

Leu Arg Ala Ala Ala Pro Leu Glu Ser Val Thr Ile Asp Arg Ser Lys
305                 310                 315                 320

Trp Lys Ala Thr Cys Asp Ser Val His Glu Gly Asp Glu Cys Gln Asn
                325                 330                 335

Ala Ile Asp Gly Asn Gly Asp Thr Ile Trp His Thr Gln Trp Glu Gly
            340                 345                 350

Thr Glu Pro Ala Pro Pro His Met Ile Thr Val Asp Met Lys Lys Val
        355                 360                 365

Tyr Asn Val Asn Gly Ile Ser Met Leu Pro Arg Gln Asp Gly Ser Gln
    370                 375                 380

Asn Gly Tyr Ile Ala Gln His Gln Val Phe Leu Ser Lys Asp Asn His
385                 390                 395                 400

Asn Trp Gly Ser Pro Val Ala Tyr Gly Thr Trp Tyr Ser Asp Tyr Thr
                405                 410                 415

Thr Lys Tyr Ala Asn Phe Asp Thr Gln Pro Ala Arg Tyr Val Arg Leu
            420                 425                 430

Val Ala Ile Thr Glu Ala Asn Gly Gly Pro Trp Thr Ser Ile Ala Glu
        435                 440                 445

Leu Asn Val Tyr Gln Gly Asn Asp Tyr Thr Ala Pro Gln Pro Ser Ser
    450                 455                 460

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

Gly Thr Val Asp Pro Lys Thr Gly Lys Val Leu Ile Trp Ser Ser Trp
                485                 490                 495
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```
Ala Arg Asp Thr Met Asp Gly Gly Pro Gly Gly Leu Thr Leu Thr Ser
            500                 505                 510

Met Trp Asp Pro Ala Thr Gly Leu Val Ala Glu Arg Asp Val Thr Glu
        515                 520                 525

Thr Asn His Asp Met Phe Cys Pro Gly Ile Ser Leu Asp Gly Asn Gly
    530                 535                 540

Gln Leu Val Val Thr Gly Gly Asn Asn Ala Glu Arg Thr Ser Leu Phe
545                 550                 555                 560

Asp Pro Val Lys Gln Ala Trp Ile Pro Gly Pro Asp Met Lys Val Ala
                565                 570                 575

Arg Gly Tyr His Ala Ser Ala Thr Thr Ser Thr Gly Lys Val Phe Thr
            580                 585                 590

Ile Gly Gly Ser Trp Ser Gly Gly Glu Tyr Phe Lys Asn Gly Glu Val
        595                 600                 605

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

Gln Lys Met Leu Thr Ala Asp Thr Gln Gly Leu Phe Arg Ser Asp Asn
625                 630                 635                 640

His Ala Trp Leu Phe Gly Trp Lys Lys Gly Thr Val Phe Gln Ala Gly
                645                 650                 655

Pro Ser Gln Ala Met Asn Trp Tyr Tyr Thr Asp Gly Lys Asp Gly Asn
            660                 665                 670

Val Lys Thr Ala Gly Lys Arg Gln Ser Asp Arg Gly Val Ala Pro Asp
        675                 680                 685

Ala Met Cys Gly Asn Ala Ile Met Phe Asp Ala Val Lys Gly Lys Ile
    690                 695                 700

Leu Thr Asn Gly Gly Thr Pro Asn Tyr Gln Asp Ser Asp Ala Thr Ala
705                 710                 715                 720

Asp Ala His Ile Ile Thr Ile Asn Asn Pro Gly Asn Lys Ala Asp Val
                725                 730                 735

Ser Tyr Ala Ser Glu Gly Leu Tyr His Ala Arg Val Phe His Ser Ser
            740                 745                 750

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

Ala Ile Pro Phe Ala Asp Ser Met Pro Val Leu Glu Pro Glu Met Tyr
    770                 775                 780

Leu Pro Asp Glu Asp Arg Phe Val Leu Met Lys Pro Asn Asn Ile Val
785                 790                 795                 800

Arg Thr Tyr His Ser Ile Ala Leu Leu Leu Pro Asp Gly Arg Val Phe
                805                 810                 815

Asn Gly Gly Gly Gly Leu Cys Gly Gly Cys Asp Thr Asn His Phe Asp
            820                 825                 830

Ala Gln Leu Tyr Thr Pro Pro Tyr Leu Tyr Asp Ser Lys Gly Arg Leu
        835                 840                 845

Ala Thr Arg Pro Lys Ile Ala Ser Val Ser Val Ser Thr Val Lys Val
    850                 855                 860

Gly Gly Thr Val Thr Val Gln Thr Ser Gly Ala Val Val Arg Ala Ser
865                 870                 875                 880

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

Arg Val Pro Leu Thr Leu Ser Asn Ala Gly Lys Asn Ser Tyr Ser Phe
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-continued

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            900                 905                 910

Gln Val Pro Ser Asp Pro Gly Val Ala Leu Pro Gly Tyr Trp Met Leu
        915                 920                 925

Phe Val Met Asp Lys Asn Gly Val Pro Ser Val Ala Ser Thr Ile Lys
    930                 935                 940

Val Thr Gly
945


<210> SEQ ID NO 59
<211> LENGTH: 684
<212> TYPE: PRT
<213> ORGANISM: Pochonia chlamydosporia 123

<400> SEQUENCE: 59

Met Glu Leu Phe Gly Ala Ile Ala Phe Val Leu Cys Gln Leu Ser Cys
1               5                   10                  15

His Val His Ala Val Thr Leu Lys Gln Thr Ser Thr Thr Ala Leu Val
            20                  25                  30

His Ala Thr Glu Gln Ala Ala Leu His Leu Leu Ala Ala Ala Pro Val
        35                  40                  45

Gly Tyr Arg Ile Asp Arg Ala Asn Trp Lys Val Thr Cys Asp Ser Gln
    50                  55                  60

Glu Ile Gly Tyr Glu Cys Gly Lys Ala Ile Asp Gly Asp Asn Ser Thr
65                  70                  75                  80

Val Trp His Thr Ala Phe Arg Ala Asp Asn Pro Lys Pro Pro His Asn
                85                  90                  95

Ile Thr Val Asp Met Gly Ser Ile Gln Asn Val Asn Gly Leu Ser Ile
            100                 105                 110

Leu Pro Arg Gln Asp Ser Asp Ser Asn Gly Trp Val Ala Arg His Gln
        115                 120                 125

Val Leu Val Ser Ala Asp Gly Gln Arg Trp Glu His Pro Val Ala Thr
    130                 135                 140

Gly Thr Trp Tyr Ala Asp Ser Thr Glu Lys Phe Ser Asn Phe Glu Pro
145                 150                 155                 160

Glu Gln Ala Arg Phe Val Arg Leu Val Ala Asp Ser Glu Val Ser Gly
                165                 170                 175

Asn Pro Trp Thr Ser Val Ala Glu Leu Asn Val Tyr Lys Ala Gly Thr
            180                 185                 190

Asp Pro Ala Pro Ala Lys Ser Ala Ser Ser Gly Lys Trp Gly Pro Thr
        195                 200                 205

Leu Asp Phe Pro Ile Val Pro Val Ala Ala Ala Val Val Pro Gln Ser
    210                 215                 220

Gly Lys Val Leu Val Trp Ser Ala Tyr Glu Asn Asp Lys Phe Glu Gly
225                 230                 235                 240

Ser Pro Gly Gly Tyr Thr Leu Thr Ser Thr Trp Asp Pro Ala Thr Gly
                245                 250                 255

Asp Val Thr Gln Arg Asn Val Thr Asn Ile Gly His Asp Met Phe Cys
            260                 265                 270

Pro Gly Ile Ser Met Asp Ser Asn Gly Gln Ile Val Val Thr Gly Gly
        275                 280                 285

Asn Asn Ala Gln Lys Thr Ser Phe Tyr Asp Ala Ala Ser Asp Ser Trp
    290                 295                 300
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Val Pro Gly Pro Asp Met Thr Val Ser Arg Gly Tyr Gln Ser Ser Ala
305                 310                 315                 320

Thr Cys Ser Asp Gly Arg Ile Phe Thr Ile Gly Gly Ser Trp Ser Gly
                325                 330                 335

Gly Gln Phe Glu Lys Asn Gly Glu Ile Tyr Asp Pro Ser Thr Lys Thr
            340                 345                 350

Trp Lys Met Leu Ser Leu Ala Ala Val Lys Pro Met Leu Thr Ala Asp
        355                 360                 365

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

Arg Asn Gly Thr Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp
385                 390                 395                 400

Tyr Phe Thr Gly Gly Asp Gly Gly Val Lys Ser Ala Gly Ser Arg Lys
                405                 410                 415

Ser Ser Arg Gly Pro Asp Pro Asp Ser Met Cys Gly Asn Ala Val Met
            420                 425                 430

Phe Asp Ala Thr Asn Gly Lys Ile Leu Thr Val Gly Gly Ser Pro Trp
        435                 440                 445

Tyr Gln Asp Asn Asp Ala Thr Ala Asn Ala His Ile Ile Thr Val Arg
    450                 455                 460

Gly Pro Gly Ser Glu Pro Ser Val Ser Phe Ala Gly Asn Gly Met His
465                 470                 475                 480

His Ala Arg Ile Phe Ala Ser Ser Val Val Leu Pro Asp Gly Ser Val
                485                 490                 495

Phe Ile Thr Gly Gly Gln Gln His Ser Ile Pro Phe Ala Asp Ser Thr
            500                 505                 510

Pro Gln Phe Thr Pro Glu Leu Tyr Asp Pro Glu Lys Asp Gln Phe Leu
        515                 520                 525

Glu Gln Ala Pro Asn Ser Ile Val Arg Val Tyr His Ser Leu Ala Leu
    530                 535                 540

Leu Leu Pro Asp Ala Thr Val Phe Asn Gly Gly Gly Gly Leu Cys Gly
545                 550                 555                 560

Gly Ser Cys Ala Thr Asn His Phe Asp Ala Gln Ile Tyr Ser Pro Arg
                565                 570                 575

Tyr Leu Phe Asp His Asp Gly Ser Pro Ala Val Arg Pro Val Ile Lys
            580                 585                 590

Ser Val Ser Arg Thr Ser Val Lys Pro Gly Asp Ser Leu Ser Phe Thr
        595                 600                 605

Thr Asp Ser Ala Val Gln His Ala Ser Leu Val Arg Tyr Gly Thr Ala
    610                 615                 620

Thr His Thr Val Asn Thr Asp Gln Arg Arg Val Pro Leu Thr Leu Asp
625                 630                 635                 640

Ala Ser Gly Ala Asn Thr Tyr Ala Val Gln Leu Pro Asn Asp Pro Gly
                645                 650                 655

Ile Met Leu Pro Gly Tyr Trp Met Leu Phe Val Met Asn Glu Arg Gly
            660                 665                 670

Thr Pro Ser Val Ala Ala Ser Ile Lys Ala His Leu
        675                 680


<210> SEQ ID NO 60
<211> LENGTH: 1073
<212> TYPE: PRT
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<213> ORGANISM: Fusarium oxysporum f. sp. cepae

<400> SEQUENCE: 60

```
Met Lys Val Val Tyr Ala Leu Thr Leu Cys Leu Gly Ile Ala Asp Ala
1               5                   10                  15

Val Val Leu Pro Val Phe Ser Ala Pro Lys Gly Gly Tyr Ala Leu Pro
            20                  25                  30

Arg Pro Asp Ser Asp Asp Thr Thr Asp Ser Ser Lys Thr Ala Ala Gly
        35                  40                  45

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

Pro Lys Thr Gly Phe Pro Ala Ser Ala Leu Ser Arg Arg Val Ala Arg
65                  70                  75                  80

Ile Glu Gln Thr Tyr Gly Ser Asp Asp Glu Ser Thr Asp Asp Ser Asp
                85                  90                  95

Asp Thr Pro Thr Asp Pro Ser Asp Ala Thr Pro Ser Ser Pro Pro Asp
            100                 105                 110

Asp Thr Pro Ser Gly Ser Ser Asp Asp Ile Asp Glu Val Val Tyr Ala
        115                 120                 125

Glu Pro Phe Met Gln Pro Thr Tyr Val Arg Phe Gly Pro Ala Pro Val
    130                 135                 140

Asp Lys Pro Glu Val Ala Pro Lys Ala Lys Ser Asn Ser Lys Asp Thr
145                 150                 155                 160

Ala Ser Val Ala Lys His Gly Val Asp Asp Asp Ser Ser Ser Gly Gly
                165                 170                 175

His Lys Gln Lys Gly Lys Asp Lys Asn Lys Gly Lys Asp Asp Ala Thr
            180                 185                 190

Lys Ser Arg Lys Lys Pro Glu Asp Ser Pro Lys Thr Ser Ser Asn Ser
        195                 200                 205

Ala Thr Asp Ser Val Ser Val Thr Ala Thr Ser Thr Ala Ala Pro Thr
    210                 215                 220

Ser Pro Pro Lys Gly Asp Asp Lys Gly Lys Ser Lys Gly Lys Gly Lys
225                 230                 235                 240

Gly Lys Gly Lys Asp Gly Gly Gly Arg His Asn Gly Asp Asp Asp Ala
                245                 250                 255

Thr Lys Ser Arg Thr Lys Val Glu Asp Ser Thr Lys Thr Arg Ser Ser
            260                 265                 270

Ala Pro Thr Lys Thr Tyr Ser Asp Asp Ser Gly Lys Gly Lys Gly Lys
        275                 280                 285

Gly Lys Gly Asp Gly Lys Gly Arg His Asp Gly Gly Val Asp Ala Thr
    290                 295                 300

Lys Ser Arg Ala Lys Ala Glu Asp Ser Glu Thr Asn Ser Lys Lys Ser
305                 310                 315                 320

Ser Lys Lys Gly Ser Lys Asp Asp Ser Lys Ser Lys Pro Ser Lys Lys
                325                 330                 335

Ser Phe Ile Thr His Gln Ser Gly Lys Thr Phe Asp Ala Asp Ser Thr
            340                 345                 350

Lys Gly Gly Gly Lys Asn Gly Pro Gly Tyr Asn Pro Ser Phe Asp Val
        355                 360                 365

Pro Lys Leu Asn Lys Gly Tyr Ile Gln Ala Ile Pro Pro Lys Ala Ser
    370                 375                 380
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Thr Ile Asn Asn Lys Phe Ser Ser Arg Val Lys Pro Arg Pro Gln Leu
385                 390                 395                 400

Asn Thr Glu Lys Val Arg Pro Leu Ser Ser Ser Ser Ser Ser Ser Ser
                405                 410                 415

Ser Ser Leu Leu Lys Arg Asp Glu Ser Lys Asn Ile Leu Ser Leu Arg
            420                 425                 430

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

Val Thr Cys Asp Ser Val His Glu Gly Asp Asp Cys Lys Asn Ala Ile
    450                 455                 460

Asp Gly Asn Gly Asp Thr Met Trp His Thr Gln Trp Glu Gly Ser Glu
465                 470                 475                 480

Pro Ala Pro Pro His Ser Ile Thr Val Asp Met Lys Lys Ser Tyr Asn
                485                 490                 495

Val Asn Gly Ile Ser Met Leu Pro Arg Gln Asp Gly Ser Gln Asn Gly
            500                 505                 510

Tyr Ile Ala Gln His Gln Ile Phe Leu Ser Lys Asp Gly Lys Thr Trp
        515                 520                 525

Gly Ser Pro Val Ala Tyr Gly Asn Trp Tyr Ser Asp Trp Thr Val Lys
    530                 535                 540

Tyr Ala Asn Phe Asp Thr Gln Pro Ala Arg Phe Val Lys Leu Val Ala
545                 550                 555                 560

Leu Thr Glu Ala Asn Gly Asn Pro Trp Thr Ser Ile Ala Glu Leu Asn
                565                 570                 575

Val Phe Gln Ala Asn Asp Tyr Val Pro Pro Gln Ala Ser Gln Gly Ala
            580                 585                 590

Trp Gly Pro Thr Ile Asn Phe Pro Ile Ile Pro Val Ala Gly Ala Val
        595                 600                 605

Asp Pro Asn Thr Gly Lys Val Leu Val Trp Ser Ser Trp Ala Arg Asp
    610                 615                 620

Thr Met Ser Gly Gly Pro Gly Gly Leu Thr Leu Thr Ser Thr Trp Asp
625                 630                 635                 640

Pro Ala Thr Gly Gln Val Ala Glu Arg Gln Val Thr Glu Thr Asn His
                645                 650                 655

Asp Met Phe Cys Pro Gly Ile Ser Leu Asp Gly Asn Gly Gln Leu Val
            660                 665                 670

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

Gln Gln Ala Trp Val Ser Gly Pro Asn Met Gln Val Ala Arg Gly Tyr
    690                 695                 700

Gln Ser Ser Ala Thr Thr Ser Thr Gly Lys Val Phe Thr Ile Gly Gly
705                 710                 715                 720

Ser Trp Ser Gly Gly Glu Ser Phe Lys Asn Gly Glu Val Tyr Asp Pro
                725                 730                 735

Lys Lys Lys Thr Trp Thr Leu Leu Asn Lys Ala Asp Val Gln Lys Met
            740                 745                 750

Leu Thr Asn Asp Ala Gln Gly Leu Phe Arg Ser Asp Asn His Ala Trp
        755                 760                 765

Leu Phe Gly Trp Lys Ser Gly Thr Val Phe Gln Ala Gly Pro Ser Lys
    770                 775                 780

Asn Met Asn Trp Tyr Tyr Thr Glu Lys Lys Asn Gly Asp Val Lys Thr
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785                 790                 795                 800

Ala Gly Gln Arg Ala Ser Asp Arg Gly Ile Ala Pro Asp Ala Met Cys
                805                 810                 815

Gly Asn Ala Ile Met Phe Asp Ala Val Lys Gly Lys Ile Leu Thr His
            820                 825                 830

Gly Gly Thr Pro Asn Tyr Gln Asp Ser Asp Ala Thr Thr Asp Ala His
        835                 840                 845

Ile Ile Thr Val Gly Asn Pro Gly Ala Asn Val Ser Val Ala Tyr Ala
    850                 855                 860

Ser Glu Gly Leu Phe Phe Pro Arg Val Phe His Ser Ser Val Val Leu
865                 870                 875                 880

Pro Asn Gly Asn Val Phe Ile Thr Gly Gly Gln Gln Tyr Ala Val Pro
                885                 890                 895

Phe Glu Asp Ser Thr Pro Gln Leu Gln Pro Glu Met Tyr Tyr Pro Asp
            900                 905                 910

Arg Asp Val Phe Glu Leu Met Lys Pro Asn Asn Ile Val Arg Thr Tyr
        915                 920                 925

His Ser Ile Ala Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly
    930                 935                 940

Gly Gly Leu Cys Gly Gly Cys Asp Thr Asn His Phe Asp Ala Gln Leu
945                 950                 955                 960

Tyr Thr Pro Pro Tyr Leu Tyr Asp Ser Lys Gly Lys Leu Ala Thr Arg
                965                 970                 975

Pro Lys Ile Thr Ser Val Ser Val Ser Thr Ile Lys Val Gly Gly Thr
            980                 985                 990

Val Thr Val Gln Thr Gly Gly Ala  Ile Val Gln Ala Ser  Leu Val Arg
        995                 1000                1005

Tyr Gly  Thr Ala Thr His Thr  Val Asn Ser Asp Gln  Arg Arg Ile
    1010                1015                1020

Pro Leu  Thr Leu Ala Asn Ala  Gly Lys Asn Ser Tyr  Ser Phe Gln
    1025                1030                1035

Val Pro  Ser Asp Pro Gly Val  Ala Leu Pro Gly Tyr  Trp Met Leu
    1040                1045                1050

Phe Val  Met Asp Lys Asn Gly  Val Pro Ser Val Ala  Ser Thr Ile
    1055                1060                1065

Lys Val  Thr Gly Ser
    1070


<210> SEQ ID NO 61
<211> LENGTH: 1074
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 61

Met Lys Val Val Tyr Ala Leu Thr Leu Cys Leu Gly Ile Ala Asp Ala
1               5                   10                  15

Val Val Leu Pro Val Phe Ser Ala Pro Lys Gly Gly Tyr Ala Leu Pro
            20                  25                  30

Arg Pro Asp Ser Asp Asp Thr Thr Asp Ser Ser Lys Thr Ala Ala Gly
        35                  40                  45

Ser Lys Thr Asn Leu Asp Ser Met Leu Pro Val Phe Gly Lys Ala Lys
    50                  55                  60
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Pro Lys Thr Gly Phe Pro Ala Ser Ala Leu Ser Arg Arg Val Ala Arg
65                  70                  75                  80

Ile Glu Gln Thr Tyr Gly Ser Asp Asp Glu Ser Thr Asp Asp Ser Asp
                85                  90                  95

Asp Thr Pro Thr Asp Pro Ser Asp Ala Thr Pro Ser Ser Pro Ser Asp
            100                 105                 110

Val Thr Pro Pro Ser Pro Pro Asp Asp Thr Pro Ser Gly Ser Ser Asp
        115                 120                 125

Asp Ile Asp Lys Val Val Tyr Ala Glu Pro Phe Met Gln Pro Thr Tyr
    130                 135                 140

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

Ala Lys Ser Asn Ser Lys Asp Thr Gly Ser Val Ala Lys His Gly Gly
                165                 170                 175

Asp Asp Asp Ser Ser Ser Gly Gly His Lys Gln Lys Gly Lys Asp Asp
            180                 185                 190

Lys Gly Arg His Asn Gly Asp Asp Asp Ala Thr Lys Ser Arg Lys Lys
        195                 200                 205

Pro Glu Asp Ser Pro Lys Thr Ser Ser Ser Ser Ala Thr Asp Ser Val
    210                 215                 220

Ser Val Thr Ala Thr Ser Thr Ala Ala Pro Thr Ser Pro Pro Thr Gly
225                 230                 235                 240

Asp Asp Lys Gly Lys Gly Lys Gly Lys Asp Gly Gly Gly Arg His Asn
                245                 250                 255

Gly Asp Asp Asp Ala Thr Lys Ser Arg Thr Lys Val Glu Asp Ser Thr
            260                 265                 270

Lys Thr Arg Ser Ser Ala Pro Thr Lys Thr Ser Ser Asp Asp Ser Gly
        275                 280                 285

Lys Gly Lys Gly Lys Gly Lys Gly Gly Gly Lys Gly Arg His Asp Gly
    290                 295                 300

Gly Asp Glu Ala Thr Lys Ser Arg Ala Lys Ala Glu Asp Ser Lys Thr
305                 310                 315                 320

Asn Ser Lys Lys Ser Ser Lys Lys Gly Ser Lys Asp Asp Ser Lys Ser
                325                 330                 335

Lys Pro Ser Lys Lys Ser Phe Ile Thr His Gln Ser Gly Lys Thr Phe
            340                 345                 350

Asp Ala Asp Ser Thr Lys Gly Gly Gly Lys Asn Gly Pro Gly Tyr Asn
        355                 360                 365

Pro Ser Phe Asp Val Pro Lys Leu Asn Lys Gly Tyr Ile Gln Ala Ile
    370                 375                 380

Pro Pro Lys Ala Ser Thr Ile Asn Asn Lys Phe Ser Ser Arg Val Lys
385                 390                 395                 400

Pro Arg Pro Gln Leu Asn Thr Glu Lys Val Arg Pro Leu Ser Ser Ser
                405                 410                 415

Ser Ser Ser Leu Leu Lys Arg Asp Glu Ser Lys Asn Ile Leu Ser Leu
            420                 425                 430

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

Ser Val Thr Cys Asp Ser Val His Glu Gly Asp Asp Cys Lys Asn Ala
    450                 455                 460

Ile Asp Gly Asn Gly Asp Thr Met Trp His Thr Gln Trp Glu Gly Ser
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465                 470                 475                 480

Glu Pro Ala Pro Pro His Ser Ile Thr Val Asp Met Lys Lys Ser Tyr
                485                 490                 495

Asn Val Asn Gly Ile Ser Met Leu Pro Arg Gln Asp Gly Ser Gln Asn
            500                 505                 510

Gly Tyr Ile Ala Gln His Gln Ile Phe Leu Ser Lys Asp Gly Lys Thr
        515                 520                 525

Trp Gly Ser Pro Val Ala Tyr Gly Asn Trp Tyr Ser Asp Trp Thr Val
    530                 535                 540

Lys Tyr Ala Asn Phe Asp Thr Gln Pro Ala Arg Phe Val Lys Leu Val
545                 550                 555                 560

Ala Leu Thr Glu Ala Asn Gly Asn Pro Trp Thr Ser Ile Ala Glu Leu
                565                 570                 575

Asn Val Phe Gln Ala Asn Asp Tyr Val Pro Pro Gln Ala Ser Gln Gly
            580                 585                 590

Ala Trp Gly Pro Thr Ile Asn Phe Pro Ile Ile Pro Val Ala Gly Thr
        595                 600                 605

Val Asp Pro Asn Thr Gly Lys Val Leu Val Trp Ser Ser Trp Ala Arg
    610                 615                 620

Asp Thr Met Ser Gly Gly Pro Gly Gly Leu Thr Leu Thr Ser Thr Trp
625                 630                 635                 640

Asp Pro Ala Thr Gly Gln Val Ala Glu Arg Gln Val Thr Glu Thr Asn
                645                 650                 655

His Asp Met Phe Cys Pro Gly Ile Ser Leu Asp Gly Asn Gly Gln Leu
            660                 665                 670

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

Val Gln Gln Ala Trp Val Ser Gly Pro Asn Met Gln Val Ala Arg Gly
    690                 695                 700

Tyr Gln Ser Ser Ala Thr Thr Ser Thr Gly Lys Val Phe Thr Ile Gly
705                 710                 715                 720

Gly Ser Trp Ser Gly Gly Glu Ser Phe Lys Asn Gly Glu Val Tyr Asp
                725                 730                 735

Pro Lys Lys Lys Thr Trp Thr Leu Leu Asn Lys Ala Asp Val Gln Lys
            740                 745                 750

Met Leu Thr Asn Asp Ala Gln Gly Leu Phe Arg Ser Asp Asn His Ala
        755                 760                 765

Trp Leu Phe Gly Trp Lys Ser Gly Thr Val Phe Gln Ala Gly Pro Ser
    770                 775                 780

Lys Asn Met Asn Trp Tyr Tyr Thr Glu Lys Lys Asn Gly Asp Val Lys
785                 790                 795                 800

Thr Ala Gly Gln Arg Ala Ser Asp Arg Gly Val Ala Pro Asp Ala Met
                805                 810                 815

Cys Gly Asn Ala Ile Met Phe Asp Ala Val Lys Gly Lys Ile Leu Thr
            820                 825                 830

His Gly Gly Thr Pro Asn Tyr Gln Asp Ser Asp Ala Thr Thr Asp Ala
        835                 840                 845

His Ile Ile Thr Val Gly Asn Pro Gly Ala Asn Val Ser Val Ala Tyr
    850                 855                 860

Ala Ser Glu Gly Leu Phe Phe Pro Arg Val Phe His Ser Ser Val Val
865                 870                 875                 880
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Leu Pro Asn Gly Asn Val Phe Ile Thr Gly Gly Gln Gln Tyr Ala Val
               885                 890                 895

Pro Phe Glu Asp Ser Thr Pro Gln Leu Gln Pro Glu Met Tyr Tyr Pro
           900                 905                 910

Asp Arg Asp Gly Phe Glu Leu Met Lys Pro Asn Asn Ile Val Arg Thr
       915                 920                 925

Tyr His Ser Ile Ala Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly
   930                 935                 940

Gly Gly Gly Leu Cys Gly Gly Cys Asp Thr Asn His Phe Asp Ala Gln
945                 950                 955                 960

Leu Tyr Thr Pro Pro Tyr Leu Tyr Tyr Ser Lys Gly Lys Leu Ala Thr
               965                 970                 975

Arg Pro Lys Ile Thr Ser Val Ser Val Ser Thr Ile Lys Val Gly Gly
           980                 985                 990

Thr Val Thr Val Gln Thr Gly Gly  Ala Ile Val Gln Ala  Ser Leu Val
       995                 1000                1005

Arg Tyr  Gly Thr Ala Thr His  Thr Val Asn Ser Asp  Gln Arg Arg
   1010                1015                1020

Ile Pro  Leu Thr Leu Ala Asn  Ala Gly Lys Asn Ser  Tyr Ser Phe
   1025                1030                1035

Gln Val  Pro Ser Asp Pro Gly  Val Ala Leu Pro Gly  Tyr Trp Met
   1040                1045                1050

Leu Phe  Val Met Asp Lys Asn  Gly Val Pro Ser Val  Ala Ser Thr
   1055                1060                1065

Ile Lys  Val Thr Gly Ser
   1070


<210> SEQ ID NO 62
<211> LENGTH: 1070
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum

<400> SEQUENCE: 62

Met Lys Val Val Tyr Ala Leu Thr Leu Cys Leu Gly Ile Ala Asp Ala
1               5                   10                  15

Val Val Leu Pro Val Phe Ser Ala Pro Lys Gly Gly Tyr Ala Leu Pro
           20                  25                  30

Arg Pro Asp Ser Asp Asp Thr Thr Asp Ser Ser Lys Thr Ala Ala Gly
       35                  40                  45

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

Pro Lys Thr Gly Phe Pro Ala Ser Ala Leu Ser Arg Arg Val Ala Arg
65                  70                  75                  80

Ile Glu Gln Thr Tyr Gly Ser Asp Asp Glu Ser Thr Asp Asp Ser Asp
               85                  90                  95

Asp Thr Pro Thr Asp Pro Ser Asp Ala Thr Pro Ser Ser Pro Pro Asp
           100                 105                 110

Asp Thr Pro Ser Gly Ser Ser Asp Asp Ile Asp Glu Val Val Tyr Ala
       115                 120                 125

Glu Pro Phe Met Gln Pro Thr Tyr Val Arg Phe Gly Pro Ala Pro Val
   130                 135                 140

Asp Lys Pro Glu Val Ala Pro Lys Ala Lys Ser Asn Ser Lys Asp Thr
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145                 150                 155                 160

Ala Ser Val Ala Lys His Gly Val Asp Asp Asp Ser Ser Ser Gly Gly
                165                 170                 175

His Lys Gln Lys Gly Lys Asp Lys Asn Lys Gly Lys Asp Asp Ala Thr
            180                 185                 190

Lys Ser Arg Lys Lys Pro Glu Asp Ser Pro Lys Thr Ser Ser Asn Ser
        195                 200                 205

Ala Thr Asp Ser Val Ser Val Thr Ala Thr Ser Thr Ala Ala Pro Thr
    210                 215                 220

Ser Pro Pro Lys Gly Asp Asp Lys Gly Lys Ser Lys Gly Lys Gly Lys
225                 230                 235                 240

Gly Lys Gly Lys Asp Gly Gly Gly Arg His Asn Gly Asp Asp Asp Ala
                245                 250                 255

Thr Lys Ser Arg Thr Lys Val Glu Asp Ser Thr Lys Thr Arg Ser Ser
            260                 265                 270

Ala Pro Thr Lys Thr Tyr Ser Asp Asp Ser Gly Lys Gly Lys Gly Lys
        275                 280                 285

Gly Lys Gly Asp Gly Lys Gly Arg His Asp Gly Gly Val Asp Ala Thr
    290                 295                 300

Lys Ser Arg Ala Lys Ala Glu Asp Ser Glu Thr Asn Ser Lys Lys Ser
305                 310                 315                 320

Ser Lys Lys Gly Ser Lys Asp Asp Ser Lys Ser Lys Pro Ser Lys Lys
                325                 330                 335

Ser Phe Ile Thr His Gln Ser Gly Lys Thr Phe Asp Ala Asp Ser Thr
            340                 345                 350

Lys Gly Gly Gly Lys Asn Gly Pro Gly Tyr Asn Pro Ser Phe Asp Val
        355                 360                 365

Pro Lys Leu Asn Lys Gly Tyr Ile Gln Ala Ile Pro Pro Lys Ala Ser
    370                 375                 380

Thr Ile Asn Asn Lys Phe Ser Ser Arg Val Lys Pro Arg Pro Gln Leu
385                 390                 395                 400

Asn Thr Glu Lys Val Arg Pro Leu Ser Ser Ser Ser Ser Ser Ser Leu
                405                 410                 415

Leu Lys Arg Asp Glu Ser Lys Asn Ile Leu Ser Leu Arg Ala Ala Ala
            420                 425                 430

Pro Phe Asn Ser Ala Ala Ile Asp Arg Lys Lys Trp Ser Val Thr Cys
        435                 440                 445

Asp Ser Val His Glu Gly Asp Asp Cys Lys Asn Ala Ile Asp Gly Asn
    450                 455                 460

Gly Asp Thr Met Trp His Thr Gln Trp Glu Gly Ser Glu Pro Ala Pro
465                 470                 475                 480

Pro His Ser Ile Thr Val Asp Met Lys Lys Ser Tyr Asn Val Asn Gly
                485                 490                 495

Ile Ser Met Leu Pro Arg Gln Asp Gly Ser Gln Asn Gly Tyr Ile Ala
            500                 505                 510

Gln His Gln Ile Phe Leu Ser Lys Asp Gly Lys Thr Trp Gly Ser Pro
        515                 520                 525

Val Ala Tyr Gly Asn Trp Tyr Ser Asp Trp Thr Val Lys Tyr Ala Asn
    530                 535                 540

Phe Asp Thr Gln Pro Ala Arg Phe Phe Lys Leu Val Ala Leu Thr Glu
545                 550                 555                 560
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```
Ala Asn Gly Asn Pro Trp Thr Ser Ile Ala Glu Leu Asn Val Phe Gln
               565                 570                 575

Ala Asn Asp Tyr Val Pro Pro Gln Ala Ser Gln Gly Ala Trp Gly Pro
            580                 585                 590

Thr Ile Asn Phe Pro Ile Ile Pro Val Ala Gly Thr Val Asp Pro Asn
        595                 600                 605

Thr Gly Lys Val Leu Val Trp Ser Ser Trp Ala Arg Asp Thr Met Ser
    610                 615                 620

Gly Gly Pro Gly Gly Leu Thr Leu Thr Ser Thr Trp Asp Pro Ala Thr
625                 630                 635                 640

Gly Gln Val Ala Glu Arg Gln Val Thr Glu Thr Asn His Asp Met Phe
               645                 650                 655

Cys Pro Gly Ile Ser Leu Asp Gly Asn Gly Gln Leu Val Val Thr Gly
            660                 665                 670

Gly Asn Asn Ala Glu Arg Thr Ser Leu Phe Asp Pro Val Lys Gln Ala
        675                 680                 685

Trp Val Ser Gly Pro Asn Met Lys Val Ala Arg Gly Tyr Gln Ser Ser
    690                 695                 700

Ala Thr Thr Ser Thr Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Ser
705                 710                 715                 720

Gly Gly Glu Ser Phe Lys Asn Gly Glu Val Tyr Asp Pro Lys Lys Lys
               725                 730                 735

Thr Trp Thr Leu Leu Asn Lys Ala Asp Val Gln Lys Met Leu Thr Asn
            740                 745                 750

Asp Ala Gln Gly Leu Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly
        755                 760                 765

Trp Lys Ser Gly Thr Val Phe Gln Ala Gly Pro Ser Lys Asn Met Asn
    770                 775                 780

Trp Tyr Tyr Thr Glu Lys Lys Asn Gly Asp Val Lys Thr Ala Gly Gln
785                 790                 795                 800

Arg Ala Ser Asp Arg Gly Ile Ala Pro Asp Ala Met Cys Gly Asn Ala
               805                 810                 815

Ile Met Phe Asp Ala Val Lys Gly Lys Ile Leu Thr His Gly Gly Thr
            820                 825                 830

Pro Asn Tyr Gln Asp Ser Asp Ala Thr Thr Asp Ala His Ile Ile Thr
        835                 840                 845

Val Gly Asn Pro Gly Ala Asn Val Ser Val Ala Tyr Ala Ser Glu Gly
    850                 855                 860

Leu Phe Phe Pro Arg Val Phe His Ser Ser Val Val Leu Pro Asn Gly
865                 870                 875                 880

Asn Val Phe Ile Thr Gly Gly Gln Gln Tyr Ala Val Pro Phe Glu Asp
               885                 890                 895

Ser Thr Pro Gln Leu Gln Pro Glu Met Tyr Tyr Pro Asp Arg Asp Val
            900                 905                 910

Phe Glu Leu Met Lys Pro Asn Asn Ile Val Arg Thr Tyr His Ser Ile
        915                 920                 925

Ala Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu
    930                 935                 940

Cys Gly Gly Cys Asp Thr Asn His Phe Asp Ala Gln Leu Tyr Thr Pro
945                 950                 955                 960
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```
Pro Tyr Leu Tyr Asp Ser Lys Gly Lys Leu Ala Thr Arg Pro Lys Ile
               965                 970                 975

Thr Ser Val Ser Val Ser Thr Ile Lys Val Gly Gly Thr Val Thr Val
           980                 985                 990

Gln Thr Gly Gly Ala Ile Val Gln  Ala Ser Leu Val Arg  Tyr Gly Thr
       995                 1000                1005

Ala Thr  His Thr Val Asn Ser  Asp Gln Arg Arg Ile  Pro Leu Thr
   1010                1015                1020

Leu Ala  Asn Ala Gly Lys Asn  Ser Tyr Ser Phe Gln  Val Pro Ser
   1025                1030                1035

Asp Pro  Gly Val Ala Leu Pro  Gly Tyr Trp Met Leu  Phe Val Met
   1040                1045                1050

Asp Lys  Asn Gly Val Pro Ser  Val Ala Ser Thr Ile  Lys Val Thr
   1055                1060                1065

Gly Ser
   1070


<210> SEQ ID NO 63
<211> LENGTH: 1071
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. narcissi

<400> SEQUENCE: 63

Met Lys Val Val Tyr Ala Leu Thr Leu Cys Leu Gly Ile Ala Asp Ala
1               5                   10                  15

Val Val Leu Pro Val Phe Ser Ala Pro Lys Gly Gly Tyr Ala Leu Pro
           20                  25                  30

Arg Pro Asp Ser Asp Asp Thr Thr Asp Ser Ser Lys Thr Ala Ala Gly
       35                  40                  45

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

Pro Lys Thr Gly Phe Pro Ala Ser Ala Leu Ser Arg Arg Val Ala Arg
65                  70                  75                  80

Ile Glu Gln Thr Tyr Gly Ser Asp Asp Glu Ser Thr Asp Asp Ser Asp
               85                  90                  95

Asp Thr Pro Thr Asp Pro Ser Asp Ala Thr Pro Ser Ser Pro Pro Asp
           100                 105                 110

Asp Thr Pro Ser Gly Ser Ser Asp Asp Ile Asp Glu Val Val Tyr Ala
       115                 120                 125

Glu Pro Phe Met Gln Pro Thr Tyr Val Arg Phe Gly Pro Ala Pro Val
   130                 135                 140

Asp Lys Pro Glu Val Ala Pro Lys Ala Lys Ser Asn Ser Lys Asp Thr
145                 150                 155                 160

Ala Ser Val Ala Lys His Gly Val Asp Asp Asp Ser Ser Ser Gly Gly
               165                 170                 175

His Lys Gln Lys Gly Lys Asp Lys Asn Lys Gly Lys Asp Asp Ala Thr
           180                 185                 190

Lys Ser Arg Lys Lys Pro Glu Asp Ser Pro Lys Thr Ser Ser Asn Ser
       195                 200                 205

Ala Thr Asp Ser Val Ser Val Thr Ala Thr Ser Thr Ala Ala Pro Thr
   210                 215                 220

Ser Pro Pro Lys Gly Asp Asp Lys Gly Lys Ser Lys Gly Lys Gly Lys
225                 230                 235                 240
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```
Gly Lys Gly Lys Asp Gly Gly Gly Arg His Asn Gly Asp Asp Asp Ala
                245                 250                 255

Thr Lys Ser Arg Thr Lys Val Glu Asp Ser Thr Lys Thr Arg Ser Ser
            260                 265                 270

Ala Pro Thr Lys Thr Tyr Ser Asp Asp Ser Gly Lys Gly Lys Gly Lys
        275                 280                 285

Gly Lys Gly Asp Gly Lys Gly Arg His Asp Gly Gly Val Asp Ala Thr
    290                 295                 300

Lys Ser Arg Ala Lys Ala Glu Asp Ser Glu Thr Asn Ser Lys Lys Ser
305                 310                 315                 320

Ser Lys Lys Gly Ser Lys Asp Asp Ser Lys Ser Lys Pro Ser Lys Lys
                325                 330                 335

Ser Phe Ile Thr His Gln Ser Gly Lys Thr Phe Asp Ala Asp Ser Thr
            340                 345                 350

Lys Gly Gly Gly Lys Asn Gly Pro Gly Tyr Asn Pro Ser Phe Asp Val
        355                 360                 365

Pro Lys Leu Asn Lys Gly Tyr Ile Gln Ala Ile Pro Pro Lys Ala Ser
    370                 375                 380

Thr Ile Asn Asn Lys Phe Ser Ser Arg Val Lys Pro Arg Pro Gln Leu
385                 390                 395                 400

Asn Thr Glu Lys Val Arg Pro Val Ser Ser Ser Ser Ser Ser Ser Ser
                405                 410                 415

Leu Leu Lys Arg Asp Glu Ser Lys Asn Ile Leu Ser Leu Arg Ala Ala
            420                 425                 430

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

Cys Asp Ser Val His Glu Gly Asp Asp Cys Lys Asn Ala Ile Asp Gly
    450                 455                 460

Asn Gly Asp Thr Met Trp His Thr Gln Trp Glu Gly Ser Glu Pro Ala
465                 470                 475                 480

Pro Pro His Ser Ile Thr Val Asp Met Lys Lys Ser Tyr Asn Val Asn
                485                 490                 495

Gly Ile Ser Met Leu Pro Arg Gln Asp Gly Ser Gln Asn Gly Tyr Ile
            500                 505                 510

Ala Gln His Gln Ile Phe Leu Ser Lys Asp Gly Lys Thr Trp Gly Ser
        515                 520                 525

Pro Val Ala Tyr Gly Asn Trp Tyr Ser Asp Trp Thr Val Lys Tyr Ala
    530                 535                 540

Asn Phe Asp Thr Gln Pro Ala Arg Phe Val Lys Leu Val Ala Leu Thr
545                 550                 555                 560

Glu Ala Asn Gly Asn Pro Trp Thr Ser Ile Ala Glu Leu Asn Val Phe
                565                 570                 575

Gln Ala Asn Asp Tyr Val Pro Pro Gln Ala Thr Gln Gly Ala Trp Gly
            580                 585                 590

Pro Thr Ile Asn Phe Pro Ile Ile Pro Val Ala Gly Thr Val Asp Pro
        595                 600                 605

Asn Thr Gly Lys Val Leu Val Trp Ser Ser Trp Ala Arg Asp Thr Met
    610                 615                 620

Ser Gly Gly Pro Gly Gly Leu Thr Leu Ile Ser Thr Trp Asp Pro Ala
625                 630                 635                 640
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Thr Gly Gln Val Ala Glu Arg Gln Val Thr Glu Thr Asn His Asp Met
                645                 650                 655

Phe Cys Pro Gly Ile Ser Leu Asp Gly Asn Gly Gln Leu Val Val Thr
            660                 665                 670

Gly Gly Asn Asn Ala Glu Arg Thr Ser Leu Phe Asp Pro Val Lys Gln
        675                 680                 685

Ala Trp Val Ser Gly Pro Asn Met Lys Val Ala Arg Gly Tyr Gln Ser
    690                 695                 700

Ser Ala Thr Thr Ser Thr Gly Lys Val Phe Thr Ile Gly Gly Ser Trp
705                 710                 715                 720

Ser Gly Gly Glu Ser Phe Lys Asn Gly Glu Val Tyr Asp Pro Lys Lys
                725                 730                 735

Lys Thr Trp Thr Leu Leu Asn Lys Ala Asp Val Gln Lys Met Leu Thr
            740                 745                 750

Asn Asp Ala Gln Gly Leu Phe Arg Ser Asp Asn His Ala Trp Leu Phe
        755                 760                 765

Gly Trp Lys Ser Gly Thr Val Phe Gln Ala Gly Pro Ser Lys Asn Met
    770                 775                 780

Asn Trp Tyr Tyr Thr Glu Lys Lys Asn Gly Asp Val Lys Thr Ala Gly
785                 790                 795                 800

Gln Arg Ala Ser Asp Arg Gly Val Ala Pro Asp Ala Met Cys Gly Asn
                805                 810                 815

Ala Ile Met Phe Asp Ala Val Lys Gly Lys Ile Leu Thr His Gly Gly
            820                 825                 830

Thr Pro Asn Tyr Gln Asp Ser Asp Ala Thr Thr Asp Ala His Ile Ile
        835                 840                 845

Thr Val Gly Asn Pro Gly Ala Asn Val Ser Val Ala Tyr Ala Ser Glu
    850                 855                 860

Gly Leu Phe Phe Pro Arg Val Phe His Ser Ser Val Val Leu Pro Asn
865                 870                 875                 880

Gly Asn Val Phe Ile Thr Gly Gly Gln Gln Tyr Ala Val Pro Phe Glu
                885                 890                 895

Asp Ser Thr Pro Gln Leu Gln Pro Glu Met Tyr Tyr Pro Asp Arg Asp
            900                 905                 910

Val Phe Glu Leu Met Lys Pro Asn Asn Ile Val Arg Thr Tyr His Ser
        915                 920                 925

Ile Ala Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly
    930                 935                 940

Leu Cys Gly Gly Cys Asp Thr Asn His Phe Asp Ala Gln Leu Tyr Thr
945                 950                 955                 960

Pro Pro Tyr Leu Tyr Asp Ser Lys Gly Lys Leu Ala Thr Arg Pro Lys
                965                 970                 975

Ile Thr Ser Val Ser Val Ser Thr Ile Lys Val Gly Gly Thr Val Thr
            980                 985                 990

Val Gln Thr Gly Gly Ala Ile Val  Gln Ala Ser Leu Val  Arg Tyr Gly
        995                 1000                1005

Thr Ala  Thr His Thr Val Asn  Ser Asp Gln Arg Arg  Ile Pro Leu
    1010                1015                1020

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

Ser Asp  Pro Gly Val Ala Leu  Pro Gly Tyr Trp Met  Leu Phe Val
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    1040                1045                1050

Met Asp  Lys Asn Gly Val Pro  Ser Val Ala Ser Thr  Ile Lys Val
    1055                1060                1065

Thr Gly  Ser
    1070


<210> SEQ ID NO 64
<211> LENGTH: 1083
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. cubense

<400> SEQUENCE: 64

Met Lys Ala Gly Tyr Ala Leu Thr Leu Cys Leu Gly Ile Ala Asp Ala
1               5                   10                  15

Val Val Leu Pro Val Phe Ser Ala Pro Lys Gly Gly Tyr Ala Leu Pro
            20                  25                  30

Arg Pro Asp Ser Asp Asp Thr Thr Asp Ser Ser Lys Thr Ala Ala Gly
        35                  40                  45

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

Pro Lys Thr Gly Phe Pro Ala Ser Ala Leu Ser Arg Arg Val Ala Arg
65                  70                  75                  80

Ile Glu Gln Thr Tyr Gly Ser Asp Asp Glu Ser Thr Asp Asp Ser Asp
                85                  90                  95

Asp Thr Pro Thr Asp Pro Ser Asp Ala Thr Pro Ser Ser Pro Ser Asp
            100                 105                 110

Val Thr Pro Pro Ser Pro Pro Asp Asp Thr Pro Ser Gly Ser Ser Asp
        115                 120                 125

Asp Ile Asp Glu Val Val Tyr Ala Glu Pro Phe Met Gln Pro Thr Tyr
    130                 135                 140

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

Ala Lys Ser Asn Ser Lys Asp Thr Ala Ser Val Ala Lys His Gly Gly
                165                 170                 175

Asp Asp Asp Ser Ser Ser Gly Gly His Lys Gln Lys Gly Lys Asp Asp
            180                 185                 190

Lys Gly Arg His Asn Gly Asp Asp Asp Ala Thr Lys Ser Arg Lys Lys
        195                 200                 205

Pro Glu Asp Ser Pro Lys Thr Ser Ser Ser Ser Ala Thr Asp Ser Val
    210                 215                 220

Ser Val Thr Ala Thr Ser Thr Ala Ala Pro Thr Ser Pro Pro Thr Gly
225                 230                 235                 240

Asp Asp Lys Gly Lys Gly Lys Gly Lys Gly Lys Gly Lys Gly Lys Asp
                245                 250                 255

Gly Gly Gly Arg His Asn Gly Asp Asp Asp Ala Thr Lys Ser Gln Thr
            260                 265                 270

Lys Val Asp Tyr Ser Thr Lys Thr Arg Ser Ser Ala Pro Thr Lys Thr
        275                 280                 285

Ser Ser Asp Asp Ser Gly Lys Gly Lys Gly Lys Gly Lys Gly Gly Gly
    290                 295                 300

Lys Gly Arg His Asp Gly Gly Asp Asp Ala Ala Lys Ser Arg Ala Lys
305                 310                 315                 320
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Ala Glu Asp Ser Lys Thr Asn Ser Lys Lys Ser Ser Lys Lys Gly Ser
                325                 330                 335

Lys Asp Asp Ser Lys Ser Lys Pro Ser Lys Lys Ser Phe Ile Thr His
            340                 345                 350

Gln Ser Gly Lys Thr Phe Asp Ala Asp Ser Thr Lys Gly Gly Gly Lys
        355                 360                 365

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

Gly Tyr Ile Gln Ala Ile Pro Pro Lys Ala Ser Thr Ile Asn Asn Lys
385                 390                 395                 400

Phe Ser Ser Arg Val Lys Pro Arg Pro Gln Leu Asn Thr Glu Lys Val
                405                 410                 415

Arg Pro Leu Ser Ser Ser Ser Ser Ser Ser Ser Ser Leu Leu Lys Arg
            420                 425                 430

Asp Glu Ser Lys Asn Ile Leu Ser Leu Arg Ala Ala Ala Pro Phe Asn
        435                 440                 445

Ser Ala Ala Ile Asp Arg Asn Lys Trp Ser Val Thr Cys Asp Ser Val
    450                 455                 460

His Glu Gly Asp Asp Cys Lys Asn Ala Ile Asp Gly Asn Gly Asp Thr
465                 470                 475                 480

Met Trp His Thr Gln Trp Glu Gly Ser Glu Pro Ala Pro Pro His Ser
                485                 490                 495

Ile Thr Val Asp Met Lys Lys Ser Tyr Asn Val Asn Gly Ile Ser Met
            500                 505                 510

Leu Pro Arg Gln Asp Gly Ser Gln Asn Gly Tyr Met Ala Gln His Gln
        515                 520                 525

Val Phe Leu Ser Lys Asp Gly Lys Thr Trp Gly Ser Pro Val Ala Tyr
    530                 535                 540

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

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

Asn Pro Trp Thr Ser Ile Ala Glu Leu Asn Val Phe Gln Ala Asn Asp
            580                 585                 590

Tyr Val Pro Pro Gln Ala Ser Gln Gly Ala Trp Gly Pro Thr Ile Asn
        595                 600                 605

Phe Pro Ile Ile Pro Val Ala Gly Thr Val Asp Pro Asn Thr Gly Lys
    610                 615                 620

Val Leu Val Trp Ser Ser Trp Ala Arg Asp Thr Met Ser Gly Gly Pro
625                 630                 635                 640

Gly Gly Leu Thr Leu Thr Ser Thr Trp Asp Pro Ala Thr Gly Gln Val
                645                 650                 655

Ala Glu Arg Gln Val Thr Glu Thr Asn His Asp Met Phe Cys Pro Gly
            660                 665                 670

Ile Ser Leu Asp Gly Asn Gly Gln Leu Val Val Thr Gly Gly Asn Asn
        675                 680                 685

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

Gly Pro Asn Met Gln Val Ala Arg Gly Tyr Gln Ser Ser Ala Thr Thr
705                 710                 715                 720

Ser Thr Gly Lys Val Phe Thr Ile Gly Gly Ser Trp Ser Gly Gly Glu
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               725                 730                 735

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

Leu Leu Asn Lys Ala Asp Val Gln Lys Met Leu Thr Asn Asp Ala Gln
        755                 760                 765

Gly Leu Phe Arg Ser Asp Asn His Ala Trp Leu Phe Gly Trp Lys Ser
    770                 775                 780

Gly Thr Val Phe Gln Ala Gly Pro Ser Lys Asn Met Asn Trp Tyr Tyr
785                 790                 795                 800

Thr Glu Lys Lys Asn Gly Asp Val Lys Thr Ala Gly Gln Arg Ala Ser
                805                 810                 815

Asp Arg Gly Val Ala Pro Asp Ala Met Cys Gly Asn Ala Ile Met Phe
            820                 825                 830

Asp Ala Val Lys Gly Arg Ile Leu Thr His Gly Gly Thr Pro Asn Tyr
        835                 840                 845

Gln Asp Ser Asp Ala Thr Thr Asp Ala His Ile Ile Thr Val Gly Asn
    850                 855                 860

Pro Gly Ala Asn Val Ser Val Ala Tyr Ala Ser Glu Gly Leu Phe Phe
865                 870                 875                 880

Pro Arg Val Phe His Ser Ser Val Val Leu Pro Asn Gly Asn Val Phe
                885                 890                 895

Ile Thr Gly Gly Gln Gln Tyr Ala Val Pro Phe Glu Asp Ser Thr Pro
            900                 905                 910

Gln Leu Gln Pro Glu Met Tyr Tyr Pro Asp Lys Asp Gly Phe Glu Leu
        915                 920                 925

Met Lys Pro Asn Asn Ile Val Arg Thr Tyr His Ser Ile Ala Leu Leu
    930                 935                 940

Leu Pro Asp Gly Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Gly
945                 950                 955                 960

Cys Asp Thr Asn His Phe Asp Ala Gln Leu Tyr Thr Pro Ser Tyr Leu
                965                 970                 975

Tyr Asp Ser Lys Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Ser Val
            980                 985                 990

Ser Val Ser Thr Ile Lys Val Gly  Gly Thr Val Thr Val  Gln Thr Gly
        995                 1000                1005

Gly Ala  Ile Val Gln Ala Ser  Leu Val Arg Tyr Gly  Thr Ala Thr
    1010                1015                1020

His Thr  Val Asn Ser Asp Gln  Arg Arg Ile Pro Leu  Thr Leu Ala
    1025                1030                1035

Asn Ala  Gly Lys Asn Ser Tyr  Ser Phe Gln Val Pro  Ser Asp Pro
    1040                1045                1050

Gly Val  Ala Leu Pro Gly Tyr  Trp Met Leu Phe Val  Ile Asp Lys
    1055                1060                1065

Asn Gly  Val Pro Ser Val Ala  Ser Thr Ile Lys Val  Thr Ser Ser
    1070                1075                1080


<210> SEQ ID NO 65
<211> LENGTH: 951
<212> TYPE: PRT
<213> ORGANISM: Fusarium oxysporum f. sp. cubense race 4

<400> SEQUENCE: 65
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Met Gln Pro Thr Tyr Val Arg Phe Gly Pro Ala Pro Val Asp Lys Pro
1               5                  10                  15

Glu Val Ala Pro Lys Ala Lys Ser Asn Ser Lys Asp Thr Ala Ser Val
            20                  25                  30

Ala Lys His Gly Gly Asp Asp Asp Ser Asn Ser Gly Gly His Lys Gln
        35                  40                  45

Lys Gly Lys Asp Lys Asn Lys Gly Lys Asp Asp Lys Gly Arg His Asn
    50                  55                  60

Gly Asp Asp Asp Ala Thr Lys Ser Arg Lys Lys Pro Glu Asp Ser Pro
65                  70                  75                  80

Lys Thr Ser Ser Ser Ser Ala Thr Asp Thr Val Ser Val Thr Ala Thr
                85                  90                  95

Ser Thr Ala Ala Pro Thr Ser Pro Pro Thr Gly Asp Asp Lys Gly Lys
            100                 105                 110

Gly Lys Gly Lys Gly Lys Gly Lys Gly Lys Asp Gly Gly Gly Arg His
        115                 120                 125

Asn Gly Asp Asp Asp Ala Thr Lys Ser Arg Thr Lys Leu Glu Asp Ser
    130                 135                 140

Thr Lys Thr Arg Ser Ser Ala Pro Thr Lys Thr Ser Ser Asp Asp Ser
145                 150                 155                 160

Gly Lys Gly Lys Gly Lys Gly Lys Gly Gly Gly Lys Gly Arg His Asp
                165                 170                 175

Gly Gly Asp Asp Ala Ala Lys Ser Gln Ala Lys Ala Glu Asp Ser Lys
            180                 185                 190

Thr Asn Ser Lys Lys Ser Ser Lys Lys Gly Ser Lys Asp Asp Ser Lys
        195                 200                 205

Ser Lys Pro Ser Lys Lys Ser Phe Ile Thr His Gln Ser Gly Lys Thr
    210                 215                 220

Phe Asp Ala Asp Ser Thr Lys Gly Gly Gly Lys Asn Gly Pro Gly Tyr
225                 230                 235                 240

Asn Pro Ser Phe Asp Val Pro Lys Leu Asn Lys Gly Tyr Ile Gln Ala
                245                 250                 255

Ile Pro Pro Lys Ala Ser Thr Ile Asn Asn Lys Phe Ser Ser Arg Val
            260                 265                 270

Lys Pro Arg Pro Gln Leu Asn Thr Glu Lys Val Arg Pro Leu Ser Ser
        275                 280                 285

Ser Ser Ser Ser Ser Phe Leu Lys Arg Asp Glu Ser Lys Asn Ile Leu
    290                 295                 300

Ser Leu Arg Ala Ala Ala Pro Phe Asn Ser Ala Ala Ile Asp Arg Lys
305                 310                 315                 320

Lys Trp Ser Val Thr Cys Asp Ser Val His Glu Gly Asp Asp Cys Lys
                325                 330                 335

Asn Ala Ile Asp Gly Asn Gly Asp Thr Met Trp His Thr Gln Trp Glu
            340                 345                 350

Gly Ser Glu Pro Ala Pro Pro His Ser Ile Thr Val Asp Met Lys Lys
        355                 360                 365

Ser Tyr Asn Val Asn Gly Ile Ser Met Leu Pro Arg Gln Asp Gly Ser
    370                 375                 380

Gln Asn Gly Tyr Ile Ala Gln His Gln Val Phe Leu Ser Lys Asp Gly
385                 390                 395                 400

Lys Thr Trp Gly Ser Pro Val Ala Tyr Gly Asn Trp Tyr Asn Asp Trp
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               405                 410                 415

Thr Val Lys Tyr Ala Asn Phe Asp Thr Gln Pro Ala Arg Phe Val Arg
            420                 425                 430

Leu Val Ala Leu Thr Glu Ala Asn Gly Asn Pro Trp Thr Ser Ile Ala
        435                 440                 445

Glu Leu Asn Val Phe Gln Ala Asn Asp Tyr Val Pro Pro Gln Ala Ser
    450                 455                 460

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

Gly Thr Val Asp Pro Asn Thr Gly Lys Val Leu Val Trp Ser Ser Trp
                485                 490                 495

Ala Arg Asp Thr Met Ser Gly Gly Pro Gly Gly Leu Thr Leu Thr Ser
            500                 505                 510

Thr Trp Asp Pro Ala Thr Gly Gln Val Ala Glu Arg Gln Val Thr Glu
        515                 520                 525

Thr Asn His Asp Met Phe Cys Pro Gly Ile Ser Ile Asp Gly Asn Gly
    530                 535                 540

Gln Leu Val Val Thr Gly Gly Asn Asn Ala Glu Arg Thr Ser Leu Phe
545                 550                 555                 560

Asp Pro Val Lys Gln Ala Trp Val Ser Gly Pro Asn Met Gln Val Ala
                565                 570                 575

Arg Gly Tyr Gln Ser Ser Ala Thr Thr Ser Thr Gly Lys Val Phe Thr
            580                 585                 590

Ile Gly Gly Ser Trp Ser Gly Gly Glu Ser Phe Lys Asn Gly Glu Val
        595                 600                 605

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

Gln Lys Met Leu Thr Asn Asp Ala Gln Gly Leu Phe Arg Ser Asp Asn
625                 630                 635                 640

His Ala Trp Leu Phe Gly Trp Lys Ser Gly Thr Ser Gly Thr Val Phe
                645                 650                 655

Gln Ala Gly Pro Ser Lys Asn Met Asn Trp Tyr Tyr Thr Glu Lys Lys
            660                 665                 670

Asn Gly Asp Ala Lys Thr Ala Gly Gln Arg Ala Ser Asp Arg Gly Val
        675                 680                 685

Ala Pro Asp Ala Met Cys Gly Asn Ala Ile Met Phe Asp Ala Val Lys
    690                 695                 700

Gly Lys Ile Leu Thr His Gly Gly Thr Pro Asn Tyr Gln Asp Ser Asp
705                 710                 715                 720

Ala Thr Thr Asp Ala His Ile Ile Thr Val Gly Asn Pro Gly Thr Asn
                725                 730                 735

Ala Ser Val Ala Tyr Ala Ser Glu Gly Leu Phe Phe Pro Arg Val Phe
            740                 745                 750

His Ser Ser Val Val Leu Pro Asn Gly Asn Val Phe Ile Thr Gly Gly
        755                 760                 765

Gln Lys Tyr Ala Val Pro Phe Glu Asp Ser Thr Pro Gln Leu Gln Pro
    770                 775                 780

Glu Met Tyr Tyr Pro Asp Lys Asp Gly Phe Glu Leu Met Lys Pro Asn
785                 790                 795                 800

Asn Ile Val Arg Thr Tyr His Ser Ile Ala Leu Leu Leu Pro Asp Gly
                805                 810                 815
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Arg Val Phe Asn Gly Gly Gly Gly Leu Cys Gly Gly Cys Asp Thr Asn
            820                 825                 830

His Phe Asp Ala Gln Leu Tyr Thr Pro Pro Tyr Leu Tyr Asp Ser Lys
        835                 840                 845

Gly Lys Leu Ala Thr Arg Pro Lys Ile Thr Ser Val Ser Val Ser Thr
    850                 855                 860

Ile Lys Val Gly Gly Thr Val Thr Val Gln Thr Gly Gly Ala Ile Val
865                 870                 875                 880

Gln Ala Ser Leu Val Arg Tyr Gly Thr Ala Thr His Thr Val Asn Ser
                885                 890                 895

Asp Gln Arg Arg Ile Pro Leu Thr Leu Ala Asn Ala Gly Lys Asn Ser
            900                 905                 910

Tyr Ser Phe Gln Val Pro Ser Asp Pro Gly Val Ala Leu Pro Gly Tyr
        915                 920                 925

Trp Met Leu Phe Val Met Asp Lys Asn Gly Val Pro Ser Val Ala Ser
    930                 935                 940

Thr Ile Lys Val Thr Gly Ser
945                 950


<210> SEQ ID NO 66
<211> LENGTH: 676
<212> TYPE: PRT
<213> ORGANISM: Metarhizium guizhouense ARSEF 977

<400> SEQUENCE: 66

Met Lys Leu Thr Thr Glu Thr Val Leu Leu Gly Ala Leu Leu Ala Gly
1               5                   10                  15

Gln Ala Ala Ala Gly Leu Val Pro Arg Ser Phe Thr Val Lys Gln His
            20                  25                  30

Tyr His Glu Asn Ser Thr Phe Ser Lys Leu Phe Ala Ala Pro Pro Ile
        35                  40                  45

Ala Asn Gly Glu Ile Asp Arg Ala Gly Trp Lys Val Thr Cys Asp Ser
    50                  55                  60

Phe Glu Pro Gly Asn Glu Cys Ser Lys Ala Ile Asp Gly Asn Asn Asp
65                  70                  75                  80

Thr Phe Trp His Thr Lys Phe Glu Gly Ser Asn Val Pro His Gln Ile
                85                  90                  95

Val Val Asp Phe Gly Ser Thr His Asn Ile Asn Gly Ile Ser Ala Leu
            100                 105                 110

Pro Arg Gln Asp Gly Asn Asp His Gly Tyr Met Ala Gln His Asp Val
        115                 120                 125

Ala Val Ser Thr Asp Gly Ser Asn Trp Glu Thr Val Ala Ala Gly Thr
    130                 135                 140

Trp Tyr Gly Gly Asp Lys Thr Leu Lys Tyr Ala Asn Phe Glu Thr Arg
145                 150                 155                 160

Thr Val Arg Tyr Val Arg Val Arg Ala Thr Ser Glu Ala Asn Gly Gly
                165                 170                 175

Pro Trp Thr Ser Leu Ala Glu Leu Lys Ala Tyr Ala Ala Lys Thr Gly
            180                 185                 190

Pro Ala Pro Tyr Ala Gly Leu Gly Lys Trp Gly Ala Thr Ile Asp Phe
        195                 200                 205

Pro Thr Val Pro Val Ala Ala Ala Val Asp Pro Val Ser Gly Lys Val
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    210                 215                 220

Leu Val Trp Ser Ser Tyr Thr Tyr Asp Asn Tyr Leu Gly Ser Thr Gln
225                 230                 235                 240

Asp Arg Val Phe Thr Ser Leu Trp Asp Pro Ala Thr Gly Ala Val Thr
                245                 250                 255

Pro Lys Leu Val Asp Asp Thr Asp His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Ile Asp Gly Ala Gly Gln Met Val Val Thr Gly Gly Asn Ser Ala
        275                 280                 285

Ser Lys Thr Thr Leu Tyr Asp Phe Ala Ser Gly Ala Trp Leu Pro Gly
    290                 295                 300

Pro Asp Met Thr Val Ala Arg Gly Tyr Gln Ala Ser Ala Thr Leu Ser
305                 310                 315                 320

Asp Gly Arg Val Phe Thr Ile Gly Gly Cys Trp Ser Gly Gly Trp Phe
                325                 330                 335

Asp Lys Asn Gly Glu Val Tyr Asp Pro Arg Ala Arg Thr Trp Thr Gly
            340                 345                 350

Leu Pro Gln Ala Leu Val Arg Pro Met Leu Thr Ala Asp Ala Gln Gly
        355                 360                 365

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

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn Trp Tyr Ala Thr
385                 390                 395                 400

Ala Gly Asn Gly Ser Val Ser Pro Ala Gly Gln Arg Arg Ser Asp Arg
                405                 410                 415

Gly Ala Asp Ala Asp Ala Met Asn Gly Asn Ala Val Met Phe Asp Ala
            420                 425                 430

Leu Ala Gly Arg Ile Leu Ala Phe Gly Gly Ala Pro Ser Tyr Gln Asp
        435                 440                 445

Ser Gln Ala Ser Ala Ala Ala His Leu Ile Thr Ile Gly Asp Pro Gly
    450                 455                 460

Lys Pro Ala Asp Val Arg Phe Ala Ser Asn Gly Leu Trp Ser Pro Arg
465                 470                 475                 480

Ala Phe His Thr Ser Ala Val Leu Pro Asp Gly Thr Val Phe Ile Thr
                485                 490                 495

Gly Gly Gln Ser Tyr Ala Val Pro Phe Ser Asp Glu Thr Pro Gln Leu
            500                 505                 510

Thr Pro Glu Leu Tyr Asp Pro Ala Ala Asp Ala Phe Tyr Lys Gln Gln
        515                 520                 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Val Ala Leu Leu Leu Pro
    530                 535                 540

Asp Ala Thr Val Leu Ser Ala Gly Gly Gly Leu Cys Gly Asp Cys Asn
545                 550                 555                 560

Thr Asn His Phe Asp Gly Gln Val Phe Thr Pro Gln Tyr Leu Leu Thr
                565                 570                 575

Lys Asp Gly Gln Pro Ala Val Arg Pro Val Ile Arg Ser Ala Thr Leu
            580                 585                 590

Ser Gly Arg Thr Val Ala Ile Glu Thr Asp Ser Ser Val Ala Ser Ala
        595                 600                 605

Ser Leu Ile Arg Phe Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln
    610                 615                 620
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Arg Arg Val Pro Leu Thr Leu Val Arg Val Gly Thr Asn Arg Tyr Thr
625                 630                 635                 640

Ala Glu Val Pro Ala Asp Thr Gly Val Val Leu Pro Gly Tyr Tyr Met
                645                 650                 655

Leu Phe Val Met Asn Glu Lys Gly Val Pro Ser Val Ser Lys Thr Leu
            660                 665                 670

Asn Phe Leu Val
        675


<210> SEQ ID NO 67
<211> LENGTH: 669
<212> TYPE: PRT
<213> ORGANISM: Metarhizium rileyi RCEF 4871

<400> SEQUENCE: 67

Met Lys Leu Thr Thr Glu Thr Cys Leu Leu Ala Ala Leu Phe Ala Gly
1               5                   10                  15

Gln Val Ser Gly Leu Val Ser Lys Glu His Tyr Arg Glu Lys Ser Thr
            20                  25                  30

Phe Ser Lys Leu Phe Ala Ala Pro Pro Ile Gly Asn Glu Leu Asn Arg
        35                  40                  45

Ala Gly Trp Lys Val Thr Cys Asp Ser Ala Glu Pro Gly Ser Glu Cys
    50                  55                  60

Gly Lys Ala Ile Asp Gly Ser Asn Glu Thr Phe Trp His Thr Ser Tyr
65                  70                  75                  80

Asp Gly Ser Asn Leu Pro His Gln Ile Val Val Asp Phe Gly Ser Arg
                85                  90                  95

His Asn Ile Asn Gly Ile Ser Ala Leu Pro Arg Gln Asp Gly Ser Asp
            100                 105                 110

His Gly Phe Ile Ala Gln His Asp Val Ala Val Ser Thr Asp Gly Arg
        115                 120                 125

Asn Trp Glu Thr Val Ala Gly Gly Thr Trp His Gly Gly Asp Ser Met
    130                 135                 140

Leu Lys Tyr Ala Asn Phe Glu Thr Arg Ser Ala Arg Tyr Val Arg Val
145                 150                 155                 160

Arg Ala Thr Ser Glu Ala Asn Gly Asn Ala Trp Thr Ser Leu Ala Glu
                165                 170                 175

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

Gly Lys Trp Gly Pro Thr Ile Asn Phe Pro Thr Val Pro Val Ala Ala
        195                 200                 205

Thr Val Asp Pro Gly Ser Gly Arg Val Ile Val Trp Ser Ser Tyr Thr
    210                 215                 220

Tyr Asp Asn Tyr Leu Gly Ser Ser Gln Asp Arg Val Phe Thr Ser Val
225                 230                 235                 240

Trp Asp Pro Ala Thr Gly Val Val Thr Pro Lys Leu Val Asp Asn Thr
                245                 250                 255

Asp His Asp Met Phe Cys Pro Gly Ile Ser Ile Asp Gly Thr Gly Ser
            260                 265                 270

Met Val Val Thr Gly Gly Asn Ser Ala Ser Lys Thr Thr Leu Tyr Asp
        275                 280                 285

Phe Ala Ser Glu Ser Trp Ile Pro Gly Pro Asp Met Asn Phe Pro Arg
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    290                 295                 300

Gly Tyr Gln Ala Ser Ala Thr Leu Ser Asp Gly Arg Val Phe Thr Ile
305                 310                 315                 320

Gly Gly Cys Trp Ser Gly Gly Trp Phe Glu Lys Asn Gly Glu Val Tyr
                325                 330                 335

Asp Pro Lys Ala Arg Ala Trp Thr Asn Leu Thr Gly Ala Arg Val Arg
            340                 345                 350

Pro Met Leu Thr Ala Asp Ala Gln Gly Ile Tyr Arg Ala Asp Asn His
        355                 360                 365

Gly Trp Leu Phe Gly Trp Lys Gly Gly Ser Val Phe Gln Ala Gly Pro
    370                 375                 380

Ser Thr Ala Met Asn Trp Tyr Thr Thr Ser Gly Asp Gly Gly Val Ser
385                 390                 395                 400

Pro Ala Gly Gln Arg Glu Ser Glu Arg Gly Ala Asp Gly Asp Ser Met
                405                 410                 415

Asn Gly Asn Ala Val Met Tyr Asp Ala Thr Gln Gly Lys Ile Leu Ala
            420                 425                 430

Val Gly Gly Ala Pro Ser Tyr Gln Asp Ser Pro Ala Thr Gly His Ala
        435                 440                 445

His Leu Ile Thr Ile Gly Asp Pro Gly Ser Glu Ala Arg Val Arg Phe
    450                 455                 460

Ala Gly Asn Gly Met Ser Ala Ala Arg Ala Phe His Asn Ser Val Val
465                 470                 475                 480

Leu Pro Asp Gly Thr Val Phe Ile Thr Gly Gly Gln Ser Tyr Ala Val
                485                 490                 495

Pro Phe Ser Asp Asp Thr Pro Asp Leu Thr Pro Glu Leu Tyr Asp Pro
            500                 505                 510

Ala Thr Asp Ala Phe Thr Gln Gln Gln Pro Asn Ser Ile Val Arg Val
        515                 520                 525

Tyr His Ser Val Ala Leu Leu Leu Pro Asp Ala Arg Val Leu Ser Ala
    530                 535                 540

Gly Gly Gly Leu Cys Gly Asp Cys Thr Thr Asn His Phe Asp Ala Gln
545                 550                 555                 560

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

Arg Pro Ala Ile Arg Ser Ala Asp Val Arg Asp Gly Asn Ile Ala Ile
            580                 585                 590

Val Thr Asp Ser Ala Val Ala Ser Ala Ser Leu Val Arg Phe Gly Thr
        595                 600                 605

Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro Leu Arg Leu
    610                 615                 620

Val Arg Ser Gly Thr Asn Arg Tyr Thr Ala Asn Val Ser Leu Asp Pro
625                 630                 635                 640

Gly Ile Leu Leu Pro Gly Tyr Tyr Met Leu Phe Val Leu Asn Ala Asn
                645                 650                 655

Gly Val Pro Ser Val Ser Lys Thr Leu Lys Phe Leu Val
            660                 665


<210> SEQ ID NO 68
<211> LENGTH: 676
<212> TYPE: PRT
<213> ORGANISM: Metarhizium brunneum ARSEF 3297
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<400> SEQUENCE: 68

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Met Lys Leu Thr Thr Glu Thr Val Leu Leu Gly Ala Leu Phe Ala Gly
1               5                  10                  15

Gln Ala Ala Gly Gly Leu Val Pro Ser Pro Leu Thr Gly Lys Gln His
            20                  25                  30

Tyr His Glu Asn Ser Thr Phe Ser Lys Leu Phe Ala Ala Pro Pro Ile
        35                  40                  45

Ala Thr Gly Glu Leu Asp Arg Ala Gly Trp Lys Val Thr Cys Asp Ser
    50                  55                  60

Phe Glu Pro Gly Asn Glu Cys Ile Lys Ala Ile Asp Gly Asn Asn Asp
65                  70                  75                  80

Thr Phe Trp His Thr Lys Phe Glu Gly Ser Asn Val Pro His Gln Ile
                85                  90                  95

Val Val Asp Phe Gly Ser Met His Asn Ile Asn Gly Ile Ser Ala Leu
            100                 105                 110

Pro Arg Gln Asp Gly Asn Asn His Gly Tyr Ile Ala Gln His Asp Val
        115                 120                 125

Ala Val Ser Thr Asp Gly Ser Asn Trp Glu Thr Val Ala Ala Gly Thr
    130                 135                 140

Trp Tyr Gly Gly Asp Lys Leu Leu Lys Tyr Ala Asn Phe Glu Thr Arg
145                 150                 155                 160

Thr Ala Arg Tyr Val Arg Leu Arg Ala Thr Ser Glu Val Ser Gly Ala
                165                 170                 175

Pro Trp Thr Ser Val Ala Glu Leu Lys Ala Tyr Ala Ala Lys Ser Gly
            180                 185                 190

Pro Ala Ala Tyr Gly Gly Val Gly Lys Trp Gly Ala Thr Ile Asp Phe
        195                 200                 205

Pro Thr Val Pro Val Ala Ala Ala Val Asp Pro Val Ser Gly Lys Val
    210                 215                 220

Leu Val Trp Ser Ser Tyr Thr Tyr Asp Asn Tyr Leu Gly Ser Thr Gln
225                 230                 235                 240

Asp Arg Val Phe Thr Ser Leu Trp Asp Pro Ala Thr Gly Ala Val Thr
                245                 250                 255

Pro Lys Leu Val Asp Asp Thr Asp His Asp Met Phe Cys Pro Gly Ile
            260                 265                 270

Ser Ile Asp Gly Thr Gly Gln Met Val Val Thr Gly Gly Asn Ser Ala
        275                 280                 285

Ser Lys Thr Thr Leu Tyr Asp Phe Ala Ser Gly Ala Trp Leu Pro Gly
    290                 295                 300

Pro Asp Met Thr Val Ala Arg Gly Tyr Gln Ala Ser Ala Thr Leu Ser
305                 310                 315                 320

Asp Gly Arg Val Phe Thr Ile Gly Gly Cys Trp Ser Gly Gly Trp Phe
                325                 330                 335

Asp Lys Asn Gly Glu Val Tyr Asp Pro Arg Ala Arg Ala Trp Ser Gly
            340                 345                 350

Leu Pro Gly Ala Leu Val Arg Pro Met Leu Thr Ala Asp Ala Gln Gly
        355                 360                 365

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

Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met His Trp Tyr Tyr Thr
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385 390 395 400

Ala Gly Asn Gly Ser Val Ala Pro Ala Gly Asp Arg Arg Ser Asp Arg
405 410 415

Gly Thr Asp Pro Asp Ala Met Asn Gly Asn Ala Val Met Phe Asp Ala
420 425 430

Arg Ala Gly Arg Ile Leu Ser Phe Gly Gly Ser Pro Ser Tyr Gln Asn
435 440 445

Ser Gln Ala Ser Ala Ala Ala His Leu Ile Thr Ile Gly Asp Pro Gly
450 455 460

Lys Pro Ala Asp Val Arg Phe Ala Ser Asn Gly Leu Trp Ser Pro Arg
465 470 475 480

Ala Phe His Thr Ser Ala Val Leu Pro Asp Gly Thr Val Phe Ile Thr
485 490 495

Gly Gly Gln Ser Tyr Ala Val Pro Phe Ser Asp Glu Thr Pro Gln Leu
500 505 510

Thr Pro Glu Leu Tyr Asp Pro Val Ala Asp Ala Phe Tyr Lys Gln Gln
515 520 525

Pro Asn Ser Ile Val Arg Val Tyr His Ser Val Ala Leu Leu Leu Pro
530 535 540

Asp Ala Thr Val Leu Ser Ala Gly Gly Gly Leu Cys Gly Asp Cys Asn
545 550 555 560

Thr Asn His Phe Asp Gly Gln Val Phe Thr Pro Gln Tyr Leu Leu Thr
565 570 575

Lys Asp Gly Gln Pro Ala Val Arg Pro Val Ile Arg Ser Ala Thr Leu
580 585 590

Ser Gly Arg Thr Val Thr Ile Glu Thr Asp Ser Ser Val Ala Ser Ala
595 600 605

Ser Leu Ile Arg Phe Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln
610 615 620

Arg Arg Val Pro Leu Thr Leu Val Arg Ala Gly Asp Asn Arg Tyr Thr
625 630 635 640

Ala Glu Val Pro Ala Asp Thr Gly Val Val Leu Pro Gly Tyr Tyr Met
645 650 655

Leu Phe Val Met Asn Asp Lys Gly Val Pro Ser Val Ser Lys Thr Leu
660 665 670

Asn Phe Leu Val
675

<210> SEQ ID NO 69
<211> LENGTH: 677
<212> TYPE: PRT
<213> ORGANISM: Metarhizium anisopliae ARSEF 549

<400> SEQUENCE: 69

Met Lys Leu Thr Thr Glu Thr Val Leu Leu Gly Ala Leu Phe Ala Gly
1 5 10 15

Gln Ala Ala Gly Gly Leu Val Pro Pro Ser Pro Leu Thr Gly Lys Gln
20 25 30

His Tyr His Glu Asn Ser Thr Phe Ser Lys Leu Phe Ala Ala Pro Pro
35 40 45

Ile Ala Thr Gly Glu Leu Asp Arg Ala Gly Trp Lys Val Thr Cys Asp
50 55 60

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Ser Phe Glu Pro Gly Asn Glu Cys Ser Leu Ala Ile Asp Gly Asn Asn
65                  70                  75                  80

Asp Thr Phe Trp His Thr Lys Phe Glu Gly Ser Asn Val Pro His Gln
                85                  90                  95

Ile Val Val Asp Phe Gly Ala Thr His Asp Ile Asn Gly Ile Ser Ala
            100                 105                 110

Leu Pro Arg Gln Asp Gly Asn Asn His Gly Tyr Ile Ala Ala His Glu
        115                 120                 125

Val Ala Val Ser Thr Asp Gly Ser Asn Trp Glu Thr Val Ala Ala Gly
    130                 135                 140

Thr Trp Tyr Gly Gly Asp Lys Leu Leu Lys Tyr Ala Asn Phe Glu Thr
145                 150                 155                 160

Arg Thr Ala Arg Tyr Val Arg Leu Arg Ala Thr Ser Glu Val Ser Gly
                165                 170                 175

Ala Ala Trp Thr Ser Val Ala Glu Leu Lys Ala Tyr Ala Ala Lys Ser
            180                 185                 190

Gly Pro Ala Ala Tyr Gly Gly Ala Gly Lys Trp Gly Ala Thr Ile Asp
        195                 200                 205

Phe Pro Thr Val Pro Val Ala Ala Ala Val Asp Pro Val Ser Gly Lys
    210                 215                 220

Val Leu Val Trp Ser Ser Tyr Thr Tyr Asp Asn Tyr Leu Gly Ser Thr
225                 230                 235                 240

Gln Asp Arg Val Phe Thr Ser Leu Trp Asp Pro Ala Thr Gly Ser Val
                245                 250                 255

Thr Pro Lys Leu Val Asp Asp Thr Asp His Asp Met Phe Cys Pro Gly
            260                 265                 270

Ile Ser Ile Asp Gly Thr Gly Gln Met Val Val Thr Gly Gly Asn Ser
        275                 280                 285

Ala Ser Lys Thr Thr Leu Tyr Asp Phe Ala Ser Gly Ala Trp Leu Pro
    290                 295                 300

Gly Pro Asp Met Thr Val Ala Arg Gly Tyr Gln Ala Ser Ala Thr Leu
305                 310                 315                 320

Ser Asp Gly Arg Val Phe Thr Ile Gly Gly Cys Trp Ser Gly Gly Trp
                325                 330                 335

Phe Asp Lys Asn Gly Glu Val Tyr Asp Pro Arg Ala Arg Ala Trp Ser
            340                 345                 350

Gly Leu Pro Gly Ala Leu Val Arg Pro Met Leu Thr Ala Asp Ala Gln
        355                 360                 365

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

Gly Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met His Trp Tyr Tyr
385                 390                 395                 400

Thr Ala Gly Asn Gly Ser Val Ala Pro Ala Gly Asp Arg Arg Ser Asp
                405                 410                 415

Arg Gly Thr Asp Pro Asp Ala Met Asn Gly Asn Ala Val Met Phe Asp
            420                 425                 430

Ala Pro Ala Gly Arg Ile Leu Ser Phe Gly Gly Ser Pro Ser Tyr Gln
        435                 440                 445

Asn Ser Asp Ala Ser Ala Ala Ala His Leu Ile Thr Ile Gly Asp Pro
    450                 455                 460

Gly Lys Pro Ala Asp Val Arg Phe Ala Ser Asn Gly Leu Trp Ser Pro
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465                 470                 475                 480

Arg Ala Phe His Thr Ser Ala Val Leu Pro Asp Gly Thr Val Phe Ile
                485                 490                 495

Thr Gly Gly Gln Ser Tyr Ala Val Pro Phe Ser Asp Glu Thr Pro Gln
            500                 505                 510

Leu Thr Pro Glu Leu Tyr Asp Pro Val Ala Asp Thr Phe Tyr Lys Gln
        515                 520                 525

Gln Pro Asn Ser Ile Val Arg Val Tyr His Ser Val Ala Leu Leu Leu
    530                 535                 540

Pro Asp Ala Thr Val Leu Ser Ala Gly Gly Gly Leu Cys Gly Asp Cys
545                 550                 555                 560

Asn Thr Asn His Phe Asp Gly Gln Val Phe Thr Pro Gln Tyr Leu Leu
                565                 570                 575

Thr Lys Asp Gly Gln Pro Ala Val Arg Pro Val Ile Arg Ser Ala Thr
            580                 585                 590

Leu Ser Gly Arg Thr Val Ala Ile Glu Thr Asp Ser Ser Val Ala Ser
        595                 600                 605

Ala Ser Leu Ile Arg Phe Gly Thr Ala Thr His Thr Val Asn Thr Asp
    610                 615                 620

Gln Arg Arg Val Pro Leu Thr Leu Val Arg Ala Gly Asp Asn Arg Tyr
625                 630                 635                 640

Thr Ala Glu Val Pro Ala Asp Pro Gly Val Val Leu Pro Gly Tyr Tyr
                645                 650                 655

Met Leu Phe Val Met Asn Asp Lys Gly Val Pro Ser Val Ser Lys Thr
            660                 665                 670

Leu Asn Phe Leu Val
        675


<210> SEQ ID NO 70
<211> LENGTH: 680
<212> TYPE: PRT
<213> ORGANISM: Moelleriella libera RCEF 2490

<400> SEQUENCE: 70

Met Ser Arg Phe Leu Leu Leu Leu Ala Leu Val Ala Val Ala Ser Ser
1               5                   10                  15

Ala Ala Val Glu Gln Gln Gln Gln Gln Gln Gln Gln Pro Arg Ala Ile
            20                  25                  30

Lys Ile Leu Glu His Tyr Arg Glu Ser Ser Thr Phe Thr Lys Leu Phe
        35                  40                  45

Ala Ala Ala Pro Ile Gly Asn Glu Ile Pro Lys Asn Ala Tyr Thr Val
    50                  55                  60

Thr Cys Asp Ser Tyr Gln Pro Gly Asn Glu Cys Ala Leu Ala Ile Asp
65                  70                  75                  80

Gly Asn Asn Asn Thr Phe Trp His Thr Ala Phe Ser Gly Ala Asn Leu
                85                  90                  95

Pro His Gln Ile Val Val Asp Leu Gly Ala Thr Arg Asn Ile Asn Gly
            100                 105                 110

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

Gln His Glu Val Ala Val Ser Thr Asp Asn Arg Asn Trp Glu Val Val
    130                 135                 140
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Ala Ser Gly Thr Trp Tyr Gly Gly Asp Ser Thr Thr Lys Phe Ala Asn
145                 150                 155                 160

Phe Glu Thr Arg Ser Ile Arg Tyr Ile Arg Leu Lys Ala Leu Ser Glu
                165                 170                 175

Ala Tyr Gly Asn Gln Trp Thr Ser Val Ala Glu Val Lys Val Tyr Glu
            180                 185                 190

Ala Lys Thr Gly Pro Ala Ala Phe Ala Gly Thr Gly Lys Trp Gly Pro
        195                 200                 205

Thr Ile Asn Phe Pro Thr Ile Pro Val Ala Gly Ala Val Asp Pro Leu
    210                 215                 220

Thr Gly Gln Val Leu Ile Trp Ser Ser Tyr Thr Tyr Asp Asn Tyr Leu
225                 230                 235                 240

Gly Ser Ser Gln Asp Arg Val Phe Thr Ser Ile Trp Asp Pro Ser Thr
                245                 250                 255

Gly Val Val Thr Pro Lys Leu Val Asp Asn Thr Asn His Asp Met Phe
            260                 265                 270

Cys Pro Gly Ile Ser Ile Asp Gly Ala Gly Arg Met Val Ile Thr Gly
        275                 280                 285

Gly Asn Ser Ala Gln Lys Thr Thr Val Tyr Gln Phe Gly Ser Gln Thr
    290                 295                 300

Trp Ile Pro Gly Pro Asp Met Asn Thr Gln Arg Gly Tyr Gln Ala Ser
305                 310                 315                 320

Ala Thr Leu Ser Asp Gly Arg Val Phe Thr Ile Gly Gly Cys Trp Ser
                325                 330                 335

Gly Gly Trp Phe Glu Lys Asn Gly Glu Val Tyr Asp Pro Lys Ala Ser
            340                 345                 350

Thr Trp Thr Ser Leu Pro Gly Ala Leu Val His Pro Met Leu Thr Asn
        355                 360                 365

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

Trp Lys Asn Gly Ser Val Phe Gln Ala Gly Pro Ser Thr Ala Met Asn
385                 390                 395                 400

Trp Tyr Thr Thr Ser Gly Asn Gly Ser Val Ala Pro Ala Gly Asn Arg
                405                 410                 415

Thr Ser Ser Arg Gly Asp Ala Pro Asp Ala Met Thr Gly Asn Ala Val
            420                 425                 430

Met Tyr Asp Ala Val Asn Gly Lys Ile Leu Ser Phe Gly Gly Ser Pro
        435                 440                 445

Ser Tyr Gln Asp Ser Ser Ala Thr Thr Asn Ala His Ile Ile Thr Ile
    450                 455                 460

Gly Ser Pro Gly Ala Pro Ala Gln Ser Arg Phe Ala Ser Asn Gly Leu
465                 470                 475                 480

Trp Ser Pro Arg Ala Phe His Thr Ser Val Ile Leu Pro Asp Gly Lys
                485                 490                 495

Thr Phe Ile Thr Gly Gly Gln Thr Tyr Ala Val Pro Phe Ser Asp Asp
            500                 505                 510

Asn Pro Asp Leu Thr Pro Glu Met Tyr Asp Pro Val Ala Asp Ser Phe
        515                 520                 525

Val Gln Gln Gln Ala Asn Thr Ile Ile Arg Val Tyr His Ser Ile Ser
    530                 535                 540

Leu Leu Leu Pro Asp Gly Arg Val Phe Asn Ala Gly Gly Gly Leu Cys
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545                 550                 555                 560

Gly Asp Cys Thr Thr Asn His Phe Asp Gly Gln Ile Phe Thr Pro Gln
                565                 570                 575

Tyr Leu Leu Thr Arg Thr Gly Gln Leu Ala Ala Arg Pro Ala Ile Asn
            580                 585                 590

Ser Val Ser Leu Ser Gly Arg Arg Leu Thr Ile Asn Thr Asn Ser Ala
        595                 600                 605

Ile Thr Ser Ala Ala Leu Met Arg Tyr Gly Ser Ala Thr His Thr Val
    610                 615                 620

Asn Thr Asp Gln Arg Arg Ile Pro Leu Lys Leu Thr Thr Thr Gly Thr
625                 630                 635                 640

Asn Arg Tyr Thr Ala Asp Ala Pro Ser Asp Pro Gly Ile Leu Leu Pro
                645                 650                 655

Gly Tyr Tyr Met Leu Phe Val Leu Asn Ser Gln Gly Val Pro Ser Val
            660                 665                 670

Ala Lys Thr Val Asn Phe Leu Val
        675                 680


<210> SEQ ID NO 71
<211> LENGTH: 672
<212> TYPE: PRT
<213> ORGANISM: Pochonia chlamydosporia 170

<400> SEQUENCE: 71

Met Lys Leu Ala Ser Gln Thr Leu Leu Ala Ile Val Ser Leu Ser Gln
1               5                   10                  15

Ala Ala Ala Ile Asn Ser Glu Ile Thr Thr Lys Gln His Tyr Arg Glu
            20                  25                  30

Asn Ser Thr Phe Ala Lys Leu Ser Ala Ala Ala Pro Ile Gly Asn Glu
        35                  40                  45

Ile Asn His Ala Gly Trp Lys Val Thr Cys Asp Ser Tyr Gln Pro Gly
    50                  55                  60

Asn Glu Cys Ile Lys Ala Ile Asp Gly Glu Gly Lys Thr Phe Trp His
65                  70                  75                  80

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

Gly Thr Thr His Asn Val Asn Gly Leu Ser Ala Leu Pro Arg Gln Asp
            100                 105                 110

Gly Asn Asn His Gly Tyr Ile Ala Gln His Asp Val Ser Val Ser Ile
        115                 120                 125

Asp Asn Glu Asn Trp Glu Thr Val Ala Arg Gly Asn Trp Tyr Ala Gly
    130                 135                 140

Asp Ser Thr Gln Lys Phe Ala Asn Phe Glu Thr Lys Leu Ile Arg Tyr
145                 150                 155                 160

Ile Arg Leu Arg Ala Met Ser Glu Ala His Gly His Gln Trp Thr Ser
                165                 170                 175

Leu Ala Glu Leu Lys Val Tyr Glu Ala Lys Gly Gly Pro Ala Ala Tyr
            180                 185                 190

Ser Gly Asn Gly Lys Trp Gly Pro Thr Ile Asp Phe Pro Thr Val Pro
        195                 200                 205

Val Ala Gly Thr Val Asp Pro Phe Thr Gly Lys Val Ile Ile Trp Ser
    210                 215                 220
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Ser Tyr Lys Tyr Asp Asn Tyr Ala Gly Thr Ser Gln Asp Arg Val Phe
225                 230                 235                 240

Thr Ser Ile Trp Asp Pro Ala Thr Gly Ile Val Thr Ser Lys Leu Val
                245                 250                 255

Asp Asp Thr Asp His Asp Met Phe Cys Pro Gly Ile Ser Ile Asp Gly
            260                 265                 270

Thr Gly Lys Met Val Val Thr Gly Gly Asn Ser Ala Arg Lys Thr Thr
        275                 280                 285

Leu Tyr Asp Tyr Gln Lys Arg Thr Trp Ile Pro Gly Pro Asp Met Asn
    290                 295                 300

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

Phe Thr Val Gly Gly Cys Trp Ser Gly Gly Trp Leu Glu Lys Asn Gly
                325                 330                 335

Glu Val Tyr Asp Pro Lys Ala Lys Ala Trp Thr Asn Leu Ser Ser Ala
            340                 345                 350

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

Asp Asn His Gly Trp Leu Phe Gly Trp Lys Ser Gly Ser Val Phe Gln
    370                 375                 380

Ala Gly Pro Ser Thr Ser Met Asn Trp Tyr Phe Thr Ala Gly Asn Gly
385                 390                 395                 400

Arg Val Ala Ser Ala Gly Ile Arg Lys Thr Ile Lys Gly Val Asp Pro
                405                 410                 415

Asp Ser Met Ser Gly Asn Ala Val Met Tyr Asp Ala Thr Asn Gly Lys
            420                 425                 430

Ile Leu Thr Phe Gly Gly Ser Pro Ser Tyr Gln Asp Ser Asn Ala Thr
        435                 440                 445

Gly His Ala His Leu Ile Thr Ile Gly Asn Pro Gly Ser Gln Ala Gln
    450                 455                 460

Val Gln Val Ala Gly Asn Gly Met Trp Ser Pro Arg Ala Phe His Thr
465                 470                 475                 480

Ser Val Val Leu Pro Asp Gly Lys Thr Phe Ile Thr Gly Gly Gln Ser
                485                 490                 495

Tyr Ala Val Pro Phe Ser Asp Asp Thr Ala Gln Leu Thr Pro Glu Leu
            500                 505                 510

Tyr Asp Pro Asn Thr Asp Thr Phe Tyr Gln Gln Gln Ser Asn Thr Ile
        515                 520                 525

Ile Arg Val Tyr His Ser Met Ser Leu Leu Leu Ser Asp Gly Arg Val
    530                 535                 540

Phe Asn Ala Gly Gly Gly Leu Cys Gly Asp Cys Lys Thr Asn His Phe
545                 550                 555                 560

Asp Gly Gln Val Phe Thr Pro Gln Tyr Leu Leu Thr Asn Asn Gly Gln
                565                 570                 575

Pro Ala Thr Arg Pro Val Ile Thr Ser Val Ile Gln Ser Gly Arg Arg
            580                 585                 590

Ile Thr Ile Thr Thr Asp Ser Ala Val Ser Thr Ala Ser Leu Ile Arg
        595                 600                 605

Phe Gly Thr Ala Thr His Thr Val Asn Thr Asp Gln Arg Arg Ile Pro
    610                 615                 620

Leu Pro Leu Asn Thr Ser Gly Thr Asn Gln Tyr Val Ala Asp Ala Pro
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625 630 635 640

Val Asp Pro Gly Ile Leu Leu Pro Gly Tyr Tyr Met Leu Phe Val Met
645 650 655

Asn Ala Asn Gly Val Pro Ser Val Ser Lys Thr Leu Thr Phe Leu Val
660 665 670

<210> SEQ ID NO 72
<211> LENGTH: 563
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 72

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

Val Asn Val Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
20 25 30

Leu Leu Asp Lys Ile Tyr Glu Val Glu Gly Met Arg Trp Ala Gly Asn
35 40 45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
50 55 60

Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser
65 70 75 80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
85 90 95

His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu
100 105 110

Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
115 120 125

Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Thr
130 135 140

Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Val Thr Gln
145 150 155 160

Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val
165 170 175

Pro Ala Lys Leu Leu Gln Thr Pro Ile Asp Met Ser Leu Lys Pro Asn
180 185 190

Asp Ala Glu Ser Glu Lys Glu Val Ile Asp Thr Ile Leu Ala Leu Val
195 200 205

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

His Asp Val Lys Ala Glu Thr Lys Lys Leu Ile Asp Leu Thr Gln Phe
225 230 235 240

Pro Ala Phe Val Thr Pro Met Gly Lys Gly Ser Ile Asp Glu Gln His
245 250 255

Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Pro Glu Val
260 265 270

Lys Glu Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu
275 280 285

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
290 295 300

Asn Ile Val Glu Phe His Ser Asp His Met Lys Ile Arg Asn Ala Thr
305 310 315 320

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Phe Pro Gly Val Gln Met Lys Phe Val Leu Gln Lys Leu Leu Thr Thr
                325                 330                 335

Ile Ala Asp Ala Ala Lys Gly Tyr Lys Pro Val Ala Val Pro Ala Arg
            340                 345                 350

Thr Pro Ala Asn Ala Ala Val Pro Ala Ser Thr Pro Leu Lys Gln Glu
        355                 360                 365

Trp Met Trp Asn Gln Leu Gly Asn Phe Leu Gln Glu Gly Asp Val Val
    370                 375                 380

Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr Phe
385                 390                 395                 400

Pro Asn Asn Thr Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly
                405                 410                 415

Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu Ile
            420                 425                 430

Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln
        435                 440                 445

Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro
    450                 455                 460

Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile
465                 470                 475                 480

His Gly Pro Lys Ala Gln Tyr Asn Glu Ile Gln Gly Trp Asp His Leu
                485                 490                 495

Ser Leu Leu Pro Thr Phe Gly Ala Lys Asp Tyr Glu Thr His Arg Val
            500                 505                 510

Ala Thr Thr Gly Glu Trp Asp Lys Leu Thr Gln Asp Lys Ser Phe Asn
        515                 520                 525

Asp Asn Ser Lys Ile Arg Met Ile Glu Ile Met Leu Pro Val Phe Asp
    530                 535                 540

Ala Pro Gln Asn Leu Val Glu Gln Ala Lys Leu Thr Ala Ala Thr Asn
545                 550                 555                 560

Ala Lys Gln


<210> SEQ ID NO 73
<211> LENGTH: 563
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 73

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

Val Asn Cys Asn Thr Val Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
            20                  25                  30

Leu Leu Asp Lys Leu Tyr Glu Val Lys Gly Met Arg Trp Ala Gly Asn
        35                  40                  45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
    50                  55                  60

Lys Gly Met Ser Cys Ile Ile Thr Thr Phe Gly Val Gly Glu Leu Ser
65                  70                  75                  80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
                85                  90                  95

His Val Val Gly Val Pro Ser Ile Ser Ser Gln Ala Lys Gln Leu Leu
            100                 105                 110
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Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
        115                 120                 125

Ser Ala Asn Ile Ser Glu Thr Thr Ala Met Ile Thr Asp Ile Ala Asn
    130                 135                 140

Ala Pro Ala Glu Ile Asp Arg Cys Ile Arg Thr Thr Tyr Thr Thr Gln
145                 150                 155                 160

Arg Pro Val Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Asn Val
                165                 170                 175

Pro Ala Lys Leu Leu Glu Thr Pro Ile Asp Leu Ser Leu Lys Pro Asn
            180                 185                 190

Asp Ala Glu Ala Glu Ala Glu Val Val Arg Thr Val Val Glu Leu Ile
        195                 200                 205

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

His Asp Val Lys Ala Glu Thr Lys Lys Leu Met Asp Leu Thr Gln Phe
225                 230                 235                 240

Pro Val Tyr Val Thr Pro Met Gly Lys Gly Ala Ile Asp Glu Gln His
                245                 250                 255

Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Arg Pro Glu Val
            260                 265                 270

Lys Lys Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Ile Gly Ala Leu
        275                 280                 285

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
    290                 295                 300

Asn Ile Val Glu Phe His Ser Asp His Ile Lys Ile Arg Asn Ala Thr
305                 310                 315                 320

Phe Pro Gly Val Gln Met Lys Phe Ala Leu Gln Lys Leu Leu Asp Ala
                325                 330                 335

Ile Pro Glu Val Val Lys Asp Tyr Lys Pro Val Ala Val Pro Ala Arg
            340                 345                 350

Val Pro Ile Thr Lys Ser Thr Pro Ala Asn Thr Pro Met Lys Gln Glu
        355                 360                 365

Trp Met Trp Asn His Leu Gly Asn Phe Leu Arg Glu Gly Asp Ile Val
    370                 375                 380

Ile Ala Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Thr Phe
385                 390                 395                 400

Pro Thr Asp Val Tyr Ala Ile Val Gln Val Leu Trp Gly Ser Ile Gly
                405                 410                 415

Phe Thr Val Gly Ala Leu Leu Gly Ala Thr Met Ala Ala Glu Glu Leu
            420                 425                 430

Asp Pro Lys Lys Arg Val Ile Leu Phe Ile Gly Asp Gly Ser Leu Gln
        435                 440                 445

Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro
    450                 455                 460

Tyr Ile Phe Val Leu Asn Asn Asn Gly Tyr Thr Ile Glu Lys Leu Ile
465                 470                 475                 480

His Gly Pro His Ala Glu Tyr Asn Glu Ile Gln Gly Trp Asp His Leu
                485                 490                 495

Ala Leu Leu Pro Thr Phe Gly Ala Arg Asn Tyr Glu Thr His Arg Val
            500                 505                 510

Ala Thr Thr Gly Glu Trp Glu Lys Leu Thr Gln Asp Lys Asp Phe Gln
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        515                 520                 525

Asp Asn Ser Lys Ile Arg Met Ile Glu Val Met Leu Pro Val Phe Asp
    530                 535                 540

Ala Pro Gln Asn Leu Val Lys Gln Ala Gln Leu Thr Ala Ala Thr Asn
545                 550                 555                 560

Ala Lys Gln


<210> SEQ ID NO 74
<211> LENGTH: 563
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 74

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

Val Asn Val Asn Thr Ile Phe Gly Leu Pro Gly Asp Phe Asn Leu Ser
            20                  25                  30

Leu Leu Asp Lys Ile Tyr Glu Val Asp Gly Leu Arg Trp Ala Gly Asn
        35                  40                  45

Ala Asn Glu Leu Asn Ala Ala Tyr Ala Ala Asp Gly Tyr Ala Arg Ile
    50                  55                  60

Lys Gly Leu Ser Val Leu Val Thr Thr Phe Gly Val Gly Glu Leu Ser
65                  70                  75                  80

Ala Leu Asn Gly Ile Ala Gly Ser Tyr Ala Glu His Val Gly Val Leu
                85                  90                  95

His Val Val Gly Val Pro Ser Ile Ser Ala Gln Ala Lys Gln Leu Leu
            100                 105                 110

Leu His His Thr Leu Gly Asn Gly Asp Phe Thr Val Phe His Arg Met
        115                 120                 125

Ser Ala Asn Ile Ser Glu Thr Thr Ser Met Ile Thr Asp Ile Ala Thr
    130                 135                 140

Ala Pro Ser Glu Ile Asp Arg Leu Ile Arg Thr Thr Phe Ile Thr Gln
145                 150                 155                 160

Arg Pro Ser Tyr Leu Gly Leu Pro Ala Asn Leu Val Asp Leu Lys Val
                165                 170                 175

Pro Gly Ser Leu Leu Glu Lys Pro Ile Asp Leu Ser Leu Lys Pro Asn
            180                 185                 190

Asp Pro Glu Ala Glu Lys Glu Val Ile Asp Thr Val Leu Glu Leu Ile
        195                 200                 205

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

His Asn Val Lys Lys Glu Thr Gln Lys Leu Ile Asp Leu Thr Gln Phe
225                 230                 235                 240

Pro Ala Phe Val Thr Pro Leu Gly Lys Gly Ser Ile Asp Glu Gln His
                245                 250                 255

Pro Arg Tyr Gly Gly Val Tyr Val Gly Thr Leu Ser Lys Gln Asp Val
            260                 265                 270

Lys Gln Ala Val Glu Ser Ala Asp Leu Ile Leu Ser Val Gly Ala Leu
        275                 280                 285

Leu Ser Asp Phe Asn Thr Gly Ser Phe Ser Tyr Ser Tyr Lys Thr Lys
    290                 295                 300

Asn Val Val Glu Phe His Ser Asp Tyr Val Lys Val Lys Asn Ala Thr
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305                 310                 315                 320

Phe Leu Gly Val Gln Met Lys Phe Ala Leu Gln Asn Leu Leu Lys Val
                325                 330                 335

Ile Pro Asp Val Val Lys Gly Tyr Lys Ser Val Pro Val Pro Thr Lys
            340                 345                 350

Thr Pro Ala Asn Lys Gly Val Pro Ala Ser Thr Pro Leu Lys Gln Glu
        355                 360                 365

Trp Leu Trp Asn Glu Leu Ser Lys Phe Leu Gln Glu Gly Asp Val Ile
    370                 375                 380

Ile Ser Glu Thr Gly Thr Ser Ala Phe Gly Ile Asn Gln Thr Ile Phe
385                 390                 395                 400

Pro Lys Asp Ala Tyr Gly Ile Ser Gln Val Leu Trp Gly Ser Ile Gly
                405                 410                 415

Phe Thr Thr Gly Ala Thr Leu Gly Ala Ala Phe Ala Ala Glu Glu Ile
            420                 425                 430

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

Leu Thr Val Gln Glu Ile Ser Thr Met Ile Arg Trp Gly Leu Lys Pro
    450                 455                 460

Tyr Leu Phe Val Leu Asn Asn Asp Gly Tyr Thr Ile Glu Lys Leu Ile
465                 470                 475                 480

His Gly Pro His Ala Glu Tyr Asn Glu Ile Gln Thr Trp Asp His Leu
                485                 490                 495

Ala Leu Leu Pro Ala Phe Gly Ala Lys Lys Tyr Glu Asn His Lys Ile
            500                 505                 510

Ala Thr Thr Gly Glu Trp Asp Ala Leu Thr Thr Asp Ser Glu Phe Gln
        515                 520                 525

Lys Asn Ser Val Ile Arg Leu Ile Glu Leu Lys Leu Pro Val Phe Asp
    530                 535                 540

Ala Pro Glu Ser Leu Ile Lys Gln Ala Gln Leu Thr Ala Ala Thr Asn
545                 550                 555                 560

Ala Lys Gln


<210> SEQ ID NO 75
<211> LENGTH: 568
<212> TYPE: PRT
<213> ORGANISM: Zymomonas mobilis

<400> SEQUENCE: 75

Met Ser Tyr Thr Val Gly Thr Tyr Leu Ala Glu Arg Leu Val Gln Ile
1               5                   10                  15

Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu
            20                  25                  30

Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys
        35                  40                  45

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

Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala
65                  70                  75                  80

Phe Asp Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu
                85                  90                  95

Ile Ser Gly Ala Pro Asn Asn Asn Asp His Ala Ala Gly His Val Leu
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           100                 105                 110

His His Ala Leu Gly Lys Thr Asp Tyr His Tyr Gln Leu Glu Met Ala
        115                 120                 125

Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala
    130                 135                 140

Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys
145                 150                 155                 160

Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala
                165                 170                 175

Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu
            180                 185                 190

Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asp
        195                 200                 205

Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly
    210                 215                 220

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

Ala Thr Met Ala Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His
                245                 250                 255

Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys
            260                 265                 270

Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn
        275                 280                 285

Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu
    290                 295                 300

Val Leu Ala Glu Pro Arg Ser Val Val Val Asn Gly Ile Arg Phe Pro
305                 310                 315                 320

Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser
                325                 330                 335

Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu
            340                 345                 350

Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala
        355                 360                 365

Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val
    370                 375                 380

Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Ile Lys Leu
385                 390                 395                 400

Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly
                405                 410                 415

Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg
            420                 425                 430

Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln
        435                 440                 445

Glu Val Ala Gln Met Val Arg Leu Lys Pro Pro Val Ile Ile Phe Leu
    450                 455                 460

Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro
465                 470                 475                 480

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

Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala
            500                 505                 510
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Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn
        515                 520                 525

Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys
    530                 535                 540

Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser
545                 550                 555                 560

Arg Lys Pro Val Asn Lys Leu Leu
                565
```

<210> SEQ ID NO 76
<211> LENGTH: 568
<212> TYPE: PRT
<213> ORGANISM: Zymomonas mobilis subsp. Mobilis

<400> SEQUENCE: 76

```
Met Ser Tyr Thr Val Gly Thr Tyr Leu Ala Glu Arg Leu Val Gln Ile
1               5                   10                  15

Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu
            20                  25                  30

Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys
        35                  40                  45

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

Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala
65                  70                  75                  80

Phe Asp Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu
                85                  90                  95

Ile Ser Gly Ala Pro Asn Asn Asn Asp His Ala Ala Gly His Val Leu
            100                 105                 110

His His Ala Leu Gly Lys Thr Asp Tyr His Tyr Gln Leu Glu Met Ala
        115                 120                 125

Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala
    130                 135                 140

Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys
145                 150                 155                 160

Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala
                165                 170                 175

Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu
            180                 185                 190

Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asn
        195                 200                 205

Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly
    210                 215                 220

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

Ala Thr Met Ala Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His
                245                 250                 255

Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys
            260                 265                 270

Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn
        275                 280                 285

Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu
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```
    290                 295                 300

Val Leu Ala Glu Pro Arg Ser Val Val Val Asn Gly Ile Arg Phe Pro
305                 310                 315                 320

Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser
                325                 330                 335

Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu
            340                 345                 350

Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala
        355                 360                 365

Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val
    370                 375                 380

Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu
385                 390                 395                 400

Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly
                405                 410                 415

Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg
            420                 425                 430

Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln
        435                 440                 445

Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu
    450                 455                 460

Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro
465                 470                 475                 480

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

Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala
            500                 505                 510

Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn
        515                 520                 525

Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys
    530                 535                 540

Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser
545                 550                 555                 560

Arg Lys Pro Val Asn Lys Leu Leu
                565


<210> SEQ ID NO 77
<211> LENGTH: 568
<212> TYPE: PRT
<213> ORGANISM: Zymomonas mobilis subsp. mobilis NRRL B-12526

<400> SEQUENCE: 77

Met Ser Tyr Thr Val Gly Thr Tyr Leu Ala Glu Arg Leu Val Gln Ile
1               5                   10                  15

Gly Leu Lys His His Phe Ala Val Ala Gly Asp Tyr Asn Leu Val Leu
            20                  25                  30

Leu Asp Asn Leu Leu Leu Asn Lys Asn Met Glu Gln Val Tyr Cys Cys
        35                  40                  45

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

Gly Ala Ala Ala Ala Val Val Thr Tyr Ser Val Gly Ala Leu Ser Ala
65                  70                  75                  80
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```
Phe Asp Ala Ile Gly Gly Ala Tyr Ala Glu Asn Leu Pro Val Ile Leu
               85                  90                  95

Ile Ser Gly Ala Pro Asn Asn Asn Asp His Ala Ala Gly His Val Leu
           100                 105                 110

His His Ala Leu Gly Lys Thr Asp Tyr His Tyr Gln Leu Glu Met Ala
       115                 120                 125

Lys Asn Ile Thr Ala Ala Ala Glu Ala Ile Tyr Thr Pro Glu Glu Ala
   130                 135                 140

Pro Ala Lys Ile Asp His Val Ile Lys Thr Ala Leu Arg Glu Lys Lys
145                 150                 155                 160

Pro Val Tyr Leu Glu Ile Ala Cys Asn Ile Ala Ser Met Pro Cys Ala
               165                 170                 175

Ala Pro Gly Pro Ala Ser Ala Leu Phe Asn Asp Glu Ala Ser Asp Glu
           180                 185                 190

Ala Ser Leu Asn Ala Ala Val Glu Glu Thr Leu Lys Phe Ile Ala Asn
       195                 200                 205

Arg Asp Lys Val Ala Val Leu Val Gly Ser Lys Leu Arg Ala Ala Gly
   210                 215                 220

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

Ala Thr Met Ala Ala Ala Lys Ser Phe Phe Pro Glu Glu Asn Pro His
               245                 250                 255

Tyr Ile Gly Thr Ser Trp Gly Glu Val Ser Tyr Pro Gly Val Glu Lys
           260                 265                 270

Thr Met Lys Glu Ala Asp Ala Val Ile Ala Leu Ala Pro Val Phe Asn
       275                 280                 285

Asp Tyr Ser Thr Thr Gly Trp Thr Asp Ile Pro Asp Pro Lys Lys Leu
   290                 295                 300

Val Leu Ala Glu Pro Arg Ser Val Val Val Asn Gly Val Arg Phe Pro
305                 310                 315                 320

Ser Val His Leu Lys Asp Tyr Leu Thr Arg Leu Ala Gln Lys Val Ser
               325                 330                 335

Lys Lys Thr Gly Ala Leu Asp Phe Phe Lys Ser Leu Asn Ala Gly Glu
           340                 345                 350

Leu Lys Lys Ala Ala Pro Ala Asp Pro Ser Ala Pro Leu Val Asn Ala
       355                 360                 365

Glu Ile Ala Arg Gln Val Glu Ala Leu Leu Thr Pro Asn Thr Thr Val
   370                 375                 380

Ile Ala Glu Thr Gly Asp Ser Trp Phe Asn Ala Gln Arg Met Lys Leu
385                 390                 395                 400

Pro Asn Gly Ala Arg Val Glu Tyr Glu Met Gln Trp Gly His Ile Gly
               405                 410                 415

Trp Ser Val Pro Ala Ala Phe Gly Tyr Ala Val Gly Ala Pro Glu Arg
           420                 425                 430

Arg Asn Ile Leu Met Val Gly Asp Gly Ser Phe Gln Leu Thr Ala Gln
       435                 440                 445

Glu Val Ala Gln Met Val Arg Leu Lys Leu Pro Val Ile Ile Phe Leu
   450                 455                 460

Ile Asn Asn Tyr Gly Tyr Thr Ile Glu Val Met Ile His Asp Gly Pro
465                 470                 475                 480

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

Asn Gly Asn Gly Gly Tyr Asp Ser Gly Ala Gly Lys Gly Leu Lys Ala
            500                 505                 510

Lys Thr Gly Gly Glu Leu Ala Glu Ala Ile Lys Val Ala Leu Ala Asn
        515                 520                 525

Thr Asp Gly Pro Thr Leu Ile Glu Cys Phe Ile Gly Arg Glu Asp Cys
    530                 535                 540

Thr Glu Glu Leu Val Lys Trp Gly Lys Arg Val Ala Ala Ala Asn Ser
545                 550                 555                 560

Arg Lys Pro Val Asn Lys Leu Leu
                565


<210> SEQ ID NO 78
<211> LENGTH: 577
<212> TYPE: PRT
<213> ORGANISM: Aspergillus parasiticus

<400> SEQUENCE: 78

Met Glu Gly Glu Thr Leu Pro Leu Ala Gln Tyr Leu Phe Lys Arg Leu
1               5                   10                  15

Leu Gln Leu Gly Val Asp Ser Ile Phe Gly Val Pro Gly Asp Tyr Asn
            20                  25                  30

Leu Thr Leu Leu Asp His Val Val Pro Ser Gly Leu Lys Trp Val Gly
        35                  40                  45

Asn Cys Asn Glu Leu Asn Ala Gly Tyr Ala Ala Asp Gly Tyr Ser Arg
    50                  55                  60

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

Ser Ala Ile Asn Ala Ile Ala Gly Ala Tyr Ala Glu Lys Ala Pro Val
                85                  90                  95

Val His Ile Val Gly Thr Pro Met Arg Ala Ser Gln Glu Ser Arg Ala
            100                 105                 110

Leu Ile His His Thr Phe Asn Asp Gly Asp Tyr Gln Arg Phe Asp Ala
        115                 120                 125

Ile Gln Glu His Val Thr Val Ala Gln Val Ser Leu Ser Asp His Arg
    130                 135                 140

Thr Ala Pro Ser Glu Ile Asp Arg Ile Leu Leu Gln Cys Leu Leu His
145                 150                 155                 160

Ser Arg Pro Val Arg Ile Ala Ile Pro Val Asp Met Val Pro Val Leu
                165                 170                 175

Val Pro Val Ala Gly Leu Ser Ser Lys Ile Gln Ile Pro Pro Ala Val
            180                 185                 190

Arg Gln Pro Gln Ala Glu Glu Ala Ala Leu Asn Ala Val Leu Lys Arg
        195                 200                 205

Ile Tyr Ser Ser Lys Lys Pro Met Ile Leu Val Asp Gly Glu Thr Arg
    210                 215                 220

Ser Phe Gly Met Leu Gln Arg Val Asn His Phe Ile Gln Thr Ile Gly
225                 230                 235                 240

Trp Pro Thr Phe Thr Ser Gly Phe Gly Lys Gly Leu Val Asp Glu Thr
                245                 250                 255

Leu Pro Asn Val Tyr Gly Val Cys Thr Leu His Gln Lys Ala Phe Val
            260                 265                 270
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Asp Ser Cys Asp Leu Val Leu Val Phe Gly Pro His Phe Ser Asn Thr
        275                 280                 285

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

Phe Ser Pro Asn Ser Ile Gln Val Asn Lys Asp Val Phe Arg Asp Leu
305                 310                 315                 320

Pro Val Gly Tyr Phe Ile Glu Gln Leu Thr Gln Gln Leu Asp Ile Ser
                325                 330                 335

Arg Ile Pro Thr His Lys His Asp Leu Val His Pro Ser Leu Arg Thr
            340                 345                 350

Leu Pro Glu Val Ser Pro Thr Asp Leu Val Thr Gln Thr Gly Gly Phe
        355                 360                 365

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

Glu Thr Gly Thr Pro Gly Tyr Gly Val Asn Asp Phe Ile Leu Pro Pro
385                 390                 395                 400

Gln Thr Arg Leu Phe Lys Pro Ala Thr Trp Leu Ser Ile Gly Tyr Met
                405                 410                 415

Leu Pro Ala Ala Leu Gly Ala Ser His Ala Gln Arg Asp Leu Val Ala
            420                 425                 430

Ser Asp Gln Tyr His Ser Leu Ser Asn Pro Arg Thr Ile Leu Phe Ile
        435                 440                 445

Gly Asp Gly Ser Phe Gln Met Thr Val Gln Glu Leu Ser Thr Ile Ile
    450                 455                 460

His Gln Lys Leu Asn Val Ile Ile Phe Leu Ile Asn Asn Asp Gly Tyr
465                 470                 475                 480

Thr Ile Glu Arg Cys Ile His Gly Arg Asn Gln Ala Tyr Asn Asp Val
                485                 490                 495

Ala Pro Trp Arg Tyr Leu Lys Ala Ala Glu Phe Phe Gly Ala Asp Gln
            500                 505                 510

Asp Gly Glu Tyr Lys Ala Ser Thr Trp Glu Val Arg Thr Trp Ala Asp
        515                 520                 525

Leu Asp Arg Val Leu Asn Asp Ser Gln Leu Ala Asp Gly Lys Gly Leu
    530                 535                 540

Arg Met Val Glu Val Phe Met Glu Arg Leu Asp Ala Pro Asp Val Leu
545                 550                 555                 560

Met Gly Leu Leu Asn Asn Gln Val Leu Arg Glu Asn Ala Gln Ser Arg
                565                 570                 575

Leu
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<210> SEQ ID NO 79
<211> LENGTH: 563
<212> TYPE: PRT
<213> ORGANISM: FLS

<400> SEQUENCE: 79

```
Met Ala Met Ile Thr Gly Gly Glu Leu Val Val Arg Thr Leu Ile Lys
1               5                   10                  15

Ala Gly Val Glu His Leu Phe Gly Leu His Gly Ile His Ile Asp Thr
            20                  25                  30

Ile Phe Gln Ala Cys Leu Asp His Asp Val Pro Ile Ile Asp Thr Arg
        35                  40                  45
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His Glu Ala Ala Ala Gly His Ala Ala Glu Gly Tyr Ala Arg Ala Gly
    50                  55                  60

Ala Lys Leu Gly Val Ala Leu Val Thr Ala Gly Gly Gly Phe Thr Asn
65                  70                  75                  80

Ala Val Thr Pro Ile Ala Asn Ala Arg Thr Asp Arg Thr Pro Val Leu
                85                  90                  95

Phe Leu Thr Gly Ser Gly Ala Leu Arg Asp Asp Glu Thr Asn Thr Leu
            100                 105                 110

Gln Ala Gly Ile Asp Gln Val Ala Met Ala Ala Pro Ile Thr Lys Trp
        115                 120                 125

Ala His Arg Val Met Ala Thr Glu His Ile Pro Arg Leu Val Met Gln
    130                 135                 140

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

Leu Pro Trp Asp Ile Leu Met Asn Gln Ile Asp Glu Asp Ser Val Ile
                165                 170                 175

Ile Pro Asp Leu Val Leu Ser Ala His Gly Ala His Pro Asp Pro Ala
            180                 185                 190

Asp Leu Asp Gln Ala Leu Ala Leu Leu Arg Lys Ala Glu Arg Pro Val
        195                 200                 205

Ile Val Leu Gly Ser Glu Ala Ser Arg Thr Ala Arg Lys Thr Ala Leu
    210                 215                 220

Ser Ala Phe Val Ala Ala Thr Gly Val Pro Val Phe Ala Asp Tyr Glu
225                 230                 235                 240

Gly Leu Ser Met Leu Ser Gly Leu Pro Asp Ala Met Arg Gly Gly Leu
                245                 250                 255

Val Gln Asn Leu Tyr Ser Phe Ala Lys Ala Asp Ala Ala Pro Asp Leu
            260                 265                 270

Val Leu Met Leu Gly Ala Arg Phe Gly Leu Asn Thr Gly His Gly Ser
        275                 280                 285

Gly Gln Leu Ile Pro His Ser Ala Gln Val Ile Gln Val Asp Pro Asp
    290                 295                 300

Ala Cys Glu Leu Gly Arg Leu Gln Gly Ile Ala Leu Gly Ile Val Ala
305                 310                 315                 320

Asp Val Gly Gly Thr Ile Glu Ala Leu Ala Gln Ala Thr Ala Gln Asp
                325                 330                 335

Ala Ala Trp Pro Asp Arg Gly Asp Trp Cys Ala Lys Val Thr Asp Leu
            340                 345                 350

Ala Gln Glu Arg Tyr Ala Ser Ile Ala Ala Lys Ser Ser Ser Glu His
        355                 360                 365

Ala Leu His Pro Phe His Ala Ser Gln Val Ile Ala Lys His Val Asp
    370                 375                 380

Ala Gly Val Thr Val Val Ala Asp Gly Gly Leu Thr Tyr Leu Trp Leu
385                 390                 395                 400

Ser Glu Val Met Ser Arg Val Lys Pro Gly Gly Phe Leu Cys His Gly
                405                 410                 415

Tyr Leu Asn Ser Met Gly Val Gly Phe Gly Thr Ala Leu Gly Ala Gln
            420                 425                 430

Val Ala Asp Leu Glu Ala Gly Arg Arg Thr Ile Leu Val Thr Gly Asp
        435                 440                 445

Gly Ser Val Gly Tyr Ser Ile Gly Glu Phe Asp Thr Leu Val Arg Lys
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    450                 455                 460

Gln Leu Pro Leu Ile Val Ile Ile Met Asn Asn Gln Ser Trp Gly Trp
465                 470                 475                 480

Thr Leu His Phe Gln Gln Leu Ala Val Gly Pro Asn Arg Val Thr Gly
                485                 490                 495

Thr Arg Leu Glu Asn Gly Ser Tyr His Gly Val Ala Ala Ala Phe Gly
            500                 505                 510

Ala Asp Gly Tyr His Val Asp Ser Val Glu Ser Phe Ser Ala Ala Leu
        515                 520                 525

Ala Gln Ala Leu Ala His Asn Arg Pro Ala Cys Ile Asn Val Ala Val
    530                 535                 540

Ala Leu Asp Pro Ile Pro Pro Glu Glu Leu Ile Leu Ile Gly Met Asp
545                 550                 555                 560

Pro Phe Ala


<210> SEQ ID NO 80
<211> LENGTH: 563
<212> TYPE: PRT
<213> ORGANISM: FLS L482S

<400> SEQUENCE: 80

Met Ala Met Ile Thr Gly Gly Glu Leu Val Val Arg Thr Leu Ile Lys
1               5                   10                  15

Ala Gly Val Glu His Leu Phe Gly Leu His Gly Ile His Ile Asp Thr
            20                  25                  30

Ile Phe Gln Ala Cys Leu Asp His Asp Val Pro Ile Ile Asp Thr Arg
        35                  40                  45

His Glu Ala Ala Ala Gly His Ala Ala Glu Gly Tyr Ala Arg Ala Gly
    50                  55                  60

Ala Lys Leu Gly Val Ala Leu Val Thr Ala Gly Gly Gly Phe Thr Asn
65                  70                  75                  80

Ala Val Thr Pro Ile Ala Asn Ala Arg Thr Asp Arg Thr Pro Val Leu
                85                  90                  95

Phe Leu Thr Gly Ser Gly Ala Leu Arg Asp Asp Glu Thr Asn Thr Leu
            100                 105                 110

Gln Ala Gly Ile Asp Gln Val Ala Met Ala Ala Pro Ile Thr Lys Trp
        115                 120                 125

Ala His Arg Val Met Ala Thr Glu His Ile Pro Arg Leu Val Met Gln
    130                 135                 140

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

Leu Pro Trp Asp Ile Leu Met Asn Gln Ile Asp Glu Asp Ser Val Ile
                165                 170                 175

Ile Pro Asp Leu Val Leu Ser Ala His Gly Ala His Pro Asp Pro Ala
            180                 185                 190

Asp Leu Asp Gln Ala Leu Ala Leu Leu Arg Lys Ala Glu Arg Pro Val
        195                 200                 205

Ile Val Leu Gly Ser Glu Ala Ser Arg Thr Ala Arg Lys Thr Ala Leu
    210                 215                 220

Ser Ala Phe Val Ala Ala Thr Gly Val Pro Val Phe Ala Asp Tyr Glu
225                 230                 235                 240

Gly Leu Ser Met Leu Ser Gly Leu Pro Asp Ala Met Arg Gly Gly Leu
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               245                 250                 255

Val Gln Asn Leu Tyr Ser Phe Ala Lys Ala Asp Ala Ala Pro Asp Leu
            260                 265                 270

Val Leu Met Leu Gly Ala Arg Phe Gly Leu Asn Thr Gly His Gly Ser
        275                 280                 285

Gly Gln Leu Ile Pro His Ser Ala Gln Val Ile Gln Val Asp Pro Asp
    290                 295                 300

Ala Cys Glu Leu Gly Arg Leu Gln Gly Ile Ala Leu Gly Ile Val Ala
305                 310                 315                 320

Asp Val Gly Gly Thr Ile Glu Ala Leu Ala Gln Ala Thr Ala Gln Asp
                325                 330                 335

Ala Ala Trp Pro Asp Arg Gly Asp Trp Cys Ala Lys Val Thr Asp Leu
            340                 345                 350

Ala Gln Glu Arg Tyr Ala Ser Ile Ala Ala Lys Ser Ser Ser Glu His
        355                 360                 365

Ala Leu His Pro Phe His Ala Ser Gln Val Ile Ala Lys His Val Asp
    370                 375                 380

Ala Gly Val Thr Val Val Ala Asp Gly Gly Leu Thr Tyr Leu Trp Leu
385                 390                 395                 400

Ser Glu Val Met Ser Arg Val Lys Pro Gly Gly Phe Leu Cys His Gly
                405                 410                 415

Tyr Leu Asn Ser Met Gly Val Gly Phe Gly Thr Ala Leu Gly Ala Gln
            420                 425                 430

Val Ala Asp Leu Glu Ala Gly Arg Arg Thr Ile Leu Val Thr Gly Asp
        435                 440                 445

Gly Ser Val Gly Tyr Ser Ile Gly Glu Phe Asp Thr Leu Val Arg Lys
    450                 455                 460

Gln Leu Pro Leu Ile Val Ile Ile Met Asn Asn Gln Ser Trp Gly Trp
465                 470                 475                 480

Thr Ser His Phe Gln Gln Leu Ala Val Gly Pro Asn Arg Val Thr Gly
                485                 490                 495

Thr Arg Leu Glu Asn Gly Ser Tyr His Gly Val Ala Ala Ala Phe Gly
            500                 505                 510

Ala Asp Gly Tyr His Val Asp Ser Val Glu Ser Phe Ser Ala Ala Leu
        515                 520                 525

Ala Gln Ala Leu Ala His Asn Arg Pro Ala Cys Ile Asn Val Ala Val
    530                 535                 540

Ala Leu Asp Pro Ile Pro Pro Glu Glu Leu Ile Leu Ile Gly Met Asp
545                 550                 555                 560

Pro Phe Ala


<210> SEQ ID NO 81
<211> LENGTH: 941
<212> TYPE: PRT
<213> ORGANISM: Vibrio vulnificus

<400> SEQUENCE: 81

Met His Asn Gly Val Met Lys Ala Trp Leu Glu Ser Ser His Leu Ala
1               5                   10                  15

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

Asp Pro Asp Leu Val Ser Glu Glu Trp Lys Arg Val Phe Glu Gly Leu
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```
        35                  40                  45

Pro Lys Pro Thr Lys Glu Val Ala Glu Gln Pro His Ser Arg Val Arg
    50                  55                  60

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

Val Ser Asp Pro Asp Val Asp Ala Lys Gln Val Lys Val Leu Gln Leu
                85                  90                  95

Ile Asn Ala Tyr Arg Phe Arg Gly His Glu Ala Ala Glu Leu Asp Pro
            100                 105                 110

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

His Asn Leu Thr Glu Asp Asp Phe Glu Glu Thr Phe Asn Val Gly Ser
    130                 135                 140

Phe Ala Val Gly Gln Glu Thr Met Pro Leu Lys Asp Ile Tyr Thr Ala
145                 150                 155                 160

Leu Lys Lys Thr Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Met
                165                 170                 175

Thr Asp Thr Glu Gln Lys Arg Trp Ile Gln Gln Arg Leu Glu Ser Val
            180                 185                 190

Val Gly Gln Pro Ser Phe Asp Lys Asp Glu Lys Arg Thr Phe Leu Ala
        195                 200                 205

Glu Leu Thr Ala Ala Glu Gly Leu Glu Arg Tyr Leu Gly Ala Lys Phe
    210                 215                 220

Pro Gly Ala Lys Arg Phe Ser Leu Glu Gly Gly Asp Ala Met Ile Pro
225                 230                 235                 240

Met Met Lys Glu Leu Ile Arg His Ala Gly Arg Ser Gly Met Arg Glu
                245                 250                 255

Val Val Ile Gly Met Ala His Arg Gly Arg Leu Asn Met Leu Val Asn
            260                 265                 270

Val Leu Gly Lys Lys Pro Gln Asp Leu Phe Asp Glu Phe Ala Gly Lys
        275                 280                 285

His Gly Glu Ser Trp Gly Thr Gly Asp Val Lys Tyr His Gln Gly Phe
    290                 295                 300

Ser Ala Asp Phe Ala Thr Pro Gly Gly Asp Val His Leu Ala Leu Ala
305                 310                 315                 320

Phe Asn Pro Ser His Leu Glu Ile Val Asn Pro Val Val Met Gly Ser
                325                 330                 335

Val Arg Ala Arg Gln Asp Arg Leu Gly Asp Asp Asp Gly Ser Lys Val
            340                 345                 350

Leu Pro Ile Thr Ile His Gly Asp Ser Ala Ile Ala Gly Gln Gly Val
        355                 360                 365

Val Ala Glu Thr Phe Asn Met Ser Gln Ala Arg Gly Phe Cys Val Gly
    370                 375                 380

Gly Thr Val Arg Val Val Val Asn Asn Gln Val Gly Phe Thr Thr Ser
385                 390                 395                 400

Asn Pro Arg Asp Thr Arg Ser Thr Met Tyr Cys Thr Asp Ile Ala Lys
                405                 410                 415

Met Val Gln Ala Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala
            420                 425                 430

Val Ala Phe Val Thr Arg Ile Ala Leu Asp Tyr Arg Asn Glu Phe Lys
        435                 440                 445
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Arg Asp Val Val Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn
    450                 455                 460

Glu Ala Asp Glu Pro Asn Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile
465                 470                 475                 480

Lys Lys His Pro Thr Pro Arg Lys Leu Tyr Ala Asp Val Leu Ile Asp
                485                 490                 495

Arg Asn Glu Cys Asp Ile Glu Thr Ala Thr Gln Met Val Asn Glu Tyr
            500                 505                 510

Arg Asp Ala Leu Asp His Gly Glu Val Val Val Lys Glu Trp Arg Pro
        515                 520                 525

Met Ala Leu His Ser Val Asp Trp Ser Pro Tyr Leu Gly His Glu Trp
    530                 535                 540

Asp Thr Pro Trp Ser Asn Thr Tyr Asp Lys Gln Arg Leu Val Glu Leu
545                 550                 555                 560

Gly Lys Arg Leu Cys Gln Tyr Pro Glu Ser His Thr Leu His Ser Arg
                565                 570                 575

Val Ser Lys Leu Tyr Asn Asp Arg Thr Ala Met Thr Asn Gly Glu Lys
            580                 585                 590

Glu Leu Asp Trp Gly Met Ala Glu Thr Leu Ala Tyr Ala Thr Leu Val
        595                 600                 605

Asp Asp Gly Lys Arg Ile Arg Ile Ser Gly Gln Asp Ser Gly Arg Gly
    610                 615                 620

Thr Phe Phe His Arg His Ala Val Leu His Asn Gln Asn Asp Ala Ser
625                 630                 635                 640

Thr Tyr Val Pro Leu Ala Asn Ile His Asp Lys Gln Gly Pro Phe Glu
                645                 650                 655

Val Phe Asp Ser Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr
            660                 665                 670

Gly Tyr Ala Thr Ala Glu Pro Ser Gly Leu Thr Leu Trp Glu Ala Gln
        675                 680                 685

Phe Gly Asp Phe Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile
    690                 695                 700

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

Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg
                725                 730                 735

Leu Glu Arg Tyr Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Val
            740                 745                 750

Val Pro Ser Thr Pro Ala Gln Val Tyr His Met Ile Arg Arg Gln Val
        755                 760                 765

Val Arg Pro Met Arg Arg Pro Leu Ile Val Met Ser Pro Lys Ser Leu
    770                 775                 780

Leu Arg His Pro Leu Cys Thr Ser Ser Leu Asp Asp Leu Ala Asn Gly
785                 790                 795                 800

Thr Phe Met Pro Ala Ile Pro Glu Ile Asp Glu Leu Asp Pro Ala Lys
                805                 810                 815

Val Lys Arg Val Val Phe Cys Ser Gly Lys Val Tyr Phe Asp Leu Leu
            820                 825                 830

Glu Gln Arg Arg Asn Asn Glu Gln Asp Asp Val Ala Ile Val Arg Ile
        835                 840                 845
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Glu Gln Leu Tyr Pro Phe Pro Met Asp Asp Val Lys Ala Ala Ile Ala
    850                 855                 860

Pro Tyr Val Asn Val Glu Asp Phe Val Trp Cys Gln Glu Glu Pro Gln
865                 870                 875                 880

Asn Gln Gly Ala Trp Tyr Cys Ser Gln His Asn Phe Arg Ala Ala Ile
                885                 890                 895

Pro Ala Gly Thr Glu Leu Lys Tyr Ala Gly Arg Pro Ala Ser Ala Ser
            900                 905                 910

Pro Ala Val Gly Tyr Met Ser Val His Leu Lys Gln Gln Lys Ala Leu
        915                 920                 925

Ile Asp Asp Ala Leu Asn Val Asn Glu Lys Thr Ser Asp
    930                 935                 940


<210> SEQ ID NO 82
<211> LENGTH: 857
<212> TYPE: PRT
<213> ORGANISM: Vibrio vulnificus

<400> SEQUENCE: 82

Asp Val Asp Ala Lys Gln Val Lys Val Leu Gln Leu Ile Asn Ala Tyr
1               5                   10                  15

Arg Phe Arg Gly His Glu Ala Ala Glu Leu Asp Pro Leu Gly Leu Trp
            20                  25                  30

Gln Arg Pro Thr Val Ala Glu Leu Asp Pro Ala Phe His Asn Leu Thr
        35                  40                  45

Glu Asp Asp Phe Glu Glu Thr Phe Asn Val Gly Ser Phe Ala Val Gly
    50                  55                  60

Gln Glu Thr Met Pro Leu Lys Asp Ile Tyr Thr Ala Leu Lys Lys Thr
65                  70                  75                  80

Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Met Thr Asp Thr Glu
                85                  90                  95

Gln Lys Arg Trp Ile Gln Gln Arg Leu Glu Ser Val Val Gly Gln Pro
            100                 105                 110

Ser Phe Asp Lys Asp Glu Lys Arg Thr Phe Leu Ala Glu Leu Thr Ala
        115                 120                 125

Ala Glu Gly Leu Glu Arg Tyr Leu Gly Ala Lys Phe Pro Gly Ala Lys
    130                 135                 140

Arg Phe Ser Leu Glu Gly Gly Asp Ala Met Ile Pro Met Met Lys Glu
145                 150                 155                 160

Leu Ile Arg His Ala Gly Arg Ser Gly Met Arg Glu Val Val Ile Gly
                165                 170                 175

Met Ala His Arg Gly Arg Leu Asn Met Leu Val Asn Val Leu Gly Lys
            180                 185                 190

Lys Pro Gln Asp Leu Phe Asp Glu Phe Ala Gly Lys His Gly Glu Ser
        195                 200                 205

Trp Gly Thr Gly Asp Val Lys Tyr His Gln Gly Phe Ser Ala Asp Phe
    210                 215                 220

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

His Leu Glu Ile Val Asn Pro Val Val Met Gly Ser Val Arg Ala Arg
                245                 250                 255

Gln Asp Arg Leu Gly Asp Asp Asp Gly Ser Lys Val Leu Pro Ile Thr
            260                 265                 270
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Ile His Gly Asp Ser Ala Ile Ala Gly Gln Gly Val Val Ala Glu Thr
        275                 280                 285

Phe Asn Met Ser Gln Ala Arg Gly Phe Cys Val Gly Gly Thr Val Arg
    290                 295                 300

Val Val Val Asn Asn Gln Val Gly Phe Thr Thr Ser Asn Pro Arg Asp
305                 310                 315                 320

Thr Arg Ser Thr Met Tyr Cys Thr Asp Ile Ala Lys Met Val Gln Ala
                325                 330                 335

Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val Ala Phe Val
            340                 345                 350

Thr Arg Ile Ala Leu Asp Tyr Arg Asn Glu Phe Lys Arg Asp Val Val
        355                 360                 365

Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu Ala Asp Glu
    370                 375                 380

Pro Asn Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys Lys His Pro
385                 390                 395                 400

Thr Pro Arg Lys Leu Tyr Ala Asp Val Leu Ile Asp Arg Asn Glu Cys
                405                 410                 415

Asp Ile Glu Thr Ala Thr Gln Met Val Asn Glu Tyr Arg Asp Ala Leu
            420                 425                 430

Asp His Gly Glu Val Val Val Lys Glu Trp Arg Pro Met Ala Leu His
        435                 440                 445

Ser Val Asp Trp Ser Pro Tyr Leu Gly His Glu Trp Asp Thr Pro Trp
    450                 455                 460

Ser Asn Thr Tyr Asp Lys Gln Arg Leu Val Glu Leu Gly Lys Arg Leu
465                 470                 475                 480

Cys Gln Tyr Pro Glu Ser His Thr Leu His Ser Arg Val Ser Lys Leu
                485                 490                 495

Tyr Asn Asp Arg Thr Ala Met Thr Asn Gly Glu Lys Glu Leu Asp Trp
            500                 505                 510

Gly Met Ala Glu Thr Leu Ala Tyr Ala Thr Leu Val Asp Asp Gly Lys
        515                 520                 525

Arg Ile Arg Ile Ser Gly Gln Asp Ser Gly Arg Gly Thr Phe Phe His
    530                 535                 540

Arg His Ala Val Leu His Asn Gln Asn Asp Ala Ser Thr Tyr Val Pro
545                 550                 555                 560

Leu Ala Asn Ile His Asp Lys Gln Gly Pro Phe Glu Val Phe Asp Ser
                565                 570                 575

Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly Tyr Ala Thr
            580                 585                 590

Ala Glu Pro Ser Gly Leu Thr Leu Trp Glu Ala Gln Phe Gly Asp Phe
        595                 600                 605

Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser Ser Gly Glu
    610                 615                 620

Gln Lys Trp Ala Arg Leu Cys Gly Leu Thr Met Leu Leu Pro His Gly
625                 630                 635                 640

Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu Glu Arg Tyr
                645                 650                 655

Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Val Val Pro Ser Thr
            660                 665                 670
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Pro Ala Gln Val Tyr His Met Ile Arg Arg Gln Val Val Arg Pro Met
        675                 680                 685

Arg Arg Pro Leu Ile Val Met Ser Pro Lys Ser Leu Leu Arg His Pro
    690                 695                 700

Leu Cys Thr Ser Ser Leu Asp Asp Leu Ala Asn Gly Thr Phe Met Pro
705                 710                 715                 720

Ala Ile Pro Glu Ile Asp Glu Leu Asp Pro Ala Lys Val Lys Arg Val
                725                 730                 735

Val Phe Cys Ser Gly Lys Val Tyr Phe Asp Leu Leu Glu Gln Arg Arg
            740                 745                 750

Asn Asn Glu Gln Asp Asp Val Ala Ile Val Arg Ile Glu Gln Leu Tyr
        755                 760                 765

Pro Phe Pro Met Asp Asp Val Lys Ala Ala Ile Ala Pro Tyr Val Asn
    770                 775                 780

Val Glu Asp Phe Val Trp Cys Gln Glu Glu Pro Gln Asn Gln Gly Ala
785                 790                 795                 800

Trp Tyr Cys Ser Gln His Asn Phe Arg Ala Ala Ile Pro Ala Gly Thr
                805                 810                 815

Glu Leu Lys Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro Ala Val Gly
            820                 825                 830

Tyr Met Ser Val His Leu Lys Gln Gln Lys Ala Leu Ile Asp Asp Ala
        835                 840                 845

Leu Asn Val Asn Glu Lys Thr Ser Asp
    850                 855


<210> SEQ ID NO 83
<211> LENGTH: 857
<212> TYPE: PRT
<213> ORGANISM: Vibrio vulnificus

<400> SEQUENCE: 83

Asp Val Asp Ala Lys Gln Val Lys Val Leu Gln Leu Ile Asn Ala Tyr
1               5                   10                  15

Arg Phe Arg Gly His Glu Ala Ala Glu Leu Asp Pro Leu Gly Leu Trp
            20                  25                  30

Gln Arg Pro Thr Val Ala Glu Leu Asp Pro Ala Phe His Asn Leu Thr
        35                  40                  45

Glu Asp Asp Phe Glu Glu Thr Phe Asn Val Gly Ser Phe Ala Val Gly
    50                  55                  60

Gln Glu Thr Met Pro Leu Lys Asp Ile Tyr Thr Ala Leu Lys Lys Thr
65                  70                  75                  80

Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Met Thr Asp Thr Glu
                85                  90                  95

Gln Lys Arg Trp Ile Gln Gln Arg Leu Glu Ser Val Val Gly Gln Pro
            100                 105                 110

Ser Phe Asp Lys Asp Glu Lys Arg Thr Phe Leu Ala Glu Leu Thr Ala
        115                 120                 125

Ala Glu Gly Leu Glu Arg Tyr Leu Gly Ala Lys Phe Pro Gly Ala Lys
    130                 135                 140

Arg Phe Ser Leu Glu Gly Gly Asp Ala Met Ile Pro Met Met Lys Glu
145                 150                 155                 160

Leu Ile Arg His Ala Gly Arg Ser Gly Met Arg Glu Val Val Ile Gly
                165                 170                 175
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Met Ala His Arg Gly Arg Leu Asn Met Leu Val Asn Val Leu Gly Lys
            180                 185                 190

Lys Pro Gln Asp Leu Phe Asp Glu Phe Ala Gly Lys His Gly Glu Ser
        195                 200                 205

Trp Gly Thr Gly Asp Val Lys Tyr His Gln Gly Phe Ser Ala Asp Phe
    210                 215                 220

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

His Leu Glu Ile Val Asn Pro Val Val Met Gly Ser Val Arg Ala Arg
                245                 250                 255

Gln Asp Arg Leu Gly Asp Asp Asp Gly Ser Lys Val Leu Pro Ile Thr
            260                 265                 270

Ile His Gly Asp Ser Ala Ile Ala Gly Gln Gly Val Val Ala Glu Thr
        275                 280                 285

Phe Asn Met Ser Gln Ala Arg Gly Phe Cys Val Gly Gly Thr Val Arg
    290                 295                 300

Val Val Val Asn Asn Gln Val Gly Phe Thr Thr Ser Asn Pro Arg Asp
305                 310                 315                 320

Thr Arg Ser Thr Met Tyr Cys Thr Asp Ile Ala Lys Met Val Gln Ala
                325                 330                 335

Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val Ala Phe Val
            340                 345                 350

Thr Arg Ile Ala Leu Asp Tyr Arg Asn Glu Phe Lys Arg Asp Val Val
        355                 360                 365

Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu Ala Asp Glu
    370                 375                 380

Pro Asn Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys Lys His Pro
385                 390                 395                 400

Thr Pro Arg Lys Leu Tyr Ala Asp Val Leu Ile Asp Arg Asn Glu Cys
                405                 410                 415

Asp Ile Glu Thr Ala Thr Gln Met Val Asn Glu Tyr Arg Asp Ala Leu
            420                 425                 430

Asp His Gly Glu Val Val Val Lys Glu Trp Arg Pro Met Ala Leu His
        435                 440                 445

Ser Val Asp Trp Ser Pro Tyr Leu Gly His Glu Trp Asp Thr Pro Trp
    450                 455                 460

Ser Asn Thr Tyr Asp Lys Gln Arg Leu Val Glu Leu Gly Lys Arg Leu
465                 470                 475                 480

Cys Gln Tyr Pro Glu Ser His Thr Leu His Ser Arg Val Ser Lys Leu
                485                 490                 495

Tyr Asn Asp Arg Thr Ala Met Thr Asn Gly Glu Lys Glu Leu Asp Trp
            500                 505                 510

Gly Met Ala Glu Thr Leu Ala Tyr Ala Thr Leu Val Asp Asp Gly Lys
        515                 520                 525

Arg Ile Arg Ile Ser Gly Gln Asp Ser Gly Arg Gly Thr Phe Phe His
    530                 535                 540

Arg His Ala Val Leu His Asn Gln Asn Asp Ala Ser Thr Tyr Val Pro
545                 550                 555                 560

Leu Ala Asn Ile His Asp Lys Gln Gly Pro Phe Glu Val Phe Asp Ser
                565                 570                 575
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Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly Tyr Ala Thr
            580                 585                 590

Ala Glu Pro Ser Gly Leu Thr Leu Trp Glu Ala Gln Phe Gly Asp Phe
        595                 600                 605

Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser Ser Gly Glu
    610                 615                 620

Gln Lys Trp Ala Arg Leu Cys Gly Leu Thr Met Leu Leu Pro His Gly
625                 630                 635                 640

Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu Glu Arg Tyr
                645                 650                 655

Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Val Val Pro Ser Thr
            660                 665                 670

Pro Ala Gln Val Tyr His Met Ile Arg Arg Gln Val Val Arg Pro Met
        675                 680                 685

Arg Arg Pro Leu Ile Val Met Ser Pro Lys Ser Leu Leu Arg His Pro
    690                 695                 700

Leu Cys Thr Ser Ser Leu Asp Asp Leu Ala Asn Gly Thr Phe Met Pro
705                 710                 715                 720

Ala Ile Pro Glu Ile Asp Glu Leu Asp Pro Ala Lys Val Lys Arg Val
                725                 730                 735

Val Phe Cys Ser Gly Lys Val Tyr Phe Asp Leu Leu Glu Gln Arg Arg
            740                 745                 750

Asn Asn Glu Gln Asp Asp Val Ala Ile Val Arg Ile Glu Gln Leu Tyr
        755                 760                 765

Pro Phe Pro Met Asp Asp Val Lys Ala Ala Ile Ala Pro Tyr Val Asn
    770                 775                 780

Val Glu Asp Phe Val Trp Cys Gln Glu Glu Pro Gln Asn Gln Gly Ala
785                 790                 795                 800

Trp Tyr Cys Ser Gln His Asn Phe Arg Ala Ala Ile Pro Ala Gly Thr
                805                 810                 815

Glu Leu Lys Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro Ala Val Gly
            820                 825                 830

Tyr Met Ser Val His Leu Lys Gln Gln Lys Ala Leu Ile Asp Asp Ala
        835                 840                 845

Leu Asn Val Asn Glu Lys Thr Ser Asp
    850                 855


<210> SEQ ID NO 84
<211> LENGTH: 857
<212> TYPE: PRT
<213> ORGANISM: Vibrio vulnificus

<400> SEQUENCE: 84

Asp Val Asp Ala Lys Gln Val Lys Val Leu Gln Leu Ile Asn Ala Tyr
1               5                   10                  15

Arg Phe Arg Gly His Glu Ala Ala Glu Leu Asp Pro Leu Gly Leu Trp
            20                  25                  30

Gln Arg Pro Thr Val Ala Glu Leu Asp Pro Ala Phe His Asn Leu Thr
        35                  40                  45

Glu Asp Asp Phe Glu Glu Thr Phe Asn Val Gly Ser Phe Ala Val Gly
    50                  55                  60

Gln Glu Thr Met Pro Leu Lys Asp Ile Tyr Thr Ala Leu Lys Lys Thr
65                  70                  75                  80
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Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Met Thr Asp Thr Glu
                85                  90                  95

Gln Lys Arg Trp Ile Gln Gln Arg Leu Glu Ser Val Val Gly Gln Pro
            100                 105                 110

Ser Phe Asp Lys Asp Glu Lys Arg Thr Phe Leu Ala Glu Leu Thr Ala
        115                 120                 125

Ala Glu Gly Leu Glu Arg Tyr Leu Gly Ala Lys Phe Pro Gly Ala Leu
    130                 135                 140

Arg Phe Ser Leu Glu Gly Gly Asp Ala Met Ile Pro Met Met Lys Glu
145                 150                 155                 160

Leu Ile Arg His Ala Gly Arg Ser Gly Met Arg Glu Val Val Ile Gly
                165                 170                 175

Met Ala His Arg Gly Arg Leu Asn Met Leu Val Asn Val Leu Gly Lys
            180                 185                 190

Lys Pro Gln Asp Leu Phe Asp Glu Phe Ala Gly Lys His Gly Glu Ser
        195                 200                 205

Trp Gly Thr Gly Asp Val Lys Tyr His Gln Gly Phe Ser Ala Asp Phe
    210                 215                 220

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

His Leu Glu Ile Val Asn Pro Val Val Met Gly Ser Val Arg Ala Arg
                245                 250                 255

Gln Asp Arg Leu Gly Asp Asp Asp Gly Ser Lys Val Leu Pro Ile Thr
            260                 265                 270

Ile His Gly Asp Ser Ala Ile Ala Gly Gln Gly Val Val Ala Glu Thr
        275                 280                 285

Phe Asn Met Ser Gln Ala Arg Gly Phe Cys Val Gly Gly Thr Val Arg
    290                 295                 300

Val Val Val Asn Asn Gln Val Gly Phe Thr Thr Ser Asn Pro Arg Asp
305                 310                 315                 320

Thr Arg Ser Thr Met Tyr Cys Thr Asp Ile Ala Lys Met Val Gln Ala
                325                 330                 335

Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val Ala Phe Val
            340                 345                 350

Thr Arg Ile Ala Leu Asp Tyr Arg Asn Glu Phe Lys Arg Asp Val Val
        355                 360                 365

Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu Ala Asp Glu
    370                 375                 380

Pro Asn Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys Lys His Pro
385                 390                 395                 400

Thr Pro Arg Lys Leu Tyr Ala Asp Val Leu Ile Asp Arg Asn Glu Cys
                405                 410                 415

Asp Ile Glu Thr Ala Thr Gln Met Val Asn Glu Tyr Arg Asp Ala Leu
            420                 425                 430

Asp His Gly Glu Val Val Val Lys Glu Trp Arg Pro Met Ala Leu His
        435                 440                 445

Ser Val Asp Trp Ser Pro Tyr Leu Gly His Glu Trp Asp Thr Pro Trp
    450                 455                 460

Ser Asn Thr Tyr Asp Lys Gln Arg Leu Val Glu Leu Gly Lys Arg Leu
465                 470                 475                 480
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Cys Gln Tyr Pro Glu Ser His Thr Leu His Ser Arg Val Ser Lys Leu
                485                 490                 495

Tyr Asn Asp Arg Thr Ala Met Thr Asn Gly Glu Lys Glu Leu Asp Trp
            500                 505                 510

Gly Met Ala Glu Thr Leu Ala Tyr Ala Thr Leu Val Asp Asp Gly Lys
        515                 520                 525

Arg Ile Arg Ile Ser Gly Gln Asp Ser Gly Arg Gly Thr Phe Phe His
    530                 535                 540

Arg His Ala Val Leu His Asn Gln Asn Asp Ala Ser Thr Tyr Val Pro
545                 550                 555                 560

Leu Ala Asn Ile His Asp Lys Gln Gly Pro Phe Glu Val Phe Asp Ser
                565                 570                 575

Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly Tyr Ala Thr
            580                 585                 590

Ala Glu Pro Ser Gly Leu Thr Leu Trp Glu Ala Gln Phe Gly Asp Phe
        595                 600                 605

Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser Ser Gly Glu
    610                 615                 620

Gln Lys Trp Ala Arg Leu Cys Gly Leu Thr Met Leu Leu Pro His Gly
625                 630                 635                 640

Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu Glu Arg Tyr
                645                 650                 655

Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Val Val Pro Ser Thr
            660                 665                 670

Pro Ala Gln Val Tyr His Met Ile Arg Arg Gln Val Val Arg Pro Met
        675                 680                 685

Arg Arg Pro Leu Ile Val Met Ser Pro Lys Ser Leu Leu Arg His Pro
    690                 695                 700

Leu Cys Thr Ser Ser Leu Asp Asp Leu Ala Asn Gly Thr Phe Met Pro
705                 710                 715                 720

Ala Ile Pro Glu Ile Asp Glu Leu Asp Pro Ala Lys Val Lys Arg Val
                725                 730                 735

Val Phe Cys Ser Gly Lys Val Tyr Phe Asp Leu Leu Glu Gln Arg Arg
            740                 745                 750

Asn Asn Glu Gln Asp Asp Val Ala Ile Val Arg Ile Glu Gln Leu Tyr
        755                 760                 765

Pro Phe Pro Met Asp Asp Val Lys Ala Ala Ile Ala Pro Tyr Val Asn
    770                 775                 780

Val Glu Asp Phe Val Trp Cys Gln Glu Glu Pro Gln Asn Gln Gly Ala
785                 790                 795                 800

Trp Tyr Cys Ser Gln His Asn Phe Arg Ala Ala Ile Pro Ala Gly Thr
                805                 810                 815

Glu Leu Lys Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro Ala Val Gly
            820                 825                 830

Tyr Met Ser Val His Leu Lys Gln Gln Lys Ala Leu Ile Asp Asp Ala
        835                 840                 845

Leu Asn Val Asn Glu Lys Thr Ser Asp
    850                 855
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<210> SEQ ID NO 85
<211> LENGTH: 857
<212> TYPE: PRT

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<213> ORGANISM: Vibrio vulnificus

<400> SEQUENCE: 85

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Asp Val Asp Ala Lys Gln Val Lys Val Leu Gln Leu Ile Asn Ala Tyr
1               5                   10                  15

Arg Phe Arg Gly His Glu Ala Ala Glu Leu Asp Pro Leu Gly Leu Trp
            20                  25                  30

Gln Arg Pro Thr Val Ala Glu Leu Asp Pro Ala Phe His Asn Leu Thr
        35                  40                  45

Glu Asp Asp Phe Glu Glu Thr Phe Asn Val Gly Ser Phe Ala Val Gly
    50                  55                  60

Gln Glu Thr Met Pro Leu Lys Asp Ile Tyr Thr Ala Leu Lys Lys Thr
65                  70                  75                  80

Tyr Cys Gly Ser Ile Gly Ala Glu Tyr Met His Met Thr Asp Thr Glu
                85                  90                  95

Gln Lys Arg Trp Ile Gln Gln Arg Leu Glu Ser Val Val Gly Gln Pro
            100                 105                 110

Ser Phe Asp Lys Asp Glu Lys Arg Thr Phe Leu Ala Glu Leu Thr Ala
        115                 120                 125

Ala Glu Gly Leu Glu Arg Tyr Leu Gly Ala Lys Phe Pro Gly Ala Leu
    130                 135                 140

Arg Phe Ser Leu Glu Gly Gly Asp Ala Met Ile Pro Met Met Lys Glu
145                 150                 155                 160

Leu Ile Arg His Ala Gly Arg Ser Gly Met Arg Glu Val Val Ile Gly
                165                 170                 175

Met Ala His Arg Gly Arg Leu Asn Met Leu Val Asn Val Leu Gly Lys
            180                 185                 190

Lys Pro Gln Asp Leu Phe Asp Glu Phe Ala Gly Lys His Gly Glu Ser
        195                 200                 205

Trp Gly Thr Gly Asp Val Lys Tyr His Gln Gly Phe Ser Ala Asp Phe
    210                 215                 220

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

His Leu Glu Ile Val Asn Pro Val Val Met Gly Ser Val Arg Ala Arg
                245                 250                 255

Gln Asp Arg Leu Gly Asp Asp Asp Gly Ser Lys Val Leu Pro Ile Thr
            260                 265                 270

Ile His Gly Asp Ser Ala Ile Ala Gly Gln Gly Val Val Ala Glu Thr
        275                 280                 285

Phe Asn Met Ser Gln Ala Arg Gly Phe Cys Val Gly Gly Thr Val Arg
    290                 295                 300

Val Val Val Asn Asn Gln Val Gly Phe Thr Thr Ser Asn Pro Arg Asp
305                 310                 315                 320

Thr Arg Ser Thr Met Tyr Cys Thr Asp Ile Ala Lys Met Val Gln Ala
                325                 330                 335

Pro Ile Phe His Val Asn Ala Asp Asp Pro Glu Ala Val Ala Phe Val
            340                 345                 350

Thr Arg Ile Ala Leu Asp Tyr Arg Asn Glu Phe Lys Arg Asp Val Val
        355                 360                 365

Ile Asp Leu Val Cys Tyr Arg Arg His Gly His Asn Glu Ala Asp Glu
    370                 375                 380
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```
Pro Asn Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys Lys His Pro
385                 390                 395                 400

Thr Pro Arg Lys Leu Tyr Ala Asp Val Leu Ile Asp Arg Asn Glu Cys
                405                 410                 415

Asp Ile Glu Thr Ala Thr Gln Met Val Asn Glu Tyr Arg Asp Ala Leu
            420                 425                 430

Asp His Gly Glu Val Val Val Lys Glu Trp Arg Pro Met Ala Leu His
        435                 440                 445

Ser Val Asp Trp Ser Pro Tyr Leu Gly His Glu Trp Asp Thr Pro Trp
    450                 455                 460

Ser Asn Thr Tyr Asp Lys Gln Arg Leu Val Glu Leu Gly Lys Arg Leu
465                 470                 475                 480

Cys Gln Tyr Pro Glu Ser His Thr Leu His Ser Arg Val Ser Lys Leu
                485                 490                 495

Tyr Asn Asp Arg Thr Ala Met Thr Asn Gly Glu Lys Glu Leu Asp Trp
            500                 505                 510

Gly Met Ala Glu Thr Leu Ala Tyr Ala Thr Leu Val Asp Asp Gly Lys
        515                 520                 525

Arg Ile Arg Ile Ser Gly Gln Asp Ser Gly Arg Gly Thr Phe Phe His
    530                 535                 540

Arg His Ala Val Leu His Asn Gln Asn Asp Ala Ser Thr Tyr Val Pro
545                 550                 555                 560

Leu Ala Asn Ile His Asp Lys Gln Gly Pro Phe Glu Val Phe Asp Ser
                565                 570                 575

Val Leu Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly Tyr Ala Thr
            580                 585                 590

Ala Glu Pro Ser Gly Leu Thr Leu Trp Glu Ala Gln Phe Gly Asp Phe
        595                 600                 605

Ala Asn Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser Ser Gly Glu
    610                 615                 620

Gln Lys Trp Ala Arg Leu Cys Gly Leu Thr Met Leu Leu Pro His Gly
625                 630                 635                 640

Tyr Glu Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu Glu Arg Tyr
                645                 650                 655

Leu Gln Leu Cys Ala Glu Gln Asn Met Gln Val Val Val Pro Ser Thr
            660                 665                 670

Pro Ala Gln Val Tyr His Met Ile Arg Arg Gln Val Val Arg Pro Met
        675                 680                 685

Arg Arg Pro Leu Ile Val Met Ser Pro Lys Ser Leu Leu Arg His Pro
    690                 695                 700

Leu Cys Thr Ser Ser Leu Asp Asp Leu Ala Asn Gly Thr Phe Met Pro
705                 710                 715                 720

Ala Ile Pro Glu Ile Asp Glu Leu Asp Pro Ala Lys Val Lys Arg Val
                725                 730                 735

Val Phe Cys Ser Gly Lys Val Tyr Phe Asp Leu Leu Glu Gln Arg Arg
            740                 745                 750

Asn Asn Glu Gln Asp Asp Val Ala Ile Val Arg Ile Glu Gln Leu Tyr
        755                 760                 765

Pro Phe Pro Met Asp Asp Val Lys Ala Ala Ile Ala Pro Tyr Val Asn
    770                 775                 780

Val Glu Asp Phe Val Trp Cys Gln Glu Glu Pro Gln Asn Gln Gly Ala
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785                 790                 795                 800

Trp Tyr Cys Ser Gln His Asn Phe Arg Ala Ala Ile Pro Ala Gly Thr
                805                 810                 815

Glu Leu Lys Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro Ala Val Gly
            820                 825                 830

Tyr Met Ser Val His Leu Lys Gln Gln Lys Ala Leu Ile Asp Asp Ala
        835                 840                 845

Leu Asn Val Asn Glu Lys Thr Ser Asp
    850                 855


<210> SEQ ID NO 86
<211> LENGTH: 855
<212> TYPE: PRT
<213> ORGANISM: Vibrio vulnificus

<400> SEQUENCE: 86

Val Asp Ala Lys Gln Val Lys Val Leu Gln Leu Ile Asn Ala Tyr Arg
1               5                   10                  15

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

Arg Pro Thr Val Ala Glu Leu Asp Pro Ala Phe His Asn Leu Thr Glu
        35                  40                  45

Asp Asp Phe Glu Glu Thr Phe Asn Val Gly Ser Phe Ala Val Gly Gln
    50                  55                  60

Glu Thr Met Pro Leu Lys Asp Ile Tyr Thr Ala Leu Lys Lys Thr Tyr
65                  70                  75                  80

Cys Gly Ser Ile Gly Ala Glu Tyr Met His Met Thr Asp Thr Glu Gln
                85                  90                  95

Lys Arg Trp Ile Gln Gln Arg Leu Glu Ser Val Val Gly Gln Pro Ser
            100                 105                 110

Phe Asp Lys Asp Glu Lys Arg Thr Phe Leu Ala Glu Leu Thr Ala Ala
        115                 120                 125

Glu Gly Leu Glu Arg Tyr Leu Gly Ala Lys Phe Pro Gly Ala Lys Arg
    130                 135                 140

Phe Ser Leu Glu Gly Gly Asp Ala Met Ile Pro Met Met Lys Glu Leu
145                 150                 155                 160

Ile Arg His Ala Gly Arg Ser Gly Met Arg Glu Val Val Ile Gly Met
                165                 170                 175

Ala His Arg Gly Arg Leu Asn Met Leu Val Asn Val Leu Gly Lys Lys
            180                 185                 190

Pro Gln Asp Leu Phe Asp Glu Phe Ala Gly Lys His Gly Glu Ser Trp
        195                 200                 205

Gly Thr Gly Asp Gly Gly Gly Gln Gly Phe Ser Ala Asp Phe Ala Thr
    210                 215                 220

Pro Gly Gly Asp Val His Leu Ala Leu Ala Phe Asn Pro Ser His Leu
225                 230                 235                 240

Glu Ile Val Asn Pro Val Val Met Gly Ser Val Arg Ala Arg Gln Asp
                245                 250                 255

Arg Leu Gly Asp Asp Asp Gly Ser Lys Val Leu Pro Ile Thr Ile His
            260                 265                 270

Gly Asp Ser Ala Ile Ala Gly Gln Gly Val Val Ala Glu Thr Phe Asn
        275                 280                 285
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Met Ser Gln Ala Arg Gly Phe Cys Val Gly Gly Thr Val Arg Val Val
    290                 295                 300

Val Asn Asn Gln Val Gly Phe Thr Thr Ser Asn Pro Arg Asp Thr Arg
305                 310                 315                 320

Ser Thr Met Tyr Cys Thr Asp Ile Ala Lys Met Val Gln Ala Pro Ile
                325                 330                 335

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

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

Leu Val Cys Tyr Arg Arg His Gly His Asn Glu Ala Asp Glu Pro Asn
    370                 375                 380

Ala Thr Gln Pro Leu Met Tyr Gln Lys Ile Lys Lys His Pro Thr Pro
385                 390                 395                 400

Arg Lys Leu Tyr Ala Asp Val Leu Ile Asp Arg Asn Glu Cys Asp Ile
                405                 410                 415

Glu Thr Ala Thr Gln Met Val Asn Glu Tyr Arg Asp Ala Leu Asp His
            420                 425                 430

Gly Glu Val Val Val Lys Glu Trp Arg Pro Met Ala Leu His Ser Val
        435                 440                 445

Asp Trp Ser Pro Tyr Leu Gly His Glu Trp Asp Thr Pro Trp Ser Asn
    450                 455                 460

Thr Tyr Asp Lys Gln Arg Leu Val Glu Leu Gly Lys Arg Leu Cys Gln
465                 470                 475                 480

Tyr Pro Glu Ser His Thr Leu His Ser Arg Val Ser Lys Leu Tyr Asn
                485                 490                 495

Asp Arg Thr Ala Met Thr Asn Gly Glu Lys Glu Leu Asp Trp Gly Met
            500                 505                 510

Ala Glu Thr Leu Ala Tyr Ala Thr Leu Val Asp Asp Gly Lys Arg Ile
        515                 520                 525

Arg Ile Ser Gly Gln Asp Ser Gly Arg Gly Thr Phe Phe His Arg His
    530                 535                 540

Ala Val Leu His Asn Gln Asn Asp Ala Ser Thr Tyr Val Pro Leu Ala
545                 550                 555                 560

Asn Ile His Asp Lys Gln Gly Pro Phe Glu Val Phe Asp Ser Val Leu
                565                 570                 575

Ser Glu Glu Ala Val Leu Ala Phe Glu Tyr Gly Tyr Ala Thr Ala Glu
            580                 585                 590

Pro Ser Gly Leu Thr Leu Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn
        595                 600                 605

Gly Ala Gln Val Val Ile Asp Gln Phe Ile Ser Ser Gly Glu Gln Lys
    610                 615                 620

Trp Ala Arg Leu Cys Gly Leu Thr Met Leu Leu Pro His Gly Tyr Glu
625                 630                 635                 640

Gly Gln Gly Pro Glu His Ser Ser Ala Arg Leu Glu Arg Tyr Leu Gln
                645                 650                 655

Leu Cys Ala Glu Gln Asn Met Gln Val Val Val Pro Ser Thr Pro Ala
            660                 665                 670

Gln Val Tyr His Met Ile Arg Arg Gln Val Val Arg Pro Met Arg Arg
        675                 680                 685

Pro Leu Ile Val Met Ser Pro Lys Ser Leu Leu Arg His Pro Leu Cys
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    690                 695                 700

Thr Ser Ser Leu Asp Asp Leu Ala Asn Gly Thr Phe Met Pro Ala Ile
705                 710                 715                 720

Pro Glu Ile Asp Glu Leu Asp Pro Ala Lys Val Lys Arg Val Val Phe
                725                 730                 735

Cys Ser Gly Lys Val Tyr Phe Asp Leu Leu Glu Gln Arg Arg Asn Asn
            740                 745                 750

Glu Gln Asp Asp Val Ala Ile Val Arg Ile Glu Gln Leu Tyr Pro Phe
        755                 760                 765

Pro Met Asp Asp Val Lys Ala Ala Ile Ala Pro Tyr Val Asn Val Glu
    770                 775                 780

Asp Phe Val Trp Cys Gln Glu Glu Pro Gln Asn Gln Gly Ala Trp Tyr
785                 790                 795                 800

Cys Ser Gln His Asn Phe Arg Ala Ala Ile Pro Ala Gly Thr Glu Leu
                805                 810                 815

Lys Tyr Ala Gly Arg Pro Ala Ser Ala Ser Pro Ala Val Gly Tyr Met
            820                 825                 830

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

Val Asn Glu Lys Thr Ser Asp
    850                 855


<210> SEQ ID NO 87
<211> LENGTH: 683
<212> TYPE: PRT
<213> ORGANISM: Syncephalastrum racemosum

<400> SEQUENCE: 87

Met Thr Leu Pro Thr Thr Ile His Pro Leu Asp Pro Leu Ser Pro Glu
1               5                   10                  15

Glu Ile Arg His Val Ser Glu Ile Ile Arg Lys Gln Arg Ala Ala Asp
            20                  25                  30

Glu Thr Thr Tyr Ile Phe Asn Ser Ile Ala Leu Arg Glu Pro Pro Lys
        35                  40                  45

Glu Gln Ile Leu Ala His Phe Gly Trp Thr Asp Gly Pro Lys Pro Val
    50                  55                  60

Gln Ile Asp Arg Gln Ala Phe Ala Val Leu Ile Asp Arg Pro Ser Gly
65                  70                  75                  80

Leu Val His Glu Ile Ile Val Ser Ile Thr Thr Ala Ser Ile Val Ser
                85                  90                  95

Trp Glu Thr Lys Glu Gly Val Gln Pro Thr Leu His Val Gln Glu Met
            100                 105                 110

Leu Glu Ala Glu Gln Val Met Leu Lys Asp Glu Arg Val Ile Glu Glu
        115                 120                 125

Cys Arg Lys Leu Gly Ile Glu Asp Met Ser Met Val Phe Ala Asp Thr
    130                 135                 140

Trp Gly Val Gly Trp His Lys Thr Lys Gly Lys Arg Leu Met Gln Ala
145                 150                 155                 160

Leu Met Tyr Met Arg Thr Ser Pro Asp Asp Asn Gln Tyr Ala His Pro
                165                 170                 175

Leu Asp Phe Thr Pro Leu Tyr Asp Val Asn Glu Gln Lys Val Ile Asp
            180                 185                 190
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Val Leu Val Ala Lys Arg Arg Asn Ser Lys Phe Glu Arg Pro Val Ile
        195                 200                 205

Pro Arg Ala Asp Arg Gln Phe Leu Pro Glu His Leu Gly Glu Glu Asn
    210                 215                 220

Leu Arg Lys Asp Ile Lys Pro Ile Glu Ile Thr Gln Pro Gln Gly Val
225                 230                 235                 240

Ser Phe Gln Ile Arg Gly His Glu Ile Asp Trp Gln Lys Trp Asn Leu
                245                 250                 255

His Val Gly Phe Asn Tyr Arg Glu Gly Leu Val Ile Asn Asn Val Ser
            260                 265                 270

Tyr Lys Asp Met Asp Gly Thr Val Arg Pro Met Phe Tyr Arg Val Ser
        275                 280                 285

Leu Ala Glu Met Val Val Pro Tyr Ala Asn Pro Tyr Glu Pro Tyr Asn
    290                 295                 300

His Lys Met Ala Phe Asp Val Gly Glu Tyr Gly Leu Gly Asn Leu Thr
305                 310                 315                 320

Asn Ser Leu Glu Leu Gly Cys Asp Cys Val Gly Ser Ile Phe Tyr Met
                325                 330                 335

Asp Gly Val Cys Ser Asp Ile Lys Gly Asp Ala Trp Val Ile Pro Asn
            340                 345                 350

Ala Ile Cys Ile His Glu Glu Asp Thr Gly Leu Leu Phe Lys His Thr
        355                 360                 365

Asp Phe Arg Asn Asn Lys Ala His Ser Ala Arg Ser Arg Arg Leu Val
    370                 375                 380

Ile Ser His Ile Val Thr Ala Ala Asn Tyr Asp Tyr Gly Leu Tyr Tyr
385                 390                 395                 400

Tyr Phe Tyr Gln Asp Gly Thr Phe Gln Tyr Glu Val Lys Ala Thr Gly
                405                 410                 415

Glu Leu Asn Thr His Val Leu Ala Glu Asp Glu Asp Pro Ala Pro Tyr
            420                 425                 430

Gly Thr Ile Val Ala Pro Gln Val Asp Ala Gln His His Gln His Leu
        435                 440                 445

Phe Ser Met Arg Ile Asp Pro Met Val Asp Gly Pro Thr Asn Ser Val
    450                 455                 460

Ala Gln Val Asp Val Val Ala Ser Asp Leu Pro Val Gly His Pro Asp
465                 470                 475                 480

Asn Ala Val Gly Asn Ala Phe Ser Pro Val Thr Thr Ile Tyr Ala Asp
                485                 490                 495

Thr Asp Glu Ala Arg Ala Arg Ala Asn Gly Glu Thr Ser Arg Tyr Trp
            500                 505                 510

Lys Ile Ile Asn Glu Thr Arg Ile His Pro Tyr Thr Lys Glu Pro Val
        515                 520                 525

Gly Phe Lys Leu Met Cys Pro Asn Thr Pro Pro Met Leu Pro Lys Pro
    530                 535                 540

Gly Ser Ile Ala Tyr Glu Arg Ala Val Phe Ala Ser Asn Thr Val Trp
545                 550                 555                 560

Val Thr Pro Tyr Asp Ala Glu Gln Leu Phe Pro Gly Gly Phe Tyr Cys
                565                 570                 575

Tyr Gln Ser Asp Pro Ala Asp Arg Leu Gly Leu Pro Glu Trp Thr Arg
            580                 585                 590

Glu Lys Lys Asp Val Lys Asn Lys Asp Ile Val Leu Trp Leu Thr Phe
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595 600 605

Gly Leu Thr His Ile Pro Arg Val Glu Asp Phe Pro Ile Met Pro Val
610 615 620

Glu Thr Cys Gly Phe Met Leu Lys Pro Cys Asn Phe Phe Leu Ala Asn
625 630 635 640

Pro Gly Ile Asp Ile Pro Ala Ser Asp Arg His Ser Ser Lys Ser Ala
645 650 655

Tyr Ala Pro Ala Val Ala Asn Gly Glu Tyr Gly Ile Thr Asn Gly Thr
660 665 670

Thr Asn Gly Ser Ser Cys Cys Ser Lys Gly His
675 680

<210> SEQ ID NO 88
<211> LENGTH: 638
<212> TYPE: PRT
<213> ORGANISM: Arthrobacter sp.

<400> SEQUENCE: 88

Met Thr Glu Thr Thr Ala Val Asn Thr Asp Phe Thr Leu Leu Ser Glu
1 5 10 15

Gln Glu Ile Ala Thr Ala Lys Gln Leu Leu Val Glu Asn Gln Leu Phe
20 25 30

Thr Gly Ser Thr Arg Ile Ala Tyr Met Gly Leu Glu Asp Pro Ser Glu
35 40 45

Gln Asn Ala Asp Arg Leu Val Arg Val Met Leu Met Asp Lys Ala Arg
50 55 60

Asn Glu Pro Lys Asp Val Val Leu Asp Leu Thr Arg Gly Glu Val Ala
65 70 75 80

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

Val Glu Glu Phe Glu Met Val Glu Ala Ile Leu Ala Glu Asp Ala Gln
100 105 110

Trp Ala Ala Ala Leu Glu Lys Arg Gly Leu Ala Val Asp Gln Val Arg
115 120 125

Val Ala Pro Leu Ser Ala Gly Val Phe Tyr Pro Glu Ser Gly Arg Arg
130 135 140

Ile Leu Arg Gly Leu Ala Phe Arg Gln Asp Phe Ala Asp Ser Ala Trp
145 150 155 160

Ala His Pro Ile Asp Gly Leu Val Val Tyr Ile Asp Thr Ile Glu Gln
165 170 175

Lys Val Asp Gln Leu Leu Asp Phe Gly Ile Val Asp Val Pro Ala Thr
180 185 190

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

Gln Lys Pro Ile Glu Ile Thr Gln Pro Glu Gly Ala Ser Phe Thr Val
210 215 220

Thr Glu Gly Asn His Val Glu Trp Glu Lys Trp Ser Leu Asp Ile Gly
225 230 235 240

Phe Asp Met Arg Glu Gly Leu Val Leu Tyr Asn Ile Gly Phe Asp Asp
245 250 255

Lys Gly Glu Arg Arg Arg Ile Leu Asp Arg Ala Ser Ile Ala Glu Met
260 265 270

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Val Val Pro Tyr Gly Asp Pro Ser Pro Val Arg Ser Trp Gln Asn Tyr
        275                 280                 285

Phe Asp Thr Gly Glu Tyr Leu Val Gly Arg Phe Ala Asn Ser Leu Glu
    290                 295                 300

Leu Gly Cys Asp Cys Leu Gly Glu Ile His Tyr Ile Ser Pro Val Ile
305                 310                 315                 320

Thr Asp Ala Asp Gly Asn Ala Gln Thr Ile Thr Asn Gly Ile Cys Met
                325                 330                 335

His Glu Glu Asp Ser Ser Ile Leu Ala Lys His Ser Asp Asp Trp Ser
            340                 345                 350

Gly Val Lys Tyr Thr Arg Arg Asn Arg Arg Leu Val Ile Ser Phe Phe
        355                 360                 365

Thr Thr Val Gly Asn Tyr Asp Tyr Gly Phe Tyr Trp Tyr Leu Tyr Leu
    370                 375                 380

Asp Gly Thr Ile Glu Phe Glu Ala Lys Ala Thr Gly Ile Val Phe Thr
385                 390                 395                 400

Ser Ala Met Arg Asp Glu Arg Phe Ala Ser Glu Met Ala Pro Gly Leu
                405                 410                 415

Gly Ala Pro Phe His Gln His Leu Phe Gly Ala Arg Leu Asp Phe Ala
            420                 425                 430

Leu Asp Gly Gly Pro Ser Arg Val Ile Glu Glu Glu Ala Val Arg Leu
        435                 440                 445

Pro Ile Ser Glu Asp Asn Pro Arg Gly Asn Ala Phe Thr Arg Ser Gln
    450                 455                 460

Thr Val Leu Ala Thr Glu Lys Gln Ala Val Arg Asp Ala Asn Gln Ala
465                 470                 475                 480

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

Gly Lys Pro Val Gly Phe Lys Leu Leu Pro Gln Gly Leu Pro Thr Leu
            500                 505                 510

Leu Ala Ala Glu Gly Ser Ser Val His Arg Arg Ala Glu Phe Ala Ser
        515                 520                 525

Lys Ala Leu Trp Val Thr Gln Arg Asp Ala Ala His Arg Tyr Pro Thr
    530                 535                 540

Gly Asp Phe Val Asn Gln Asn Pro Gly Val Asp Gly Ile Gly Ser Trp
545                 550                 555                 560

Ile Glu Asp Asp Lys Ser Ile Asp Gly Glu Lys Ile Ser Leu Trp His
                565                 570                 575

Thr Phe Ala Leu Thr His Phe Pro Arg Thr Glu Asp Trp Pro Ile Met
            580                 585                 590

Pro Val Asp Thr Val Gly Phe Lys Ile Arg Pro Glu Gly Phe Phe Asp
        595                 600                 605

Arg Ser Pro Val Leu Asp Val Pro Glu Pro Ala Lys His Gly Cys Cys
    610                 615                 620

Ala Thr Thr Thr Glu Ala Asp Gly Cys Cys Gly Ser Asn Gly
625                 630                 635


<210> SEQ ID NO 89
<211> LENGTH: 472
<212> TYPE: PRT
<213> ORGANISM: Bacillus megaterium (strain ATCC 12872 / QMB1551)

<400> SEQUENCE: 89
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Met Leu Gln Lys Trp Ile Thr Ser Ile Gly Leu Asp Ile Gly Thr Ser
1               5                  10                  15

Thr Thr Lys Leu Ile Val Ser Lys Leu Leu Ile Ala Asn Gln Gln Asn
            20                  25                  30

Gln Phe Thr Leu Pro Gly Cys Gln Ile Ile Asp Arg Arg Val Thr Tyr
        35                  40                  45

Ala Ser Ser Ile Tyr Thr Thr Pro Met Leu Asn Asp Val Glu Ile Asp
    50                  55                  60

Val Gln Arg Leu Thr Val Leu Leu Glu Gln Glu Tyr Lys Asn Ala Gly
65                  70                  75                  80

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

Thr Ala Arg Lys Gln Asn Ala Glu Ser Ile Val His Tyr Leu Ala Glu
            100                 105                 110

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

Ile Leu Ala Ala Lys Gly Ser Gly Ala Ile Glu Arg Ser Ala Glu Thr
    130                 135                 140

Asn Ala Val Ile Ala Asn Ile Asp Val Gly Gly Gly Thr Ala Asn Ile
145                 150                 155                 160

Ala Leu Cys Gln Asn Gly Lys Val Ile Glu Thr Phe Thr Leu His Val
                165                 170                 175

Gly Gly Arg Leu Ile Arg Leu Asn Glu Asp Gly Leu Val Thr Tyr Val
            180                 185                 190

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

Glu Gly Glu Lys Ala Thr Phe Glu Lys Leu Ser Ser Ile Cys Gln Leu
    210                 215                 220

Leu Ala Glu Glu Thr Val Asn Tyr Val Lys Ala Leu Asn Gln Asn Ser
225                 230                 235                 240

Ser Leu Leu Val Ser Pro His Thr Arg Ser Ser Thr Pro Pro Glu Thr
                245                 250                 255

Ile Met Val Ser Gly Gly Val Gly Ala Met Met Glu Lys Gln Lys Pro
            260                 265                 270

Lys Thr Val Lys Glu Val Ala Ile His Gly Asp Val Gly Pro Leu Leu
        275                 280                 285

Ala Asp His Phe Gln Ser Ile Gln Val Ser Gln Ala Ala Glu Thr Thr
    290                 295                 300

Arg Ala Thr Val Ile Gly Ala Gly Met Gln Asn Thr Glu Val Ser Gly
305                 310                 315                 320

Ser Thr Val Tyr Ile Lys Ser Lys Lys Leu Pro Leu Lys Asn Ile Pro
                325                 330                 335

Ile Ile Glu Ile Pro Val Gln Pro Glu Glu Glu Trp Asn Pro Gln Leu
            340                 345                 350

Phe Gln Glu Arg Ala Arg Ala Ser Cys Met Gln Ala Ser Thr Ile Phe
        355                 360                 365

Ser Ala Glu Asp Pro Pro Val Ala Ile Ala Leu Ser His Phe Pro Tyr
    370                 375                 380

Cys Ser Tyr Lys Met Leu Gln Glu Leu Ala Lys Val Ile Ser Ala Glu
385                 390                 395                 400
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Phe Ile Ala Cys Phe Lys Arg Ala Lys Cys Leu Val Val Leu Cys Glu
                405                 410                 415

Gln Asp Ile Ala Lys Ala Leu Gly Gln Ala Leu Ala Lys Gln Arg Lys
            420                 425                 430

Glu Leu Glu Ile Ile Cys Leu Asp Gln Ile Asp Phe Thr His Gly Asp
        435                 440                 445

Tyr Ile Asp Leu Gly Leu Pro Val Ala Gly Glu Ala Ile Ser Val Ser
    450                 455                 460

Val Lys Thr Leu Ala Phe Ser Ser
465                 470


<210> SEQ ID NO 90
<211> LENGTH: 472
<212> TYPE: PRT
<213> ORGANISM: Bacillus megaterium (A0A380XUP7)

<400> SEQUENCE: 90

Met Leu Gln Lys Trp Ile Thr Ser Ile Gly Leu Asp Ile Gly Thr Ser
1               5                   10                  15

Thr Thr Lys Leu Ile Val Ser Lys Leu Leu Ile Ala Asn Gln Gln Asn
            20                  25                  30

Gln Phe Thr Leu Pro Gly Cys Gln Ile Ile Asp Arg Gln Val Thr Tyr
        35                  40                  45

Ala Ser Ser Ile Tyr Thr Thr Pro Met Leu Asn Glu Val Glu Ile Asp
    50                  55                  60

Val Gln Arg Leu Thr Val Leu Leu Glu Gln Glu Tyr Lys Asn Ala Glu
65                  70                  75                  80

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

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

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

Ile Leu Ala Ala Lys Gly Ser Gly Ala Ile Gln His Ser Ala Glu Thr
    130                 135                 140

Asn Ala Val Ile Ala Asn Ile Asp Val Gly Gly Gly Thr Ala Asn Ile
145                 150                 155                 160

Ala Leu Cys Gln Asn Gly Lys Val Ile Glu Thr Phe Thr Leu His Val
                165                 170                 175

Gly Gly Arg Leu Ile Arg Leu Asn Ser Asp Gly Phe Val Thr Tyr Val
            180                 185                 190

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

Glu Gly Glu Lys Ala Thr Phe Glu Lys Leu Ser Ser Ile Cys Gln Leu
    210                 215                 220

Leu Ala Glu Glu Thr Val Asn Tyr Val Arg Ala Leu Ile Gln Thr Ser
225                 230                 235                 240

Ser Leu Leu Val Ser Pro His Thr Arg Ser Ser Ile Gln Pro Glu Thr
                245                 250                 255

Ile Met Ile Ser Gly Gly Val Gly Ala Met Met Glu Lys Gln Lys Pro
            260                 265                 270

Lys Thr Val Arg Glu Val Ala Val His Gly Asp Ile Gly Pro Leu Leu
        275                 280                 285
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```
Ala Tyr Gln Phe Gln Ser Ile His Val Ser Gln Ala Ala Glu Thr Thr
    290                 295                 300

Arg Ala Thr Val Ile Gly Ala Gly Met Gln Asn Thr Glu Val Ser Gly
305                 310                 315                 320

Ser Thr Val Tyr Ile Lys Ser Lys Lys Leu Pro Leu Lys Asn Ile Pro
                325                 330                 335

Ile Ile Glu Ile Pro Val Gln Pro Glu Glu Glu Trp Asn Thr Gln Leu
            340                 345                 350

Phe Gln Glu Arg Ala Arg Ala Ser Cys Met Gln Ala Ser Thr Ile Phe
        355                 360                 365

Ser Ala Glu Asp Pro Pro Val Ala Ile Ala Leu Ser His Phe Pro Tyr
    370                 375                 380

Cys Ser Tyr Lys Met Leu Gln Glu Leu Ala Lys Val Ile Ser Ala Glu
385                 390                 395                 400

Phe Gly Ala Cys Phe Lys Gly Ala Lys Cys Leu Val Val Leu Cys Glu
                405                 410                 415

Gln Asp Ile Ala Lys Ala Leu Gly Gln Ala Leu Ala Lys Gln Lys Lys
            420                 425                 430

Glu Leu Glu Ile Ile Cys Leu Asp Gln Ile Asp Phe Thr His Gly Asp
        435                 440                 445

Tyr Ile Asp Leu Gly Leu Pro Val Ala Gly Glu Ala Ile Ser Val Ser
    450                 455                 460

Val Lys Thr Leu Ala Phe Ser Ser
465                 470


<210> SEQ ID NO 91
<211> LENGTH: 438
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 91

Met Ala Ser Ser Ser Leu Cys His Arg Tyr Phe Asn Lys Ile Thr Val
1               5                   10                  15

Thr Pro Phe Phe Asn Thr Lys Lys Leu His His Tyr Ser Pro Arg Arg
            20                  25                  30

Ile Ser Leu Arg Val Asn Arg Arg Ser Phe Ser Ile Ser Ala Thr Met
        35                  40                  45

Ser Ser Ser Thr Lys Lys Val Leu Ile Pro Val Ala His Gly Thr Glu
    50                  55                  60

Pro Phe Glu Ala Val Val Met Ile Asp Val Leu Arg Arg Gly Gly Ala
65                  70                  75                  80

Asp Val Thr Val Ala Ser Val Glu Asn Gln Val Gly Val Asp Ala Cys
                85                  90                  95

His Gly Ile Lys Met Val Ala Asp Thr Leu Leu Ser Asp Ile Thr Asp
            100                 105                 110

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

Thr Leu Lys Asn Cys Lys Pro Leu Glu Lys Met Val Lys Lys Gln Asp
    130                 135                 140

Thr Asp Gly Arg Leu Asn Ala Ala Ile Cys Cys Ala Pro Ala Leu Ala
145                 150                 155                 160

Phe Gly Thr Trp Gly Leu Leu Glu Gly Lys Lys Ala Thr Cys Tyr Pro
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                165                 170                 175

Val Phe Met Glu Lys Leu Ala Ala Cys Ala Thr Ala Val Glu Ser Arg
            180                 185                 190

Val Glu Ile Asp Gly Lys Ile Val Thr Ser Arg Gly Pro Gly Thr Thr
        195                 200                 205

Met Glu Phe Ser Val Thr Leu Val Glu Gln Leu Leu Gly Lys Glu Lys
    210                 215                 220

Ala Val Glu Val Ser Gly Pro Leu Val Met Arg Pro Asn Pro Gly Asp
225                 230                 235                 240

Glu Tyr Thr Ile Thr Glu Leu Asn Gln Val Ser Trp Ser Phe Glu Gly
                245                 250                 255

Thr Pro Gln Ile Leu Val Pro Ile Ala Asp Gly Ser Glu Glu Met Glu
            260                 265                 270

Ala Val Ala Ile Ile Asp Val Leu Lys Arg Ala Lys Ala Asn Val Val
        275                 280                 285

Val Ala Ala Leu Gly Asn Ser Leu Glu Val Val Ala Ser Arg Lys Val
    290                 295                 300

Lys Leu Val Ala Asp Val Leu Leu Asp Glu Ala Glu Lys Asn Ser Tyr
305                 310                 315                 320

Asp Leu Ile Val Leu Pro Gly Gly Leu Gly Gly Ala Glu Ala Phe Ala
                325                 330                 335

Ser Ser Glu Lys Leu Val Asn Met Leu Lys Lys Gln Ala Glu Ser Asn
            340                 345                 350

Lys Pro Tyr Gly Ala Ile Cys Ala Ser Pro Ala Leu Val Phe Glu Pro
        355                 360                 365

His Gly Leu Leu Lys Gly Lys Lys Ala Thr Ala Phe Pro Ala Met Cys
    370                 375                 380

Ser Lys Leu Thr Asp Gln Ser His Ile Glu His Arg Val Leu Val Asp
385                 390                 395                 400

Gly Asn Leu Ile Thr Ser Arg Gly Pro Gly Thr Ser Leu Glu Phe Ala
                405                 410                 415

Leu Ala Ile Val Glu Lys Phe Tyr Gly Arg Glu Lys Gly Leu Gln Leu
            420                 425                 430

Ser Lys Ala Thr Leu Val
        435


<210> SEQ ID NO 92
<211> LENGTH: 388
<212> TYPE: PRT
<213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 92

Met Ala Asn Ser Arg Thr Val Leu Ile Leu Cys Gly Asp Tyr Met Glu
1               5                   10                  15

Asp Tyr Glu Val Met Val Pro Phe Gln Ala Leu Gln Ala Phe Gly Ile
            20                  25                  30

Thr Val His Thr Val Cys Pro Gly Lys Lys Ala Gly Asp Ser Cys Pro
        35                  40                  45

Thr Ala Val His Asp Phe Cys Gly His Gln Thr Tyr Phe Glu Ser Arg
    50                  55                  60

Gly His Asn Phe Thr Leu Asn Ala Thr Phe Asp Glu Val Asp Leu Ser
65                  70                  75                  80
```

-continued

```
Lys Tyr Asp Gly Leu Val Ile Pro Gly Gly Arg Ala Pro Glu Tyr Leu
                85                  90                  95

Ala Leu Thr Ala Ser Val Val Glu Leu Val Lys Glu Phe Ser Arg Ser
            100                 105                 110

Gly Lys Pro Ile Ala Ser Ile Cys His Gly Gln Leu Ile Leu Ala Ala
        115                 120                 125

Ala Asp Thr Val Asn Gly Arg Lys Cys Thr Ala Tyr Ala Thr Val Gly
    130                 135                 140

Pro Ser Leu Val Ala Ala Gly Ala Lys Trp Val Glu Pro Ile Thr Pro
145                 150                 155                 160

Asp Val Cys Val Val Asp Gly Ser Leu Ile Thr Ala Ala Thr Tyr Glu
                165                 170                 175

Gly His Pro Glu Phe Ile Gln Leu Phe Val Lys Ala Leu Gly Gly Lys
            180                 185                 190

Ile Thr Gly Ala Asn Lys Arg Ile Leu Phe Leu Cys Gly Asp Tyr Met
        195                 200                 205

Glu Asp Tyr Glu Val Lys Val Pro Phe Gln Ser Leu Gln Ala Leu Gly
    210                 215                 220

Cys Gln Val Asp Ala Val Cys Pro Glu Lys Lys Ala Gly Asp Arg Cys
225                 230                 235                 240

Pro Thr Ala Ile His Asp Phe Glu Gly Asp Gln Thr Tyr Ser Glu Lys
                245                 250                 255

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

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

Leu Ala Leu Asn Glu His Val Leu Asn Ile Val Lys Glu Phe Met Asn
    290                 295                 300

Ser Glu Lys Pro Val Ala Ser Ile Cys His Gly Gln Gln Ile Leu Ala
305                 310                 315                 320

Ala Ala Gly Val Leu Lys Gly Arg Lys Cys Thr Ala Tyr Pro Ala Val
                325                 330                 335

Lys Leu Asn Val Val Leu Gly Gly Gly Thr Trp Leu Glu Pro Asp Pro
            340                 345                 350

Ile Asp Arg Cys Phe Thr Asp Gly Asn Leu Val Thr Gly Ala Ala Trp
        355                 360                 365

Pro Gly His Pro Glu Phe Val Ser Gln Leu Met Ala Leu Leu Gly Ile
    370                 375                 380

Gln Val Ser Phe
385


<210> SEQ ID NO 93
<211> LENGTH: 186
<212> TYPE: PRT
<213> ORGANISM: Caenorhabditis elegans

<400> SEQUENCE: 93

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

Glu Glu Ile Glu Val Ile Val Thr Gly Asp Val Leu Val Arg Gly Gly
            20                  25                  30

Leu Gln Val Leu Tyr Ala Gly Ser Ser Thr Glu Pro Val Lys Cys Ala
        35                  40                  45
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Lys Gly Ala Arg Ile Val Pro Asp Val Ala Leu Lys Asp Val Lys Asn
    50                  55                  60

Lys Thr Phe Asp Ile Ile Ile Ile Pro Gly Gly Pro Gly Cys Ser Lys
65                  70                  75                  80

Leu Ala Glu Cys Pro Val Ile Gly Glu Leu Leu Lys Thr Gln Val Lys
                85                  90                  95

Ser Gly Gly Leu Ile Gly Ala Ile Cys Ala Gly Pro Thr Val Leu Leu
            100                 105                 110

Ala His Gly Ile Val Ala Glu Arg Val Thr Cys His Tyr Thr Val Lys
        115                 120                 125

Asp Lys Met Thr Glu Gly Gly Tyr Lys Tyr Leu Asp Asp Asn Val Val
    130                 135                 140

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

Phe Ala Leu Lys Ile Val Glu Thr Leu Glu Gly Pro Glu Lys Thr Asn
                165                 170                 175

Ser Leu Leu Lys Pro Leu Cys Leu Ala Lys
            180                 185


<210> SEQ ID NO 94
<211> LENGTH: 236
<212> TYPE: PRT
<213> ORGANISM: Candida albicans

<400> SEQUENCE: 94

Met Val Lys Val Leu Leu Ala Leu Thr Ser Tyr Asn Glu Thr Phe Tyr
1               5                   10                  15

Ser Asp Gly Lys Lys Thr Gly Val Phe Val Val Glu Ala Leu His Pro
            20                  25                  30

Phe Glu Val Phe Arg Lys Lys Gly Tyr Glu Ile Gln Leu Ala Ser Glu
        35                  40                  45

Thr Gly Thr Phe Gly Trp Asp Asp His Ser Val Val Pro Asp Phe Leu
    50                  55                  60

Asn Gly Glu Asp Lys Glu Ile Phe Asp Asn Val Asn Ser Glu Phe Asn
65                  70                  75                  80

Val Ala Leu Lys Asn Leu Lys Lys Ala Ser Asp Leu Asp Pro Asn Asp
                85                  90                  95

Tyr Asp Ile Phe Phe Gly Ser Ala Gly His Gly Thr Leu Phe Asp Tyr
            100                 105                 110

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

Gly Gly Val Val Ser Ala Val Cys His Gly Pro Ala Ile Phe Glu Asn
    130                 135                 140

Leu Asn Asp Pro Lys Thr Gly Glu Pro Leu Ile Lys Gly Lys Lys Ile
145                 150                 155                 160

Thr Gly Phe Thr Asp Ile Gly Glu Asp Ile Leu Gly Val Thr Asp Ile
                165                 170                 175

Met Lys Lys Gly Asn Leu Leu Thr Ile Lys Gln Val Ala Glu Lys Glu
            180                 185                 190

Gly Ala Thr Tyr Ile Glu Pro Glu Gly Pro Trp Asp Asn Phe Thr Val
        195                 200                 205

Thr Asp Gly Arg Ile Val Thr Gly Val Asn Pro Gln Ser Ala Val Lys
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    210                 215                 220

Thr Ala Glu Asp Val Ile Ala Ala Phe Glu Cys Asn
225                 230                 235


<210> SEQ ID NO 95
<211> LENGTH: 217
<212> TYPE: PRT
<213> ORGANISM: Drosophila melanogaster

<400> SEQUENCE: 95

Met Leu Ser Val Leu Arg Lys Ser Phe Pro Asn Gly Val Thr His Ala
1               5                   10                  15

His Arg Val Ile Arg Cys Lys Ser Asn Gln Asp Lys Cys Ala Lys Asn
            20                  25                  30

Ala Leu Ile Ile Leu Ala Pro Gly Ala Glu Glu Met Glu Phe Thr Ile
        35                  40                  45

Ser Ala Asp Val Leu Arg Arg Gly Lys Ile Leu Val Thr Val Ala Gly
    50                  55                  60

Leu His Asp Cys Glu Pro Val Lys Cys Ser Arg Ser Val Val Ile Val
65                  70                  75                  80

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

Val Val Leu Pro Gly Gly Leu Ala Gly Asn Lys Ala Leu Met Asn Ser
            100                 105                 110

Ser Ala Val Gly Asp Val Leu Arg Cys Gln Glu Ser Lys Gly Gly Leu
        115                 120                 125

Ile Ala Ala Ile Cys Ala Ala Pro Thr Ala Leu Ala Lys His Gly Ile
    130                 135                 140

Gly Lys Gly Lys Ser Ile Thr Ser His Pro Asp Met Lys Pro Gln Leu
145                 150                 155                 160

Lys Glu Leu Tyr Cys Tyr Ile Asp Asp Lys Thr Val Val Gln Asp Gly
                165                 170                 175

Asn Ile Ile Thr Ser Arg Gly Pro Gly Thr Thr Phe Asp Phe Ala Leu
            180                 185                 190

Lys Ile Thr Glu Gln Leu Val Gly Ala Glu Val Ala Lys Glu Val Ala
        195                 200                 205

Lys Ala Met Leu Trp Thr Tyr Lys Pro
    210                 215


<210> SEQ ID NO 96
<211> LENGTH: 187
<212> TYPE: PRT
<213> ORGANISM: Drosophila melanogaster

<400> SEQUENCE: 96

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

Glu Phe Ile Ile Ala Ala Asp Val Leu Arg Arg Ala Gly Ile Lys Val
            20                  25                  30

Thr Val Ala Gly Leu Asn Gly Gly Glu Ala Val Lys Cys Ser Arg Asp
        35                  40                  45

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

Phe Asp Val Val Val Leu Pro Gly Gly Leu Gly Gly Ser Asn Ala Met
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65                  70                  75                  80

Gly Glu Ser Ser Leu Val Gly Asp Leu Leu Arg Ser Gln Glu Ser Gly
                85                  90                  95

Gly Gly Leu Ile Ala Ala Ile Cys Ala Ala Pro Thr Val Leu Ala Lys
            100                 105                 110

His Gly Val Ala Ser Gly Lys Ser Leu Thr Ser Tyr Pro Ser Met Lys
        115                 120                 125

Pro Gln Leu Val Asn Asn Tyr Ser Tyr Val Asp Asp Lys Thr Val Val
    130                 135                 140

Lys Asp Gly Asn Leu Ile Thr Ser Arg Gly Pro Gly Thr Ala Tyr Glu
145                 150                 155                 160

Phe Ala Leu Lys Ile Ala Glu Glu Leu Ala Gly Lys Glu Lys Val Gln
                165                 170                 175

Glu Val Ala Lys Gly Leu Leu Val Ala Tyr Asn
            180                 185


<210> SEQ ID NO 97
<211> LENGTH: 283
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 97

Met Thr Val Gln Thr Ser Lys Asn Pro Gln Val Asp Ile Ala Glu Asp
1               5                   10                  15

Asn Ala Phe Phe Pro Ser Glu Tyr Ser Leu Ser Gln Tyr Thr Ser Pro
            20                  25                  30

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

His Lys Ile Leu Val Ile Ala Ala Asp Glu Arg Tyr Leu Pro Thr Asp
    50                  55                  60

Asn Gly Lys Leu Phe Ser Thr Gly Asn His Pro Ile Glu Thr Leu Leu
65                  70                  75                  80

Pro Leu Tyr His Leu His Ala Ala Gly Phe Glu Phe Glu Val Ala Thr
                85                  90                  95

Ile Ser Gly Leu Met Thr Lys Phe Glu Tyr Trp Ala Met Pro Gln Lys
            100                 105                 110

Asp Glu Lys Val Met Pro Phe Phe Glu Gln His Lys Ser Leu Phe Arg
        115                 120                 125

Asn Pro Lys Lys Leu Ala Asp Val Val Ala Ser Leu Asn Ala Asp Ser
    130                 135                 140

Glu Tyr Ala Ala Ile Phe Val Pro Gly Gly His Gly Ala Leu Ile Gly
145                 150                 155                 160

Leu Pro Glu Ser Gln Asp Val Ala Ala Ala Leu Gln Trp Ala Ile Lys
                165                 170                 175

Asn Asp Arg Phe Val Ile Ser Leu Cys His Gly Pro Ala Ala Phe Leu
            180                 185                 190

Ala Leu Arg His Gly Asp Asn Pro Leu Asn Gly Tyr Ser Ile Cys Ala
        195                 200                 205

Phe Pro Asp Ala Ala Asp Lys Gln Thr Pro Glu Ile Gly Tyr Met Pro
    210                 215                 220

Gly His Leu Thr Trp Tyr Phe Gly Glu Glu Leu Lys Lys Met Gly Met
225                 230                 235                 240
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Asn Ile Ile Asn Asp Asp Ile Thr Gly Arg Val His Lys Asp Arg Lys
                245                 250                 255

Leu Leu Thr Gly Asp Ser Pro Phe Ala Ala Asn Ala Leu Gly Lys Leu
            260                 265                 270

Ala Ala Gln Glu Met Leu Ala Ala Tyr Ala Gly
        275                 280


<210> SEQ ID NO 98
<211> LENGTH: 291
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 98

Met Thr Val Gln Thr Ser Lys Asn Pro Gln Val Asp Ile Ala Glu Asp
1               5                   10                  15

Asn Ala Phe Phe Pro Ser Glu Tyr Ser Leu Ser Gln Tyr Thr Ser Pro
            20                  25                  30

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

His Lys Ile Leu Val Ile Ala Ala Asp Glu Arg Tyr Leu Pro Thr Asp
    50                  55                  60

Asn Gly Lys Leu Phe Ser Thr Gly Asn His Pro Ile Glu Thr Leu Leu
65                  70                  75                  80

Pro Leu Tyr His Leu His Ala Ala Gly Phe Glu Phe Glu Val Ala Thr
                85                  90                  95

Ile Ser Gly Leu Met Thr Lys Phe Glu Tyr Trp Ala Met Pro His Lys
            100                 105                 110

Asp Glu Lys Val Met Pro Phe Phe Glu Gln His Lys Ser Leu Phe Arg
        115                 120                 125

Asn Pro Lys Lys Leu Ala Asp Val Val Ala Ser Leu Asn Ala Asp Ser
    130                 135                 140

Glu Tyr Ala Ala Ile Phe Val Pro Gly Gly His Gly Ala Leu Ile Gly
145                 150                 155                 160

Leu Pro Glu Ser Gln Asp Val Ala Ala Ala Leu Gln Trp Ala Ile Lys
                165                 170                 175

Asn Asp Arg Phe Val Ile Ser Leu Cys His Gly Pro Ala Ala Phe Leu
            180                 185                 190

Ala Leu Arg His Gly Asp Asn Pro Leu Asn Gly Tyr Ser Ile Cys Ala
        195                 200                 205

Phe Pro Asp Ala Ala Asp Lys Gln Thr Pro Glu Ile Gly Tyr Met Pro
    210                 215                 220

Gly His Leu Thr Trp Tyr Phe Gly Glu Glu Leu Lys Lys Met Gly Met
225                 230                 235                 240

Asn Ile Ile Asn Asp Asp Ile Thr Gly Arg Val His Lys Asp Arg Lys
                245                 250                 255

Leu Leu Thr Gly Asp Ser Pro Phe Ala Ala Asn Ala Leu Gly Lys Leu
            260                 265                 270

Ala Ala Gln Glu Met Leu Ala Ala Tyr Ala Gly Leu Glu His His His
        275                 280                 285

His His His
    290


<210> SEQ ID NO 99
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<211> LENGTH: 196
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 99

Met Ser Ala Ser Ala Leu Val Cys Leu Ala Pro Gly Ser Glu Glu Thr
1 5 10 15

Glu Ala Val Thr Thr Ile Asp Leu Leu Ile Arg Gly Gly Ile Lys Val
            20 25 30

Thr Thr Ala Ser Val Ala Ser Asp Gly Asn Leu Ala Ile Thr Cys Ser
        35 40 45

Arg Gly Val Lys Leu Leu Ala Asp Ala Pro Leu Val Glu Val Ala Asp
    50 55 60

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

Cys Phe Arg Asp Ser Thr Leu Leu Val Glu Thr Val Lys Gln Phe His
                85 90 95

Arg Ser Gly Arg Ile Val Ala Ala Ile Cys Ala Ala Pro Ala Thr Val
            100 105 110

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

Thr Leu Lys Asp Lys Ile Pro Ala Glu Gln Trp Gln Asp Lys Arg Val
    130 135 140

Val Trp Asp Ala Arg Val Lys Leu Leu Thr Ser Gln Gly Pro Gly Thr
145 150 155 160

Ala Ile Asp Phe Gly Leu Lys Ile Ile Asp Leu Leu Val Gly Arg Glu
                165 170 175

Lys Ala His Glu Val Ala Ser Gln Leu Val Met Ala Ala Gly Ile Tyr
            180 185 190

Asn Tyr Tyr Glu
        195

<210> SEQ ID NO 100
<211> LENGTH: 172
<212> TYPE: PRT
<213> ORGANISM: Escherichia coli

<400> SEQUENCE: 100

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

Glu Phe Thr Ser Pro Ala Asp Glu Phe Arg Lys Ala Gly His Glu Val
            20 25 30

Ile Thr Ile Glu Lys Gln Ala Gly Lys Thr Val Lys Gly Lys Lys Gly
        35 40 45

Glu Ala Ser Val Thr Ile Asp Lys Ser Ile Asp Glu Val Thr Pro Ala
    50 55 60

Glu Phe Asp Ala Leu Leu Leu Pro Gly Gly His Ser Pro Asp Tyr Leu
65 70 75 80

Arg Gly Asp Asn Arg Phe Val Thr Phe Thr Arg Asp Phe Val Asn Ser
                85 90 95

Gly Lys Pro Val Phe Ala Ile Cys His Gly Pro Gln Leu Leu Ile Ser
            100 105 110

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

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Ile Asp Val Lys Asn Ala Gly Ala Glu Phe Tyr Asp Gln Glu Val Val
    130                 135                 140

Val Asp Lys Asp Gln Leu Val Thr Ser Arg Thr Pro Asp Asp Leu Pro
145                 150                 155                 160

Ala Phe Asn Arg Glu Ala Leu Arg Leu Leu Gly Ala
                165                 170


<210> SEQ ID NO 101
<211> LENGTH: 329
<212> TYPE: PRT
<213> ORGANISM: Glycine max

<400> SEQUENCE: 101

Met Ala Pro Lys Lys Val Leu Leu Leu Cys Gly Asp Phe Met Glu Asp
1               5                   10                  15

Tyr Glu Ala Met Val Pro Phe Gln Ala Leu Gln Ala Phe Gly Leu Ala
            20                  25                  30

Val Asp Ala Val Cys Pro Gly Lys Lys Ser Gly Asp Val Cys Arg Thr
        35                  40                  45

Ala Val His Val Leu Ala Gly Ala Gln Thr Tyr Ser Glu Thr Val Gly
    50                  55                  60

His Asn Phe Ser Leu Asn Ala Thr Phe Asp Glu Val Asp Ala Ala Ser
65                  70                  75                  80

Tyr Asp Gly Leu Trp Val Pro Gly Gly Arg Ala Pro Glu Tyr Leu Ala
                85                  90                  95

His Val Pro Gly Val Val Glu Leu Val Thr Lys Phe Val Ser Leu Gly
            100                 105                 110

Lys Gln Ile Ala Ser Ile Cys His Gly Gln Leu Ile Leu Ala Ala Ala
        115                 120                 125

Gly Val Val Lys Gly Arg Thr Cys Thr Ala Phe Pro Pro Val Lys Pro
    130                 135                 140

Val Leu Val Ala Ala Gly Ala His Trp Val Glu Pro Asp Thr Glu Ala
145                 150                 155                 160

Ala Thr Val Val Asp Gly Asp Leu Ile Thr Ala Ala Thr Tyr Glu Gly
                165                 170                 175

His Pro Glu Leu Ile Arg His Phe Val Lys Ala Leu Gly Gly Lys Ile
            180                 185                 190

Ser Gly Phe Asp Lys Lys Ile Leu Phe Ile Cys Gly Asp Tyr Met Glu
        195                 200                 205

Asp Tyr Glu Val Lys Val Pro Phe Gln Ser Leu Gln Ala Leu Gly Cys
    210                 215                 220

His Val Asp Ala Val Cys Pro Ser Lys Lys Ala Gly Asp Thr Cys Pro
225                 230                 235                 240

Thr Ala Val His Asp Phe Glu Gly Asp Gln Thr Tyr Ser Glu Lys Pro
                245                 250                 255

Gly His Thr Phe Ala Leu Thr Ala Thr Phe Asp Asp Val Asp Pro Ser
            260                 265                 270

Gly Tyr Asp Ala Leu Val Ile Pro Gly Gly Arg Ala Pro Glu Tyr Leu
        275                 280                 285

Ala Leu Asn Glu Ser Val Ile Ala Leu Val Lys Tyr Phe Phe Glu Asn
    290                 295                 300

Lys Lys Pro Val Ala Ser Ile Cys His Gly Gln Gln Ile Leu Ser Ala
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305                 310                 315                 320

Ala Gly Val Leu Lys Val Leu Leu Leu
                325


<210> SEQ ID NO 102
<211> LENGTH: 169
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 102

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

Met Glu Thr Val Ile Pro Val Asp Val Met Arg Arg Ala Gly Ile Lys
            20                  25                  30

Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys Ser Arg
        35                  40                  45

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

Ser Ala Ala Val Lys Glu Ile Leu Lys Glu Gln Glu Asn Arg Lys Gly
65                  70                  75                  80

Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr Ala Leu Leu Ala His Glu
                85                  90                  95

Ile Gly Phe Gly Ser Lys Val Thr Thr His Pro Leu Ala Lys Asp Lys
            100                 105                 110

Met Met Asn Gly Gly His Tyr Thr Tyr Ser Glu Asn Arg Val Glu Lys
        115                 120                 125

Asp Gly Leu Ile Leu Thr Ser Arg Gly Pro Gly Thr Ser Phe Glu Phe
    130                 135                 140

Ala Leu Ala Ile Val Glu Ala Leu Asn Gly Lys Glu Val Ala Ala Gln
145                 150                 155                 160

Val Lys Ala Pro Leu Val Leu Lys Asp
                165


<210> SEQ ID NO 103
<211> LENGTH: 135
<212> TYPE: PRT
<213> ORGANISM: Mus musculus

<400> SEQUENCE: 103

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

Met Glu Thr Val Ile Pro Val Asp Val Met Arg Arg Ala Gly Ile Lys
            20                  25                  30

Val Thr Val Ala Gly Leu Ala Gly Lys Asp Pro Val Gln Cys Ser Arg
        35                  40                  45

Asp Val Met Ile Cys Pro Asp Thr Ser Leu Glu Asp Ala Lys Thr Gln
    50                  55                  60

Gly Pro Tyr Asp Val Val Val Leu Pro Gly Gly Asn Leu Gly Ala Gln
65                  70                  75                  80

Asn Leu Ser Glu Ser Pro Met Val Lys Glu Ile Leu Lys Glu Gln Glu
                85                  90                  95

Ser Arg Lys Gly Leu Ile Ala Ala Ile Cys Ala Gly Pro Thr Ala Leu
            100                 105                 110

Leu Ala His Glu Val Gly Phe Gly Cys Lys Val Thr Thr His Pro Leu
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        115                 120                 125

Ala Lys Asp Lys Met Met Asn
    130                 135


<210> SEQ ID NO 104
<211> LENGTH: 454
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 104

Met Leu Pro Ser Ser Arg Tyr Leu Leu Ala Pro Ala Pro Leu Pro Ala
1               5                   10                  15

Met Val Val Arg Pro Pro Pro Pro His Pro Pro Ser Arg Gly Thr Ser
            20                  25                  30

Pro Leu Ala Arg Pro Pro Leu Cys Arg Ala Met Ala Arg Ala Ala Pro
        35                  40                  45

Ser Leu Ser Ala Ala Ala Ser Thr Ala Ala Ser Ser Ser Thr Thr Pro
    50                  55                  60

Ala Lys Lys Lys Val Leu Leu Pro Ile Ala Met Gly Thr Glu Glu Met
65                  70                  75                  80

Glu Ala Val Ile Leu Ala Gly Val Leu Arg Arg Ala Gly Ala Asp Val
                85                  90                  95

Thr Leu Ala Ser Val Glu Asp Gly Leu Glu Val Glu Ala Ser Arg Gly
            100                 105                 110

Ser His Ile Val Ala Asp Lys Arg Ile Ala Ala Cys Ala Asp Gln Val
        115                 120                 125

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

Arg Asp Ser Val Ile Leu Gln Arg Ile Thr Val Arg Gln Ala Glu Glu
145                 150                 155                 160

Lys Arg Leu Tyr Gly Ala Ile Cys Ala Ala Pro Ala Val Val Leu Met
                165                 170                 175

Pro Trp Gly Leu His Lys Arg Lys Lys Ile Thr Cys His Pro Ser Phe
            180                 185                 190

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

Ser Gly Glu Leu Thr Thr Ser Arg Gly Pro Gly Thr Ala Phe Gln Phe
    210                 215                 220

Ala Leu Ser Phe Val Glu Gln Leu Phe Gly Pro Cys Lys Ala Glu Asp
225                 230                 235                 240

Met Asp Asn Thr Leu Leu Thr Lys Val Asp Asp Asn Leu Glu Arg Ser
                245                 250                 255

Ile Glu Val Asn Glu Ile Glu Trp Ser Ser Asp His Asn Pro His Val
            260                 265                 270

Leu Ile Pro Ile Ala Asn Gly Ser Glu Glu Met Glu Ile Ile Met Leu
        275                 280                 285

Thr Asp Val Leu Arg Arg Ala Asn Val Asn Val Val Leu Ala Ser Val
    290                 295                 300

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

Asp Lys Cys Ile Ser Asp Ala Ser Ala Leu Glu Tyr Asp Leu Ile Ile
                325                 330                 335
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Leu Pro Gly Gly Pro Ala Gly Ala Glu Arg Leu His Lys Ser Ser Val
            340                 345                 350

Leu Lys Lys Leu Leu Lys Glu Gln Lys Gln Thr Gly Arg Met Tyr Gly
        355                 360                 365

Gly Ile Cys Ser Ser Pro Val Ile Leu Gln Lys Gln Gly Leu Leu Gln
    370                 375                 380

Asp Lys Thr Val Thr Ala His Pro Ser Ile Val Asn Gln Leu Thr Cys
385                 390                 395                 400

Glu Val Ile Asp Arg Ser Lys Val Val Ile Asp Gly Asn Leu Ile Thr
                405                 410                 415

Gly Met Gly Leu Gly Thr Val Ile Asp Phe Ser Leu Ala Ile Ile Lys
            420                 425                 430

Lys Phe Phe Gly His Gly Arg Ala Lys Gly Val Ala Asn Gly Met Val
        435                 440                 445

Phe Glu Tyr Pro Lys Ser
    450


<210> SEQ ID NO 105
<211> LENGTH: 238
<212> TYPE: PRT
<213> ORGANISM: Oryza sativa

<400> SEQUENCE: 105

Met Leu Pro Ser Ser Arg Tyr Leu Leu Ala Pro Ala Pro Leu Pro Ala
1               5                   10                  15

Met Val Val Arg Pro Pro Pro Pro His Pro Pro Ser Arg Gly Thr Ser
            20                  25                  30

Pro Leu Ala Arg Pro Pro Leu Cys Arg Ala Met Ala Arg Ala Ala Pro
        35                  40                  45

Ser Leu Ser Ala Ala Ala Ser Thr Ala Ala Ser Ser Ser Thr Thr Pro
    50                  55                  60

Ala Lys Lys Lys Val Leu Leu Pro Ile Ala Met Gly Thr Glu Glu Met
65                  70                  75                  80

Glu Ala Val Ile Leu Ala Gly Val Leu Arg Arg Ala Gly Ala Asp Val
                85                  90                  95

Thr Leu Ala Ser Val Glu Asp Gly Leu Glu Val Glu Ala Ser Arg Gly
            100                 105                 110

Ser His Ile Val Ala Asp Lys Arg Ile Ala Ala Cys Ala Asp Gln Val
        115                 120                 125

Phe Asp Leu Val Ala Leu Pro Leu Thr Lys Val Asp Asp Asn Leu Glu
    130                 135                 140

Arg Ser Ile Glu Val Asn Glu Ile Glu Trp Ser Ser Asp His Asn Pro
145                 150                 155                 160

His Val Leu Ile Pro Ile Ala Asn Gly Ser Glu Glu Met Glu Ile Ile
                165                 170                 175

Met Leu Thr Asp Val Leu Arg Arg Ala Asn Val Asn Val Val Leu Ala
            180                 185                 190

Ser Val Glu Lys Ser Thr Ser Ile Val Gly Ser Gln Arg Met Arg Ile
        195                 200                 205

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

Ile Ile Leu Pro Val Ser Tyr Phe Ser Phe His Ile Phe Ile
225                 230                 235
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<210> SEQ ID NO 106
<211> LENGTH: 189
<212> TYPE: PRT
<213> ORGANISM: Plasmodium falciparum 3D7

<400> SEQUENCE: 106

Met Ser Gly Lys Lys Thr Ala Leu Val Ala Val Ala Ser Gly Ser Glu
1 5 10 15

Asp Val Glu Tyr Ile Thr Val Val Asp Val Leu Arg Arg Ala Gly Val
            20 25 30

His Val Thr Thr Ala Ser Val Glu Lys Ser Glu Gln Val Cys Leu Gln
        35 40 45

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

Asn Ile Tyr Asp Val Leu Val Ile Pro Gly Gly Met Lys Gly Ser Asn
65 70 75 80

Thr Ile Ser Glu Cys Ser Glu Phe Ile Asp Met Leu Lys Glu Gln Lys
                85 90 95

Ala Asn Asn Arg Leu Tyr Ala Ala Ile Cys Ala Ala Pro Glu Thr Val
            100 105 110

Leu Asp Arg His Ser Leu Ile Asp Asp Val Glu Ala Val Ala Tyr Pro
        115 120 125

Ser Phe Glu Arg Asn Phe Lys His Ile Gly Lys Gly Arg Val Cys Val
    130 135 140

Ser Lys Asn Cys Ile Thr Ser Val Gly Pro Gly Ser Ala Val Glu Phe
145 150 155 160

Gly Leu Lys Ile Val Glu His Leu Leu Gly Arg Gln Val Ala Leu Ser
                165 170 175

Leu Ala Ser Gly Phe Leu Leu His Pro Ala Val Thr Phe
            180 185

<210> SEQ ID NO 107
<211> LENGTH: 215
<212> TYPE: PRT
<213> ORGANISM: Pseudomonas aeruginosa

<400> SEQUENCE: 107

Met Gly Arg Ala Ser Thr Gly Lys Ala Ala Pro Gly Asn Gly His Gly
1 5 10 15

Thr Phe Pro Ala Ala Ala Arg Val Gly Met Asn Thr Pro Ser Asp Ile
            20 25 30

Gly Arg His Ala Met Thr Gln Ser Leu His Gly Lys Val Val Ala Ala
        35 40 45

Leu Val Thr Asp Gly Phe Glu Gln Val Glu Leu Thr Gly Pro Lys Lys
    50 55 60

Ala Leu Glu Asp Ala Gly Ala Thr Val Arg Ile Leu Ser Asp Lys Ala
65 70 75 80

Gly Glu Val Arg Gly Trp Asn His His Gln Pro Ala Glu Ala Phe Arg
                85 90 95

Val Asp Gly Thr Phe Glu Asp Ala Ser Leu Asp Asp Tyr Asp Ala Leu
            100 105 110

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

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

Ala Val Ile Cys His Gly Ala Trp Leu Leu Ile Ser Ala Gly Leu Val
145                 150                 155                 160

Gln Gly Arg Thr Leu Thr Ser Trp Pro Ser Leu Lys Asp Asp Ile Asn
                165                 170                 175

Asn Ala Gly Gly His Trp Val Asp Gln Glu Val Ala Val Asp Gly Lys
            180                 185                 190

Leu Val Ser Ser Arg Lys Pro Glu Asp Ile Pro Ala Phe Asn Arg Arg
        195                 200                 205

Phe Ile Glu Ile Leu Ala Gly
    210                 215


<210> SEQ ID NO 108
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Pyrococcus furiosus

<400> SEQUENCE: 108

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

Ile Tyr Pro Tyr His Arg Leu Lys Glu Glu Gly His Glu Val Tyr Ile
            20                  25                  30

Ala Ser Phe Glu Lys Gly Val Ile Thr Gly Lys His Gly Tyr Ser Val
        35                  40                  45

Lys Val Asp Leu Thr Phe Asp Glu Val Asn Pro Asp Glu Phe Asp Ala
    50                  55                  60

Leu Val Leu Pro Gly Gly Arg Ala Pro Glu Arg Val Arg Leu Asn Glu
65                  70                  75                  80

Lys Ala Val Glu Ile Ala Arg Lys Met Phe Thr Glu Gly Lys Pro Val
                85                  90                  95

Ala Thr Ile Cys His Gly Pro Gln Ile Leu Ile Ser Ala Gly Val Leu
            100                 105                 110

Lys Gly Arg Lys Gly Thr Ser Tyr Ile Gly Ile Arg Asp Asp Met Ile
        115                 120                 125

Asn Ala Gly Val Glu Trp Ile Asp Arg Glu Val Val Val Asp Gly Asn
    130                 135                 140

Trp Val Ser Ser Arg His Pro Gly Asp Leu Tyr Ala Trp Met Arg Glu
145                 150                 155                 160

Phe Val Lys Leu Leu Lys
                165


<210> SEQ ID NO 109
<211> LENGTH: 166
<212> TYPE: PRT
<213> ORGANISM: Pyrococcus horikoshii

<400> SEQUENCE: 109

Met Lys Val Leu Phe Leu Thr Ala Asn Glu Phe Glu Asp Val Glu Leu
1               5                   10                  15

Ile Tyr Pro Tyr His Arg Leu Lys Glu Glu Gly His Glu Val Tyr Ile
            20                  25                  30

Ala Ser Phe Glu Arg Gly Thr Ile Thr Gly Lys His Gly Tyr Ser Val
        35                  40                  45
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Lys Val Asp Leu Thr Phe Asp Lys Val Asn Pro Glu Glu Phe Asp Ala
    50                  55                  60

Leu Val Leu Pro Gly Gly Arg Ala Pro Glu Arg Val Arg Leu Asn Glu
65                  70                  75                  80

Lys Ala Val Ser Ile Ala Arg Lys Met Phe Ser Glu Gly Lys Pro Val
                85                  90                  95

Ala Ser Ile Cys His Gly Pro Gln Ile Leu Ile Ser Ala Gly Val Leu
            100                 105                 110

Arg Gly Arg Lys Gly Thr Ser Tyr Pro Gly Ile Lys Asp Asp Met Ile
        115                 120                 125

Asn Ala Gly Val Glu Trp Val Asp Ala Glu Val Val Val Asp Gly Asn
    130                 135                 140

Trp Val Ser Ser Arg Val Pro Ala Asp Leu Tyr Ala Trp Met Arg Glu
145                 150                 155                 160

Phe Val Lys Leu Leu Lys
                165


<210> SEQ ID NO 110
<211> LENGTH: 245
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 110

Met Ala Pro Lys Lys Val Leu Leu Ala Leu Thr Ser Tyr Asn Asp Val
1               5                   10                  15

Phe Tyr Ser Asp Gly Ala Lys Thr Gly Val Phe Val Val Glu Ala Leu
            20                  25                  30

His Pro Phe Asn Thr Phe Arg Lys Glu Gly Phe Glu Val Asp Phe Val
        35                  40                  45

Ser Glu Thr Gly Lys Phe Gly Trp Asp Glu His Ser Leu Ala Lys Asp
    50                  55                  60

Phe Leu Asn Gly Gln Asp Glu Thr Asp Phe Lys Asn Lys Asp Ser Asp
65                  70                  75                  80

Phe Asn Lys Thr Leu Ala Lys Ile Lys Thr Pro Lys Glu Val Asn Ala
                85                  90                  95

Asp Asp Tyr Gln Ile Phe Phe Ala Ser Ala Gly His Gly Thr Leu Phe
            100                 105                 110

Asp Tyr Pro Lys Ala Lys Asp Leu Gln Asp Ile Ala Ser Glu Ile Tyr
        115                 120                 125

Ala Asn Gly Gly Val Val Ala Ala Val Cys His Gly Pro Ala Ile Phe
    130                 135                 140

Asp Gly Leu Thr Asp Lys Lys Thr Gly Arg Pro Leu Ile Glu Gly Lys
145                 150                 155                 160

Ser Ile Thr Gly Phe Thr Asp Val Gly Glu Thr Ile Leu Gly Val Asp
                165                 170                 175

Ser Ile Leu Lys Ala Lys Asn Leu Ala Thr Val Glu Asp Val Ala Lys
            180                 185                 190

Lys Tyr Gly Ala Lys Tyr Leu Ala Pro Val Gly Pro Trp Asp Asp Tyr
        195                 200                 205

Ser Ile Thr Asp Gly Arg Leu Val Thr Gly Val Asn Pro Ala Ser Ala
    210                 215                 220

His Ser Thr Ala Val Arg Ser Ile Val Ala Leu Lys Asn Leu Glu His
```

-continued

225 230 235 240

His His His His His
245

<210> SEQ ID NO 111
<211> LENGTH: 237
<212> TYPE: PRT
<213> ORGANISM: Saccharomyces cerevisiae

<400> SEQUENCE: 111

Met Ala Pro Lys Lys Val Leu Leu Ala Leu Thr Ser Tyr Asn Asp Val
1 5 10 15

Phe Tyr Ser Asp Gly Met Lys Thr Gly Val Phe Val Val Glu Ala Leu
20 25 30

His Pro Phe Asn Thr Phe Arg Lys Glu Gly Phe Glu Val Asp Phe Val
35 40 45

Ser Glu Thr Gly Lys Phe Gly Trp Asp Glu His Ser Leu Ala Lys Asp
50 55 60

Phe Leu Asn Gly Gln Asp Glu Thr Asp Phe Lys Asn Lys Asp Ser Asp
65 70 75 80

Phe Asn Lys Thr Leu Ala Lys Ile Lys Thr Pro Lys Glu Val Asn Ala
85 90 95

Asp Asp Tyr Gln Ile Phe Met Ala Ser Ala Gly His Gly Thr Leu Phe
100 105 110

Asp Tyr Pro Lys Ala Lys Asp Leu Gln Asp Ile Ala Ser Glu Ile Tyr
115 120 125

Ala Asn Gly Gly Val Val Ala Ala Val Cys His Gly Pro Ala Met Phe
130 135 140

Asp Gly Leu Thr Asp Lys Lys Thr Gly Arg Pro Leu Ile Glu Gly Lys
145 150 155 160

Ser Ile Thr Gly Phe Thr Asp Val Gly Glu Thr Ile Met Gly Val Asp
165 170 175

Ser Ile Leu Lys Ala Lys Asn Leu Ala Thr Val Glu Asp Val Ala Lys
180 185 190

Lys Tyr Gly Ala Lys Tyr Leu Ala Pro Val Gly Pro Trp Asp Asp Tyr
195 200 205

Ser Ile Thr Asp Gly Arg Leu Val Thr Gly Val Asn Pro Ala Ser Ala
210 215 220

His Ser Thr Ala Val Arg Ser Ile Asp Ala Leu Lys Asn
225 230 235

<210> SEQ ID NO 112
<211> LENGTH: 191
<212> TYPE: PRT
<213> ORGANISM: Schizosaccharomyces pombe

<400> SEQUENCE: 112

Met Val Lys Val Cys Leu Phe Val Ala Asp Gly Thr Asp Glu Ile Glu
1 5 10 15

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

Ser Val Tyr Val Gly Glu Asn Lys Asp Arg Leu Val Lys Met Ser Arg
35 40 45

Asp Val Glu Met Tyr Ala Asn Arg Ser Tyr Lys Glu Ile Pro Ser Ala

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    50                  55                  60

Asp Asp Phe Ala Lys Gln Tyr Asp Ile Ala Ile Ile Pro Gly Gly Gly
65                  70                  75                  80

Leu Gly Ala Lys Thr Leu Ser Thr Thr Pro Phe Val Gln Gln Val Val
                85                  90                  95

Lys Glu Phe Tyr Lys Lys Pro Asn Lys Trp Ile Gly Met Ile Cys Ala
            100                 105                 110

Gly Thr Leu Thr Ala Lys Thr Ser Gly Leu Pro Asn Lys Gln Ile Thr
        115                 120                 125

Gly His Pro Ser Val Arg Gly Gln Leu Glu Glu Gly Gly Tyr Lys Tyr
    130                 135                 140

Leu Asp Gln Pro Val Val Leu Glu Glu Asn Leu Ile Thr Ser Gln Gly
145                 150                 155                 160

Pro Gly Thr Ala Met Leu Phe Gly Leu Lys Leu Leu Glu Gln Val Ala
                165                 170                 175

Ser Lys Asp Lys Tyr Asn Ala Val Tyr Lys Ser Leu Ser Met Pro
            180                 185                 190


<210> SEQ ID NO 113
<211> LENGTH: 547
<212> TYPE: PRT
<213> ORGANISM: Lactococcus lactis

<400> SEQUENCE: 113

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

Ile Glu Glu Ile Phe Gly Val Pro Gly Asp Tyr Asn Leu Gln Phe Leu
            20                  25                  30

Asp Gln Ile Ile Ser Arg Glu Asp Met Lys Trp Ile Gly Asn Ala Asn
        35                  40                  45

Glu Leu Asn Ala Ser Tyr Met Ala Asp Gly Tyr Ala Arg Thr Lys Lys
    50                  55                  60

Ala Ala Ala Phe Leu Thr Thr Phe Gly Val Gly Glu Leu Ser Ala Ile
65                  70                  75                  80

Asn Gly Leu Ala Gly Ser Tyr Ala Glu Asn Leu Pro Val Val Glu Ile
                85                  90                  95

Val Gly Ser Pro Thr Ser Lys Val Gln Asn Asp Gly Lys Phe Val His
            100                 105                 110

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

Pro Val Thr Ala Ala Arg Thr Leu Leu Thr Ala Glu Asn Ala Thr Tyr
    130                 135                 140

Glu Ile Asp Arg Val Leu Ser Gln Leu Leu Lys Glu Arg Lys Pro Val
145                 150                 155                 160

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

Ala Leu Ser Leu Glu Lys Glu Ser Ser Thr Thr Asn Thr Thr Glu Gln
            180                 185                 190

Val Ile Leu Ser Lys Ile Glu Glu Ser Leu Lys Asn Ala Gln Lys Pro
        195                 200                 205

Val Val Ile Ala Gly His Glu Val Ile Ser Phe Gly Leu Glu Lys Thr
    210                 215                 220
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Val Thr Gln Phe Val Ser Glu Thr Lys Leu Pro Ile Thr Thr Leu Asn
225                 230                 235                 240

Phe Gly Lys Ser Ala Val Asp Glu Ser Leu Pro Ser Phe Leu Gly Ile
                245                 250                 255

Tyr Asn Gly Lys Leu Ser Glu Ile Ser Leu Lys Asn Phe Val Glu Ser
            260                 265                 270

Ala Asp Phe Ile Leu Met Leu Gly Val Lys Leu Thr Asp Ser Ser Thr
        275                 280                 285

Gly Ala Phe Thr His His Leu Asp Glu Asn Lys Met Ile Ser Leu Asn
    290                 295                 300

Ile Asp Glu Gly Ile Ile Phe Asn Lys Val Val Glu Asp Phe Asp Phe
305                 310                 315                 320

Arg Ala Val Val Ser Ser Leu Ser Glu Leu Lys Gly Ile Glu Tyr Glu
                325                 330                 335

Gly Gln Tyr Ile Asp Lys Gln Tyr Glu Glu Phe Ile Pro Ser Ser Ala
            340                 345                 350

Pro Leu Ser Gln Asp Arg Leu Trp Gln Ala Val Glu Ser Leu Thr Gln
        355                 360                 365

Ser Asn Glu Thr Ile Val Ala Glu Gln Gly Thr Ser Phe Phe Gly Ala
    370                 375                 380

Ser Thr Ile Phe Leu Lys Ser Asn Ser Arg Phe Ile Gly Gln Pro Leu
385                 390                 395                 400

Trp Gly Ser Ile Gly Tyr Thr Phe Pro Ala Ala Leu Gly Ser Gln Ile
                405                 410                 415

Ala Asp Lys Glu Ser Arg His Leu Leu Phe Ile Gly Asp Gly Ser Leu
            420                 425                 430

Gln Leu Thr Val Gln Glu Leu Gly Leu Ser Ile Arg Glu Lys Leu Asn
        435                 440                 445

Pro Ile Cys Phe Ile Ile Asn Asn Asp Gly Tyr Thr Val Glu Arg Glu
    450                 455                 460

Ile His Gly Pro Thr Gln Ser Tyr Asn Asp Ile Pro Met Trp Asn Tyr
465                 470                 475                 480

Ser Lys Leu Pro Glu Thr Phe Gly Ala Thr Glu Asp Arg Val Val Ser
                485                 490                 495

Lys Ile Val Arg Thr Glu Asn Glu Phe Val Ser Val Met Lys Glu Ala
            500                 505                 510

Gln Ala Asp Val Asn Arg Met Tyr Trp Ile Glu Leu Val Leu Glu Lys
        515                 520                 525

Glu Asp Ala Pro Lys Leu Leu Lys Lys Met Gly Lys Leu Phe Ala Glu
    530                 535                 540

Gln Asn Lys
545
```

1. A system for the production of high value chemicals, comprising:

(a) an input selected from the group consisting of ethylene glycol, glycerol, ethanol methanol and a combination thereof;

(b) an oxidation biocatalyst comprising an alcohol oxidase, a copper radical oxidase, a glycerol oxidase, an alditol oxidase or a combination thereof;

(c) an oxidized intermediate;

(d) a finishing catalyst comprising a supported metal catalyst, a carboligating catalyst, an amine oxidase, a glyoxalase, an acid catalyst, a base catalyst, an isomerization catalyst or a combination thereof; and

(e) an output.

2. The system of claim **1**, wherein the alcohol oxidase has any of SEQ ID NO: 1 to SEQ ID NO: 71.

3. The system of claim **1**, wherein the carboligating catalyst has any of SEQ ID NO: 72 to SEQ ID NO: 86.

4. The system of claim **1**, wherein the carboligating catalyst has SEQ ID NO: 113.

5. The system of claim **1**, wherein the amine oxidase has any of SEQ ID NO: 87 to SEQ ID NO: 90.

6. The system of claim **1**, wherein the glyoxalase has any of SEQ ID NO: 91 to SEQ ID NO: 112.

7. The system of claim **1**, wherein the supported metal catalyst comprises a nanoparticle support.

8. The system of claim **1**, wherein the support of the supported metal catalyst comprises the support comprises carbon, silica, surface treated alumina, titania (TiO_2), zirconia (ZrO_2), a zeolite, montmorillonites, or a combination thereof.

9. The system of claim **1**, wherein the supported metal catalyst comprises a Group 8 metal, a 3d transition metal, an early transition metal, or combinations thereof.

10. The system of claim **1**, wherein the supported metal catalyst comprises gold, platinum or a combination thereof.

11. The system of claim **1**, wherein the carboligating catalyst comprises pyruvate decarboxylase, formolase, the E1 component of α-ketoglutarate dehydrogenase complex from SucA, the KdcA gene product of *Lactococcus lactis*, a cofactor, or a combination thereof.

12. The system of claim **1**, wherein (i) the input comprises methanol; (ii) the oxidation biocatalyst comprises an alcohol oxidase; (iii) the intermediate comprises formaldehyde; (iv) the finishing catalyst comprises urea; and (v) the output comprises a urea formaldehyde polymer.

13. The system of claim **1**, further comprising a catalase.

14. The system of claim **1**, wherein (i) the input comprises glycerol; (ii) the oxidation biocatalyst comprises a glycerol oxidase; (iii) the oxidized intermediate comprises L-glyceraldehyde; (iv) the finishing catalyst comprises an acid catalyst; and (v) the output comprises D-lactate.

15. The system of claim **1**, wherein (i) the input comprises ethylene glycol; (ii) the oxidation biocatalyst comprises a copper radical oxidase, a galactose oxidase, an alcohol oxidase, a glycerol oxidase or a combination thereof; (iii) the oxidized intermediate comprises a glycolaldehyde; (iv) the finishing catalyst comprises an amine monooxidase; and (v) the output comprises ethanolamine.

16. The system of claim **1**, wherein (i) the input comprises ethylene glycol; (ii) the oxidation biocatalyst comprises an ethylene glycol oxidase; (iii) the oxidized intermediate comprises a glycolaldehyde; (iv) the finishing catalyst comprises a carboligating catalyst, a supported metal catalyst or a combination thereof; and (v) the output comprises glycerol.

17. The system of claim **1**, wherein (i) the input comprises ethanol; (ii) the oxidation biocatalyst comprises an alcohol oxidase; (iii) the oxidized intermediate and (iv) the output comprises an acetaldehyde.

18. The system of claim **17**, further comprising a catalase.

19. The system of claim **1**, wherein (i) the input comprises glycerol; (ii) the oxidation biocatalyst comprises an alcohol oxidase, an alditol oxidase, a copper-radical oxidase, a glycerol oxidase or a combination thereof; (iii) the oxidized intermediate comprises glyceraldehyde; (iv) the finishing catalyst comprises an isomerization catalyst; and (v) the output comprises dihydroxyacetone.

20. The system of claim **1**, wherein the output has a percentage purity of from about 60% to about 95%.

21. A method for the production of high value chemicals, comprising:

(a) contacting an input selected from the group consisting of ethylene glycol, glycerol, ethanol methanol and a combination thereof with an oxidation biocatalyst comprising an alcohol oxidase, a copper radical oxidase, a glycerol oxidase, an alditol oxidase or a combination thereof to form an oxidized intermediate;

(b) contacting the oxidized intermediate with a finishing catalyst comprising a supported metal catalyst, a carboligating catalyst, an amine oxidase, a glyoxalase, an acid catalyst, a base catalyst, an isomerization catalyst or a combination thereof to form an output.

22. The method of claim **21**, wherein the alcohol oxidase has any of SEQ ID NO: 1 to SEQ ID NO: 71.

23. The method of claim **21**, wherein the carboligating catalyst has any of SEQ ID NO: 72 to SEQ ID NO: 86.

24. The method of claim **21**, wherein the carboligating catalyst has SEQ ID NO: 113.

25. The method of claim **21**, wherein the amine oxidase has any of SEQ ID NO: 87 to SEQ ID NO: 90.

26. The method of claim **21**, wherein the glyoxalase has any of SEQ ID NO: 91 to SEQ ID NO: 112.

27. The method of claim **21**, wherein the supported metal catalyst comprises a nanoparticle support.

28. The method of claim **21**, wherein the carboligating catalyst comprises pyruvate decarboxylase, formolase, the E1 component of α-ketoglutarate dehydrogenase complex from SucA, the KdcA gene product of *Lactococcus lactis*, a cofactor, or a combination thereof.

29. The method of claim **21**, wherein the output has a percentage purity of from about 60% to about 95%.

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