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(19) **United States**(12) **Patent Application Publication** (10) **Pub. No.: US 2025/0261668 A1****LIU et al.**(43) **Pub. Date:** **Aug. 21, 2025**(54) **ANIMAL FEED COMPOSITION AND USES  
THEREOF**

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**ABSTRACT**

Recombinant host cells comprising a nucleic acid construct or expression vector comprising a polynucleotide encoding a polypeptide having lysozyme activity and at least 80% sequence identity to SEQ ID NO: 264, as well as methods of producing polypeptides having lysozyme activity and at least 80% sequence identity to SEQ ID NO: 264 and compositions comprising polypeptides having lysozyme activity and at least 80% sequence identity to SEQ ID NO: 264.

**Specification includes a Sequence Listing.**

## ANIMAL FEED COMPOSITION AND USES THEREOF

### CROSS-REFERENCE TO RELATED APPLICATIONS

[0001] This application is a continuation of U.S. patent application Ser. No. 17/153,096, filed Jan. 20, 2021, which is a divisional of U.S. patent application Ser. No. 15/579,769, filed Dec. 5, 2017, and issued as U.S. Pat. No. 10,945,449 on Mar. 16, 2021, which is a national stage entry of PCT/CN2016/088362, filed Jul. 4, 2016, which claims priority to European Patent Application No. 15175030.4, filed Jul. 2, 2015. The contents of the aforementioned applications are fully incorporated herein by reference.

### REFERENCE TO A SEQUENCE LISTING

[0002] This application contains a Sequence Listing in computer readable form, which is incorporated herein by reference. The name of the file containing the Sequence Listing is "SQ.xml", which was created on May 7, 2025, and which contains 337,671 bytes.

### BACKGROUND OF THE INVENTION

#### Field of the Invention

[0003] The present invention relates animal feed or animal feed additives comprising one or more polypeptides having lysozyme activity. The invention also relates to polypeptides having lysozyme activity, polynucleotides encoding the polypeptides nucleic acid constructs, vectors, and host cells comprising the polynucleotides as well as methods of producing and using the polypeptides.

#### Description of the Related Art

[0004] Lysozyme is an O-glycosyl hydrolase produced as a defensive mechanism against bacteria by many organisms. The enzyme causes the hydrolysis of bacterial cell walls by cleaving the glycosidic bonds of peptidoglycan; an important structural molecule in bacteria. After having their cell walls weakened by lysozyme action, bacterial cells lyse as a result of unbalanced osmotic pressure.

[0005] Lysozyme naturally occurs in many organisms such as viruses, plants, insects, birds, reptiles and mammals. In mammals, Lysozyme has been isolated from nasal secretions, saliva, tears, intestinal content, urine and milk. The enzyme cleaves the glycosidic bond between carbon number 1 of N-acetylmuramic acid and carbon number 4 of N-acetyl-D-glucosamine. In vivo, these two carbohydrates are polymerized to form the cell wall polysaccharide of many microorganisms.

[0006] Lysozyme has been classified into five different glycoside hydrolase (GH) families (CAZy, cazy.org): hen egg-white lysozyme (GH22), goose egg-white lysozyme (GH23), bacteriophage T4 lysozyme (GH24), *Sphingomonas* flagellar protein (GH73) and *Chalaropsis* lysozymes (GH25). Lysozymes from the families GH23 and GH24 are primarily known from bacteriophages and have only recently been identified in fungi. The lysozyme family GH25 has been found to be structurally unrelated to the other lysozyme families.

[0007] Lysozyme extracted from hen egg white is the primary product available on the commercial market, but does not cleave N,6-O-diacetylmuramic acid in, e.g.,

*Staphylococcus aureus* cell walls and is thus unable to lyse this important human pathogen among others (Masschalck B, Deckers D, Michiels C W (2002), "Lytic and nonlytic mechanism of inactivation of gram-positive bacteria by lysozyme under atmospheric and high hydrostatic pressure", *J Food Prot.* 65 (12): 1916-23).

[0008] WO 2012/035103 discloses variants of a GH22 lysozyme from the bird *Opisthocomus hoazin*. WO 2013/076253 and WO 2013/076259 disclose single domain GH24 and GH25 lysozymes for use in animal feed. GB 2002780 discloses the use of a lysozyme in the prophylaxis treatment of chickens. The lysozyme used was the same as isolated by Flemming in 1922 which is a GH22 lysozyme from hen egg white.

[0009] CN 101912048 discloses the use of a bacteriophage T4 lysozyme in animal feed. Bacteriophage T4 lysozymes do not comprise the same domain structure as the lysozymes of the present invention. CN 103385366 discloses the use of a lysozyme (unknown type, but based on the activity assay most likely the GH22 lysozyme from hen egg white) for use in animal feed.

[0010] Antimicrobial growth promoters (AGP's) have traditionally been used for growth promotion in animals, and probably work by preventing low level infections by pathogens such as *Clostridium perfringens*. However, AGP's are increasingly being banned worldwide and therefore new solutions to promote animal growth but which are not AGP's are of interest. The object of the present invention is to provide new and effective solutions to this problem.

### SUMMARY OF THE INVENTION

[0011] The present invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains and wherein:

[0012] (a) GH24 catalytic domain gives a domT score of at least 200 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOs: 1 to 122 and hmmbuild software program, and wherein the query is carried out using hmmscan software program with default settings; and

[0013] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of at least 100 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOs: 123 to 251 and hmmbuild software program, and wherein the query is carried out using the hmmscan software program with default settings.

[0014] The invention also relates to a polypeptide having lysozyme activity, selected from the group consisting of:

[0015] (a) a polypeptide having at least 80% sequence identity to SEQ ID NO: 257;

[0016] (b) a polypeptide having at least 95% sequence identity to SEQ ID NO: 267;

[0017] (c) a polypeptide having at least 80% sequence identity to SEQ ID NO: 291;

[0018] (d) a polypeptide having at least 80% sequence identity to SEQ ID NO: 294;

[0019] (e) a polypeptide having at least 82% sequence identity to SEQ ID NO: 297;

[0020] (f) a polypeptide having at least 80% sequence identity to SEQ ID NO: 300;

- [0021] (g) a polypeptide having at least 80% sequence identity to SEQ ID NO: 303; (g)
- [0022] (h) a polypeptide having at least 80% sequence identity to SEQ ID NO: 306;
- [0023] (i) a polypeptide encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions or very-high stringency conditions with:
- [0024] (i) the mature polypeptide coding sequence of SEQ ID NO: 255;
- [0025] (ii) the mature polypeptide coding sequence of SEQ ID NO: 287;
- [0026] (iii) the mature polypeptide coding sequence of SEQ ID NO: 292;
- [0027] (iv) the mature polypeptide coding sequence of SEQ ID NO: 295;
- [0028] (v) the mature polypeptide coding sequence of SEQ ID NO: 298;
- [0029] (vi) the mature polypeptide coding sequence of SEQ ID NO: 301;
- [0030] (vii) the mature polypeptide coding sequence of SEQ ID NO: 304;
- [0031] (viii) the cDNA sequence thereof; or
- [0032] (ix) the full-length complement of (i), (ii), (iii), (iv) (v), (vi), (vii) or (viii);
- [0033] (j) a polypeptide encoded by a polynucleotide that hybridizes under very-high stringency conditions with:
- [0034] (i) the mature polypeptide coding sequence of SEQ ID NO: 265;
- [0035] (ii) the full-length complement of (i);
- [0036] (k) a polypeptide encoded by a polynucleotide having at least 80% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 255;
- [0037] (l) a polypeptide encoded by a polynucleotide having at least 95% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 265;
- [0038] (m) a polypeptide encoded by a polynucleotide having at least 80% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 287;
- [0039] (n) a polypeptide encoded by a polynucleotide having at least 80% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 292;
- [0040] (o) a polypeptide encoded by a polynucleotide having at least 80% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 295;
- [0041] (p) a polypeptide encoded by a polynucleotide having at least 82% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 298;
- [0042] (q) a polypeptide encoded by a polynucleotide having at least 80% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 301;
- [0043] (r) a polypeptide encoded by a polynucleotide having at least 80% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 304;
- [0044] (s) a variant of SEQ ID NO: 257, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions; and
- [0045] (t) a variant of SEQ ID NO: 267, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions; and
- [0046] (u) a variant of SEQ ID NO: 291, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0047] (v) a variant of SEQ ID NO: 294, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0048] (w) a variant of SEQ ID NO: 297, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0049] (x) a variant of SEQ ID NO: 300, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0050] (y) a variant of SEQ ID NO: 303, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0051] (z) a variant of SEQ ID NO: 306, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions; and
- [0052] (aa) a fragment of the polypeptide of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k), (l), (m), (n), (o), (p), (q), (r), (s), (t), (u), (v), (w), (x), (y) or (z) that has lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids.
- [0053] The invention further relates to compositions comprising the lysozyme of the invention; use of the lysozyme of the invention in animal feed, in animal feed additives, in

the preparation of a composition for use in animal feed, for improving one or more performance parameters in an animal, for the treatment of *Clostridium perfringens* infection in an animal; for the treatment of *necrotic enteritis*, and as a medicament; methods of treatment of a *Clostridium perfringens* infection and/or *necrotic enteritis* in an animal; method of improving the performance of an animal; and isolated polynucleotides encoding the polypeptides of the invention.

#### Overview of Sequence Listing

- [0054] SEQ ID NO: 1 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A6R5W4 from *Ajellomyces Capsulatus*.
- [0055] SEQ ID NO: 2 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A8PEU5 from *Coprinopsis cinerea*.
- [0056] SEQ ID NO: 3 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:Q0CMX2 from *Aspergillus terreus*.
- [0057] SEQ ID NO: 4 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:QOD1K1 from *Aspergillus terreus*.
- [0058] SEQ ID NO: 5 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:Q2TXN3 from *Aspergillus oryzae*.
- [0059] SEQ ID NO: 6 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:Q2UFQ2 from *Aspergillus oryzae*.
- [0060] SEQ ID NO: 7 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:Q5B9R 1 from *Emericella nidulans*.
- [0061] SEQ ID NO: 8 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:B0DQF 7 from *Laccaria bicolor*.
- [0062] SEQ ID NO: 9 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:B8NGV0 from *Aspergillus flavus*.
- [0063] SEQ ID NO: 10 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:B8NVG8 from *Aspergillus flavus*.
- [0064] SEQ ID NO: 11 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C0NHY3 from *Ajellomyces capsulatus*.
- [0065] SEQ ID NO: 12 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C5FQ03 from *Arthroderma otiae*.
- [0066] SEQ ID NO: 13 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C5FZ72 from *Arthroderma otiae*.
- [0067] SEQ ID NO: 14 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C5GQK2 from *Ajellomyces dermatitidis*.
- [0068] SEQ ID NO: 15 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C6H5Y9 from *Ajellomyces capsulatus*.
- [0069] SEQ ID NO: 16 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:D4AT26 from *Arthroderma benhamiae*.
- [0070] SEQ ID NO: 17 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:D4CZH0 from *Trichophyton verrucosum*.
- [0071] SEQ ID NO: 18 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:D4DKV0 from *Trichophyton verrucosum*.
- [0072] SEQ ID NO: 19 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:E4UVW7 from *Arthroderma gypseum*.
- [0073] SEQ ID NO: 20 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:E4V546 from *Arthroderma gypseum*.
- [0074] SEQ ID NO: 21 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:G9N4L5 from *Hypocrea virens*.
- [0075] SEQ ID NO: 22 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:E 9F1Z9 from *Metarhizium robertsii*.
- [0076] SEQ ID NO: 23 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:F0UVK8 from *Ajellomyces capsulatus*.
- [0077] SEQ ID NO: 24 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:F2RV71 from *Trichophyton tonsurans*.
- [0078] SEQ ID NO: 25 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:F2PV65 from *Trichophyton equinum*.
- [0079] SEQ ID NO: 26 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:F2SGL6 from *Trichophyton rubrum*.
- [0080] SEQ ID NO: 27 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:F2SJH3 from *Trichophyton rubrum*.
- [0081] SEQ ID NO: 28 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:L7ZJC4 from *Serratia marcescens*.
- [0082] SEQ ID NO: 29 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:J5TH48 from *Trichosporon asahii*.
- [0083] SEQ ID NO: 30 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:J4UH35 from *Trichosporon asahii*.
- [0084] SEQ ID NO: 31 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:K1VMN5 from *Trichosporon asahii*.
- [0085] SEQ ID NO: 32 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:K1WL46 from *Trichosporon asahii*.
- [0086] SEQ ID NO: 33 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:U9T5J9 from *Rhizophagus irregularis*.
- [0087] SEQ ID NO: 34 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:U9TCU3 from *Rhizophagus irregularis*.
- [0088] SEQ ID NO: 35 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:U9UUS9 from *Rhizophagus irregularis*.
- [0089] SEQ ID NO: 36 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:R7Z482 from *Coniosporium apollinis*.
- [0090] SEQ ID NO: 37 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A015K155 from *Rhizophagus irregularis*.
- [0091] SEQ ID NO: 38 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:W6PQ31 from *Penicillium roqueforti*.

- [0092] SEQ ID NO: 39 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A017SCH5 from *Aspergillus ruber*.
- [0093] SEQ ID NO: 40 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A022UIH6 from *Trichophyton interdigitale*.
- [0094] SEQ ID NO: 41 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A015LDX8 from *Rhizophagus irregularis*.
- [0095] SEQ ID NO: 42 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A015L2T0 from *Rhizophagus irregularis*.
- [0096] SEQ ID NO: 43 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A086NFK5 from *Metarhizium anisopliae*.
- [0097] SEQ ID NO: 44 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0A2V9H7 from *Beauveria bassiana*.
- [0098] SEQ ID NO: 45 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0A2W020 from *Beauveria bassiana*.
- [0099] SEQ ID NO: 46 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0A2W5I8 from *Beauveria bassiana*.
- [0100] SEQ ID NO: 47 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0B4HPE0 from *Metarhizium guizhouense*.
- [0101] SEQ ID NO: 48 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0B4HHE 7 from *Metarhizium majus*.
- [0102] SEQ ID NO: 49 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0B4FYT8 from *Metarhizium brunneum*.
- [0103] SEQ ID NO: 50 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A8PEP0 from *Coprinopsis cinerea*.
- [0104] SEQ ID NO: 51 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A8PEP 4 from *Coprinopsis cinerea*.
- [0105] SEQ ID NO: 52 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A8PEQ3 from *Coprinopsis cinerea*.
- [0106] SEQ ID NO: 53 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:B0DQ11 from *Laccaria bicolor*.
- [0107] SEQ ID NO: 54 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:B0DUH4 from *Laccaria bicolor*.
- [0108] SEQ ID NO: 55 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C7Z8W0 from *Nectria haematococca*.
- [0109] SEQ ID NO: 56 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C7ZQ20 from *Nectria haematococca*.
- [0110] SEQ ID NO: 57 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:GORP87 from *Hypocreja jecorina*.
- [0111] SEQ ID NO: 58 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A8PEQ1 from *Coprinopsis cinerea*.
- [0112] SEQ ID NO: 59 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:D6RMD2 from *Coprinopsis cinerea*.
- [0113] SEQ ID NO: 60 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:K91708 from *Agaricus bisporus*.
- [0114] SEQ ID NO: 61 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:E9DUC 1 from *Metarhizium acridum*.
- [0115] SEQ ID NO: 62 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:E9FAC9 from *Metarhizium robertsii*.
- [0116] SEQ ID NO: 63 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:F9GF09 from *Fusarium oxysporum*.
- [0117] SEQ ID NO: 64 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A067NV59 from *Pleurotus ostreatus*.
- [0118] SEQ ID NO: 65 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A067NBT7 from *Pleurotus ostreatus*.
- [0119] SEQ ID NO: 66 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A067NLC3 from *Pleurotus ostreatus*.
- [0120] SEQ ID NO: 67 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A067TC 70 from *Galerina marginata*.
- [0121] SEQ ID NO: 68 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A067T7N7 from *Galerina marginata*.
- [0122] SEQ ID NO: 69 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:K5VNL0 from *Agaricus bisporus*.
- [0123] SEQ ID NO: 70 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:W9Z992 from *Fusarium oxysporum*.
- [0124] SEQ ID NO: 71 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:W 9ZZW9 from *Fusarium oxysporum*.
- [0125] SEQ ID NO: 72 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:X0A5V9 from *Fusarium oxysporum*.
- [0126] SEQ ID NO: 73 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:N4UD22 from *Fusarium oxysporum*.
- [0127] SEQ ID NO: 74 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:N4UKT7 from *Fusarium oxysporum*.
- [0128] SEQ ID NO: 75 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:W9KX02 from *Fusarium oxysporum*.
- [0129] SEQ ID NO: 76 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:X0MM97 from *Fusarium oxysporum*.
- [0130] SEQ ID NO: 77 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:W7N5Q6 from *Gibberella moniliformis*.
- [0131] SEQ ID NO: 78 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:X0BI18 from *Fusarium oxysporum*.
- [0132] SEQ ID NO: 79 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:W9NXR 4 from *Fusarium oxysporum*.
- [0133] SEQ ID NO: 80 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:W9LDD0 from *Fusarium oxysporum*.

- [0134] SEQ ID NO: 81 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:W9HEM8 from *Fusarium oxysporum*.
- [0135] SEQ ID NO: 82 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:S0EP16 from *Gibberella fujikuroi*.
- [0136] SEQ ID NO: 83 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:S3D2D9 from *Glarea lozoyensis*.
- [0137] SEQ ID NO: 84 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:R7Z235 from *Coniosporium apollinis*.
- [0138] SEQ ID NO: 85 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:U4LG 64 from *Pyronema omphalodes*.
- [0139] SEQ ID NO: 86 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:U1HSJ9 from *Endocarpon pusillum*.
- [0140] SEQ ID NO: 87 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:U4LQS4 from *Pyronema omphalodes*.
- [0141] SEQ ID NO: 88 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:X0IVL1 from *Fusarium oxysporum*.
- [0142] SEQ ID NO: 89 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A086T9F0 from *Acremonium chrysogenum*.
- [0143] SEQ ID NO: 90 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A086NUM9 from *Metarhizium anisopliae*.
- [0144] SEQ ID NO: 91 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0A1TCW0 from *Torrubiella hemipterigena*.
- [0145] SEQ ID NO: 92 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A093ZCQ3 from *Pseudogymnoascus pannorum*.
- [0146] SEQ ID NO: 93 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0B4HLN8 from *Metarhizium majus*.
- [0147] SEQ ID NO: 94 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0B4H8G 1 from *Metarhizium guizhouense*.
- [0148] SEQ ID NO: 95 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A4UCC9 from *Magnaporthe oryzae*.
- [0149] SEQ ID NO: 96 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:Q2GND9 from *Chaetomium globosum*.
- [0150] SEQ ID NO: 97 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C7Z967 from *Nectria haematococca*.
- [0151] SEQ ID NO: 98 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:C9SY46 from *Verticillium alfalfaef*.
- [0152] SEQ ID NO: 99 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:G2RG69 from *Thielavia terrestris*.
- [0153] SEQ ID NO: 100 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:G2QNE9 from *Thielavia heterothallica*.
- [0154] SEQ ID NO: 101 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:J 9NQV9 from *Fusarium oxysporum*.
- [0155] SEQ ID NO: 102 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:F9F2K4 from *Fusarium oxysporum*.
- [0156] SEQ ID NO: 103 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:GORZV2 from *Chaetomium thermophilum*.
- [0157] SEQ ID NO: 104 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:G2XHC2 from *Verticillium dahliae*.
- [0158] SEQ ID NO: 105 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:N1RWA4 from *Fusarium oxysporum*.
- [0159] SEQ ID NO: 106 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:X0B4J3 from *Fusarium oxysporum*.
- [0160] SEQ ID NO: 107 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A084PYR3 from *Stachybotrys chartarum*.
- [0161] SEQ ID NO: 108 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A086TBZ4 from *Acremonium chrysogenum*.
- [0162] SEQ ID NO: 109 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A086SUF8 from *Acremonium chrysogenum*.
- [0163] SEQ ID NO: 110 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A084R 326 from *Stachybotrys chlorohalonata*.
- [0164] SEQ ID NO: 111 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A093Z6Z8 from *Pseudogymnoascus pannorum*.
- [0165] SEQ ID NO: 112 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A094IML3 from *Pseudogymnoascus pannorum*.
- [0166] SEQ ID NO: 113 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A094GY79 from *Pseudogymnoascus pannorum*.
- [0167] SEQ ID NO: 114 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A093XPZ7 from *Pseudogymnoascus pannorum*.
- [0168] SEQ ID NO: 115 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A093XAS9 from *Pseudogymnoascus pannorum*.
- [0169] SEQ ID NO: 116 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A0A1TNV6 from *Torrubiella hemipterigena*.
- [0170] SEQ ID NO: 117 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A094DVF4 from *Pseudogymnoascus pannorum*.
- [0171] SEQ ID NO: 118 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A094IE 25 from *Pseudogymnoascus pannorum*.
- [0172] SEQ ID NO: 119 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A094HNM8 from *Pseudogymnoascus pannorum*.
- [0173] SEQ ID NO: 120 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A094EPJ 7 from *Pseudogymnoascus pannorum*.
- [0174] SEQ ID NO: 121 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A094BWD6 from *Pseudogymnoascus pannorum*.
- [0175] SEQ ID NO: 122 is the amino acid sequence of the GH24 catalytic domain of SWISSPROT:A0A093ZTZ8 from *Pseudogymnoascus pannorum*.

- [0176] SEQ ID NO: 123 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:B2ASY2 from *Podospora anserina*.
- [0177] SEQ ID NO: 124 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:B6GZX8 from *Penicillium chrysogenum*.
- [0178] SEQ ID NO: 125 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:C7ZQ22 from *Nectria haematococca*.
- [0179] SEQ ID NO: 126 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:E9DSA6 from *Metarhizium acridum*.
- [0180] SEQ ID NO: 127 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:E9F1Z9 from *Metarhizium robertsii*.
- [0181] SEQ ID NO: 128 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:E9FC42 from *Metarhizium robertsii*.
- [0182] SEQ ID NO: 129 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:F9F2K5 from *Fusarium oxysporum*.
- [0183] SEQ ID NO: 130 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:F9GF09 from *Fusarium oxysporum*.
- [0184] SEQ ID NO: 131 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G2QV10 from *Thielavia terrestris*.
- [0185] SEQ ID NO: 132 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G2QV26 from *Thielavia terrestris*.
- [0186] SEQ ID NO: 133 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:J 5TH48 from *Trichosporon asahii* var. *Asahii*.
- [0187] SEQ ID NO: 134 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:J 4UH35 from *Trichosporon asahii* var. *Asahii*.
- [0188] SEQ ID NO: 135 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:J 9NQ28 from *Fusarium oxysporum* f. sp. *Lycopersici*.
- [0189] SEQ ID NO: 136 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:J 9NQW0 from *Fusarium oxysporum* f. sp. *Lycopersici*.
- [0190] SEQ ID NO: 137 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:K1VMN5 from *Trichosporon asahii* var. *Asahii*.
- [0191] SEQ ID NO: 138 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:K1WL46 from *Trichosporon asahii* var. *Asahii*.
- [0192] SEQ ID NO: 139 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9Z045 from *Fusarium oxysporum* f. sp. *Melonis*.
- [0193] SEQ ID NO: 140 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:X0A5V9 from *Fusarium oxysporum* f. sp. *Melonis*.
- [0194] SEQ ID NO: 141 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:N1S551 from *Fusarium oxysporum* f. sp. *Cubense*.
- [0195] SEQ ID NO: 142 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:N4UD22 from *Fusarium oxysporum* f. sp. *Cubense*.
- [0196] SEQ ID NO: 143 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:N4UT47 from *Fusarium oxysporum* f. sp. *Cubense*.
- [0197] SEQ ID NO: 144 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9KWW4 from *Fusarium oxysporum*.
- [0198] SEQ ID NO: 145 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:X0MM97 from *Fusarium oxysporum* f. sp. *Vasinfectum*.
- [0199] SEQ ID NO: 146 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W7N5Q6 from *Gibberella moniliformis*.
- [0200] SEQ ID NO: 147 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:X0BE07 from *Fusarium oxysporum* f. sp. *Raphani*.
- [0201] SEQ ID NO: 148 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:X0BII8 from *Fusarium oxysporum*.
- [0202] SEQ ID NO: 149 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9NW59 from *Fusarium oxysporum* f. sp. *Pisi*.
- [0203] SEQ ID NO: 150 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9NXR4 from *Fusarium oxysporum* f. sp. *Pisi*.
- [0204] SEQ ID NO: 151 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:S7ZNE7 from *Penicillium oxalicum*.
- [0205] SEQ ID NO: 152 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:S7Z5Z6 from *Penicillium oxalicum*.
- [0206] SEQ ID NO: 153 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9LDD0 from *Fusarium oxysporum* f. sp. *Lycopersici*.
- [0207] SEQ ID NO: 154 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9HEM8 from *Fusarium oxysporum*.
- [0208] SEQ ID NO: 155 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9JDH4 from *Fusarium oxysporum*.
- [0209] SEQ ID NO: 156 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:S0EP16 from *Gibberella fujikuroi*.
- [0210] SEQ ID NO: 157 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W6QLN2 from *Penicillium roqueforti*.
- [0211] SEQ ID NO: 158 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:U4LJD9 from *Pyronema omphalodes*.
- [0212] SEQ ID NO: 159 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:U4LG64 from *Pyronema omphalodes*.
- [0213] SEQ ID NO: 160 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:A0A094AK50 from *Pseudogymnoascus pannorum*.
- [0214] SEQ ID NO: 161 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9JIH2 from *Fusarium oxysporum*.
- [0215] SEQ ID NO: 162 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:X0FW82 from *Fusarium oxysporum* f. sp. *radicis-lycopersici*.
- [0216] SEQ ID NO: 163 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:A0A086TBY7 from *Acremonium chrysogenum*.
- [0217] SEQ ID NO: 164 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:A0A086T755 from *Acremonium chrysogenum*.

[0218] SEQ ID NO: 165 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A086T4C8 from *Acremonium chrysogenum*.

[0219] SEQ ID NO: 166 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A086NNR4 from *Metarhizium anisopliae*.

[0220] SEQ ID NO: 167 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A086NFK5 from *Metarhizium anisopliae*.

[0221] SEQ ID NO: 168 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094FY19 from *Pseudogymnoascus pannorum*.

[0222] SEQ ID NO: 169 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094G1N0 from *Pseudogymnoascus pannorum*.

[0223] SEQ ID NO: 170 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094GEA0 from *Pseudogymnoascus pannorum*.

[0224] SEQ ID NO: 171 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094GJR5 from *Pseudogymnoascus pannorum*.

[0225] SEQ ID NO: 172 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094G660 from *Pseudogymnoascus pannorum*.

[0226] SEQ ID NO: 173 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A093YBN4 from *Pseudogymnoascus pannorum*.

[0227] SEQ ID NO: 174 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094FSZ5 from *Pseudogymnoascus pannorum*.

[0228] SEQ ID NO: 175 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094FBW1 from *Pseudogymnoascus pannorum*.

[0229] SEQ ID NO: 176 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094H0G2 from *Pseudogymnoascus pannorum*.

[0230] SEQ ID NO: 177 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094H7M1 from *Pseudogymnoascus pannorum*.

[0231] SEQ ID NO: 178 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A093Y8W3 from *Pseudogymnoascus pannorum*.

[0232] SEQ ID NO: 179 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094GYN9 from *Pseudogymnoascus pannorum*.

[0233] SEQ ID NO: 180 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A093XAD4 from *Pseudogymnoascus pannorum*.

[0234] SEQ ID NO: 181 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094H7J6 from *Pseudogymnoascus pannorum*.

[0235] SEQ ID NO: 182 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094E0I1 from *Pseudogymnoascus pannorum*.

[0236] SEQ ID NO: 183 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094CC50 from *Pseudogymnoascus pannorum*.

[0237] SEQ ID NO: 184 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A0941195 from *Pseudogymnoascus pannorum*.

[0238] SEQ ID NO: 185 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094IAA0 from *Pseudogymnoascus pannorum*.

[0239] SEQ ID NO: 186 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094IBC0 from *Pseudogymnoascus pannorum*.

[0240] SEQ ID NO: 187 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094E946 from *Pseudogymnoascus pannorum*.

[0241] SEQ ID NO: 188 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094A3A0 from *Pseudogymnoascus pannorum*.

[0242] SEQ ID NO: 189 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A1C4L9 from *Aspergillus clavatus*.

[0243] SEQ ID NO: 190 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A1CBV9 from *Aspergillus clavatus*.

[0244] SEQ ID NO: 191 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A1DA80 from *Neosartorya fischeri*.

[0245] SEQ ID NO: 192 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A1DBW2 from *Neosartorya fischeri*.

[0246] SEQ ID NO: 193 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A1DDF2 from *Neosartorya fischeri*.

[0247] SEQ ID NO: 194 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q0CED1 from *Aspergillus terreus*.

[0248] SEQ ID NO: 195 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q0CED2 from *Aspergillus terreus*.

[0249] SEQ ID NO: 196 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q0CV85 from *Aspergillus terreus*.

[0250] SEQ ID NO: 197 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q2GND8 from *Chaetomium globosum*.

[0251] SEQ ID NO: 198 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q2GND9 from *Chaetomium globosum*.

[0252] SEQ ID NO: 199 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q2H6W7 from *Chaetomium globosum*.

[0253] SEQ ID NO: 200 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q4WAY2 from *Neosartorya fumigata*.

[0254] SEQ ID NO: 201 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q4WBR4 from *Neosartorya fumigata*.

[0255] SEQ ID NO: 202 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: Q4WVY3 from *Neosartorya fumigata*.

[0256] SEQ ID NO: 203 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: B6H9X5 from *Penicillium chrysogenum*.

[0257] SEQ ID NO: 204 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: B6 HR 38 from *Penicillium chrysogenum*.

[0258] SEQ ID NO: 205 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: C7Z8W0 from *Nectria haematococca*.

[0259] SEQ ID NO: 206 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: C7ZQ20 from *Nectria haematococca*.

[0260] SEQ ID NO: 207 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G0RP87 from *Hypocrea jecorina*.

[0261] SEQ ID NO: 208 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G2RG69 from *Thielavia terrestris*.

[0262] SEQ ID NO: 209 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G2QNE9 from *Thielavia heterothallica*.

[0263] SEQ ID NO: 210 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G0RM22 from *Hypocrea jecorina*.

[0264] SEQ ID NO: 211 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G0SG36 from *Chaetomium thermophilum* var. *Thermophilum*.

[0265] SEQ ID NO: 212 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G0RZV3 from *Chaetomium thermophilum* var. *Thermophilum*.

[0266] SEQ ID NO: 213 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:J9NQV9 from *Fusarium oxysporum* f. sp. *Lycopersici*.

[0267] SEQ ID NO: 214 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G2QD02 from *Thielavia heterothallica*.

[0268] SEQ ID NO: 215 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G2QNF0 from *Thielavia heterothallica*.

[0269] SEQ ID NO: 216 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G9MHR1 from *Hypocrea virens*.

[0270] SEQ ID NO: 217 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:E9ELX9 from *Metarhizium robertsii*.

[0271] SEQ ID NO: 218 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:F9F2K4 from *Fusarium oxysporum*.

[0272] SEQ ID NO: 219 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G0RZV2 from *Chaetomium thermophilum* var. *Thermophilum*.

[0273] SEQ ID NO: 220 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:G2RG70 from *Thielavia terrestris*.

[0274] SEQ ID NO: 221 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9Z992 from *Fusarium oxysporum* f. sp. *Melonis*.

[0275] SEQ ID NO: 222 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9ZZW9 from *Fusarium oxysporum* f. sp. *Melonis*.

[0276] SEQ ID NO: 223 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9ZAE8 from *Fusarium oxysporum* f. sp. *Melonis*.

[0277] SEQ ID NO: 224 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:N1RWA4 from *Fusarium oxysporum* f. sp. *Cubense*.

[0278] SEQ ID NO: 225 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:N4UKT7 from *Fusarium oxysporum* f. sp. *Cubense*.

[0279] SEQ ID NO: 226 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W9KX02 from *Fusarium oxysporum*.

[0280] SEQ ID NO: 227 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:X0B4J3 from *Fusarium oxysporum* f. sp. *Raphani*.

[0281] SEQ ID NO: 228 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W 6QE02 from *Penicillium roqueforti*.

[0282] SEQ ID NO: 229 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:W 6R4X8 from *Penicillium roqueforti*.

[0283] SEQ ID NO: 230 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT:A0A02459B8 from *Trichoderma reesei*.

[0284] SEQ ID NO: 231 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A086NN36 from *Metarhizium anisopliae*.

[0285] SEQ ID NO: 232 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094GA03 from *Pseudogymnoascus pannorum*.

[0286] SEQ ID NO: 233 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094C8U1 from *Pseudogymnoascus pannorum*.

[0287] SEQ ID NO: 234 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A093Z6Z8 from *Pseudogymnoascus pannorum*.

[0288] SEQ ID NO: 235 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094IML3 from *Pseudogymnoascus pannorum*.

[0289] SEQ ID NO: 236 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094GY79 from *Pseudogymnoascus pannorum*.

[0290] SEQ ID NO: 237 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A093XPZ7 from *Pseudogymnoascus pannorum*.

[0291] SEQ ID NO: 238 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A093XAS9 from *Pseudogymnoascus pannorum*.

[0292] SEQ ID NO: 239 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A09418J6 from *Pseudogymnoascus pannorum*.

[0293] SEQ ID NO: 240 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094FTL0 from *Pseudogymnoascus pannorum*.

[0294] SEQ ID NO: 241 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094AT39 from *Pseudogymnoascus pannorum*.

[0295] SEQ ID NO: 242 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A093XSP5 from *Pseudogymnoascus pannorum*.

[0296] SEQ ID NO: 243 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094BAE6 from *Pseudogymnoascus pannorum*.

[0297] SEQ ID NO: 244 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094IE25 from *Pseudogymnoascus pannorum*.

[0298] SEQ ID NO: 245 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094HNM8 from *Pseudogymnoascus pannorum*.

[0299] SEQ ID NO: 246 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094ETJ5 from *Pseudogymnoascus pannorum*.

[0300] SEQ ID NO: 247 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094EPJ7 from *Pseudogymnoascus pannorum*.

[0301] SEQ ID NO: 248 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094E9W0 from *Pseudogymnoascus pannorum*.

[0302] SEQ ID NO: 249 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094BWD6 from *Pseudogymnoascus pannorum*.

[0303] SEQ ID NO: 250 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A094BTS1 from *Pseudogymnoascus pannorum*.

[0304] SEQ ID NO: 251 is the amino acid sequence of the lysozyme enhancing domain of SWISSPROT: A0A093TZ8 from *Pseudogymnoascus pannorum*.

[0305] SEQ ID NO: 252 is conserved motif I [TAS][VIL][GAC][YFI]GHX[CAYIV].

[0306] SEQ ID NO: 253 is conserved motif II [LV][NDST]XN[QE][YFW][GASND]ALXS[WFLY]X[FY]N.

[0307] SEQ ID NO: 254 is conserved motif III [CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN].

[0308] SEQ ID NO: 255 is the cDNA sequence of the GH24 lysozyme as isolated from *Trichophaea saccata*.

[0309] SEQ ID NO: 256 is the amino acid sequence as deduced from SEQ ID NO: 255.

[0310] SEQ ID NO: 257 is the amino acid sequence of the mature GH24 lysozyme from *Trichophaea saccata*.

[0311] SEQ ID NO: 258 is primer F-80470.

[0312] SEQ ID NO: 259 is primer R-80470.

[0313] SEQ ID NO: 260 is primer 8643.

[0314] SEQ ID NO: 261 is primer 8654.

[0315] SEQ ID NO: 262 is the cDNA sequence of the GH24 lysozyme as isolated from *Chaetomium thermophilum*.

[0316] SEQ ID NO: 263 is the amino acid sequence as deduced from SEQ ID NO: 262.

[0317] SEQ ID NO: 264 is the amino acid sequence of the mature GH24 lysozyme from *Chaetomium thermophilum*.

[0318] SEQ ID NO: 265 is the DNA sequence of the GH24 lysozyme as isolated from *Trichoderma harzianum*.

[0319] SEQ ID NO: 266 is the amino acid sequence as deduced from SEQ ID NO: 265.

[0320] SEQ ID NO: 267 is the amino acid sequence of the mature GH24 lysozyme from *Trichoderma harzianum*.

[0321] SEQ ID NO: 268 is the codon optimised DNA sequence of the GH24 catalytic domain from SEQ ID NO: 255 with QCVG-linker and Savinase signal peptide.

[0322] SEQ ID NO: 269 is the amino acid sequence as deduced from SEQ ID NO: 268.

[0323] SEQ ID NO: 270 is the amino acid sequence of the mature GH24 catalytic domain from *Trichophaea saccata* with QCVG-linker.

[0324] SEQ ID NO: 271 is the DNA sequence of the lysozyme enhancing domain from SEQ ID NO: 255.

[0325] SEQ ID NO: 272 is the amino acid sequence as deduced from SEQ ID NO: 271.

[0326] SEQ ID NO: 273 is the amino acid sequence of the mature LED from *Trichophaea saccata*.

[0327] SEQ ID NO: 274 is primer P 348F9-R.

[0328] SEQ ID NO: 275 is primer A00611-F.

[0329] SEQ ID NO: 276 is primer A00611-R.

[0330] SEQ ID NO: 277 is primer CBS 14450-F.

[0331] SEQ ID NO: 278 is primer CBS 14450-R.

[0332] SEQ ID NO: 279 is the amino acid sequence of the mature GH24 lysozyme from *Acremonium alcalophilum* corresponding to the mature sequence of SEQ ID NO: 4 of WO 2013/076259.

[0333] SEQ ID NO: 280 is the amino acid sequence of the mature GH24 lysozyme from *Acremonium alcalophilum* corresponding to the mature sequence of SEQ ID NO: 6 of WO 2013/076259.

[0334] SEQ ID NO: 281 is conserved motif I-B [TAS][VIL][GAC][YFI]GHX[CAYIV].

[0335] SEQ ID NO: 282 is conserved motif I-C T[VII]GYGHXC.

[0336] SEQ ID NO: 283 is conserved motif II-B LNXN [QE][YFW][GA]ALXS[W FL]X[YF]N.

[0337] SEQ ID NO: 284 is conserved motif III-B C[YF][VI][AST]D[YKF][YF][VI]XTG.

[0338] SEQ ID NO: 285 is conserved motif IV [GEV]LXXRXXE.

[0339] SEQ ID NO: 286 is conserved motif IV-B GLXXRXXE.

[0340] SEQ ID NO: 287 is the gene sequence of the GH24 lysozyme as isolated from *Trichophaea minuta*.

[0341] SEQ ID NO: 288 is the amino acid sequence as deduced from SEQ ID NO: 287.

[0342] SEQ ID NO: 289 is the codon optimised DNA sequence of SEQ ID NO: 287.

[0343] SEQ ID NO: 290 is the amino acid sequence as deduced from SEQ ID NO: 287.

[0344] SEQ ID NO: 291 is the amino acid sequence of the mature GH24 lysozyme from *Trichophaea minuta*.

[0345] SEQ ID NO: 292 is the gene sequence of the GH24 lysozyme as isolated from *Chaetomium* sp. ZY 287.

[0346] SEQ ID NO: 293 is the amino acid sequence as deduced from SEQ ID NO: 292.

[0347] SEQ ID NO: 294 is the amino acid sequence of the mature GH24 lysozyme from *Chaetomium* sp. ZY 287.

[0348] SEQ ID NO: 295 is the gene sequence of the GH24 lysozyme as isolated from *Mortierella* sp. ZY 002.

[0349] SEQ ID NO: 296 is the amino acid sequence as deduced from SEQ ID NO: 295.

[0350] SEQ ID NO: 297 is the amino acid sequence of the mature GH24 lysozyme from *Mortierella* sp. ZY 002.

[0351] SEQ ID NO: 298 is the gene sequence of the GH24 lysozyme as isolated from *Metarhizium* sp. XZ2431.

[0352] SEQ ID NO: 299 is the amino acid sequence as deduced from SEQ ID NO: 298.

[0353] SEQ ID NO: 300 is the amino acid sequence of the mature GH24 lysozyme from *Metarhizium* sp. XZ2431.

[0354] SEQ ID NO: 301 is the gene sequence of the GH24 lysozyme as isolated from *Geomyces auratus*.

[0355] SEQ ID NO: 302 is the amino acid sequence as deduced from SEQ ID NO: 301.

[0356] SEQ ID NO: 303 is the amino acid sequence of the mature GH24 lysozyme from *Geomyces auratus*.

[0357] SEQ ID NO: 304 is the gene sequence of the GH24 lysozyme as isolated from *Ilyonectria rufa*.

[0358] SEQ ID NO: 305 is the amino acid sequence as deduced from SEQ ID NO: 304.

[0359] SEQ ID NO: 306 is the amino acid sequence of the mature GH24 lysozyme from *Ilyonectria rufa*.

#### Definitions

[0360] 50% MHB, pH 6: The term “50% MHB, pH 6” means that the antimicrobial activity of the lysozyme was tested using an RDA plate wherein the media used was ½ Mueller-Hinton broth (MHB) (Sigma/Fluka, 90922) (i.e., adjusted to pH 6 with 4 M HCl and diluted 1:1 with water) with 1.5% agarose.

[0361] Allelic variant: The term “allelic variant” means any of two or more alternative forms of a gene occupying the same chromosomal locus. Allelic variation arises naturally through mutation, and may result in polymorphism within populations. Gene mutations can be silent (no change in the encoded polypeptide) or may encode polypeptides having altered amino acid sequences. An allelic variant of a polypeptide is a polypeptide encoded by an allelic variant of a gene.

[0362] Animal: The term “animal” refers to any animal except humans. Examples of animals are non-ruminants and ruminants. Ruminant animals include, for example, animals such as sheep, goats, cattle, e.g., beef cattle, cows, and young calves, deer, yank, camel, llama and kangaroo. Non-ruminant animals include monogastric animals, including but not limited to pigs or swine (including, but not limited to, piglets, growing pigs, and sows); poultry such as turkeys, ducks, quail, guinea fowl, geese, pigeons (including squabs) and chicken (including but not limited to broiler chickens (referred to herein as broiles), chicks, layer hens (referred to herein as layers)); horses (including but not limited to hotbloods, coldbloods and warm bloods) crustaceans (including but not limited to shrimps and prawns) and fish (including but not limited to amberjack, arapaima, barb, bass, bluefish, bocachico, bream, bullhead, cachama, carp, catfish, catla, chanos, char, cichlid, cobia, cod, crappie, dorada, drum, eel, goby, goldfish, gourami, grouper, guapote, halibut, java, labeo, lai, loach, mackerel, milkfish, mojarra, mudfish, mullet, paco, pearlspot, pejerrey, perch, pike, pompano, roach, salmon, sampa, sauger, sea bass, seabream, shiner, sleeper, snakehead, snapper, snook, sole, spinefoot, sturgeon, sunfish, sweetfish, tench, terror, tilapia, trout, tuna, turbot, vendace, walleye and whitefish).

[0363] Animal feed: The term “animal feed” refers to any compound, preparation, or mixture suitable for, or intended for intake by an animal. Animal feed for a monogastric animal typically comprises concentrates as well as vitamins, minerals, enzymes, direct fed microbial, amino acids and/or other feed ingredients (such as in a premix) whereas animal feed for ruminants generally comprises forage (including roughage and silage) and may further comprise concentrates as well as vitamins, minerals, enzymes direct fed microbial, amino acid and/or other feed ingredients (such as in a premix).

[0364] Antimicrobial activity: The term “antimicrobial activity” is defined herein as an activity that kills or inhibits the growth of microorganisms, such as, algae, archaea, bacteria, fungi and/or protozoans. The antimicrobial activity can, for example, be bactericidal meaning the killing of bacteria or bacteriostatic meaning the prevention of bacterial growth. The antimicrobial activity can include catalyzing the hydrolysis of 1,4-beta-linkages between N-acetylmuramic acid and N-acetyl-D-glucosamine residues in a peptidoglycan and between N-acetyl-D-glucosamine residues in chitodextrins. Antimicrobial activity can also include the lysozyme binding to the surface of the microorganism and inhibiting its growth. The antimicrobial effect can also include the use of the lysozymes of the present invention for activation of bacterial autolysins, as an immunostimulator, by inhibiting or reducing bacterial toxins and by an opsonin effect.

[0365] For the purpose of the present invention, antimicrobial activity is determined according to the antimicrobial assay described in Example 12 (“Determination of antimicrobial activity”). Antimicrobial activity is determined if there is a clearing zone when using 50% Mueller-Hinton broth, pH 6. Preferably the diameter of the clearing zone is 4 mm or more.

[0366] Thus, the term “antimicrobial activity of SEQ ID NO: x against *Clostridium perfringens* using the conditions 50% MHB, pH 6” mean that the polypeptide shows antimicrobial activity (i.e., clearing zone) against *Clostridium perfringens* DSM756 when the conditions 50% Mueller-Hinton broth, pH 6 are used, when the experiment is performed as described in example 12.

[0367] Body Weight Gain: The term “body weight gain” means an increase in live weight of an animal during a given period of time, e.g., the increase in weight from day 1 to day 21.

[0368] cDNA: The term “cDNA” means a DNA molecule that can be prepared by reverse transcription from a mature, spliced, mRNA molecule obtained from a eukaryotic or prokaryotic cell. cDNA lacks intron sequences that may be present in the corresponding genomic DNA. The initial, primary RNA transcript is a precursor to mRNA that is processed through a series of steps, including splicing, before appearing as mature spliced mRNA.

[0369] Coding sequence: The term “coding sequence” means a polynucleotide, which directly specifies the amino acid sequence of a polypeptide. The boundaries of the coding sequence are generally determined by an open reading frame, which begins with a start codon such as ATG, GTG, or TTG and ends with a stop codon such as TAA, TAG, or TGA. The coding sequence may be a genomic DNA, cDNA, synthetic DNA, or a combination thereof.

[0370] Concentrates: The term “concentrates” means feed with high protein and energy concentrations, such as fish meal, molasses, oligosaccharides, sorghum, seeds and grains (either whole or prepared by crushing, milling, etc. from, e.g., corn, oats, rye, barley, wheat), oilseed press cake (e.g., from cottonseed, safflower, sunflower, soybean (such as soybean meal), rapeseed/canola, peanut or groundnut), palm kernel cake, yeast derived material and distillers grains (such as wet distillers grains (WDS) and dried distillers grains with solubles (DDGS)).

[0371] Control sequences: The term “control sequences” means nucleic acid sequences necessary for expression of a polynucleotide encoding a mature polypeptide of the present invention. Each control sequence may be native (i.e., from the same gene) or foreign (i.e., from a different gene) to the polynucleotide encoding the polypeptide or native or foreign to each other. Such control sequences include, but are not limited to, a leader, polyadenylation sequence, propeptide sequence, promoter, signal peptide sequence, and transcription terminator. At a minimum, the control sequences include a promoter, and transcriptional and translational stop signals. The control sequences may be provided with linkers for the purpose of introducing specific restriction sites facilitating ligation of the control sequences with the coding region of the polynucleotide encoding a polypeptide.

[0372] domT score: The term “domT score” or domain score means the score for the best scoring domain when aligning the query sequence to the HMM.

[0373] European Production Efficacy Factor (EPEF): The “European Production Efficacy Factor” is a way of comparing the performance of animals. This single-figure facilitates comparison of performance within and among farms and can be used to assess environmental, climatic and managemental

variables. The EPEF is calculated as  $[(\text{livability} \%) \times (\text{Liveweight (kg)}) / (\text{Age at depletion (days)} \times \text{FCR})] \times 100$ , wherein livability is the percentage of animals alive at slaughter, Liveweight is the average weight of the animals at slaughter, age of depletion is the age of the animals at slaughter and FCR is the feed conversion ratio at slaughter.

[0374] Expression: The term “expression” includes any step involved in the production of a polypeptide including, but not limited to, transcription, post-transcriptional modification, translation, post-translational modification, and secretion.

[0375] Expression vector: The term “expression vector” means a linear or circular DNA molecule that comprises a polynucleotide encoding a polypeptide and is operably linked to control sequences that provide for its expression.

[0376] Feed Conversion Ratio (FCR): FCR is a measure of an animal's efficiency in converting feed mass into increases of the desired output. Animals raised for meat—such as swine, poultry and fish—the output is the mass gained by the animal. Specifically FCR is calculated as feed intake divided by weight gain, all over a specified period. Improvement in FCR means reduction of the FCR value. A FCR improvement of 2% means that the FCR was reduced by 2%.

[0377] Feed efficiency: The term “feed efficiency” means the amount of weight gain per unit of feed when the animal is fed ad-libitum or a specified amount of food during a period of time. By “increased feed efficiency” it is meant that the use of a feed additive composition according the present invention in feed results in an increased weight gain per unit of feed intake compared with an animal fed without said feed additive composition being present.

[0378] Forage: The term “forage” as defined herein also includes roughage. Forage is fresh plant material such as hay and silage from forage plants, grass and other forage plants, seaweed, sprouted grains and legumes, or any combination thereof. Examples of forage plants are Alfalfa (lucerne), birdsfoot trefoil, brassica (e.g., kale, rapeseed (canola), rutabaga (swede), turnip), clover (e.g., alsike clover, red clover, subterranean clover, white clover), grass (e.g., Bermuda grass, brome, false oat grass, fescue, heath grass, meadow grasses, orchard grass, ryegrass, Timothy-grass), corn (maize), millet, barley, oats, rye, sorghum, soybeans and wheat and vegetables such as beets. Forage further includes crop residues from grain production (such as corn stover; straw from wheat, barley, oat, rye and other grains); residues from vegetables like beet tops; residues from oil-seed production like stems and leaves from soy beans, rapeseed and other legumes; and fractions from the refining of grains for animal or human consumption or from fuel production or other industries.

[0379] Fragment: The term “fragment” means a polypeptide having one or more (e.g., several) amino acids absent from the amino and/or carboxyl terminus of a mature polypeptide or domain; wherein the fragment has lysozyme activity. In one aspect, a fragment contains at least 215 amino acid residues (e.g., amino acids 16 to 230 of SEQ ID NO: 257), at least 225 amino acid residues (e.g., amino acids 11 to 235 of SEQ ID NO: 257), or at least 235 amino acid residues (e.g., amino acids 6 to 240 of SEQ ID NO: 257). In another aspect, a fragment contains at least 215 amino acid residues (e.g., amino acids 16 to 230 of SEQ ID NO: 264), at least 225 amino acid residues (e.g., amino acids 11 to 235 of SEQ ID NO: 264), or at least 235 amino acid residues (e.g., amino acids 6 to 240 of SEQ ID NO: 264). In another

aspect, a fragment contains at least 218 amino acid residues (e.g., amino acids 16 to 233 of SEQ ID NO: 267), at least 228 amino acid residues (e.g., amino acids 11 to 238 of SEQ ID NO: 267), or at least 238 amino acid residues (e.g., amino acids 6 to 243 of SEQ ID NO: 267).

[0380] In one aspect, the fragment comprises at least 90% of the length of the mature polypeptide, such as at least 220 amino acids of SEQ ID NO: 288, at least 220 amino acids of SEQ ID NO: 290, at least 220 amino acids of SEQ ID NO: 291, at least 224 amino acids of SEQ ID NO: 293, at least 224 amino acids of SEQ ID NO: 294, at least 220 amino acids of SEQ ID NO: 296, at least 220 amino acids of SEQ ID NO: 297, at least 222 amino acids of SEQ ID NO: 299, at least 222 amino acids of SEQ ID NO: 300, at least 225 amino acids of SEQ ID NO: 302, at least 225 amino acids of SEQ ID NO: 303, at least 216 amino acids of SEQ ID NO: 305 or at least 216 amino acids of SEQ ID NO: 306.

[0381] In another aspect, the fragment comprises at least 92% of the length of the mature polypeptide, such as at least 225 amino acids of SEQ ID NO: 288, at least 225 amino acids of SEQ ID NO: 290, at least 225 amino acids of SEQ ID NO: 291, at least 229 amino acids of SEQ ID NO: 293, at least 229 amino acids of SEQ ID NO: 294, at least 225 amino acids of SEQ ID NO: 296, at least 225 amino acids of SEQ ID NO: 297, at least 227 amino acids of SEQ ID NO: 299, at least 227 amino acids of SEQ ID NO: 300, at least 230 amino acids of SEQ ID NO: 302, at least 230 amino acids of SEQ ID NO: 303, at least 220 amino acids of SEQ ID NO: 305 or at least 220 amino acids of SEQ ID NO: 306.

[0382] In another aspect, the fragment comprises at least 94% of the length of the mature polypeptide, such as at least 230 amino acids of SEQ ID NO: 288, at least 230 amino acids of SEQ ID NO: 290, at least 230 amino acids of SEQ ID NO: 291, at least 234 amino acids of SEQ ID NO: 293, at least 234 amino acids of SEQ ID NO: 294, at least 230 amino acids of SEQ ID NO: 296, at least 230 amino acids of SEQ ID NO: 297, at least 232 amino acids of SEQ ID NO: 299, at least 232 amino acids of SEQ ID NO: 300, at least 235 amino acids of SEQ ID NO: 302, at least 235 amino acids of SEQ ID NO: 303, at least 225 amino acids of SEQ ID NO: 305 or at least 225 amino acids of SEQ ID NO: 306.

[0383] In another aspect, the fragment comprises at least 96% of the length of the mature polypeptide, such as at least 235 amino acids of SEQ ID NO: 288, at least 235 amino acids of SEQ ID NO: 290, at least 235 amino acids of SEQ ID NO: 291, at least 239 amino acids of SEQ ID NO: 293, at least 239 amino acids of SEQ ID NO: 294, at least 235 amino acids of SEQ ID NO: 296, at least 235 amino acids of SEQ ID NO: 297, at least 237 amino acids of SEQ ID NO: 299, at least 237 amino acids of SEQ ID NO: 300, at least 240 amino acids of SEQ ID NO: 302, at least 240 amino acids of SEQ ID NO: 303, at least 230 amino acids of SEQ ID NO: 305 or at least 230 amino acids of SEQ ID NO: 306.

[0384] In another aspect, the fragment comprises at least 98% of the length of the mature polypeptide, such as at least 240 amino acids of SEQ ID NO: 288, at least 240 amino acids of SEQ ID NO: 290, at least 240 amino acids of SEQ ID NO: 291, at least 244 amino acids of SEQ ID NO: 293, at least 244 amino acids of SEQ ID NO: 294, at least 240 amino acids of SEQ ID NO: 296, at least 240 amino acids of SEQ ID NO: 297, at least 242 amino acids of SEQ ID NO: 299, at least 242 amino acids of SEQ ID NO: 300, at least 245 amino acids of SEQ ID NO: 302, at least 245 amino

acids of SEQ ID NO: 303, at least 235 amino acids of SEQ ID NO: 305 or at least 235 amino acids of SEQ ID NO: 306.

[0385] In another aspect, the fragment comprises at least 99% of the length of the mature polypeptide, such as at least 242 amino acids of SEQ ID NO: 288, at least 242 amino acids of SEQ ID NO: 290, at least 242 amino acids of SEQ ID NO: 291, at least 246 amino acids of SEQ ID NO: 293, at least 246 amino acids of SEQ ID NO: 294, at least 242 amino acids of SEQ ID NO: 296, at least 242 amino acids of SEQ ID NO: 297, at least 244 amino acids of SEQ ID NO: 299, at least 244 amino acids of SEQ ID NO: 300, at least 247 amino acids of SEQ ID NO: 302, at least 247 amino acids of SEQ ID NO: 303, at least 237 amino acids of SEQ ID NO: 305 or at least 237 amino acids of SEQ ID NO: 306.

[0386] hmmbuild: The term “hmmbuild” is a program from the package HMMER 3.0 (March 2010) ([hmmer.org/](http://hmmer.org/)) that builds a profile HMM from an input multiple alignment.

[0387] hmmcan: The term “hmmcan” is a program from the package HMMER 3.0 (March 2010) ([hmmer.org/](http://hmmer.org/)) that searches a protein sequence against a protein profile HMM database.

[0388] Host cell: The term “host cell” means any cell type that is susceptible to transformation, transfection, transduction, or the like with a nucleic acid construct or expression vector comprising a polynucleotide of the present invention. The term “host cell” encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication.

[0389] Isolated: The term “isolated” means a substance in a form or environment that does not occur in nature. Non-limiting examples of isolated substances include (1) any non-naturally occurring substance, (2) any substance including, but not limited to, any enzyme, variant, nucleic acid, protein, peptide or cofactor, that is at least partially removed from one or more or all of the naturally occurring constituents with which it is associated in nature; (3) any substance modified by the hand of man relative to that substance found in nature; or (4) any substance modified by increasing the amount of the substance relative to other components with which it is naturally associated (e.g., recombinant production in a host cell; multiple copies of a gene encoding the substance; and use of a stronger promoter than the promoter naturally associated with the gene encoding the substance).

[0390] Lysozyme activity: The term “lysozyme activity” means the hydrolysis of the 1,4-beta-linkages between N-acetylmuramic acid and N-acetyl-D-glucosamine residues in a peptidoglycan or between N-acetyl-D-glucosamine residues in chitodextrins, resulting in bacteriolysis. Lysozyme belongs to the enzyme class EC 3.2.1.17. Lysozyme activity is typically measured by turbidimetric determination, such as the changes in turbidity of a suspension of *Micrococcus luteus* ATCC 4698 or *Exiguobacterium undea* (DSM14481) induced by the lytic action of the lysozyme. In appropriate experimental conditions these changes are proportional to the amount of lysozyme in the medium (c.f. INS 1105 of the Combined Compendium of Food Additive Specifications of the Food and Agriculture Organisation of the UN ([fao.org](http://fao.org))). For the purpose of the present invention, lysozyme activity is determined according to the turbidity assay described in example 11 (“Determination of Lysozyme Activity”) and the polypeptide has lysozyme activity if it shows activity against one or more bacteria, such as *Micrococcus luteus* ATCC 4698 and/or

*Exiguobacterium undea* (DSM14481). In one aspect, the polypeptides of the present invention have at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 100% of the lysozyme activity of SEQ ID NO: 257. In another aspect, the polypeptides of the present invention have at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 100% of the lysozyme activity of SEQ ID NO: 264. In another aspect, the polypeptides of the present invention have at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 100% of the lysozyme activity of SEQ ID NO: 267.

[0391] Mature polypeptide: The term “mature polypeptide” means a polypeptide in its final form following translation and any post-translational modifications, such as N-terminal processing, C-terminal truncation, glycosylation, phosphorylation, etc. In one aspect, the mature polypeptide amino acids 1 to 245 of SEQ ID NO: 257 based on EDMAN N-terminal sequencing data, intact molecular weight analysis and proteomic analysis. In another aspect, the mature polypeptide amino acids 1 to 245 of SEQ ID NO: 264. In another aspect, the mature polypeptide amino acids 1 to 248 of SEQ ID NO: 267.

[0392] In one aspect, the mature polypeptide is amino acids 1 to 245 of SEQ ID NO: 288 and amino acids -17 to -1 of SEQ ID NO: 288 are a signal peptide. In another aspect, the mature polypeptide is amino acids 1 to 245 of SEQ ID NO: 290. In an alternative aspect, the mature polypeptide is amino acids 1 to 245 of SEQ ID NO: 291.

[0393] In one aspect, the mature polypeptide is amino acids 1 to 249 of SEQ ID NO: 293 and amino acids -18 to -1 of SEQ ID NO: 293 are a signal peptide. In an alternative aspect, the mature polypeptide is amino acids 1 to 249 of SEQ ID NO: 294.

[0394] In one aspect, the mature polypeptide is amino acids 1 to 245 of SEQ ID NO: 296 and amino acids -19 to -1 of SEQ ID NO: 296 are a signal peptide. In an alternative aspect, the mature polypeptide is amino acids 1 to 245 of SEQ ID NO: 297.

[0395] In one aspect, the mature polypeptide is amino acids 1 to 247 of SEQ ID NO: 299 and amino acids -19 to -1 of SEQ ID NO: 299 are a signal peptide. In an alternative aspect, the mature polypeptide is amino acids 1 to 247 of SEQ ID NO: 300.

[0396] In one aspect, the mature polypeptide is amino acids 1 to 250 of SEQ ID NO: 302 and amino acids -18 to -1 of SEQ ID NO: 302 are a signal peptide. In an alternative aspect, the mature polypeptide is amino acids 1 to 250 of SEQ ID NO: 303.

[0397] In one aspect, the mature polypeptide is amino acids 1 to 240 of SEQ ID NO: 305 and amino acids -18 to -1 of SEQ ID NO: 305 are a signal peptide. In an alternative aspect, the mature polypeptide is amino acids 1 to 240 of SEQ ID NO: 306.

[0398] It is known in the art that a host cell may produce a mixture of two or more different mature polypeptides (i.e., with a different C-terminal and/or N-terminal amino acid) expressed by the same polynucleotide. It is also known in the art that different host cells process polypeptides differently, and thus, one host cell expressing a polynucleotide may produce a different mature polypeptide (e.g., having a

different C-terminal and/or N-terminal amino acid) as compared to another host cell expressing the same polynucleotide.

**[0399]** Mature polypeptide coding sequence: The term “mature polypeptide coding sequence” means a polynucleotide that encodes a mature polypeptide having lysozyme activity. In one aspect, the mature polypeptide coding sequence is the joined sequence of nucleotides 52 to 347, nucleotides 401 to 615, nucleotides 668 to 772 and nucleotides 825 to 943 of SEQ ID NO: 255 or the cDNA sequence thereof and nucleotides 1 to 51 of SEQ ID NO: 255 are the signal peptide. In another aspect, the mature polypeptide coding sequence is the joined sequence of nucleotides 55 to 367, nucleotides 425 to 555 and nucleotides 630 to 920 of SEQ ID NO: 262 or the cDNA sequence thereof and nucleotides 1 to 54 of SEQ ID NO: 262 are the signal peptide. In another aspect, the mature polypeptide coding sequence is nucleotides 55 to 798 of SEQ ID NO: 265 and nucleotides 1 to 54 of SEQ ID NO: 265 are the signal peptide.

**[0400]** Nucleic acid construct: The term “nucleic acid construct” means a nucleic acid molecule, either single- or double-stranded, which is isolated from a naturally occurring gene or is modified to contain segments of nucleic acids in a manner that would not otherwise exist in nature or which is synthetic, which comprises one or more control sequences.

**[0401]** Obtained or obtainable from: The term “obtained or obtainable from” means that the polypeptide may be found in an organism from a specific taxonomic rank. In one embodiment, the polypeptide is obtained or obtainable from the kingdom Fungi, wherein the term kingdom is the taxonomic rank. In a preferred embodiment, the polypeptide is obtained or obtainable from the phylum Ascomycota, wherein the term phylum is the taxonomic rank. In another preferred embodiment, the polypeptide is obtained or obtainable from the subphylum Pezizomycotina, wherein the term subphylum is the taxonomic rank.

**[0402]** If the taxonomic rank of a polypeptide is not known, it can easily be determined by a person skilled in the art by performing a BLASTP search of the polypeptide (using, e.g., the National Center for Biotechnology Information (NCIB) website: [ncbi.nlm.nih.gov/](http://ncbi.nlm.nih.gov/)) and comparing it to the closest homologues. An unknown polypeptide which is a fragment of a known polypeptide is considered to be of the same taxonomic species. An unknown natural polypeptide or artificial variant which comprises a substitution, deletion and/or insertion in up to 10 positions is considered to be from the same taxonomic species as the known polypeptide.

**[0403]** Operably linked: The term “operably linked” means a configuration in which a control sequence is placed at an appropriate position relative to the coding sequence of a polynucleotide such that the control sequence directs expression of the coding sequence.

**[0404]** Profile Hidden Markov Model: “Profile Hidden Markov Model” are statistical models of multiple sequence alignments. They capture position-specific information about how conserved each column of the alignment is, and which residues are likely (see [ftp://ftp.hgc.jp/pub/mirror/wustl/hmmr3/3.1b1/Userguide.pdf](http://ftp.hgc.jp/pub/mirror/wustl/hmmr3/3.1b1/Userguide.pdf)).

**[0405]** Roughage: The term “roughage” means dry plant material with high levels of fiber, such as fiber, bran, husks

from seeds and grains and crop residues (such as stover, copra, straw, chaff, sugar beet waste).

**[0406]** Sequence identity: The relatedness between two amino acid sequences or between two nucleotide sequences is described by the parameter “sequence identity”.

**[0407]** For purposes of the present invention, the sequence identity between two amino acid sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, *J. Mol. Biol.* 48:443-453) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et al., 2000, *Trends Genet.* 16:276-277), preferably version 5.0.0 or later. The parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EBLO-SUM62 (EMBOSS version of BLOSUM62) substitution matrix. The output of Needle labelled “longest identity” (obtained using the-nobrief option) is used as the percent identity and is calculated as follows:

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

**[0408]** For purposes of the present invention, the sequence identity between two deoxyribonucleotide sequences is determined using the Needleman-Wunsch algorithm (Needleman and Wunsch, 1970, *supra*) as implemented in the Needle program of the EMBOSS package (EMBOSS: The European Molecular Biology Open Software Suite, Rice et al., 2000, *supra*), preferably version 5.0.0 or later. The parameters used are gap open penalty of 10, gap extension penalty of 0.5, and the EDNAFULL (EMBOSS version of NCBI NUC4.4) substitution matrix. The output of Needle labelled “longest identity” (obtained using the-no-brief option) is used as the percent identity and is calculated as follows:

$$\frac{\text{Identical Deoxyribonucleotides} \times 100}{\text{Length of Alignment} - \text{Total Number of Gaps in Alignment}}$$

**[0409]** Stringency conditions: The different stringency conditions are defined as follows.

**[0410]** The term “very low stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 25% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 0.8×SSC, 0.2% SDS at 55° C.

**[0411]** The term “low stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 25% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 0.8×SSC, 0.2% SDS at 60° C.

**[0412]** The term “medium stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 35% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 0.8×SSC, 0.2% SDS at 65° C.

**[0413]** The term “medium-high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 35% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 0.8×SSC, 0.2% SDS at 70° C.

**[0414]** The term “high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 50% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 0.4×SSC, 0.2% SDS at 70° C.

**[0415]** The term “very high stringency conditions” means for probes of at least 100 nucleotides in length, prehybridization and hybridization at 42° C. in 5×SSPE, 0.3% SDS, 200 micrograms/ml sheared and denatured salmon sperm DNA, and 50% formamide, following standard Southern blotting procedures for 12 to 24 hours. The carrier material is finally washed three times each for 15 minutes using 0.4×SSC, 0.2% SDS at 75° C.

**[0416]** Subsequence: The term “subsequence” means a polynucleotide having one or more (e.g., several) nucleotides absent from the 5' and/or 3' end of a mature polypeptide coding sequence; wherein the subsequence encodes a fragment having lysozyme activity. In one aspect, a subsequence contains at least 645 nucleotides (e.g., the joined sequence of nucleotides 97 to 347, nucleotides 401 to 615, nucleotides 668 to 772 and nucleotides 825 to 898 of SEQ ID NO: 255 or the cDNA sequence thereof), at least 675 nucleotides (e.g., the joined sequence of nucleotides 82 to 347, nucleotides 401 to 615, nucleotides 668 to 772 and nucleotides 825 to 913 of SEQ ID NO: 255 or the cDNA sequence thereof), or at least 705 nucleotides (e.g., the joined sequence of nucleotides 67 to 347, nucleotides 401 to 615, nucleotides 668 to 772 and nucleotides 825 to 928 of SEQ ID NO: 255 or the cDNA sequence thereof).

**[0417]** Substantially pure polypeptide: The term “substantially pure polypeptide” means a preparation that contains at most 10%, at most 8%, at most 6%, at most 5%, at most 4%, at most 3%, at most 2%, at most 1%, and at most 0.5% by weight of other polypeptide material with which it is natively or recombinantly associated. Preferably, the polypeptide is at least 92% pure, e.g., at least 94% pure, at least 95% pure, at least 96% pure, at least 97% pure, at least 98% pure, at least 99%, at least 99.5% pure, and 100% pure by weight of the total polypeptide material present in the preparation. The polypeptides of the present invention are preferably in a substantially pure form. This can be accomplished, for example, by preparing the polypeptide by well known recombinant methods or by classical purification methods.

**[0418]** Variant: The term “variant” means a polypeptide having lysozyme activity comprising an alteration, i.e., a substitution, insertion, and/or deletion, of one or more (several) amino acid residues at one or more (e.g., several) positions. A substitution means replacement of the amino acid occupying a position with a different amino acid; a deletion means removal of the amino acid occupying a

position; and an insertion means adding 1, 2, or 3 amino acids adjacent to and immediately following the amino acid occupying the position.

**[0419]** In one aspect, a lysozyme variant according to the invention may comprise from 1 to 5; from 1 to 10; from 1 to 15; from 1 to 20; from 1 to 25; from 1 to 30; from 1 to 35; from 1 to 40; from 1 to 45; or from 1-50, i.e., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 alterations and have at least 20%, e.g., at least 40%, at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 100% of the lysozyme activity of the parent lysozyme, such as SEQ ID NO: 257, SEQ ID NO: 264 or SEQ ID NO: 267.

#### Nomenclature

**[0420]** For purposes of the present invention, the nomenclature [E/Q] means that the amino acid at this position may be a glutamic acid (Glu, E) or a glutamine (Gln, Q). Likewise the nomenclature [V/G/A/I] means that the amino acid at this position may be a valine (Val, V), glycine (Gly, G), alanine (Ala, A) or isoleucine (Ile, I), and so forth for other combinations as described herein. Unless otherwise limited further, the amino acid X is defined such that it may be any of the 20 natural amino acids.

#### DETAILED DESCRIPTION OF THE INVENTION

##### Animal Feed and Animal Feed Additives Comprising Polypeptides Having Lysozyme Activity

**[0421]** The inventors have discovered that some polypeptides that comprise one or more Glycosyl Hydrolase family 24 (GH24) catalytic domains also comprise sections of polypeptide which until now has not been known to have any function and have therefore not been annotated. The inventors have herein annotated these sections of polypeptide, which is referred to herein as a lysozyme enhancing domain (LED), and have surprisingly discovered that this lysozyme enhancing domain significantly enhances antimicrobial activity against *Clostridium perfringens*.

**[0422]** For example, the polypeptide of SEQ ID NO: 257 which comprises a GH24 domain and a lysozyme enhancing domain has significant activity against *Clostridium perfringens* (see table 3 of example 12). However, when the polypeptide is expressed without the lysozyme enhancing domain being present (SEQ ID NO: 270), there is no activity against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0423]** Two other polypeptides comprising a GH24 domain and a lysozyme enhancing domain (SEQ ID NO: 264 and 267) also have significant activity against *Clostridium perfringens* (see table 3) using the conditions 50% MHB, pH 6. However, two known GH24 lysozymes (SEQ ID NO: 279 and SEQ ID NO: 280) which do not comprise a lysozyme enhancing domain do not have any activity against *Clostridium perfringens*.

**[0424]** The inventors have also discovered that the LED protein (SEQ ID NO: 273) binds to *M. lysodiektikus* cells under the buffer conditions tested while crystalline cellulose did not bind the LED protein. This demonstrates that the LED protein is an important feature of the lysozymes of the

invention and possibly explains why said lysozymes are more active against *Clostridium perfringens* under the tested conditions compared to GH24 lysozymes lacking the LED. [0425] Thus, in one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains and wherein:

[0426] (a) GH24 catalytic domain gives a domT score of at least 200 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 1 to 122 and hmmbuild software program, and wherein the query is carried out using hmmscan software program with default settings; and

[0427] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of at least 100 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 123 to 251 and hmmbuild software program, and wherein the query is carried out using the hmmscan software program with default settings.

[0428] In another aspect, the present invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein:

[0429] (a) the polypeptide comprises one or more GH24 catalytic domains, wherein the GH24 catalytic domain gives a domT score of 200 or more when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 1 to 122 inclusive using the software program hmmbuild, the query being carried out using the hmmscan software program with default settings; and

[0430] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of 100 or more when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 123 to 251 inclusive using the software program hmmbuild, the query being carried out using the hmmscan software program with default settings.

[0431] In another aspect, the present invention relates to an animal feed or animal feed additive comprising one or more vitamins and one or more polypeptides having lysozyme activity, wherein the polypeptide comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains and wherein:

[0432] (a) GH24 catalytic domain gives a domT score of at least 200 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 1 to 122 and hmmbuild software program, and wherein the query is carried out using hmmscan software program with default settings; and

[0433] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of at least 100 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 123 to 251 and hmmbuild software program, and wherein the query is carried out using the hmmscan software program with default settings.

[0434] In another aspect, the present invention relates to an animal feed or animal feed additive comprising one or more minerals and one or more polypeptides having lysozyme activity, wherein the polypeptide comprises one or

more GH24 catalytic domains and one or more lysozyme enhancing domains and wherein:

[0435] (a) GH24 catalytic domain gives a domT score of at least 200 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 1 to 122 and hmmbuild software program, and wherein the query is carried out using hmmscan software program with default settings; and

[0436] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of at least 100 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 123 to 251 and hmmbuild software program, and wherein the query is carried out using the hmmscan software program with default settings.

[0437] In another aspect, the present invention relates to an animal feed or animal feed additive comprising one or more amino acids and one or more polypeptides having lysozyme activity, wherein the polypeptide comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains and wherein:

[0438] (a) GH24 catalytic domain gives a domT score of at least 200 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 1 to 122 and hmmbuild software program, and wherein the query is carried out using hmmscan software program with default settings; and

[0439] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of at least 100 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 123 to 251 and hmmbuild software program, and wherein the query is carried out using the hmmscan software program with default settings.

[0440] In another aspect, the present invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains and wherein:

[0441] (a) GH24 catalytic domain gives a domT score of at least 200 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 1 to 122 and hmmbuild software program, and wherein the query is carried out using hmmscan software program with default settings; and

[0442] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of at least 100 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 123 to 251 and hmmbuild software program, and wherein the query is carried out using the hmmscan software program with default settings; and

[0443] one or more components selected from the list consisting of:

[0444] one or more additional enzymes;

[0445] one or more microbes;

[0446] one or more vitamins;

[0447] one or more minerals;

[0448] one or more amino acids; and

[0449] one or more other feed ingredients.

[0450] In another aspect, the present invention relates to a pelleted animal feed comprising plant based material and one or more polypeptides having lysozyme activity, wherein the polypeptide comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains and wherein:

[0451] (a) GH24 catalytic domain gives a domT score of at least 200 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 1 to 122 and hmmbuild software program, and wherein the query is carried out using hmmcan software program with default settings; and

[0452] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of at least 100 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 123 to 251 and hmmbuild software program, and wherein the query is carried out using the hmmcan software program with default settings.

[0453] The theory behind Profile HMMs as described in Durbin et al. (*Biological sequence analysis: probabilistic models of proteins and nucleic acids*, Cambridge University Press, 1998) and Krogh et al. (*J. Mol. Biol.* 235:1501-1531 (1994)), both incorporated herein by reference, is characterization of a set of proteins based on the probability of each amino acid occurring at each position in the alignment of the proteins of the set.

[0454] Specifically, profile HMMs are statistical models of multiple sequence alignments, or even of single sequences. They capture position-specific information about how conserved each column of the alignment is, and which residues are likely. All profile methods are more or less statistical descriptions of the consensus of a multiple sequence alignment. They use position-specific scores for amino acids or nucleotides (residues) and position specific penalties for opening and extending an insertion or deletion. Traditional pairwise alignment (for example, BLAST, FASTA or the Smith/Waterman algorithm) uses position-independent scoring parameters. This property of profiles captures important information about the degree of conservation at various positions in the multiple alignment, and the varying degree to which gaps and insertions are permitted.

[0455] The advantage of using HMMs is that HMMs have a formal probabilistic basis. Probability theory is used to guide how all the scoring parameters should be set. One of the most important aspect is that HMMs have a consistent theory for setting position-specific gap and insertion scores. The methods are consistent and therefore highly automatable, allowing hundreds of profile HMMs to be applied to, e.g., whole genome analysis. An example of a protein domain model database is Pfam (Sonnhammer et al., 1997, 'A comprehensive database of protein families based on seed alignments', *Proteins* 28:405-420; Finn et al., 2010, 'The Pfam protein families database', *Nucl. Acids Res.* 38: D211-D222), which is a significant part of the Interpro protein domain annotation system. The construction and use of Pfam is tightly tied to the HMMER software package (see en.wikipedia.org/wiki/HMMER).

[0456] The GH24 domain is defined in the following manner. SEQ ID NOS: 1 to 122, which are partial sequences of the UniProt entries as explained in the 'overview of sequence listing' section herein, are aligned using the software program MUSCLE v3.8.31 with the default settings.

Using this alignment, a hidden Markov model (HMM) is built for the GH24 domain. The HMM is constructed using the software program 'hmmbuild' from the package HMMER 3.0 (March 2010) (hmmer.org/) and the software is invoked using the default settings.

[0457] A GH24 domain is defined to match the above mentioned HMM using the software program 'hmmscan' from the package HMMER 3.0 (March 2010) (hmmer.org/) using the default settings if the domT score is at least 200. In a preferred embodiment, the domT score is at least 220, preferably at least 230, more preferably at least 240, even more preferably at least 250, even more preferably at least 255, or most preferably at least 260.

[0458] The HMM profile of the GH24 domain as generated using SEQ ID NOS: 1 to 122 according to the procedure above is given in example 15. The HMM profile can be copied into a text file which is subsequently loaded into the software program 'hmmscan' so that other polypeptides can be tested to see whether said polypeptide comprises one or more GH24 catalytic domains.

[0459] The Lysozyme Enhancing Domain (LED) is defined in the following manner. SEQ ID NOS: 123 to 251, which are partial sequences of the UniProt entries as explained in the 'overview of sequence listing' section herein, are aligned using the software program MUSCLE v3.8.31 with the default settings. Using this alignment, a hidden Markov model (HMM) is built for the LED. The HMM is constructed using the software program 'hmmbuild' from the package HMMER 3.0 (March 2010) (hmmer.org/) and the software is invoked using the default settings.

[0460] A LED is defined to match the above mentioned HMM using the software program 'hmmscan' from the package HMMER 3.0 (March 2010) (hmmer.org/) using the default settings if the domT score is at least 100. In a preferred embodiment, the domT score is at least 103, preferably at least 106, more preferably at least 109, more preferably at least 112, more preferably at least 115, more preferably at least 118, even more preferably at least 121, or most preferably at least 124.

[0461] The HMM profile of the LED as generated using SEQ ID NOS: 123 to 251 according to the procedure above is given in example 16. The HMM profile can be copied into a text file which is subsequently loaded into the software program 'hmmscan' so that other polypeptides can be tested to see whether said polypeptide comprises one or more LED.

[0462] In an embodiment, the GH24 catalytic domain gives a domT score of at least 220 and the lysozyme enhancing domain gives a domT score of at least 100. In an embodiment, the GH24 catalytic domain gives a domT score of at least 230 and the lysozyme enhancing domain gives a domT score of at least 100. In an embodiment, the GH24 catalytic domain gives a domT score of at least 240 and the lysozyme enhancing domain gives a domT score of at least 100. In an embodiment, the GH24 catalytic domain gives a domT score of at least 250 and the lysozyme enhancing domain gives a domT score of at least 100.

[0463] In an embodiment, the GH24 catalytic domain gives a domT score of at least 220 and the lysozyme enhancing domain gives a domT score of at least 103. In an embodiment, the GH24 catalytic domain gives a domT score of at least 230 and the lysozyme enhancing domain gives a domT score of at least 103. In an embodiment, the GH24 catalytic domain gives a domT score of at least 240 and the

lysozyme enhancing domain gives a domT score of at least 103. In an embodiment, the GH24 catalytic domain gives a domT score of at least 250 and the lysozyme enhancing domain gives a domT score of at least 103.

[0464] In an embodiment, the GH24 catalytic domain gives a domT score of at least 220 and the lysozyme enhancing domain gives a domT score of at least 106. In an embodiment, the GH24 catalytic domain gives a domT score of at least 230 and the lysozyme enhancing domain gives a domT score of at least 106. In an embodiment, the GH24 catalytic domain gives a domT score of at least 240 and the lysozyme enhancing domain gives a domT score of at least 106. In an embodiment, the GH24 catalytic domain gives a domT score of at least 250 and the lysozyme enhancing domain gives a domT score of at least 106.

[0465] In an embodiment, the GH24 catalytic domain gives a domT score of at least 220 and the lysozyme enhancing domain gives a domT score of at least 109. In an embodiment, the GH24 catalytic domain gives a domT score of at least 230 and the lysozyme enhancing domain gives a domT score of at least 109. In an embodiment, the GH24 catalytic domain gives a domT score of at least 240 and the lysozyme enhancing domain gives a domT score of at least 109. In an embodiment, the GH24 catalytic domain gives a domT score of at least 250 and the lysozyme enhancing domain gives a domT score of at least 109.

[0466] In an embodiment, the GH24 catalytic domain gives a domT score of at least 220 and the lysozyme enhancing domain gives a domT score of at least 112. In an embodiment, the GH24 catalytic domain gives a domT score of at least 230 and the lysozyme enhancing domain gives a domT score of at least 112. In an embodiment, the GH24 catalytic domain gives a domT score of at least 240 and the lysozyme enhancing domain gives a domT score of at least 112. In an embodiment, the GH24 catalytic domain gives a domT score of at least 250 and the lysozyme enhancing domain gives a domT score of at least 112.

[0467] In an embodiment, the GH24 catalytic domain gives a domT score of at least 220 and the lysozyme enhancing domain gives a domT score of at least 115. In an embodiment, the GH24 catalytic domain gives a domT score of at least 230 and the lysozyme enhancing domain gives a domT score of at least 115. In an embodiment, the GH24 catalytic domain gives a domT score of at least 240 and the lysozyme enhancing domain gives a domT score of at least 115. In an embodiment, the GH24 catalytic domain gives a domT score of at least 250 and the lysozyme enhancing domain gives a domT score of at least 115.

[0468] In an embodiment, the GH24 catalytic domain gives a domT score of at least 220 and the lysozyme enhancing domain gives a domT score of at least 118. In an embodiment, the GH24 catalytic domain gives a domT score of at least 230 and the lysozyme enhancing domain gives a domT score of at least 118. In an embodiment, the GH24 catalytic domain gives a domT score of at least 240 and the lysozyme enhancing domain gives a domT score of at least 118. In an embodiment, the GH24 catalytic domain gives a domT score of at least 250 and the lysozyme enhancing domain gives a domT score of at least 118.

[0469] In an embodiment, the polypeptide having lysozyme activity is obtained or obtainable from the kingdom Fungi, preferably from the phylum Ascomycota.

[0470] In an embodiment, the polypeptide having lysozyme activity has at least 30% of the antimicrobial

activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 50% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 60% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0471] In an embodiment, the polypeptide having lysozyme activity has at least 70% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 75% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 80% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0472] In an embodiment, the polypeptide having lysozyme activity has at least 85% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 90% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 95% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 100% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0473] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0474] (a) the GH24 catalytic domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252) and/or one or more motif II [LV][NDST]XN[QE][YFW][GASND]ALXS[FLY]X[FY]N (SEQ ID NO: 253); and

[0475] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 254)  
[CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN].

[0476] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0477] (a) the catalytic GH24 domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 281) and/or one or more motif II LNXN[QE][YFW][GA]ALXS[WFL]X[YF]N (SEQ ID NO: 283); and

[0478] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 284)  
C[YF][VI][AST]D[YKF][YF][VI]XTG.

[0479] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0480] (a) the GH24 catalytic domain comprises one or more motif I: T[VI]GYGHXC (SEQ ID NO: 282) and/or one or more motif II LNXN[QE][YFW][GA] ALXS[WFL]X[YF]N (SEQ ID NO: 283); and

[0481] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 284)  
C[YF][VI][AST]D[YKF][YF][VI]XTG.

[0482] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0483] (a) the GH24 catalytic domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252), one or more motif I [LV][NDST] XN[QE][YFW][GASND]ALXS[WFL]X[YF]N (SEQ ID NO: 253) and/or one or more motif IV [GEV]LXXRRXXE (SEQ ID NO: 285); and

[0484] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 254)  
C[CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN].

[0485] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0486] (a) the GH24 catalytic domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 282), one or more motif II LNXN[QE][YFW][GA]ALXS[WFL]X[YF]N (SEQ ID NO: 283) and/or one or more motif IV GLXXRRXXE (SEQ ID NO: 286); and

[0487] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 284)  
C[YF][VI][AST]D[YKF][YF][VI]XTG.

[0488] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide

having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0489] (a) the GH24 catalytic domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252) and one or more motif II [LV][NDST]XN[QE][YFW][GASND]ALXS[WFL]X[YF]N (SEQ ID NO: 253); and

[0490] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 254)  
C[CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN].

[0491] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0492] (a) the GH24 catalytic domain comprises one or more motif I [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 281) and one or more motif II LNXN[QE][YFW][GA]ALXS[WFL]X[YF]N (SEQ ID NO: 283); and

[0493] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 284)  
C[CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN].

[0494] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0495] (a) the GH24 catalytic domain comprises one or more motif I: T[VI]GYGHXC (SEQ ID NO: 282) and one or more motif II LNXN[QE][YFW][GA]ALXS[WFL]X[YF]N (SEQ ID NO: 283); and

[0496] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 284)  
C[YF][VI][AST]D[YKF][YF][VI]XTG.

[0497] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0498] (a) the GH24 catalytic domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252), one or more motif II [LV][NDST]XN[QE][YFW][GASND]ALXS[WFL]X[YF]N (SEQ ID NO: 253) and one or more motif IV [GEV]LXXRRXXE (SEQ ID NO: 285); and

[0499] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 254)  
[CGY][Y F][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN].

[0500] In one aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0501] (a) the GH24 catalytic domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 281), one or more motif II LNXN[QE] [YFW][GA]ALXS[WFL]X[YF]N (SEQ ID NO: 283) and one or more motif IV GLXXRRXXE (SEQ ID NO: 286); and

[0502] (b) the lysozyme enhancing domain comprises one or more motif III:

(SEQ ID NO: 284)  
C[YF][VI][AST]D[YKE][YF][VI]XTG.

[0503] In an embodiment, the polypeptide having lysozyme activity is obtained or obtainable from the kingdom Fungi, preferably from the phylum Ascomycota.

[0504] In an embodiment, the polypeptide having lysozyme activity has at least 30% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 50% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 60% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0505] In an embodiment, the polypeptide having lysozyme activity has at least 70% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 75% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 80% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0506] In an embodiment, the polypeptide having lysozyme activity has at least 85% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 90% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 100% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0507] In another aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0508] (a) the GH24 catalytic domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252), one or more motif II [LV][NDST] XN[QE][YFW][GASND]ALXS[WFL]X[FY]N (SEQ ID NO: 253) and has at least 50%, e.g., at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 14; and

[0509] (b) the GH24 lysozyme enhancing domain comprises one or more motif I: [TAS][VIL][GAC][YFI] GHX[CAYIV] (SEQ ID NO: 252), one or more motif II [LV][NDST]XN[QE][YFW][GASND]ALXS [WFL]X[FY]N (SEQ ID NO: 253) and has at least 45%, e.g., at least 50%, at least 55%, at least 60%, at least 65%, at least 70%, at least 75%, at least 80%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 180.

[0510] In an embodiment, the polypeptide having lysozyme activity is obtained or obtainable from the kingdom Fungi, preferably from the phylum Ascomycota.

[0511] In an embodiment, the polypeptide having lysozyme activity has at least 30% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 50% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 60% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0512] In an embodiment, the polypeptide having lysozyme activity has at least 70% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 75% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 80% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0513] In an embodiment, the polypeptide having lysozyme activity has at least 85% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 90% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 95% of the antimicrobial activity of SEQ

ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 100% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0514] In another aspect, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains, wherein:

[0515] (b) the GH24 catalytic domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252), one or more motif II [LV][NDST] XN[QE][YFW][GASND]ALXS[WFLY]X[FY]N (SEQ ID NO: 253) and has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to one or more of SEQ ID NO: 1 to 122; and

[0516] (b) the lysozyme enhancing domain comprises one or more motif I: [TAS][VIL][GAC][YFI]GHX [CAYIV] (SEQ ID NO: 252), one or more motif II [LV][NDST]XN[QE][YFW][GASND]ALXS[WFLY] X[FY]N (SEQ ID NO: 253) and has at least 65%, e.g., at least 70%, at least 75%, at least 80%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to one or more of SEQ ID NO: 123 to 251.

[0517] In an embodiment, the polypeptide having lysozyme activity is obtained or obtainable from the kingdom Fungi, preferably from the phylum Ascomycota.

[0518] In an embodiment, the polypeptide having lysozyme activity has at least 30% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 50% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 60% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0519] In an embodiment, the polypeptide having lysozyme activity has at least 70% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 75% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 80% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0520] In an embodiment, the polypeptide having lysozyme activity has at least 85% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 90% of

the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 95% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6. In an embodiment, the polypeptide having lysozyme activity has at least 100% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0521] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 257.

[0522] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 257 and at least 70% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0523] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 257 and at least 80% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0524] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 257 and at least 90% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0525] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 257 and at least 95% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0526]** In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 257 and at least 100% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0527]** In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 257. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0528]** In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 257 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 257 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 245 of SEQ ID NO: 257 and has lysozyme activity.

**[0529]** In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 264.

**[0530]** In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 264 and at least 70% of the antimicrobial activity of SEQ ID NO: 264 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0531]** In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 264 and at least 80% of the antimicrobial activity of SEQ ID NO: 264 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0532]** In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 264 and at least 90% of the antimicrobial activity of SEQ ID NO: 264 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0533]** In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 264 and at least 95% of the antimicrobial activity of SEQ ID NO: 264 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0534]** In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 264 and at least 100% of the antimicrobial activity of SEQ ID NO: 264 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0535]** In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 264. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 264 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0536]** In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 264 or an allelic variant thereof having lysozyme activity; comprises or consists of the

amino acid sequence of SEQ ID NO: 264 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 245 of SEQ ID NO: 264 and has lysozyme activity.

[0537] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 267.

[0538] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 267 and at least 70% of the antimicrobial activity of SEQ ID NO: 267 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0539] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 267 and at least 80% of the antimicrobial activity of SEQ ID NO: 267 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0540] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 267 and at least 90% of the antimicrobial activity of SEQ ID NO: 267 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0541] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID

NO: 267 and at least 95% of the antimicrobial activity of SEQ ID NO: 267 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0542] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 267 and at least 100% of the antimicrobial activity of SEQ ID NO: 267 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0543] In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 267. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 267 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0544] In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 267 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 267 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 248 of SEQ ID NO: 267 and has lysozyme activity.

[0545] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 291.

[0546] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID

NO: 291 and at least 70% of the antimicrobial activity of SEQ ID NO: 291 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0547] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 291 and at least 80% of the antimicrobial activity of SEQ ID NO: 291 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0548] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 291 and at least 90% of the antimicrobial activity of SEQ ID NO: 291 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0549] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 291 and at least 95% of the antimicrobial activity of SEQ ID NO: 291 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0550] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 291 and at least 100% of the antimicrobial activity of SEQ ID NO: 291 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0551] In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 291. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 291 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0552] In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having

lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 291 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 291 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 245 of SEQ ID NO: 291 and has lysozyme activity.

[0553] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 294 and at least 70% of the antimicrobial activity of SEQ ID NO: 294 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0554] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 294 and at least 80% of the antimicrobial activity of SEQ ID NO: 294 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0555] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 294 and at least 90% of the antimicrobial activity of SEQ ID NO: 294 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0556] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 294 and at least 90% of the antimicrobial activity of SEQ ID NO: 294 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0557] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least

98%, at least 99%, or 100% sequence identity to SEQ ID NO: 294 and at least 95% of the antimicrobial activity of SEQ ID NO: 294 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0558] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 294 and at least 100% of the antimicrobial activity of SEQ ID NO: 294 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0559] In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 294. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 294 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0560] In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 294 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 294 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 245 of SEQ ID NO: 294 and has lysozyme activity.

[0561] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 297.

[0562] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID

NO: 297 and at least 70% of the antimicrobial activity of SEQ ID NO: 297 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0563] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 297 and at least 80% of the antimicrobial activity of SEQ ID NO: 297 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0564] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 297 and at least 90% of the antimicrobial activity of SEQ ID NO: 297 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0565] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 297 and at least 95% of the antimicrobial activity of SEQ ID NO: 297 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0566] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 297 and at least 100% of the antimicrobial activity of SEQ ID NO: 297 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0567] In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 297. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 297 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0568] In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having

lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 297 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 297 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 249 of SEQ ID NO: 297 and has lysozyme activity.

[0569] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 300.

[0570] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 300 and at least 70% of the antimicrobial activity of SEQ ID NO: 300 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0571] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 300 and at least 80% of the antimicrobial activity of SEQ ID NO: 300 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0572] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 300 and at least 90% of the antimicrobial activity of SEQ ID NO: 300 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0573] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least

98%, at least 99%, or 100% sequence identity to SEQ ID NO: 300 and at least 95% of the antimicrobial activity of SEQ ID NO: 300 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0574] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 300 and at least 100% of the antimicrobial activity of SEQ ID NO: 300 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0575] In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 300. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 300 against *Clostridium perfringens* using the conditions 50% MHB, PH 6.

[0576] In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 300 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 300 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 247 of SEQ ID NO: 300 and has lysozyme activity.

[0577] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 303.

[0578] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID

NO: 303 and at least 70% of the antimicrobial activity of SEQ ID NO: 303 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0579] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 303 and at least 80% of the antimicrobial activity of SEQ ID NO: 303 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0580] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 303 and at least 90% of the antimicrobial activity of SEQ ID NO: 303 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0581] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 303 and at least 95% of the antimicrobial activity of SEQ ID NO: 303 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0582] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 303 and at least 100% of the antimicrobial activity of SEQ ID NO: 303 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0583] In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 303. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 303 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0584] In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having

lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 303 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 303 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 250 of SEQ ID NO: 303 and has lysozyme activity.

[0585] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 306 and at least 70% of the antimicrobial activity of SEQ ID NO: 306 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0586] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 306 and at least 80% of the antimicrobial activity of SEQ ID NO: 306 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0587] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 306 and at least 90% of the antimicrobial activity of SEQ ID NO: 306 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0588] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 306 and at least 90% of the antimicrobial activity of SEQ ID NO: 306 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

[0589] In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least

98%, at least 99%, or 100% sequence identity to SEQ ID NO: 306 and at least 95% of the antimicrobial activity of SEQ ID NO: 306 against *Clostridium perfringens* using the conditions 50% MHB, PH 6.

**[0590]** In a further embodiment, the invention relates to an animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity has at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 306 and at least 100% of the antimicrobial activity of SEQ ID NO: 306 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

**[0591]** In a further embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity differs by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 306. In an embodiment, the polypeptide has at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the antimicrobial activity of SEQ ID NO: 306 against *Clostridium perfringens* using the conditions 50% MHB, PH 6.

**[0592]** In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of the amino acid sequence of SEQ ID NO: 306 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 306 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In a preferred embodiment, the animal feed or animal feed additive comprises one or more polypeptides having lysozyme activity, wherein the polypeptide having lysozyme activity comprising or consists of amino acids 1 to 240 of SEQ ID NO: 306 and has lysozyme activity.

#### Novel Lysozymes of the Invention

**[0593]** The invention further relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 256 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have lysozyme activity. In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from the mature polypeptide of SEQ ID NO: 256. In an embodiment, the polypeptide has been isolated. In an embodiment, the

polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of the mature polypeptide of SEQ ID NO: 256.

**[0594]** A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 256 or an allelic variant thereof; comprises or consists of the amino acid sequence of SEQ ID NO: 256 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO: 256. In another aspect, the polypeptide comprises or consists of amino acids 1 to 245 of SEQ ID NO: 256.

**[0595]** The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 257 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 70% of the lysozyme activity of SEQ ID NO: 257.

**[0596]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 257 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 80% of the lysozyme activity of SEQ ID NO: 257.

**[0597]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 257 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 90% of the lysozyme activity of SEQ ID NO: 257.

**[0598]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 257 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 95% of the lysozyme activity of SEQ ID NO: 257.

**[0599]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 257 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 100% of the lysozyme activity of SEQ ID NO: 257.

**[0600]** In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 257. In an embodiment,

the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 257.

[0601] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 257 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 257 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of amino acids 1 to 245 of SEQ ID NO: 257 and has lysozyme activity.

[0602] In another aspect, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 255, (ii) the cDNA sequence thereof; or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). In an embodiment, the polypeptide has been isolated.

[0603] In another embodiment, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 255 or the cDNA sequence thereof of at least 80%, e.g., at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%. In a further embodiment, the polypeptide has been isolated.

[0604] In another embodiment, the present invention relates to variants of the mature polypeptide of SEQ ID NO: 257 comprising a substitution, and/or deletion, and/or insertion at one or more (e.g., several) positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 257 is not more than 49, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49. In another embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 257 is between 1 and 45, such as 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 257 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In another embodiment, the number of substitutions and/or deletions and/or insertions in SEQ ID NO: 257 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of substitutions in SEQ ID NO: 257 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of conservative substitutions in SEQ ID NO: 257 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In an embodiment, the variant has

at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 257.

[0605] The invention further relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 266 of at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have lysozyme activity. In one aspect, the polypeptides differ by up to 12 amino acids, e.g., between 1 and 12 amino acids, such as 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acids from the mature polypeptide of SEQ ID NO: 266. In an embodiment, the polypeptide has been isolated. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of the mature polypeptide of SEQ ID NO: 266.

[0606] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 266 or an allelic variant thereof; comprises or consists of the amino acid sequence of SEQ ID NO: 266 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids, at least 240 amino acids or at least 245 amino acids. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO: 266. In another aspect, the polypeptide comprises or consists of amino acids 1 to 248 of SEQ ID NO: 266.

[0607] The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 267 of at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 70% of the lysozyme activity of SEQ ID NO: 267.

[0608] The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 267 of at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 80% of the lysozyme activity of SEQ ID NO: 267.

[0609] The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 267 of at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 90% of the lysozyme activity of SEQ ID NO: 267.

[0610] The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 267 of at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 95% of the lysozyme activity of SEQ ID NO: 267.

[0611] The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 267 of at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 100% of the lysozyme activity of SEQ ID NO: 267.

[0612] In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 12 amino acids, such as 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 amino acids from SEQ ID NO: 267. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 267.

[0613] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID

NO: 267 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 267 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids, at least 240 amino acids or at least 245 amino acids. In another aspect, the polypeptide comprises or consists of amino acids 1 to 248 of SEQ ID NO: 267 and has lysozyme activity.

[0614] In another aspect, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide that hybridizes under very high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 265, (ii) the cDNA sequence thereof; or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). In an embodiment, the polypeptide has been isolated.

[0615] In another embodiment, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 265 or the cDNA sequence thereof of at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100%. In a further embodiment, the polypeptide has been isolated.

[0616] In another embodiment, the present invention relates to variants of the mature polypeptide of SEQ ID NO: 267 comprising a substitution, and/or deletion, and/or insertion at one or more (e.g., several) positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 267 is not more than 12, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12. In another embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 267 is between 1 and 12, such as 1-10 or 1-5 positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 267 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In another embodiment, the number of substitutions and/or deletions and/or insertions in SEQ ID NO: 267 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of substitutions in SEQ ID NO: 267 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of conservative substitutions in SEQ ID NO: 267 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In an embodiment, the variant has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 267.

[0617] The amino acid changes in the mature polypeptide of SEQ ID NO: 256, SEQ ID NO: 257, the mature polypeptide of SEQ ID NO: 266 or the mature polypeptide of SEQ ID NO: 267 described above may be of a minor nature, that is conservative amino acid substitutions or insertions that do not significantly affect the folding and/or activity of the protein; small deletions, typically of 1-30 amino acids; small amino- or carboxyl-terminal extensions, such as an

amino-terminal methionine residue; a small linker peptide of up to 20-25 residues; or a small extension that facilitates purification by changing net charge or another function, such as a poly-histidine tract, an antigenic epitope or a binding domain.

[0618] Examples of conservative substitutions are within the groups of basic amino acids (arginine, lysine and histidine), acidic amino acids (glutamic acid and aspartic acid), polar amino acids (glutamine and asparagine), hydrophobic amino acids (leucine, isoleucine and valine), aromatic amino acids (phenylalanine, tryptophan and tyrosine), and small amino acids (glycine, alanine, serine, threonine and methionine). Amino acid substitutions that do not generally alter specific activity are known in the art and are described, for example, by H. Neurath and R. L. Hill, 1979, In, *The Proteins*, Academic Press, New York. Common substitutions are Ala/Ser, Val/Ile, Asp/Glu, Thr/Ser, Ala/Gly, Ala/Thr, Ser/Asn, Ala/Val, Ser/Gly, Tyr/Phe, Ala/Pro, Lys/Arg, Asp/Asn, Leu/Ile, Leu/Val, Ala/Glu, and Asp/Gly.

[0619] Essential amino acids in a polypeptide can be identified according to procedures known in the art, such as site-directed mutagenesis or alanine-scanning mutagenesis (Cunningham and Wells, 1989, *Science* 244:1081-1085). In the latter technique, single alanine mutations are introduced at every residue in the molecule, and the resultant mutant molecules are tested for lysozyme activity to identify amino acid residues that are critical to the activity of the molecule. See also, Hilton et al., 1996, *J. Biol. Chem.* 271:4699-4708. The active site of the enzyme or other biological interaction can also be determined by physical analysis of structure, as determined by such techniques as nuclear magnetic resonance, crystallography, electron diffraction, or photoaffinity labelling, in conjunction with mutation of putative contact site amino acids. See, for example, de Vos et al., 1992, *Science* 255:306-312; Smith et al., 1992, *J. Mol. Biol.* 224:899-904; Wlodaver et al., 1992, *FEBS Lett.* 309:59-64. The identity of essential amino acids can also be inferred from an alignment with a related polypeptide.

[0620] Single or multiple amino acid substitutions, deletions, and/or insertions can be made and tested using known methods of mutagenesis, recombination, and/or shuffling, followed by a relevant screening procedure, such as those disclosed by Reidhaar-Olson and Sauer, 1988, *Science* 241: 53-57; Bowie and Sauer, 1989, *Proc. Natl. Acad. Sci. USA* 86:2152-2156; WO 95/17413; or WO 95/22625. Other methods that can be used include error-prone PCR, phage display (e.g., Lowman et al., 1991, *Biochemistry* 30:10832-10837; U.S. Pat. No. 5,223,409; WO 92/06204), and region-directed mutagenesis (Derbyshire et al., 1986, *Gene* 46:145; Ner et al., 1988, *DNA* 7:127).

[0621] Mutagenesis/shuffling methods can be combined with high-throughput, automated screening methods to detect activity of cloned, mutagenized polypeptides expressed by host cells (Ness et al., 1999, *Nature Biotechnology* 17:893-896). Mutagenized DNA molecules that encode active polypeptides can be recovered from the host cells and rapidly sequenced using standard methods in the art. These methods allow the rapid determination of the importance of individual amino acid residues in a polypeptide.

[0622] The polypeptide may be a hybrid polypeptide in which a region of one polypeptide is fused at the N-terminus or the C-terminus of a region of another polypeptide.

[0623] The polypeptide may be a fusion polypeptide or cleavable fusion polypeptide in which another polypeptide is fused at the N-terminus or the C-terminus of the polypeptide of the present invention. A fusion polypeptide is produced by fusing a polynucleotide encoding another polypeptide to a polynucleotide of the present invention. Techniques for producing fusion polypeptides are known in the art, and include ligating the coding sequences encoding the polypeptides so that they are in frame and that expression of the fusion polypeptide is under control of the same promoter(s) and terminator. Fusion polypeptides may also be constructed using intein technology in which fusion polypeptides are created post-translationally (Cooper et al., 1993, *EMBO J.* 12:2575-2583; Dawson et al., 1994, *Science* 266:776-779).

[0624] A fusion polypeptide can further comprise a cleavage site between the two polypeptides. Upon secretion of the fusion protein, the site is cleaved releasing the two polypeptides. Examples of cleavage sites include, but are not limited to, the sites disclosed in Martin et al., 2003, *J. Ind. Microbiol. Biotechnol.* 3:568-576; Svetina et al., 2000, *J. Biotechnol.* 76:245-251; Rasmussen-Wilson et al., 1997, *Appl. Environ. Microbiol.* 63:3488-3493; Ward et al., 1995, *Biotechnology* 13:498-503; and Contreras et al., 1991, *Biotechnology* 9:378-381; Eaton et al., 1986, *Biochemistry* 25:505-512; Collins-Racie et al., 1995, *Biotechnology* 13:982-987; Carter et al., 1989, *Proteins: Structure, Function, and Genetics* 6:240-248; and Stevens, 2003, *Drug Discovery World* 4:35-48.

[0625] The invention further relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 288 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have lysozyme activity. In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from the mature polypeptide of SEQ ID NO: 288. In an embodiment, the polypeptide has been isolated. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of the mature polypeptide of SEQ ID NO: 288.

[0626] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 288 or an allelic variant thereof; comprises or consists of the amino acid sequence of SEQ ID NO: 288 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO: 288. In another aspect, the polypeptide comprises or consists of amino acids 1 to 245 of SEQ ID NO: 288.

[0627] The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 291 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least

92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 70% of the lysozyme activity of SEQ ID NO: 291.

[0628] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 291 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 80% of the lysozyme activity of SEQ ID NO: 291.

[0629] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 291 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 90% of the lysozyme activity of SEQ ID NO: 291.

[0630] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 291 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 95% of the lysozyme activity of SEQ ID NO: 291.

[0631] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 291 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 100% of the lysozyme activity of SEQ ID NO: 291.

[0632] In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 291. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 291.

[0633] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 291 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 291 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of amino acids 1 to 245 of SEQ ID NO: 291 and has lysozyme activity.

[0634] In another aspect, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) the mature polypeptide coding

sequence of SEQ ID NO: 287, (ii) the cDNA sequence thereof; or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). In an embodiment, the polypeptide has been isolated.

[0635] In another embodiment, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 287 or the cDNA sequence thereof of at least 80%, e.g., at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%. In a further embodiment, the polypeptide has been isolated.

[0636] In another embodiment, the present invention relates to variants of the mature polypeptide of SEQ ID NO: 291 comprising a substitution, and/or deletion, and/or insertion at one or more (e.g., several) positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 291 is not more than 49, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49. In another embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 291 is between 1 and 45, such as 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 291 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In another embodiment, the number of substitutions and/or deletions and/or insertions in SEQ ID NO: 291 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of substitutions in SEQ ID NO: 291 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of conservative substitutions in SEQ ID NO: 291 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In an embodiment, the variant has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 291.

[0637] The invention further relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 293 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have lysozyme activity. In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from the mature polypeptide of SEQ ID NO: 293. In an embodiment, the polypeptide has been isolated. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of the mature polypeptide of SEQ ID NO: 293.

[0638] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 293 or an allelic variant thereof; comprises or consists of the amino acid sequence of SEQ ID NO: 293 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO: 293. In another aspect, the polypeptide comprises or consists of amino acids 1 to 249 of SEQ ID NO: 293.

[0639] The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 294 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 70% of the lysozyme activity of SEQ ID NO: 294.

[0640] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 294 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 80% of the lysozyme activity of SEQ ID NO: 294.

[0641] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 294 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 90% of the lysozyme activity of SEQ ID NO: 294.

[0642] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 294 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 95% of the lysozyme activity of SEQ ID NO: 294.

[0643] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 294 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 100% of the lysozyme activity of SEQ ID NO: 294.

[0644] In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 294. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 294.

**[0645]** A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 294 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 294 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of amino acids 1 to 249 of SEQ ID NO: 294 and has lysozyme activity.

**[0646]** In another aspect, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 292, (ii) the cDNA sequence thereof; or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). In an embodiment, the polypeptide has been isolated.

**[0647]** In another embodiment, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 292 or the cDNA sequence thereof of at least 80%, e.g., at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%. In a further embodiment, the polypeptide has been isolated.

**[0648]** In another embodiment, the present invention relates to variants of the mature polypeptide of SEQ ID NO: 294 comprising a substitution, and/or deletion, and/or insertion at one or more (e.g., several) positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 294 is not more than 49, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49. In another embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 294 is between 1 and 45, such as 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 294 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In another embodiment, the number of substitutions and/or deletions and/or insertions in SEQ ID NO: 294 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of substitutions in SEQ ID NO: 294 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of conservative substitutions in SEQ ID NO: 294 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In an embodiment, the variant has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 294.

**[0649]** The invention further relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 296 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have lysozyme activity. In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from the mature polypeptide of SEQ ID NO: 296. In an embodiment, the polypeptide has been isolated. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of the mature polypeptide of SEQ ID NO: 296.

**[0650]** A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 296 or an allelic variant thereof; comprises or consists of the amino acid sequence of SEQ ID NO: 296 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO: 296. In another aspect, the polypeptide comprises or consists of amino acids 1 to 245 of SEQ ID NO: 296.

**[0651]** The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 297 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 70% of the lysozyme activity of SEQ ID NO: 297.

**[0652]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 297 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 80% of the lysozyme activity of SEQ ID NO: 297.

**[0653]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 297 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 90% of the lysozyme activity of SEQ ID NO: 297.

**[0654]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 297 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 95% of the lysozyme activity of SEQ ID NO: 297.

**[0655]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 297 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 100% of the lysozyme activity of SEQ ID NO: 297.

**[0656]** In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 297. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 297.

**[0657]** A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 297 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 297 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of amino acids 1 to 245 of SEQ ID NO: 297 and has lysozyme activity.

**[0658]** In another aspect, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 295, (ii) the cDNA sequence thereof; or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). In an embodiment, the polypeptide has been isolated.

**[0659]** In another embodiment, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 295 or the cDNA sequence thereof of at least 80%, e.g., at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%. In a further embodiment, the polypeptide has been isolated.

**[0660]** In another embodiment, the present invention relates to variants of the mature polypeptide of SEQ ID NO: 297 comprising a substitution, and/or deletion, and/or insertion at one or more (e.g., several) positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 297 is not more than 49, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49. In another embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid

insertions or any combination thereof in SEQ ID NO: 297 is between 1 and 45, such as 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 297 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In another embodiment, the number of substitutions and/or deletions and/or insertions in SEQ ID NO: 297 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of substitutions in SEQ ID NO: 297 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of conservative substitutions in SEQ ID NO: 297 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In an embodiment, the variant has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 297.

**[0661]** The invention further relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 299 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have lysozyme activity. In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from the mature polypeptide of SEQ ID NO: 299. In an embodiment, the polypeptide has been isolated. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of the mature polypeptide of SEQ ID NO: 299.

**[0662]** A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 299 or an allelic variant thereof; comprises or consists of the amino acid sequence of SEQ ID NO: 299 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO: 299. In another aspect, the polypeptide comprises or consists of amino acids 1 to 247 of SEQ ID NO: 299.

**[0663]** The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 300 of at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 70% of the lysozyme activity of SEQ ID NO: 300.

**[0664]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 300 of at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and

wherein the polypeptide has at least at least 80% of the lysozyme activity of SEQ ID NO: 300.

[0665] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 300 of at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 90% of the lysozyme activity of SEQ ID NO: 300.

[0666] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 300 of at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 95% of the lysozyme activity of SEQ ID NO: 300.

[0667] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 300 of at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 100% of the lysozyme activity of SEQ ID NO: 300.

[0668] In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 300. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 300.

[0669] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 300 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 300 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of amino acids 1 to 247 of SEQ ID NO: 300 and has lysozyme activity.

[0670] In another aspect, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 298, (ii) the cDNA sequence thereof; or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). In an embodiment, the polypeptide has been isolated.

[0671] In another embodiment, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 298 or the cDNA sequence thereof of at least 80%, e.g., at least 85%,

at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%. In a further embodiment, the polypeptide has been isolated.

[0672] In another embodiment, the present invention relates to variants of the mature polypeptide of SEQ ID NO: 300 comprising a substitution, and/or deletion, and/or insertion at one or more (e.g., several) positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 300 is not more than 49, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49. In another embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 300 is between 1 and 45, such as 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 300 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In another embodiment, the number of substitutions and/or deletions and/or insertions in SEQ ID NO: 300 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of substitutions in SEQ ID NO: 300 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of conservative substitutions in SEQ ID NO: 300 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In an embodiment, the variant has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 300.

[0673] The invention further relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 302 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have lysozyme activity. In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from the mature polypeptide of SEQ ID NO: 302. In an embodiment, the polypeptide has been isolated. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of the mature polypeptide of SEQ ID NO: 302.

[0674] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 302 or an allelic variant thereof; comprises or consists of the amino acid sequence of SEQ ID NO: 302 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another

aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO: 302. In another aspect, the polypeptide comprises or consists of amino acids 1 to 250 of SEQ ID NO: 302.

**[0675]** The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 303 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 70% of the lysozyme activity of SEQ ID NO: 303.

**[0676]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 303 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 80% of the lysozyme activity of SEQ ID NO: 303.

**[0677]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 303 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 90% of the lysozyme activity of SEQ ID NO: 303.

**[0678]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 303 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 95% of the lysozyme activity of SEQ ID NO: 303.

**[0679]** In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 303 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 100% of the lysozyme activity of SEQ ID NO: 303.

**[0680]** In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 303. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 303.

**[0681]** A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 303 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 303 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or

at least 240 amino acids. In another aspect, the polypeptide comprises or consists of amino acids 1 to 250 of SEQ ID NO: 303 and has lysozyme activity.

**[0682]** In another aspect, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 301, (ii) the cDNA sequence thereof; or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). In an embodiment, the polypeptide has been isolated.

**[0683]** In another embodiment, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 301 or the cDNA sequence thereof of at least 80%, e.g., at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%. In a further embodiment, the polypeptide has been isolated.

**[0684]** In another embodiment, the present invention relates to variants of the mature polypeptide of SEQ ID NO: 303 comprising a substitution, and/or deletion, and/or insertion at one or more (e.g., several) positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 303 is not more than 49, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49. In another embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 303 is between 1 and 45, such as 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 303 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In another embodiment, the number of substitutions and/or deletions and/or insertions in SEQ ID NO: 303 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of substitutions in SEQ ID NO: 303 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of conservative substitutions in SEQ ID NO: 303 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In an embodiment, the variant has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 303.

**[0685]** The invention further relates to polypeptides having a sequence identity to the mature polypeptide of SEQ ID NO: 305 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, which have lysozyme activity. In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as 1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49 or 50 amino acids from SEQ ID NO: 305. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 305.

9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from the mature polypeptide of SEQ ID NO: 305. In an embodiment, the polypeptide has been isolated. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of the mature polypeptide of SEQ ID NO: 305.

[0686] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 305 or an allelic variant thereof; comprises or consists of the amino acid sequence of SEQ ID NO: 305 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of the mature polypeptide of SEQ ID NO: 305. In another aspect, the polypeptide comprises or consists of amino acids 1 to 240 of SEQ ID NO: 305.

[0687] The present invention further relates to polypeptides having a sequence identity to SEQ ID NO: 306 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 70% of the lysozyme activity of SEQ ID NO: 306.

[0688] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 306 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 80% of the lysozyme activity of SEQ ID NO: 306.

[0689] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 306 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 90% of the lysozyme activity of SEQ ID NO: 306.

[0690] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 306 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 95% of the lysozyme activity of SEQ ID NO: 306.

[0691] In a particular embodiment, the invention relates to polypeptides having a sequence identity to SEQ ID NO: 306 of at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%, and wherein the polypeptide has at least at least 100% of the lysozyme activity of SEQ ID NO: 306.

[0692] In one aspect, the polypeptides differ by up to 49 amino acids, e.g., between 1 and 49 amino acids, such as

1-45, 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 amino acids, or 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 amino acids from SEQ ID NO: 306. In an embodiment, the polypeptide has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 306.

[0693] A polypeptide of the present invention preferably comprises or consists of the amino acid sequence of SEQ ID NO: 306 or an allelic variant thereof having lysozyme activity; comprises or consists of the amino acid sequence of SEQ ID NO: 306 and a N-terminal and/or C-terminal His-tag and/or HQ-tag; or is a fragment thereof having lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids. In another aspect, the polypeptide comprises or consists of amino acids 1 to 240 of SEQ ID NO: 306 and has lysozyme activity.

[0694] In another aspect, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions, or very high stringency conditions with (i) the mature polypeptide coding sequence of SEQ ID NO: 304, (ii) the cDNA sequence thereof; or (iii) the full-length complement of (i) or (ii) (Sambrook et al., 1989, *Molecular Cloning, A Laboratory Manual*, 2d edition, Cold Spring Harbor, New York). In an embodiment, the polypeptide has been isolated.

[0695] In another embodiment, the present invention relates to a polypeptide having lysozyme activity encoded by a polynucleotide having a sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 304 or the cDNA sequence thereof of at least 80%, e.g., at least 85%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100%. In a further embodiment, the polypeptide has been isolated.

[0696] In another embodiment, the present invention relates to variants of the mature polypeptide of SEQ ID NO: 306 comprising a substitution, and/or deletion, and/or insertion at one or more (e.g., several) positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 306 is not more than 49, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49. In another embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 306 is between 1 and 45, such as 1-40, 1-35, 1-30, 1-25, 1-20, 1-15, 1-10 or 1-5 positions. In an embodiment, the number of positions comprising one or more amino acid substitutions, and/or one or more amino acid deletions, and/or one or more amino acid insertions or any combination thereof in SEQ ID NO: 306 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In another embodiment, the number of substitutions and/or deletions and/or insertions in SEQ ID NO: 306 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further

embodiment, the number of substitutions in SEQ ID NO: 306 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In a further embodiment, the number of conservative substitutions in SEQ ID NO: 306 is not more than 10, e.g., 1, 2, 3, 4, 5, 6, 7, 8, 9 or 10. In an embodiment, the variant has at least at least 70%, e.g., at least 80%, at least 90%, at least 95% or at least 100% of the lysozyme activity of SEQ ID NO: 306.

#### Sources of Polypeptides Having Lysozyme Activity

[0697] A polypeptide having lysozyme activity of the present invention may be obtained from microorganisms of any genus. For purposes of the present invention, the term "obtained from" as used herein in connection with a given source shall mean that the polypeptide encoded by a polynucleotide is produced by the source or by a strain in which the polynucleotide from the source has been inserted. In one aspect, the polypeptide obtained from a given source is secreted extracellularly.

[0698] The polypeptide may be a fungal polypeptide. In one aspect, the polypeptide is a polypeptide having lysozyme activity from a fungus of the class Pezizomycetes, such as from the order Pezizales, or from the family Pyronemataceae, or from the genus *Trichophaea* or from the species *Trichophaea saccata* or *Trichophaea minuta*. In another aspect, the polypeptide is a polypeptide having lysozyme activity from a fungus of the class Sordariomycetes, such as from the order Hypocreales, or from the family Hypocreaceae, or from the genus *Trichoderma* or from the species *Trichoderma harzianum*.

[0699] In another aspect, the polypeptide is a polypeptide having lysozyme activity from a fungus of the class Sordariomycetes, such as from the order Sordariales, or from the family Chaetomiaceae, or from the genus *Chaetomium* or from the species *Chaetomium* sp. ZY 287.

[0700] In another aspect, the polypeptide is a polypeptide having lysozyme activity from a fungus of the order Mortierellales, or from the family Mortierellaceae, or from the genus *Mortierella* or from the species *Mortierella* sp. ZY 002.

[0701] In another aspect, the polypeptide is a polypeptide having lysozyme activity from a fungus of the class Sordariomycetes, such as from the order Hypocreales, or from the family Clavicipitaceae, or from the genus *Metarhizium* or from the species *Metarhizium* sp. XZ2431.

[0702] In another aspect, the polypeptide is a polypeptide having lysozyme activity from a fungus of the class Leotiomycetes, such as from the family Pseudeurotiaceae, or from the genus *Geomyces* or from the species *Geomyces auratus*.

[0703] In another aspect, the polypeptide is a polypeptide having lysozyme activity from a fungus of the class Sordariomycetes, such as from the order Hypocreales, or from the family Nectriaceae, or from the genus *Ilyonectria* or from the species *Ilyonectria rufa*.

[0704] It will be understood that for the aforementioned species, the invention encompasses both the perfect and imperfect states, and other taxonomic equivalents, e.g., anamorphs, regardless of the species name by which they are known. Those skilled in the art will readily recognize the identity of appropriate equivalents.

[0705] Strains of these species are readily accessible to the public in a number of culture collections, such as the American Type Culture Collection (ATCC), Deutsche Sam-

mlung von Mikroorganismen und Zellkulturen GmbH (DSMZ), Centraalbureau Voor Schimmelcultures (CBS), and Agricultural Research Service Patent Culture Collection, Northern Regional Research Center (NRRL).

[0706] The polypeptide may be identified and obtained from other sources including microorganisms isolated from nature (e.g., soil, composts, water, etc.) or DNA samples obtained directly from natural materials (e.g., soil, composts, water, etc.) using the above-mentioned probes. Techniques for isolating microorganisms and DNA directly from natural habitats are well known in the art. A polynucleotide encoding the polypeptide may then be obtained by similarly screening a genomic DNA or cDNA library of another microorganism or mixed DNA sample. Once a polynucleotide encoding a polypeptide has been detected with the probe(s), the polynucleotide can be isolated or cloned by utilizing techniques that are known to those of ordinary skill in the art (see, e.g., Sambrook et al., 1989, *supra*).

#### Polynucleotides

[0707] The present invention also relates to polynucleotides encoding a polypeptide of the present invention, as described herein. In an embodiment, the polynucleotide encoding the polypeptide of the present invention has been isolated.

[0708] The techniques used to isolate or clone a polynucleotide are known in the art and include isolation from genomic DNA or cDNA, or a combination thereof. The cloning of the polynucleotides from genomic DNA can be effected, e.g., by using the well-known polymerase chain reaction (PCR) or antibody screening of expression libraries to detect cloned DNA fragments with shared structural features. See, e.g., Innis et al., 1990, *PCR: A Guide to Methods and Application*, Academic Press, New York. Other nucleic acid amplification procedures such as ligase chain reaction (LCR), ligation activated transcription (LAT) and polynucleotide-based amplification (NASBA) may be used. The polynucleotides may be cloned from a strain of *Trichophaea* or a strain of *Trichoderma*, or a related organism and thus, for example, may be an allelic or species variant of the polypeptide encoding region of the polynucleotide.

[0709] Modification of a polynucleotide encoding a polypeptide of the present invention may be necessary for synthesizing polypeptides substantially similar to the polypeptide. The term "substantially similar" to the polypeptide refers to non-naturally occurring forms of the polypeptide. These polypeptides may differ in some engineered way from the polypeptide isolated from its native source, e.g., variants that differ in specific activity, thermostability, pH optimum, or the like. The variants may be constructed on the basis of the polynucleotide presented as the mature polypeptide coding sequence of SEQ ID NO: 255, SEQ ID NO: 265, SEQ ID NO: 287, SEQ ID NO: 292, SEQ ID NO: 295, SEQ ID NO: 298, SEQ ID NO: 301, SEQ ID NO: 304, or the cDNA sequence thereof, e.g., a subsequence thereof, and/or by introduction of nucleotide substitutions that do not result in a change in the amino acid sequence of the polypeptide, but which correspond to the codon usage of the host organism intended for production of the enzyme, or by introduction of nucleotide substitutions that may give rise to a different amino acid sequence. For a general description of nucleotide substitution, see, e.g., Ford et al., 1991, *Protein Expression and Purification* 2:95-107.

### Nucleic Acid Constructs

[0710] The present invention also relates to nucleic acid constructs comprising a polynucleotide of the present invention operably linked to one or more control sequences that direct the expression of the coding sequence in a suitable host cell under conditions compatible with the control sequences.

[0711] The polynucleotide may be manipulated in a variety of ways to provide for expression of the polypeptide. Manipulation of the polynucleotide prior to its insertion into a vector may be desirable or necessary depending on the expression vector. The techniques for modifying polynucleotides utilizing recombinant DNA methods are well known in the art.

[0712] The control sequence may be a promoter, a polynucleotide that is recognized by a host cell for expression of a polynucleotide encoding a polypeptide of the present invention. The promoter contains transcriptional control sequences that mediate the expression of the polypeptide. The promoter may be any polynucleotide that shows transcriptional activity in the host cell including mutant, truncated, and hybrid promoters, and may be obtained from genes encoding extracellular or intracellular polypeptides either homologous or heterologous to the host cell.

[0713] Examples of suitable promoters for directing transcription of the nucleic acid constructs of the present invention in a bacterial host cell are the promoters obtained from the *Bacillus amyloliquefaciens* alpha-amylase gene (amyQ), *Bacillus licheniformis* alpha-amylase gene (amyL), *Bacillus licheniformis* penicillinase gene (penP), *Bacillus stearothermophilus* maltogenic amylase gene (amyM), *Bacillus subtilis* levansucrase gene (sacB), *Bacillus subtilis* xyIA and xyIB genes, *Bacillus thuringiensis* cryIIIA gene (Agaisse and Lereclus, 1994, *Molecular Microbiology* 13: 97-107), *E. coli* lac operon, *E. coli* trc promoter (Egon et al., 1988, *Gene* 69:301-315), *Streptomyces coelicolor* agarase gene (dagA), and prokaryotic beta-lactamase gene (Villa-Kamaroff et al., 1978, *Proc. Natl. Acad. Sci. USA* 75:3727-3731), as well as the tac promoter (DeBoer et al., 1983, *Proc. Natl. Acad. Sci. USA* 80:21-25). Further promoters are described in "Useful proteins from recombinant bacteria" in Gilbert et al., 1980, *Scientific American* 242:74-94; and in Sambrook et al., 1989, supra. Examples of tandem promoters are disclosed in WO 99/43835.

[0714] Examples of suitable promoters for directing transcription of the nucleic acid constructs of the present invention in a filamentous fungal host cell are promoters obtained from the genes for *Aspergillus nidulans* acetamidase, *Aspergillus niger* neutral alpha-amylase, *Aspergillus niger* acid stable alpha-amylase, *Aspergillus niger* or *Aspergillus awamori* glucoamylase (glaA), *Aspergillus oryzae* TAKA amylase, *Aspergillus oryzae* alkaline protease, *Aspergillus oryzae* triose phosphate isomerase, *Fusarium oxysporum* trypsin-like protease (WO 96/00787), *Fusarium venenatum* amyloglucosidase (WO 00/56900), *Fusarium venenatum* Daria (WO 00/56900), *Fusarium venenatum* Quinn (WO 00/56900), *Rhizomucor miehei* lipase, *Rhizomucor miehei* aspartic proteinase, *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase I, *Trichoderma reesei* cellobiohydrolase II, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* xylanase III, *Trichoderma reesei* translation elongation factor.

[0715] In a yeast host, useful promoters are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* galactokinase (GAL1), *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH1, ADH2/GAP), *Saccharomyces cerevisiae* triose phosphate isomerase (TPI), *Saccharomyces cerevisiae* metallothionein (CUP 1), and *Saccharomyces cerevisiae* 3-phosphoglycerate kinase. Other useful promoters for yeast host cells are described by Romanos et al., 1992, *Yeast* 8:423-488.

[0716] The control sequence may also be a transcription terminator, which is recognized by a host cell to terminate transcription. The terminator is operably linked to the 3'-terminus of the polynucleotide encoding the polypeptide. Any terminator that is functional in the host cell may be used in the present invention.

[0717] Preferred terminators for bacterial host cells are obtained from the genes for *Bacillus clausii* alkaline protease (aprH), *Bacillus licheniformis* alpha-amylase (amyL), and *Escherichia coli* ribosomal RNA (rmnB).

[0718] Preferred terminators for filamentous fungal host cells are obtained from the genes for *Aspergillus nidulans* acetamidase, *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* glucoamylase, *Aspergillus niger* alpha-glucosidase, *Aspergillus oryzae* TAKA amylase, *Fusarium oxysporum* trypsin-like protease, *Trichoderma reesei* beta-glucosidase, *Trichoderma reesei* cellobiohydrolase I, *Trichoderma reesei* cellobiohydrolase II, *Trichoderma reesei* endoglucanase I, *Trichoderma reesei* endoglucanase II, *Trichoderma reesei* endoglucanase III, *Trichoderma reesei* endoglucanase V, *Trichoderma reesei* xylanase I, *Trichoderma reesei* xylanase II, *Trichoderma reesei* xylanase III, *Trichoderma reesei* beta-xylanidase, and *Trichoderma reesei* translation elongation factor.

[0719] Preferred terminators for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase, *Saccharomyces cerevisiae* cytochrome C (CYC1), and *Saccharomyces cerevisiae* glyceraldehyde-3-phosphate dehydrogenase. Other useful terminators for yeast host cells are described by Romanos et al., 1992, supra.

[0720] The control sequence may also be an mRNA stabilizer region downstream of a promoter and upstream of the coding sequence of a gene which increases expression of the gene.

[0721] Examples of suitable mRNA stabilizer regions are obtained from a *Bacillus thuringiensis* cryIIIA gene (WO 94/25612) and a *Bacillus subtilis* SP 82 gene (Hue et al., 1995, *Journal of Bacteriology* 177:3465-3471).

[0722] The control sequence may also be a leader, a nontranslated region of an mRNA that is important for translation by the host cell. The leader is operably linked to

the 5'-terminus of the polynucleotide encoding the polypeptide. Any leader that is functional in the host cell may be used.

[0723] Preferred leaders for filamentous fungal host cells are obtained from the genes for *Aspergillus oryzae* TAKA amylase and *Aspergillus nidulans* triose phosphate isomerase.

[0724] Suitable leaders for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae* enolase (ENO-1), *Saccharomyces cerevisiae* 3-phosphoglycerate kinase, *Saccharomyces cerevisiae* alpha-factor, and *Saccharomyces cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH2/GAP).

[0725] The control sequence may also be a polyadenylation sequence, a sequence operably linked to the 3'-terminus of the polynucleotide and, when transcribed, is recognized by the host cell as a signal to add polyadenosine residues to transcribed mRNA. Any polyadenylation sequence that is functional in the host cell may be used.

[0726] Preferred polyadenylation sequences for filamentous fungal host cells are obtained from the genes for *Aspergillus nidulans* anthranilate synthase, *Aspergillus niger* glucoamylase, *Aspergillus niger* alpha-glucosidase *Aspergillus oryzae* TAKA amylase, and *Fusarium oxysporum* trypsin-like protease.

[0727] Useful polyadenylation sequences for yeast host cells are described by Guo and Sherman, 1995, *Mol. Cellular Biol.* 15:5983-5990.

[0728] The control sequence may also be a signal peptide coding region that encodes a signal peptide linked to the N-terminus of a polypeptide and directs the polypeptide into the cell's secretory pathway. The 5'-end of the coding sequence of the polynucleotide may inherently contain a signal peptide coding sequence naturally linked in translation reading frame with the segment of the coding sequence that encodes the polypeptide. Alternatively, the 5'-end of the coding sequence may contain a signal peptide coding sequence that is foreign to the coding sequence. A foreign signal peptide coding sequence may be required where the coding sequence does not naturally contain a signal peptide coding sequence. Alternatively, a foreign signal peptide coding sequence may simply replace the natural signal peptide coding sequence in order to enhance secretion of the polypeptide. However, any signal peptide coding sequence that directs the expressed polypeptide into the secretory pathway of a host cell may be used.

[0729] Effective signal peptide coding sequences for bacterial host cells are the signal peptide coding sequences obtained from the genes for *Bacillus* NCIB 11837 malto-*genic* amylase, *subtilisin*, *Bacillus licheniformis* *Bacillus licheniformis* beta-lactamase, *Bacillus stearothermophilus* alpha-amylase, *Bacillus stearothermophilus* neutral proteases (nprT, nprS, nprM), and *Bacillus subtilis* prsA. Further signal peptides are described by Simonen and Palva, 1993, *Microbiological Reviews* 57:109-137.

[0730] Effective signal peptide coding sequences for filamentous fungal host cells are the signal peptide coding sequences obtained from the genes for *Aspergillus niger* neutral amylase, *Aspergillus niger* glucoamylase, *Aspergillus oryzae* TAKA amylase, *Humicola insolens* cellulase, *Humicola insolens* endoglucanase V, *Humicola lanuginosa* lipase, and *Rhizomucor miehei* aspartic proteinase.

[0731] Useful signal peptides for yeast host cells are obtained from the genes for *Saccharomyces cerevisiae*

alpha-factor and *Saccharomyces cerevisiae* invertase. Other useful signal peptide coding sequences are described by Romanos et al., 1992, supra. The control sequence may also be a propeptide coding sequence that encodes a propeptide positioned at the N-terminus of a polypeptide. The resultant polypeptide is known as a proenzyme or propolypeptide (or a zymogen in some cases). A propolypeptide is generally inactive and can be converted to an active polypeptide by catalytic or autocatalytic cleavage of the propeptide from the propolypeptide. The propeptide coding sequence may be obtained from the genes for *Bacillus subtilis* alkaline protease (aprE), *Bacillus subtilis* neutral protease (nprT), *Myceliophthora thermophila* laccase (WO 95/33836), *Rhizomucor miehei* aspartic proteinase, and *Saccharomyces cerevisiae* alpha-factor.

[0732] Where both signal peptide and propeptide sequences are present, the propeptide sequence is positioned next to the N-terminus of a polypeptide and the signal peptide sequence is positioned next to the N-terminus of the propeptide sequence.

[0733] It may also be desirable to add regulatory sequences that regulate expression of the polypeptide relative to the growth of the host cell. Examples of regulatory sequences are those that cause expression of the gene to be turned on or off in response to a chemical or physical stimulus, including the presence of a regulatory compound. Regulatory sequences in prokaryotic systems include the lac, tac, and trp operator systems. In yeast, the ADH2 system or GAL1 system may be used. In filamentous fungi, the *Aspergillus niger* glucoamylase promoter, *Aspergillus oryzae* TAKA alpha-amylase promoter, and *Aspergillus oryzae* glucoamylase promoter, *Trichoderma reesei* cellobiohydrolase I promoter, and *Trichoderma reesei* cellobiohydrolase II promoter may be used. Other examples of regulatory sequences are those that allow for gene amplification. In eukaryotic systems, these regulatory sequences include the dihydrofolate reductase gene that is amplified in the presence of methotrexate, and the metallothionein genes that are amplified with heavy metals. In these cases, the polynucleotide encoding the polypeptide would be operably linked to the regulatory sequence.

#### Expression Vectors

[0734] The present invention also relates to recombinant expression vectors comprising a polynucleotide of the present invention, a promoter, and transcriptional and translational stop signals. The various nucleotide and control sequences may be joined together to produce a recombinant expression vector that may include one or more convenient restriction sites to allow for insertion or substitution of the polynucleotide encoding the polypeptide at such sites. Alternatively, the polynucleotide may be expressed by inserting the polynucleotide or a nucleic acid construct comprising the polynucleotide into an appropriate vector for expression. In creating the expression vector, the coding sequence is located in the vector so that the coding sequence is operably linked with the appropriate control sequences for expression.

[0735] The recombinant expression vector may be any vector (e.g., a plasmid or virus) that can be conveniently subjected to recombinant DNA procedures and can bring about expression of the polynucleotide. The choice of the vector will typically depend on the compatibility of the

vector with the host cell into which the vector is to be introduced. The vector may be a linear or closed circular plasmid.

[0736] The vector may be an autonomously replicating vector, i.e., a vector that exists as an extrachromosomal entity, the replication of which is independent of chromosomal replication, e.g., a plasmid, an extrachromosomal element, a minichromosome, or an artificial chromosome. The vector may contain any means for assuring self-replication. Alternatively, the vector may be one that, when introduced into the host cell, is integrated into the genome and replicated together with the chromosome(s) into which it has been integrated. Furthermore, a single vector or plasmid or two or more vectors or plasmids that together contain the total DNA to be introduced into the genome of the host cell, or a transposon, may be used.

[0737] The vector preferably contains one or more selectable markers that permit easy selection of transformed, transfected, transduced, or the like cells. A selectable marker is a gene the product of which provides for biocide or viral resistance, resistance to heavy metals, prototrophy to auxotrophs, and the like.

[0738] Examples of bacterial selectable markers are *Bacillus licheniformis* or *Bacillus subtilis* dal genes, or markers that confer antibiotic resistance such as ampicillin, chloramphenicol, kanamycin, neomycin, spectinomycin, or tetracycline resistance. Suitable markers for yeast host cells include, but are not limited to, ADE2, HIS3, LEU2, LYS2, MET3, TRP1, and URA3. Selectable markers for use in a filamentous fungal host cell include, but are not limited to, adeA (phosphoribosylaminoimidazole-succinocarboxamide synthase), adeB (phosphoribosyl-aminoimidazole synthase), amdS (acetamidase), argB (ornithine carbamoyltransferase), bar (phosphinothricin acetyltransferase), hph (hygromycin phosphotransferase), niaD (nitrate reductase), pyrG (orotidine-5'-phosphate decarboxylase), sc (sulfate adenyltransferase), and trpC (anthranilate synthase), as well as equivalents thereof. Preferred for use in an *Aspergillus* cell are *Aspergillus nidulans* or *Aspergillus oryzae* amdS and pyrG genes and a *Streptomyces hygroscopicus* bar gene. Preferred for use in a *Trichoderma* cell are adeA, adeB, amdS, hph, and pyrG genes.

[0739] The selectable marker may be a dual selectable marker system as described in WO 2010/039889. In one aspect, the dual selectable marker is an hph-tk dual selectable marker system.

[0740] The vector preferably contains an element(s) that permits integration of the vector into the host cell's genome or autonomous replication of the vector in the cell independent of the genome.

[0741] For integration into the host cell genome, the vector may rely on the polynucleotide's sequence encoding the polypeptide or any other element of the vector for integration into the genome by homologous or non-homologous recombination. Alternatively, the vector may contain additional polynucleotides for directing integration by homologous recombination into the genome of the host cell at a precise location(s) in the chromosome(s). To increase the likelihood of integration at a precise location, the integrational elements should contain a sufficient number of nucleic acids, such as 100 to 10,000 base pairs, 400 to 10,000 base pairs, and 800 to 10,000 base pairs, which have a high degree of sequence identity to the corresponding target sequence to enhance the probability of homologous

recombination. The integrational elements may be any sequence that is homologous with the target sequence in the genome of the host cell. Furthermore, the integrational elements may be non-encoding or encoding polynucleotides. On the other hand, the vector may be integrated into the genome of the host cell by non-homologous recombination.

[0742] For autonomous replication, the vector may further comprise an origin of replication enabling the vector to replicate autonomously in the host cell in question. The origin of replication may be any plasmid replicator mediating autonomous replication that functions in a cell. The term "origin of replication" or "plasmid replicator" means a polynucleotide that enables a plasmid or vector to replicate in vivo.

[0743] Examples of bacterial origins of replication are the origins of replication of plasmids pBR 322, pUC 19, pACYC177, and pACYC184 permitting replication in *E. coli*, and pUB110, pE194, pTA1060, and pAMβ1 permitting replication in *Bacillus*.

[0744] Examples of origins of replication for use in a yeast host cell are the 2 micron origin of replication, ARS1, ARS4, the combination of ARS1 and CEN3, and the combination of ARS4 and CEN6.

[0745] Examples of origins of replication useful in a filamentous fungal cell are AMA1 and ANS1 (Gems et al., 1991, *Gene* 98:61-67; Cullen et al., 1987, *Nucleic Acids Res.* 15:9163-9175; WO 00/24883). Isolation of the AMA1 gene and construction of plasmids or vectors comprising the gene can be accomplished according to the methods disclosed in WO 00/24883.

[0746] More than one copy of a polynucleotide of the present invention may be inserted into a host cell to increase production of a polypeptide. An increase in the copy number of the polynucleotide can be obtained by integrating at least one additional copy of the sequence into the host cell genome or by including an amplifiable selectable marker gene with the polynucleotide where cells containing amplified copies of the selectable marker gene, and thereby additional copies of the polynucleotide, can be selected for by cultivating the cells in the presence of the appropriate selectable agent.

[0747] The procedures used to ligate the elements described above to construct the recombinant expression vectors of the present invention are well known to one skilled in the art (see, e.g., Sambrook et al., 1989, *supra*).

#### Host Cells

[0748] The present invention also relates to recombinant host cells, comprising a polynucleotide of the present invention operably linked to one or more control sequences that direct the production of a polypeptide of the present invention. A construct or vector comprising a polynucleotide is introduced into a host cell so that the construct or vector is maintained as a chromosomal integrant or as a self-replicating extra-chromosomal vector as described earlier. The term "host cell" encompasses any progeny of a parent cell that is not identical to the parent cell due to mutations that occur during replication. The choice of a host cell will to a large extent depend upon the gene encoding the polypeptide and its source.

[0749] The host cell may be any cell useful in the recombinant production of a polypeptide of the present invention, e.g., a prokaryote or a eukaryote.

[0750] The prokaryotic host cell may be any Gram-positive or Gram-negative bacterium. Gram-positive bacteria include, but are not limited to, *Bacillus*, *Clostridium*, *Enterococcus*, *Geobacillus*, *Lactobacillus*, *Lactococcus*, *Oceanobacillus*, *Staphylococcus*, *Streptococcus*, and *Streptomyces*. Gram-negative bacteria include, but are not limited to, *Campylobacter*, *E. coli*, *Flavobacterium*, *Fusobacterium*, *Helicobacter*, *Ilyobacter*, *Neisseria*, *Pseudomonas*, *Salmonella*, and *Ureaplasma*.

[0751] The bacterial host cell may be any *Bacillus* cell including, but not limited to, *Bacillus alkalophilus*, *Bacillus amyloliquefaciens*, *Bacillus brevis*, *Bacillus circulans*, *Bacillus clausii*, *Bacillus coagulans*, *Bacillus firmus*, *Bacillus laetus*, *Bacillus lenthus*, *Bacillus licheniformis*, *Bacillus megaterium*, *Bacillus pumilus*, *Bacillus stearothermophilus*, *Bacillus subtilis*, and *Bacillus thuringiensis* cells.

[0752] The bacterial host cell may also be any *Streptococcus* cell including, but not limited to, *Streptococcus equisimilis*, *Streptococcus pyogenes*, *Streptococcus uberis*, and *Streptococcus equi* subsp. *Zooepidemicus* cells.

[0753] The bacterial host cell may also be any *Streptomyces* cell including, but not limited to, *Streptomyces achromogenes*, *Streptomyces avermitilis*, *Streptomyces coelicolor*, *Streptomyces griseus*, and *Streptomyces lividans* cells.

[0754] The introduction of DNA into a *Bacillus* cell may be effected by protoplast transformation (see, e.g., Chang and Cohen, 1979, *Mol. Gen. Genet.* 168:111-115), competent cell transformation (see, e.g., Young and Spizizen, 1961, *J. Bacteriol.* 81:823-829, or Dubnau and Davidoff-Abelson, 1971, *J. Mol. Biol.* 56:209-221), electroporation (see, e.g., Shigekawa and Dower, 1988, *Biotechniques* 6:742-751), or conjugation (see, e.g., Koehler and Thorne, 1987, *J. Bacteriol.* 169:5271-5278). The introduction of DNA into an *E. coli* cell may be effected by protoplast transformation (see, e.g., Hanahan, 1983, *J. Mol. Biol.* 166:557-580) or electroporation (see, e.g., Dower et al., 1988, *Nucleic Acids Res.* 16:6127-6145). The introduction of DNA into a *Streptomyces* cell may be effected by protoplast transformation, electroporation (see, e.g., Gong et al., 2004, *Folia Microbiol.* (Praha) 49:399-405), conjugation (see, e.g., Mazodier et al., 1989, *J. Bacteriol.* 171:3583-3585), or transduction (see, e.g., Burke et al., 2001, *Proc. Natl. Acad. Sci. USA* 98:6289-6294). The introduction of DNA into a *Pseudomonas* cell may be effected by electroporation (see, e.g., Choi et al., 2006, *J. Microbiol. Methods* 64:391-397) or conjugation (see, e.g., Pinedo and Smets, 2005, *Appl. Environ. Microbiol.* 71:51-57). The introduction of DNA into a *Streptococcus* cell may be effected by natural competence (see, e.g., Perry and Kuramitsu, 1981, *Infect. Immun.* 32:1295-1297), protoplast transformation (see, e.g., Catt and Jolllick, 1991, *Microbios* 68:189-207), electroporation (see, e.g., Buckley et al., 1999, *Appl. Environ. Microbiol.* 65:3800-3804), or conjugation (see, e.g., Clewell, 1981, *Microbiol. Rev.* 45:409-436). However, any method known in the art for introducing DNA into a host cell can be used.

[0755] The host cell may also be a eukaryote, such as a mammalian, insect, plant, or fungal cell.

[0756] The host cell may be a fungal cell. "Fungi" as used herein includes the phyla Ascomycota, Basidiomycota, Chytridiomycota, and Zygomycota as well as the Oomycota and all mitosporic fungi (as defined by Hawksworth et al., In, *Ainsworth and Bisby's Dictionary of The Fungi*, 8th edition, 1995, CAB International, University Press, Cambridge, UK).

[0757] The fungal host cell may be a yeast cell. "Yeast" as used herein includes ascosporogenous yeast (Endomycetales), basidiosporogenous yeast, and yeast belonging to the Fungi Imperfecti (Blastomycetes). Since the classification of yeast may change in the future, for the purposes of this invention, yeast shall be defined as described in Biology and Activities of Yeast (Skinner, Passmore, and Davenport, editors, *Soc. App. Bacteriol. Symposium Series No. 9*, 1980).

[0758] The yeast host cell may be a *Candida*, *Hansenula*, *Kluyveromyces*, *Pichia*, *Saccharomyces*, *Schizosaccharomyces*, or *Yarrowia* cell, such as a *Kluyveromyces lactis*, *Saccharomyces carlsbergensis*, *Saccharomyces cerevisiae*, *Saccharomyces diastaticus*, *Saccharomyces douglasii*, *Saccharomyces kluyveri*, *Saccharomyces norbensis*, *Saccharomyces oviformis*, or *Yarrowia lipolytica* cell.

[0759] The fungal host cell may be a filamentous fungal cell. "Filamentous fungi" include all filamentous forms of the subdivision Eumycota and Oomycota (as defined by Hawksworth et al., 1995, supra). The filamentous fungi are generally characterized by a mycelial wall composed of chitin, cellulose, glucan, chitosan, mannan, and other complex polysaccharides. Vegetative growth is by hyphal elongation and carbon catabolism obligately aerobic. In contrast, vegetative growth by yeasts such as *Saccharomyces cerevisiae* is by budding of a unicellular thallus and carbon catabolism may be fermentative.

[0760] The filamentous fungal host cell may be an *Acremonium*, *Aspergillus*, *Aureobasidium*, *Bjerkandera*, *Ceriporiopsis*, *Chrysosporium*, *Coprinus*, *Coriolus*, *Cryptococcus*, *Filibasidium*, *Fusarium*, *Humicola*, *Magnaporthe*, *Mucor*, *Myceliophthora*, *Neocallimastix*, *Neurospora*, *Paecilomyces*, *Penicillium*, *Phanerochaete*, *Phlebia*, *Piromyces*, *Pleurotus*, *Schizophyllum*, *Talaromyces*, *Thermoascus*, *Thielavia*, *Tolypocladium*, *Trametes*, or *Trichoderma* cell.

[0761] For example, the filamentous fungal host cell may be an *Aspergillus awamori*, *Aspergillus foetidus*, *Aspergillus fumigatus*, *Aspergillus japonicus*, *Aspergillus nidulans*, *Aspergillus niger*, *Aspergillus oryzae*, *Bjerkandera adusta*, *Ceriporiopsis aneirina*, *Ceriporiopsis caregiae*, *Ceriporiopsis gilvescens*, *Ceriporiopsis pannocinta*, *Ceriporiopsis rivulosa*, *Ceriporiopsis subrufa*, *Ceriporiopsis subvermispora*, *Chrysosporium inops*, *Chrysosporium keratinophilum*, *Chrysosporium lucknowense*, *Chrysosporium merdarium*, *Chrysosporium pannicola*, *Chrysosporium queenslandicum*, *Chrysosporium tropicum*, *Chrysosporium zonatum*, *Coprinus cinereus*, *Coriolus hirsutus*, *Fusarium bactridioides*, *Fusarium cerealis*, *Fusarium crookwellense*, *Fusarium culmorum*, *Fusarium graminearum*, *Fusarium graminum*, *Fusarium heterosporum*, *Fusarium negundi*, *Fusarium oxysporum*, *Fusarium reticulatum*, *Fusarium roseum*, *Fusarium sambucinum*, *Fusarium sarcochroum*, *Fusarium sporotrichioides*, *Fusarium sulphureum*, *Fusarium torulosum*, *Fusarium trichothecoides*, *Fusarium venenatum*, *Humicola insolens*, *Humicola lanuginosa*, *Mucor miehei*, *Myceliophthora thermophila*, *Neurospora crassa*, *Penicillium purpurogenum*, *Phanerochaete chrysosporium*, *Phlebia radiata*, *Pleurotus eryngii*, *Thielavia terrestris*, *Trametes villosa*, *Trametes versicolor*, *Trichoderma harzianum*, *Trichoderma koningii*, *Trichoderma longibrachiatum*, *Trichoderma reesei*, or *Trichoderma viride* cell.

[0762] Fungal cells may be transformed by a process involving protoplast formation, transformation of the protoplasts, and regeneration of the cell wall in a manner known

per se. Suitable procedures for transformation of *Aspergillus* and *Trichoderma* host cells are described in EP 238023, Yelton et al., 1984, *Proc. Natl. Acad. Sci. USA* 81:1470-1474, and Christensen et al., 1988, *Bio/Technology* 6:1419-1422. Suitable methods for transforming *Fusarium* species are described by Malardier et al., 1989, *Gene* 78:147-156, and WO 96/00787. Yeast may be transformed using the procedures described by Becker and Guarente, In Abelson, J. N. and Simon, M. I., editors, *Guide to Yeast Genetics and Molecular Biology, Methods in Enzymology*, Volume 194, pp 182-187, Academic Press, Inc., New York; Ito et al., 1983, *J. Bacteriol.* 153:163; and Hinnen et al., 1978, *Proc. Natl. Acad. Sci. USA* 75:1920.

#### Methods of Production

[0763] The present invention also relates to methods of producing a polypeptide of the present invention, comprising (a) cultivating a cell, which in its wild-type form produces the polypeptide, under conditions conducive for production of the polypeptide; and optionally, (b) recovering the polypeptide. In one aspect, the cell is a *Trichophaea* cell. In another aspect, the cell is a *Trichophaea saccata* cell. In another aspect, the cell is a *Trichoderma* cell. In another aspect, the cell is a *Trichoderma harzianum* cell. In another aspect, the cell is a *Trichoderma minuta* cell. In another aspect, the cell is a *Chaetomium* cell. In another aspect, the cell is a *Chaetomium* sp. ZY287 cell. In another aspect, the cell is a *Mortierella* sp. ZY 002 cell. In another aspect, the cell is a *Metarhizium* cell. In another aspect, the cell is a *Metarhizium* sp. XZ2431 cell. In another aspect, the cell is a *Geomyces* cell. In another aspect, the cell is a *Geomyces auratus* cell. In another aspect, the cell is a *Ilyonectria* cell. In another aspect, the cell is a *Ilyonectria rufa* cell.

[0764] The present invention also relates to methods of producing a polypeptide of the present invention, comprising (a) cultivating a recombinant host cell of the present invention under conditions conducive for production of the polypeptide; and optionally, (b) recovering the polypeptide.

[0765] The host cells are cultivated in a nutrient medium suitable for production of the polypeptide using methods known in the art. For example, the cells may be cultivated by shake flask cultivation, or small-scale or large-scale fermentation (including continuous, batch, fed-batch, or solid state fermentations) in laboratory or industrial fermenters in a suitable medium and under conditions allowing the polypeptide to be expressed and/or isolated. The cultivation takes place in a suitable nutrient medium comprising carbon and nitrogen sources and inorganic salts, using procedures known in the art. Suitable media are available from commercial suppliers or may be prepared according to published compositions (e.g., in catalogues of the American Type Culture Collection). If the polypeptide is secreted into the nutrient medium, the polypeptide can be recovered directly from the medium. If the polypeptide is not secreted, it can be recovered from cell lysates.

[0766] The polypeptide may be detected using methods known in the art that are specific for the polypeptides. These detection methods include, but are not limited to, use of specific antibodies, formation of an enzyme product, or disappearance of an enzyme substrate. For example, an enzyme assay may be used to determine the activity of the polypeptide.

[0767] The polypeptide may be recovered using methods known in the art. For example, the polypeptide may be recovered from the nutrient medium by conventional procedures including, but not limited to, collection, centrifugation, filtration, extraction, spray-drying, evaporation, or precipitation. In one aspect, a fermentation broth comprising the polypeptide is recovered.

[0768] The polypeptide may be purified by a variety of procedures known in the art including, but not limited to, chromatography (e.g., ion exchange, affinity, hydrophobic, chromatofocusing, and size exclusion), electrophoretic procedures (e.g., preparative isoelectric focusing), differential solubility (e.g., ammonium sulfate precipitation), SDS-PAGE, or extraction (see, e.g., *Protein Purification*, Janson and Ryden, editors, VCH Publishers, New York, 1989) to obtain substantially pure polypeptides.

[0769] In an alternative aspect, the polypeptide is not recovered, but rather a host cell of the present invention expressing the polypeptide is used as a source of the polypeptide.

#### Production in Plants

[0770] The present invention also relates to isolated plants, e.g., a transgenic plant, plant part, or plant cell, comprising a polynucleotide of the present invention so as to express and produce a polypeptide or domain in recoverable quantities. The polypeptide or domain may be recovered from the plant or plant part. Alternatively, the plant or plant part containing the polypeptide or domain may be used as such for improving the quality of a food or feed, e.g., improving nutritional value, palatability, and rheological properties, or to destroy an antinutritive factor.

[0771] The transgenic plant can be dicotyledonous (a dicot) or monocotyledonous (a monocot). Examples of monocot plants are grasses, such as meadow grass (blue grass, *Poa*), forage grass such as *Festuca*, *Lolium*, temperate grass, such as *Agrostis*, and cereals, e.g., wheat, oats, rye, barley, rice, sorghum, and maize (corn).

[0772] Examples of dicot plants are tobacco, legumes, such as lupins, potato, sugar beet, pea, bean and soybean, and cruciferous plants (family Brassicaceae), such as cauliflower, rape seed, and the closely related model organism *Arabidopsis thaliana*.

[0773] Examples of plant parts are stem, callus, leaves, root, fruits, seeds, and tubers as well as the individual tissues comprising these parts, e.g., epidermis, mesophyll, parenchyme, vascular tissues, meristems.

[0774] Plant cells and specific plant cell compartments, such as chloroplasts, apoplasts, mitochondria, vacuoles, peroxisomes and cytoplasm are also considered to be a plant part. Also included within the scope of the present invention are the progeny of such plants, plant parts, and plant cells.

[0775] The transgenic plant or plant cell expressing the polypeptide or domain may be constructed in accordance with methods known in the art.

[0776] The present invention also relates to methods of producing a polypeptide or domain of the present invention comprising (a) cultivating a transgenic plant or a plant cell comprising a polynucleotide encoding the polypeptide or domain under conditions conducive for production of the polypeptide or domain; and (b) recovering the polypeptide or domain.

### Fermentation Broth Formulations or Cell Compositions

[0777] The present invention also relates to a fermentation broth formulation or a cell composition comprising a polypeptide of the present invention. The fermentation broth product further comprises additional ingredients used in the fermentation process, such as, for example, cells (including, the host cells containing the gene encoding the polypeptide of the present invention which are used to produce the polypeptide of interest), cell debris, biomass, fermentation media and/or fermentation products. In some embodiments, the composition is a cell-killed whole broth containing organic acid(s), killed cells and/or cell debris, and culture medium.

[0778] The term "fermentation broth" as used herein refers to a preparation produced by cellular fermentation that undergoes no or minimal recovery and/or purification. For example, fermentation broths are produced when microbial cultures are grown to saturation, incubated under carbon-limiting conditions to allow protein synthesis (e.g., expression of enzymes by host cells) and secretion into cell culture medium. The fermentation broth can contain unfractionated or fractionated contents of the fermentation materials derived at the end of the fermentation. Typically, the fermentation broth is unfractionated and comprises the spent culture medium and cell debris present after the microbial cells (e.g., filamentous fungal cells) are removed, e.g., by centrifugation. In some embodiments, the fermentation broth contains spent cell culture medium, extracellular enzymes, and viable and/or nonviable microbial cells.

[0779] In an embodiment, the fermentation broth formulation and cell compositions comprise a first organic acid component comprising at least one 1-5 carbon organic acid and/or a salt thereof and a second organic acid component comprising at least one 6 or more carbon organic acid and/or a salt thereof. In a specific embodiment, the first organic acid component is acetic acid, formic acid, propionic acid, a salt thereof, or a mixture of two or more of the foregoing and the second organic acid component is benzoic acid, cyclohexanecarboxylic acid, 4-methylvaleric acid, phenylacetic acid, a salt thereof, or a mixture of two or more of the foregoing.

[0780] In one aspect, the composition contains an organic acid(s), and optionally further contains killed cells and/or cell debris. In one embodiment, the killed cells and/or cell debris are removed from a cell-killed whole broth to provide a composition that is free of these components.

[0781] The fermentation broth formulations or cell compositions may further comprise a preservative and/or antimicrobial (e.g., bacteriostatic) agent, including, but not limited to, sorbitol, sodium chloride, potassium sorbate, and others known in the art.

[0782] The cell-killed whole broth or composition may contain the unfractionated contents of the fermentation materials derived at the end of the fermentation. Typically, the cell-killed whole broth or composition contains the spent culture medium and cell debris present after the microbial cells (e.g., filamentous fungal cells) are grown to saturation, incubated under carbon-limiting conditions to allow protein synthesis. In some embodiments, the cell-killed whole broth or composition contains the spent cell culture medium, extracellular enzymes, and killed filamentous fungal cells. In some embodiments, the microbial cells present in the cell-killed whole broth or composition can be permeabilized and/or lysed using methods known in the art.

[0783] A whole broth or cell composition as described herein is typically a liquid, but may contain insoluble components, such as killed cells, cell debris, culture media components, and/or insoluble enzyme(s). In some embodiments, insoluble components may be removed to provide a clarified liquid composition.

[0784] The whole broth formulations and cell compositions of the present invention may be produced by a method described in WO 90/15861 or WO 2010/096673.

### Enzyme Compositions

[0785] The present invention also relates to compositions comprising a lysozyme of the present invention. Preferably, the compositions are enriched in the lysozyme of the invention. The term "enriched" indicates that the lysozyme activity of the composition has been increased, e.g., with an enrichment factor of at least 1.1, such as at least 1.2, at least 1.3, at least 1.4, at least 1.5, at least 2.0, at least 3.0, at least 4.0, at least 5.0, at least 10.

[0786] The compositions may comprise a polypeptide of the present invention as the major enzymatic component, e.g., a mono-component composition. Such a composition may further comprise a formulating agent, as described below. Alternatively, the compositions may comprise multiple enzymatic activities.

[0787] In an embodiment, the composition comprises the polypeptide of the invention and one or more formulating agents as described below.

### Formulating Agent

[0788] The enzyme of the invention may be formulated as a liquid or a solid. For a liquid formulation, the formulating agent may comprise a polyol (such as, e.g., glycerol, ethylene glycol or propylene glycol), a salt (such as, e.g., sodium chloride, sodium benzoate, potassium sorbate) or a sugar or sugar derivative (such as, e.g., dextrin, glucose, sucrose, and sorbitol). Thus in one embodiment, the composition is a liquid composition comprising the polypeptide of the invention and one or more formulating agents selected from the list consisting of glycerol, ethylene glycol, 1,2-propylene glycol, 1,3-propylene glycol, sodium chloride, sodium benzoate, potassium sorbate, dextrin, glucose, sucrose, and sorbitol. The liquid formulation may be sprayed onto the feed after it has been pelleted or may be added to drinking water given to the animals.

[0789] For a solid formulation, the formulation may be for example as a granule, spray dried powder or agglomerate. The formulating agent may comprise a salt (organic or inorganic zinc, sodium, potassium or calcium salts such as, e.g., calcium acetate, calcium benzoate, calcium carbonate, calcium chloride, calcium citrate, calcium sorbate, calcium sulfate, potassium acetate, potassium benzoate, potassium carbonate, potassium chloride, potassium citrate, potassium sorbate, potassium sulfate, sodium acetate, sodium benzoate, sodium carbonate, sodium chloride, sodium citrate, sodium sulfate, zinc acetate, zinc benzoate, zinc carbonate, zinc chloride, zinc citrate, zinc sorbate, zinc sulfate), starch or a sugar or sugar derivative (such as, e.g., sucrose, dextrin, glucose, lactose, sorbitol).

[0790] In an embodiment, the solid composition is in granulated form. The granule may have a matrix structure where the components are mixed homogeneously. However, the granule typically comprises a core particle and one or

more coatings, which typically are salt and/or wax coatings. Examples of waxes are polyethylene glycols; polypropylenes; Carnauba wax; Candelilla wax; bees wax; hydrogenated plant oil or animal tallow such as hydrogenated ox tallow, hydrogenated palm oil, hydrogenated cotton seeds and/or hydrogenated soy bean oil; fatty acid alcohols; monoglycerides and/or di-glycerides, such as glyceryl stearate, wherein stearate is a mixture of stearic and palmitic acid; micro-crystalline wax; paraffin's; and fatty acids, such as hydrogenated linear long chained fatty acids and derivatives thereof. A preferred wax is palm oil or hydrogenated palm oil. The core particle can either be a homogeneous blend of lysozyme of the invention optionally combined with one or more additional enzymes and optionally together with one or more salts or an inert particle with the lysozyme of the invention optionally combined with one or more additional enzymes applied onto it.

[0791] In an embodiment, the material of the core particles are selected from the group consisting of inorganic salts (such as calcium acetate, calcium benzoate, calcium carbonate, calcium chloride, calcium citrate, calcium sorbate, calcium sulfate, potassium acetate, potassium benzoate, potassium carbonate, potassium chloride, potassium citrate, potassium sorbate, potassium sulfate, sodium acetate, sodium benzoate, sodium carbonate, sodium chloride, sodium citrate, sodium sulfate, zinc acetate, zinc benzoate, zinc carbonate, zinc chloride, zinc citrate, zinc sorbate, zinc sulfate), starch or a sugar or sugar derivative (such as, e.g., sucrose, dextrin, glucose, lactose, sorbitol), sugar or sugar derivative (such as, e.g., sucrose, dextrin, glucose, lactose, sorbitol), small organic molecules, starch, flour, cellulose and minerals and clay minerals (also known as hydrous aluminium phyllosilicates). In a preferred embodiment, the core comprises a clay mineral such as kaolinite or kaolin. [0792] The salt coating is typically at least 1 µm thick and can either be one particular salt or a mixture of salts, such as Na<sub>2</sub>SO<sub>4</sub>, K<sub>2</sub>SO<sub>4</sub>, MgSO<sub>4</sub> and/or sodium citrate. Other examples are those described in, e.g., WO 2008/017659, WO 2006/034710, WO 97/05245, WO 98/54980, WO 98/55599, WO 00/70034 or polymer coating such as described in WO 01/00042.

[0793] In another embodiment, the composition is a solid composition comprising the lysozyme of the invention and one or more formulating agents selected from the list consisting of sodium chloride, sodium benzoate, potassium sorbate, sodium sulfate, potassium sulfate, magnesium sulfate, sodium thiosulfate, calcium carbonate, sodium citrate, dextrin, glucose, sucrose, sorbitol, lactose, starch and cellulose. In a preferred embodiment, the formulating agent is selected from one or more of the following compounds: sodium sulfate, dextrin, cellulose, sodium thiosulfate and calcium carbonate. In a preferred embodiment, the solid composition is in granulated form. In an embodiment, the solid composition is in granulated form and comprises a core particle, an enzyme layer comprising the lysozyme of the invention and a salt coating.

[0794] In a further embodiment, the formulating agent is selected from one or more of the following compounds: glycerol, ethylene glycol, 1,2-propylene glycol or 1,3-propylene glycol, sodium chloride, sodium benzoate, potassium sorbate, sodium sulfate, potassium sulfate, magnesium sulfate, sodium thiosulfate, calcium carbonate, sodium citrate, dextrin, glucose, sucrose, sorbitol, lactose, starch, kaolin and cellulose. In a preferred embodiment, the formulating agent

is selected from one or more of the following compounds: 1,2-propylene glycol, 1,3-propylene glycol, sodium sulfate, dextrin, cellulose, sodium thiosulfate, kaolin and calcium carbonate.

#### Animal Feed and Animal Feed Additives

[0795] The present invention also relates to animal feed compositions and animal feed additives. Animal feed compositions or diets have a relatively high content of protein. Poultry and pig diets can be characterised as indicated in Table B of WO 01/58275, columns 2-3. Fish diets can be characterised as indicated in column 4 of this Table B. Furthermore, such fish diets usually have a crude fat content of 200-310 g/kg.

[0796] An animal feed composition according to the invention has a crude protein content of 50-800 g/kg, and furthermore comprises at least one lysozyme as described herein or more than one lysozyme as described herein.

[0797] Furthermore, or in the alternative (to the crude protein content indicated above), the animal feed composition of the invention has a content of metabolisable energy of 10-30 MJ/kg; and/or a content of calcium of 0.1-200 g/kg; and/or a content of available phosphorus of 0.1-200 g/kg; and/or a content of methionine of 0.1-100 g/kg; and/or a content of methionine plus cysteine of 0.1-150 g/kg; and/or a content of lysine of 0.5-50 g/kg.

[0798] In particular embodiments, the content of metabolisable energy, crude protein, calcium, phosphorus, methionine, methionine plus cysteine, and/or lysine is within any one of ranges 2, 3, 4 or 5 in Table B of WO 01/58275 (R. 2-5).

[0799] Crude protein is calculated as nitrogen (N) multiplied by a factor 6.25, i.e., Crude protein (g/kg)=N (g/kg)×6.25. The nitrogen content is determined by the Kjeldahl method (A.O.A.C., 1984, Official Methods of Analysis 14th ed., Association of Official Analytical Chemists, Washington DC).

[0800] Metabolisable energy can be calculated on the basis of the NRC publication Nutrient requirements in swine, ninth revised edition 1988, subcommittee on swine nutrition, committee on animal nutrition, board of agriculture, national research council. National Academy Press, Washington, D.C., pp. 2-6, and the European Table of Energy Values for Poultry Feed-stuffs, Spelderholt centre for poultry research and extension, 7361 DA Beekbergen, The Netherlands. Grafisch bedrijf Ponsen & looijen bv, Wageningen. ISBN 90-71463-12-5.

[0801] The dietary content of calcium, available phosphorus and amino acids in complete animal diets is calculated on the basis of feed tables such as Veevoedertabel 1997, gegevens over chemische samenstelling, verterbaarheid en voederwaarde van voedermiddelen, Central Veevoederbureau, Runderweg 6, 8219 pk Lelystad. ISBN 90-72839-13-7.

[0802] In a particular embodiment, the animal feed composition of the invention contains at least one vegetable protein as defined above.

[0803] The animal feed composition of the invention may also contain animal protein, such as Meat and Bone Meal, Feather meal, and/or Fish Meal, typically in an amount of 0-25%. The animal feed composition of the invention may also comprise Dried Distillers Grains with Solubles (DDGS), typically in amounts of 0-30%.

[0804] In still further particular embodiments, the animal feed composition of the invention contains 0-80% maize;

and/or 0-80% sorghum; and/or 0-70% wheat; and/or 0-70% Barley; and/or 0-30% oats; and/or 0-40% soybean meal; and/or 0-25% fish meal; and/or 0-25% meat and bone meal; and/or 0-20% whey.

[0805] The animal feed may comprise vegetable proteins. In particular embodiments, the protein content of the vegetable proteins is at least 10, 20, 30, 40, 50, 60, 70, 80, or 90% (w/w). Vegetable proteins may be derived from vegetable protein sources, such as legumes and cereals, for example, materials from plants of the families Fabaceae (Leguminosae), Cruciferaceae, Chenopodiaceae, and Poaceae, such as soy bean meal, lupin meal, rapeseed meal, and combinations thereof.

[0806] In a particular embodiment, the vegetable protein source is material from one or more plants of the family Fabaceae, e.g., soybean, lupine, pea, or bean. In another particular embodiment, the vegetable protein source is material from one or more plants of the family Chenopodiaceae, e.g., beet, sugar beet, spinach or quinoa. Other examples of vegetable protein sources are rapeseed, and cabbage. In another particular embodiment, soybean is a preferred vegetable protein source. Other examples of vegetable protein sources are cereals such as barley, wheat, rye, oat, maize (corn), rice, and sorghum.

[0807] Animal diets can, e.g., be manufactured as mash feed (non-pelleted) or pelleted feed. Typically, the milled feed-stuffs are mixed and sufficient amounts of essential vitamins and minerals are added according to the specifications for the species in question. Enzymes can be added as solid or liquid enzyme formulations. For example, for mash feed a solid or liquid enzyme formulation may be added before or during the ingredient mixing step. For pelleted feed the (liquid or solid) lysozyme/enzyme preparation may also be added before or during the feed ingredient step. Typically, a liquid lysozyme/enzyme preparation comprises the lysozyme of the invention optionally with a polyol, such as glycerol, ethylene glycol or propylene glycol, and is added after the pelleting step, such as by spraying the liquid formulation onto the pellets. The enzyme may also be incorporated in a feed additive or premix.

[0808] Alternatively, the lysozyme can be prepared by freezing a mixture of liquid enzyme solution with a bulking agent such as ground soybean meal, and then lyophilizing the mixture.

[0809] In an embodiment, the composition comprises one or more additional enzymes. In an embodiment, the composition comprises one or more microbes. In an embodiment, the composition comprises one or more vitamins. In an embodiment, the composition comprises one or more minerals. In an embodiment, the composition comprises one or more amino acids. In an embodiment, the composition comprises one or more other feed ingredients.

[0810] In another embodiment, the composition comprises one or more of the polypeptides of the invention, one or more formulating agents and one or more additional enzymes. In an embodiment, the composition comprises one or more of the polypeptides of the invention, one or more formulating agents and one or more microbes. In an embodiment, the composition comprises one or more of the polypeptides of the invention, one or more formulating agents and one or more vitamins. In an embodiment, the composition comprises one or more of the polypeptides of the invention and one or more minerals. In an embodiment, the composition comprises the polypeptide of the invention, one

or more formulating agents and one or more amino acids. In an embodiment, the composition comprises one or more of the polypeptides of the invention, one or more formulating agents and one or more other feed ingredients.

[0811] In a further embodiment, the composition comprises one or more of the polypeptides of the invention, one or more formulating agents and one or more components selected from the list consisting of: one or more additional enzymes; one or more microbes; one or more vitamins; one or more minerals; one or more amino acids; and one or more other feed ingredients.

[0812] The final lysozyme concentration in the diet is within the range of 0.01-200 ppm enzyme protein per kg animal feed, such as 0.1 to 150 ppm, 0.5 to 100 ppm, 1 to 75 ppm, 2 to 50 ppm, 3 to 25 ppm, 2 to 80 ppm, 5 to 60 ppm, 8 to 40 ppm or 10 to 30 ppm enzyme protein per kg animal feed, or any combination of these intervals.

[0813] It is at present contemplated that the lysozyme is administered in one or more of the following amounts (dosage ranges): 0.01-200; 0.01-100; 0.5-100; 1-50; 5-100; 5-50; 10-100; 0.05-50; 5-25; or 0.10-10-all these ranges being in mg lysozyme per kg feed (ppm).

[0814] For determining mg lysozyme protein per kg feed, the lysozyme is purified from the feed composition, and the specific activity of the purified lysozyme is determined using a relevant assay (see under lysozyme activity). The lysozyme activity of the feed composition as such is also determined using the same assay, and on the basis of these two determinations, the dosage in mg lysozyme protein per kg feed is calculated.

[0815] In a particular embodiment, the animal feed additive of the invention is intended for being included (or prescribed as having to be included) in animal diets or feed at levels of 0.01 to 10.0%; more particularly 0.05 to 5.0%; or 0.2 to 1.0% (% meaning g additive per 100 g feed). This is so in particular for premixes.

[0816] The same principles apply for determining mg lysozyme protein in feed additives. Of course, if a sample is available of the lysozyme used for preparing the feed additive or the feed, the specific activity is determined from this sample (no need to purify the lysozyme from the feed composition or the additive).

#### Additional Enzymes

[0817] In another embodiment, the compositions described herein optionally include one or more enzymes. Enzymes can be classified on the basis of the handbook Enzyme Nomenclature from NC-IUBMB, 1992), see also the ENZYME site at the internet: expasy.ch/enzyme/. ENZYME is a repository of information relative to the nomenclature of enzymes. It is primarily based on the recommendations of the Nomenclature Committee of the International Union of Biochemistry and Molecular Biology (IUB-MB), Academic Press, Inc., 1992, and it describes each type of characterized enzyme for which an EC (Enzyme Commission) number has been provided (Bairoch, 2000, "The ENZYME Database", *Nucleic Acids Res.* 28:304-305). This IUB-MB Enzyme nomenclature is based on their substrate specificity and occasionally on their molecular mechanism; such a classification does not reflect the structural features of these enzymes.

[0818] Another classification of certain glycoside hydrolase enzymes, such as endoglucanase, xylanase, galactanase, mannanase, dextranase, lysozyme and galactosidase is

described in Henrissat et al, "The carbohydrate-active enzymes database (CAZy) in 2013", *Nucl. Acids Res.* (1 Jan. 2014) 42 (D1): D490-D495; see also [cazy.org](http://cazy.org).

**[0819]** Thus the composition of the invention may also comprise at least one other enzyme selected from the group comprising of phytase (EC 3.1.3.8 or 3.1.3.26); xylanase (EC 3.2.1.8); galactanase (EC 3.2.1.89); alpha-galactosidase (EC 3.2.1.22); protease (EC 3.4); phospholipase A1 (EC 3.1.1.32); phospholipase A2 (EC 3.1.1.4); lysophospholipase (EC 3.1.1.5); phospholipase C (3.1.4.3); phospholipase D (EC 3.1.4.4); amylase such as, for example, alpha-amylase (EC 3.2.1.1); arabinofuranosidase (EC 3.2.1.55); beta-xylosidase (EC 3.2.1.37); acetyl xylan esterase (EC 3.1.1.72); feruloyl esterase (EC 3.1.1.73); cellulase (EC 3.2.1.4); cellobiohydrolases (EC 3.2.1.91); beta-glucosidase (EC 3.2.1.21); pullulanase (EC 3.2.1.41), alpha-mannosidase (EC 3.2.1.24), mannanase (EC 3.2.1.25) and beta-glucanase (EC 3.2.1.4 or EC 3.2.1.6), or any mixture thereof.

**[0820]** In a particular embodiment, the composition of the invention comprises a phytase (EC 3.1.3.8 or 3.1.3.26). Examples of commercially available phytases include Bio-Feed™ Phytase (Novozymes), Ronozyme® P, Ronozyme® NP and Ronozyme® HiPhos (DSM Nutritional Products), Natuphos™ (BASF), Finase® and Quantum® Blue (AB Enzymes), OptiPhos® (Huvepharma) Phyzyme® XP (Verenium/DuPont) and Axta® PHY (DuPont). Other preferred phytases include those described in, e.g., WO 98/28408, WO 00/43503, and WO 03/066847.

**[0821]** In a particular embodiment, the composition of the invention comprises a xylanase (EC 3.2.1.8). Examples of commercially available xylanases include Ronozyme® WX and Ronozyme® G2 (DSM Nutritional Products), Econase® XT and Barley (AB Vista), Xylathin® (Verenium), Hostazym® X (Huvepharma) and Axta® XB (Xylanase/beta-glucanase, DuPont).

**[0822]** In a particular embodiment, the composition of the invention comprises a protease (EC 3.4). Examples of commercially available proteases include Ronozyme® Pro-Act (DSM Nutritional Products).

#### Microbes

**[0823]** In an embodiment, the animal feed composition further comprises one or more additional microbes. In a particular embodiment, the animal feed composition further comprises a bacterium from one or more of the following genera: *Lactobacillus*, *Lactococcus*, *Streptococcus*, *Bacillus*, *Pediococcus*, *Enterococcus*, *Leuconostoc*, *Carnobacterium*, *Propionibacterium*, *Bifidobacterium*, *Clostridium* and *Megasphaera* or any combination thereof.

**[0824]** In a preferred embodiment, animal feed composition further comprises a bacterium from one or more of the following strains: *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus pumilus*, *Bacillus polymyxa*, *Bacillus megaterium*, *Bacillus coagulans*, *Bacillus circulans*, *Enterococcus faecium*, *Enterococcus* spp., and *Pediococcus* spp., *Lactobacillus* spp., *Bifidobacterium* spp., *Lactobacillus acidophilus*, *Pediococcus acidilactici*, *Lactococcus lactis*, *Bifidobacterium bifidum*, *Propionibacterium thoenii*, *Lactobacillus farcimimus*, *Lactobacillus rhamnosus*, *Clostridium butyricum*, *Bifidobacterium animalis* spp. *animalis*, *Lactobacillus reuteri*, *Lactobacillus salivarius* spp. *salivarius*, *Megasphaera elsdenii*, *Propionibacteria* sp.

**[0825]** In a more preferred embodiment, composition, animal feed additive or animal feed further comprises a bacterium from one or more of the following strains of *Bacillus subtilis*: 3A-P4 (PTA-6506), 15A-P4 (PTA-6507), 22C-P1 (PTA-6508), 2084 (NRRL B-500130), LSSA01 (NRRL-B-50104), BS27 (NRRL B-501 05), BS 18 (NRRL B-50633), BS 278 (NRRL B-50634), DSM 29870, DSM 29871, NRRL B-50136, NRRL B-50605, NRRL B-50606, NRRL B-50622 and PTA-7547.

**[0826]** In a more preferred embodiment, composition, animal feed additive or animal feed further comprises a bacterium from one or more of the following strains of *Bacillus pumilus*: NRRL B-50016, ATCC 700385, NRRL B-50885 or NRRL B-50886.

**[0827]** In a more preferred embodiment, composition, animal feed additive or animal feed further comprises a bacterium from one or more of the following strains of *Bacillus licheniformis*: NRRL B 50015, NRRL B-50621 or NRRL B-50623.

**[0828]** In a more preferred embodiment, composition, animal feed additive or animal feed further comprises a bacterium from one or more of the following strains of *Bacillus amyloliquefaciens*: DSM 29869, DSM 29869, NRRL B 50607, PTA-7543, PTA-7549, NRRL B-50349, NRRL B-50606, NRRL B-50013, NRRL B-50151, NRRL B-50141, NRRL B-50147 or NRRL B-50888.

**[0829]** The bacterial count of each of the bacterial strains in the animal feed composition is between  $1 \times 10^4$  and  $1 \times 10^{14}$  CFU/kg of dry matter, preferably between  $1 \times 10^6$  and  $1 \times 10^{12}$  CFU/kg of dry matter, and more preferably between  $1 \times 10^7$  and  $1 \times 10^{11}$  CFU/kg of dry matter. In a more preferred embodiment the bacterial count of each of the bacterial strains in the animal feed composition is between  $1 \times 10^8$  and  $1 \times 10^{10}$  CFU/kg of dry matter.

**[0830]** The bacterial count of each of the bacterial strains in the animal feed composition is between  $1 \times 10^5$  and  $1 \times 10^{15}$  CFU/animal/day, preferably between  $1 \times 10^7$  and  $1 \times 10^{13}$  CFU/animal/day, and more preferably between  $1 \times 10^8$  and  $1 \times 10^{12}$  CFU/animal/day. In a more preferred embodiment the bacterial count of each of the bacterial strains in the animal feed composition is between  $1 \times 10^9$  and  $1 \times 10^{11}$  CFU/animal/day.

**[0831]** In another embodiment, the one or more bacterial strains are present in the form of a stable spore.

#### Premix

**[0832]** In an embodiment, the animal feed may include a premix, comprising, e.g., vitamins, minerals, enzymes, amino acids, preservatives, antibiotics, other feed ingredients or any combination thereof which are mixed into the animal feed.

#### Amino Acids

**[0833]** The composition of the invention may further comprise one or more amino acids. Examples of amino acids which are used in animal feed are lysine, alanine, beta-alanine, threonine, methionine and tryptophan.

#### Vitamins and Minerals

**[0834]** In another embodiment, the animal feed may include one or more vitamins, such as one or more fat-soluble vitamins and/or one or more water-soluble vitamins. In another embodiment, the animal feed may optionally

include one or more minerals, such as one or more trace minerals and/or one or more macro minerals.

[0835] Usually fat- and water-soluble vitamins, as well as trace minerals form part of a so-called premix intended for addition to the feed, whereas macro minerals are usually separately added to the feed.

[0836] Non-limiting examples of fat-soluble vitamins include vitamin A, vitamin D3, vitamin E, and vitamin K, e.g., vitamin K3.

[0837] Non-limiting examples of water-soluble vitamins include vitamin B12, biotin and choline, vitamin B1, vitamin B2, vitamin B6, niacin, folic acid and panthothenate, e.g., Ca-D-panthothenate.

[0838] Non-limiting examples of trace minerals include boron, cobalt, chloride, chromium, copper, fluoride, iodine, iron, manganese, molybdenum, selenium and zinc.

[0839] Non-limiting examples of macro minerals include calcium, magnesium, potassium and sodium.

[0840] The nutritional requirements of these components (exemplified with poultry and piglets/pigs) are listed in Table A of WO 01/58275. Nutritional requirement means that these components should be provided in the diet in the concentrations indicated.

[0841] In the alternative, the animal feed additive of the invention comprises at least one of the individual components specified in Table A of WO 01/58275. At least one means either of, one or more of, one, or two, or three, or four and so forth up to all thirteen, or up to all fifteen individual components. More specifically, this at least one individual component is included in the additive of the invention in such an amount as to provide an in-feed-concentration within the range indicated in column four, or column five, or column six of Table A.

[0842] In a still further embodiment, the animal feed additive of the invention comprises at least one of the below vitamins, preferably to provide an in-feed-concentration within the ranges specified in the below Table 1 (for piglet diets, and broiler diets, respectively).

TABLE 1

Typical vitamin recommendations		
Vitamin	Piglet diet	Broiler diet
Vitamin A	10,000-15,000 IU/kg feed	8-12,500 IU/kg feed
Vitamin D3	1800-2000 IU/kg feed	3000-5000 IU/kg feed
Vitamin E	60-100 mg/kg feed	150-240 mg/kg feed
Vitamin K3	2-4 mg/kg feed	2-4 mg/kg feed
Vitamin B1	2-4 mg/kg feed	2-3 mg/kg feed
Vitamin B2	6-10 mg/kg feed	7-9 mg/kg feed
Vitamin B6	4-8 mg/kg feed	3-6 mg/kg feed
Vitamin B12	0.03-0.05 mg/kg feed	0.015-0.04 mg/kg feed
Niacin (Vitamin B3)	30-50 mg/kg feed	50-80 mg/kg feed
Pantothenic acid	20-40 mg/kg feed	10-18 mg/kg feed
Folic acid	1-2 mg/kg feed	1-2 mg/kg feed
Biotin	0.15-0.4 mg/kg feed	0.15-0.3 mg/kg feed
Choline chloride	200-400 mg/kg feed	300-600 mg/kg feed

#### Other Feed Ingredients

[0843] The composition of the invention may further comprise colouring agents, stabilisers, growth improving additives and aroma compounds/flavourings, polyunsatu-

rated fatty acids (PUFAs); reactive oxygen generating species, anti-microbial peptides and anti-fungal polypeptides.

[0844] Examples of colouring agents are carotenoids such as beta-carotene, astaxanthin, and lutein.

[0845] Examples of aroma compounds/flavourings are creosol, anethol, deca-, undeca- and/or dodeca-lactones, ionones, irone, gingerol, piperidine, propylidene phthalide, butylidene phthalide, capsaicin and tannin.

[0846] Examples of stabilizing agents (e.g., acidifiers) are organic acids. Examples of these are benzoic acid (VevoVitall®, DSM Nutritional Products), formic acid, butyric acid, fumaric acid and propionic acid.

[0847] Examples of antimicrobial peptides (AMP's) are CAP18, Leucocin A, Trypticin, Protegrin-1, Thanatin, Defensin, Lactoferrin, Lactoferricin, and Ovispirin such as Novispirin (Robert Lehrer, 2000), Plectasins, and Statins, including the compounds and polypeptides disclosed in WO 03/044049 and WO 03/048148, as well as variants or fragments of the above that retain antimicrobial activity.

[0848] Examples of antifungal polypeptides (AFP's) are the *Aspergillus giganteus*, and *Aspergillus niger* peptides, as well as variants and fragments thereof which retain antifungal activity, as disclosed in WO 94/01459 and WO 02/090384.

[0849] Examples of polyunsaturated fatty acids are C18, C20 and C22 polyunsaturated fatty acids, such as arachidonic acid, docosohexaenoic acid, eicosapentaenoic acid and gamma-linoleic acid.

[0850] Examples of reactive oxygen generating species are chemicals such as perborate, persulphate, or percarbonate; and enzymes such as an oxidase, an oxygenase or a syntethase.

[0851] The composition of the invention may further comprise at least one amino acid. Examples of amino acids which are used in animal feed are lysine, alanine, beta-alanine, threonine, methionine and tryptophan.

#### Uses

##### Use in Animal Feed

[0852] A lysozyme of the invention may also be used in animal feed, wherein the term "animal" refers to all animals except humans. Examples of animals are non-ruminants, and ruminants. Ruminant animals include, for example, animals such as sheep, goats, cattle, e.g., beef cattle, cows, and young calves, deer, yank, camel, llama and kangaroo. Non-ruminant animals include mono-gastric animals, e.g., pigs or swine (including, but not limited to, piglets, growing pigs, and sows); poultry such as turkeys, ducks and chicken (including but not limited to broiler chicks, layers); horses (including but not limited to hotbloods, coldbloods and warm bloods), young calves; fish (including but not limited to amberjack, arapaima, barb, bass, bluefish, bocachico, bream, bullhead, cachama, carp, catfish, catla, chanos, char, cichlid, cobia, cod, crappie, dorada, drum, eel, goby, goldfish, gourami, grouper, guapote, halibut, java, labeo, lai, loach, mackerel, milkfish, mojarra, mudfish, mullet, paco, pearlspot, pejerrey, perch, pike, pompano, roach, salmon, sampa, sauger, sea bass, seabream, shiner, sleeper, snakehead, snapper, snook, sole, spinefoot, sturgeon, sunfish, sweetfish, tench, terror, tilapia, trout, tuna, turbot, vendace, walleye and whitefish); and crustaceans (including but not limited to shrimps and prawns).

**[0853]** In the use according to the invention the lysozymes can be fed to the animal before, after, or simultaneously with the diet. The latter is preferred.

**[0854]** In a particular embodiment, the lysozyme, in the form in which it is added to the feed, or when being included in a feed additive, is well-defined. Well-defined means that the lysozyme preparation is at least 50% pure as determined by Size-exclusion chromatography (see Example 12 of WO 01/58275). In other particular embodiments the lysozyme preparation is at least 60, 70, 80, 85, 88, 90, 92, 94, or at least 95% pure as determined by this method.

**[0855]** A well-defined lysozyme preparation is advantageous. For instance, it is much easier to dose correctly to the feed a lysozyme that is essentially free from interfering or contaminating other lysozymes. The term dose correctly refers in particular to the objective of obtaining consistent and constant results, and the capability of optimizing dosage based upon the desired effect.

**[0856]** For the use in animal feed, however, the lysozyme need not be pure; it may, e.g., include other enzymes, in which case it could be termed a lysozyme preparation.

**[0857]** The lysozyme preparation can be (a) added directly to the feed, or (b) it can be used in the production of one or more intermediate compositions such as feed additives or premixes that is subsequently added to the feed (or used in a treatment process). The degree of purity described above refers to the purity of the original lysozyme preparation, whether used according to (a) or (b) above.

#### Methods of Improving Animal Performance

**[0858]** In an embodiment, the present invention also relates to a method of improving the performance of an animal comprising administering to the animal the animal feed or an animal feed additive of the invention.

**[0859]** In a preferred embodiment, the method of improving the performance of an animal comprises administering to the animal an animal feed or an animal feed additive comprising the lysozyme of SEQ ID NO: 257, SEQ ID NO: 264, SEQ ID NO: 267, SEQ ID NO: 291, SEQ ID NO: 294, SEQ ID NO: 297, SEQ ID NO: 300, SEQ ID NO: 303 and/or SEQ ID NO: 306.

**[0860]** In an embodiment, the present invention also relates to the use of the animal feed or an animal feed additive of the invention for improving the performance of an animal. In another embodiment, the invention relates to the use of one or more lysozymes of the invention for improving the performance of an animal.

**[0861]** In one embodiment, ‘improving the performance of an animal’ means that there is an increase in body weight gain. In another embodiment, ‘improving the performance of an animal’ means that there is an improved feed conversion ratio. In a further embodiment, ‘improving the performance of an animal’ means that there is an increased feed efficiency. In a further embodiment, ‘improving the performance of an animal’ means that there is an increase in body weight gain and/or an improved feed conversion ratio and/or an increased feed efficiency.

#### Methods of Preparing an Animal Feed

**[0862]** In an embodiment, the present invention provides a method for preparing an animal feed comprising adding one or more lysozymes of the present invention to one or more animal feed ingredients. Animal feed ingredients

include, but are not limited to, concentrates (as defined herein), forage (as defined herein), enzymes, microbe, vitamins, minerals and amino acids.

**[0863]** In a preferred embodiment, the method of preparing an animal feed comprises mixing the lysozyme of SEQ ID NO: 257, SEQ ID NO: 264, SEQ ID NO: 267, SEQ ID NO: 291, SEQ ID NO: 294, SEQ ID NO: 297, SEQ ID NO: 300, SEQ ID NO: 303 and/or SEQ ID NO: 306 with concentrate and/or forage.

Methods of Treatment of *Clostridium perfringens* and/or *Necrotic enteritis*

**[0864]** In another aspect, the present invention provides a method of treatment of *necrotic enteritis* comprising the steps of administering the animal feed or animal feed additive to one or more animals with *necrotic enteritis*. In an embodiment, the present invention provides a method of treatment of a *Clostridium perfringens* infection comprising the steps of administering the animal feed or animal feed additive to one or more animals with a *Clostridium perfringens* infection.

**[0865]** In another aspect, the present invention provides a method of treatment of *necrotic enteritis* comprising the steps of administering one or more lysozymes of the invention to one or more animals with *necrotic enteritis*. In an embodiment, the present invention provides a method of treatment of a *Clostridium perfringens* infection comprising the steps of administering one or more lysozymes of the invention to one or more animals with a *Clostridium perfringens* infection.

**[0866]** In a further aspect, the invention relates to the animal feed or animal feed additive of the invention for the treatment of *necrotic enteritis* in an animal. In an embodiment, the invention relates to composition comprising the lysozyme of SEQ ID NO: 257, SEQ ID NO: 264, SEQ ID NO: 267, SEQ ID NO: 291, SEQ ID NO: 294, SEQ ID NO: 297, SEQ ID NO: 300, SEQ ID NO: 303 and/or SEQ ID NO: 306 for the treatment of *Necrotic enteritis* in an animal.

**[0867]** In a further aspect, the invention relates to the animal feed or animal feed additive of the invention for the treatment of a *Clostridium perfringens* infection in an animal. In an embodiment, the invention relates to composition comprising the lysozyme of SEQ ID NO: 257, SEQ ID NO: 264, SEQ ID NO: 267, SEQ ID NO: 291, SEQ ID NO: 294, SEQ ID NO: 297, SEQ ID NO: 300, SEQ ID NO: 303 and/or SEQ ID NO: 306 for the treatment of a *Clostridium perfringens* infection in an animal.

**[0868]** Antimicrobial activity towards *Clostridium perfringens* can be determined according to the antimicrobial assay described in Example 12.

#### PREFERRED EMBODIMENTS

**[0869]** Herein follows a list if preferred embodiments of the invention.

1. An animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein the polypeptide comprises one or more GH24 catalytic domains and one or more lysozyme enhancing domains and wherein:

**[0870]** (a) GH24 catalytic domain gives a domT score of at least 200 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOS: 1 to 122 and hmmbuild software program, and wherein the query is carried out using hmmscan software program with default settings; and

- [0871] (b) the polypeptide comprises one or more lysozyme enhancing domains, wherein the lysozyme enhancing domain gives a domT score of at least 100 when queried using a Profile Hidden Markov Model prepared using SEQ ID NOs: 123 to 251 and hmmbuild software program, and wherein the query is carried out using the hmmcan software program with default settings.
2. The animal feed or animal feed additive of item 1, wherein the GH24 catalytic domain gives a domT score of 220 or more and the lysozyme enhancing domain gives a domT score of 100 or more.
3. The animal feed or animal feed additive of item 1, wherein the GH24 catalytic domain gives a domT score of 230 or more and the lysozyme enhancing domain gives a domT score of 100 or more.
4. The animal feed or animal feed additive of item 1, wherein the GH24 catalytic domain gives a domT score of 240 or more and the lysozyme enhancing domain gives a domT score of 100 or more.
5. The animal feed or animal feed additive of item 1, wherein the GH24 catalytic domain gives a domT score of 250 or more and the lysozyme enhancing domain gives a domT score of 103 or more.
6. An animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein:
- [0872] (a) the polypeptide comprises one or more GH24 catalytic domain comprising one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252) and/or one or more motif II [LV][NDST]XN[QE][YFW][GASND]ALXS[WFLY]X[FY]N (SEQ ID NO: 253); and
- [0873] (b) the polypeptide comprises one or more lysozyme enhancing domain comprising one or more motif III: [CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN] (SEQ ID NO: 254).
7. An animal feed or animal feed additive comprising one or more polypeptides having lysozyme activity, wherein:
- [0874] (a) the polypeptide comprises one or more GH24 catalytic domain comprising one or more motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252) and one or more motif II [LV][NDST]XN[QE][YFW][GASND]ALXS[WFLY]X[FY]N (SEQ ID NO: 253); and
- [0875] (b) the polypeptide comprises one or more lysozyme enhancing domain comprising one or more motif III: [CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN] (SEQ ID NO: 254).
8. The animal feed or animal feed additive of item 6 or 7, wherein the one or more motif I is [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 281).
9. The animal feed or animal feed additive item 6 or 7, wherein the one or more motif I is T[VI]GYGHXC (SEQ ID NO: 282).
10. The animal feed or animal feed additive of any of items 6 to 9, wherein the one or more motif II LNXN[QE][YFW][GA]ALXS[WFL]X[YF]N (SEQ ID NO: 283).
11. The animal feed or animal feed additive of any of items 6 to 10, wherein the one or more motif III C [YF][VI][AST]D[YKF][YF][VI]XTG (SEQ ID NO: 284).
12. The animal feed or animal feed additive of any of items 6 to 11, wherein the GH24 catalytic domain further comprises one or more motif IV: [GEV]LXXRRXXE (SEQ ID NO: 285).
13. The animal feed or animal feed additive of any of items 6 to 12, wherein the GH24 catalytic domain further comprises one or more motif IV: GLXXRRXXE (SEQ ID NO: 286).
14. The animal feed or animal feed additive of any of items 1 to 13, wherein the lysozyme enhancing domain has at least 45% sequence identity to SEQ ID NO: 180.
15. The animal feed or animal feed additive of any of items 1 to 14, wherein the lysozyme enhancing domain has at least 65% sequence identity to one or more of SEQ ID NO: 123 to 251.
16. The animal feed or animal feed additive of any of items 1 to 15, wherein the GH24 catalytic domain has at least 55% sequence identity to SEQ ID NO: 14.
17. The animal feed or animal feed additive of any of items 1 to 16, wherein the GH24 catalytic domain has at least 65% sequence identity to one or more of SEQ ID NO: 1 to 122.
18. The animal feed or animal feed additive of any of items 1 to 17, wherein the polypeptide is obtained or obtainable from the kingdom Fungi.
19. The animal feed or animal feed additive of any of items 1 to 18, wherein the polypeptide is obtained or obtainable from the phylum Ascomycota.
20. The animal feed or animal feed additive of any of items 1 to 19, wherein the polypeptide is selected from the group consisting of:
- [0876] (a) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 257;
- [0877] (b) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 264;
- [0878] (c) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 267;
- [0879] (d) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 291;
- [0880] (e) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 294;
- [0881] (f) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at

least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 297;

[0882] (g) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 300;

[0883] (h) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 303;

[0884] (i) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 306;

[0885] (j) a variant of SEQ ID NO: 257, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0886] (k) a variant of SEQ ID NO: 264, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0887] l) a variant of SEQ ID NO: 267, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0888] (m) a variant of SEQ ID NO: 291, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0889] (n) a variant of SEQ ID NO: 294, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18,

19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0890] (o) a variant of SEQ ID NO: 297, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0891] (p) a variant of SEQ ID NO: 300, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0892] (q) a variant of SEQ ID NO: 303, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0893] (r) a variant of SEQ ID NO: 306, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;

[0894] (s) a fragment of the polypeptide of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k), (l), (m), (n), (o), (p), (q) or (r) that has lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids.

21. The animal feed or animal feed additive of any of items 1 to 20, wherein the polypeptide having lysozyme activity has at least 30% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

22. The animal feed or animal feed additive of any of items 1 to 20, wherein the polypeptide having lysozyme activity has at least 30%, e.g., at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 100% of the antimicrobial activity of SEQ ID NO: 257 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

23. The animal feed or animal feed additive of any of items 1 to 20, wherein the polypeptide having lysozyme activity has at least 30%, e.g., at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 100% of the antimicrobial activity of SEQ ID NO: 264 against *Clostridium perfringens* using the conditions 50% MHB, PH 6.

24. The animal feed or animal feed additive of any of items 1 to 20, wherein the polypeptide having lysozyme activity

has at least 30%, e.g., at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, at least 95%, or at least 100% of the antimicrobial activity of SEQ ID NO: 267 against *Clostridium perfringens* using the conditions 50% MHB, pH 6.

25. The animal feed or animal feed additive of any of items 1 to 24 further comprising one or more components selected from the list consisting of:

- [0895] one or more additional enzymes;
- [0896] one or more microbes;
- [0897] one or more vitamins;
- [0898] one or more minerals;
- [0899] one or more amino acids; and
- [0900] one or more other feed ingredients.

26. The animal feed or animal feed additive of item 25, wherein the one or more additional enzymes is selected from the group consisting of phytase, xylanase, galactanase, alpha-galactosidase, protease, phospholipase A1, phospholipase A2, lysophospholipase, phospholipase C, phospholipase D, amylase, lysozyme, arabinofuranosidase, beta-xylosidase, acetyl xylan esterase, feruloyl esterase, cellulase, cellobiohydrolases, beta-glucosidase, pullulanase, and beta-glucanase or any combination thereof.

27. The animal feed or animal feed additive of item 25, wherein the one or more microbes is selected from the group consisting of *Bacillus subtilis*, *Bacillus licheniformis*, *Bacillus amyloliquefaciens*, *Bacillus cereus*, *Bacillus pumilus*, *Bacillus polymyxa*, *Bacillus megaterium*, *Bacillus coagulans*, *Bacillus circulans*, *Bifidobacterium bifidum*, *Bifidobacterium animalis*, *Bifidobacterium* sp., *Carnobacterium* sp., *Clostridium butyricum*, *Clostridium* sp., *Enterococcus faecium*, *Enterococcus* sp., *Lactobacillus* sp., *Lactobacillus acidophilus*, *Lactobacillus* *farcinimuis*, *Lactobacillus rhamnosus*, *Lactobacillus reuteri*, *Lactobacillus salivarius*, *Lactococcus lactis*, *Lactococcus* sp., *Leuconostoc* sp., *Megasphaera elsdenii*, *Megasphaera* sp., *Pediococcus acidilactici*, *Pediococcus* sp., *Propionibacterium thoenii*, *Propionibacterium* sp. and *Streptococcus* sp. or any combination thereof.

28. A pelleted animal feed comprising plant based material and the animal feed or animal feed additive of any of items 1 to 27.

29. The pelleted animal feed of item 28, wherein the plant based material comprises oats, rye, barley, wheat, maize, corn, sorghum, switchgrass, millet, pearl millet, foxtail millet, soybean, wild soybean, beans, lupin, tepary bean, scarlet runner bean, slimjim bean, lima bean, French bean, Broad bean (fava bean), chickpea, lentil, peanut, Spanish peanut, canola, rapeseed (oilseed rape) or pea, in a processed form thereof or any combination thereof.

30. A polypeptide having lysozyme activity, selected from the group consisting of:

- [0901] (a) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 257;
- [0902] (b) a polypeptide having at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 267;
- [0903] (c) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 291;

least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 291;

[0904] (d) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 294;

[0905] (e) a polypeptide having at least 82%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 297;

[0906] (f) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 300;

[0907] (g) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 303;

[0908] (h) a polypeptide having at least 80%, e.g., at least 81%, at least 82%, at least 83%, at least 84%, at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to SEQ ID NO: 306;

[0909] (i) a polypeptide encoded by a polynucleotide that hybridizes under medium-high stringency conditions, high stringency conditions or very-high stringency conditions with:

[0910] (i) the mature polypeptide coding sequence of SEQ ID NO: 255;

[0911] (ii) the mature polypeptide coding sequence of SEQ ID NO: 287;

[0912] (iii) the mature polypeptide coding sequence of SEQ ID NO: 292;

[0913] (iv) the mature polypeptide coding sequence of SEQ ID NO: 295;

[0914] (v) the mature polypeptide coding sequence of SEQ ID NO: 298;

[0915] (vi) the mature polypeptide coding sequence of SEQ ID NO: 301;

[0916] (vii) the mature polypeptide coding sequence of SEQ ID NO: 304;

[0917] (viii) the cDNA sequence thereof; or

[0918] (ix) the full-length complement of (i), (ii), (iii), (iv) (v), (vi), (vii) or (viii);

[0919] (j) a polypeptide encoded by a polynucleotide that hybridizes under very-high stringency conditions with:

- [0920] (i) the mature polypeptide coding sequence of SEQ ID NO: 265;
- [0921] (ii) the full-length complement of (i);
- [0922] (k) a polypeptide encoded by a polynucleotide having at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 255;
- [0923] (l) a polypeptide encoded by a polynucleotide having at least 95%, e.g., at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 265;
- [0924] (m) a polypeptide encoded by a polynucleotide having at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 287;
- [0925] (n) a polypeptide encoded by a polynucleotide having at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 292;
- [0926] (o) a polypeptide encoded by a polynucleotide having at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 295;
- [0927] (p) a polypeptide encoded by a polynucleotide having at least 82%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 298;
- [0928] (q) a polypeptide encoded by a polynucleotide having at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 301;
- [0929] (r) a polypeptide encoded by a polynucleotide having at least 80%, e.g., at least 85%, at least 86%, at least 87%, at least 88%, at least 89%, at least 90%, at least 91%, at least 92%, at least 93%, at least 94%, at least 95%, at least 96%, at least 97%, at least 98%, at least 99%, or 100% sequence identity to the mature polypeptide coding sequence of SEQ ID NO: 304;
- [0930] (s) a variant of SEQ ID NO: 257, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions; and
- [0931] (t) a variant of SEQ ID NO: 267, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11 or 12 positions; and
- [0932] (u) a variant of SEQ ID NO: 291, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0933] (v) a variant of SEQ ID NO: 294, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0934] (w) a variant of SEQ ID NO: 297, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0935] (x) a variant of SEQ ID NO: 300, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0936] (y) a variant of SEQ ID NO: 303, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions;
- [0937] (z) a variant of SEQ ID NO: 306, wherein the variant has lysozyme activity and comprises one or more substitutions and/or one or more deletions and/or one or more insertions or any combination thereof in 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48 or 49 positions; and
- [0938] (aa) a fragment of the polypeptide of (a), (b), (c), (d), (e), (f), (g), (h), (i), (j), (k), (l), (m), (n), (o), (p), (q), (r), (s), (t), (u), (v), (w), (x), (y) or (z) that has lysozyme activity wherein the fragment comprises at least 200 amino acids, such as at least 210 amino acids, at least 215 amino acids, at least 220 amino acids, at least 225 amino acids, at least 230 amino acids, at least 235 amino acids or at least 240 amino acids.

31. The polypeptide according to item 30, wherein the polypeptide comprises or consists of amino acids 1 to 245 of SEQ ID NO: 257, amino acids 1 to 248 of SEQ ID NO: 267, amino acids 1 to 245 of SEQ ID NO: 291, amino acids 1 to 249 of SEQ ID NO: 294, amino acids 1 to 245 of SEQ ID NO: 297, amino acids 1 to 247 of SEQ ID NO: 300, amino acids 1 to 250 of SEQ ID NO: 303 or amino acids 1 to 240 of SEQ ID NO: 306.
32. A composition comprising one or more polypeptides of any of items 30 to 31 and one or more formulating agents.
33. The composition of item 32 wherein the formulating agent comprises one or more of the following compounds: glycerol, ethylene glycol, 1,2-propylene glycol or 1, 3-propylene glycol, sodium chloride, sodium benzoate, potassium sorbate, sodium sulfate, potassium sulfate, magnesium sulfate, sodium thiosulfate, calcium carbonate, sodium citrate, dextrin, maltodextrin, glucose, sucrose, sorbitol, lactose, wheat flour, wheat bran, corn gluten meal, starch, kaolin and cellulose or any combination thereof.
34. A granule comprising one or more polypeptides of item 30 or 31 or the composition of item 32 or 33.
- 35 The granule of item 34 wherein the granule is coated.
36. The granule of item 35 wherein the coating comprises a salt and/or wax and/or a flour.
37. Use of the polypeptide of item 30 or 31, the animal feed or animal feed additive of any of items 1 to 27, the pelleted animal feed of item 28 or 29, the composition of item 32 or 33 or the granule of any of items 34 to 36:
- [0939] in animal feed;
  - [0940] in animal feed additives;
  - [0941] in the preparation of a composition for use in animal feed;
  - [0942] for improving one or more performance parameters in an animal;
  - [0943] for the treatment of *Clostridium perfringens* infection in an animal; and/or for the treatment of *necrotic enteritis* in an animal.
38. A method of treatment of a *Clostridium perfringens* infection and/or *necrotic enteritis* in an animal comprising the steps of administering the polypeptide of item 30 or 31, the animal feed or animal feed additive of any of items 1 to 27, the pelleted animal feed of item 28 or 29, the composition of item 32 or 33 or the granule of any of items 34 to 36 to one or more animals.
39. The polypeptide of item 30 or 31, the animal feed or animal feed additive of any of items 1 to 27, the pelleted animal feed of item 28 or 29, the composition of item 32 or 33 or the granule of any of items 34 to 36 for use as a medicament.
40. The polypeptide of item 30 or 31, the animal feed or animal feed additive of any of items 1 to 27, the pelleted animal feed of item 28 or 29, the composition of item 32 or 33 or the granule of any of items 34 to 36 for use in treatment of a *Clostridium perfringens* infection and/or *necrotic enteritis* in an animal.
41. A method of improving the performance of an animal comprising administering to the animal the polypeptide of item 30 or 31, the animal feed or animal feed additive of any of items 1 to 27, the pelleted animal feed of item 28 or 29, the composition of item 32 or 33 or the granule of any of items 34 to 36.
42. An isolated polynucleotide encoding the polypeptide of item 30 or 31.
43. A nucleic acid construct or expression vector comprising the polynucleotide of item 42 operably linked to one or more control sequences that direct the production of the polypeptide in an expression host cell.
44. A recombinant expression host cell comprising the polynucleotide of item 42 operably linked to one or more control sequences that direct the production of the polypeptide.
45. A method of producing the polypeptide of item 30 or 31, comprising:
- [0944] (a) cultivating a cell, which in its wild-type form produces the polypeptide, under conditions conducive for production of the polypeptide; and
  - [0945] (b) recovering the polypeptide.
46. A method of producing the polypeptide of item 30 or 31, comprising:
- [0946] (a) cultivating a host cell of item 44 under conditions conducive for production of the polypeptide; and
  - [0947] (b) recovering the polypeptide.
47. A transgenic plant, plant part or plant cell transformed with a polynucleotide encoding the polypeptide of item 30 or 31.
48. A whole broth formulation or cell culture composition comprising a polypeptide of item 30 or 31.
- [0948] The present invention is further described by the following examples that should not be construed as limiting the scope of the invention.

## EXAMPLES

### Strains

[0949] *Trichophaea saccata* CBS804.70 was purchased from the Centraalbureau voor Schimmelcultures (Utrecht, the Netherlands). According to CBS, the strain was obtained from coal spoil tip soil, with high surface temperatures from Staffordshire, England in May 1968.

[0950] *Trichoderma harzianum*, originally named A00611 was deposited at the Centraalbureau voor Schimmelcultures, Utrecht, Netherlands under the code: CBS223.93.

[0951] *Chaetomium thermophilum* var. *thermophilum* was purchased from Centraalbureau voor Schimmelcultures, Utrecht, Netherlands under the code CBS 144.50. According to CBS, the strain was obtained from decaying wheat straw from Leeds, England on or before 1950.

[0952] *Chaetomium* sp. ZY 287 was obtained from a soil sample from Beijing, China in August 2013. *Mortierella* sp. ZY 002 were obtained from a soil sample from Shanxi province, China in December 2012. *Metarhizium* sp. XZ2431 and *Geomyces auratus* were obtained from soil samples from Guizhou province, China in July 2014. *Ilyonectria rufa* was obtained from Tibet in August 2011.

### Media and Solutions

[0953] YP+2% glucose medium was composed of 1% yeast extract, 2% peptone and 2% glucose.

[0954] YP+2% maltodextrin medium was composed of 1% yeast extract, 2% peptone and 2% maltodextrin.

[0955] PDA agar plates were composed of potato infusion (potato infusion was made by boiling 300 g of sliced (washed but unpeeled) potatoes in water for 30 minutes and then decanting or straining the broth through cheesecloth. Distilled water was then added until the total volume of the

suspension was one liter, followed by 20 g of dextrose and 20 g of agar powder. The medium was sterilized by autoclaving at 15 psi for 15 minutes (Bacteriological Analytical Manual, 8th Edition, Revision A, 1998).

[0956] LB plates were composed of 10 g of Bacto-Tryptone, 5 g of yeast extract, 10 g of sodium chloride, 15 g of Bacto-agar, and deionized water to 1 liter.

[0957] LB medium was composed of 10 g of Bacto-Tryptone, 5 g of yeast extract, 10 g of sodium chloride, and deionized water to 1 liter.

[0958] COVE sucrose plates were composed of 342 g of sucrose, 20 g of agar powder, 20 ml of COVE salts solution, and deionized water to 1 liter. The medium was sterilized by autoclaving at 15 psi for 15 minutes (Bacteriological Analytical Manual, 8th Edition, Revision A, 1998). The medium was cooled to 60° C. and 10 mM acetamide, 15 mM CsCl, TRITON® X-100 (50 µl/500 ml) were added.

[0959] COVE salts solution was composed of 26 g of MgSO<sub>4</sub>·7H<sub>2</sub>O, 26 g of KCl, 26 g of KH<sub>2</sub>PO<sub>4</sub>, 50 ml of COVE trace metals solution, and deionized water to 1 liter. COVE trace metals solution was composed of 0.04 g of Na<sub>2</sub>B<sub>4</sub>O<sub>7</sub>·10H<sub>2</sub>O, 0.4 g of CuSO<sub>4</sub>·5H<sub>2</sub>O, 1.2 g of FeSO<sub>4</sub>·7H<sub>2</sub>O, 0.7 g of MnSO<sub>4</sub>·H<sub>2</sub>O, 0.8 g of Na<sub>2</sub>MoO<sub>4</sub>·2H<sub>2</sub>O, 10 g of ZnSO<sub>4</sub>·7H<sub>2</sub>O, and deionized water to 1 liter.

[0960] Dap-4C medium was composed of 20 g Dextrose, 10 g Maltose, 11 g MgSO<sub>4</sub>·7H<sub>2</sub>O, 1 g KH<sub>2</sub>PO<sub>4</sub>, 2 g Citric Acid, 5.2 g K<sub>3</sub>PO<sub>4</sub>·H<sub>2</sub>O, 0.5 g Yeast Extract (Difco), 1 ml Dowfax 63N10 (Dow Chemical Company), 0.5 ml KU6 trace metals solution, 2.5 g CaCO<sub>3</sub>, and deionized water to 1 liter. The medium was sterilized by autoclaving at 15 psi for 15 minutes (Bacteriological Analytical Manual, 8th Edition, Revision A, 1998). Before use, Dap-4C medium was added 3.5 ml sterile 50% (NH<sub>4</sub>)<sub>2</sub>HPO<sub>4</sub> and 5 ml sterile 20% Lactic Acid per 150 ml medium.

[0961] Dap-2C medium was composed of 20 g maltodextrin, 11 g MgSO<sub>4</sub>·7H<sub>2</sub>O, 1 g KH<sub>2</sub>PO<sub>4</sub>, 2 g Citric Acid, 5.2 g K<sub>3</sub>PO<sub>4</sub>·H<sub>2</sub>O, 0.5 g Yeast Extract (Difco), 1 ml Dowfax 63N10 (Dow Chemical Company), 0.5 ml KU6 trace metals solution, 2.5 g CaCO<sub>3</sub>, and deionized water to 1 liter. The medium was sterilized by autoclaving at 15 psi for 15 minutes (Bacteriological Analytical Manual, 8th Edition, Revision A, 1998). Before use, Dap-4C medium was added 3.5 ml sterile 50% (NH<sub>4</sub>)<sub>2</sub>HPO<sub>4</sub> and 5 ml sterile 20% Lactic Acid per 150 ml medium.

[0962] KU6 trace metals solution was composed of 0.13 g NiCl<sub>2</sub>, 2.5 g CuSO<sub>4</sub>·5H<sub>2</sub>O, 13.9 g FeSO<sub>4</sub>·7H<sub>2</sub>O, 8.45 g MnSO<sub>4</sub>·H<sub>2</sub>O, 6.8 g ZnCl<sub>2</sub>, 3 g Citric Acid, and deionized water to 1 liter.

[0963] PDA medium was composed of 39 g of potato dextrose agar and deionized water to 1 liter.

[0964] Horikoshi medium contained 10 g of glucose, 5 g of peptone, 5 g of yeast extract, 1 g of K<sub>2</sub>HPO<sub>4</sub>, 0.2 g of MgSO<sub>4</sub>·7H<sub>2</sub>O, 15 g of agar in 900 ml of distilled water. Autoclave at 121° C. for 15 minutes. After autoclaving, aseptically add 100.0 ml of sterile 10% Na<sub>2</sub>CO<sub>3</sub> to the medium. Adjust for final pH of 10.0.

[0965] YPM medium contained 1% of Yeast extract, 2% of Peptone and 2% of Maltose.

[0966] Selective medium was composed of 342 g of sucrose, 20 ml of salt solution, 20 g of agar.

[0967] Salt solution was composed of 26 g of KCl, 26 g of MgSO<sub>4</sub>·7H<sub>2</sub>O, 76 g of KH<sub>2</sub>PO<sub>4</sub>, 50 ml of trace element solution, in water with final volume of 1 L.

[0968] Trace element solution was composed of 400 mg of Na<sub>2</sub>B<sub>4</sub>O<sub>7</sub>·10H<sub>2</sub>O, 400 mg of CuSO<sub>4</sub>·5H<sub>2</sub>O, 800 mg of FeSO<sub>4</sub>·7H<sub>2</sub>O, 800 mg of MnSO<sub>4</sub>·2H<sub>2</sub>O, 800 mg of Na<sub>2</sub>MoO<sub>4</sub>·2H<sub>2</sub>O, 8 g of ZnSO<sub>4</sub>·7H<sub>2</sub>O in water with final volume of 1 L.

[0969] Slant medium was composed of 30 g of sucrose, 20 ml of salt solution, 20 g of agar.

Example 1: Expression of the GH24 Lysozyme  
from *Trichophaea saccata*

[0970] The fungal strain was cultivated in 100 ml of YP+2% glucose medium in 1000 ml Erlenmeyer shake flasks for 5 days at 20° C. Mycelia were harvested from the flasks by filtration of the medium through a Buchner vacuum funnel lined with MIRACLOTH® (EMD Millipore, Billerica, MA, USA). Mycelia were frozen in liquid nitrogen and stored at -80° C. until further use. Genomic DNA was isolated using a DNEASY® Plant Maxi Kit (QIAGEN GMBH, Hilden Germany) according to the manufacturer's instructions.

[0971] Genomic sequence information was generated by Illumina MySeq (Illumina Inc., San Diego, CA). The polypeptide coding sequence for the entire coding region was cloned from *Trichophaea saccata* CBS804.70 genomic DNA by PCR using the primers F-80470 and R-80470 (SEQ ID NO: 258 and SEQ ID NO: 259 respectively) as described below.

(SEQ ID NO: 258)  
5' -ACACAACTGGGGATCCACC**A**TGCACGCTCTCACCCTTCT-3'

(SEQ ID NO: 259)  
5' -CTAGATCTCGAGAAGCTT**T**AGCACTGGGAGGGTGGG-3'

[0972] Bold letters represent *Trichophaea saccata* enzyme coding sequence. Restriction sites are underlined. The sequence to the left of the restriction sites is homologous to the insertion sites of pDau109 (WO 2005/042735).

[0973] Extensor HIFI PCR mix, 2x concentration (Thermo Scientific cat no AB-0795) was used for experiment.

[0974] The amplification reaction (25 µl) was performed according to the manufacturer's instructions (Thermo Scientific cat no AB-0795) with the following final concentrations:

PCR Mix:

[0975] 0.5 µM Primer F-80470

[0976] 0.5 µM Primer R-80470

[0977] 12.5 µl Extensor HIFI PCR mix, 2xconc.

[0978] 11.0 µl H<sub>2</sub>O

[0979] 10 ng of *Trichophaea saccata* CBS 804.70 genomic DNA.

[0980] The PCR reaction was incubated in a DYAD® Dual-Block Thermal Cycler (BioRad, USA) programmed for 1 cycle at 94° C. for 30 seconds; 30 cycles each at 94° C. for 30 seconds, 52° C. for 30 seconds and 68° C. for 60 seconds followed by 1 cycle at 68° C. for 6 minutes. Samples were cooled to 10° C. before removal and further processing.

[0981] Three µl of the PCR reaction were analyzed by 1% agarose gel electrophoresis using 40 mM Tris base, 20 mM sodium acetate, 1 mM disodium EDTA (TAE) buffer. A major band of about 946 bp was observed. The remaining

PCR reaction was purified directly with an ILLUSTRATM GFX™ PCR DNA and Gel Band Purification Kit (GE Healthcare, Piscataway, NJ, USA) according to the manufacturer's instructions.

[0982] Two µg of plasmid pDau109 was digested with Bam HI and Hind III and the digested plasmid was run on a 1% agarose gel using 50 mM Tris base-50 mM boric acid-1 mM disodium EDTA (TBE) buffer in order to remove the stuffer fragment from the restricted plasmid. The bands were visualized by the addition of SYBR® Safe DNA gel stain (Life Technologies Corporation, Grand Island, NY, USA) and use of a 470 nm wavelength transilluminator. The band corresponding to the restricted plasmid was excised and purified using an ILLUSTRATM GFX™ PCR DNA and Gel Band Purification Kit. The plasmid was eluted into 10 mM Tris pH 8.0 and its concentration adjusted to 20 ng per µl. An IN-FUSION® PCR Cloning Kit (Clontech Laboratories, Inc., Mountain View, CA, USA) was used to clone the 983 bp PCR fragment into pDau109 digested with Bam HI and Hind III (20 ng). The IN-FUSION® total reaction volume was 10 µl. The IN-FUSION® total reaction volume was 10 µl. The IN-FUSION® reaction was transformed into FUSION-BLUE™ *E. coli* cells (Clontech Laboratories, Inc., Mountain View, CA, USA) according to the manufacturer's protocol and plated onto LB agar plates supplemented with 50 µg of ampicillin per ml. After incubation overnight at 37° C., transformant colonies were observed growing under selection on the LB plates supplemented with 50 µg of ampicillin per ml.

[0983] Several colonies were selected for analysis by colony PCR using the pDau10<sup>9</sup> vector primers described below. Four colonies were transferred from the LB plates supplemented with 50 µg of ampicillin per ml with a yellow inoculation pin (Nunc A/S, Denmark) to new LB plates supplemented with 50 µg of ampicillin per ml and incubated overnight at 37° C.

Primer 8653 :  
 (SEQ ID NO: 260)  
 5' -GCAAGGGATGCCATGCTTGG-3'

Primer 8654 :  
 (SEQ ID NO: 261)  
 5' -CATATAACCAATTGCCCTC-3'

[0984] Each of the three colonies were transferred directly into 200 µl PCR tubes composed of 5 µl of 2x Extensor HIFI PCR mix, (Thermo Fisher Scientific, Rockford, IL, USA), 0.5 µl of primer 8653 (10 pm/µl), 0.5 µl of primer 8654 (10 pm/µl), and 4 µl of deionized water. Each colony PCR was incubated in a DYAD® Dual-Block Thermal Cycler programmed for 1 cycle at 94° C. for 60 seconds; 30 cycles each at 95° C. for 30 seconds, 60° C. for 45 seconds, 72° C. for 60 seconds, 68° C. for 10 minutes, and 10° C. for 10 minutes.

[0985] Three µl of each completed PCR reaction were submitted to 1% agarose gel electrophoresis using TAE buffer. All four *E. coli* transformants showed a PCR band of about 980 bp. Plasmid DNA was isolated from each of the four colonies using a QIAprep Spin Miniprep Kit (QIAGEN GMBH, Hilden Germany). The resulting plasmid DNA was sequenced with primers 8653 and 8654 (SEQ ID NO: 260 and 261) using an Applied Biosystems Model 3730 Automated DNA Sequencer using version 3.1 BIG-DYE™ terminator chemistry (Applied Biosystems, Inc., Foster City,

CA, USA). One plasmid, designated pKKSC0312-2, was chosen for transforming *Aspergillus oryzae* MT3568. *A. oryzae* MT3568 is an amdS (acetamidase) disrupted gene derivative of *Aspergillus oryzae* JaL355 (WO 2002/40694) in which pyrG auxotrophy was restored by inactivating the *A. oryzae* amdS gene. Protoplasts of *A. oryzae* MT3568 were prepared according to the method described in EP 0238023, pages 14-15.

[0986] *E. coli* 3701 containing pKKSC0312-2 was grown overnight according to the manufacturer's instructions (Genomed) and plasmid DNA of pKKSC0312-2 was isolated using a Plasmid Midi Kit (Genomed J ETquick kit, cat.nr. 400250, GENOMED GmbH, Germany) according to the manufacturer's instructions. The purified plasmid DNA was transformed into *Aspergillus oryzae* MT3568. *A. oryzae* MT3568 protoplasts were prepared according to the method of Christensen et al., 1988, *Bio/Technology* 6:1419-1422. The selection plates consisted of COVE sucrose with+10 mM acetamide+15 mM CsCl+TRITON® X-100 (50 µl/500 ml). The plates were incubated at 37° C. Briefly, 8 µl of plasmid DNA representing 3 ugs of DNA was added to 100 µl MT3568 protoplasts. 250 µl of 60% PEG solution was added and the tubes were gently mixed and incubate at 37° for 30 minutes. The mix was added to 10 ml of pre melted Cove top agarose (The top agarose melted and then the temperature equilibrated to 40 C in a warm water bath before being added to the protoplast mixture). The combined mixture was then plated on two Cove-sucrose selection petri plates with 10 mM Acetamide. The plates were incubated at 37° C. for 4 days. Single *Aspergillus* transformed colonies were identified by growth on plates using the selection Acetamide as a carbon source. Each of the four *A. oryzae* transformants were inoculated into 750 µl of YP medium supplemented with 2% glucose and also 750 µl of 2% maltodextrin and also DAP4C in 96 well deep plates and incubated at 37° C. stationary for 4 days. At the same time the four transformants were restreaked on COVE-2 sucrose agar medium.

[0987] Culture broth from the *Aspergillus oryzae* transformants were then analyzed for production of the GH24 polypeptide by SDS-PAGE using NUPAGE® 10% Bis-Tris SDS gels (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's recommendations. A protein band at approximately 27 kDa was observed for each of the *Aspergillus oryzae* transformants. One *A. oryzae* transformant was cultivated in 1000 ml Erlenmeyer shake flasks containing 100 ml of DAP4C medium at 26° C. for 4 days with agitation at 85 rpm and purified as described in example 2.

#### Example 2: Purification of the GH24 Lysozyme from *Trichophaea saccata*

[0988] The fermentation supernatant with the GH24 lysozyme was filtered through a Fast PES Bottle top filter with a 0.22 µm cut-off. The resulting solution was diafiltrated with 5 mM Na-acetate, pH 4.5 and concentrated (volume reduced by a factor of 10) on an Ultra Filtration Unit (Sartorius) with a 10 kDa cut-off membrane.

[0989] After pretreatment about 275 ml of the lysozyme containing solution was purified by chromatography on SP Sepharose (approximately 60 mL) in a XK26 column eluting the bound lysozyme with 0 to 100% gradient of buffer A (50 mM Na-acetate pH 4.5) and buffer B (50 mM Na-acetate+1 M NaCl pH 4.5) over 10 column volumes. The fractions

from the column were pooled based on the chromatogram (absorption at 280 and 254 nm) and SDS-PAGE analysis.

[0990] The molecular weight, as estimated from SDS-PAGE, was approximately 27 kDa and the purity was >90%. Characteristics for the GH24 Lysozyme from *Trichophaea saccata*

[0991] Determination of the N-terminal sequence was: YPVKTDL.

[0992] The calculated molecular weight from this mature sequence is 26205.5 Da (M+H)<sup>+</sup>.

[0993] The molecular weight determined by intact molecular weight analysis was 26205.3 Da. (M+H)<sup>+</sup>.

[0994] The mature sequence (from EDMAN N-terminal sequencing data, intact molecular weight analysis and proteomic analysis with 92% amino acid coverage):

```
(SEQ ID NO: 257)
YPVKTDLHCRSSPSTSASIVRTYSSGTEVQIQCQTTGTSVQGSNV
WDKTQHGCYVADYYVKTGHSGIFTTKCGSSSSGGSKPPPIAAT
VALIKEFEGFVPKPAPDPIGLPTVGYGHLCCTKGCKEVPSFPLT
QETATKLLQSDIKFTFTSCSVNPKDSVKLNDNQYGALASWAFNVG
CGNVQTSSLIKRLNAGENPNTVAAQELPKWKYAGGKVMPGLVRRR
NAEVALFKKPSSVQAHPPKC.
```

**Example 3: Expression of the LED Alone from *Trichophaea saccata***

[0995] In order to establish the properties of the newly defined lysozyme enhancing domain, an expression construct in which the N-terminal portion of the GH24 polypeptide coding sequence from example 1 was expressed.

[0996] The amino acid sequence shown below represents the signal peptide and the NZ4 domain. The signal peptide is underlined.

```
(SEQ ID NO: 272)
MHALTLLTATLFGLAAYPVKTDLHCRSSPSTSASIVRTYSSGTE
VQIQCQTTGTSVQGSNVWDKTQHGCYVADYYVKTGHSGIFTTKCG
```

[0997] The DNA representing SEQ ID NO: 272 is shown below as SEQ ID NO: 271 wherein the signal peptide is underlined.

```
(SEQ ID NO: 271)
ATGCACGCCTCTCACCCCTCTCACCGCAACCCCTCTCGGTCTCGCA
GCGGCCTACCCAGTGAAAGACCGACCTTCACTGCCGCTCTCTCCC
AGCACTTCCGCCAGCATCGTCCGACCTACTCCAGTGGAACGGAA
GTCCAGATCCAGTGCCAGACCACGGGCACTTCGGTCCAAGGATCC
AATGTCTGGACAAGACCCAGCACGGTTGCTACGTCGCAAGACTAC
TACGTCAAGACCGGGCATTCTGGGATTTCACCAAGTGGGT
```

[0998] PCR primers were designed in order to amplify the DNA fragment SEQ ID NO: 271 from pKKSC0312-2 of example 1. The forward primer from example 1 (SEQ ID NO: 258) could be reused. For the reverse primer, a TAA

stop codon was added to the DNA sequence of the above and then the Infusion cloning site for the HindIII site was added to create the primer below:

```
(SEQ ID NO: 274)
AGATCTCGAGAAGCTTATACCGCACTTGGGTGAAA.
```

[0999] The amplification reaction (25 μl) was performed according example 1. The 270 base pair PCR product was cloned into vector pDau222 also as described in example 1.

[1000] Culture broth from the *Aspergillus oryzae* transformants were then analyzed for production of the LED polypeptide by SDS-PAGE using NUPAGE® 8% Bis-Tris SDS gels (Invitrogen, Carlsbad, CA, USA) according to the manufacturer. A band at approximately 14 kDa was observed for each of the *Aspergillus oryzae* transformants. The actual size appears larger than the predicted size of 8.4 kDa possibly because of post translational modification. One *A. oryzae* transformant producing the LED polypeptide was cultivated in 1000 ml Erlenmeyer shake flasks containing 100 ml of DAP4C medium at 30° C. for 4 days with agitation at 150 rpm and purified as described in example 4.

**Example 4: Expression of the LED Alone from *Trichophaea saccata***

[1001] The fermentation supernatant with the LED alone from *Trichophaea saccata* was filtered through a Fast PES Bottle top filter with a 0.22 μm cut-off. The resulting solution was desalted on a G25 Sephadex column (approximately 500 mL) into 50 mM Na-acetate, pH 4.5. Following this the protein containing solution (approximately 125 ml) was purified by chromatography on SP Sepharose (approximately 50 mL) in a XK26 column eluting the bound lysozyme with 0 to 100% gradient of buffer A (50 mM Na-acetate pH 4.5) and buffer B (50 mM Na-acetate+1 M NaCl pH 4.5) over 10 column volumes. The fractions from the column were pooled based on the chromatogram (absorption at 280 and 254 nm) and SDS-PAGE analysis.

[1002] The molecular weight, as estimated from SDS-PAGE, was 6-10 kDa and the purity was >95%. The calculated molecular weight from this mature sequence is 7906.64 Da.

[1003] The mature sequence (from proteomic analysis with 97% amino acid coverage) was determined to be:

```
(SEQ ID NO: 273)
YPVKTDLHCRSSPSTSASIVRTYSSGTEVQIQCQTTGTSVQGSNV
WDKTQHGCYVADYYVKTGHSGIFTTKCG.
```

**Example 5: Expression of the GH24 Domain of *Trichophaea saccata* CBS804.70**

[1004] In order to determine if the lysozyme enhancing domain has functional or enhancing properties for the associated GH24 lysozyme, a construct was cloned and protein expressed in which the LED had been removed from the GH24 lysozyme. The construct was made as follows:

[1005] A synthetic gene was created as described below.

[1006] Based on multiple sequence alignments, QCVG or similar appears to be fairly well conserved in the GH24 fungal lysozymes without the LED domain. Therefor the signal and the sequence downstream QCVG sequence from

SEQ ID NO: 279 (GH24 from *Acremonium acalophilum*) was used in part of the construct. This peptide sequence was then added directly to the mature peptide fragment containing only the GH24 lysozyme region of SEQ ID NO: 257 resulting in the amino acid sequence below:

(SEQ ID NO: 269)  
MAKVSTLTIALLTMASQARAQCVGCKPPPIAATVALIKEFEGFV  
PKPAP DPIGLPTVGYGHLCRKGCKEVPYSFPLTQETATKLLQS  
DIKTFTSCSVNSYVKDSVKLNDNQY GALASWAFNVGCGNVQTSSLI  
KRLNAGENPNTVAAQELPKWKYAGGKVMPGLVRRAEVALKKP  
SSVOAHPPK .

[1007] A synthetic DNA (SEQ ID NO: 268) that had been codon optimised for expression in *Aspergillus oryzae* was ordered from GeneArt® Gene Synthesis, Life Technologies. The synthetic DNA conveniently had BamHII and HindIII restriction sites added to the ends so as to make a BamHII-HindIII restricted fragment compatible with the cloning vector pDau109 used in example 1.

[1008] The fragment was received from GeneArt in kanamycin resistant vector pMK and the plasmid was dissolved DNA in 50 µls in 10 mM Tris, pH7.5. 20 µls of the mixture with BamHI-HindIII according to the protocol below:

Plasmid	20 µl
Cut smart buffer: 10x #B7204S	4.0 µl
Milli-Q H <sub>2</sub> O:	14.0 µl
Hind III HF: NEB #R3104S	1 µl
BamH HF: NEB #R3136S	1 µl
Total volume	40 µl

**[1009]** The reaction was incubated for 3 hours at 37° C. The restriction digest was purified with the GFX PCR DNA and Gel Band purification Kit (Cat. no 28-9034-71) from GE Healthcare and eluted in 40 µls 10 mM Tris, pH 7.5. The purified restriction digest was then used in a simple ligation with BamHI-HindIII restricted pDau109 (example 1) according to the T4 DNA ligase manufacturer's instructions (New England Biolabs., [neb.com](http://neb.com)).

[1010] 2.5  $\mu$ l of the 10  $\mu$ l ligation was used to transform 25  $\mu$ l Stellar<sup>TM</sup> (Life Technologies) Competent cells according to the manufacturer's instructions and the treated cells plated on LB agar plates with 50 mg/ml ampicillin. Colony PCR of select transformants was performed according to example 1 and the PCR fragments sequenced. A single plasmid, selected as being PCR error free, was transformed into *Aspergillus oryzae* MT3568 according to example 1. Among the several transformants that produced the secreted product of about 20 kDa, one was chosen and cultivated in 1000 ml Erlenmeyer shake flasks containing 100 ml of DAP4C medium at 30° C. for 4 days with agitation at 150 rpm and purified as described in example 6.

### Example 6: Purification of the GH24 Domain of *Trichophaea saccata* CBS804.70

[1011] The fermentation supernatant with the GH24 domain was filtered through a Fast PES Bottle top filter with a 0.22  $\mu$ m cut-off. The resulting solution was diafiltrated

with 50 mM Na-acetate, pH 4.5 on an Ultra Filtration Unit (Sartorius) with a 10 kDa cut-off membrane.

[1012] After pretreatment about 500 ml of the lysozyme containing solution was purified by chromatography on SP Sepharose (approximately 50 mL) in a XK26 column eluting the bound protein with 0 to 100% gradient of buffer A (50 mM Na-acetate pH 4.5) and buffer B (50 mM Na-acetate+1 M NaCl pH 4.5) over 10 column volumes. The fractions from the column were pooled based on the chromatogram (absorption at 280 and 254 nm) and SDS-PAGE analysis.

[1013] The molecular weight, as estimated from SDS-PAGE, was approximately 20 kDa and the purity was >90%.

[1014] The calculated molecular weight from this mature sequence is 18182.86 Da.

[1015] The mature sequence (from proteomic analysis with 72% amino acid coverage) was determined to be:

(SEQ ID NO: 270)  
QCVGCKPPPINAATVALIKEFEGFVPKPAPDPIGLPTVGYGHLC  
TKGCKEVPSFPLTQETATKLLQSDIKTFTSCVSNYVKDSVKLND  
NQYGALASWAFNVCGNVQTSSLIKRLNAGENPNTVAQQELPKWK  
YAGGKVMPGLVRRRNAEVALFKKPSSVQAHPPKC .

### Example 7: Cloning and Expression of GH24 Lysozyme from *Trichoderma harzianum* A00611

[1016] *Trichoderma harzianum*, originally named A00611 was deposited at the Centraalbureau voor Schimmelcultures, Utrecht, Netherlands under the code: CBS223.93. *Trichoderma harzianum* A00611 was grown on Potato Dextrose Agar at 26° C. for several days. Mycelia was harvested directly from the inoculated PDA agar plate and the DNA prepared as in example 1.

[1017] The polypeptide coding sequence for the entire coding region was cloned from *Trichoderma harzianum* A00611 genomic DNA by PCR using primers SEQ ID NO: 275 and SEQ ID NO: 276 as given below.

F SEQ ID NO: 275  
5' -ACACAACTGGGGATCCACCATGAAGACTGCCTTGCTG-3'  
  
R SEQ ID NO: 276  
5' -AGATCTCGAGAAGCTTATCACTGGCAGTTGGATAGGC-3'

[1018] Bold letters represent *Trichoderma harzianum* enzyme coding sequence. Restriction sites are underlined. The sequence to the left of the restriction sites is homologous to the insertion sites of pDau109 (WO 2005/042735).

**[1019]** Cloning of the 800 bp PCR fragment, transformation into *Aspergillus oryzae* and production of culture fluid for purification of the GH24 lysozyme was performed according to example 1.

[1020] A band at approximately 27 kDa was observed for each of the *Aspergillus oryzae* transformants. One *A. oryzae* transformant producing the polypeptide was chosen and cultivated in 1000 ml Erlenmeyer shake flasks containing 100 ml of DAP4C medium at 30° C. for 4 days with agitation at 150 rpm and purified as described in example 8.

**Example 8: Purification of the GH24 Lysozyme from *Trichoderma harzianum* A00611**

[1021] The fermentation supernatant with the GH24 lysozyme from *Trichoderma harzianum* A00611 was filtered through a Fast PES Bottle top filter with a 0.22 µm cut-off. About one liter was obtained and the pH was adjusted to 4.5 with diluted acetic acid. The sample was diluted to two liters with Milli-Q water.

[1022] After pretreatment about 1000 ml of the lysozyme containing solution was purified by chromatography on SP Sepharose (approximately 30 mL) in a XK26 column eluting the bound lysozyme with 0 to 100% gradient of buffer A (50 mM Na-acetate pH 4.5) and buffer B (50 mM Na-acetate+1 M NaCl pH 4.5) over 10 column volumes. The fractions from the column were pooled based on the chromatogram (absorption at 280 and 254 nm) and SDS-PAGE analysis.

[1023] The molecular weight, as estimated from SDS-PAGE, was approximately 27 kDa and the purity was >90%.

**Example 9: Cloning and Expression of the GH24 Lysozyme from *Chaetomium thermophilum* var. *thermophilum***

[1024] *Chaetomium thermophilum* var. *thermophilum* was purchased from Centraalbureau voor Schimmelcultures, Utrecht, Netherlands under the code CBS 144.50. The strain was grown on Potato Dextrose Agar at 37° C. for several days. Mycelia was harvested directly from the inoculated PDA agar plate and the DNA prepared as in example 1.

[1025] The polypeptide coding sequence for the entire coding region was cloned from *Chaetomium thermophilum* CBS 144.50 genomic DNA by PCR using primers SEQ ID NO: 277 and SEQ ID NO: 278 as given below.

F	SEQ ID NO: 277
5' -ACACA <u>ACTGGGGATCCACC</u> <b>A</b> TGAAGTTGCCATCCTCGC-3'	
R	SEQ ID NO: 278
5' -AGAT <u>CTCGAGAAGCTTATCAGCACTTAACAGGAAGAGCC</u> -3'	

[1026] Bold letters represent GH24 enzyme coding sequence. Restriction sites are underlined. The sequence to the left of the restriction sites is homologous to the insertion sites of pDau109 (WO 2005/042735).

[1027] Cloning of the 960 bp PCR fragment, transformation into *Aspergillus oryzae* and production of culture fluid for purification of the GH24 lysozyme was performed according to example 1. A band at approximately 26 kDa was observed for each of the *Aspergillus oryzae* transformants. One *A. oryzae* transformant producing the polypeptide was chosen and cultivated in 1000 ml Erlenmeyer shake flasks containing 100 ml of DAP4C medium at 30° C. for 4 days with agitation at 150 rpm and purified as described in example 10.

**Example 10: Purification of the GH24 Lysozyme from *Chaetomium thermophilum* Var. *thermophilum***

[1028] The fermentation supernatant with the GH24 lysozyme from *Chaetomium thermophilum* var. *thermophilum* was filtered through a Fast PES Bottle top filter with a 0.22 µm cut-off. The resulting solution was diafiltrated with 50 mM Na-acetate, pH 4.5 and concentrated (volume

reduced by a factor of 10) on an Ultra Filtration Unit (Sartorius) with a 10 kDa cut-off membrane.

[1029] After pretreatment about 300 mL of the lysozyme containing solution was purified by chromatography on SP Sepharose (approximately 60 mL) in a XK26 column eluting the bound lysozyme with 0 to 100% gradient of buffer A (50 mM Na-acetate pH 4.5) and buffer B (50 mM Na-acetate+1 M NaCl pH 4.5) over 10 column volumes. The fractions from the column were pooled based on the chromatogram (absorption at 280 and 254 nm) and SDS-PAGE analysis.

[1030] The molecular weight, as estimated from SDS-PAGE, was approximately 27 kDa and the purity was >90%.

**Example 11: Determination of Lysozyme Activity**

[1031] Lysozyme activity was determined by measuring the decrease (drop) in absorbance/optical density of a solution of resuspended *Micrococcus lysodeikticus* ATTC No. 4698 (Sigma-Aldrich M3770) or *Exiguobacterium undae* (DSM14481) measured in a spectrophotometer at 540 nm.

**Preparation of *Micrococcus lysodeikticus* Substrate**

[1032] Before use, the cells were resuspended in citric acid-phosphate buffer pH 6.5 to a concentration of 0.5 mg cells/mL and the optical density (OD) at 540 nm was measured. The cell suspension was then adjusted so that the cell concentration equalled an OD<sub>540</sub>=1.0. The adjusted cell suspension was then stored cold before use. Resuspended cells were used within 4 hours.

**Preparation of Dried Cells of *Exiguobacterium undae* Substrate**

[1033] A culture of *E. undae* (DSM14481) was grown in 100 mL LB medium (Fluka 51208, 25 g/L) in a 500 mL shake-flask at 30° C., 250 rpm overnight. The overnight culture was then centrifuged at 20° C. and 5000 g for 10 minutes, and the pellet was then washed twice with sterile milliQ water, and resuspended in Milli-Q water. The washed cells were centrifuged for 1 minute at 13000 rpm and as much as possible of the supernatant was decanted. The washed cells were dried in a vacuum centrifuge for 1 hour. The cell pellet was resuspended in citric acid-phosphate buffer pH 4, 5 or 6 so that the optical density (OD) at 540 nm=1.

**Measurement of Lysozyme Antimicrobial Activity in the Turbidity Assay**

[1034] The lysozyme sample to be measured was diluted to a concentration of 100-200 mg enzyme protein/L in citric acid-phosphate buffer pH 4, 5 or 6, and kept on ice until use. In a 96 well microtiterplate (Nunc) 200 µL of the substrate was added to each well, and the plate was incubated at 37° C. for 5 minutes in a VERSAmax microplate reader (Molecular Devices). Following incubation, the absorbance of each well was measured at 540 nm (start value). To start the activity measurement, 20 µL of the diluted lysozyme sample was added to each substrate (200 µL) and kinetic measurement of absorbance at 540 nm was initiated for minimum 30 minutes up to 24 hours at 37° C. The measured absorbance at 540 nm was monitored for each well and over time a drop in absorbance is seen if the lysozyme has lysozyme activity. The results are presented in table 2 below.

TABLE 2

Lysozyme Activity against <i>Micrococcus lysodeikticus</i> and <i>Exiguobacterium undae</i> as measured by Optical Density Drop		
GH24 Lysozyme	<i>Micrococcus lysodeikticus</i> <sup>1</sup>	<i>Exiguobacterium undae</i> <sup>1</sup>
GH24 Lysozyme from <i>Trichophaea saccata</i> (SEQ ID NO: 257)	++ (pH 6)	++ (pH 6)
GH24 lysozyme from <i>Chaetomium thermophilum</i> (SEQ ID NO: 264)	++++ (pH 5)	++++ (pH 6)
GH24 lysozyme from <i>Trichophaea saccata</i> lacking LED (SEQ ID NO: 270)	- (pH 6)	Not tested
GH24 lysozyme from <i>Acremonium alcalophilum</i> (SEQ ID NO: 280)	+ (pH 4.5)	- (pH 3-7)

<sup>1</sup>Means no significant effect; + means small effect; ++ means medium effect; +++ means large effect; ++++ means very large effect.

The pH value in the brackets lists the assay pH based on lysozyme-substrate combination.

[1035] The data shows that the two GH24 lysozymes that naturally comprise the lysozyme enhancing domain (LED) (SEQ ID NO: 257 and 264) showed good activity against both substrates. In comparison, SEQ ID NO: 270 (which is SEQ ID NO: 257 but lacking the LED) demonstrated no lysozyme activity against *Micrococcus lysodeikticus* and the GH24 lysozyme which does not natively comprise a LED (SEQ ID NO: 280) showed a small amount of activity.

#### Example 12: Determination of Antimicrobial Activity

[1036] The antimicrobial activity of 3 GH24 lysozymes also comprising the lysozyme enhancing domain (LED) (SEQ ID NO: 257, 264 and 267), two GH24 lysozymes which natively do not comprise the LED (SEQ ID NO: 279 and 280) and the GH24 lysozyme of SEQ ID NO. 257 for which the LED was removed (resulting in SEQ ID NO: 269) against *Clostridium perfringens* DSM756 was tested using an RDA as described previously by Lehrer et al. ("Ultrasensitive assays for endogenous antimicrobial polypeptides", *J. Immunol. Methods* 137:167-73 (1991)), but with several modifications.

[1037] Briefly, RDA bacteria were prepared by streaking *C. perfringens* DSM756 from freeze stocks on Luria-Bertani agar plates (Sigma L3027) and the plates were incubated overnight at 37° C. under anaerobic conditions (Anaerogen, Oxoid) in a jar. The following day colonies were suspended in 0.9% NaCl and the suspensions were adjusted to McFarland std. 1. 87% sterile glycerol was added to give a final glycerol concentration of 20% and the cells were frozen at -80° C. until use. For estimation of colony forming units (CFU) per milliliter of the RDA bacteria 10-fold dilution series were prepared of the freeze stock in 0.9% NaCl and 100 µl of the dilutions were plated on Luria-Bertani agar plates (Sigma L3027) and incubated overnight at 37° C. under anaerobic conditions (Anaerogen, Oxoid) in a jar.

[1038] When preparing the RDA plates broth media with agar was melted and cooled to 42° C. Two media were tested in the experiment:

[1039] a) ½ Mueller-Hinton broth (MHB) (Sigma/ Fluka, 90922) (i.e., adjusted to pH 6 with 4 M HCl and diluted 1:1 with water) with 1.5% agarose, and

[1040] b) ½ Mueller-Hinton broth (MHB) (Sigma/ Fluka, 90922) (i.e., diluted 1:9 with water) with 1% agarose.

[1041] For each assay plate 30 ml of melted media was added to achieve around 5.0×10<sup>5</sup> cfu/mL *C. perfringens* DSM756 and this was poured into a single-well omnitrays (Nunc) plate. The omnitrays plate was overlaid with a TSP plate (Nunc) and left to solidify (at room temperature or below). Afterwards, the TSP plate was removed; leaving 96 wells, in which 10 µL of the compound of interest could be tested.

[1042] 10 µL of the test solutions were spotted pr. well and the plates were incubated over night at 37° C. in a jar under anaerobic condition (Anaerogen, Oxoid). The following day a clearing zone indicated inhibition of growth of test bacteria and thereby antimicrobial activity. For the RDA plates with ½ MHB, the clearing zones were visualized by coloring with MTT (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide, a yellow tetrazole), that is reduced to purple formazan in living cells (Mosmann, 1983, "Rapid colorimetric assay for cellular growth and survival: application to proliferation and cytotoxicity assays", *Journal of Immunological Methods* 65 (1-2): 55-63). This coloring provides for a dark coloring of living cells and no coloring of the clearing zones without living cells.

[1043] Bacitracin zinc salt (Sigma B-8800) (50 µg/ml) was included as a positive control and lysozymes were tested using a solution of 100 µg/ml. The results are presented in table 3 below.

TABLE 3

Antimicrobial Activity against <i>Clostridium perfringens</i> as measured by RDA			
Experiment	Diameter of clearing zone (mm)		
	1	2	1
Lysozyme	1/10 MHB pH 7 9	1/10 MHB pH 7 8	1/2 MHB pH 6 11
GH24 Lysozyme from <i>Trichophaea saccata</i> (SEQ ID NO: 257)	9	7	10
GH24 lysozyme from <i>Chaetomium thermophilum</i> (SEQ ID NO: 264)	10	8	12
GH24 lysozyme from <i>Trichoderma harzianum</i> (SEQ ID NO: 267)	(8)*	(5)*	0
GH24 lysozyme from <i>Trichophaea saccata</i> lacking LED (SEQ ID NO: 270)	0	0	0
GH24 lysozyme from <i>Acremonium alcalophilum</i> (SEQ ID NO: 279)	0	0	0
GH24 lysozyme from <i>Acremonium alcalophilum</i> (SEQ ID NO: 280)	0	0	0
Bacitracin zinc salt	22	18	11

\*Incomplete inhibition of growth visible after MTT colouring

[1044] The 3 GH24 lysozymes also comprising the lysozyme enhancing domain (LED) (SEQ ID NO: 257, 264 and 267) all showed antimicrobial activity against viable cells of *C. perfringens* DSM756 under both tested conditions. In comparison, the two GH24 lysozymes which natively do not comprise the LED (SEQ ID NO: 279 and 280) did not inhibit growth under the test conditions. Fur-

thermore, the GH24 lysozyme for which the LED was removed (SEQ ID NO: 269) also showed no inhibition of growth in  $\frac{1}{2}$  MHB, pH 6, although incomplete inhibition of growth was observed when using  $\frac{1}{10}$  MBH, PH 7.

**[1045]** Thus, the results show that GH24 lysozymes tested which comprise a LED show significant activity *Clostridium perfringens* using the conditions 50% MHB, pH 6 whereas the GH24 lysozymes without the LED (either naturally or when the LED has been removed) do not show activity *Clostridium perfringens* using the conditions 50% MHB, PH 6.

#### Example 13: Temperature Stability

**[1046]** Temperature stability was determined for the GH24 lysozyme from *Trichophaea saccata* (SEQ ID NO: 257) by incubating the lysozyme at different temperatures (60-99° C.) for a short period of time (30, 60 and 90 seconds) after which the residual activity was measured for 1 h at 37° C. using *M. lysodeikticus* substrate prepared as described in Example 11.

#### Heat Treatment

**[1047]** The samples to be evaluated were diluted to a lysozyme concentration of 0.05 mg enzyme protein/mL in milliQ water. Initially 40  $\mu$ L of each lysozyme sample was pipetted into PCR tubes (3 replicates) and the closed tubes were then kept on ice. The PCR tubes were placed in a preheated PCR machine for 30, 60 or 90 seconds at 60, 65, 70, 75, 80, 85, 90, 95 or 99° C. and then put back on ice for instant cooling. Non heated control samples corresponding to the heated samples were prepared and kept on ice.

#### Activity Measurement

**[1048]** The OD drop assay using *M. lysodeikticus* as substrate was used to determine lysozyme activity in heated and non-heated samples. Initially 20  $\mu$ L of each sample (control and heat treated) was transferred to a 96-well microtiter plate, then 180  $\mu$ L assay buffer (pH 6) and 20  $\mu$ L *M. lysodeikticus* substrate was added to each well. The plate was immediately placed in an absorbance reader preheated to 37° C. and OD540 recorded for 1 hour. The difference between the absorbance at T=0 and the time points was calculated as the AOD. The percentage residual activity was calculated by comparing the AOD of the heat treated sample with the corresponding AOD of the sample which was not heat treated (Table 5).

TABLE 5

Residual activity (%) of the GH24 lysozyme from <i>Trichophaea saccata</i> (SEQ ID NO: 257) measured by OD drop after heat treatment at different temperatures									
Time (Sec)	Temperature (° C.)								
	60	65	70	75	80	85	90	95	99
30	93	99	94	101	94	98	94	98	93
60	99	97	93	96	98	94	99	94	97
90	96	99	98	98	97	100	97	102	89

**[1049]** The results show that the GH24 lysozyme from *Trichophaea saccata* (SEQ ID NO: 257) is stable for at least 90 seconds at temperatures as high as 99° C.

#### Example 13: Thermostability Determined Using DSC

**[1050]** The thermostability of GH24 lysozyme from *Trichophaea saccata* (SEQ ID NO: 257) at different pH values was determined by Differential Scanning calorimetry (DSC) using a VP-capillary DSC instrument (MicroCal Inc., Piscataway, NJ, USA) equipped with an auto sampler. Aliquots of the GH24 lysozyme, purified as described in Example 2, were buffer-changed (see buffer in table 6 below) using prepak NAP-5 columns. The samples were diluted with the corresponding buffer to approximately 0.5 mg/ml and the buffer was used as reference solution. Sample and reference solutions (approx. 0.5 ml) were thermally pre-equilibrated for 10 minutes at 20° C. and the DSC scan was performed from 20 to 100° C. at a scan rate of 200 K/hour. Data-handling was performed using the MicroCal Origin software (version 7.0383). The thermal denaturation temperature, Td (° C.), was taken as the top of denaturation peak (major endothermic peak) in thermograms (Cp vs. T) obtained after heating the lysozyme solution in the buffer at a constant programmed heating rate. Denaturation temperatures were determined at an accuracy of approximately  $\pm 0.5$ ° C. and are given in table 6 below.

TABLE 6

Denaturation Temperature of the GH24 lysozyme from *Trichophaea saccata* (SEQ ID NO: 257) at various pH's

Buffer	Td (° C.)
50 mM Na-acetate, pH 4.5	70.0
50 mM Na-acetate, pH 5.5	70.8
50 mM Na-acetate, pH 6.5	69.7

#### Example 14: Lysozyme Enhancing Domain Binds to Bacterial Cells

**[1051]** 250 mg *Micrococcus lysodeikticus* ATCC No. 4698 (Sigma M3770) cells were resuspended in 2.5 ml distilled H<sub>2</sub>O with 0.1% Tween 80. Cells were soaked at 4° C. overnight.

**[1052]** Avicel® PH-101 is a microcrystalline cellulose powder trademarked by FMC Corporation (Philadelphia, Pennsylvania) and sold by Sigma Aldrich (cat no. 11365). 250 mg Avicel was suspended in H<sub>2</sub>O with 0.1% Tween 80. This was also left hydrating overnight.

**[1053]** After overnight hydrations, 50  $\mu$ l of each suspension was taken out and this was washed once in 50  $\mu$ l H<sub>2</sub>O with 0.1% Tween 80. The purified LED (SEQ ID NO: 273) had a concentration of 0.23 mg/ml in a buffer consisting of 50 mM Na-Acetate, pH 4.5+50 mM NaCl. For the experiment, 50  $\mu$ l of Avicel suspension or 50  $\mu$ l of *M. lysodeikticus* suspension were aliquoted into 1.5 ml Eppendorf tubes. 50  $\mu$ l (11.5 mgs) of purified LED protein were then added to each tube, mixed by vortexing and then incubated at room temperature for 30 minutes. The samples were then centrifuged, and the liquid decanted to a 1.5 ml Eppendorf tube.

**[1054]** For each sample, 8  $\mu$ l 4xE-PAGE Loading Buffer (EPBUF-01, Life Technologies), 1  $\mu$ l (10x) NuPAGE® Sample Reducing Agent (Life Technologies), were added to 24  $\mu$ l supernatant. The two samples were then vortex mixed and heated in a heating block at 70° C. for 10 minutes. 20  $\mu$ l of each prepared sample were then loaded on to a Criterion XT 8-16% gradient BIS-Tris SDS gel and run in

Criterion XT MOPS buffer according to the manufacturer's instructions (BioRad Laboratories). A Rainbow recombinant molecular weight marker was also run in the gel (RPN800, GE Healthcare). The SDS gel was stained with Simply Blue Coomassie stain (Life Technologies) and the results visualized as shown in table 7.

TABLE 7

Binding of LED to Avicel or <i>M. lysodeikticus</i> suspension			
Sample	Lysozyme enhancing domain	Suspension	Result
1	SEQ ID NO: 273	Avicel	+++
2	SEQ ID NO: 273	<i>M. lysodeikticus</i>	+
3	SEQ ID NO: 273	None	+++

+ represents band intensity on an SDS gel.

[1055] The results show that the LED protein migrates on the SDS gel at about 8 kDa as expected. The LED protein SDS band intensity is approximately equal in the Avicel and

the untreated samples (samples 1 and 3) while the SDS band intensity was substantially reduced in the *M. lysodeikticus* cells treated sample (sample 2). This means that the *M. lysodeikticus* cells were able to bind the LED protein under the buffer conditions tested (25 mM Na-Acetate, pH 4.5, 25 mM NaCl) while crystalline cellulose could not bind LED protein. It should be noted that it is unknown which component of the *Micrococcus* cells that LED binds to.

#### Example 15: The Lysozyme Enhancing Domain HMM

[1056] SEQ ID NOS: 123 to 251 were aligned using the software program MUSCLE v3.8.31 with the default settings. Using this alignment, the HMM was constructed using the software program 'hmmbuild' from the package HMMER 3.0 (March 2010) (hmmer.org/) and the software was invoked using the default settings. The lysozyme enhancing domain HMM profile thereby generated for subsequent loading into the software program 'hmmscan' is given below.

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HMMER3/b [3.0 | March 2010]
NAME lysozyme_enhancing_domain
LENG 73
ALPH amino
RF no
CS no
MAP yes
DATE Tue Feb 3 15:29:15 2015
NSEQ 129
EFFN 1.263702
CKSUM 3302514446
STATS LOCAL MSV -9.1036 0.71868
STATS LOCAL VITERBI -9.7357 0.71868
STATS LOCAL FORWARD -3.7686 0.71868
HMM A C D E F G H I K L M N
P Q R S T V W Y
    m->m m->i m->d i->m i->i d->m d->d
    COMPO 2.64236 3.16005 2.87141 2.79417 3.60706 2.63596 3.86157 2.94229
2.65279 2.95816 3.97690 3.11757 3.46392 3.12498 3.11011 2.56828 2.58627 2.58086
4.17029 3.04296
    2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354 2.67741
2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518 4.58477
3.61503
    0.17958 4.32413 1.88959 0.61958 0.77255 0.00000 *
    1 3.80107 5.04040 4.67499 4.39045 1.81828 4.48873 3.56285 3.50991
4.23379 2.82560 4.11380 4.16131 4.81340 4.22617 4.28030 3.87997 4.03091
3.43577 3.70270 0.73371 1 -
    2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354
2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518
4.58477 3.61503
    0.02327 4.16783 4.89017 0.61958 0.77255 0.67437 0.71228
    2 2.33952 4.44593 3.23890 3.02979 4.35083 3.16321 4.20776 3.67603
3.02584 3.40031 4.31198 3.32021 1.10553 3.46227 3.39562 2.64660 2.86963
3.24503 5.70138 4.44714 2 -
    2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354
2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518
4.58477 3.61503
    0.02327 4.16783 4.89017 0.61958 0.77255 0.58149 0.81886
    3 2.99224 4.47028 5.00531 4.50059 3.72470 4.59877 5.18674 1.10701
4.40105 2.19903 3.51509 4.69439 4.89181 4.65354 4.58483 3.98375 3.44715
1.21838 5.67709 4.47722 3 -
    2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354
2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518
4.58477 3.61503
    0.02218 4.21548 4.93783 0.61958 0.77255 0.62351 0.76800
    4 2.67119 4.76820 3.04982 2.54195 4.12069 3.43519 3.75916 3.51149
2.19874 3.13703 3.97428 2.96845 3.89558 2.93360 2.89915 2.57877 1.61288
3.10281 5.38435 4.08520 4 -
    2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354
2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518
4.58477 3.61503
    0.02491 4.21548 4.62159 0.61958 0.77255 0.52151 0.90048

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5	2.37234	5.08464	2.49824	2.21575	4.41120	1.99198	3.58111	3.86677	
2.52882	3.41126	4.20120	2.81325	3.86140	2.84200	3.02691	2.42476	2.83819	
3.48001	5.60144	4.21122	5	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.02114	4.26301	4.98536	0.61958	0.77255	0.56183	0.84436		
6	2.63301	5.17310	2.09015	2.17272	4.49463	3.27178	3.65545	3.97097	
2.38584	3.47241	4.23433	2.52660	3.34330	2.76874	2.94084	2.41690	2.44683	
3.55393	5.62559	4.21427	6	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.07099	4.26555	2.90975	0.61958	0.77255	0.56422	0.84119		
7	2.61111	4.85146	2.70126	2.41033	4.02944	2.66646	3.65077	3.52514	
2.43178	3.11934	3.92649	2.77281	3.83428	2.77300	2.91547	2.42718	2.41739	2.79685
5.35415	3.75427	7	--						
	2.68618	4.42226	2.77521	2.73124	3.46355	2.40511	3.72496	3.29355	
2.67742	2.69356	4.24691	2.90348	2.73741	3.18147	2.89802	2.37888	2.77504	2.98519
4.58478	3.61504								
	0.09494	2.48394	4.93906	0.38374	1.14353	0.52245	0.89910		
8	3.16563	4.52406	5.00410	4.47860	3.59477	4.61318	5.11093	1.75130	
4.36399	1.66390	3.39589	4.68330	4.88103	4.58179	4.52924	3.98371	3.48258	0.98654
5.56065	4.39116	9	--						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.02108	4.26555	4.98790	0.61958	0.77255	0.56422	0.84119		
9	2.74568	5.18103	2.62071	2.37499	4.50785	3.44148	3.43386	3.97009	
2.14487	3.46738	4.24084	1.77122	3.86903	2.77625	2.44752	2.65464	2.97757	3.56615
5.60976	4.22640	10	--						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.02108	4.26555	4.98790	0.61958	0.77255	0.43965	1.03356		
10	3.21633	3.35479	4.79708	4.65548	4.57914	3.72194	5.20787	3.82938	
4.49870	3.70850	4.85167	4.53077	4.45916	4.82584	4.53365	3.48556	3.72159	3.53505
5.86530	4.85631	11	--						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510		
11	3.30119	5.31389	3.73668	3.09114	4.51121	3.86969	3.13217	4.16018	
2.10415	3.58751	4.49408	3.45992	4.26052	2.99924	0.83233	3.31264	3.47550	3.85705
5.50391	4.26079	12	--						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510		
12	2.24421	4.51545	3.30473	2.81428	4.39051	3.23670	4.14928	3.77491	
3.04692	3.44962	4.27960	3.30747	3.89875	3.36729	3.42822	1.05895	2.51437	3.31859
5.70279	4.43964	13	--						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510		
13	2.69468	4.75034	2.89429	2.56341	4.66767	0.94912	4.20148	4.12822	
3.15097	3.75743	4.60332	3.20872	3.96757	3.42394	3.55601	2.47312	3.12631	3.62410
5.94365	4.63448	14	--						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510		
14	2.69468	4.75034	2.89429	2.56341	4.66767	0.94912	4.20148	4.12822	
3.15097	3.75743	4.60332	3.20872	3.96757	3.42394	3.55601	2.47312	3.12631	3.62410
5.94365	4.63448	14	--						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510		
15	2.67424	4.69741	3.65691	3.53445	4.63811	3.40395	4.65858	4.09486	
3.63150	3.77181	4.76683	3.75211	0.59051	3.99224	3.88152	2.99980	3.31792	3.64480
5.92609	4.77080	15	--						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510		
15	2.26323	4.51933	3.21961	2.94036	4.47411	1.38422	4.14822	3.91245	
3.06085	3.54037	4.34588	2.97288	3.87499	3.35219	3.46854	1.96711	2.52323	3.40350
5.76384	4.49002	16	--						

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2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
16	2.20668	4.36145	3.82003	3.56662	4.41076	3.20360	4.55272 3.51597
3.53768	3.41304	4.35967	3.64187	3.96341	3.86648	3.78744	2.68079 0.81042 3.10831
5.83931	4.64399	17	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
17	2.61570	5.10849	2.62653	2.38205	4.43252	2.78078	3.60811 3.89018
2.47426	3.42628	4.20945	2.71231	3.87390	2.61734	2.99949	1.64993 2.94705 3.49936
5.60799	4.21799	18	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
18	2.58292	4.58689	3.02231	2.68583	3.00245	3.32285	2.97170 3.14564
2.67302	2.81683	3.67939	2.99852	3.79428	3.00246	3.09283	2.65865 2.82740 2.88473
5.11794	2.25478	19	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
19	2.02971	5.05961	2.68453	2.36019	4.37471	3.26819	3.65420 3.83090
2.10672	3.36092	4.13132	2.92980	3.45060	2.77060	2.82369	2.16905 2.88648 3.43886
5.53518	4.15201	20	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
20	3.16684	4.47509	4.98151	4.48359	3.78153	4.52597	5.13073 1.23357
4.37208	2.38350	3.60515	4.64947	4.86068	4.63385	4.54770	3.62858 3.43521 1.03896
5.65865	4.43929	21	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
21	2.67985	4.50015	3.40866	2.83947	3.66095	3.60615	3.61051 2.50038
2.12953	2.71143	3.59755	3.27678	3.98763	2.81347	3.06211	2.85030 2.83675 1.92294
5.06195	3.81377	22	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
22	2.57540	5.16214	3.25351	2.63376	4.54584	3.62294	3.69980 3.93939
1.30635	3.43432	4.24813	3.13299	4.00544	2.78831	2.11440	2.89381 2.74985 3.58326
5.55169	4.27942	23	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
23	2.54445	4.73655	3.02733	2.59505	4.05985	3.44683	3.70095 3.46466
2.60056	3.09418	3.92399	3.08417	3.89235	2.67009	3.04116	2.11836 1.78482 2.95974
5.35882	4.04770	24	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
24	3.40982	4.75103	4.67192	4.22624	1.97308	4.35966	3.81417 3.04888
4.07862	2.38151	3.72579	4.16721	4.67838	4.14717	4.17038	3.68839 3.63576 2.47365
4.02768	0.99393	25	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510
25	2.33607	5.05721	2.94517	2.24042	4.36369	3.44673	3.55543 3.81754
1.82729	3.31948	4.11325	2.80831	3.17764	2.75227	2.78214	2.58400 2.65726 3.32087
5.51479	4.13659	26	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958 0.77255 0.48576 0.95510

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26	2.36555	5.04925	3.04993	2.35049	4.35720	3.51989	3.68369	3.71551
1.45376	3.06828	4.12214	3.00561	3.91721	2.74243	2.72409	2.73518	2.95391
5.49677	4.16815	27	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
27	2.61202	4.80098	2.75023	2.62858	4.42906	1.32629	3.93435	3.86483
2.78346	3.46292	4.27988	3.09911	3.91159	3.10786	2.85440	2.43819	2.91018
5.68001	4.35178	28	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
2.98518	4.58477	3.61503						
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
28	2.39518	5.06692	2.42469	2.35324	4.15968	3.22653	3.04826	3.83188
2.39351	3.35617	4.12096	2.82671	3.83411	2.52507	2.87979	2.43622	2.35726
5.52582	4.13893	29	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
29	2.56098	5.10975	1.84700	2.22610	4.41970	3.43432	3.64564	3.82090
2.31577	3.39892	4.16246	2.88269	3.84241	2.68525	2.69153	2.62766	2.81515
5.56120	3.47482	30	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
30	2.71289	4.20867	4.05384	3.08944	3.32534	3.70711	4.11635	2.10460
3.37170	2.31376	3.31881	3.74286	4.18005	3.62760	3.59433	3.09939	2.94743
4.85949	3.10435	31	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
31	2.56066	3.98356	2.83917	2.26935	4.26245	3.45019	3.65582	3.70207
1.96206	3.26063	4.04582	2.95679	3.84786	2.75603	2.89654	2.30158	2.29348
5.46026	4.09624	32	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
32	2.98261	4.34033	4.74407	4.16222	2.74015	4.19374	4.48870	1.33722
4.00888	1.70186	3.16247	4.27271	4.50036	4.14592	4.09048	3.51345	3.21313
4.93581	3.15765	33	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
33	2.50714	4.52249	3.32761	2.73441	3.99413	2.87824	3.93263	3.37611
2.83014	3.05077	3.89907	3.20556	3.90546	3.15647	3.23473	2.09891	1.66153
5.34950	4.08041	34	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
34	2.73372	0.86170	4.21080	3.82223	3.72250	3.51687	4.43487	3.14732
3.50989	2.93675	3.97687	3.88251	4.17078	3.93344	3.44432	2.99564	3.14856
5.25169	3.70577	35	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
35	2.72821	4.93521	3.15849	2.72873	3.66991	3.61431	3.78500	3.57206
2.57323	3.13265	4.05241	3.20038	4.05162	1.36867	2.92156	2.93601	3.12692
5.09768	2.57435	36	--					
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
36	2.39232	4.68655	3.16574	2.46000	3.89951	3.51768	3.74742	2.86223
2.34831	2.93724	3.78511	3.11031	3.91433	2.90991	3.00803	2.69966	1.85059
5.23226	3.93826	37	--					

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2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
37	2.38712	4.95526	2.95139	2.14292	4.22581	3.30071	3.48757	3.66208	
2.41922	3.22834	4.01725	2.96015	3.42523	2.64575	2.85382	2.40915	2.33462	3.08668
5.43599	3.59495	38	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	
2.98518	4.58477	3.61503							
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
38	3.32493	5.03100	4.08842	4.05521	5.14287	0.28143	5.12256	4.87721	
4.29611	4.46333	5.45951	4.25516	4.43330	4.58529	4.45932	3.51325	3.84001	4.31766
6.09414	5.26815	39	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
39	2.77845	5.16916	2.50798	1.90461	4.47239	3.42576	3.73520	3.92893	
2.55535	3.46812	4.26082	2.91770	3.47218	2.74953	3.05304	2.74879	1.68968	3.54385
5.65411	4.25701	40	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
40	2.55637	3.36322	2.86419	2.49420	4.07854	3.43147	3.53651	3.49427	
2.36324	3.10007	3.91410	2.51497	3.86778	2.83786	2.95074	2.24490	2.43049	3.00556
5.34651	3.93774	41	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
41	3.32262	4.56891	5.24679	4.77118	3.84175	4.81012	5.48421	1.14831	
4.68143	2.30177	3.60891	4.94823	5.08094	4.93596	4.85577	4.22682	3.58792	0.99460
5.88795	4.67682	42	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
42	2.65825	5.10541	2.72992	2.15627	3.98363	3.31023	3.53625	3.89170	
2.18852	3.23731	4.15424	2.23857	3.82936	2.65748	2.86654	2.25743	2.79796	3.48165
5.55380	4.15800	43	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
43	2.61182	4.52680	3.60621	3.51889	4.78008	0.61583	4.68006	4.23876	
3.72062	3.95294	4.83622	3.66170	4.02536	4.00392	3.97409	2.79132	2.85714	3.64017
6.05621	4.90618	44	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
44	2.79049	5.22667	2.25221	2.33027	4.53369	3.27947	3.53614	4.00930	
2.56097	3.52971	4.31450	1.59788	3.89352	2.86397	3.06987	2.39242	3.03945	3.49407
5.69864	4.13140	45	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
45	2.49378	3.36932	2.74714	2.42229	4.10830	3.46961	3.68039	3.52770	
2.44255	3.12654	3.93602	2.51463	3.86384	2.82770	2.94369	2.19290	2.51568	3.13211
5.36588	3.76024	46	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			
46	2.69732	4.16858	4.15640	3.57668	3.28068	3.80998	4.13366	1.644485	
3.45403	1.84904	3.26899	3.79253	3.96991	3.68559	3.64246	2.81777	2.62992	2.15853
4.82146	3.52063	47	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510			

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47	4.19233	5.38393	4.84605	4.67977	3.27817	4.29458	4.57157	4.26819
4.41284	3.57367	4.87507	4.74845	4.85287	4.77414	4.45256	4.39169	4.52083
0.32020	3.26075	48 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
48	3.20149	5.67973	0.78816	2.34486	4.76934	3.43076	3.17601	4.55895
3.07436	4.04716	4.94146	2.92732	4.07402	3.21129	3.65781	3.08955	3.50632
6.03658	4.51417	49 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
49	2.76346	4.98544	3.15831	2.56957	4.01057	3.55403	3.68400	3.67589
1.47331	2.89158	4.05158	3.07047	3.93382	2.56322	2.45400	2.78078	2.98070
5.41794	3.49426	50 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
50	2.64257	4.43619	3.56736	3.08202	3.77537	3.52079	4.05811	2.42620
3.00927	2.79176	3.72810	2.99222	4.03030	3.35753	3.34645	2.85418	1.35329
5.23131	3.98292	51 - -						
	2.68618	4.42225	2.77521	2.73124	3.46340	2.40514	3.72496	3.29355
2.67742	2.69356	4.24691	2.90348	2.73741	3.18148	2.89802	2.37888	2.77521
4.58478	3.61472							
	0.08832	2.54971	5.04648	0.37639	1.15942	0.48576	0.95510	
51	2.52068	4.47414	3.35565	2.74391	3.33968	3.48613	3.81115	3.00228
2.76056	2.69538	3.20591	3.24034	3.68619	2.82417	3.12828	2.08694	2.32290
4.31681	3.78415	53 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
52	2.77860	4.87789	1.42239	2.56155	3.13731	3.54366	3.74371	3.49507
2.67769	3.09585	3.97167	3.06454	3.97169	2.99708	3.12924	2.82286	3.01884
4.04928	3.59798	54 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
53	2.94931	5.28328	2.08563	2.39481	4.84632	1.16425	4.00151	4.36230
3.01231	3.90219	4.74326	2.45548	3.99074	3.18038	3.56729	2.91382	3.29175
6.06470	4.62009	55 - -						
	2.68621	4.42228	2.77522	2.73126	3.46357	2.40509	3.72497	3.29357
2.67727	2.69358	4.24693	2.90346	2.73742	3.18149	2.89804	2.37878	2.77522
4.58480	3.61506							
	0.08509	2.58845	5.04648	0.73284	0.65497	0.48576	0.95510	
54	3.21633	0.35479	4.79708	4.65548	4.57914	3.72194	5.20787	3.82938
4.49870	3.70850	4.85167	4.53077	4.45916	4.82584	4.53365	3.48556	3.72159
5.86530	4.85631	59 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58480	3.61506							
	0.08509	2.58845	5.04648	0.73284	0.65497	0.48576	0.95510	
55	3.21633	0.35479	4.79708	4.65548	4.57914	3.72194	5.20787	3.82938
4.49870	3.70850	4.85167	4.53077	4.45916	4.82584	4.53365	3.48556	3.72159
5.86530	4.85631	59 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58480	3.61506							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
56	4.07603	5.22780	4.94333	4.71701	1.81696	4.70604	3.64405	3.73694
4.54415	3.00155	4.31962	4.34626	5.01267	4.44587	4.52415	4.10863	4.29875
3.75731	0.60600	60 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58480	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
57	3.29932	4.57114	5.13914	4.65306	3.79025	4.73170	5.36042	1.62171
4.54419	2.21256	3.57888	4.84627	5.01963	4.80796	4.72647	4.13701	3.56571
5.80720	4.58938	61 - -						
	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58480	3.61503							
	0.01987	4.32413	5.04648	0.61958	0.77255	0.48576	0.95510	
58	3.45708	3.61908	4.43729	3.53676	3.86941	3.73557	3.76041	1.18441
5.86901	4.67381	62 - -						

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2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958
					0.77255	0.48576	0.95510
58	3.16638	5.52729	0.80512	2.42994	5.07620	2.30005	4.12607
					4.65042		
3.22647	4.16769	5.05164	2.99972	4.08759	3.32219	3.82773	3.09290
					3.51563	4.17606	
6.23444	4.80691	63	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958
					0.77255	0.48576	0.95510
59	3.11990	4.36544	4.32127	3.81191	2.17745	4.09367	3.78203
					3.04592		
3.23806	2.64903	3.67717	3.91110	4.44159	3.85035	3.84946	3.39383
					3.34718	2.77912	
3.74216	1.06936	64	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958
					0.77255	0.48576	0.95510
60	3.51146	4.91649	4.45325	4.08004	2.02567	4.31163	3.69403
					3.46524		
3.96389	2.92976	4.07889	4.05659	4.68281	4.07537	4.10672	2.99801
					3.75887	3.31559	
3.91189	0.78971	65	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958
					0.77255	0.48576	0.95510
61	2.72553	4.31253	4.16671	3.66674	3.67680	3.72642	4.41126
					2.29394		
3.56150	2.58708	3.60951	3.86666	4.24179	3.84789	3.80334	2.76599
					2.38224	1.10833	
5.25833	4.04936	66	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958
					0.77255	0.48576	0.95510
62	2.51216	5.16569	2.33791	2.35923	4.49437	3.19374	3.66109
					3.96480		
1.64210	3.46558	4.22781	2.83561	3.85394	2.71011	2.84192	2.54559
					2.88860	3.55105	
5.61534	4.21583	67	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.32413	5.04648	0.61958
					0.77255	0.48576	0.95510
63	2.49188	4.38955	3.59551	3.16295	4.09719	3.28177	4.17679
					3.38911		
3.04040	3.15453	4.02841	3.43067	3.92288	3.44894	3.44644	2.11805
					1.20176	2.68117	
5.48692	4.25411	68	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.31435	5.03670	0.61958
					0.77255	0.48576	0.95510
64	2.51216	5.16569	2.33791	2.35923	4.49437	3.19374	3.66109
					3.96480		
3.58485	3.73760	4.55934	3.55250	3.87506	3.84242	3.86415	2.56592
					2.50453	3.40204	
5.97883	4.79808	69	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.31435	5.03670	0.61958
					0.77255	0.48576	0.95510
65	2.63597	3.39258	3.14566	2.45530	3.91792	3.49097	3.54341
					3.31288		
2.40023	2.95698	3.79792	3.08785	3.89316	2.92081	3.00148	1.97899
					2.29007	2.96915	
5.24220	3.94276	70	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.31435	5.03670	0.61958
					0.77255	0.48576	0.95510
66	2.59137	4.97540	2.68695	2.29850	4.05453	3.34590	3.64946
					3.59380		
2.42308	3.26160	4.04572	2.57932	3.83844	2.77492	2.90216	1.98570
					2.44689	3.22530	
5.46068	4.09334	71	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.31435	5.03670	0.61958
					0.77255	0.48576	0.95510
67	2.36239	3.82492	3.07537	2.52645	4.05085	1.94430	3.77137
					3.45853		
2.53920	3.08721	3.91418	2.86394	3.87403	2.94691	3.05153	2.46988
					2.65768	3.12923	
5.35184	4.04208	72	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.29528	5.01763	0.61958
					0.77255	0.52575	0.89432
68	2.59137	4.97540	2.68695	2.29850	4.05453	3.34590	3.64946
					3.59380		
2.42308	3.26160	4.04572	2.57932	3.83844	2.77492	2.90216	1.98570
					2.44689	3.22530	
5.46068	4.09334	71	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.29528	5.01763	0.61958
					0.77255	0.52575	0.89432
69	2.36239	3.82492	3.07537	2.52645	4.05085	1.94430	3.77137
					3.45853		
2.53920	3.08721	3.91418	2.86394	3.87403	2.94691	3.05153	2.46988
					2.65768	3.12923	
5.35184	4.04208	72	--				
				2.68618	4.42225	2.77519	2.73123
					3.46354	2.40513	3.72494
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503			0.01987	4.29528	5.01763	0.61958
					0.77255	0.52575	0.89432

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68	2.51473	4.23017	3.73065	3.15738	2.96324	3.66009	3.93184	2.62617			
3.08387	2.43082	2.74387	3.49391	3.33993	3.35931	3.14679	2.64784	2.86016	2.49302		
4.81896	2.22311	73	--	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518		
4.58477	3.61503			0.02046	4.29528	5.01763	0.61958	0.77255	0.52575	0.89432	
69	2.33893	4.26290	4.21737	3.66773	3.27773	3.87203	4.32579	2.12233			
3.56960	2.41061	3.43058	3.89614	4.28394	3.82133	3.79298	2.87144	3.03565	1.21453		
5.06701	3.86005	74	--	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518		
4.58477	3.61503			0.02293	4.29528	4.70670	0.61958	0.77255	0.52575	0.89432	
70	2.49593	4.60476	3.23381	2.52485	3.79749	3.53767	3.76569	3.14297			
2.26081	2.40764	3.70182	3.15412	3.92810	2.98301	3.03430	2.76728	2.09050	2.55846		
5.16115	3.88294	75	--	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518		
4.58477	3.61503			0.02051	4.29287	5.01521	0.61958	0.77255	0.52898	0.88967	
71	2.60687	5.12624	2.52016	2.23382	4.44833	2.55208	3.64005	3.91884			
2.12896	3.37075	4.18386	2.86694	3.03933	2.74997	2.89501	2.33562	2.83629	3.50672		
5.58015	4.17955	76	--	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518		
4.58477	3.61503			0.02051	4.29287	5.01521	0.61958	0.77255	0.52898	0.88967	
72	2.57816	5.12677	2.87095	2.24649	4.45454	3.41210	3.40077	3.91086			
1.59193	3.41242	4.17909	2.90547	3.85681	2.60853	2.68264	2.65653	2.67555	3.50960		
5.55782	4.18309	77	--	2.68618	4.42225	2.77520	2.73117	3.46354	2.40513	3.72495	3.29354
2.67741	2.69355	4.24690	2.90347	2.73740	3.18147	2.89801	2.37887	2.77520	2.98519		
4.58477	3.61503			0.09497	3.41028	2.85473	0.52137	0.90068	0.52898	0.88967	
73	3.08258	0.42515	4.66004	4.49479	4.42412	3.61311	5.06351	3.64868			
4.33208	3.53771	4.67608	4.38809	4.34603	4.66309	4.38494	3.35266	3.58099	3.36315		
5.74041	4.70439	79	--	2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518		
4.58477	3.61503			0.01461	4.23357	*	0.61958	0.77255	0.00000	*	
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#### Example 16: The GH24 Catalytic Domain HMM

[1057] SEQ ID NOS: 1 to 122 were aligned using the software program MUSCLE v3.8.31 with the default settings. Using this alignment, the HMM was constructed using the software program ‘hmmbuild’ from the package

HMMER 3.0 (March 2010) ([hmmer.org/](http://hmmer.org/)) and the software was invoked using the default settings. The GH24 catalytic domain HMM profile thereby generated for subsequent loading into the software program ‘hmmscan’ is given below.

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HMMER3/b [3.0 | March 2010]
NAME GH24_catalytic_domain
LENG 161
ALPH amino
RF no
CS no
MAP yes
DATE Tue Apr 14 10:23:27 2015
NSEQ 122
EFFN 1.567444
CKSUM 3253961472
STATS LOCAL MSV -10.1203 0.70833
STATS LOCAL VITERBI -10.9320 0.70833
STATS LOCAL FORWARD -4.4787 0.70833
HMM A C D E F G H I K L M N
P Q R S T V W Y
m->m m->i m->d i->m i->i d->m d->d
COMPO 2.44048 3.93467 3.01702 2.62301 3.43295 2.77445 3.69252 3.04117
2.65511 2.46463 3.77377 2.92042 3.46380 3.02561 2.94926 2.63867 2.77262 2.69908
4.58415 3.55522

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2.68613	4.42197	2.77528	2.73121	3.46362	2.40507	3.72503	3.29362
2.67741	2.69347	4.24698	2.90355	2.73748	3.18155	2.89786	2.37893
4.58485	3.61511						
0.42529	0.202566	1.53938	0.94684	0.49097	0.00000	*	
1	2.72350	4.81830	3.16936	2.62649	4.11581	3.51252	3.71942
2.24998	2.85999	3.95362	3.10351	1.86600	2.88649	2.42995	2.74652
5.34619	4.06251	6	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.02197	4.22496	4.94731	0.61958	0.77255	0.75070	0.63873	
2	2.54350	5.09272	2.65636	2.29098	4.41602	2.99758	3.47346
2.05017	3.38851	4.14035	2.65877	3.36878	2.57545	2.80210	2.49808
5.53830	4.14000	7	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.02165	4.23928	4.96162	0.61958	0.77255	0.55400	0.85483	
3	2.29319	4.21840	3.95914	3.39016	3.37768	3.73291	4.08404
3.30131	2.30451	3.36148	3.66722	3.96097	3.55864	3.55098	2.44506
4.88856	3.68459	8	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01947	4.34420	5.06654	0.61958	0.77255	0.61386	0.77927	
4	2.74772	4.85695	2.87194	2.73668	4.63295	3.30941	4.14345
3.05642	3.80763	4.64806	0.00956	3.98834	3.35260	3.47426	2.10780
5.91048	4.53618	9	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01917	4.35956	5.08190	0.61958	0.77255	0.63061	0.75986	
5	2.12850	5.12616	2.51993	2.17045	4.44916	3.31679	3.63665
2.17180	3.42224	4.17456	2.91475	3.69539	2.47321	2.87406	2.49141
5.57266	4.17399	10	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01917	4.35956	5.08190	0.61958	0.77255	0.63061	0.75986	
6	1.46486	5.07291	2.62203	2.24830	4.37269	3.31665	3.74063
2.50756	3.37686	4.17647	2.86466	3.60033	2.87945	2.92672	2.74276
5.58151	4.20704	11	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01917	4.35956	5.08190	0.61958	0.77255	0.63061	0.75986	
7	2.17549	4.36144	3.73727	3.42594	4.53253	1.83798	4.46965
3.46881	3.62766	4.44736	3.54831	3.90736	3.74497	3.77756	2.51903
5.87792	4.67921	12	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01917	4.35956	5.08190	0.61958	0.77255	0.59794	0.79839	
8	2.17549	4.36144	3.73727	3.42594	4.53253	1.83798	4.46965
3.46881	3.62766	4.44736	3.54831	3.90736	3.74497	3.77756	2.51903
5.87792	4.67921	12	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01891	4.37321	5.09556	0.61958	0.77255	0.61277	0.78055	
9	3.21972	4.50196	5.08099	4.54710	3.67073	4.61619	5.10917
4.43636	1.72834	3.48636	4.70971	4.89148	4.64075	4.57635	3.97953
5.56354	4.38821	13	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01891	4.37321	5.09556	0.61958	0.77255	0.61277	0.78055	
10	2.21875	3.46186	4.20895	2.47286	3.84197	2.71978	2.70252
5.60290	4.19720	14	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01891	4.37321	5.09556	0.61958	0.77255	0.47193	0.97763	
11	3.10702	4.52363	4.59128	3.76793	2.82202	4.24456	4.31533
3.86137	0.84608	2.77098	4.22984	4.53874	4.04360	4.00636	3.55360
4.98174	3.78454	15	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887
4.58477	3.61503						
0.01780	4.43314	5.15549	0.61958	0.77255	0.52727	0.89212	

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11	3.43901	4.67793	5.35556	4.83217	3.64816	4.91195	5.41930	0.86797
4.72910	1.79405	3.18234	5.01743	5.11165	4.88087	4.84705	4.30046	3.68194
5.72096	4.59690	16	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.43314	5.15549	0.61958	0.77255	0.52727	0.89212		
12	2.25468	5.11708	2.95136	2.31419	4.43742	2.93886	3.67050	3.89862
1.79270	3.41419	4.17655	2.95628	3.57244	2.54460	2.89046	2.49672	2.70342
5.57506	4.18857	17	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.43314	5.15549	0.61958	0.77255	0.52727	0.89212		
13	2.67371	5.19058	2.65415	1.77278	4.52357	2.97916	3.37968	4.00320
2.29480	3.45227	4.23628	2.89789	3.86090	2.69304	2.74143	2.20291	2.82697
5.62881	4.22137	18	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.43314	5.15549	0.61958	0.77255	0.52727	0.89212		
14	2.81579	4.22364	4.47018	3.89188	1.48290	3.93522	4.09383	2.62540
3.73020	1.92295	3.15573	3.97226	4.29103	3.88937	3.82500	2.90865	3.04647
3.69273	3.08017	19	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.43314	5.15549	0.61958	0.77255	0.52727	0.89212		
15	3.18472	5.59003	2.51116	0.73356	4.97137	3.49635	4.05433	4.46680
2.91869	4.01079	4.89285	3.02135	4.12423	3.23170	3.44861	2.94448	3.49165
6.14660	4.69845	20	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.44584	5.16819	0.61958	0.77255	0.50746	0.92136		
16	2.63285	4.65582	3.05809	2.95774	4.52790	0.99566	4.22427	3.96361
3.15170	3.35882	4.43654	3.32975	3.98358	3.44306	3.48471	2.26849	2.95946
5.83543	4.54966	21	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.44584	5.16819	0.61958	0.77255	0.50746	0.92136		
17	2.85632	3.37564	4.60322	4.02460	1.39485	3.99023	4.14489	2.59011
3.84632	2.15449	3.18679	4.06005	4.34070	3.98159	3.90687	3.30078	3.08762
3.05451	3.20082	22	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.44584	5.16819	0.61958	0.77255	0.50746	0.92136		
18	2.66729	4.65691	3.26612	2.63248	3.59907	3.57768	3.79390	3.22463
2.58508	2.88889	3.74552	3.18306	3.96288	2.76398	2.21227	2.49586	2.92028
5.19804	3.45436	23	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.44584	5.16819	0.61958	0.77255	0.50746	0.92136		
19	2.15329	4.93377	2.72392	2.45038	4.18602	3.46029	3.70858	3.61065
2.39726	2.85937	4.00284	3.02169	2.29781	2.84985	2.92083	2.61534	2.92011
5.42832	3.51133	24	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.44584	5.16819	0.61958	0.77255	0.50746	0.92136		
20	2.60039	5.14177	2.40424	2.39661	4.46473	3.46452	3.22687	3.82146
2.34703	3.43742	4.18905	2.53509	3.85931	2.76069	2.48112	2.15943	2.56736
5.58781	3.98848	25	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01780	4.44584	5.16819	0.61958	0.77255	0.50746	0.92136		
21	2.67842	4.25530	3.93960	3.30296	2.65434	3.76986	4.06743	2.34859
3.16231	2.41816	3.35928	3.66250	1.99709	3.53911	3.53118	3.04669	2.94335
4.87521	3.66773	26	--					

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2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01758	4.44584	5.16819	0.61958	0.77255	0.50746	0.92136			
22	2.35693	4.72401	3.20434	2.57805	3.89878	3.59542	3.83415	3.30513	
2.45060	2.96490	3.82939	3.20409	4.00721	3.02410	3.01463	2.73830	2.99846	3.03825
5.25060	1.65974	27	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.04783	4.44584	3.35315	0.61958	0.77255	0.50746	0.92136			
23	2.67429	5.03904	2.71552	2.42815	3.42871	3.47139	3.66503	3.56736	
2.12738	3.11366	4.09499	2.80474	2.49274	2.58565	2.81632	2.65515	2.70589	3.31018
5.50599	3.32956	28	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01811	4.41613	5.13847	0.61958	0.77255	0.46783	0.98447			
24	2.80258	3.80314	1.07544	2.73853	4.22664	3.51752	4.00892	3.12191	
2.89547	3.24952	4.16749	3.22350	4.04459	3.20256	3.34582	2.88238	3.10901	3.14052
5.59573	4.24511	29	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.02905	4.45025	4.07730	0.61958	0.77255	0.50044	0.93208			
25	2.25512	4.65074	3.26511	2.72356	3.93527	3.14982	3.83757	3.32426	
2.65175	2.98376	3.43732	3.00233	1.89086	3.04409	3.13107	2.60570	2.91688	2.73040
5.28256	3.99674	30	--						
2.68618	4.42225	2.77520	2.73123	3.46354	2.40510	3.72495	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73740	3.18146	2.89801	2.37887	2.77520	2.98518
4.58477	3.61503								
0.09269	3.75476	2.73149	0.54795	0.86306	0.48896	0.95001			
26	2.20760	4.20273	3.79874	3.31128	3.16594	3.51238	4.00110	2.04422	
3.04865	2.40223	3.06460	3.46501	4.08831	3.47948	3.47692	2.91568	2.45698	2.12142
4.80701	3.37658	32	--						
2.68618	4.42225	2.77520	2.73123	3.46354	2.40510	3.72495	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77520	2.98518
4.58477	3.61503								
0.01860	4.38973	5.11208	0.61958	0.77255	0.44606	1.02206			
27	2.89429	4.80561	3.58134	3.54304	4.97183	0.46686	4.80272	4.62849	
3.86637	4.26878	5.14633	3.40192	4.22316	4.13479	4.14184	3.05434	3.41253	3.99006
6.18155	5.02899	33	--						
2.68620	4.42227	2.77521	2.73125	3.46355	2.40514	3.72472	3.29356		
2.67742	2.69356	4.24691	2.90348	2.73732	3.18134	2.89802	2.37888	2.77521	2.98520
4.58478	3.61505								
0.04293	3.31454	5.17259	0.77558	0.61699	0.50044	0.93208			
28	2.68018	4.37382	3.60152	3.03271	3.37749	3.67013	2.87447	2.64539	
2.70815	1.83610	3.47768	2.80710	4.04839	3.27708	3.31669	2.91878	2.91175	2.35117
4.95200	3.30164	37	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01750	4.45025	5.17259	0.61958	0.77255	0.50044	0.93208			
29	2.59450	4.66219	3.27040	2.59506	3.84655	3.58175	3.79708	3.14848	
2.36788	2.60330	3.75125	3.18753	2.01907	2.93847	3.06156	2.80580	2.85294	2.96388
3.37709	3.92228	38	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01750	4.45025	5.17259	0.61958	0.77255	0.50044	0.93208			
30	2.38332	4.46240	3.96391	3.74958	4.56460	3.29443	4.72276	3.67520	
3.71927	3.57098	4.53007	3.78193	4.07155	4.04991	3.94677	2.78605	0.65157	3.25220
5.99515	4.80793	39	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510			
31	2.99096	4.42944	4.70942	4.15218	3.57105	4.31482	4.71076	1.65507	
4.01113	2.14494	3.46003	4.34534	4.64055	3.56162	4.17763	3.64279	3.30622	1.03756
5.29753	4.10999	40	--						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510			

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32	2.68716	3.00522	4.44310	4.24828	4.84005	0.50716	5.03457	4.26978
4.19629	4.02594	4.89944	4.06659	4.16496	4.45125	4.33862	2.90519	3.23060
6.12241	5.07039	41	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
33	3.88807	5.12914	4.96349	4.62971	2.07646	4.68858	3.80768	2.95192
4.45489	2.84188	4.11936	4.39032	4.99014	4.43288	4.48511	4.04965	4.11066
3.94943	0.62936	42	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
34	3.55261	5.22999	4.34030	4.32810	5.38495	0.21258	5.36943	5.16848
4.58491	4.72792	5.73557	4.50771	4.63301	4.86357	4.71836	3.74664	4.07606
6.28543	5.51964	43	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
35	3.87327	5.50886	3.92890	3.78212	3.89799	4.10572	0.35257	4.67985
3.62123	4.07577	5.19561	4.15242	4.70480	4.16744	3.83107	3.95140	4.21270
5.33871	3.84015	44	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
36	2.55850	4.67610	2.85436	2.69895	3.86374	3.57559	3.81417	3.24443
2.55253	1.61527	3.72651	3.02186	3.97376	2.93710	3.10915	2.81523	2.56702
5.22462	3.94128	45	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
37	2.36682	1.08021	4.17330	3.72135	3.82769	2.87004	4.41678	2.93056
3.59066	2.91000	3.83458	3.78442	4.07632	3.86713	3.80034	2.83912	2.97220
5.31748	3.88653	46	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
38	2.44867	5.13209	2.74120	2.37534	4.45129	3.13883	3.37571	3.81639
2.09231	3.25691	4.17977	2.88681	3.86250	2.39570	2.69695	2.32020	2.78438
5.58043	4.18603	47	--					
2.68605	4.42230	2.77519	2.73128	3.46359	2.40494	3.72500	3.29359	
2.67735	2.69360	4.24695	2.90338	2.73745	3.18151	2.89806	2.37892	2.77525
4.58482	3.61508							
0.20624	2.21113	2.56670	0.73716	0.65099	0.48576	0.95510		
39	2.38824	5.13667	2.46225	2.33995	4.46125	3.44638	3.64321	3.93304
1.96184	3.43315	4.18470	2.59657	3.84499	2.58355	2.85687	2.53095	2.55813
5.58195	4.18304	52	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01868	4.38546	5.10781	0.61958	0.77255	0.59629	0.80040		
40	2.52969	5.03587	2.97654	2.42115	4.32785	3.46441	3.53193	3.77619
2.02445	3.31736	4.09206	2.74547	2.84178	2.54513	2.88744	2.19787	2.76245
4.74099	3.94803	53	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01868	4.38546	5.10781	0.61958	0.77255	0.59629	0.80040		
41	2.60675	5.16003	2.52146	2.30324	4.48997	2.73454	3.64845	3.96623
2.17370	3.45896	4.20601	2.47959	3.85066	2.56867	2.84590	2.41657	2.61213
5.60178	4.19843	54	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01868	4.38546	5.10781	0.61958	0.77255	0.52092	0.90134		
42	2.65287	1.19275	3.40429	3.38996	3.71368	3.53484	4.23292	2.66477
3.32728	2.80149	3.73937	3.41343	4.09824	3.63311	3.60222	2.91375	2.99822
5.20557	3.95872	55	--					

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2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01810 4.41655 5.13890 0.61958 0.77255 0.55221 0.85726  
     43  2.11988 4.99095 2.69229 2.46032 4.29867 3.20836 3.70173 3.73910  
 2.41197 3.30074 4.08762 2.99012 3.49720 2.83041 2.93503 1.83660 2.75199 3.37089  
 5.50311 3.91158  56 --  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01810 4.41655 5.13890 0.61958 0.77255 0.44635 1.02155  
     44  2.97807 5.54822 1.79883 1.40119 4.86180 2.66411 3.85669 4.37053  
 2.55019 3.84442 4.63047 2.91417 3.99223 2.98875 3.29382 2.51970 3.23747 3.92819  
 5.98719 4.51765  57 --  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.03941 4.45929 3.60927 0.61958 0.77255 0.48576 0.95510  
     45  2.61240 4.24725 4.16179 3.58472 3.39505 3.87860 4.19991 1.92349  
 3.14424 2.34125 3.37288 3.82971 4.24684 3.71715 3.49381 3.16925 2.66754 1.39907  
 4.93254 3.73395  58 --  
     2.68618 4.42225 2.77520 2.73124 3.46355 2.40514 3.72495 3.29355  
 2.67742 2.69356 4.24691 2.90347 2.73740 3.18139 2.89802 2.37888 2.77515 2.98519  
 4.58478 3.61504  
     0.25671 3.65255 1.60702 0.72234 0.66479 0.46471 0.98972  
     46  2.58330 4.92802 2.97235 2.46773 4.31534 2.58226 3.69110 3.75176  
 1.87863 3.30755 4.09886 2.98123 2.63799 2.82333 2.81087 2.53970 2.76486 3.37093  
 5.49792 4.14980  62 --  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.02147 4.24787 4.97022 0.61958 0.77255 0.55284 0.85640  
     47  2.77665 4.24510 4.17142 3.60737 2.13407 3.57711 3.73827 2.35069  
 3.48227 2.34958 3.36160 3.78414 4.21156 3.69055 3.54299 3.02842 3.00774 2.51180  
 4.48419 1.75453  63 --  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.03412 4.34809 3.88173 0.61958 0.77255 0.48868 0.95045  
     48  2.64793 5.13223 2.68703 2.40086 4.44996 3.45949 3.57898 3.91234  
 1.96012 3.42866 4.19439 2.88878 2.24549 2.73197 2.91333 2.37138 2.77466 3.51110  
 5.59115 4.20105  64 --  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.04971 4.40314 3.31713 0.61958 0.77255 0.57163 0.83150  
     49  2.37672 4.18835 3.56611 3.33942 2.17161 3.71892 4.00701 2.08833  
 3.02370 2.38402 3.30016 3.62106 4.09164 3.49901 3.49065 2.99304 2.64183 2.38390  
 4.79262 3.11868  65 --  
     2.68620 4.42227 2.77521 2.73125 3.46356 2.40514 3.72496 3.29356  
 2.67728 2.69357 4.24691 2.90348 2.73728 3.18148 2.89802 2.37888 2.77521 2.98520  
 4.58479 3.61505  
     0.10921 2.32965 5.09470 0.32898 1.27175 0.41324 1.08324  
     50  2.36036 4.48294 3.68434 3.32162 3.85852 3.33505 4.35926 3.56334  
 3.31819 3.31552 4.22296 3.55561 0.98977 3.63840 3.64294 2.75832 2.58704 3.18303  
 5.67820 4.43472  67 --  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     51  3.33618 4.66932 5.03266 4.45397 3.21894 4.56404 4.81904 1.85917  
 4.29340 0.83078 3.04538 4.61993 4.79371 4.38871 4.36938 3.89649 3.55725 2.44200  
 5.15478 3.19773  68 --  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     52  2.63866 4.70838 2.85148 2.85343 4.48197 3.34287 4.11038 3.90212  
 3.00292 3.53870 4.35671 3.26563 3.96589 3.30138 3.43429 1.61544 3.45306  
 5.76856 4.46367  69 --  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510

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53	2.60942	5.07136	2.96029	1.86628	4.36808	3.48244	3.67378	3.41756
2.01165	2.96531	4.12545	2.81630	3.87448	2.70253	2.69783	2.64352	2.83702
5.53327	3.97650	70	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
54	1.73678	5.05920	2.76019	2.19606	4.34746	3.40699	3.38009	3.79477
2.40682	3.34131	4.11991	2.97912	3.88458	2.75025	2.94159	2.52476	2.67210
5.53093	4.15658	71	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
55	2.74043	5.24631	2.40465	1.98907	4.58049	3.38842	3.68829	4.06538
2.30593	3.54649	4.29373	2.38561	3.88263	2.43061	2.89904	2.64727	2.26054
5.68162	4.26599	72	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
56	1.08787	3.11680	4.26466	3.92702	4.56744	1.40507	4.74478	3.93820
3.86529	3.68181	4.51094	3.79343	3.96845	4.09724	4.08049	2.63816	2.94685
5.59490	4.80790	73	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
57	2.41449	5.12942	2.78064	2.08572	4.44698	3.23509	3.61872	3.91373
2.08441	3.01887	4.17771	2.90972	3.86400	2.67091	2.76247	2.56463	2.37385
5.57871	4.18533	74	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
58	2.35618	5.15466	2.90683	2.02302	4.48230	3.47099	3.65791	3.95381
1.95514	3.38590	3.74147	2.87799	3.86418	2.42507	2.64313	2.58222	2.72135
5.59647	4.19971	75	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
59	2.82048	4.31441	3.59911	3.58912	3.26417	3.91044	4.18415	2.46874
3.46903	1.09245	3.07229	3.84330	4.26181	3.60727	3.67712	3.19562	3.05032
4.07413	3.66480	76	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
60	3.81742	5.05913	5.53372	4.96642	2.73032	5.13111	5.29889	2.41979
4.82530	0.53749	2.78402	5.19788	5.17474	4.75171	4.83127	4.50985	4.01876
5.35596	4.27056	77	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
61	2.18353	5.08325	2.76302	2.42575	4.38435	3.47806	3.51762	3.56262
2.08507	3.12651	3.85720	2.82327	3.87031	2.36589	2.66671	2.51935	2.91708
5.54292	4.16091	78	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
62	2.69830	5.20991	2.17874	2.32825	4.54673	3.35646	3.67029	4.02682
1.91955	3.50995	4.25567	2.93721	3.87314	2.41655	2.73200	2.29314	2.77110
5.64478	4.23801	79	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
63	3.48091	5.78050	0.48398	2.64029	5.32183	3.22187	4.38302	4.97741
3.56135	4.48508	5.42901	3.21673	4.30207	3.60605	4.17838	3.38965	3.84278
6.42296	5.06153	80	--					

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2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
64	2.89612	4.42362	4.83116	4.24658	3.32561	4.29064	4.63708 2.02632
4.09588	1.20988	2.20498	4.37598	4.59093	4.23666	4.18320	3.48664 3.29831 1.90263
5.10096	3.96543	81	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
65	2.20468	5.00834	3.02460	2.46700	4.28538	3.22809	3.68956 3.72332
2.07471	3.22745	4.06994	2.99846	3.13955	2.71422	2.40530	2.55367 2.81763 2.91995
5.48516	3.93946	82	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.02786	4.45929	4.14114	0.61958	0.77255	0.48576	0.95510	
66	2.57606	4.97328	3.01298	2.37658	4.23859	2.99122	3.69147 3.38775
2.24029	3.15189	3.89305	2.89169	3.40567	2.76365	2.64345	2.34850 2.54841 2.73885
5.45700	4.10045	83	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01752	4.44895	5.17130	0.61958	0.77255	0.50251	0.92889	
67	2.13166	4.25308	3.90762	3.34403	2.05039	3.72688	4.02347 2.73125
3.25999	2.46542	3.38226	3.63057	3.61807	3.51702	3.51516	2.92597 2.67380 2.52551
4.81288	2.35249	84	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01752	4.44895	5.17130	0.61958	0.77255	0.50251	0.92889	
68	2.51295	5.09054	2.98184	1.72812	4.39612	3.48435	3.67785 3.73881
2.41954	3.37739	4.14803	2.97394	3.88052	2.28202	2.67212	2.46700 3.25830
5.55010	4.17304	85	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01752	4.44895	5.17130	0.61958	0.77255	0.50251	0.92889	
69	2.66132	5.17285	2.66986	2.39540	4.50725	3.46839	3.65551 3.76967
1.96543	3.47208	4.21733	2.37317	3.86241	2.33907	2.51152	2.47816 2.84664 3.35597
5.61061	4.20948	86	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01752	4.44895	5.17130	0.61958	0.77255	0.47543	0.97185	
70	2.40476	1.44095	3.96481	3.44698	3.67421	2.80450	4.21141 3.02108
3.36628	2.76284	3.66000	3.64693	4.04722	3.63180	3.63000	2.52077 2.78604 2.59026
5.14211	3.50924	87	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
71	3.14464	4.45336	5.03021	4.46417	3.35819	4.45790	4.86159 1.42980
4.32230	1.69292	2.86587	4.38080	4.74701	4.47359	4.40409	3.79830 3.38213 1.35681
5.29927	4.14289	88	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
72	2.30011	3.73407	3.03761	2.41231	4.07806	3.34217	3.55224 3.48929
2.54009	3.10364	3.92326	2.86753	3.54726	2.88785	2.87570	2.44080 2.13433 3.07048
5.35921	3.53834	89	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
73	2.14048	5.14694	2.67449	2.30248	4.47134	3.40113	3.65777 3.94253
2.17125	2.97837	4.13264	2.74458	3.76417	2.57571	2.52099	2.46181 2.82539 3.52649
5.59184	4.19432	90	--				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	

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74	2.33987	3.97918	2.71800	2.68393	3.66274	3.56899	3.79046	3.23575
2.52458	2.58207	2.74593	2.97884	3.95502	2.69024	3.09550	2.49450	2.91310
5.20705	3.47237	91	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
75	2.72508	4.24130	3.63475	3.45984	3.36239	3.81026	4.11532	2.14147
3.36542	1.74492	3.34959	3.73067	3.64897	3.61353	3.59970	3.09084	2.24848
4.88118	3.68107	92	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.11347	4.45929	2.34657	0.61958	0.77255	0.48576	0.95510		
76	2.44605	5.08758	2.70732	2.38750	4.40669	3.21874	3.64649	3.86979
2.21274	3.38705	4.14749	2.21702	3.28711	2.75638	2.85771	2.36598	2.63424
5.55021	4.16021	93	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.09636	4.36489	2.53639	0.61958	0.77255	0.62371	0.76777		
77	2.52140	5.19229	1.93533	2.18979	4.51146	3.30655	3.67579	3.98696
2.38932	3.49150	4.25802	2.75360	3.76248	2.79221	2.91679	2.09509	2.83845
5.64795	4.23568	94	--					
2.68618	4.42225	2.77512	2.73124	3.46355	2.40511	3.72495	3.29355	
2.67741	2.69356	4.24691	2.90347	2.73740	3.18147	2.89802	2.37886	2.77520
4.58478	3.61504							
0.13745	2.78775	2.70509	0.42399	1.06256	0.37095	1.17143		
78	2.36341	5.11547	2.88923	2.38557	4.43588	3.12293	3.65240	3.90110
1.86565	3.41125	4.16867	2.81154	3.56873	2.61972	2.78323	2.22914	2.70573
5.56793	4.17668	96	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01833	4.40410	5.12644	0.61958	0.77255	0.56252	0.84344		
79	2.28762	4.29763	3.88020	3.31128	3.45344	3.77121	4.08077	2.37703
2.80959	2.48145	3.28647	3.63489	3.92261	3.50644	3.49947	3.04725	2.88061
4.95908	3.74730	97	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01827	4.40717	5.12952	0.61958	0.77255	0.49049	0.94759		
80	2.49336	4.91866	3.06468	2.50610	4.16905	3.50622	3.47926	3.59090
2.04052	3.18152	3.98708	2.87458	3.40359	2.84700	2.63414	2.70907	2.30092
5.41218	3.71728	98	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01772	4.43760	5.15995	0.61958	0.77255	0.46471	0.98972		
81	3.45413	4.80651	5.06351	4.52310	3.14668	4.66315	5.03497	2.37248
4.37178	6.05498	3.13154	4.73925	4.90613	4.49133	4.48329	4.02717	3.33601
5.35929	4.25227	99	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
82	2.73939	4.83330	3.00723	2.83344	4.71960	3.34320	4.20357	4.19656
3.09807	3.81073	4.63710	0.93081	4.01975	3.40262	3.51075	2.36222	2.79342
5.97881	4.64405	100	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
83	2.04424	5.17228	2.45633	2.07839	4.50311	3.46548	3.65902	3.97943
2.19774	3.32071	4.21748	2.93804	3.60950	2.58020	2.72229	2.50774	2.92631
5.61278	4.10566	101	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
84	2.94884	5.24796	2.66241	2.49038	4.31917	3.52589	3.86118	3.97970
2.71091	3.53375	4.37214	1.14648	4.03010	2.78537	3.17219	2.92497	3.20366
5.61132	3.34532	102	--					

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2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
85	3.04248	5.24204	2.96062	2.60820	4.65653	3.59476	3.94929 4.07361
2.56705	3.61817	4.49759	3.18876	4.11995	0.96272	2.89157	3.04418 2.94698 3.72218
5.79098	4.47565	103	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
86	3.15528	4.57797	4.44504	3.93193	1.85137	4.15122	3.86565 3.06977
3.40619	2.70190	3.70726	4.00202	4.49914	3.94620	3.42969	3.27245 3.38207 2.89093
2.96247	1.23585	104	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
87	1.91388	4.74994	2.64175	2.83276	4.65908	1.23026	4.17545 4.11077
3.11125	3.71800	4.52370	3.25060	3.97313	3.36530	3.56454	2.36795 3.06739 3.59931
5.92594	4.60838	105	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
88	0.42105	4.60486	4.18172	4.04773	4.75980	3.40644	4.98013 3.98668
4.08316	3.83537	4.82707	4.00997	4.20267	4.37016	4.26066	2.96393 3.28352 3.52613
6.11697	5.00536	106	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
89	2.94731	4.79718	4.85811	4.40161	3.41462	4.43006	5.01217 2.43392
4.20104	0.64102	3.23863	4.59387	4.80786	4.42809	4.33978	3.84144 3.64619 2.39900
5.44657	4.32673	107	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
90	2.69295	3.98202	4.44440	3.88309	3.49385	3.95542	4.41654 1.88586
3.76101	2.45692	3.45424	4.04259	4.36196	3.98345	3.92955	2.88509 2.53539 1.21450
5.07315	3.87854	108	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
91	2.23020	4.52728	3.33461	3.29998	4.71681	3.23321	4.50469 4.14576
3.50163	3.83741	4.66077	3.52242	3.99178	3.76238	3.84265	0.70612 3.04592 3.56218
6.04302	4.79944	109	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
92	4.05064	5.18728	5.18918	4.93015	1.30934	4.79876	3.74116 3.69305
4.72772	2.64779	4.25890	4.46765	5.07773	4.56292	4.64571	4.16664 4.25926 3.61933
1.17959	1.95218	110	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
93	1.28536	3.49665	3.98287	3.48773	3.94001	3.37174	4.32499 3.24593
3.42157	3.01829	3.90186	3.64596	4.01208	3.68988	3.70737	2.34460 1.97075 2.43625
5.38426	4.18438	111	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	
94	4.32746	5.37697	5.24755	5.08968	0.67847	4.92310	3.72282 3.90894
4.89259	3.12203	4.46331	4.52796	5.19934	4.66186	4.77457	4.32624 4.53605 3.86568
3.81270	1.39600	112	-				
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887 2.77519 2.98518
4.58477	3.61503						
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510	

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95	2.96563	5.03414	2.96147	2.89269	4.69467	3.45494	4.31635	4.30858
3.22879	3.95664	4.87223	0.68215	4.15542	3.55820	3.60524	3.03479	3.16772
5.99932	4.61384	113	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
96	2.69438	4.19269	4.25987	3.56878	3.31680	3.86774	4.19014	2.37254
3.54681	2.01345	2.82578	3.75808	4.23400	3.76804	3.71685	2.96995	2.77903
4.85178	3.66032	114	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
97	2.84079	3.93256	4.40616	4.26397	4.98754	0.39355	5.11403	4.49447
4.25980	4.21665	5.11067	4.15445	4.26046	4.53706	4.40205	3.05226	3.38675
6.18922	5.18548	115	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
98	2.56290	1.46178	3.90788	3.37708	3.63161	3.17695	4.15838	2.97148
3.29073	2.63206	3.61432	3.36809	3.48256	3.56931	3.49641	2.86742	2.68116
5.09846	3.89390	116	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
99	2.54148	5.04654	2.70539	2.37565	4.49775	1.34409	3.89783	3.94239
2.76174	3.51789	4.32880	2.93324	3.97003	3.05438	3.18788	2.57266	2.88542
5.73092	4.36307	117	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
100	1.70557	4.79988	3.14657	2.65009	4.21466	2.82353	3.84500	3.42042
2.59544	3.24327	4.06100	1.96080	3.93084	3.00954	3.10889	2.73130	2.86940
5.48983	4.17058	118	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
101	2.00483	4.12604	4.25448	3.66225	2.77296	3.75391	4.11010	2.48130
3.52384	2.03969	2.75516	3.82391	4.16685	3.59884	3.66689	2.88608	2.76467
4.74141	3.24653	119	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01734	4.45929	5.18164	0.61958	0.77255	0.48576	0.95510		
102	2.39869	4.21435	2.90223	2.24202	4.43514	2.98780	3.65947	3.89880
2.09993	3.22037	4.16856	2.93058	3.86386	2.09592	2.58555	2.64666	2.91791
5.56867	4.17940	120	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.03303	4.45929	3.86691	0.61958	0.77255	0.48576	0.95510		
103	2.23097	4.22037	2.87691	3.85914	2.63441	2.47196	1.93702	2.57645
2.23601	3.40681	4.16467	2.87691	3.85914	2.63441	2.47196	1.93702	2.57645
5.56559	4.17529	121	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.03161	4.44387	3.94438	0.61958	0.77255	0.51058	0.91665		
103	2.65435	5.11517	2.88355	2.35449	4.19901	3.13016	3.36182	3.89436
2.23601	3.40681	4.16467	2.87691	3.85914	2.63441	2.47196	1.93702	2.57645
5.56559	4.17529	121	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01786	4.43012	5.15246	0.61958	0.77255	0.48058	0.96345		
104	2.41340	4.51586	3.64272	3.20902	3.96433	3.40133	4.18341	3.53981
3.13494	3.21340	4.09895	3.49607	4.02251	3.49050	3.46406	0.91626	3.00878
4.01968	4.06003	122	--					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01750	4.45022	5.17257	0.61958	0.77255	0.47667	0.96981		
105	2.54090	4.85452	2.71842	2.54794	4.08758	3.52137	3.73124	3.35427
2.53920	3.11249	3.93155	3.06305	3.91306	2.75440	2.85634	2.18869	1.95817
3.86953	4.03850	123	--					

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2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     106 2.89313 4.34581 4.36083 3.78021 3.00250 4.01068 3.73906 2.43845  
 3.64357 1.03448 3.21890 3.99265 4.35163 3.85444 3.81380 3.30755 2.87425 2.34644  
 4.89798 3.69665 124 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     107 2.38886 4.16785 4.23962 3.65212 3.27942 3.49631 4.14953 1.93787  
 3.52117 1.96618 3.08994 3.83908 4.20151 3.73674 3.19737 3.12692 2.88453 1.75092  
 4.80522 3.61535 125 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     108 2.18860 5.09773 3.01081 2.41645 4.40890 3.02601 3.68034 3.70590  
 1.98541 3.38487 4.15581 2.98738 3.88981 2.71530 2.19915 2.40384 2.85715 3.47177  
 5.55249 4.18095 126 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     109 2.88848 5.01007 3.36359 2.70440 4.28892 3.67769 3.76628 3.67046  
 2.13438 2.83550 3.27792 3.21417 4.04788 2.78880 1.37591 2.92736 2.91052 3.36660  
 5.44614 4.18169 127 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     110 3.01550 4.50647 4.29320 3.35689 3.38082 4.10807 4.41212 2.46129  
 3.56171 0.92330 3.04014 4.02324 4.44436 3.85149 3.77877 3.41276 2.95071 2.45376  
 5.11441 3.95652 128 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     111 2.93246 5.26208 2.83845 2.51972 4.59855 3.53909 3.83421 4.05395  
 2.41041 3.41162 4.39541 1.22702 4.02054 2.58739 2.94782 2.68984 3.17979 3.67765  
 5.73531 4.37438 129 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     112 1.88527 5.12970 3.02339 2.46506 4.44856 3.51148 3.58652 3.89850  
 1.94584 3.41349 3.98691 2.52080 3.90280 2.52008 2.59054 2.68296 2.96264 3.50769  
 5.57002 4.20272 130 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01734 4.45929 5.18164 0.61958 0.77255 0.48576 0.95510  
     113 2.74124 4.71833 3.14766 2.56164 4.15454 1.48155 3.79728 3.56948  
 2.55233 3.04403 4.01264 2.75713 3.96322 2.96545 2.76272 2.79611 2.99003 3.24999  
 5.18738 4.10961 131 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01752 4.44892 5.17127 0.61958 0.77255 0.50256 0.92882  
     114 2.78829 5.27067 2.39544 1.43884 3.52342 3.39995 3.72836 4.06474  
 2.49027 3.56292 4.32709 2.73652 3.90878 2.43899 3.02346 2.74367 3.02799 3.64666  
 5.71376 4.29711 132 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01752 4.44892 5.17127 0.61958 0.77255 0.50256 0.92882  
     115 2.58656 5.08616 1.97465 2.39675 4.38521 3.47529 3.67325 3.84095  
 2.19218 3.37163 4.14005 2.49894 3.87169 2.78755 2.91440 2.60276 2.70141 3.45224  
 4.35740 3.44083 133 - -  
     2.68618 4.42225 2.77519 2.73123 3.46354 2.40513 3.72494 3.29354  
 2.67741 2.69355 4.24690 2.90347 2.73739 3.18146 2.89801 2.37887 2.77519 2.98518  
 4.58477 3.61503  
     0.01752 4.44892 5.17127 0.61958 0.77255 0.50256 0.92882

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116	2.36408	4.93399	3.05515	2.41820	4.19006	3.28886	3.70715	3.53115
2.35589	3.20126	4.00416	3.02568	2.28335	2.65312	2.79254	2.53358	2.91948
5.42832	4.08366	134	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
117	2.47921	5.15398	2.61824	2.37031	4.47665	3.08217	3.69410	3.94314
2.47045	3.45936	4.22669	1.75974	3.87627	2.54232	2.92200	2.53173	2.86250
5.62343	4.22533	135	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
118	2.47352	4.43682	3.41083	2.85816	3.65814	3.53539	3.85691	2.85096
2.62235	2.70516	3.52326	3.27951	3.95603	3.10614	3.16295	2.71586	1.69391
5.07488	3.82615	136	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
119	3.12393	4.58092	4.64216	4.33325	3.86300	4.10675	5.08066	2.11143
4.20840	2.49287	3.78444	4.45840	4.65799	4.54804	4.38259	3.64748	3.48352
5.70632	4.45559	137	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
120	1.52970	4.31242	4.27636	3.70359	3.15057	3.97419	4.29716	1.75553
3.59501	2.15161	3.34066	3.94036	4.33244	3.82618	3.79879	3.27010	3.08534
4.97587	3.57672	138	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
121	2.00921	3.05304	3.07103	2.43399	4.07708	3.27326	3.62893	3.48743
2.55372	3.10420	3.92537	3.02189	3.60524	2.90180	2.72153	2.18932	2.85663
5.36146	4.03760	139	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
122	2.38800	5.20369	2.45901	1.93151	4.53281	3.41096	3.67622	4.01159
2.41230	3.32407	4.25203	2.80676	3.87283	2.05963	2.92660	2.50851	2.91530
5.64462	4.23622	140	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
123	2.80442	5.57008	2.32768	1.01424	4.88079	2.93753	3.89581	4.38320
2.81015	3.87205	4.67758	2.92022	4.01617	2.76513	3.36230	2.93852	3.29333
6.02758	4.55781	141	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
124	3.65291	4.92987	5.28841	4.75290	2.09973	4.85851	4.79616	2.49842
4.59706	0.68663	3.08443	4.86508	5.00895	4.57855	4.61939	4.21526	3.86249
4.95107	3.43578	142	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
125	2.68163	4.78103	3.25910	2.74134	4.08738	3.29345	3.84411	3.27298
2.47216	3.00438	3.96065	3.20761	1.46271	3.03322	2.77484	2.83542	3.00539
5.37921	4.09799	143	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
126	2.97837	5.31590	3.32617	2.68999	4.72425	3.69304	3.27951	4.12761
1.41978	3.15207	4.36950	2.95852	4.05870	2.29333	1.88668	2.95013	3.17244
5.64414	4.36966	144	-	2.68618	4.42225	2.77519	2.73123	3.46354
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503	0.07281	4.44892	2.83821	0.61958	0.77255	0.50256	0.92882
127	2.97837	5.31590	3.32617	2.68999	4.72425	3.69304	3.27951	4.12761

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2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.02051	4.44892	4.75533	0.61958	0.77255	0.50256	0.92882			
127	3.24053	4.68626	4.42354	3.93390	2.40064	4.19011	3.87268	3.13732	
3.77092	2.69167	3.77020	4.01866	4.54932	3.96154	3.93737	3.50591	2.78389	2.98596
1.09473	2.38377	145	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01757	4.44599	5.16833	0.61958	0.77255	0.50723	0.92171			
128	2.69906	4.81576	3.08565	2.57557	4.04005	3.53963	3.74869	3.22744	
2.40032	3.06681	3.89789	1.97993	3.93159	2.91813	2.73517	2.75677	2.74275	2.22386
5.33397	4.02105	146	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.02207	4.44599	4.59455	0.61958	0.77255	0.50723	0.92171			
129	2.67905	4.57309	3.32994	2.76622	3.73883	3.59300	3.19938	3.01028	
2.15094	2.56209	3.22488	3.09606	3.97668	3.06418	2.85128	2.81906	2.63816	2.82377
4.30953	2.58633	147	-						
2.68618	4.42225	2.77515	2.73123	3.46354	2.40513	3.72495	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73740	3.18146	2.89801	2.37887	2.77520	2.98518
4.58477	3.61503								
0.02949	3.75743	5.16391	0.54795	0.86306	0.51420	0.91124			
130	1.37236	4.40095	3.68215	3.15295	3.75592	2.52271	4.08407	2.92930	
3.10149	2.47905	3.70955	3.48452	4.03143	3.40599	3.44185	2.76304	2.93611	2.46504
5.20046	3.97096	149	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01765	4.44156	5.16391	0.61958	0.77255	0.51420	0.91124			
131	2.92571	5.41476	2.40274	2.25750	4.73426	1.59137	3.83505	4.22032	
2.46966	3.72284	4.51462	2.12442	3.97518	2.96959	3.22426	2.64902	3.18355	3.80226
5.88395	4.44532	150	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77520	2.98518
4.58477	3.61503								
0.01765	4.44156	5.16391	0.61958	0.77255	0.51420	0.91124			
132	2.91871	5.13022	2.71064	2.58530	4.61395	1.08952	3.96281	4.05904	
2.60237	3.62616	4.46295	2.92155	4.04062	3.13339	2.89835	2.92929	3.22159	3.66933
5.81419	4.46718	151	-						
2.68618	4.42225	2.77520	2.73124	3.46354	2.40513	3.72495	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73732	3.18147	2.89801	2.37887	2.77520	2.98519
4.58477	3.61503								
0.01765	4.44156	5.16391	0.61958	0.77255	0.51420	0.91124			
133	2.55415	5.12827	2.99700	2.37401	4.45513	3.42989	3.22630	3.91005	
1.66425	3.41408	4.09517	2.82365	3.87578	2.41406	2.56728	2.66166	2.93780	3.15862
5.56110	4.18910	154	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.08528	3.78188	2.83085	0.63047	0.76001	0.51420	0.91124			
133	2.55415	5.12827	2.99700	2.37401	4.45513	3.42989	3.22630	3.91005	
1.66425	3.41408	4.09517	2.82365	3.87578	2.41406	2.56728	2.66166	2.93780	3.15862
5.56110	4.18910	154	-						
2.68618	4.42225	2.77519	2.73124	3.46354	2.40513	3.72495	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73732	3.18147	2.89801	2.37887	2.77520	2.98519
4.58477	3.61503								
0.01865	4.38685	5.10920	0.61958	0.77255	0.59439	0.80274			
134	2.68757	4.69832	3.24582	2.59317	3.89741	3.57072	3.77065	3.17298	
2.28857	2.93278	3.78681	3.16345	3.22761	2.80999	2.72847	2.80064	2.93185	1.75884
5.22736	3.94700	155	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01865	4.38685	5.10920	0.61958	0.77255	0.59439	0.80274			
135	2.66448	4.14616	4.10629	3.52046	3.11519	3.76324	4.05895	2.53934	
3.39922	1.42345	3.09375	3.35986	4.13201	3.56974	3.58549	2.72565	2.89692	2.25748
3.72072	3.54295	156	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01865	4.38685	5.10920	0.61958	0.77255	0.59439	0.80274			
136	2.54947	5.15494	2.81817	2.27071	4.47196	3.45438	3.67320	3.93783	
2.18117	3.44723	4.21076	2.61053	2.15770	2.48927	2.90923	2.63558	2.81969	3.53198
5.60426	4.20964	157	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01865	4.38685	5.10920	0.61958	0.77255	0.46370	0.99143			

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137	2.48424	4.64364	3.23983	2.74683	4.45646	0.95630	4.24608	3.78460
3.16682	3.50936	4.37248	3.36772	4.01139	3.48004	3.54078	2.79397	3.07496
5.79263	4.52277	158	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01765	4.44156	5.16391	0.61958	0.77255	0.51420	0.91124		
138	3.30920	4.75420	4.61173	4.11127	3.12041	4.38915	4.69609	2.54917
3.90653	0.68230	3.16405	4.37109	4.69955	3.81654	4.07332	3.74605	3.29083
5.18905	3.99579	159	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01765	4.44156	5.16391	0.61958	0.77255	0.51420	0.91124		
139	2.64297	4.51540	3.13915	2.58066	3.67426	3.43890	3.84982	2.79669
2.71873	2.72061	3.40686	3.27646	3.99414	3.11806	3.19182	2.71823	2.35387
5.08364	3.82661	160	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.02149	4.44156	4.65848	0.61958	0.77255	0.51420	0.91124		
140	2.64854	5.18440	3.10682	2.54595	4.52943	3.57236	3.59991	3.96071
2.19829	3.42661	4.24551	2.43253	3.96199	2.65206	1.54852	2.67222	2.94271
5.59352	4.26198	161	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01772	4.43780	5.16014	0.61958	0.77255	0.52008	0.90256		
141	3.44190	5.32458	4.00047	3.46399	4.96977	3.41557	4.22078	4.46813
2.52378	3.92894	4.85429	3.79058	4.42887	3.40774	0.52734	3.51113	3.71233
5.83836	4.76025	162	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01772	4.43780	5.16014	0.61958	0.77255	0.52008	0.90256		
142	3.44190	5.32458	4.00047	3.46399	4.96977	3.41557	4.22078	4.46813
2.52378	3.92894	4.85429	3.79058	4.42887	3.40774	0.52734	3.51113	3.71233
5.83836	4.76025	163	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.02519	4.43780	4.33842	0.61958	0.77255	0.52008	0.90256		
143	1.90653	5.22931	2.62762	2.14830	4.55055	3.46127	3.70649	4.02504
2.07812	3.52458	4.28677	2.20792	3.89414	2.79487	2.97073	2.72114	2.99769
5.67510	4.26740	164	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.02519	4.43780	4.33842	0.61958	0.77255	0.52008	0.90256		
144	1.66693	4.90314	2.79419	2.43720	4.14970	3.50399	3.70716	3.38051
2.26779	3.16514	3.57851	2.96848	3.89556	2.85254	2.83650	2.70887	2.91240
5.40141	4.06201	165	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01785	4.43045	5.15280	0.61958	0.77255	0.53138	0.88623		
144	1.66693	4.90314	2.79419	2.43720	4.14970	3.50399	3.70716	3.38051
2.26779	3.16514	3.57851	2.96848	3.89556	2.85254	2.83650	2.70887	2.91240
5.40141	4.06201	165	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.02074	4.43045	4.75450	0.61958	0.77255	0.53138	0.88623		
145	3.57909	5.69383	2.89268	0.43731	5.13396	3.74413	4.42879	4.71520
3.39551	4.25239	5.24212	3.42136	4.38610	3.65781	3.83675	3.52400	3.90016
6.18972	4.96810	166	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.02074	4.43045	4.75450	0.61958	0.77255	0.53138	0.88623		
145	3.57909	5.69383	2.89268	0.43731	5.13396	3.74413	4.42879	4.71520
3.39551	4.25239	5.24212	3.42136	4.38610	3.65781	3.83675	3.52400	3.90016
6.18972	4.96810	166	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.02361	4.42762	4.47474	0.61958	0.77255	0.53569	0.88012		
146	2.53815	4.23541	3.89256	3.31415	3.35365	3.43314	4.01926	2.27305
3.13182	2.36020	3.34809	3.61467	4.10930	3.48366	2.78779	3.00792	2.91165
4.84488	3.36475	167	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.01800	4.42201	5.14436	0.61958	0.77255	0.54412	0.86835		
147	1.80943	5.17035	2.62157	2.07449	4.49100	3.42292	3.67419	3.96118
2.17043	3.46432	4.22212	2.93630	3.87161	2.56527	2.84559	2.64670	2.88453
5.61623	4.21716	168	-					

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2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01800	4.42201	5.14436	0.61958	0.77255	0.54412	0.86835			
148	3.71568	4.98323	5.39542	4.83916	2.79356	5.00269	5.20401	2.41032	
4.69620	0.57295	2.93926	5.06411	5.09914	4.67653	4.73417	4.37793	3.92780	2.46918
5.32073	4.20270	169	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.01800	4.42201	5.14436	0.61958	0.77255	0.54412	0.86835			
149	1.99327	2.70853	4.08451	3.52864	1.85792	3.42232	3.91516	2.71735	
3.41997	2.46283	3.37905	3.72050	4.10390	3.65301	3.62210	2.80539	2.90591	2.50317
4.85301	3.64388	170	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.03954	4.42201	3.62092	0.61958	0.77255	0.54412	0.86835			
150	2.52034	5.07675	2.86686	2.34451	4.38139	3.46473	3.58228	3.83719	
1.82596	2.91213	3.78433	2.90755	3.85707	2.33901	2.80894	2.51619	2.74142	3.44564
5.53279	4.15171	171	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.05269	4.40086	3.24268	0.61958	0.77255	0.54412	0.86835			
151	2.56841	4.80930	3.10084	2.47522	4.03593	3.39038	3.70967	3.30280	
2.05479	3.06154	3.82459	3.05201	3.89470	2.71798	2.95896	2.58812	1.96719	3.08959
4.39727	4.00056	172	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.03303	4.36720	3.92179	0.61958	0.77255	0.62070	0.77126			
152	2.00712	4.80326	3.04608	2.51290	4.16635	3.12701	3.47637	3.58373	
2.58766	3.19402	4.01252	3.03841	2.06845	2.94568	3.05479	2.54694	2.74358	3.23947
5.43985	4.11489	173	-						
2.68618	4.42228	2.77522	2.73117	3.46357	2.40515	3.72476	3.29338		
2.67743	2.69358	4.24692	2.90349	2.73734	3.18149	2.89803	2.37884	2.77522	2.98521
4.58480	3.61506								
0.11549	2.35531	4.25417	0.54335	0.86941	0.63840	0.75107			
153	2.16030	4.62913	3.21138	2.59079	4.25901	2.76297	3.94367	3.67658	
2.80049	3.30378	4.12023	3.18454	3.88643	3.12635	3.23166	1.76272	1.88963	3.27351
5.54965	4.25166	176	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.03127	4.34547	4.02732	0.61958	0.77255	0.64844	0.73995			
154	2.66792	5.11177	2.56371	2.33718	4.43052	3.12411	3.63758	3.76704	
2.24610	3.40665	4.16392	2.51360	3.83618	2.72460	2.75418	2.00063	2.60055	3.48912
5.56277	4.16722	177	-						
2.68618	4.42225	2.77520	2.73123	3.46354	2.40510	3.72495	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73740	3.18146	2.89801	2.37887	2.77520	2.98518
4.58477	3.61503								
0.20910	3.75741	1.79972	0.56129	0.84507	0.66269	0.72456			
155	2.55143	4.81591	2.81468	2.31661	3.92133	3.34474	3.63569	3.47575	
2.37389	3.07571	3.88637	2.95949	3.82254	2.66149	2.66956	2.47706	2.52334	2.53039
5.31632	3.83266	179	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.03176	4.16074	4.15646	0.61958	0.77255	0.76695	0.62442			
156	2.55523	4.93315	2.94860	2.24014	4.20806	3.11633	3.48685	3.19520	
2.09238	3.20688	3.99407	2.92490	3.24954	2.58362	2.75119	2.50501	2.80774	3.04779
5.40950	4.04862	180	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73740	3.18146	2.89801	2.37887	2.77520	2.98518
4.58477	3.61503								
0.02276	4.19001	4.91235	0.61958	0.77255	0.81337	0.58584			
157	1.20660	4.40759	3.35604	2.93272	3.95893	3.20449	3.52467	3.34303	
2.90686	3.04070	3.90878	3.27859	3.58791	3.25408	3.26247	2.65317	2.85764	2.78550
5.33854	4.07865	181	-						
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354		
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519	2.98518
4.58477	3.61503								
0.02276	4.19001	4.91235	0.61958	0.77255	0.68268	0.70372			

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158	2.67140	4.29203	3.70746	3.13942	2.86196	3.68163	2.96310	2.76890
3.05716	1.69286	3.39392	3.48105	3.86490	2.82577	3.35631	2.94264	2.90223
3.97407	3.25518	182	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.02128	4.25624	4.97858	0.61958	0.77255	0.74947	0.63982		
159	2.63798	4.48996	3.51982	3.04228	3.81419	3.47372	4.04467	3.03664
2.92137	2.64518	3.23372	3.40240	1.41997	3.31178	3.25344	2.82205	2.74199
5.29179	4.03651	183	-					
2.68618	4.42225	2.77519	2.73123	3.46354	2.40513	3.72494	3.29354	
2.67741	2.69355	4.24690	2.90347	2.73739	3.18146	2.89801	2.37887	2.77519
4.58477	3.61503							
0.14151	4.25624	2.13899	0.61958	0.77255	0.74947	0.63982		
160	2.46470	3.83575	3.23523	2.67393	3.66999	3.49642	3.73458	3.04690
2.43613	2.64675	3.59308	3.01880	3.25014	2.84868	2.98138	2.59083	2.70116
5.05478	3.78583	184	-					
2.68617	4.42231	2.77511	2.73129	3.46360	2.40503	3.72497	3.29360	
2.67725	2.69361	4.24696	2.90353	2.73733	3.18150	2.89795	2.37891	2.77523
4.58483	3.61509							
0.49613	0.96883	4.45773	0.15588	1.93562	0.80876	0.58953		
161	2.60601	0.74299	4.28430	4.02298	4.16889	3.28957	4.69398	3.40236
3.85046	3.26155	3.28085	3.92541	3.45640	4.17512	3.98128	2.85611	3.09926
5.57309	4.44623	186	-					
2.68617	4.42226	2.77521	2.73125	3.46355	2.40514	3.72496	3.29355	
2.67738	2.69356	4.24691	2.90348	2.73741	3.18131	2.89802	2.37887	2.77517
4.58478	3.61504							
0.09408	2.41030	*	0.42020	1.06978	0.00000	*		
//								

#### Example 17: In Vivo Broiler Trial

##### Materials and Methods

**[1058]** The trial was performed at the Research Center for Animal Nutrition (DSM Nutritional Products France, F-68305 Village-Neuf) according to the official French guidelines for experiments with live animals. Day-old male broiler chickens ("ROSS PM3"), were supplied by a commercial hatchery (Joseph Grelier S. A., Elevage avicole de la Bohadière, F-49290 Saint-Laurent de la Plaine, France).

##### Animals and Housing

**[1059]** On the day of arrival (day 1), the chickens were divided by weight into groups of 20 birds. Each group was placed in one floor-pen littered with wood shavings and allocated to one of the different treatments.

**[1060]** Each treatment was replicated with 8 groups. The chickens were housed in an environmentally controlled room. The room temperature was adapted to the age of the birds. In the first few days an additional infra-red electric heating lamp was placed in each pen. Moreover, in the first week feed was offered to the birds as crumbled pellets, afterwards as pelleted feed. The birds had free access to feed and water.

##### Feeding and Treatments

**[1061]** The experimental diets (Starter, Grower and Finisher) were based on soybean meal, wheat and rye (12%) as main ingredients (Table 8). The diets were formulated to contain 225 g crude protein and 12.5 MJ/kg MEN for the starter period, 215 g crude protein and 12.8 MJ/kg MEN for the grower period and 205 g crude protein and 13.0 MJ/kg MEN for the finisher period.

TABLE 8

Composition and nutrient contents of the basal experimental diets			
	Starter (d 1-22)	Grower (d 22-36)	Finisher (d 36-42)
<b>Ingredients (%)</b>			
Soybean meal	38.00	35.40	33.00
Corn	22.55	20.20	21.40
Wheat	20.00	24.50	25.00
Rye	12.00	12.00	12.00
Soya oil	3.80	4.30	4.85
DL-Methionine	0.20	0.15	0.15
NaCl	0.15	0.15	0.15
DCP	1.70	1.85	1.95
CaCO <sub>3</sub>	0.54	0.39	0.34
Premix <sup>1</sup>	1.00	1.00	1.00
Coccidiostat	0.06	—	—
<b>Calculated content</b>			
Crude protein (%)	22.5	21.5	20.5
Metabolizable energy (MJ/kg) <sup>2</sup>	12.6	12.8	13.0
<b>Analyzed content</b>			
Crude protein (%)	21.9	21.5	20.8
Metabolizable energy (MJ/kg) <sup>3</sup>	12.5	12.6	12.9

<sup>1</sup>Vitamin-mineral premix provided per kilogram of diet: Vitamin A: 10'000 IU; vitamin E: 40 IU.; vitamin K3: 3.0 mg; vitamin C: 100 mg; vitamin B1: 2.50 mg; vitamin B2: 8.00 mg; vitamin B6: 5.00 mg; vitamin B12: 0.03 mg; niacin: 50.0 mg; pantothenate calcium: 12.0 mg; folic acid: 1.50 mg; biotin 0.15 mg; cholin: 450 mg; ethoxyquine: 54 mg; Na: 1.17 g; Mg: 0.8 g; Mn: 80 mg; Fe: 60 mg; Cu: 30 mg; Zn: 54 mg; I: 1.24 mg; Co: 0.6 mg; Se: 0.3 mg.

<sup>2</sup>Without coccidiostat;

<sup>3</sup>Calculated with EC-equation;

<sup>3</sup>Calculated with EC-equation based on analysed crude nutrients.

**[1062]** The diets were fed either unsupplemented (negative control, C), supplemented with the GH24 lysozyme (SEQ ID NO: 257) at 25 mg per kg feed or with Avilamycin at an inclusion level of 10 mg/kg. No additional enzymes (e.g., phytase) were added to the feed.

**[1063]** Appropriate amounts of the solid product (Avilamycin) was mixed with a small quantity of the basal feed as a premix which was then added to the feed to get the final concentration, according to the treatment. After mixing the feed was pelleted (3×25 mm) at about 70° C.

**[1064]** Appropriate amount of the liquid preparations of Lysozyme was diluted in water and sprayed onto the respective pelleted feed to get the final concentrations in the feed corresponding to the different treatments. For procedural balance of all treatments the same volume of water were also sprayed onto the pellets of the control diets.

#### Experimental Parameters and Analyses

**[1065]** For the two experiments, the birds were weighed (as replicate group) on days 1, 22 and 36. The feed consumption for the intermediate periods was determined. Body weight gain and feed conversion ratio (feed/gain) were calculated.

**[1066]** The analyses of the nutrient content in the feed samples were performed according to standard methods (VDLUFA 1976). Nitrogen analysis was carried out with a Leco N analyzer (CP=N\*6.25).

#### Statistical Analysis

**[1067]** For the statistical evaluation of performance data, a one-factorial analysis of variance (factor: treatment) was carried out. The software 'Stat Box Pro Agri', version 7.1.9 (Grimmer soft, 1985-2011) was used. Where significant treatment effects ( $p<0.05$ ) were indicated, the differences among treatment means were subsequently determined with the Newman-Keuls test.

#### Results and Discussion

**[1068]** Based on the analyzed chemical compositions of the diets, the content of crude protein was close to the calculated content but the metabolizable energy was higher than expected in all the three diets (starter-grower and finisher) (Table 8).

**[1069]** The results of the growth performance are summarized in table 9 for the two periods (starter period, day 1-22; grower period, day 22-36, finisher period, day 36-42) and for the whole experimental period from day 1 to day 42 (table 10).

TABLE 9

Growth performance data of male broiler chickens fed graded inclusion levels of microbial lysozyme

Treatment/Product	Starter (d 1-22)			Grower (d 22-36)			Finisher (d 36-42)		
	Weight gain (g/b)	Feed intake (g/b)	FCR	Weight gain (g/b)	Feed intake (g/b)	FCR	Weight gain (g/b)	Feed intake (g/b)	FCR
Control (C)	1096	1578	1.440	1328	2285	1.723	761	1487	1.960
Avilamycin (10 mg/kg)	1102	1593	1.452	1334	2242	1.683	738	1460	1.982
Relative to C (%)	100.6	101.0	100.8	100.4	98.1	97.7	97.0	98.2	101.1
SEQ ID NO: 257 (25 mg/kg)	1133	1603	1.414	1364	2336	1.714	800	1524	1.919
Relative to C (%)	103.4	101.6	98.1	102.7	102.2	99.5	105.1	102.5	97.9

TABLE 10

Growth performance summary of male broiler chickens fed graded inclusion levels of microbial lysozyme

Treatment/ Product	Whole period				
	Weight gain (g/b)	Feed intake (g/b)	FCR	Mortality	EPEF
Control (C)	3186	5351	1.680	7.5	418
Avilamycin (10 mg/kg)	3184	5312	1.669	12.5	397
Relative to C (%)	99.9	99.3	99.3		95.0
SEQ ID NO: 257 (25 mg/kg)	3290	5450	1.657	10.0	425
Relative to C (%)	103.3	101.9	98.6		101.7

**[1070]** Over the whole period, the GH24 supplemented at 25 mg/kg resulted in a FCR improvement of 1.4% compared to NC diet. Furthermore, the GH24 lysozyme supplemented at 25 mg/kg resulted in an EPEF improvements of 1.7% compared to NC diet. Whilst the positive control Avilamycin showed a slight FCR improvement of 0.7%, the EPEF was worse by 5.0%.

#### Conclusion

**[1071]** The results obtained in the study showed that the inclusion of a microbial lysozyme at 25 mg/kg was effective in improving the FCR and the EPEF of broilers fed diets formulated with coccidiostat in the starter period and based on soybean meal, corn, wheat and rye. In addition, the microbial lysozyme at 25 mg/kg was markedly better in improving the EPEF over the positive control (Avilamycin).

#### Example 18: In Vivo Piglet Trial

#### Materials and Methods

**[1072]** The trial was performed from Oct. 23 to Dec. 4, 2014 at the Research Center for Animal Nutrition (DSM Nutritional Products France, F-68305 Village-Neuf) according to the official French guidelines for experiments with live animals.

## Animals and Housing

[1073] One hundred and four castrated male crossbred (Large-White (female)×Redon (male)) weaned piglets having 28 days of age supplied by the commercial farm “Elevage de la Plaine du Rhin” located in Balgau (France), were used in a 42-day experiment. The initial bodyweight of the piglets was  $7.88\pm0.675$  kg. They were sorted by body weight into 32 groups of 3 or 4 piglets and randomly allotted to each dietary treatment. Each group of animals was placed in one flat-deck cages and allocated to one of the different treatments.

[1074] Each treatment was replicated with 8 cages using a total of 26 animals (6 cages of 3 animals/treatment and 2 cages of 4 animals/treatment) per treatment. Each cage had a plastic-coated welded wire floor and was equipped with two water nipples and two stainless-steel individualised feeders. Animals were housed in an environmentally controlled room. Room temperature was initially 27° C. and was lowered weekly by about 2° C. until 21-22° C. and relative humidity percentage was 50%.

## Feeding and Treatments

[1075] The experimental diets (Pre-Starter and Starter) were fed ad libitum in two feeding phases from day 0 to 14 (phase 1, Pre-starter) and day 14 to 42 (phase 2, Starter). The ingredient composition and the calculated nutrient levels of the experimental diets for phases 1 and 2 are presented in table 11. The analysed content is presented in table 12. Both diets were formulated to meet the animals' requirements according NRC (2012) and were fed in pelleted form. Pelleting conditions were at 70° C. for 30 seconds.

TABLE 11

Composition and nutrient contents of the basal experimental diets		
	Pre-starter (%)	Starter (%)
<u>Ingredients</u>		
Barley	38.00	38.00
Wheat	22.10	17.50
Soybean meal 48%	24.00	22.00
Maize	6.00	16.20
Soybean oil	1.00	2.00
Dried whey	5.00	—
Vermiculite	—	1.00
Calcium carbonate	0.30	0.30
L-Lysine HCl	0.10	—
Vitamin-mineral Premix 3136 <sup>1</sup>	3.50	3.00
<u>Estimated nutrient content</u>		
Crude protein (%)	19.47	17.95
Lysine (%)	1.24	1.03
Threonine (%)	0.67	0.61
Methionine + cysteine (%)	0.70	0.66
Total P (%)	0.71	0.64
Total Ca (%)	0.84	0.71
Estimated digestible energy (MJ/kg)	13.62	13.87

<sup>1</sup>Vitamin-mineral premix 3136 provided per kilogram of diet: Vitamin A: 20'000 I.U.; Vitamin E: 100 mg.; Vitamin K: 4.0 mg.; Vitamin C: 200 mg.; Vitamin B1: 5.00 mg.; Vitamin B2: 10.00 mg.; Vitamin B6: 8.00 mg.; Vitamin B12: 0.07 mg.; Niacin: 60.0 mg.; Pantothenic acid: 40.0 mg.; Folic acid: 3.00 mg.; Biotin 0.4 mg.; Choline: 800 mg.; Mn: 60.5 mg.; Fe: 162 mg.; Cu: 9.5 mg.; Zn: 100 mg.; I: 0.9 mg.; Se: 0.3 mg.

TABLE 12

Analysed nutrient contents of the basal diets		
Analyzed nutrient content	Pre-starter	Starter
Dry matter (%)	87.89	87.42
Crude protein (% DM)	21.69	19.63
Crude Ash (% DM)	6.41	6.37
Fat (% DM)	4.15	5.42
Starch (% DM)	44.63	49.54
Total P (mg/g DM)	8.24	7.50
Total Ca (mg/g DM)	9.01	7.69
Total Zn (mg/g DM)	0.28	0.25
Gross energy (MJ/kg DM)	18.42	18.67

[1076] The diets were fed either unsupplemented (negative control) or supplemented with the GH24 lysozyme (SEQ ID NO: 257) at 50 mg per kg feed or VevoVital at 5000 mg per kg feed. No additional enzymes (e.g., phytase) were added to the feed.

Treatment	Product	Inclusion level (mg/kg)
A	Negative control	—
B	VevoVital	5000
C	SEQ ID NO: 257	50

[1077] VevoVital was mixed to the premixed mash diet before pelleting the diet.

[1078] Appropriate amount of the liquid preparations of lysozyme was diluted in water and sprayed onto the respective pelleted feed to get the final concentrations in the feed corresponding to the different treatments. For procedural balance of all treatments the same volume of water were also sprayed onto the pellets of the control diets.

## Experimental Parameters and Analyses

[1079] The health status of the animals was controlled daily.

[1080] Body weight of the individual animals and feed consumption per pen were recorded on days 14 and 42 of the study. Performance, average daily weight gain (ADWG), average daily feed intake (ADFI) and feed conversion ratio (FCR) was calculated for phases 1 and 2, and the whole experimental period.

## Statistical Analysis

[1081] The experimental unit was the piglet, except for ADFI and FCR which were measured by cage, and in both cases, treatment was used as class variable.

[1082] Statistical analyses were performed using the Stat-Graphics Centurion XVI statistical software package (Manugistics, Rockville, MD).

[1083] One-factorial ANOVA and Student-Newman-Keuls test was used to assess differences among means in treatment groups.

[1084] Variability in the data was expressed as the pooled standard error. In all instances, differences were reported as significant at  $P<0.05$ .

## Results and Discussion

[1085] Based on the analyzed chemical compositions of the diets, the content of crude protein (19.07% and 17.16% as is, in pre-starter and starter periods, respectively) was

close to the calculated content (19.47% and 17.95% as is, in pre-starter and starter periods, respectively) (Table 12).

[1086] All piglets remained healthy throughout the study. During the enzyme supplementation, none of the animals showed any symptoms of illness or toxicosis due to the test compounds. Mortality rate was equal to zero.

[1087] Results of the growth performance are summarized for the two periods (pre-starter period, days 0-14, and starter period, days 14-42) and for the whole experimental periods from day 0 to day 42 (Table 12).

[1088] In general, excellent animal growth performance was obtained for all treatments.

[1089] No significant difference among the supplemented treatments was recorded in terms of body weight. However, the supplementation of GH24 lysozyme (SEQ ID NO: 257) at 50 mg/kg resulted in numerical improvement of the ADWG by 11.8% during the starter period, and 7.8% during the whole period, compared to the negative control diet.

[1090] Over the pre-starter, starter and whole periods the supplementation of VovoVital resulted in an improvement of ADWG by 4.8, 5.8 and 5.4% compared to NC.

[1091] The results of FCR showed a statistically significant effect ( $p < 0.05$ ) of treatment in the pre-starter, starter and overall periods.

[1092] Over the starter period, from day 15 to day 42, piglets, which received VovoVital (PC) or the GH24 lysozyme (SEQ ID NO: 257) included at 50 mg/kg showed an improvement to FCR by 9.5% and 9.1% compared to NC.

[1093] As presented in Table 13, during the overall period (day 0 to day 42) piglets receiving feed added with VovoVital (PC) at 5000 mg/kg, the GH24 lysozyme (SEQ ID NO: 4) included at 50 mg/kg showed an improvement on FCR by 9.6% and 7.1% respectively compared to the negative control.

not statistically significant. Improvement of BWG with the GH24 lysozyme (SEQ ID NO: 257) at 50 mg/kg feed was even higher than the positive control. Of importance, nevertheless, was to observe a statistically significant effect of the GH24 lysozyme (SEQ ID NO: 257) included at 50 mg/kg feed treatment on ADFI and FCR in the starter and overall periods.

Example 19: Expression of the GH24 Lysozyme  
from *Trichophaea minuta*

[1095] The gene from *Trichophaea minuta* was codon optimized using Gene designer and synthesized by Geneart. The gene of interest was cut out using BamHI and XhoI from NEB and the gel purified using Sigma Agarose gel purification Kit. An expression vector pDAU222 was also made, digested with BamHI and XhoI from NEB, and the larger fragment gel purified.

[1096] Finally, the construct of interest was made using Clontech In-Fusion® HD PCR Cloning Kit. In the construct, the gene of interest was under the influence of NA2TPI promoter of the vector pDAU222 and it had its native signal for secretion. The gene of interest was having its own terminator codon TAA made to it. The positive clone grown on LB-ampicillin plate in *E. coli* was re-confirmed by colony PCR and then one positive clone was picked to put into *Aspergillus oryzae* MT3568 strain. The positive clone in *Aspergillus* was selected through AMDS selection by plating the transformants on sucrose agar with 1 M acetamide. One positive transformant was then grown in 300 ml DAP-4C media in 1 liter baffled flask at 30° C. for 4 days and then purified as described in example 20.

TABLE 13

Growth performance data of piglets fed graded inclusion levels of microbial lysozyme										
Treatment	day 0-14			day 14-42			day 0-42			FCR (2)
	ADFI (g/d) (2)	ADWG (g/d) (1)	FCR (2)	ADFI (g/d) (2)	ADWG (g/d) (1)	FCR (2)	ADFI (g/d) (2)	ADWG (g/d) (1)		
	Mean	360	290	1.240 <sup>a,b</sup>	930 <sup>b,c</sup>	603	1.544 <sup>b</sup>	734 <sup>b</sup>	499	1.484 <sup>b</sup>
Negative control (NC)	SD	20	66	0.053	34	79	0.096	23	69	0.072
VovoVital (PC)	%	100	100	100	100	100	100	100	100	
	Mean	355	304	1.168 <sup>a</sup>	886 <sup>a,b</sup>	638	1.398 <sup>a</sup>	709 <sup>a,b</sup>	526	1.342 <sup>a</sup>
	SD	26	56	0.041	33	62	0.103	30	52	0.079
	% relative	98.6	104.8	94.2	95.3	105.8	90.5	96.6	105.4	90.4
NC + SEQ ID NO: 257 (50 ppm)	Mean	333	265	1.272 <sup>b</sup>	944 <sup>c</sup>	674	1.404 <sup>a</sup>	740 <sup>b</sup>	538	1.379 <sup>a</sup>
	SD	42	53	0.049	62	89	0.044	49	69	0.040
	% relative	92.5	91.4	102.6	101.5	111.8	90.9	100.8	107.8	92.9
NC	P value	0.317	0.346	0.014	0.013	0.068	0.009	0.034	0.341	0.004

(1) Mean ± mean deviation of 18 determinations;

(2) Mean ± mean deviation of 6 determinations;

<sup>a,b</sup>Different superscripts in the same column indicate a significant difference ( $p < 0.05$ );

ADFI: average daily feed intake;

ADWG: average daily weight gain.

## Conclusion

[1094] It can be concluded that in the present study and at the tested dosages and conditions, the GH24 lysozyme supplemented at 50 mg per kg feed to soybean meal, maize, wheat and barley based diet had a numerically improvement on growth performance of piglets although this effect was

Example 20: Purification of the GH24 Lysozyme  
from *Trichophaea minuta* (SEQ ID NO: 291)

[1097] The target molecule was purified using a Phenyl Toyo column. The purification was carried out at pH 8 using HEPES (50 mM)+1.5 M ammonium sulphate for equilibration, HEPES (50 mM)+1 M ammonium sulphate

to wash and HEPES, pH8 to elute. The purity of the purified enzymes was checked by SDS-PAGE and the concentration of the enzyme determined by Abs 280 nm after a buffer exchange. The purified protein was also MS verified.

**Example 21: Genomic DNA Extraction from Strains of *Chaetomium* sp., *Mortierella* sp., *Metarhizium* sp., *Geomyces auratus* and *Ilyonectria rufa***

[1098] Strain *Chaetomium* sp. and *Mortierella* sp. were inoculated onto a PDA plate and incubated for 7 days at 37° C. in the darkness. Several mycelia-PDA plugs were inoculated into 500 ml shake flasks containing 100 ml of YPG medium. The flasks were incubated for 4-5 days at 37° C. with shaking at 160 rpm.

[1099] Strain *Metarhizium* sp. and *Geomyces auratus* were inoculated onto a PDA plate and incubated for 7 days at 25° C. in the darkness. Several mycelia-PDA plugs were inoculated into 500 ml shake flasks containing 100 ml of YPG medium. The flasks were incubated for 3 days at 25° C. with shaking at 160 rpm.

[1100] Strain *Ilyonectria rufa* were inoculated onto a PDA plate and incubated for 7 days at 25° C. in the darkness. Several mycelia-PDA plugs were inoculated into 500 ml shake flasks containing 100 ml of YPG medium. The flasks were incubated for 11 days at 25° C. with shaking at 160 rpm.

[1101] The mycelia were collected by filtration through MIRACLOTH® (Calbiochem, La Jolla, CA, USA) and frozen under liquid nitrogen. Frozen mycelia were ground, by a mortar and a pestle, to a fine powder, and genomic DNA was isolated using DNeasy® Plant Maxi Kit (24) (QIAGEN GmbH, Hilden, Germany) following the manufacturer's instruction.

**Example 22: Genome Sequencing, Assembly and Annotation**

[1102] The extracted genomic DNA samples were genome sequenced using an ILLUMINA® HiSeq 2000 System (Illumina, Inc., San Diego, CA, USA).

[1103] The raw reads of *Mortierella* sp. and *Ilyonectria rufa* were assembled using program Idba (Peng Yu et al., 2010, *Research in Computational Molecular Biology* 6044: 426-440. Springer Berlin Heidelberg.). The raw reads of *Chaetomium* sp., *Metarhizium* sp. and *Geomyces auratus* were assembled using program Spades (Bankevich et al., 2012, *Journal of Computational Biology* 19 (5): 455-477). The assembled sequences were analyzed using standard bioinformatics methods for gene identification and function prediction. GeneMark-ES fungal version (Ter-Hovhannissyan et al., 2008, *Genome Research* 18 (12): 1979-1990) was used for gene prediction. Blastall version 2.2.10 (Altschul et al., 1990, *Journal of Molecular Biology* 215 (3): 403-410, ncbi.nlm.nih.gov/blast/executables/release/2.2.10/) and HMMER version 2.1.1 (National Center for Biotechnology Information (NCBI), Bethesda, MD, USA) were used to predict function based on structural homology. The GH24 family lysozyme polypeptides were identified directly by analysis of the Blast results. The Agene program (Munch and Krogh, 2006, *BMC Bioinformatics* 7:263) and SignalP program (Nielsen et al., 1997, *Protein Engineering* 10:1-6) were used to identify start codons. SignalP program was further used to predict signal peptides. Pepstats (Rice et al.,

2000, *Trends in Genetics* 16 (6): 276-277) was used to predict isoelectric points and molecular weights.

**Example 23: Cloning of GH24 Lysozymes (SEQ ID NO: 292, 295, 298, 301, 304)**

[1104] Five fungal GH24 lysozyme wild type sequences were cloned from *Chaetomium* sp. (SEQ ID NO: 292), *Mortierella* sp. (SEQ ID NO: 295), *Metarhizium* sp. (SEQ ID NO: 298), *Geomyces auratus* (SEQ ID NO: 301) and *Ilyonectria rufa* (SEQ ID NO: 304).

[1105] The fungal GH24 lysozymes were cloned into an *Aspergillus oryzae* expression vector pCaHj505 as described in WO 2013/029496. The transcription of the GH24 lysozyme coding sequence with the native secretion signal was under the control of an *Aspergillus oryzae* alpha-amylase gene promoter.

[1106] The final expression plasmids, p505-GH24\_Chaet287, p505-GH24\_Mort, p505-GH24\_Metar, p505-GH24\_Geau, and p505-GH24\_Ilyru (SEQ ID NO: 292, 295, 298, 301, 304), were individually transformed into an *Aspergillus oryzae* expression host. The GH24 lysozyme genes were integrated by homologous recombination into the *Aspergillus oryzae* host genome upon transformation. Four transformants of each transformation were selected from the selective media agar plate and inoculated to 3 ml of YPM medium in 24-well plate and incubated at 30° C., 150 rpm. After 3 days incubation, 20 µl of supernatant from each transformant were analyzed on NuPAGE Novex 4-12% Bis-Tris Gel w/MES according to the manufacturer's instructions. The resulting gel was stained with Instant Blue. SDS-PAGE profiles of the cultures showed that all 5 genes were expressed with 1 or 2 protein bands each detected at 30 KD, 28 KD & 30 KD, 28 KD, 25 KD & 28 KD and 28 KD respectively. The recombinant *Aspergillus oryzae* strain with the strongest protein band were selected for shaking flask culturing and were inoculated on slant made of slant medium and incubated at 37° C. for 6-7 days. When strains were well grown to fully sporulated, they were inoculated to 2 L shaking flasks each containing 400 ml of YPM and 4-8 flasks for each strain. Flasks were shaking at 80 rpm, 30° C. Cultures were harvested on day 3 and filtered using a 0.45 µm DURAPORE Membrane and were purified as described in example 24 to 28.

**Example 24: Purification of the GH24 Lysozyme from *Chaetomium* sp. ZY287 (SEQ ID NO: 294)**

[1107] The culture supernatant was firstly precipitated with ammonium sulfate (80% saturation), then dialyzed with 20 mM PBS at pH 6.5. The solution was filtered with 0.45 um filter and then loaded into SP Fast Flow column (GE Healthcare) equilibrated with 20 mM PBS at pH 6.5. A gradient of NaCl concentration was applied as elution buffer from zero to 1 M, and then elution fractions and flow-through fraction were collected to detect lysozyme activity. The fractions with lysozyme activity were pooled and analyzed by SDS-PAGE, and then concentrated for further evaluation. The protein concentration was determined by Qubit® Protein Assay Kit (Invitrogen, cat Q33212).

**Example 25: Purification of the GH24 Lysozyme from *Mortierella* sp. ZY002 (SEQ ID NO: 297)**

[1108] The culture supernatant was firstly precipitated with ammonium sulfate (80% saturation), then dialyzed with

20 mM PBS at pH 7.0. The solution was filtered with 0.45 um filter and then loaded into SP Fast Flow column (GE Healthcare) equilibrated with 20 mM PBS at pH 7.0. A gradient of NaCl concentration was applied as elution buffer from zero to 1 M, and then elution fractions and flow-through fraction were collected to detect lysozyme activity. The fractions with lysozyme activity were pooled and analyzed by SDS-PAGE, and then concentrated for further evaluation. The protein concentration was determined by Qubit® Protein Assay Kit (Invitrogen, cat Q33212).

**Example 26:** Purification of the GH24 Lysozyme from *Metarhizium* sp. XZ2431 (SEQ ID NO: 300)

[1109] The culture supernatant was firstly precipitated with ammonium sulfate (80% saturation), then dialyzed with 20 mM PBS at pH 7.0. The solution was filtered with 0.45 um filter and then loaded into SP Fast Flow column (GE Healthcare) equilibrated with 20 mM PBS at pH 7.0. A gradient of NaCl concentration was applied as elution buffer from zero to 1 M, and then elution fractions and flow-through fraction were collected to detect lysozyme activity. The fractions with lysozyme activity were pooled and analyzed by SDS-PAGE, and then concentrated for further evaluation. The protein concentration was determined by Qubit® Protein Assay Kit (Invitrogen, cat Q33212).

**Example 27:** Purification of the GH24 Lysozyme from *Geomyces auratus* (SEQ ID NO: 303)

[1110] The culture supernatant was firstly precipitated with ammonium sulfate (80% saturation), then dialyzed with 20 mM PBS at pH 7.0. The solution was filtered with 0.45 um filter and then loaded into SP Fast Flow column (GE Healthcare) equilibrated with 20 mM PBS at pH 7.0. A gradient of NaCl concentration was applied as elution buffer from zero to 1 M, and then elution fractions and flow-through fraction were collected to detect lysozyme activity. The fractions with lysozyme activity were pooled and analyzed by SDS-PAGE, and then concentrated for further evaluation.

[1111] Since the purified sample has two bands, the collected sample was added ammonium sulfate with a final conductivity with 180 mS/cm, and then loaded into a Phenyl Sepharose 6 Fast Flow column (GE Healthcare) equilibrated with 20 mM PBS at pH 7.0 with 1.8 M (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub>. A concentration gradient of (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> was applied as elution buffer from 1.8 M to zero. The fractions with lysozyme activity were collected and carried out for SDS-PAGE. The sample also contains two bands, but MS data showed both bands are target proteins. The protein concentration was determined by Qubit® Protein Assay Kit (Invitrogen, cat Q33212).

**Example 28:** Purification of the GH24 Lysozyme from *Ilyonectria rufa* (SEQ ID NO: 306)

[1112] The culture supernatant was firstly precipitated with ammonium sulfate (80% saturation), then dialyzed with 20 mM PBS at pH 7.5. The solution was filtered with 0.45 um filter and then loaded into SP Fast Flow column (GE Healthcare) equilibrated with 20 mM PBS at pH 7.5. A gradient of NaCl concentration was applied as elution buffer from zero to 1 M, and then elution fractions and flow-through fraction were collected to detect lysozyme activity. The fractions with lysozyme activity were pooled and ana-

lyzed by SDS-PAGE, and then concentrated for further evaluation. The protein concentration was determined by Qubit® Protein Assay Kit (Invitrogen, cat Q33212).

**Example 29:** Determination of Lysozyme Activity

[1113] Lysozyme activity was determined as described in example 11 herein and is presented in table 14.

TABLE 14

GH24 Lysozyme	Lysozyme Activity against <i>Micrococcus lysodeikticus</i> and <i>Exiguobacterium undae</i> as measured by Optical Density Drop	
	<i>Micrococcus lysodeikticus</i> <sup>1</sup>	<i>Exiguobacterium undae</i> <sup>1</sup>
GH24 lysozyme from <i>Trichoderma harzianum</i> (SEQ ID NO: 267)	+++ (pH 6)	++++ (pH 6)
GH24 lysozyme from <i>Trichophaea minuta</i> (SEQ ID NO: 291)	++++ (pH 6)	++++ (pH 6)
GH24 lysozyme from <i>Chaetomium sp.</i>	+++ (pH 7)	+++ (pH 7)
ZY287 (SEQ ID NO: 294)		
GH24 lysozyme from <i>Mortierella</i> sp.	++++ (pH 6)	+++ (pH 6)
ZY002 (SEQ ID NO: 297)		
GH24 lysozyme from <i>Metarhizium</i> sp.	+++ (pH 6)	+++ (pH 6)
XZ2431 (SEQ ID NO: 300)		
GH24 lysozyme from <i>Geomyces auratus</i> (SEQ ID NO: 303)	+++ (pH 6)	++++ (pH 6)
GH24 lysozyme from <i>Ilyonectria rufa</i> (SEQ ID NO: 306)	++ (pH 6)	++++ (pH 6)

<sup>1</sup>Means no significant effect; + means small effect; ++ means medium effect; +++ means large effect; ++++ means very large effect.  
The pH value in the brackets lists the assay pH based on lysozyme-substrate combination.

[1114] The data shows that all of the GH24 lysozymes that naturally comprise the lysozyme enhancing domain (LED) (SEQ ID NO: 267, 291, 294, 297, 300, 303 and 306) showed good activity against both substrates.

**Example 30:** Determination of DomT Scores

[1115] The DomT scores for the GH24 domain and the LED domain of the lysozymes of the invention were determined using the Lysozyme Enhancing Domain HMM from example 15 and the GH24 catalytic domain HMM from example 16 as described herein. The DomT scores for other prior art lysozyme sequences were also calculated and are presented in table 15 below.

TABLE 15

Sequence	Domains	DomT scores for GH24 catalytic and Lysozyme Enhancing Domains	
		DomT score of LED <sup>1</sup>	DomT score for GH24 domain
SEQ ID NO: 257	LED + GH24	103.0	265.9
SEQ ID NO: 264	LED + GH24	127.0	257.2
SEQ ID NO: 267	LED + GH24	125.0	249.6
SEQ ID NO: 279	GH24	—	251.9
SEQ ID NO: 280	GH24	—	229.8
SEQ ID NO: 291	LED + GH24	103.1	263.2

TABLE 15-continued

DomT scores for GH24 catalytic and Lysozyme Enhancing Domains			
Sequence	Domains	DomT score of LED <sup>1</sup>	DomT score for GH24 domain
SEQ ID NO: 294	LED + GH24	113.1	254.0
SEQ ID NO: 297	LED + GH24	103.1	246.3
SEQ ID NO: 300	LED + GH24	117.8	242.2
SEQ ID NO: 303	LED + GH24	119.8	246.9
SEQ ID NO: 306	LED + GH24	116.7	257.5
Lactococcus c2 phage from WO 95/31562 (GENESEQP: AAR85295)	GH24 phage	—	74.5
Enterobacteria phage T4 lysozyme, SEQ ID NO: 24 of WO 2013/021206 (BAK49017)	GH24 phage	—	34.9

<sup>1</sup>No score means that there was no alignment to the HMM and thus no score could be generated

[1116] No DomT scores could be generated for the lysozyme enhancing domain or the GH24 domain (i.e., there was no sequence alignment) for the other lysozymes tested, including GH25 lysozymes disclosed in WO 2005/080559, WO 2009/102755, WO 2013/076253, WO 2013/076259,

GH22 lysozyme such as hen egg white lysozyme and a GH23 lysozyme disclosed in WO 2013/076259 demonstrating that the HMMs are selective for the GH24 catalytic domain and the lysozyme enhancing domain respectively.

[1117] Unsurprisingly the prior art GH24 phage lysozymes did not align very well with the HMM of the GH24 catalytic domain as disclosed herein. These phage lysozymes are structurally and taxonomically very different from the fungal GH24 lysozymes of the invention and furthermore do not comprise a LED. In comparison, all of the GH24 lysozymes of the invention gave a domT score of at least 200 for the GH24 catalytic domain and a domT score of at least 100 for the lysozyme enhancing domain indicating good alignment to the HMMs.

[1118] The invention described and claimed herein is not to be limited in scope by the specific aspects herein disclosed, since these aspects are intended as illustrations of several aspects of the invention. Any equivalent aspects are intended to be within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description. Such modifications are also intended to fall within the scope of the appended claims. In the case of conflict, the present disclosure including definitions will control.

## SEQUENCE LISTING

```

Sequence total quantity: 306
SEQ ID NO: 1      moltype = AA length = 157
FEATURE           Location/Qualifiers
source            1..157
mol_type = protein
organism = Ajellomyces capsulatus

SEQUENCE: 1
PHVNKTALAI IKEFEGFVPR PEPDPIGLPT VGYGHLCKTK GCKEVKFPPLS KGTATTLLKK 60
DLRSFQQAII LSTKTAVKLN ANYQGALVSW AYNVGPNAAR SSSLISRLNQ GEDPNQVIAQ 120
ELPKWRLAGG KVFEGLVRRA KAEVKLAKTP TKSKALP 157

SEQ ID NO: 2      moltype = AA length = 159
FEATURE           Location/Qualifiers
source            1..159
mol_type = protein
organism = Coprinopsis cinerea

SEQUENCE: 2
INKKTLDDLK EFEQWAASPY KDVAGYPTVG YGHKCSKND CSELGYKFPMT KAQGEELLAK 60
DVKGFEKCIS DYINDTIKLN DNQYQGALVSW SFNVGCCAAK DSTLISRLNK GDSPNTVAGE 120
ELPRWNKAGG KVVVDGLTNRR KKEVELFKTS STVIAHPPC 159

SEQ ID NO: 3      moltype = AA length = 154
FEATURE           Location/Qualifiers
source            1..154
mol_type = protein
organism = Aspergillus terreus

SEQUENCE: 3
GKLLRRGISD AAVELIGSLG GFRPDFYYIN GHKTVGYGHD CVAKQDCDSI DTPLTKEEGA 60
ALLKKDLAGY ENCVCEMDNA KYLNANQYGA LVSFAYNSGC GGVQSWWHGA MEQKNFKGIC 120
SALPNTNTLG GELSSRRAKE GAFCAKPTNQ TSGC 154

SEQ ID NO: 4      moltype = AA length = 166
FEATURE           Location/Qualifiers
source            1..166
mol_type = protein
organism = Aspergillus terreus

SEQUENCE: 4
ACSGPNVNEA TIKLMKGYES WEADVYDDGY GNPTVGYGHL CDDWSCSDVS YDIPLSESOG 60
EKLFAEDIVA YQNGVVAALS DDVTLNNDQY GALVSWCFNV GTGAVAESTL AKRLNNGEDP 120
DTVAEEELPK WVYANGAPSE GLKNRRAEL KLFTTSSDTE ALPVDC 166

SEQ ID NO: 5      moltype = AA length = 154

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-continued

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FEATURE	Location/Qualifiers
source	1..154
	mol_type = protein
	organism = Aspergillus oryzae
SEQUENCE: 5	
ATVVRGASA ATVSLIGEVE GFRADFYDMM GHKTIGYGH CVAKQDCDSI KAPISNAQGD	60
EILQKDLAGF EQCVCALPNA KALNANQYGA LVSYAFNTGC GGLQQAWTAA MTSKNFDSIC	120
ADLPHTNRTLN GVLDNRRKKE AALCSTPTTQ MCFC	154
SEQ ID NO: 6	moltype = AA length = 163
FEATURE	Location/Qualifiers
source	1..163
	mol_type = protein
	organism = Aspergillus oryzae
SEQUENCE: 6	
GPPVNQNGLN LIKSFESFQP SVYDDGFGNP TIGYGHLCGD ATCSEVTYPK PLSEADASRL	60
LADDLVSYQD ALTNALADPV TLNDNQYAAAL VSWTFNIGNG NMQKSDLVAR MNKGENVATV	120
AHDELPQWNK ANGQVVNGLT RRRKAELDLF DAPAIY GALP VPC	163
SEQ ID NO: 7	moltype = AA length = 162
FEATURE	Location/Qualifiers
source	1..162
	mol_type = protein
	organism = Emericella nidulans
SEQUENCE: 7	
PDVNTATTDL MKAFESWEPD VYDDGYGNPT IGYGHLCSDW SCSDVAYDIP LSEEDGVKLF	60
AEDIAVYQDG VVSALDSSVT LNDNQY GALV SWCYNVGAGA VAESTLAARL NAGEDPNTVA	120
EEELIKWVYA NGEVSEGLKR RRNAEIELFQ TSSDGEALPV SC	162
SEQ ID NO: 8	moltype = AA length = 159
FEATURE	Location/Qualifiers
source	1..159
	mol_type = protein
	organism = Laccaria bicolor
SEQUENCE: 8	
ISSATVNLIK GS ESLVPIPS PDPIGLLTVG YGHKCLKPQC SEVTFPFPPLS SSTASQLFAQ	60
DMTQYINCLH RSISKS VVVLN DNQFGALVSW TYNAGCEGMG TSTLVKRLNN GEDPNTVVAQ	120
ELPKWNIAKK KISKGLVNRR NREISFFQTP SNVVAHPLC	159
SEQ ID NO: 9	moltype = AA length = 160
FEATURE	Location/Qualifiers
source	1..160
	mol_type = protein
	organism = Laccaria bicolor
SEQUENCE: 9	
PPANADTINL IERFEGFVPS PRPDPIGLPT VG YGHLCQTK GCSEVPFKFP VTKNAVTL	60
HSDLTTFQNC VNSDIKRSVH LNDNQY GALV SWAYNVGGCN IKTSSLVRRRL NAGEDPNTVA	120
AQELPKQWNKG GGKVLPGLVR RRAEEVKLFK TPSSVSAHPC	160
SEQ ID NO: 10	moltype = AA length = 162
FEATURE	Location/Qualifiers
source	1..162
	mol_type = protein
	organism = Laccaria bicolor
SEQUENCE: 10	
PAVNAATIAL IKKFEGFVAS PSPDPIGLPT VG YGHLCQTK NCAEVPSFSP LTEAEASTLL	60
NSDLKTYEAC ITKDIVSSVR LNDNQY GALC SWAFNECGGA AGSSTLIARL NAGQDPDAV	120
AQELPKWDIA GGKVLPGLVN RRAEVALFK TPSSVIAHPP HC	162
SEQ ID NO: 11	moltype = AA length = 163
FEATURE	Location/Qualifiers
source	1..163
	mol_type = protein
	organism = Aspergillus flavus
SEQUENCE: 11	
GPPVNQNGLN LIKSFESFQP SVYDDGFGNP TIGYGHLCGD ATCSEVTYPK PLSEADASRL	60
LADDLVSYQD ALTNALADPV TLNDNQYAAAL VSWTFNIGNG NMQKSDLVAR MNKGENVATV	120
AHDELPQWNK ANGQVVNGLT RRRKAELDLF DAPAIY GALP VPC	163
SEQ ID NO: 12	moltype = AA length = 154
FEATURE	Location/Qualifiers
source	1..154
	mol_type = protein
	organism = Aspergillus flavus
SEQUENCE: 12	
ATVVRGASA ATVSLIGEVE GFRADFYDMM GHKTIGYGH CVAKQDCDSI KAPISNAQGD	60

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EILQKDLAGF	EQCVCALPNA	KALNANQYGA	LVSYAFNTGC	GGLQQAWTAA	MTSKNFDSIC	120
ADLPHTNTLN	GVLDNRKKE	AALCATPTTQ	MCGC			154
<hr/>						
SEQ ID NO: 13	moltype = AA length = 157					
FEATURE	Location/Qualifiers					
source	1..157					
	mol_type = protein					
	organism = Ajellomyces capsulatus					
SEQUENCE: 13						
PVNWKATLTL	IKEFEGFVPR	PEPDPIGLPT	VGYGHLCKTK	GCKEVKFPLS	KETATTLLKK	60
DILRSFQQAIT	LSTKTAVKLN	ANQY GALVSW	AYNVGPNAAR	SSSLISRLNK	GEDPNKVIHQ	120
ELPKWRLAGG	KVFKGLVRRR	KAEVKLAKTP	TKSKALP			157
<hr/>						
SEQ ID NO: 14	moltype = AA length = 162					
FEATURE	Location/Qualifiers					
source	1..162					
	mol_type = protein					
	organism = Arthroderma otae					
SEQUENCE: 14						
PDVNDETI	IKHFEGLVPR	PAPDPIGLPT	VGYGHLCRTK	GCGEVGFPPFP	LTEESATELL	60
HQDVVKSPQQS	ITLSTADSVV	LNANQY GALV	SWAFNVGGGA	AKKSSLIKRL	NQGQDVDTVI	120
REELPLWNKA	GGHVLPGGLVR	RRKAEVELAM	EHTDDGALPV	DC		162
<hr/>						
SEQ ID NO: 15	moltype = AA length = 162					
FEATURE	Location/Qualifiers					
source	1..162					
	mol_type = protein					
	organism = Arthroderma otae					
SEQUENCE: 15						
PDVNAATISL	VKEFERFVPS	PSPDPIGLPT	VGYGHLQSK	NCGEVGFPFFP	LTEDTATQLL	60
AQDIKAPQQT	ITLKTVNGVH	LNENQY GALV	SWTFNVGPNN	VATSSLKRL	NALEDVNTVL	120
REELPKWRYA	GGKVLPGGLVR	RRAEVALGE	TPSNVGA LPV	DC		162
<hr/>						
SEQ ID NO: 16	moltype = AA length = 160					
FEATURE	Location/Qualifiers					
source	1..160					
	mol_type = protein					
	organism = Ajellomyces dermatitidis					
SEQUENCE: 16						
PVNWKATLAL	IKEFEGFVPR	PAPDPIGLPT	VGYGHLCKTK	GCKEVKFPLT	KKTATALLKK	60
DILRSFQQAIT	LSTKKA VKL N	ANQY GALVSW	AYNVGPNAAR	SSSLIRRLNR	GENPNKVIHQ	120
ELPKWRLAGG	KVFKGLVRRR	KAEVKLAKTP	TKKKALPV			160
<hr/>						
SEQ ID NO: 17	moltype = AA length = 157					
FEATURE	Location/Qualifiers					
source	1..157					
	mol_type = protein					
	organism = Ajellomyces capsulatus					
SEQUENCE: 17						
PVNWKATLAL	IKEFEGFVPR	PEPDPIGLPT	VGYGHLQSK	NCAEV KYKFP	LTKTTAKELL	60
DILRSFQQAIT	LSTKTA VKL N	ANQY GALVSW	AYNVGPNAAR	SSSLISRLNK	GEDPNKVIHQ	120
ELPKWRLAGG	KVFKGLVRRR	KAEVKLAKTP	TKSKALP			157
<hr/>						
SEQ ID NO: 18	moltype = AA length = 163					
FEATURE	Location/Qualifiers					
source	1..163					
	mol_type = protein					
	organism = Hypocrea jecorina					
SEQUENCE: 18						
KTINGAGVLDL	IAKWE GFVAS	PKPDPIGLPT	VGYGHLQSK	NC AEV KYKFP	LTKTTAKELL	60
LDDLPKVTKC	LADVLNSKPK	LNANQY WAALS	SWFNV GCGN	AKTSTLVKRL	NNGEAPNTVA	120
AQELPKWRM A	GGKVMPGLEA	RRKDEVKLFK	TASSKEAYPK	CQA		163
<hr/>						
SEQ ID NO: 19	moltype = AA length = 162					
FEATURE	Location/Qualifiers					
source	1..162					
	mol_type = protein					
	organism = Arthroderma benhamiae					
SEQUENCE: 19						
PDVNPATI	IKEFEGFVPA	PAPDPVGLPT	VGYGHLQSK	NCGEVGFPFFP	LTEDTATQLL	60
IQDVVKAPQQT	ITLKTA DVGH	LNENQY GALV	SWTFNVGPNN	VATSSLQRL	NALEDVNTVL	120
REELPKWRYA	GGKVLPGGLVR	RRAEVALGE	TASDVP ALPV	AC		162
<hr/>						
SEQ ID NO: 20	moltype = AA length = 162					
FEATURE	Location/Qualifiers					
source	1..162					

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mol_type = protein
organism = Trichophyton verrucosum
SEQUENCE: 20
PDVNPATIAL IKFEGFVPA PAPDPVGLPT VGYGHLCQSK NCGEVGFPPF LTEDTATQLL 60
IQDVKAPQQT ITLKTADGVH LNENQY GALV SWTFNVGPGN VATSSLQRL NALEDVNTVL 120
REELPKWKG GGGVLPGLVR RRAAEVALGE TASDVPALPV AC 162

SEQ ID NO: 21      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Trichophyton verrucosum
SEQUENCE: 21
PDVNDETLI IKHFEFGVPR PAPDPIGLPT VGYGHLCRTN GCSEVPFSFP LTEETATELL 60
MQDVKSQQS ITLSTTDQVV LNANQY GALV SWAYNVGGDA AKKSSLISRL NQGQDVDVVI 120
REELPLWNKA GGHVLPGLVR RRAAEVELAS ENTDQPALPV DC 162

SEQ ID NO: 22      moltype = AA length = 161
FEATURE           Location/Qualifiers
source            1..161
mol_type = protein
organism = Coprinopsis cinerea
SEQUENCE: 22
NTATVNLQEQ FEGFVASPEP DPIGLPTVGF GHLCRQPNCNA EVTAQGLSFPL LSRAQAEQLL 60
QSDVQTFTNC LARFIIDSVV LNENQFGALT SWAFNVGCNN VQRSTLRRRL NAGQDPNTVA 120
AQELPRFNRA GGRVNLNGLTR RRRAEVALFQ TPSNTVALPV C 161

SEQ ID NO: 23      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Arthroderma gypseum
SEQUENCE: 23
PDVNAATIAL VKEFEGFVPS PAPDPIGLPT VGYGHLCQSK NCGEVGFPPF LTEDTATQLL 60
SQDIKAPQQT ITLKTADGVH LNENQY GALV SWTFNVGPGN VATSSLKRL NALEDVNTVL 120
REELPKWKG GGGVLPGLVR RRAAEVALGE TPSDVPALPV DC 162

SEQ ID NO: 24      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Arthroderma gypseum
SEQUENCE: 24
PDVNEATISL IKHFEFGVPR PAPDPIGLPT VGYGHACRTK GCAEVPPFPF LTEDTATELL 60
MQDVKSQQS ITLSTTDEVV LNANEY GALV SWAFNIGGGA AKKSSLIRRL NQGQDVNTVL 120
REELPLWNKA GGGVLPGLVR RRAAEVELAS EHTDEPALPV DC 162

SEQ ID NO: 25      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Hypocrea virens
SEQUENCE: 25
KTINGAGVDL IAKWEGFVAS PKPDPIGLPT VGYGHLCQKK NCREVKYKFP LTAKTTAKELL 60
LDDLPKVTKC LADYLNTPKLN LNDNQWAAALT SWFVNVCNN AKTSTLVKRL NNGEAANTVA 120
AEELPKWRLA GGGVLPGLEA RRKDEVKLFK TASSKQAYPK CQ 162

SEQ ID NO: 26      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Agaricus bisporus
SEQUENCE: 26
PRVNSATISL IKFEGFVKS PSPDPIGLPT VGYGHLCQKK GCAEVPYKFP LTEANAGKLL 60
QTDIKSFTKC VSDNIKDAV LNANQFGALS SWAFNVGCNN VKASALVARL NRGEKPNTVA 120
AEELPKWRLA GGGVLPGLEA RRKDEVKLFK TASKAIHPP KC 162

SEQ ID NO: 27      moltype = AA length = 163
FEATURE           Location/Qualifiers
source            1..163
mol_type = protein
organism = Metarhizium robertsii
SEQUENCE: 27
KTLNKAGTDL ITRWEGFVDR PKPDPIGLPT VGYGHLCQKK SCAEVKYTFP LTAKTALQLL 60
NDDLPVSYTKC LGKVLDAKGK KLNENQWAAAL TSWFVNVCNN AAQSSSLVKR LNRGENANTV 120
ASEELPKWKM GGGRVLPGLV KRRAEVALF KIASSRSAPP QCQ 163

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SEQ ID NO: 28      moltype = AA  length = 157
FEATURE          Location/Qualifiers
source           1..157
                 mol_type = protein
                 organism = Ajellomyces capsulatus
SEQUENCE: 28
PNVNKATLAL IKFEGFVPR PEPDPIGLPT VGYGHLCKTK GCKEVKFPLS KGTATTLLKK 60
DLRSFQQAIT LSTKTAVKLN ANQY GALVSW AYNVGPNAAR SSSLISRLNK GEDPNKVIAQ 120
ELPKWRLASG KVFKGLVRRR KAEVKLAKTP TKSALP                         157

SEQ ID NO: 29      moltype = AA  length = 162
FEATURE          Location/Qualifiers
source           1..162
                 mol_type = protein
                 organism = Trichophyton tonsurans
SEQUENCE: 29
PDVNDETIAL IKHFEFGFVPR PAPDPIGLPT VGYGHLCRTK GCSEVPFPFPF LTEETATELL 60
MQDVVKSPQOS ITLSTTDQVV LNANQY GALV SWAYNVGGSA AKKSSLISRL NQGDQDVAI 120
REELPLWNKA GGHVLSGLVR RRAAEVELAS EHTDQPALPV DC                         162

SEQ ID NO: 30      moltype = AA  length = 159
FEATURE          Location/Qualifiers
source           1..159
                 mol_type = protein
                 organism = Trichophyton equinum
SEQUENCE: 30
PDVNPATIAL IKFEGFVPS PAPDPVGLPT VGYGHLQSK NCGEVGFPFPF LTEDTATQLL 60
LQDVVKAPQQT ITLK TADGVH LNENQY GALV SWTFNVGPQN VATSSLQRL NALEDVNNTVL 120
REELPQWKYG GGKVLPGGLVR RRAAEVALGE TPSNVAALP                         159

SEQ ID NO: 31      moltype = AA  length = 162
FEATURE          Location/Qualifiers
source           1..162
                 mol_type = protein
                 organism = Trichophyton rubrum
SEQUENCE: 31
PDVNPATIAL IKFEGFVPA PAPDPVGLPT VGYGHLQSK NCGEVGFPFPF LTEDTATQLL 60
IQDVVKAPQQT ITLK TADGVH LNENQY GALV SWTFNVGPQN VATSSLQRL NALEDVNNTVL 120
REELPQWKYG GGKVLPGGLVR RRAAEVALGE TASDVPALPV AC                         162

SEQ ID NO: 32      moltype = AA  length = 161
FEATURE          Location/Qualifiers
source           1..161
                 mol_type = protein
                 organism = Trichophyton rubrum
SEQUENCE: 32
VNNDETIGLI KHFEFGFVLRP APDPIGLPTV GYGHLCRTKG CSEVSFPFFL TEETATELLI 60
QDVKSSQOSI TLSTTDQVF NANQSGALVS WAYTVGGATA KKSSLISRLN REQDQDAIR 120
EELPLWNKAG RHVLPQVRR RAAEVELASG HTDQPPPLLVD C                         161

SEQ ID NO: 33      moltype = AA  length = 150
FEATURE          Location/Qualifiers
source           1..150
                 mol_type = protein
                 organism = Pleurotus ostreatus
SEQUENCE: 33
MKSFESFVSPAPDPVGKL TVGYGHKCIQ PGCSEAGAPP LTEAGAVALM HRDLRIATTC 60
LSPAISSTVR LNDNQFGALA DWAFNVGCGA MRRSTLVSRL NSGENPNTVA AQELPKWNVA 120
EGHVSNGLIR RRAAEVALFQ TASSVIAHPC                         150

SEQ ID NO: 34      moltype = AA  length = 150
FEATURE          Location/Qualifiers
source           1..150
                 mol_type = protein
                 organism = Pleurotus ostreatus
SEQUENCE: 34
LIKFEFGVAPAPDPIGLP TVGYGHLQCT TSCSEAGAPP LTEARATLL LSDSRVATSC 60
LNTAISRNRV LNAQFGALT SWTFNVGCGN MRSSSLLSRL NAGEAPNTVA AQELPKWNKA 120
GGQVLAGLTR RRAAEVVLFQ TASSVIAHPC                         150

SEQ ID NO: 35      moltype = AA  length = 150
FEATURE          Location/Qualifiers
source           1..150
                 mol_type = protein
                 organism = Pleurotus ostreatus

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SEQUENCE: 35  
 LIKSSEGVP SPAPDPIGL P TVGYGHLCQT SSCSEAGPFP LTEARATTLL LADSRTATSC 60  
 LNTAISSSVR LNDNQFGALT SWTFNVCAN MRSSTLVSRL NAGETPNTVA AQELPRWNLA 120  
 GGVVQPGLV T RRA NEVKLFQ TASSVVAHPC 150

SEQ ID NO: 36 moltype = AA length = 146  
 FEATURE Location/Qualifiers  
 source 1..146  
 mol\_type = protein  
 organism = *Serratia marcescens*

SEQUENCE: 36  
 ELQTSEAGLR LIADLEGCR L SPYQCSAGVW T QGIGHTAGV IPGKAIDEHK AAMDLVDDVR 60  
 RTERGMAACL PDTLSQQTYD AAI AFAFNVG VSAACHSTLV ALLQQRQRQ ACDQLPRWVY 120  
 VN GKKKNKGL E QRAMERALC LQGIAS 146

SEQ ID NO: 37 moltype = AA length = 162  
 FEATURE Location/Qualifiers  
 source 1..162  
 mol\_type = protein  
 organism = *Galerina marginata*

SEQUENCE: 37  
 PEVNAATISL IKKFEGFVSK PAPDPIGLPT VG YGHLCKTT GCAEVPFSSFP LTEAEATTLL 60  
 NTDLKTFTAC ITKDISSSKIK LNDNQYGALS SWAFNEGCN VGSSTLIARL NAGDNPNTVA 120  
 A QELPKWDIA GGMVLQGLVN RRVAEVKLFQ TPSSVIAHPP QC 162

SEQ ID NO: 38 moltype = AA length = 161  
 FEATURE Location/Qualifiers  
 source 1..161  
 mol\_type = protein  
 organism = *Galerina marginata*

SEQUENCE: 38  
 TPPNAATVSL IKSFEGFVAS PKPDPIGLPT AGPGHKCVKA NCAEVPFSSFP LSQDTATQLL 60  
 QSDAQKFVTC LHGLISKVVT LNDNQFGALT SFAFNLCGCA VQSSTLLKRL NN GEDPNTVA 120  
 AAEIPRFNKA GGKVSSGLAR RRAAEVQLFQ TPSSTTAQPL C 161

SEQ ID NO: 39 moltype = AA length = 163  
 FEATURE Location/Qualifiers  
 source 1..163  
 mol\_type = protein  
 organism = *Agaricus bisporus*

SEQUENCE: 39  
 PRVNSATISL IKEFEGFVKS PSPDPIGLPT VGF GHLCKSK GCAEVPYKFP LTEANAGKLL 60  
 QTDI KSFTKC VSDNIKDAVK LNANQFGALS SWAFNVGCN VKASALVARL NRGEKPNTVA 120  
 AEELPKWRLA GGKV LKGLVR RRAAEVQLFK TASSAIAHPP KCS 163

SEQ ID NO: 40 moltype = AA length = 167  
 FEATURE Location/Qualifiers  
 source 1..167  
 mol\_type = protein  
 organism = *Trichosporon asahii*

SEQUENCE: 40  
 VNADGIALIQ EFESFQPRPY KDPKG LWTVG YGHLCANGK DSTCSGTGFK YPLTLATAGE 60  
 LLKKDIPRYT KCLRDNLNED KVKL NKNQWA ALSFV FN LGCFQ RSDLM ARLNKGEDVN 120  
 TVIAAEFPRW NKADGA VL TG LVRRRAAEVA LAKKTS HGTS KAFPTCT 167

SEQ ID NO: 41 moltype = AA length = 164  
 FEATURE Location/Qualifiers  
 source 1..164  
 mol\_type = protein  
 organism = *Trichosporon asahii*

SEQUENCE: 41  
 CPSINDAGIA LIKEFEGFFK NPYKD PVGLW TVGYGHLCAN GGKDSSCSGT GF KYPLTEAT 60  
 ATELLKKDLP SYTSCP PKYL TSGAKLNK NQ YAALT SFTFN LGCGV LKDF A GR LNKG EDAS 120  
 TVFAQEFPKY VHAGGNV LQG LVRRRNAEVA LAKKAG STEA WP KC 164

SEQ ID NO: 42 moltype = AA length = 160  
 FEATURE Location/Qualifiers  
 source 1..160  
 mol\_type = protein  
 organism = *Trichosporon asahii*

SEQUENCE: 42  
 INDAGVELIK SFEGCVANPY QDAGGKWTVG YGHLC SGGD STCS DTGF SY PLTE ETATEL 60  
 FKRD LPN VS CMPQ YLT DGA KLN KNQ WAAL TSFC YN LGGC IL SD FAG RL AGED ANVIG 120  
 EEF PKY TLAE GVELEG TGAG GDEEVALA QS PGSTEAWP NC 160

SEQ ID NO: 43 moltype = AA length = 168

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FEATURE	Location/Qualifiers
source	1..168
	mol_type = protein
	organism = Trichosporon asahii
SEQUENCE: 43	
VNADGITALIQ EFESFQPRPY KDPKGLWTVG YGHLCANGKK DSTCSTGFK YPLTLATAGE	60
LLKKDIPRYT KCLRDNLNED KVKLKNQWA ALSSFVFNLG CGNFQRSDLR ARLNKGEDVN	120
TVIAAEFFRW NKADGAVLTG LVRRRAAEVA LAKKTSHGTS KAFPTAPK	168
SEQ ID NO: 44	moltype = AA length = 131
FEATURE	Location/Qualifiers
source	1..131
	mol_type = protein
	organism = Rhizophagus irregularis
SEQUENCE: 44	
MSLFKENFYD DPVGITTIGY GHNCKANKDS DKIKAPISIK EAEELLRKDL VKFEDYVVKQ	60
VPELNSNQFS AVVSFAYNLG CDKLRSTSILL KKLKAGDTQG ASEEFGRWVH AKRKRLPGLV	120
RRREDERQLF L	131
SEQ ID NO: 45	moltype = AA length = 141
FEATURE	Location/Qualifiers
source	1..141
	mol_type = protein
	organism = Rhizophagus irregularis
SEQUENCE: 45	
VNKEGLLDIE GPEGFYPNFX KDPVGIKTIG YGHACHVHDC SKIQAPISLA EGETLLKSDL	60
AVFESCVESL TRTNLNPDQF SALVSFTFNL GCGAYQKSTL RRKLNAGDTK GASLEFAKWV	120
YGGGKKLPGL VRRRNAERDL F	141
SEQ ID NO: 46	moltype = AA length = 105
FEATURE	Location/Qualifiers
source	1..105
	mol_type = protein
	organism = Rhizophagus irregularis
SEQUENCE: 46	
INKAGLKLK KPEGFRSRFY VDKGIITIGY GHACHVYDCS KIHPPISRAK GEALLKKDLV	60
VFEKCVDSL QIKLNSNQFS ALVSFTYNLC CEAYRRSTLR RKLNA	105
SEQ ID NO: 47	moltype = AA length = 155
FEATURE	Location/Qualifiers
source	1..155
	mol_type = protein
	organism = Coniosporium apollinis
SEQUENCE: 47	
PTVNDGTIIM LKELEGFSAT PYLDVNKAII GYGHQCNEPE CAGLSPPITE VEATEMLQD	60
LRTYRDCLTA KLGSVTLNEN QYGALASWTF NVGCGNMRRGS TLVIRLLAGE DPNTVAADEL	120
PWRLVNGQV SQALVRRREK EIALFKTESG VQVLP	155
SEQ ID NO: 48	moltype = AA length = 114
FEATURE	Location/Qualifiers
source	1..114
	mol_type = protein
	organism = Rhizophagus irregularis
SEQUENCE: 48	
TIGYGHNCEA NNDGDKINAP ISIAQAEDLL RRDLSMYENY VNSQVPGLNS NQFSALVSFT	60
FNVGCGNLGS STLLKKLKAG DTQGAANEGF RWVYANKKKL PGLIRRREAEE KRLF	114
SEQ ID NO: 49	moltype = AA length = 163
FEATURE	Location/Qualifiers
source	1..163
	mol_type = protein
	organism = Penicillium roqueforti
SEQUENCE: 49	
GPAVNTNGLD LIKSFESFQA NVYDDGYGNP TIGYGHLCSD STCSEVTFSK PLTEDTASQL	60
LAKDLVTYQN GVTNALATAV TLNDNQYAL VSWTFNVGNG NMQSSLVSR MNAGENVETV	120
ASEELPKWNK ANGAVVAGLT RRRADEVKLF EEASQTKALP VGC	163
SEQ ID NO: 50	moltype = AA length = 163
FEATURE	Location/Qualifiers
source	1..163
	mol_type = protein
	organism = Aspergillus ruber
SEQUENCE: 50	
GPPANIPTLD LLKGFETMQP DPYDDGFGNP TIGYGHLCTN KACSDVFFSK PLSEDSATRL	60
LQGDLTSAQD AVTNALADPV TLNDNQY GAL ISWTFNVGNG NMQSSLVSR MNAGEEIVAV	120
ANNEPLWNLK ANGKVVNGLV RRRKAEVDLF NTPSNFGALP VPC	163

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SEQ ID NO: 51      moltype = AA  length = 162
FEATURE          Location/Qualifiers
source           1..162
mol_type = protein
organism = Pyronema omphalodes

SEQUENCE: 51
INATATISLIK SFEQGVPSPK PDPPIGLPTVG YGHLCKKKGC AEVKYKFPLT EATAAQLLQD 60
DAYTFRKCVAAIKDSVTLT DNQY GALVSW AFNV GCGVQ TSTLVKRLNR GENKNIVASQ 120
ELIKWNKAGN PP KPMNGLTR RR NAEIALFK KASSVQA HPP KC 162

SEQ ID NO: 52      moltype = AA  length = 161
FEATURE          Location/Qualifiers
source           1..161
mol_type = protein
organism = Pyronema omphalodes

SEQUENCE: 52
PPVNTATVNL IKFEGFVPS PAPDPIGLPT VGYGHLCRKT NCAEVYPYPFP LTTTAAALL 60
QTDLKTYTKC ISDYIVDSVR LNDNQY GALS SWAFNV GCGN AKTSTLISRL NAGQNPNTVA 120
SEELPKWNKA GGSVLPGLTR RRAAEVTLFK TASTKIAHPA C 161

SEQ ID NO: 53      moltype = AA  length = 144
FEATURE          Location/Qualifiers
source           1..144
mol_type = protein
organism = Trichophyton interdigitale

SEQUENCE: 53
PDVNDETIAL IKHFE GFVPR PAPDPIGLPT VGYGHLCRKT GCSEVPFPFP LTEETATELL 60
MQDVVKSPQQS ITLSTTDQVV LNANQY GALV SWAYNVGGSA AKKSSLISRL NQGQDVDAVI 120
REELPLWNKA GGHVLPGLVR RRAA 144

SEQ ID NO: 54      moltype = AA  length = 134
FEATURE          Location/Qualifiers
source           1..134
mol_type = protein
organism = Rhizophagus irregularis

SEQUENCE: 54
INKEGLALIE RPEGFSPNPFY KDPVGIKTIG YGHAYHVND SKIRPPISRA EGEALLKKDL 60
ARFEKCVESL TRVKLNSNQF SALCSFTFN GCGAYQKSTL RRKLNAGDTK GASLEYRKWV 120
YGGGKLPGL VKRR 134

SEQ ID NO: 55      moltype = AA  length = 141
FEATURE          Location/Qualifiers
source           1..141
mol_type = protein
organism = Rhizophagus irregularis

SEQUENCE: 55
VNKEGLLDIE GPEGFYPNPFY KDPVGIKTIG YGHACHVHD SKIQAPISLA EG ETLKSDL 60
AVFESCVESL TRTNLNPQDF SALVSFTFN GCGAYQKSTL RRKLNAGDTK GASLEFAKWN 120
YGGGKKLPGL VRRRNAERDL F 141

SEQ ID NO: 56      moltype = AA  length = 163
FEATURE          Location/Qualifiers
source           1..163
mol_type = protein
organism = Metarhizium anisopliae

SEQUENCE: 56
KTLNKAGTDL ITRWEGFVDR PQDPPIGLPT VGYGHLCQKK SCAEVKYTFP LTKATALQLL 60
NDDLPSYTKC LGKVLDAGKV KLNENQWAAL TSWVFNVGCG AAQSSSLVKR LNRGENANTV 120
ASEELPKWKM GGGRVLPGLV KRADEVALF KMASSRSAAF QCQ 163

SEQ ID NO: 57      moltype = AA  length = 132
FEATURE          Location/Qualifiers
source           1..132
mol_type = protein
organism = Beauveria bassiana

SEQUENCE: 57
MLTDLEGVRY TPYYDVAGVL TVCYGHTGAD IIKTKTYSAT ECQAMLDKDL VP FARSVERS 60
VKVPTTTEYQK AALISFSYNV GVTAFERS SSL LRQLNAGNYQ AACDGLRQWT YAGGKQWKGL 120
MNRRDIEREV CM 132

SEQ ID NO: 58      moltype = AA  length = 137
FEATURE          Location/Qualifiers
source           1..137
mol_type = protein
organism = Beauveria bassiana

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SEQUENCE: 58
GVDLIKSFEG LRLAKYKDAV GKWTIGYGLH ILATENYDRP LTEQEAEINLL RSDLALTERG 60
VYRQVSMALN QNQFDALVAF AFNVGLGNLQ NSTLLRLLNQ GNYSAADEF LRWNKAGGNV 120
LAGLTRRREA ERKLFLS 137

SEQ ID NO: 59      moltype = AA length = 138
FEATURE           Location/Qualifiers
source            1..138
                  mol_type = protein
                  organism = Beauveria bassiana

SEQUENCE: 59
LILPELEGVSY TPYYDVAGVL TVCYGHTGQD IIPDKTYTLS ECRRWLDQDL RPAAQVVSR 60
VTVPVSEYQR AALISFTYNV GTAAFLRSSV LRTLNAGDYE QACAGLKWI WAGGKPWQGL 120
INRREVEYQL CTWPEPEK 138

SEQ ID NO: 60      moltype = AA length = 163
FEATURE           Location/Qualifiers
source            1..163
                  mol_type = protein
                  organism = Metarhizium guizhouense

SEQUENCE: 60
KTLINKAGTDL VTRWEGFVDR PKPDPIGLPT VGYGHLCKKK SCAEVKYTFPP LTKTTALQL 60
NDDLPNTYTKC LGEVLDASKV KLNENQWAAL TSWVFNVGCG AAQSSSLVVR LNHGENANTV 120
ASEELPKWKM GGGRVLPGLV KRRADEVALF KIASSRSAFP QCQ 163

SEQ ID NO: 61      moltype = AA length = 163
FEATURE           Location/Qualifiers
source            1..163
                  mol_type = protein
                  organism = Metarhizium majus

SEQUENCE: 61
KTLINKAGTDL VTRWEGFVDR PKPDPIGLPT VGYGHLCKKK SCAEVKYTFPP LTKATALQL 60
NDDLPNTYTKC LGEVLDASKV KLNENQWAAL TSWVFNVGCG AAQSSSLVVR LNHGENANTV 120
ASEELPKWRM GGGKVLPGLV KRRADEVALF KIASSRSAFP QCQ 163

SEQ ID NO: 62      moltype = AA length = 163
FEATURE           Location/Qualifiers
source            1..163
                  mol_type = protein
                  organism = Metarhizium brunneum

SEQUENCE: 62
KTLINKAGTDL ITRWEGFVDR PKPDPIGLPT VGYGHLCKKK GCAEVKYTFPP LTKATALQL 60
NDDLPNTYTKC LGRALDAGKV KLNENQWAAL TSWVFNVGCG AAQSSSLVVR LNRGENANTV 120
ASEELPKWKM GGGRVLPGLV KRRADEVGLF KIASSRSAFP QCQ 163

SEQ ID NO: 63      moltype = AA length = 163
FEATURE           Location/Qualifiers
source            1..163
                  mol_type = protein
                  organism = Magnaporthe oryzae

SEQUENCE: 63
PKLNQASLDL VKEFEGWFDPD IYLDPVLGPT VGYGHLCSNP TCSEVPYPIP LSVANGEALL 60
QSDLGIARRC LSADLVDSVV LNPNQYGLAV SWFVNMGCGA QKSSTLTARL NAGEDKSVVA 120
RQELPRWWYVA GGQVLNGLVR RRAEVALFD TPAEGVAHPP RPC 163

SEQ ID NO: 64      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
                  mol_type = protein
                  organism = Coprinopsis cinerea

SEQUENCE: 64
TTVNARTVRE IKSSEGFVKS PAPDPIGLPT VGYGHLCKTK GCAEVPYKFP LTDAQATSLL 60
KSDLKTFQNC ISKDLRDTVR LNENQYGLAV SWAFNVGCRA TGSSTLIARL NRGDNPAKVA 120
EEELPKWNKA NGKVLQGLVN RRKREIAMFK TPSKVIHHPP KC 162

SEQ ID NO: 65      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
                  mol_type = protein
                  organism = Coprinopsis cinerea

SEQUENCE: 65
TNVNSKTVEH IKQWEGFVKS PAPDPIGLPT VGYGHLCKTK GCSEVPYKFP LTEAQATSLL 60
KTDLKTFQNC ISSQLKDSVR LNANQYGLAV SWAFNVGCGR TSGSALISRL NKGESPNTVA 120
SQELPKWNKA GGKVLQGLVN RRKAEVTLFK TSSSVIHHPP TC 162

SEQ ID NO: 66      moltype = AA length = 162

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FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Coprinopsis cinerea
SEQUENCE: 66
SPVNSRTVQE IKNSEGFVRS PAPDPIGLPT VGYGHLCKNK GCSEVPYSSFP LTEAQATSSL 60
MTDLKTFQKC ISDQINDSIR LNENQY GALV SWAFNVGCGN TASSALISRL NKGESPNKVA 120
EEELPRWKYI GGQVLPGLVA RRNRREIALFK TAASSVVGHPHRC 162

SEQ ID NO: 67      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Chaetomium globosum
SEQUENCE: 67
PKSNSATVDSL IAKSEGFRAN VYNDPAGHPT VGYGHLCTKA KCAEIKYKIP LSTTDGKKLL 60
ADDMKKFEKC ITAMLNSKAK LNLNQY GALV SWSFNVGCGA AQGSQVLKRL NKGENVNTVL 120
SNELPKWVNA GGKKLPGGLVT RRNRNEIALAK KSGSGAALPV KC 162

SEQ ID NO: 68      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Nectria haematococca
SEQUENCE: 68
PKSNQATVNL IASFEGFRAN IYKDAAGYPT VGYGHLCSN KCTDVKYSIP LSQANGKKLL 60
ASDMAKFEKC ITAMVKSIVK LNKNQY GALV SWSFNNCGGA AKTSTLIKRL NKGEAPNTVI 120
SQELPKWVYA GGKKLNGLVR RRKAEVNALAK KATTEKALPK SC 162

SEQ ID NO: 69      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Nectria haematococca
SEQUENCE: 69
PPVNQATLISL VEEFEGFRAD VYIDATGNPT VGYGHLCKQS GCSEIPYPPIP LSQADGQKLL 60
QDDIKVAAQC ITLDTTSAVV LNANQY GALV SWAFNVGCGA SGDSTLIIRR NNGEDANTVA 120
SEELPKWNKG NGQPIAGLTR RRAAEVELFK APTDVGALPV GC 162

SEQ ID NO: 70      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Nectria haematococca
SEQUENCE: 70
PSSNQATVDSL IGEFEGFVPH IYKDAAGYPT VGYGHLCSNS KCTDVKYPIP LSKTNGKKLL 60
ADDMRKFEKC IAKMVSSKVLT LNKNFEGALV SWSFNVGCGA AEGSQLIKRL NKGEKPNTVI 120
SGELPKWVYA GKRKLPGGLVR RRNAEIALAK KATSEKALPV KC 162

SEQ ID NO: 71      moltype = AA length = 155
FEATURE          Location/Qualifiers
source           1..155
                  mol_type = protein
                  organism = Verticillium alfalfae
SEQUENCE: 71
PNVNAATISL ITEFEGWYPN IYIDPVLPT VGYGHLCADS SCSDVRYPIP LSRANGEQLL 60
RDDIAGFQNC ITLQTASSVV LNANQY GALV SWAFNVGCGA TKTSTLIQRL NAGGNPNTVA 120
AEELPKWNRG GGQVLPGLTR RRAAEVALHR TATSA 155

SEQ ID NO: 72      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Thielavia terrestris
SEQUENCE: 72
PKSNQATVNL IAEYEGFVDH VYTDATGHPT VGYGHLCSNS KCSDVPYHIP LSQADGKKLL 60
ADDMKKYEKC ITAMLTSKAV VNLNQY GALV SWAFNMCGCA AESSTLVKRL NAGENVNTVL 120
SQELPKWVHG DGKVLPGGLVR RRNAEIALAK TPTSDKALPV KC 162

SEQ ID NO: 73      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Thielavia heterothallica
SEQUENCE: 73
PKSNSATVDSL IAKSEGFRSK IYTDATGHAT VGYGHMCTKP KCAEVKYKIP LSTADGKKLL 60

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AEDMRKFEKC ITNMLNSKAV LNYNQFGALV SWSFNVGCGA AQSSQLVKRL NKGENVNKL	120
SEELPKWVHG GGKVLPGGLVT RRKNEVALAK KPGSSKALPV KC	162
SEQ ID NO: 74	moltype = AA length = 162
FEATURE	Location/Qualifiers
source	1..162
	mol_type = protein
	organism = Coprinopsis cinerea
SEQUENCE: 74	
PVNNTTRTLDL IKLSEGFVAS PEPDPIGLPT VGYGHLCQRT GCTEVYPYSFP LTQAQAHALL	60
ISDLRKYQNC IARDIVDSVR LNNDQYQALV SWAFNVGCTN TASSTLIRRL NAGENPNTVA	120
EQELPRWNMA GGQVLPGLVT RRAREVTLFK TASSVIAHPP PC	162
SEQ ID NO: 75	moltype = AA length = 162
FEATURE	Location/Qualifiers
source	1..162
	mol_type = protein
	organism = Fusarium oxysporum
SEQUENCE: 75	
PSSNQATVDSL IGEFEGFVPH IYKDAAGYPT VGYGHLCNS KCTDVKYAIP LSKANGKKLL	60
ADDMRKFEKC IAKMVSSKVT LNKNQFGALV SWSFNLGCGA AEGSQLLKRL NKGEKPNTVI	120
SQELPKWVYA GGRKLPGLVR RRNAEVALAK KATSEKALPV KC	162
SEQ ID NO: 76	moltype = AA length = 162
FEATURE	Location/Qualifiers
source	1..162
	mol_type = protein
	organism = Metarhizium acridum
SEQUENCE: 76	
PKANEDTVKF ISGFEGFWSDH VYRDPGPQHL ETLGYGHLCCK KPNCAEVKYP FPPLSKADGL	60
KLLSDDMSVA ENCIYKDVPN KVALNANQYG ALVSWAFNVG CGNVASSRLI RRLNAGEDPN	120
TVAAQELPW NKAGGKVLPG LTRRRNAEVE LFKTPTNPDA LP	162
SEQ ID NO: 77	moltype = AA length = 162
FEATURE	Location/Qualifiers
source	1..162
	mol_type = protein
	organism = Metarhizium robertsii
SEQUENCE: 77	
PKANEATVKF ISTFEGWYDH VYPDPGPQHL ETLGYGHLCK KPNCAEVKYP FPPLSKADGL	60
KLLSDDMSVA ENCIYQDTSA KVTLNANQYG ALVSWAFNVG CGNVASSRLI RRLNAGEDPN	120
TVAAQELPW NRAGGKVLPG LTRRRNAEVE LFKTPTNPDA LP	162
SEQ ID NO: 78	moltype = AA length = 162
FEATURE	Location/Qualifiers
source	1..162
	mol_type = protein
	organism = Fusarium oxysporum
SEQUENCE: 78	
PSSNQATVDSL IGEFEGFVPH IYKDAAGYPT VGYGHLCNS KCTDVKYPPIP LSKANGKKLL	60
ADDMRKFEKC IAKMVSSKVT LNKNQFGALV SWSFNLGCGA AEGSQLLKRL NKGEKPNTVI	120
SQELPKWVYA GGRKLPGLVR RRNAEVALAK KATSEKALPV KC	162
SEQ ID NO: 79	moltype = AA length = 161
FEATURE	Location/Qualifiers
source	1..161
	mol_type = protein
	organism = Fusarium oxysporum
SEQUENCE: 79	
PKSNAATVKL ISSFEGFRPD VYNDPTGNPT VGYGHLCDAP QCSEVKYPVP LSVANGKKLL	60
ADDMKEFEVC ITAMLNSKAR LNRNQYQALI SWAFNMGCNN AESTLVGRLN NGEDPNTVIS	120
QELPQWVYAS QORLPGLVHR RNAEIELAQK PTRRSALPKR C	161
SEQ ID NO: 80	moltype = AA length = 162
FEATURE	Location/Qualifiers
source	1..162
	mol_type = protein
	organism = Chaetomium thermophilum
SEQUENCE: 80	
PKSNQATVDSL IAEFEGFRAN IYTDAAGYAT VGYGHKCQKA KCAEVKYKIP LSKADGKKLL	60
ADDMRSFEVC ITNMLNSKAK LNYNQFGALV SWSFNVGCGA AKSSTLIKRL NNGENVNKL	120
SEELPKWNKA GGKVLQGLVR RRAAEVALAK KSGSSQALPV KC	162
SEQ ID NO: 81	moltype = AA length = 154
FEATURE	Location/Qualifiers
source	1..154

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mol_type = protein
organism = Verticillium dahliae
SEQUENCE: 81
PNNQAATISL ITEFEGWYPN IYIDPVGLPT VGYGHLCADS SCSDVRYPPIP LSRANGEQLL 60
RDDIAGFQNC ITLQTASSVV LNKNQY GALV SWAFNVGCGA TRTSTLIQRL NAGGDPNTVA 120
AEELPKWNRG GGQVLPGGLTR RRAAEVALHR TATS 154

SEQ ID NO: 82      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 82
PSSNQATVDL IGEFEGFVPH IYKDAAGYPT VGYGHLCSNS KCTDVKYAPIP LSKANGKKLL 60
ADDMRKFEKC IAKMISSKVT LNKNQY GALV SWSFNLGCGA AEGSQLLKRL NKGEKPNTVI 120
SQELPKWVYA GGRKLPGGLVR RRNAEVALAK KATSEKALPV KC 162

SEQ ID NO: 83      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 83
PSSNQATVDL IGEFEGFVPH IYKDAAGYPT VGYGHLCSNS KCTDVKYAPIP LSKANGKKLL 60
ADDMRKFEKC IAKMVSSKV LNKNQY GALV SWSFNLGCGA AEGSQLLKRL NKGEKPNTVI 120
SQELPKWVYA GGRKLPGGLVR RRNAEVALAK KATSEKALPV KC 162

SEQ ID NO: 84      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 84
PKSNAATVNL IASFKGFRPD VYNDPTGNPT VGYGHLCDAP QCSEAKYPIP LSIVNGKKLL 60
ADGMKEFEIC ITAMLN SKAN LNRNQY GALI SWAFNMGCN ADSSTLVGRL NNGEDPNTVI 120
SQELPKWVYA SGQR LPGLVR RRNAEIELAQ KPTRRRALPK RC 162

SEQ ID NO: 85      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 85
PSSNQATVDL IGEFEGFVPH IYKDAAGYPT VGYGHLCSNS KCTDVKYAPIP LSKANGKKLL 60
ADDMRKFEKC IAKMVSSKV LNKNQY GALV SWSFNLGCGA AEGSQLLKRL NKGEKPNTVI 120
SQELPKWVYA GGRKLPGGLVR RRNAEVALAK KATSEKALPV KC 162

SEQ ID NO: 86      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 86
PKSNAATVNL IASFEGFRPD VYNDPTGNPT VGYGHLCDAP QCSEVKYPVP LSVANGKKLL 60
ADDMKEFEVC ITAMLN SKAN LNRNQY GALI SWAFNMGCN AESSIONVGRL NNGEDPN SVI 120
SQELPKWVYA SGQR LPGLVL RRNAEIELAQ KPTRRRALPK RC 162

SEQ ID NO: 87      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 87
PSSNQATVDL IGEFEGFVPH IYKDAAGYPT VGYGHLCSNS KCTDVKYAPIP LSKANGKKLL 60
ADDMRKFEKC IAKMVSSKV LNKNQY GALV SWSFNLGCGA AEGSQLLKRL NKGEKPNTVI 120
SQELPKWVYA GGRKLPGGLVR RRNAEVALAK KATSEKALPV KC 162

SEQ ID NO: 88      moltype = AA length = 162
FEATURE           Location/Qualifiers
source            1..162
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 88
PSSNQATVDL IGEFEGFVPH IYKDAAGYPT VGYGHLCSNS KCTDVKYAPIP LSKANGKKLL 60
ADDMRKFEKC IAQMVS SKVT LNKNQY GALV SWSFNLGCGA AEGSQLLKRL NKGEKPNTVI 120
SQELPKWVYA GGRKLPGGLVR RRNAEVALAK KATSEKALPV KC 162

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SEQ ID NO: 89      moltype = AA length = 126
FEATURE          Location/Qualifiers
source           1..126
                  mol_type = protein
                  organism = Fusarium oxysporum
SEQUENCE: 89
PKSNAATINL IASFEGFRPD VYNDPTGNPT VGYGHLCDAP QCSEVKYPPIP LSIVNGKLL 60
ADGMKEFEIC ITAMLNSKAN LNRNQYGALI SWAFNMGCN ADSSTLVGRL NNGEDPNIVI 120
SQELPQ          126

SEQ ID NO: 90      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Gibberella moniliformis
SEQUENCE: 90
PKSNAATVNL IASFEGFRPD VYNDPTGNPT VGYGHLCDAP QCSEVKYPPIP LSVVNGKLL 60
ADDMKEFEVC ITAMLNSKAK LNRNQYGALI SWAFNMGCN AESSTLIGRL NNCEDPNTVI 120
SQELPQWEYA SGQRRLPGLLR RRNAEIELAQ KPTRRRRALPK RC          162

SEQ ID NO: 91      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Fusarium oxysporum
SEQUENCE: 91
PSSNQATVDL IGEFEGFVPH IYKDAAGYPT VGYGHLCNS KCTDVKYPPIP LSKANGKLL 60
ADDMRKFEKC IAKMVSSKVT LNKNQFGALV SWSFNLGCGA AEGSQLKRL NKGEKPNTVI 120
SQELPKWVYA GGRKLPGGLR RRNAEVALAK KATSEKALPV KC          162

SEQ ID NO: 92      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Fusarium oxysporum
SEQUENCE: 92
PKSNAATVNL IASFEGFRPD VYNDPTGNPT VGYGHQCDAP QCSEVKYPVP LSVANGKLL 60
ADDMKEFEVC ITAMLNSKAR LNRNQYGALI SWAFNMGCN GESSTLVGRL KNGEDPNTVI 120
SQELPQWVYA SGQRRLPGLVH RRNAEIELAQ KPTRRSALPK RC          162

SEQ ID NO: 93      moltype = AA length = 161
FEATURE          Location/Qualifiers
source           1..161
                  mol_type = protein
                  organism = Fusarium oxysporum
SEQUENCE: 93
PKSNAATVKL ISSFEGFRPD VYNDPTGNPT VGYGHLCDAP QCSEVKYPVP LSVANGKLL 60
ADDMKEFEVC ITAMLNSKAR LNRNQYGALI SWAFNMGCN AESTLVGRLN NGEDPNTVIS 120
QELPQWVYAS GQRRLPGLVHR RNAEIELAQ PTRRSALPK C          161

SEQ ID NO: 94      moltype = AA length = 139
FEATURE          Location/Qualifiers
source           1..139
                  mol_type = protein
                  organism = Fusarium oxysporum
SEQUENCE: 94
PKSNVATINL IASFEGFRPD FYNDPTGNPT VGYGHLCDAP QCSEVKYPPIP LSIVNGKLL 60
ADGMKEFEIC ITAMLNSKAN LNRNQYGALI SWAFNMGCN ANSSTLVGRL NNEEDPNTVI 120
SQELPQWVNV SGQRRLPGLV 139

SEQ ID NO: 95      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Fusarium oxysporum
SEQUENCE: 95
PKSNAATVNL VASFEGFKPD VYNDPTGNPT VGYGHLCDAP QCSEVRYPVP LSVANGKLL 60
ADDMKGFAVC ISAMLN SKAR LNRNQYGALI SWAFNMGCN AESSTLIGRL NNWEDPNTVI 120
SQELPRWVYA SGKRRLPGLVR RRNAEIELAQ KPTRRRRALPK RC          162

SEQ ID NO: 96      moltype = AA length = 162
FEATURE          Location/Qualifiers
source           1..162
                  mol_type = protein
                  organism = Gibberella fujikuroi

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SEQUENCE: 96  
 PKSNAATVNL IASFEGFRPD VYSDPTGNPT VGYGHLCADAP QCSEVKYPIP LSVANGKLL 60  
 VDDMKDFEVC LTAMLNSKAK LNRNQYGALI SWAFNMGCQN AQSSLVGRN NNGEDPNTVI 120  
 SQELPHWVYA SGQRPLPGLVR RRNAEIELAQ KPTRRRALPK RC 162

SEQ ID NO: 97            moltype = AA length = 145  
 FEATURE                Location/Qualifiers  
 source                1..145  
 mol\_type = protein  
 organism = Glarea lozoyensis

SEQUENCE: 97  
 PKVNTATLKL IEGFEGWSAT AYKDPDGNP TIGYGHLCSSA SCKEIKYSIP LSRAEGDSL 60  
 QDDLAVERKC IAKQIKDSIK LNANQFGALV SWAFNVGCGN SGDSTLIRRL NAGEAPNTVA 120  
 AQELPKWNRG KNGVLPGLTR RRNAE 145

SEQ ID NO: 98            moltype = AA length = 160  
 FEATURE                Location/Qualifiers  
 source                1..160  
 mol\_type = protein  
 organism = Coniosporium apollinis

SEQUENCE: 98  
 PDVNAATVAL IKEFEGFVRS PAPDPIGLPT VGFGLCCTA GCAEVPYKFP LTEAQAAALL 60  
 QTDLKTYEK C LADKVADSVR LNDNQYGALV SWTFNVGCGN MGSSTLVRL NAGEAPNTVA 120  
 AQELPKWNKA GGNVLAGLTR RRAAEVQLFQ TASGTQALPS 160

SEQ ID NO: 99            moltype = AA length = 162  
 FEATURE                Location/Qualifiers  
 source                1..162  
 mol\_type = protein  
 organism = Endocarpon pusillum

SEQUENCE: 99  
 PDVNAATVAL IKEFEGFVKS PAPDPIGLPT VGYGHLCKTN GCSEVPYPFF LSEAQAALL 60  
 QTDLKSYEKC LADKVSDSVK LSDNQYGALV SWTFNVGCGN MGGSTLVTRL NNGESPNTVA 120  
 AQELPKWNKA GGSALAGLTR RRAAEVQLFQ TASGTQALPA KC 162

SEQ ID NO: 100            moltype = AA length = 105  
 FEATURE                Location/Qualifiers  
 source                1..105  
 mol\_type = protein  
 organism = Fusarium oxysporum

SEQUENCE: 100  
 DPTGNPTVGY GHLCDAAQCS EVKYPIPLSI VNGKKLLADG MKEFEICNPA MLNSKANLNR 60  
 NQY GALISWA FNMGRGNADS STLVRNLNN EDPNTVISQE LPQWV 105

SEQ ID NO: 101            moltype = AA length = 150  
 FEATURE                Location/Qualifiers  
 source                1..150  
 mol\_type = protein  
 organism = Stachybotrys chartarum

SEQUENCE: 101  
 PTINSATVSL IQEFEWSPT IYLDPSGYPT VGYGHLCANS RCTDVYPPIP LSTANGNLL 60  
 QSDMLVARRC IAQDVNVRLN ANQY GALVSW AFNVGCGASG SSSLVRLNA GENPNTVAEE 120  
 ELP RWVNNSGG VQLPGLVRRR NAEVALFRTA 150

SEQ ID NO: 102            moltype = AA length = 160  
 FEATURE                Location/Qualifiers  
 source                1..160  
 mol\_type = protein  
 organism = Acremonium chrysogenum

SEQUENCE: 102  
 PKNKATVDSL ISEFEGFRAD IYIDATGHPT VGYGHLCSDK KCSDVSYPPIP LSKANGKLL 60  
 AKDMRRFEKC ITNMVDAKVN KNQY GALVSW SFNVGCGAAQ GSQLVKRLNK GQKVNKLSE 120  
 ELP KWVHGGG QVL PGLVRRR KAEIALAKKK TDAKALPPC 160

SEQ ID NO: 103            moltype = AA length = 150  
 FEATURE                Location/Qualifiers  
 source                1..150  
 mol\_type = protein  
 organism = Acremonium chrysogenum

SEQUENCE: 103  
 PEVNQPALNL VQQFEDFRAT IYKDPAGHPA VGYGHLCSDS ACSDVPTIP LSYTDAERLL 60  
 RDDLADCTN DTGNNVVLA NQY GALVSWA FNVCENSGF SALIERLNMG EDPTSVATDE 120  
 LPRWNMIGDE VVPAFERRA AEVDLFLAPS 150

SEQ ID NO: 104            moltype = AA length = 155  
 FEATURE                Location/Qualifiers

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source          1..155
               mol_type = protein
               organism = Acremonium chrysogenum

SEQUENCE: 104
PAANAATVSL VAEFEGFSPD IYDDPSGYPT VGYGHLCGDP SCSEVPYPPIP LSEEDGRKLL 60
ASDMAVAQNC ITMQTAESVV LNNDQY GALV SWAFNVGCGN SGSSTLISRL NAGEDPNTVA 120
AEELPKWKYS GGVELPGLVR RRAAEVDLHK TPSDV                         155

SEQ ID NO: 105      moltype = AA length = 157
FEATURE          Location/Qualifiers
source           1..157
               mol_type = protein
               organism = Metarhizium anisopliae

SEQUENCE: 105
PKANEATVKF ISTFEGWYDH VYPDGPQHL ETLGYGHLC KPNCAEVKYP FPPLSKADGL 60
KLLSDDMSVA ENCIYQDTSA KVTLNANQY ALVSWAFNVG CGNVASSRLI RRLNAGEDPD 120
TVAAQELPOW NRAGGKVLPG LTRRRNAEVE LFKPTPTN                         157

SEQ ID NO: 106      moltype = AA length = 150
FEATURE          Location/Qualifiers
source           1..150
               mol_type = protein
               organism = Stachybotrys chlorohalonata

SEQUENCE: 106
PTTNSATVSL IAEFEGWSST IYLDPSGYPT VGYGHLCANS RCTDVPYPPIP LSTANGNLL 60
QSMDMLVARRC IAQDVNVRNL ANQY GALV AFNVGCGASG SSSLVRLNA GENPNTVAAE 120
ELPRWWNSGG VQLPGLVRRR NAEVALFRTA                                     150

SEQ ID NO: 107      moltype = AA length = 158
FEATURE          Location/Qualifiers
source           1..158
               mol_type = protein
               organism = Pseudogymnoascus pannorum

SEQUENCE: 107
PKSNGATVDL IAEFEGFVPN VYTDATGHAT VGYGHLCQKS KCSEVPYHIP LTKANGKKLL 60
ASDIGVYEKC VTAMLN SKAK VNLNQY GALV SLTFNMGC GA IKSSAI VTRL NKGEKATTVI 120
SSEFPKWWHG GGKVLPG LVR RRKA EVALAK KTAGKALP                         158

SEQ ID NO: 108      moltype = AA length = 158
FEATURE          Location/Qualifiers
source           1..158
               mol_type = protein
               organism = Pseudogymnoascus pannorum

SEQUENCE: 108
PKSNAATVNL IAEFEGFVPH VYTDATGHPT VGYGHLCNS KS DAGYPIP ISKANGKKLL 60
AKDMGKAEC K ITAMVNSKVT LNANEY GALV SLAFNVGCGA MKSSTLVKRL NN GEKASVYY 120
PKEFPKWWHG NGKVLPG LVR RRKA EVALSK KAAGKALP                         158

SEQ ID NO: 109      moltype = AA length = 158
FEATURE          Location/Qualifiers
source           1..158
               mol_type = protein
               organism = Pseudogymnoascus pannorum

SEQUENCE: 109
PKSNAATVDL IAEFEGFVPK VYTDATGHPT VGYGHLCNS KS DAGYPIP LSKANGKKLL 60
AKDMGKAEC K VTAMVNSKVT LNANEY GALV SLAFNVGCGA MQSSSLV KRL NN GEKASVYY 120
PVEFPKWWHG NGKVLPG LVR RRKA EVALSK KAAGKALP                         158

SEQ ID NO: 110      moltype = AA length = 158
FEATURE          Location/Qualifiers
source           1..158
               mol_type = protein
               organism = Pseudogymnoascus pannorum

SEQUENCE: 110
PHSNTATVNL IAEFEGFVPN VYTDATGHPT VGYGHLCNS KCSGIGYPIP LSVANGKKLL 60
AKDMGVAERC ITAMTSKAV LNANQY GALV SLTFNMGC GA IQSSAI KRI NN GEKASVVF 120
PNEFPKWWHG GGVLPGLVR RRNAEIALSK KAADKVLP                         158

SEQ ID NO: 111      moltype = AA length = 158
FEATURE          Location/Qualifiers
source           1..158
               mol_type = protein
               organism = Pseudogymnoascus pannorum

SEQUENCE: 111
PHSNTATVNL IAEFEGFVPN VYTDATGHPT VGYGHLCNS KCSGIGYPIP LSVANGKKLL 60
AKDMGVAEC K ITAMTSKAV LNANEY GALV SLTFNMGC GA IQSSDI KRI NKGEKASVVF 120

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PSEFPKWWHG GGVVLPGLVR RRNAEIALSK KAADKVLP	158
 SEQ ID NO: 112 moltype = AA length = 162	
FEATURE Location/Qualifiers	
source 1..162	
mol_type = protein	
organism = Torrubiella hemipterigena	
 SEQUENCE: 112	
PAVNQATVNL VAEFEGFRAS EYTDATGHPT IGYGHLCTAK GCADVAYPKP LSEADGKKQL 60	
AKDLAVAQNC ITTMTANPVT LNANQY GALV SWAFNVCGGA AKSSTLikel NAGKDARTVI 120	
DTELPKWNKG NGKPIAGLTR RRKAEVDSLH VATSQGALPA KC 162	
 SEQ ID NO: 113 moltype = AA length = 164	
FEATURE Location/Qualifiers	
source 1..164	
mol_type = protein	
organism = Torrubiella hemipterigena	
 SEQUENCE: 113	
PVANAATVVF VSGFEGWRDY VYRD PGNGFQ TLGYGHLCKK PNCAEV PYKF PPLSKADGLK 60	
LlssDMAIAE NCVT KDIKDK IVLNANQYGA LVSWAFNVGC GNVASSSLIR RLNA GENPNV 120	
VAA SELPKWN KDAKGHVLPG LTRRRAAEVK LFQTPTSEHA LPAC 164	
 SEQ ID NO: 114 moltype = AA length = 158	
FEATURE Location/Qualifiers	
source 1..158	
mol_type = protein	
organism = Pseudogymnoascus pannorum	
 SEQUENCE: 114	
PHSNTATVNL IAEFEGFVPN VYTDATGHPT VGYGHLCSNS KCSGIGYPPIP LSVANGKKLL 60	
AKDMGVAERC ITAMTNSKAV LNANQY GALV SLTFNMCGGA IQSSDIKRI NNGEKASVVF 120	
PKEFPRWVHG GGVVLPGLVR RRNAEIALSK KAADKVLP 158	
 SEQ ID NO: 115 moltype = AA length = 158	
FEATURE Location/Qualifiers	
source 1..158	
mol_type = protein	
organism = Pseudogymnoascus pannorum	
 SEQUENCE: 115	
PKSNAATVDL IAEFEGFVPK VYTDATGHPT VGYGHLCSNS KCSDAGYPPIP LSKANGKKLL 60	
AKDMGKAEC K VTAMVNSKVT LNANEY GALV SLAFNVCGA MQSSSLVKRL NNGEKASVY 120	
PVEFPKWWHG NGKVLPG LVR RRNAEVALAK KAAGKALP 158	
 SEQ ID NO: 116 moltype = AA length = 158	
FEATURE Location/Qualifiers	
source 1..158	
mol_type = protein	
organism = Pseudogymnoascus pannorum	
 SEQUENCE: 116	
PKSNAATVDL IAEFEGFVAK VYIDATGHPT VGYGHLCTKS KCAEVGYPPIP LSKANGKKLL 60	
ATDMAKAEC K VTAMLNSKAV LNANQY GALV SLAFNVCGA VQSSSI VTRL NKGEKAATVY 120	
PQEFPKWWHG GGKVLPG LVR RRNAEVALAK KAAGKALP 158	
 SEQ ID NO: 117 moltype = AA length = 158	
FEATURE Location/Qualifiers	
source 1..158	
mol_type = protein	
organism = Pseudogymnoascus pannorum	
 SEQUENCE: 117	
PKSNAATVDL IAEFEGFVAK VYIDATGHPT VGYGHLCTKS KCAEVGYPPIP LSKANGKKLL 60	
ATDMAKAEC K VTAMLNSKAV LNANQY GALV SLAFNVCGA VQSSSI VTRL NKGEKAATVY 120	
PQEFPKWWHG GGKVLPG LVR RRNAEVALAK KAAGKALP 158	
 SEQ ID NO: 118 moltype = AA length = 158	
FEATURE Location/Qualifiers	
source 1..158	
mol_type = protein	
organism = Pseudogymnoascus pannorum	
 SEQUENCE: 118	
PKSNAATVDL IAEFEGFVPN VYTDATGHAT VGYGHLQKS KCSEV PYHIP LTKANGKKLL 60	
ASDIGHVYEKC VTAMLNSKAK LNLNQY GALV SLTFNMCGGA IKSSAI VTRL NKGEKATTVI 120	
SQEFPKWWHG GGKVLPG LVR RRNAEVALAK KTAGKALP 158	
 SEQ ID NO: 119 moltype = AA length = 158	
FEATURE Location/Qualifiers	
source 1..158	
mol_type = protein	

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SEQUENCE: 119          organism = Pseudogymnoascus pannorum
PKSNAATVDSL IAEFEGFVPN VYIDATGHPT VGYGHLCTKS KCAEIGYPPIP LSKANGKKLL 60
AKDIAKFEKC VTAMLKSKAV LNLNQYGLAV SLAFNVGGGA VQSSSIVTRL NKGEKAATVF 120
PQEFPKWWHG NGKVLPLGLVR RRKAEEVALAK KAAGKALP 158

SEQ ID NO: 120          moltype = AA length = 162
FEATURE
source
1..162
mol_type = protein
organism = Pseudogymnoascus pannorum

SEQUENCE: 120          organism = Pseudogymnoascus pannorum
PASNQATIDL IAGSEGFSGD VYTDPTGNPT VGYGHLQDS TCADTGFPPIP LSEEDGKLL 60
AGDMKQFESC ITTMTGDAVT LNLNQYGLAV SWSFNNGCGA AQSSTLISRL NNGEDPNTVI 120
EQELPQWVYG NGQILDGLVK RRQAEIDLAK TPTSDGALPA PC 162

SEQ ID NO: 121          moltype = AA length = 162
FEATURE
source
1..162
mol_type = protein
organism = Metarhizium majus

SEQUENCE: 121          organism = Metarhizium majus
PKANEATVKF ISTFEGWYDH VYPDPGPQHL ETLGYGHLC KPNCAEVKYP FPPLSKADGL 60
KLLSDDMSVA ENCIYQDTNA KVTLNANQYG ALVSWAFNVG CGNVASSRLI RRLNAGEDPN 120
MVAAQELPW NRADGKVLPG LTRRRNAEVE LFKTPTNNDPA LP 162

SEQ ID NO: 122          moltype = AA length = 162
FEATURE
source
1..162
mol_type = protein
organism = Metarhizium guizhouense

SEQUENCE: 122          organism = Metarhizium guizhouense
PKANEATVKF ISTFEGWYDH VYPDPGPQHL ETLGYGHLC KPNCAEVKYP FPPLSKADGL 60
KLLSDDMSVA ENCIYQDTNA KVTLNANQYG ALVSWAFNVG CGNVASSRLI RRLNAGEDPN 120
TVAAQELPW NRADGKVLPG LTRRRNAEVE LFKTPTNNDPA LP 162

SEQ ID NO: 123          moltype = AA length = 74
FEATURE
source
1..74
mol_type = protein
organism = Podospora anserina

SEQUENCE: 123          organism = Podospora anserina
YPITGDVVNC RSGPGTSYSV VKQYTQGQDV TITCQTEGTN VNGVTIWDKT ADGNCYVSDY 60
YVQTGVNGYV TERC 74

SEQ ID NO: 124          moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein
organism = Penicillium chrysogenum

SEQUENCE: 124          organism = Penicillium chrysogenum
YPITGDGVNC RSGPGTSYSV VKSYKQGADV AITCQTAGTS VNGNEIWDKT EDGCYITDYY 60
IRTGSSSYVT KKC 73

SEQ ID NO: 125          moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein
organism = Nectria haematococca

SEQUENCE: 125          organism = Nectria haematococca
YPVTSNLNC RSGPGTAFAI KKSYKNGQDV TITCQTEGDN IEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK GKC 73

SEQ ID NO: 126          moltype = AA length = 61
FEATURE
source
1..61
mol_type = protein
organism = Metarhizium acridum

SEQUENCE: 126          organism = Metarhizium acridum
YPITGTTVNC RAGPATDPAI VRAYKKDDKV SIARQTQGPD INGGTIWDKT ADGCYVSDYF 60
V 61

SEQ ID NO: 127          moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein

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SEQUENCE: 127          organism = Metarhizium robertsii
FPVTADSLNC RAEPNTSSAV KKTYKKTDDV KISCQTEGPS INGNSIWDKT QDGCYVADYY 60
IKTGSSGYVT GKC          73

SEQ ID NO: 128          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Metarhizium robertsii

SEQUENCE: 128          moltype = AA length = 73
YAIIEADGVNC RSGPSTSDKV VRTYNKGNDV KLECQTAGQA IHGDSLWDKT TDGCYVADYY 60
VKTGTTNMVT GQC          73

SEQ ID NO: 129          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 129          moltype = AA length = 69
YPTVTSNLNC RSGPGTAFAI KKSYKKGQDV TITCQTQGDN VEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK GKC          73

SEQ ID NO: 130          moltype = AA length = 69
FEATURE          Location/Qualifiers
source           1..69
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 130          moltype = AA length = 73
DEGVRCRSGP TTSHAIQRQF TKGTDVTITC QIEGTNIEGN ALWDKTTFGC YVSDYYVATG 60
SSGYVTSKC          69

SEQ ID NO: 131          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Thielavia terrestris

SEQUENCE: 131          moltype = AA length = 73
YPVKADTLNC RSGPGTSYKV IKTYKKGTDL KITCQTPGTS VNGDNLWDKT SDGCYVADYY 60
VKTGTSGYVT AHC          73

SEQ ID NO: 132          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Thielavia terrestris

SEQUENCE: 132          moltype = AA length = 73
YPIKGDGVNC RTGPGTSYKV VKSYAKGVDV KITCQTHGES INGDTLWDKT SDGCYVADYY 60
VKTGTTNMVT GQC          73

SEQ ID NO: 133          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Trichosporon asahii

SEQUENCE: 133          moltype = AA length = 73
YPIKTDGVRC RSGPGTSYDI KKYSAGDKV TLSCYKTGTS VEGNTYWDKT GDGCYVSDYY 60
VKTGSTTPVV SKC          73

SEQ ID NO: 134          moltype = AA length = 72
FEATURE          Location/Qualifiers
source           1..72
mol_type = protein
organism = Trichosporon asahii

SEQUENCE: 134          moltype = AA length = 72
YPVKETLHCR SSPSTSGKIV KDYPKGTKIK LSCYSRGQSI GGNTIWDKT DGCFVADYYV 60
TTGTTNPVVA AC          72

SEQ ID NO: 135          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 135          moltype = AA length = 73
YPITGNNVNC REGPSTGYEV VKTYHKGDDV KLTCQTSGEG VLGNSLWDKT SDGCYVADYY 60
VKTGTSGMVT KDC          73

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SEQ ID NO: 136      moltype = AA  length = 73
FEATURE
source
1..73
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 136
YPVTSNLNC RSGPGTAFAI KKSYKKGQDV TITCQTQGDK VEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK GKC          73

SEQ ID NO: 137      moltype = AA  length = 72
FEATURE
source
1..72
mol_type = protein
organism = Trichosporon asahii
SEQUENCE: 137
YPVKEGLNCR SEPNTGGGIV TSYAAGTQVT ITCATHGEAV NGHDVWDKTT DGCFVSDWYV 60
STGTAEFVAS EC          72

SEQ ID NO: 138      moltype = AA  length = 73
FEATURE
source
1..73
mol_type = protein
organism = Trichosporon asahii
SEQUENCE: 138
YPIKTDGVRC RSGPGTSYDI KKTYSAGDKV TLSCYKTGTS VEGNTYWDKT GDGCYVSDYY 60
VKTGSTTPVV SKC          73

SEQ ID NO: 139      moltype = AA  length = 73
FEATURE
source
1..73
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 139
YPVTSNLNC RSGPGTAFAI KKSYKKGQDV TINCQTQGDN VEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK GKC          73

SEQ ID NO: 140      moltype = AA  length = 69
FEATURE
source
1..69
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 140
DEGVRCRSGP TTSNAIQRF AKGTDVAITC QTEGTHIKGN ALWDKTTFGC YVSDCYVATG 60
SSGYVTSKC          69

SEQ ID NO: 141      moltype = AA  length = 73
FEATURE
source
1..73
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 141
YPVTSNLNC RSGPGTAFAI KKSYKKGQDV TITCQTQGDN VEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK GKC          73

SEQ ID NO: 142      moltype = AA  length = 69
FEATURE
source
1..69
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 142
DEGVRCRSGP TTSHAIQRQF TKGTDVTITC QIEGTNIEGN ALWDKTTFGC YVSDYYVATG 60
SSGYVTSKC          69

SEQ ID NO: 143      moltype = AA  length = 73
FEATURE
source
1..73
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 143
YPVTSNLNC RSGPGTAFAI KKSYKKGQDV TITCQTQGDN VEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK GKC          73

SEQ ID NO: 144      moltype = AA  length = 73
FEATURE
source
1..73

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mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 144
YPVTSNLNC RSGPGTAFAI KKSYKKGQDV TITCQTQGDK VEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK GKC 73

SEQ ID NO: 145      moltype = AA length = 69
FEATURE          Location/Qualifiers
source           1..69
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 145
DEGVRCRSGP TTSNAIQRQF AKGTDVAITC QTEGTHIKGN VPWDKTTFGC YVSDYYVATG 60
SSGYVTSKC 69

SEQ ID NO: 146      moltype = AA length = 69
FEATURE          Location/Qualifiers
source           1..69
mol_type = protein
organism = Gibberella moniliformis
SEQUENCE: 146
DEGVRCRSGP TTSNAIQRQF TKGTDGTITY QTEGTNIEGN TLWDKTTFGC FVSDYYVATG 60
SSGYVTSKC 69

SEQ ID NO: 147      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 147
YPVTSNLNC RSGPGTAFAI KKSYKKGQDV TITCQTQGDN VEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK DKC 73

SEQ ID NO: 148      moltype = AA length = 69
FEATURE          Location/Qualifiers
source           1..69
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 148
DEGVRCRSGP TTSNAIQRQF TKGTDVTITC QIEGTNIEGN ALWDKTTFGC YVSDYYVATG 60
SSGYVTSKC 69

SEQ ID NO: 149      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 149
YPVTSNLNC RSGPGTAFAI KKSYKKGQDV TITCQTQGDN VEGNSIWDKT SDGCYVADKY 60
VKTGKDGYVK GKC 73

SEQ ID NO: 150      moltype = AA length = 69
FEATURE          Location/Qualifiers
source           1..69
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 150
DEGVRCRSGP TTSNAIQRQF TKGTDVTITC QIEGTNIEGN ALWDKTTFGC YVSDYYVATG 60
SSGYVTSKC 69

SEQ ID NO: 151      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Penicillium oxalicum
SEQUENCE: 151
YPVKTDLHC RSGPGTSYSI VKTYNTGTL TITCQTPGPV INGDELWDKT SDGCYVSDYY 60
VKTGTSGYVA PHC 73

SEQ ID NO: 152      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Penicillium oxalicum
SEQUENCE: 152
YPVKTDLHC RSGPGTNYAV VKSYKIGTDL TITCQAPGTV VSGDELWDKT SDGCYVSDYY 60

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VKTGTSGYVT KQC	73
SEQ ID NO: 153	moltype = AA length = 69
FEATURE	Location/Qualifiers
source	1..69
	mol_type = protein
	organism = Fusarium oxysporum
SEQUENCE: 153	
DEGVRCRSGP TTSNAIQRQF AKGTDVAITC QTEGTHIKGN VPWDKTTFGC YISDYYVAKG	60
SSGYVTSKC	69
SEQ ID NO: 154	moltype = AA length = 69
FEATURE	Location/Qualifiers
source	1..69
	mol_type = protein
	organism = Fusarium oxysporum
SEQUENCE: 154	
DEGVRCRSGP TTSHAIQRQF TKGTDVTITC QIEGTNIEGN ALWDKTTFGC YLSDYYVATG	60
SSGYVTSKC	69
SEQ ID NO: 155	moltype = AA length = 73
FEATURE	Location/Qualifiers
source	1..73
	mol_type = protein
	organism = Fusarium oxysporum
SEQUENCE: 155	
YPVTSNDNLNC RSGPGTGFAI KKSYKKQDI TITCQTQGDN VEGNSIWDT SNGCYVADKY	60
VKTGKDGYVK GKC	73
SEQ ID NO: 156	moltype = AA length = 69
FEATURE	Location/Qualifiers
source	1..69
	mol_type = protein
	organism = Gibberella fujikuroi
SEQUENCE: 156	
DEGVRCRSGP TTSHAIQTHF VKGTDVTITC QTEGTYIGGS TLWDKTTFGC YVSDYYVATG	60
SSGYVTSKC	69
SEQ ID NO: 157	moltype = AA length = 59
FEATURE	Location/Qualifiers
source	1..59
	mol_type = protein
	organism = Penicillium roqueforti
SEQUENCE: 157	
YPVTGSVIDC HSGPGASHSV VKTYEERADI EIVCQATGTT VDGSDIWHQT VDDCYVSDF	59
SEQ ID NO: 158	moltype = AA length = 74
FEATURE	Location/Qualifiers
source	1..74
	mol_type = protein
	organism = Pyronema omphalodes
SEQUENCE: 158	
YPLVHTDTLN CRSSPSTSSS ITKTYKKSDD IKITCQTYGD TIKGNNIWDK TPDGCYVSDY	60
YVKTGKSGFV VGKC	74
SEQ ID NO: 159	moltype = AA length = 72
FEATURE	Location/Qualifiers
source	1..72
	mol_type = protein
	organism = Pyronema omphalodes
SEQUENCE: 159	
YPAKETLRCR TSPSTSASIH KTYPAGADIK ITCQTTGTVK LTSNVWDKTS DGCYVSDYYV	60
STGHSGIFLS KC	72
SEQ ID NO: 160	moltype = AA length = 73
FEATURE	Location/Qualifiers
source	1..73
	mol_type = protein
	organism = Pseudogymnoascus pannorum
SEQUENCE: 160	
FPITGNTVNC RSGPGTDFSI KQTYAKGEAV AITCQTSGTK INGNDIWLDT TDGCYVTDFY	60
VKTGSISYVL PKC	73
SEQ ID NO: 161	moltype = AA length = 68
FEATURE	Location/Qualifiers
source	1..68

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mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 161
DKGVRCRSGP TTSHAIQRQF TKGTDVTITC QIEGTNIEGN ALWDKTTFGC YVSDYYVATG 60
SSGYVTLK 68

SEQ ID NO: 162      moltype = AA length = 68
FEATURE          Location/Qualifiers
source           1..68
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 162
DKGVRCRSGP TTSHAIQRQF TKGTDVTITC QIEGTNIEGN ALWDKTTFGC YVSDYYVATG 60
SSGYVTLK 68

SEQ ID NO: 163      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Acremonium chrysogenum
SEQUENCE: 163
YPITGNEVNC RSGPSTSSDI VTSYKKGDEV QVTCQIDGED IFGNTIWDQT EDGCYVADFY 60
VKTGSNAFVT EAC 73

SEQ ID NO: 164      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Acremonium chrysogenum
SEQUENCE: 164
YPITADDVKC RAGPSTSHDI VTAFAAEGHEV ELECQIVGEN IFGNSIWDKT TDGCYVSDYY 60
VRTGSDGMVV DNC 73

SEQ ID NO: 165      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Acremonium chrysogenum
SEQUENCE: 165
YPVTADSLNC REGAGTDTAV VTTYTAGTDV EVVCQAEGEV IEGSSIWDQT QDGCYVSDVY 60
VDTGSDGYVA DKC 73

SEQ ID NO: 166      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Metarhizium anisopliae
SEQUENCE: 166
YAIEADGVNC RSGPSTSDKV VRTYNKGNDV KLECQTAGQA IHGDSLWDKT TDGCYVADYY 60
VKTGTTNMVT GQC 73

SEQ ID NO: 167      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Metarhizium anisopliae
SEQUENCE: 167
FPVTADSLNC RAEPNTSSAV KKTYKKTDDV KISCQTEGPS INGNSIWDKT QDGCYVADYY 60
IKTGSSGYVT GKC 73

SEQ ID NO: 168      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 168
YPITGTYVNC RTGPSTSFDI VRSYELGDEV DLTCQIAGET VTGDNLWDFT TDGCYVADYF 60
VKTGTFGMVV DEC 73

SEQ ID NO: 169      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 169
YPITGTYVNC RSGPSTSFDI VRSYELGDEV SLTCQIAGET VEGDYLWDLT TDGCYVADYF 60

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VKTGTVGMVA EEC		73
SEQ ID NO: 170	moltype = AA length = 74	
FEATURE	Location/Qualifiers	
source	1..74	
	mol_type = protein	
	organism = Pseudogymnoascus pannorum	
SEQUENCE: 170		
YPIISGDSVNC RSGPATSYKV IKTYAKGHDV KVTCQTVGET VKGDNLWDKT ADGCYVADYY	60	
VKTGTTGRVV KTEC	74	
SEQ ID NO: 171	moltype = AA length = 73	
FEATURE	Location/Qualifiers	
source	1..73	
	mol_type = protein	
	organism = Pseudogymnoascus pannorum	
SEQUENCE: 171		
VTSPPTTVKCR SGPGTQYKIV KTYPASGREC YSCYESGTCI NGNCSWDYNY MDNCYISGYY	60	
TGSACTTAAL GKC	73	
SEQ ID NO: 172	moltype = AA length = 74	
FEATURE	Location/Qualifiers	
source	1..74	
	mol_type = protein	
	organism = Pseudogymnoascus pannorum	
SEQUENCE: 172		
YPIISGTSVNC RSGPATSYKV IKTYKKGQDV KITCQTVGET VSGDNLWDKT SDGCYVADYY	60	
VKTGTTGRVV KTEC	74	
SEQ ID NO: 173	moltype = AA length = 73	
FEATURE	Location/Qualifiers	
source	1..73	
	mol_type = protein	
	organism = Pseudogymnoascus pannorum	
SEQUENCE: 173		
YPIKGGSVNC RAGPGTNFPI VKTFKKGDTV DITCQTPGTS ISGNSIWDLI PDNCFITDYY	60	
VKTGTGKYIK PRC	73	
SEQ ID NO: 174	moltype = AA length = 64	
FEATURE	Location/Qualifiers	
source	1..64	
	mol_type = protein	
	organism = Pseudogymnoascus pannorum	
SEQUENCE: 174		
VTMPTTVKCR SGPGTQYRIV KTYRAGDREC YSCYESGTCI NGNCSWDYNY MDNCYISGYY	60	
TDSG	64	
SEQ ID NO: 175	moltype = AA length = 73	
FEATURE	Location/Qualifiers	
source	1..73	
	mol_type = protein	
	organism = Pseudogymnoascus pannorum	
SEQUENCE: 175		
VTSPPTTVKCR SGPGTQYKIV KTYPASGREC YSCYESGTCI NGNCSWDYNY MDNCYISGYY	60	
TGSACTTAAL GKC	73	
SEQ ID NO: 176	moltype = AA length = 73	
FEATURE	Location/Qualifiers	
source	1..73	
	mol_type = protein	
	organism = Pseudogymnoascus pannorum	
SEQUENCE: 176		
YPITGNTVNC RSGPGTDFPI KKTFAKGSIV SITCQTPGTK INGNEIWDLT SDGCFVSDFY	60	
VKTGSITYVK PKC	73	
SEQ ID NO: 177	moltype = AA length = 73	
FEATURE	Location/Qualifiers	
source	1..73	
	mol_type = protein	
	organism = Pseudogymnoascus pannorum	
SEQUENCE: 177		
YPITGTSVNC RSGPSTKFDV VRSYVLGDEV TLTCQIAGET VTGDLWDLT TDGCYVADYF	60	
VKTGTVGMVT EAC	73	
SEQ ID NO: 178	moltype = AA length = 73	
FEATURE	Location/Qualifiers	

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source          1..73
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 178
YPITGTYVNC RSGPSTSVDI IRSYELGDEV DLTCQIAGET VTGDNLWDFT TDGCYVADYF 60
VKTGTFGMVV DEC                                73

SEQ ID NO: 179      moltype = AA  length = 74
FEATURE          Location/Qualifiers
source           1..74
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 179
YPISGDSVNC RSGPATSYKV IKTYAKGHDV KVTCQTVGET VKGDNLWDKT ADGCYVADYY 60
VKTGTTGRVV KTEC                                74

SEQ ID NO: 180      moltype = AA  length = 73
FEATURE          Location/Qualifiers
source           1..73
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 180
YPITGTYVNC RTGPSTSFDI VRSYELGDEV DLTCQIAGET VTGDNLWDFT TDGCYVADYF 60
VKTGTFGMVV DEC                                73

SEQ ID NO: 181      moltype = AA  length = 73
FEATURE          Location/Qualifiers
source           1..73
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 181
YPITGTYVNC RSGPSTSFDI VRSYELGDEV SLTCQIAGET VEGDYLWDLT TDGCYVADYF 60
VKTGTVGMVA EEC                                73

SEQ ID NO: 182      moltype = AA  length = 72
FEATURE          Location/Qualifiers
source           1..72
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 182
YPISGDSVNC RSGPATSYKV IKTYLKGDHV DLTCQTVGET VKGDSLWDKT TDGCYVADYY 60
VKTGTTGRVV KK                                 72

SEQ ID NO: 183      moltype = AA  length = 73
FEATURE          Location/Qualifiers
source           1..73
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 183
YPIKGGSVNC RSGPGTNFAI VKTFKKGDTV DITCQTPGTS ISGNSIWDLT PDNCFITDYY 60
VKTGTGKYIK PRC                                73

SEQ ID NO: 184      moltype = AA  length = 67
FEATURE          Location/Qualifiers
source           1..67
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 184
CRSGPGTGYS VIATVKKGSY YSFGCYKTGT CVSGNCTWDR IFWDGKSCYV SGYYTDSACS 60
ASALGKC                                         67

SEQ ID NO: 185      moltype = AA  length = 73
FEATURE          Location/Qualifiers
source           1..73
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 185
YPITGTFVNC RSGPSTKFV D VRSYVLGDEV TLTCQIAGET VTGDLWDLT TDGCYVADYF 60
VKTGTVGMVT EAC                                73

SEQ ID NO: 186      moltype = AA  length = 67
FEATURE          Location/Qualifiers
source           1..67
               mol_type = protein
               organism = Pseudogymnoascus pannorum
SEQUENCE: 186

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CRSGPGTGYS VIATVKKGSY YSFGCYKTGT CVSGNCTWDR IFWDGKSCYV SGYYTDSACS ASALGKC	60 67
SEQ ID NO: 187 moltype = AA length = 73 FEATURE Location/Qualifiers source 1..73 mol_type = protein organism = Pseudogymnoascus pannorum	
SEQUENCE: 187 YPITGTVNC RTGPSTSFEI IRSYKLGDEV SLTCQIAGET VQGNYLWDLT TDGCYVADYF VKTGSDGMVT EGC	60 73
SEQ ID NO: 188 moltype = AA length = 73 FEATURE Location/Qualifiers source 1..73 mol_type = protein organism = Aspergillus clavatus	
SEQUENCE: 188 YPITGDGVNC RSGPGTSYKV VKSYPKGHQV SIVCQATGTD VKGDSLWDKT SDGCYVADYY VKTGTTGYVT KHC	60 73
SEQ ID NO: 189 moltype = AA length = 73 FEATURE Location/Qualifiers source 1..73 mol_type = protein organism = Aspergillus clavatus	
SEQUENCE: 189 YPITGDTVNC RSGPGTSHAV VKSYKKGEDV KIVCQAPGTD VKGESIWDKT SDGCYVADYY VKTGTTGYVT KKC	60 73
SEQ ID NO: 190 moltype = AA length = 73 FEATURE Location/Qualifiers source 1..73 mol_type = protein organism = Neosartorya fischeri	
SEQUENCE: 190 YPITGNEVNC RAGPSTNDKV VKSYHKGDDV KLSCQTYGEN VQGNSIWDKT TDGCYVSDFY VKTGSNSMVT KEC	60 73
SEQ ID NO: 191 moltype = AA length = 73 FEATURE Location/Qualifiers source 1..73 mol_type = protein organism = Neosartorya fischeri	
SEQUENCE: 191 YPITGDGVNC RSGPGTNHPV VKSYPKGHDV SIVCQAPGTD VKGDKLWDKT SDGCYVADYY VKTGSTDYVT KHC	60 73
SEQ ID NO: 192 moltype = AA length = 73 FEATURE Location/Qualifiers source 1..73 mol_type = protein organism = Neosartorya fischeri	
SEQUENCE: 192 YPITGDGVNC RSGPGTNHPV VKSYPKGHDV SIVCQAPGTD VKGDKLWDKT SDGCYVADYY VKTGSSDYVT KHC	60 73
SEQ ID NO: 193 moltype = AA length = 73 FEATURE Location/Qualifiers source 1..73 mol_type = protein organism = Aspergillus terreus	
SEQUENCE: 193 YPITGDGVNC RSGPGTSHAV VKSYPKGHEI SIVCQAAGTD VKGDNLWDKT SDGCYVADYY VKTGSTGYVT KHC	60 73
SEQ ID NO: 194 moltype = AA length = 64 FEATURE Location/Qualifiers source 1..64 mol_type = protein organism = Aspergillus terreus	
SEQUENCE: 194 CRTGPSTNDG ITKTYKKGDD VKLSCQTYGE SIQGSTIWDK TTDGCYVADY YVKTGTSGMV TGEC	60 64
SEQ ID NO: 195 moltype = AA length = 73	

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FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Aspergillus terreus
SEQUENCE: 195
YITADGVNC RSGPGTSNKS VKTYAKGTDV KISCQQAGES IFGNSLWDKT SDGCYVSDYY 60
VKTGSTGYVT DKC                                         73

SEQ ID NO: 196      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Chaetomium globosum
SEQUENCE: 196
YPITGSVVNC RSGPGTSYAV KKSYAKGADV KISCQTSCTS VNGNNIWDKT QDGCYVADYY 60
VKTGTNGYVT KKC                                         73

SEQ ID NO: 197      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Chaetomium globosum
SEQUENCE: 197
YPITGSVVNC RSGPGTSYAV KKSYAKGADV TISCQTTGTS VNGNSIWDKT QDGCYVADYY 60
VKTGTNGYVT KKC                                         73

SEQ ID NO: 198      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Chaetomium globosum
SEQUENCE: 198
YPITGNDVNC RSGPDTSYKS VKTYKKGADV KLTCQTYGES INGNNAIWDTK SDGCYVSDYY 60
VKTGSNSMVT KEC                                         73

SEQ ID NO: 199      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Neosartorya fumigata
SEQUENCE: 199
YPITGNGVNC RAGPSTNDKV IKSYAKGTDV KLSCQTYGEN INGNSIWDKT TDGCYVADYY 60
VKTGSNSMVT KEC                                         73

SEQ ID NO: 200      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Neosartorya fumigata
SEQUENCE: 200
YPITGNGVNC RSGPGTNYPV VKSYPKGHEV SIVCQAPGTD IKGDKLWDKT SDGCYVADYY 60
VKTGTTGYVT KHC                                         73

SEQ ID NO: 201      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Neosartorya fumigata
SEQUENCE: 201
YPITGDNVNC RSGPGTNYPV VKSYPKGHEV SIVCQAPGTD IKGDKLWDKT SDGCYVADYY 60
VKTGTTNYVA KHC                                         73

SEQ ID NO: 202      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Penicillium chrysogenum
SEQUENCE: 202
YPITGDSVNC RSGPGTTHAV VKSYKKAQDV TVTCQTAGES IFGDNLWDKT SDGCYVADYY 60
VQTGTSNYVT TKC                                         73

SEQ ID NO: 203      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
                  mol_type = protein
                  organism = Penicillium chrysogenum

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SEQUENCE: 203
YPITSDQLNC RSGPSTSVDV VKTYKSGADV KVSCQTYGES INGNTIWDKT SDNCYVADYY 60
VKTGSDSMVT ESC 73

SEQ ID NO: 204      moltype = AA length = 73
FEATURE
source
Location/Qualifiers
1..73
mol_type = protein
organism = Nectria haematococca

SEQUENCE: 204
YPITGDDVRC RSGPGTSYAI KKTFKKGTNV KITCQTTGTN IKGNNIWDKV SEGCYVSDYY 60
VKTGSSGFVT KKC 73

SEQ ID NO: 205      moltype = AA length = 73
FEATURE
source
Location/Qualifiers
1..73
mol_type = protein
organism = Nectria haematococca

SEQUENCE: 205
YPITGDDVVC RSGPGTSYAV KKVLKKGTDV TITCQTEGTN ISGNTIWDKI SDGCYVSDYY 60
VKTGSNGYVK PKC 73

SEQ ID NO: 206      moltype = AA length = 73
FEATURE
source
Location/Qualifiers
1..73
mol_type = protein
organism = Hypocrea jecorina

SEQUENCE: 206
YPITGDDVNC RTGPGTSYAI KTSYKKSHDI SISCQTTGTS VNGNNIWDKT ADGCYVADYY 60
VKTGSSGFVT KKC 73

SEQ ID NO: 207      moltype = AA length = 73
FEATURE
source
Location/Qualifiers
1..73
mol_type = protein
organism = Thielavia terrestris

SEQUENCE: 207
YAITGDTVNC RSGPGTNYAV KKTYAKGHDV TLSCQTTSGTT VNGNSIWDKT SDGCYVSDYY 60
VKTGSNSYVT KKC 73

SEQ ID NO: 208      moltype = AA length = 74
FEATURE
source
Location/Qualifiers
1..74
mol_type = protein
organism = Thielavia heterothallica

SEQUENCE: 208
YPTANGGLS CRSGPGTSYP VKKYKKGFD IKISCQTTGT SVNGYNIWDK TQDGCVSDY 60
VVKTGKSGFV TTKC 74

SEQ ID NO: 209      moltype = AA length = 73
FEATURE
source
Location/Qualifiers
1..73
mol_type = protein
organism = Hypocrea jecorina

SEQUENCE: 209
YPITGDTVNC RSGPGTSFAI KKTYKKSQDV SVTCQTTSGTS VNGNSIWDKT SDGCYVADYY 60
VKTGSSSYVT KKC 73

SEQ ID NO: 210      moltype = AA length = 73
FEATURE
source
Location/Qualifiers
1..73
mol_type = protein
organism = Chaetomium thermophilum

SEQUENCE: 210
YPITGEGVNC RSGPGTSYKV IKSYKKGTDV KISCOIKGES INGNNLWDKT QDGCVSDYY 60
VKTGSNSMVT KQC 73

SEQ ID NO: 211      moltype = AA length = 73
FEATURE
source
Location/Qualifiers
1..73
mol_type = protein
organism = Chaetomium thermophilum

SEQUENCE: 211
YKITGNNVNC RSGPGTSYSV KKTYAKGTDV KITCQTTGTN INGNNIWDKT SDGCYVSDYY 60
VKTGTNGYVT TKC 73

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SEQ ID NO: 212      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 212
YPITGNDVKC RSGPGTSYAV KKVLKKGTDV KITCQTEGTN ISGNTIWDKI SDGCYVSDYY 60
VKTGSSGYIK PKC               73

SEQ ID NO: 213      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Thielavia heterothallica
SEQUENCE: 213
YPITGDDVNC RTGPGTSFKS VKTYPKGTDV KLSCQTYGEV IFGNSIWDKT QDGNCYVSDYY 60
VKTGSNNMVT GEC               73

SEQ ID NO: 214      moltype = AA length = 74
FEATURE          Location/Qualifiers
source           1..74
mol_type = protein
organism = Thielavia heterothallica
SEQUENCE: 214
YPVTANGGLS CRSGPGBTSYA VKKTYKKGFD VKISCQTTGT SVNGNNIWDK TQDGNCYVADYY 60
YVKTGKNGFV TSKC               74

SEQ ID NO: 215      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Hypocrea virens
SEQUENCE: 215
YPITGEAVNC RTGPGTSFAI KKTYKKSQDV SVTCQTSCTS VNGNSIWDKT SDGCYVADYY 60
VKTGSSSYVT KKC               73

SEQ ID NO: 216      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Metarhizium robertsii
SEQUENCE: 216
YPITGTTVNC RSGPSTHDKV IKTYNKGNDI KISCQVAGET VSGNNLWDKT QDGCFVSDYY 60
VKTGSNGMVT GQC               73

SEQ ID NO: 217      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum
SEQUENCE: 217
YPITGNDVKC RSGPGTSYAV KKVLKKGTDV KITCQTEGTN ISGNTIWDKI SDGCYVSDYY 60
VKTGSSGYIK PKC               73

SEQ ID NO: 218      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Chaetomium thermophilum
SEQUENCE: 218
YAITGDNVNC RSGPGTSYAV KKVKYKKGTDV KISCQTTGTN INGNNLWDKT SDGCYVSDYY 60
VKTGSNGYVT SKC               73

SEQ ID NO: 219      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Thielavia terrestris
SEQUENCE: 219
YPITGNGVNC RSGPGTSHAV KKVKYAKGTDI KVTCQTEGTS INGNSIWDKT SDGCYVADYY 60
VKTGSNSYVT KKC               73

SEQ ID NO: 220      moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein

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SEQUENCE: 220          organism = Fusarium oxysporum
YPITGNDVKC RSGPGTSYAV KKVLKKGTDV KITCQTEGTN ISGNTIWDKT SDGCYVSDYY 60
VKTGSSGYIK PKC          73

SEQ ID NO: 221          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 221          moltype = AA length = 73
YPITGNDVKC RSGPGTSYAV KEVLKKGTDV KITCQTEGTN ISGNTIWDKI SDGCYVSDYY 60
VKTGSSGYIK PKC          73

SEQ ID NO: 222          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 222          moltype = AA length = 73
FPITGNTVNC RSGPGTSYSV KRTYKKGQDV SITCQTYGTN VNGNSIWDKT SDGCYVADYY 60
VKTGSDEFVT KKC          73

SEQ ID NO: 223          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 223          moltype = AA length = 73
YPITGNDVKC RSGPGTSYAV KKVLKKGTDV KITCQTEGTN ISGNTIWDKI SDGCYVSDYY 60
VKTGSNGYIK PKC          73

SEQ ID NO: 224          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 224          moltype = AA length = 73
YPITGNDVKC RSGPGTSYAV KKVLKKGTDV KITCQTEGTN ISGNTIWDKI SDGCYVSDYY 60
VKTGSSGYIK PKC          73

SEQ ID NO: 225          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 225          moltype = AA length = 73
YPITGNDVKC RSGPGTSYAV KKVLKKGTDV KITCQTEGTN ISGNTIWDKI SDGCYVSDYY 60
VKTGSSGYIK PKC          73

SEQ ID NO: 226          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Fusarium oxysporum

SEQUENCE: 226          moltype = AA length = 73
YPITGNDVKC RSGPGTSYAV KKVLKKGTDV KITCQTEGTN ISGNTIWDKI SDGCYVSDYY 60
VKTGSSGYIK PKC          73

SEQ ID NO: 227          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Penicillium roqueforti

SEQUENCE: 227          moltype = AA length = 73
YPITGDTVNC RSGPGTSHTV VKTYKKAHDV KITCQTTGDS ISGNNIWDKT SDGCYVADYY 60
VKTGSNSYVT AKC          73

SEQ ID NO: 228          moltype = AA length = 73
FEATURE          Location/Qualifiers
source           1..73
mol_type = protein
organism = Penicillium roqueforti

SEQUENCE: 228          moltype = AA length = 73
YAITASVANC RTGPSTSNAV VTTYKKGADV KITCQTYGEN IQGNSIWDKT SDGCYVADYY 60
VKTGSNSMVT KDC          73

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SEQ ID NO: 229      moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein
organism = Trichoderma reesei
SEQUENCE: 229
YPIITGDTVNC RSGPGTSFAI KKTYKKSQDV SVTCQTSGTS VNGNSIWDKT SDGCYVADYY 60
VKTGSSSYVT KKC 73

SEQ ID NO: 230      moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein
organism = Metarhizium anisopliae
SEQUENCE: 230
YPIITGTTVNC RSGPSTHDKV IKTYNKGNDI KISCQVAGEN VSGNNLWDKT RDGCYVSDYY 60
VKTGSNGMVT GQC 73

SEQ ID NO: 231      moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 231
YPIITGSTVNC RSGPGTSYAV KKTYKKGDAV TITCQKEGPV VSGNSIWDKT SDGCYVADYY 60
VKTGSNGYVK PKC 73

SEQ ID NO: 232      moltype = AA length = 72
FEATURE
source
1..72
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 232
YPISGDSVNC RSGPATSYKV IKTYKKGHDV KITCQTVGET IKGGNLWDKT SDGCYVTDYY 60
VKTGTTGRVV KK 72

SEQ ID NO: 233      moltype = AA length = 72
FEATURE
source
1..72
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 233
FPVTATVNCR SGPGTGFAVK KSYTKGHAVT ISCQTGGTSV QGNSIWDKTS DGCVADYYV 60
KTGSSGYVKP KC 72

SEQ ID NO: 234      moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 234
FPITGDTVNC RSGPGTSYAV KKSYNKGHSV TITCQTAGTS VKGNSIWDKT SDGCYVADYY 60
VKTGSSGYVK PKC 73

SEQ ID NO: 235      moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 235
FPITGDSVNC RSGPGTSYAV KKSYAKGHSV TITCQTAGTS VNGNSIWDKT SDGCYVADYY 60
VKTGSSGYVK PKC 73

SEQ ID NO: 236      moltype = AA length = 73
FEATURE
source
1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 236
YPIINAAGVNC RSGPGTSYAV KKSYAKDHAV TVTCQTAGTS VNGNSIWDKT SDGCYVADYY 60
VNTGSSGYVK PKC 73

SEQ ID NO: 237      moltype = AA length = 73
FEATURE
source
1..73

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mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 237
YPINAAGVNC RSGPGTGYAV KKSYAKDHAV TVTCQTAGTT VNGNSIWDKT SDGCYVADYY 60
VNTGSSGYVK PKC 73

SEQ ID NO: 238      moltype = AA length = 73
FEATURE           Location/Qualifiers
source            1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 238
YPITGTTVNC RSGPGTSYAV KKTYKKGDAV TITCQKEGPV ISGNSIWDKT SDGCYVADYY 60
VKTGSNGYVK PKC 73

SEQ ID NO: 239      moltype = AA length = 73
FEATURE           Location/Qualifiers
source            1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 239
YPITGKTVNC RAGPGTSYPV KKTYSKGDTV TITCQTSGTK VNGNAIWDLT SDGCYLTDYY 60
VKTGTTSKYIK PQC 73

SEQ ID NO: 240      moltype = AA length = 69
FEATURE           Location/Qualifiers
source            1..69
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 240
YPISGTDVNC RSGPATSYKV VKTYKKGHDV KVTCQTVGET IKGDNLWDKT SDGCYVADYY 60
VKTGTTGRV 69

SEQ ID NO: 241      moltype = AA length = 73
FEATURE           Location/Qualifiers
source            1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 241
YPINTAGVNC RSGPGTSYAV KKSYAKDHAV TVTCQTAGTS VNGNAIWDKT SDGCYVADYY 60
VNTGSSGYVK PKC 73

SEQ ID NO: 242      moltype = AA length = 73
FEATURE           Location/Qualifiers
source            1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 242
YPINAAGVNC RSGPGTGYAV KKSYAKDHAV TVTCQTAGTS VNGNSIWDKT SDGCYVADYY 60
VNTGSSGYVK PKC 73

SEQ ID NO: 243      moltype = AA length = 74
FEATURE           Location/Qualifiers
source            1..74
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 243
YPISGTSVNC RSGPATSYKV IKAYKKGQDV KITCQTVGET VSGDNLWDKT TDGCYVADYY 60
VKTGTTGRVV NAEC 74

SEQ ID NO: 244      moltype = AA length = 73
FEATURE           Location/Qualifiers
source            1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 244
FPITGDSVNC RSGPGTSYAV KKSYAKGHSV TITCQTAGGS VNGNSIWDKT SDGCYVADYY 60
VKTGSSGYVK PKC 73

SEQ ID NO: 245      moltype = AA length = 73
FEATURE           Location/Qualifiers
source            1..73
mol_type = protein
organism = Pseudogymnoascus pannorum
SEQUENCE: 245
FPITGDTVNC RSGPGTSYAV KKSYAKGHDV TITCQTAGGS VSGNSIWDKT SDGCYVADYY 60

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VKTGSSGYVK PKC	73
SEQ ID NO: 246	moltype = AA length = 64
FEATURE	Location/Qualifiers
source	1..64
	mol_type = protein
	organism = Pseudogymnoascus pannorum
SEQUENCE: 246	
YPITGKTVNC RAGPGTSYPV KKTYSKGDTV TITCQTSGTK VNGNAIWDLT SDGCYLTDDY	60
VKTG	64
SEQ ID NO: 247	moltype = AA length = 73
FEATURE	Location/Qualifiers
source	1..73
	mol_type = protein
	organism = Pseudogymnoascus pannorum
SEQUENCE: 247	
FPITGDSVNC RSGPGTSYAV KKSYAKGHDV TITCQGGTS VSGNSIWDKT SDGCYVADYY	60
VKTGSSGYVK PKC	73
SEQ ID NO: 248	moltype = AA length = 72
FEATURE	Location/Qualifiers
source	1..72
	mol_type = protein
	organism = Pseudogymnoascus pannorum
SEQUENCE: 248	
FPVTETVNCR SGPGGTSYGVK KSYTKGHAVT ISCQTGGTSV KGNSIWDKTS DGCYVADYYV	60
KTGSSGYVKP KC	72
SEQ ID NO: 249	moltype = AA length = 72
FEATURE	Location/Qualifiers
source	1..72
	mol_type = protein
	organism = Pseudogymnoascus pannorum
SEQUENCE: 249	
FPVTATVNCR SGPGGTGYAVK KSYTKGNAVT ISCQTGGTSV NGNSIWDKTS DGCYVADYYV	60
KTGSSGYVKP KC	72
SEQ ID NO: 250	moltype = AA length = 73
FEATURE	Location/Qualifiers
source	1..73
	mol_type = protein
	organism = Pseudogymnoascus pannorum
SEQUENCE: 250	
YPINAAGVNC RSGPGTSYAV KKSYAKDHAV TVTCQTAGTS VNGNAIWDLT SDGCYVADYY	60
VNTGSNGYVK PKC	73
SEQ ID NO: 251	moltype = AA length = 73
FEATURE	Location/Qualifiers
source	1..73
	mol_type = protein
	organism = Pseudogymnoascus pannorum
SEQUENCE: 251	
FPITGATVNC RSGPGTSYAV KKSYAKGHDV TITCQGGTS VNGNSIWDKT SDGCYVADYY	60
VKTGSSGYVK PKC	73
SEQ ID NO: 252	moltype = length =
SEQUENCE: 252	
000	
SEQ ID NO: 253	moltype = AA length = 15
FEATURE	Location/Qualifiers
REGION	1..15
	note = Synthetic construct
REGION	1
	note = NON_CONS - The amino acid in position 1 of the conserved motif is leucine or valine.
REGION	2
	note = NON_CONS - The amino acid in position 2 of the conserved motif is asparagine, aspartic acid, serine or threonine.
REGION	3
	note = NON_CONS - The amino acid in position 3 of the conserved motif is any amino acid.
REGION	5
	note = NON_CONS - The amino acid in position 5 of the

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REGION           conserved motif is glutamic acid or glutamine.
6               note = NON_CONS - The amino acid in position 6 of the
                  conserved motif is phenylalanine, tyrosine or tryptophan.

REGION           note = NON_CONS - The amino acid in position 7 of the
7               conserved motif is alanine, aspartic acid, asparagine,
                  glycine or serine.

REGION           note = NON_CONS - The amino acid in position 10 of the
10              conserved motif is any amino acid.

REGION           note = NON_CONS - The amino acid in position 12 of the
12              conserved motif is leucine, phenylalanine, tyrosine or
                  tryptophan.

REGION           note = NON_CONS - The amino acid in position 13 of the
13              conserved motif is any amino acid.

REGION           note = NON_CONS - The amino acid in position 14 of the
14              conserved motif is phenylalanine or tyrosine.

source          1..15
                mol_type = protein
                organism = synthetic construct

SEQUENCE: 253
XXXNXXXALX SXXXN                                         15

SEQ ID NO: 254      moltype = length =
SEQUENCE: 254
000

SEQ ID NO: 255      moltype = DNA length = 946
FEATURE          Location/Qualifiers
sig_peptide      1..51
mat_peptide      52..943
source          1..946
                mol_type = genomic DNA
                organism = Trichophaea saccata

CDS             1..347
CDS             401..615
CDS             668..772
CDS             825..943

SEQUENCE: 255
atgcacgctc tcacccttct caccgcaacc ctcttcggc tcgcagcgcc ctaccagg 60
aagaccgacc ttcaactggcg ctccctctcc agcacttccg ccagcatcgt ccgcacctac 120
tccagtggaa cggaaagtccca gatccagtgc cagaccacgg gcacttcggt ccaaggatcc 180
aatgtctggg acaaagaccca gcacgggtgc tacgtccacg actactacgt caagaccggg 240
catttcggga ttttcacacc caagtggcg agcagctcgg gtggagggtc ctgcaaggct 300
cccccgatca atgctgctac tgccgatcg atcaaggagg ttgaggggta agtgacagct 360
ctgagtgagg tggatgagg attaaagactg acgaggatag attcgttct aagccccc 420
cggatcttat tggatggcg accgtggat acgggcatct ttgcaagact aagggctgca 480
aagaagtgcc ttacagctt cctctcaccc agggactgc cacaaggttt cttcagacgc 540
atatacaagac ttccacctt tgcgttagca acatcgtcaa ggactctgtt aagtcacg 600
ataaaccatg cggagggtgag ttccagtgtt acagtgaatt tattgtatgatttctaagta 660
attttagtgc tggcgcttgc ggcttcaac gtcggctgc gaaaactcca gacttctcg 720
ctgatcaaga gattgaacgc tggggagaac cctaacaactg tgcgtgtca gggtaagata 780
tttatccccc atttgcctt gacacatggc tgaaaaagt gcaacttcc ccaactggaa 840
gtacgcttgtt ggaaagggtt tgcctggctt ggtccggccg cgcaatgtt aggtcgccgt 900
cttcaagaag cccagcagcg ttcaaggccca ccctcccaag tgctaa                                         946

SEQ ID NO: 256      moltype = AA length = 262
FEATURE          Location/Qualifiers
source          1..262
                mol_type = protein
                organism = Trichophaea saccata

SEQUENCE: 256
MHALTLLTAT LFGLAAAYPV KTDLHCRSSP STSASIVRTY SSGTEVQIQC QTTGTSVQGS 60
NVWDKTOHGC YVADYYVKTG HSGIFTTKCG SSSGGGSCKP PPINAATVAL IKEFEGFVPK 120
PAPDPIGLPT VGYGHLCCTK GCKEVPPYSFP LTQETATKLL QSDIKTFTSC VSNYVKDSVK 180
LNDNQYGALA SWAFNVGCGN VQTSSLIKRL NAGENPNTVA AQELPKWKYA GGKVMPGLVR 240
RNAEVALFK KPSSVQAHPK KC                                         262

SEQ ID NO: 257      moltype = AA length = 245
FEATURE          Location/Qualifiers
source          1..245
                mol_type = protein

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SEQUENCE: 257          organism = Trichophaea saccata
YPVKTDLHCR SSPSTSASIV RTYSSGTEVQ IQCQTTGTSV QGSNVWDKTQ HGCYVADYYV 60
KTHSGIFTT KCGSSGGGS CKPPPINAAAT VALIKEFEGF VPKPAPDPPIG LPTVGYGHLC 120
KTKGCKEVPI SFPLTQETAT KLLQSDIKTF TSCVSNYVKD SVKLNDNQYG ALASWAFNVG 180
CGNVQTSSLI KRLNAGENPN TVAAQELPKW KYAGGKVMPG LVRRRNAEVA LFKKPSSVQA 240
HPPKC                                         245

SEQ ID NO: 258          moltype = DNA length = 39
FEATURE                 Location/Qualifiers
misc_feature            1..39
note = Synthetic construct
source                  1..39
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 258          acacaactgg ggatccacca tgcacgctct cacccttctc 39

SEQ ID NO: 259          moltype = DNA length = 38
FEATURE                 Location/Qualifiers
misc_feature            1..38
note = Synthetic construct
source                  1..38
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 259          cttagatctcg agaagctttt agcaattggg aggggtggg 38

SEQ ID NO: 260          moltype = DNA length = 20
FEATURE                 Location/Qualifiers
misc_feature            1..20
note = Synthetic construct
source                  1..20
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 260          gcaaggaggatc ccatgcttgg 20

SEQ ID NO: 261          moltype = DNA length = 19
FEATURE                 Location/Qualifiers
misc_feature            1..19
note = Synthetic construct
source                  1..19
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 261          catataacca attgccctc 19

SEQ ID NO: 262          moltype = DNA length = 923
FEATURE                 Location/Qualifiers
sig_peptide             1..54
mat_peptide              55..920
source                  1..923
mol_type = genomic DNA
organism = Chaetomium thermophilum
CDS                      1..367
CDS                      425..555
CDS                      630..920

SEQUENCE: 262          atgaagttcg ccattcctcgc cgccgttgc tccttccttg ctccccccag cgcctatgcc 60
attaccggcg acaaactcaa ctgtcgacgg ggcggcaggca ctagctacgc ggtcaagaag 120
gtctacaaga agggcaccga cgtcaagatc agtgcgcaga ctactggcac caatatcaac 180
ggcaacaatc ttgggacaa gacctctgac ggctgtatg ttccggacta ttacgtcaag 240
actggcagca acggctatgt gaccggcaag tgcaagtctca gtggaggccag cacctgcgt 300
gcggccaaagt ctaaccaagc cactgtcgat ctcatcgctg agtggaggcc 360
aatatctgtt tggatataca acctcgccatt gtacttaaga acaaggcttc aactcgtaa 420
caagacaccc atgcagctgg atacgcccact gtccggatacg gccacaaggcc 480
aagtgcgtc aggtcaagta caagattccc ctttccaagg ccgtatggcaaa gaagcttctg 540
gcggatgata tgagggtatc ttcccccctt cataaaaaacc ataccatctc tggaagctc 600
atcaatttcg actaacccca aatctacaga gcttcgaagt ctgcattaaac aacatgtca 660
atagcaaggc caagctgaac tacaaccgt tcggctgactc ggtcaatgg tccttcaatg 720
tcggctgcgg cgctgccaag tcggctgactc tcatcaagcc cctaaacaac ggcggaaatg 780
tcaacaaggc tctttccgag gagctgccc agtggacaa ggctgggca aaggttctc 840
aaggcccttgt ccggccgggt gctgtcgagg tcgctctggc taagaaggctc ggcagctctc 900
aggcttcc tggtaagtgc tga                                         923

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SEQ ID NO: 263      moltype = AA length = 263
FEATURE          Location/Qualifiers
source           1..263
mol_type = protein
organism = Chaetomium thermophilum

SEQUENCE: 263
MKFAILAAVA SFLAPASAYA ITGDNVNCRS GPGTSYAVKK VYKKGTDVKI SCQTTGNIN 60
GNNLWDKTSD GCYVSDYYVK TGSNGYVTSK CSSGGTCA APKSQNATVD LIAEPEGFRA 120
NIYTDAAGYA TVGYGHKCQK AKCAEVKYKI PLSKADGKKL LADDMRSFEV CITNMLNSKA 180
KLNNYNQFGAL VSWSFNVGCG AAKSSTLIKR LNNGENVNKV LSEELPKWNK AGGKVLOGLV 240
RRAAEVALA KKGSSQALP VKC                                263

SEQ ID NO: 264      moltype = AA length = 249
FEATURE          Location/Qualifiers
source           1..249
mol_type = protein
organism = Chaetomium thermophilum

SEQUENCE: 264
PASAYAITGD NVNCRSGPGT SYAVKKVYKK GTDVKISCQT TGTINGNNL WDKTSDGCYV 60
SDYVVKTSN GYVTSKCSSS GGSTCAAPKS NQATVDLIAE FEGFRANIYT DAAGYATVGY 120
GHKCQKAKCA EVKYKIPLSK ADGKLLADD MRSFEVCITN MLNSKAKLNY NQFGALVWS 180
FNVGCQAALKS STLIKRLNNG ENVNKVLSEE LPKWNKAGGK VLQGLVRRRA AEVALAKKSG 240
SSQALPVKC                                249

SEQ ID NO: 265      moltype = DNA length = 801
FEATURE          Location/Qualifiers
sig_peptide     1..54
mat_peptide     55..798
source          1..801
mol_type = genomic DNA
organism = Trichoderma harzianum
CDS              1..798

SEQUENCE: 265
atgaagactg cttttgtc tccctggcat ccatcgtag cgccatcccc 60
atcaactggc atgttgtca ctcggcttggc ccacgtacgc catcaagaag 120
tcctacaaga agaacaaga catctccata acgtgtcaga cagcggaaac cagcgtcaat 180
ggcaacacgca ttgggataa gaccggccgac gggtgtcact tcgcccacta ctacgtcaag 240
acgggctcca gcggttacgt gaccaagaag tgcaactgtt cctccgggg cggctccctcg 300
tcaggactact gcaagaccat caacagcggc gggtgtcact tcatcgccaa gtggggaggc 360
ttcgtcggca cggccaaagcc cgacccatt gggttgccta cggccatctc 420
tgccagcaga agaactgtcag aggggtcaag tacaagtcc ccctgaccaa gaccaccc 480
aaggagatgc tgctggacga cctggccaaag tacacaaagt gcctcgccga ctaccta 540
gacaaggccca actcaatgc caacaggatgg gggccctgca cgtccctgggt cttaacatgc 600
ggctgcggca acgcaaaagac atcgacttc gtgaagcgc tcaacaacgg cgaggctgc 660
aacactgtt ctgcagagga actcccaag tggcgcattgg caggggaaa agtctggcc 720
ggctctcgagg ctgcggaaa ggacgaggtc aagtgttca agacggcgatc atcgaaggc 780
gcctatccaa atgtccatgt a                                801

SEQ ID NO: 266      moltype = AA length = 266
FEATURE          Location/Qualifiers
source           1..266
mol_type = protein
organism = Trichoderma harzianum

SEQUENCE: 266
MTATAAALVF SLASIVSAYP ITGDNVNCRT GPGTSYAIKK SYKKNQDISI SCQTAGTSVN 60
GNSIWDKTAD GCYVADYYVK TGSSGYVTKK CTASSGGSS SSYCKTINSV GVDLIAKWE 120
FVASPKPDPI GLPTVGYGHL CQQKNCREVK YKPLTLKTTA KELLDDLPK YTCKLADYL 180
DKPKLNANQW AALTSLWVFNV GCGNAKTSTL VKRLLNNGEA NTVAEEELPK WRMAGGKVLP 240
GLEARRKDEV KLFKTASSKQ AYPKQ                                266

SEQ ID NO: 267      moltype = AA length = 248
FEATURE          Location/Qualifiers
source           1..248
mol_type = protein
organism = Trichoderma harzianum

SEQUENCE: 267
YPITGDNVNC RTGPGTSYAI KKSYKKNQDI SISCQTAGTS VNGNSIWDTK ADGCYVADYY 60
VKTGSSGYVT KKCTASSGGG SSSYCKTIN SAGVDLIAKW EGFVASPKPD PIGLPTVGYG 120
HLCQQKNCRE VKYKFPLTKT TAKELLDDL PKYTKCLADY LNDKPKLNAN QWAALTSWVF 180
NVGCGNAKTS TLVKRLNNGE AANTVAAEEL PKWRMAGGKV LPGLEARRKD EVKLFKTASS 240
KQAYPKQ                                248

SEQ ID NO: 268      moltype = DNA length = 585
FEATURE          Location/Qualifiers
misc_feature    1..585
note = Synthetic construct

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sig_peptide          10..69
mat_peptide          70..576
source               1..585
mol_type = other DNA
organism = synthetic construct
CDS                  10..576
SEQUENCE: 268
ggatccacca tggcgaagt ctccactctc accatcgcat tgctcacgat ggcgtcgag 60
gcaaggccac agtgtgtggg ctgttaaacct ctcgcgatca acgcagccac agtggcggtg 120
atcaaagagt tccaaggctt cgtgcctaaa cctgcacccc atccgatccg ctcctctaca 180
gtcggctacg gccatctctg taaaactaaag ggtatgtaaag aggtccccata ctcttcct 240
ttgacccagg agactgccac gaaattgtctc cagtcggata tcaagacctt caccttcgt 300
gtctccaact acgtcaaaga ctcggctcaag ctcaacgaca accagttatgg agccttgcc 360
tgcgtggcct tcaacgtggg atgtgcgaaac gtgcagacat cgtgcgtcat taagcgctt 420
aacgcaggcg aacaaaaaaa caccgtcgca gcccaggagt tgccgaagtg gaagtatgcg 480
ggaggcaagg tcatgcctgg tctcgctcg aggaggaaacg cagagggtggc ccttcctaaag 540
aaggccttcgtt ccgtccaggc gcacccctctt aaatgtttaaa agctt 585

SEQ ID NO: 269      moltype = AA length = 189
FEATURE
REGION             1..189
source              note = Synthetic Construct
1..189
mol_type = protein
organism = synthetic construct
SEQUENCE: 269
MAKVSTLTIA LLTMASQARA QCVGCKPPPI NAATVALIKE FEGFVPKPAP DPIGLPTVGY 60
GHLCCKTKGCK EVPYSFPLTQ ETATKLLQSD IKTFTSCVSN YVKDSVKLND NQYGALASWA 120
FNVGCGNVQT SSLIKRLNAG ENPNTVAAQE LPKWKYAGGK VMPGLVRRRN AEVALFKKPS 180
SVQAHPPKC          189

SEQ ID NO: 270      moltype = AA length = 169
FEATURE
REGION             1..169
source              note = Synthetic construct
1..169
mol_type = protein
organism = synthetic construct
SEQUENCE: 270
QCVGCKPPPI NAATVALIKE FEGFVPKPAP DPIGLPTVGY GHLCCKTKGCK EVPYSFPLTQ 60
ETATKLLQSD IKTFTSCVSN YVKDSVKLND NQYGALASWA FNVGCGNVQT SSLIKRLNAG 120
ENPNTVAAQE LPKWKYAGGK VMPGLVRRRN AEVALFKKPS SVQAHPPKC          169

SEQ ID NO: 271      moltype = DNA length = 270
FEATURE
misc_feature        1..270
source              note = Synthetic construct
1..51
52..270
mol_type = other DNA
organism = synthetic construct
CDS                 1..270
SEQUENCE: 271
atgcacgttc tcccccttc caccgcaccc ctcttcggtc tcgcacggc ctaccatgt 60
aagaccgacc ttcaactggc ctccctcccg agcaacttcccg ccgcacatgt ccgcaccc 120
tccatgtggaa cggaaatcca gatccaggc tcgcacccgg gcacttcggc ccaaggatcc 180
aatgtctggg acaagaccca gcacgggttc tacgtcgacg actactatgt caagaccgg 240
cattctggaa ttttccaccac caagtgcggc 270

SEQ ID NO: 272      moltype = AA length = 90
FEATURE
REGION             1..90
source              note = Synthetic Construct
1..90
mol_type = protein
organism = synthetic construct
SEQUENCE: 272
MHALTLLTAT LFGLAAAYPV KTDLHCRSSP STSASIVRTY SSGTEVQIQC QTTGTQVQGS 60
NVWDKTKHGC YVADYYVKTG HSGIFTTKCG          90

SEQ ID NO: 273      moltype = AA length = 73
FEATURE
source              Location/Qualifiers
1..73
mol_type = protein
organism = Synthetic construct

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SEQUENCE: 273
YVKTDLHCR SSPSTSASIV RTYSSGTEVQ IQCQTTGTSV QGSNVWDKTQ HGCYVADYYV 60
KTGHSGIFTT KCG 73

SEQ ID NO: 274      moltype = DNA length = 37
FEATURE
misc_feature        Location/Qualifiers
1..37
note = Synthetic construct
source              1..37
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 274
agatctcgag aagcttatac cgcacttggt ggtgaaa 37

SEQ ID NO: 275      moltype = DNA length = 39
FEATURE
misc_feature        Location/Qualifiers
1..39
note = Synthetic construct
source              1..39
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 275
acacaactgg ggatccacca tgaagactgc ctttgctgc 39

SEQ ID NO: 276      moltype = DNA length = 38
FEATURE
misc_feature        Location/Qualifiers
1..38
note = Synthetic construct
source              1..38
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 276
agatctcgag aagcttatac ctggcacttt ggataggc 38

SEQ ID NO: 277      moltype = DNA length = 39
FEATURE
misc_feature        Location/Qualifiers
1..39
note = Synthetic construct
source              1..39
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 277
acacaactgg ggatccacca tgaagttcgc catcctcgc 39

SEQ ID NO: 278      moltype = DNA length = 39
FEATURE
misc_feature        Location/Qualifiers
1..39
note = Synthetic construct
source              1..39
mol_type = other DNA
organism = synthetic construct

SEQUENCE: 278
agatctcgag aagcttatac gcacttaaca ggaagagcc 39

SEQ ID NO: 279      moltype = AA length = 166
FEATURE
source              Location/Qualifiers
1..166
mol_type = protein
organism = Acremonium alcalophilum

SEQUENCE: 279
QCVGPEVNSA SINLIKEFEG WYPDIYVDPA GYPTVGYGHL CSDSSCSDVS YSIPLSEADG 60
ENLLRDDITN FQNCITWQTA SSVVLANQY GALVSWAFNV GCGASESSL IARLNAGEDP 120
NTVAEEELPR WNQGGGQVLP GLVRRRAAEV ELHQIPTDVA ALPACS 166

SEQ ID NO: 280      moltype = AA length = 157
FEATURE
source              Location/Qualifiers
1..157
mol_type = protein
organism = Acremonium alcalophilum

SEQUENCE: 280
QCVGPAINS A LNLIKEFEG WRPNIYRDPV GLPTVGYGHL CRDSSCSDVP YPIPLSVANG 60
ERLLRSIDLAT ASSVVLNANQ YGALVSWAFN VCGCATSTST LIRRLNAGES PNTVAAQELP 120
RWNKAGGQVL PGLVRRRAAE VELHRTSTSV RALPACS 157

SEQ ID NO: 281      moltype = length =
SEQUENCE: 281

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SEQ ID NO: 282      moltype = AA  length = 8
FEATURE
REGION
1..8
note = Synthetic construct
2
note = NON_CONS - The amino acid in position 2 of the
conserved motif is valine or isoleucine.
REGION
7
note = NON_CONS - The amino acid in position 7 of the
conserved motif is any amino acid.
source
1..8
mol_type = protein
organism = synthetic construct
SEQUENCE: 282
TXGYGHXC

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8

  

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SEQ ID NO: 283      moltype = AA  length = 15
FEATURE
REGION
1..15
note = Synthetic construct
3
note = NON_CONS - The amino acid in position 3 of the
conserved motif is any amino acid.
REGION
5
note = NON_CONS - The amino acid in position 5 of the
conserved motif is glutamic acid or glutamine.
REGION
6
note = NON_CONS - The amino acid in position 6 of the
conserved motif is phenylalanine, tryptophan or tyrosine.
REGION
7
note = NON_CONS - The amino acid in position 7 of the
conserved motif is alanine or glycine.
REGION
10
note = NON_CONS - The amino acid in position 10 of the
conserved motif is any amino acid.
REGION
12
note = NON_CONS - The amino acid in position 12 of the
conserved motif is leucine, phenylalanine or tryptophan.
REGION
13
note = NON_CONS - The amino acid in position 13 of the
conserved motif is any amino acid.
REGION
14
note = NON_CONS - The amino acid in position 14 of the
conserved motif is phenylalanine or tyrosine.
source
1..15
mol_type = protein
organism = synthetic construct
SEQUENCE: 283
LNXNXXXALX SXXXN

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15

  

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SEQ ID NO: 284      moltype = AA  length = 11
FEATURE
REGION
1..11
note = Synthetic construct
2
note = NON_CONS - The amino acid in position 2 of the
conserved motif is phenylalanine or tyrosine.
REGION
3
note = NON_CONS - The amino acid in position 3 of the
conserved motif is isoleucine or valine.
REGION
4
note = NON_CONS - The amino acid in position 4 of the
conserved motif is alanine, serine or threonine.
REGION
6
note = NON_CONS - The amino acid in position 6 of the
conserved motif is lysine, phenylalanine or tyrosine.
REGION
7
note = NON_CONS - The amino acid in position 7 of the
conserved motif is phenylalanine or tyrosine.
REGION
8
note = NON_CONS - The amino acid in position 8 of the
conserved motif is isoleucine or valine.
REGION
9
note = NON_CONS - The amino acid in position 9 of the

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source           conserved motif is any amino acid.
               1..11
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 284
CXXXDXXXXT G                               11

SEQ ID NO: 285      moltype = AA length = 9
FEATURE          Location/Qualifiers
REGION           1..9
note = Synthetic construct
REGION           1
note = NON_CONS - The amino acid in position 1 of the
               conserved motif is glutamic acid, glycine or valine.
REGION           3
note = NON_CONS - The amino acid in position 3 of the
               conserved motif is any amino acid.
REGION           4
note = NON_CONS - The amino acid in position 4 of the
               conserved motif is any amino acid.
REGION           7
note = NON_CONS - The amino acid in position 7 of the
               conserved motif is any amino acid.
REGION           8
note = NON_CONS - The amino acid in position 8 of the
               conserved motif is any amino acid.
source           1..9
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 285
XLXXRXXE                               9

SEQ ID NO: 286      moltype = AA length = 9
FEATURE          Location/Qualifiers
REGION           1..9
note = Synthetic construct
REGION           3
note = NON_CONS - The amino acid in position 3 of the
               conserved motif is any amino acid.
REGION           4
note = NON_CONS - The amino acid in position 4 of the
               conserved motif is any amino acid.
REGION           7
note = NON_CONS - The amino acid in position 7 of the
               conserved motif is any amino acid.
REGION           8
note = NON_CONS - The amino acid in position 8 of the
               conserved motif is any amino acid.
source           1..9
               mol_type = protein
               organism = synthetic construct
SEQUENCE: 286
GLXXRXXE                               9

SEQ ID NO: 287      moltype = DNA length = 961
FEATURE          Location/Qualifiers
sig_peptide      1..51
mat_peptide      52..958
source           1..961
               mol_type = genomic DNA
               organism = Trichophaea minuta
CDS              1..347
CDS              410..624
CDS              683..787
CDS              840..958
SEQUENCE: 287
atgcacgccc tcggccctcc cgccagcaacc ctcttcggtc tccgagggc ctacccagcg 60
aaagttgacc tccgctgccc ttccctctccc agcacctccg cgagcgtagt ccgcacctac 120
tccaaaggct cccaaatcca gatctcttcg cagaccacgg gcactccgt cgaaggctcc 180
aatgtctggg acaagaccca gcatggctgc tacgtcgccc actactacgt caagaccggg 240
cattctggaa ttccacaac caagtgcggc agcagcttg gtgggtgtc ttcaagccg 300
cccccgatca atgcggctac tggccgttg attaaggagt ttgagggtta agtggccgc 360
ggacttgggg agttagagact atggagctgg atgctgacgg gactactaga ttttgtcta 420
agcccgacc ggatccatt ggattgccga ctgtgggata tggtcatctt tgcaagacta 480
ggggctgcaa ggaggtgcct tacagttcc cgctcaccca gactaccgg accaagtgtc 540
tgcagagcga tatcaagact ttccacccctt gtgttagcaa ctacgtcaag gactctgtta 600

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agcttaacga taaccaggatc ggaggtaatt tccagtattc cccgttgc tgcataata	660
taatgattt gacgaaatgg agcttatacg tcgtgggtt tcaacgttgg ttgcggaaat	720
atccagactt ctccgtat caagagactg aatgtggaa agaacccaa cactgttgc	780
gctcagggtt agacccatctc actggatgtt atttggggg ggagctgaca aagtgcaga	840
actccctaag tggaaatatg ctggatggaaa ggttcttccc ggcttggtcc gcccggaa	900
ggctgagggtc ggcgtttca agaagccag cagcgtccag gcccacccctc ccaagtgtca	960
g	961

SEQ ID NO: 288	moltype = AA length = 262
FEATURE	Location/Qualifiers
source	1..262
	mol_type = protein
	organism = Trichophaea minuta
SEQUENCE: 288	
MHALALLAAT LFGLAAAYPA KVDLRCRSSP STSASVVRTY SKGSEIQISC QTTGTSVEGS	60
NWWDKTOHGC YVADYYVKTG HSGIFTTKG SSSGGGCKP PPINAATVAL IKEFEGFVAK	120
PAPDPIGLPT VGYGHLCKTK GCKEVPYSFP LTQTTATKLL QSDIKFTSC VSNYVKDSVK	180
LNDNQFGALS SWAFNVCGN IQTSSLIKRL NAGENPNTVA AQELPKWKYA GGKVLPGLVR	240
RRKAEVALFK KPSSVQAHPK KC	262

SEQ ID NO: 289	moltype = DNA length = 789
FEATURE	Location/Qualifiers
sig_peptide	1..51
source	1..789
	mol_type = other DNA
	organism = synthetic construct
mat_peptide	52..789
SEQUENCE: 289	
atgcacgcac tcgcgtctt ggcagccact ctcttcggc tcgcgcgcg ctatccgc	60
aagggtggacc tcgcgtgtcg ttctgtccctt tccacatccg cttccgtcg caggactt	120
tccaaaggccctt ccggatcca gattctgtcg cagaccacgg gcacatcggtt ggaaggctcc	180
aacgtgtggg acaagacgcgcac gcaaggctgt tacgtcgccg attactacgtt caagaccgg	240
cattcgggca tcttcacaac caagtgtgtt tccctcgccg gaggaggctc ctgttaacct	300
cctccgcgtaca acgcgcacac agtcgccttc atcaaggagt tcgaaggctt cgtggcaaaa	360
cctgcgcggccatccatcggtt tttggccactt gtggatactcg gccacttggtaa gacgaaaa	420
ggctgttaagg aggtgcctta ctccctccggtt ttagactcaga caacggcgcac gaaatttttgc	480
cagtgcggaca tcaaaatctt cacatccgtt gtgttcaactt acgtcaaggat ttcggtcaaa	540
ctcaacgata accagtccgg agcgtgtcg tcgtggccct tcaacgttgg atgtggcaac	600
atccagacgtt cgtcgatcat caagcgatcc aacgcggggaa cactgtcgca	660
gcccaggaaatcccgaaatggatatcggtt ggtggcaagg tccctccgggtt tttggtccga	720
aggcggaaagg cagaagtgcgcgtt aagccgtcg cggccggc acatccctccg	780
aagtgttaa	789

SEQ ID NO: 290	moltype = AA length = 262
FEATURE	Location/Qualifiers
REGION	1..262
source	note = Synthetic Construct
	1..262
	mol_type = protein
	organism = synthetic construct
SEQUENCE: 290	
MHALALLAAT LFGLAAAYPA KVDLRCRSSP STSASVVRTY SKGSEIQISC QTTGTSVEGS	60
NWWDKTOHGC YVADYYVKTG HSGIFTTKG SSSGGGCKP PPINAATVAL IKEFEGFVAK	120
PAPDPIGLPT VGYGHLCKTK GCKEVPYSFP LTQTTATKLL QSDIKFTSC VSNYVKDSVK	180
LNDNQFGALS SWAFNVCGN IQTSSLIKRL NAGENPNTVA AQELPKWKYA GGKVLPGLVR	240
RRKAEVALFK KPSSVQAHPK KC	262

SEQ ID NO: 291	moltype = AA length = 245
FEATURE	Location/Qualifiers
source	1..245
	mol_type = protein
	organism = Trichophaea minuta
SEQUENCE: 291	
YPAKVDLRCR SSPSTSASVV RTYSKGSEIQ ISCQTTGTSV EGSNWWDKTQ HGCVADYYV	60
KTGHSGIFTT KCGSSGGGS CKPPPINAAAT VALIKEFEGF VAKPAPDPIG LPTVGYGHLC	120
KTKGCKEVPT SFPLTQTTAT KLLQSDIKTF TSCVSNVVKD SVKLNDNQFG ALSSWFNVG	180
CGNIQTSSLI KRLNAGENPN TVAAQELPKW KYAGGKVLPG LVRRRKAeva LFKKPSSVQA	240
HPPKC	245

SEQ ID NO: 292	moltype = DNA length = 935
FEATURE	Location/Qualifiers
sig_peptide	1..54
mat_peptide	55..932
source	1..935
	mol_type = genomic DNA
	organism = Chaetomium sp.

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CDS	1..379	
CDS	448..578	
CDS	642..932	
<b>SEQUENCE: 292</b>		
atgaagttcg ctatcatcgc cgccgtcggtt cccttcctgg cccccgcctc ggcctacaag	60	
atctcgggca gtcgtcaaa ctgcggctcc gggcccgccca ccaactaccc cgtcaagaag	120	
acatacgcca acggtgacga ggtcaccatt agctgccaga ccacccggcac gaacgtggag	180	
ggcaacaaca tctggacaa gacccagcac gggtgtacg tcgcccacaa gtatgtcaag	240	
accggcaagg acgggttgtt cacaagaag tgccggcgtt ccgggtgggg tgggtggc	300	
aagacactgca aggcccaac gtcacacgcg gtatccgtt attgatgtc ttccgtc	360	
ggcttcgggg ccaatatccgtt tgatgtaccc cccgaaaggaa aagtggcat aagtgtgca	420	
gactcctaaac gactgtaccc ctttcagaca cggatgcac tggccacccc accgttggt	480	
acggccacat gtgcaccaag tccaggtcgcc cgaggtcaaa gtacaagatc ccgtctcc	540	
aggccgcacgg caagaactgtt ctcggccatcg acatggcggtt gagtcccatc catccctcc	600	
ttcacagact aacttactga cgcgccttc ccaatccatc gaaattcgag aagtgcata	660	
aggagatgtt caactcacaag gccaagctca acctgaacca gtaacggccc ctcgtca	720	
ggtccttcaa ctgcggctgc ggcgcgcaca agggctccca gtcgtcaac cgcctcaaca	780	
aggggcagaaa ccccaacacg gtccctctca acagagctcc caagtgggtc cacggcaacg	840	
gcaagggtgtt gcccgggttc gtcgcgcgcg gcaacgcgcgaa gattgcgcctc gccaagaaga	900	
gcccgcacgg cgcgcgcctg cccgtcaagt gctag	935	
<b>SEQ ID NO: 293</b>	moltype = AA length = 267	
<b>FEATURE</b>	Location/Qualifiers	
source	1..267	
	mol_type = protein	
	organism = Chaetomium sp.	
<b>SEQUENCE: 293</b>		
MKFAIIIAAVV PFLAPASAYK ISGSSVNCRS GPGTNYPVKY TYANGDEVTI SCQTTGTNVE	60	
GNNIWDKTQH GCYVADKYVK TGKDGFTKK CGSSGGGGG KTKCAPNSA ATVDLIASFE	120	
GFRANIYTDA TGHPTVGYGH MCTKSRCABV KYKIPLSKAD GKKLLADMA KFEKCIKEML	180	
NSKAKLNLNQ YGALVWSWFN VGCGAAKGSQ LVSLNKGPN PNTVLSNELP KWVGNGKVL	240	
PGLVRRRRAE IALAKKSGSG AALPVKC	267	
<b>SEQ ID NO: 294</b>	moltype = AA length = 249	
<b>FEATURE</b>	Location/Qualifiers	
source	1..249	
	mol_type = protein	
	organism = Chaetomium sp.	
<b>SEQUENCE: 294</b>		
YKISGSSVNC RSGPGTNYPV KKTYANGDEV TISCQTTGTN VEGNNIWDKT QHGCYVADKY	60	
VTKGKDGFVTK KKGCGGGGG GGKTKCAPKS NAATVDLIAS FEGFRANIYT DATGHPTVGY	120	
GHMCTKSRC A VKYKIPLSK ADGKLLADD MAKPEKCIKE MLNSKAQLNL NQYGALVWS	180	
FNVGCGAAKG SQLVSRLNKG ENPNTVLSNE LPKWVHGNGK VLPGLVRRRN AEIALAKKSG	240	
SGAALPVKC	249	
<b>SEQ ID NO: 295</b>	moltype = DNA length = 795	
<b>FEATURE</b>	Location/Qualifiers	
sig_peptide	1..57	
mat_peptide	58..792	
source	1..795	
	mol_type = genomic DNA	
	organism = Mortierella sp.	
CDS	1..792	
<b>SEQUENCE: 295</b>		
atgaagttca cgccgtccct tgctgccttg gctgcctcta tccccgcac gctggccat	60	
cccatcagg gtccgtatgc tctgcattgc cgttccggcc ctggtaatc gtacccatc	120	
aaaaagacgc tgcgtctcc ttaggatata aagatccat gccaggagcc tggtaacgtc	180	
gtcaacggcg tttagcgttg ggacaagacc cagttggct gtaacgtgtc cgattattat	240	
gtcaagactg tgcacggcaat ctacgtcgcc cctcgctgca acagegggtt cagctctagc	300	
gcttcactg ctgcgtacgc tgctggatcc aacttgcata aggagtttg aggcttcgtc	360	
cctccgcctc cgccggatcc cattggctt cccacgttgc gtaacgttca ttgtgc	420	
accaagggtt gcccggaggt caagtactca ttcccttta ccacccgcac cgccaccgt	480	
ttgctcaagg acgacccccc caagtacaca tgcgtcttg ccaaggccctt gaatggcaaa	540	
ccaaaactgaa cacaacca gtcggccgccc ctgcgtctgtt ggacgtttaa tggggctgt	600	
ggcaacatgaa aatcctcgat ctttgcatacg cggccatgtt ccccaact	660	
gtcgccaccc aggactccc caagtggaaa ctggctgtt gcaaggctt ccccggtct	720	
gtccgtctgtt gtcgtccgaa ggtcaagctg ttcaagacgg ccaacttcc ccagggttat	780	
cctaagtgtt cttaa	795	
<b>SEQ ID NO: 296</b>	moltype = AA length = 264	
<b>FEATURE</b>	Location/Qualifiers	
source	1..264	
	mol_type = protein	
	organism = Mortierella sp.	
<b>SEQUENCE: 296</b>		
MKFTLALAAL AASIPATLAY PITGADALHC RSGPGTSYPI QKTLRPPQDI KIQCQEPGT	60	

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VNGVSLWDKT QFGCYVSDYY VKTGTGNYVA PRCNSGGSSS ACTGLNDAGI NLIKEFEGFV	120
PRPAPDPIGL PTVGYGHLCQ TKCGCEVKYS FPLTTATATA LLKDDLPKYT SCLAKALNGK	180
PKLKNKNQWA LASWTFNVGC GNMKSSSLIT RLNAGQNPNT VATEELPKWK LAGGKVLPGL	240
VRRRAAEVKL FKTANSSQGY PKCA	264
SEQ ID NO: 297	moltype = AA length = 245
FEATURE	Location/Qualifiers
source	1..245
	mol_type = protein
	organism = Mortierella sp.
SEQUENCE: 297	
YPITGADALH CRSGPGTSYP IQKTLRPPQD IKIQCQEPTG VVNGVSLWDK TQFGCYVSDY	60
YVKTGTGNYV APRCNSSGGSS SACTGLNDAG INLIKEFEGF VPRPAPDPIG LPTVGYGHLC	120
QTKGCGEVKY SFPLTTATAT ALLKDSDLPK TSCLAKALNG KPKLNKNQWA ALASWTFNVG	180
CGNMKSSSLI TRLNAGQNPNT TVATEELPKW KLGGKVLPG LVRRRAAEVK LFKTANSSQG	240
YPKCA	245
SEQ ID NO: 298	moltype = DNA length = 801
FEATURE	Location/Qualifiers
sig_peptide	1..57
mat_peptide	58..798
source	1..801
	mol_type = genomic DNA
	organism = Metarhizium sp.
CDS	1..798
SEQUENCE: 298	
atgaagtttc tggctgttgc aaatgtcttg gcaatgacat ccactgttgt agttgcctac	60
ccaggtttctg ctgatagtct caactgcccga gcccggccaa acaccaggc tcggcatcaaa	120
acacacctaca agaagggtga agatgtcaaa atttcctgcg agaccgaggg tccctccatc	180
aacggcaaca ccatctggga caaagcccaa gatggttgtc acgtcgccga ctactacgtc	240
aaaacccggat cctctggcata cgtcaactggc aaatgcggcg sttagcagttt cccaaagcgg	300
tccggctttt gcaagacggt aaacaaggcg ggccctcgatc tcatcaccaa gtggaaaggc	360
tttggttcca gcccccgggg cgaccatcggc ggccctgcata ctgttgccca tgccatctc	420
tgccagaaga agggctgcgc cgaagtcaag tacaagtcc ctttgaccaa ggccactgcc	480
ctgcagtc tcaacqacga tctccccaaq tataccggctt gcctcggccaa gctccctcaac	540
agcaaggtaa acgttcaatgaa caatcgtggc gggctctgtt cttccctgggt ttcaacgtt	600
ggatgtggca acgctcagtc ttccctctttt gtcagacgtc tcaacaatgg cgagaacccc	660
aacacagttt ctcccagtga gcttccaaag tggaaaatgg ccgggtggtaa ggtgtggag	720
ggcttggtaa aacgcggcgtc tgacgagggtc agacttctca aggtttcttc ttccaaggc	780
gcattccca aatgccatgt g	801
SEQ ID NO: 299	moltype = AA length = 266
FEATURE	Location/Qualifiers
source	1..266
	mol_type = protein
	organism = Metarhizium sp.
SEQUENCE: 299	
MKFLAVANVL AMTSTVVVAY PVSADSLNCR AEPNTSSAIK TTYKKGEDVK ISCQTEGPSI	60
NGNTIWDKTQ DGCYVADYYV KTGSSEYVIG KCGGSSPPSG SGFCCKTVNKA GLDLITKWE	120
FVSSPRGDPI GLPTVGYGH CQKKGCAEVK YKFPLTKATA LQLLNDDLPK YTGCLGKLLN	180
SVKVLNDNQW AALT SWVFNV GCGNAQSSSL VRRLNNNGENP NTVAPSELPK WKMAGGKVLE	240
GLVKRRADEV RLFKVSSSKG AFPKCQ	266
SEQ ID NO: 300	moltype = AA length = 247
FEATURE	Location/Qualifiers
source	1..247
	mol_type = protein
	organism = Metarhizium sp.
SEQUENCE: 300	
YPVSAIDLNC RAEPNTSSAI KTTYKKGEDV KISCQTEGPS INGNTIWDKT QDGCVADYY	60
VTKGSSGYVT GKCGGSSPPS GSGFCCKTVNKA AGLDLITKWE GFVSSPRGDPI IGLPTVGYGH	120
LCQKKGCAEVK KYKFPLTKAT ALQLLNDDLPK KYTGCLGKLL NSKVVLNDNQ WAALT SWVFN	180
VGGGNAQSSS LVRRRLNNGEN PNTVAPSELPK KWKMAGGKVLE EGLVKRRADEV VRLFKVSSSK	240
GAFPKCQ	247
SEQ ID NO: 301	moltype = DNA length = 921
FEATURE	Location/Qualifiers
sig_peptide	1..54
mat_peptide	55..918
source	1..921
	mol_type = genomic DNA
	organism = Geomyces auratus
CDS	1..382
CDS	440..570
CDS	628..918
SEQUENCE: 301	

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cccattaccg	gcagacttgt	caactgcgc	actggggcag	gaacgagcca	tggcgtaag	120
acatcataca	agaagggcc	cgaagtaacg	gtatctcg	agaccggagg	aaccatgtg	180
aacggcaat	caatctgg	taagacatc	gatggcttt	atgttgcga	ttaactatgtt	240
aagactgggt	caagcgcta	cgtgaagccc	aagtgcgggt	cctcttcgg	aggtggaggc	300
ggaagcagt	gtgggtcac	taaatctaa	gctgtactg	tcaacctgt	tgcgaattt	360
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actggccaaac	ttgtatgata	taccgcacgt	actggtaacc	ctactgtccg	ctatggccat	480
ctctgcgcga	actcgaagt	ctctggcata	ggataactaa	ttccatatctc	caaggccat	540
gctaagaagg	ttctcgccaa	ggacatgggt	gtaaatgtc	accgtatgtt	gaagatcccc	600
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agcaactgtca	ttccctcaaga	gcttccaaag	tgggtatatg	gtgggagcag	cgtcttctt	840
ggtttggttc	ggctctgtca	cgctgagatt	gctgttgcta	aaaaggctac	atcgagcaag	900
qactccqqq	ctactgtcta	a				921

SEQ ID NO: 302 moltype = AA length = 268  
FEATURE Location/Qualifiers  
source 1..268  
mol\_type = protein  
organism = Geomyces auratus

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SEQUENCE: 302
MKLSLLAVGA VACSFVSAAF PITGSTVNCR TPGTSHGVK TSYKKHGHEVT VSCQGGTSV 60
NGNSIWDKTS DGCYVADYYYV KTGSSSGVKP KCGSSSSGGG GSASCAPKSN AATVLNIAE 120
EGFVSHVYTD ATGHPTVGYH HLCNSNSKCSG IGYSIPISKA NAKKLAKDM AIAEKCITAM 180
INKSRTLNIN QYQALVSWAF NEGGCAAKS TLKRINNGE KPSTVIPQEL PKWVYGGSSV 240
LPGLVRRRNA EIALAKKATS SKALPAHC 268

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SEQ ID NO: 303 moltype = AA length = 250  
FEATURE Location/Qualifiers  
source 1..250  
mol\_type = protein  
organism = Geomyces auratus

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SEQUENCE: 303
A1F2I3T4G5S6T7V8N9C10R11G12P13G14T15S16H17G18K19G20H21E22V23T24S25C26Q27T28G29G30T31V32N33G34N35S36I37W38D39K40T41S42D43G44C45Y46V47A48D49Y50V51A52D53Y54V55Y5660
Y57V58K59T60G61S62G63S64G65C66G67A68P69K70A71T72N73A74T75V76L77I78N79A80T81G82H83P84T85G86V87H88S89V90T91D92A93T94G95H96P97T98V99H100120
Y101G102H103Y104G105S106C107N108S109C110N111S112G113S114C115N116I117K118R119L120A121K122L123L124K125A126E127A128E129K130C131I132M133A134N135K136S137R138T139L140N141Q142Y143G144A145V146L147W148Q149S150V151R152R153S154V155R156A157K158A159L160180
A161F162N163E164G165C166A167K168G169A170K171Q172A173E174K175C176I177M178N179K180R181T182L183N184Q185Y186G187A188K189A190K191Q192180
A193F194N195E196G197C198A199K200G201A202K203Q204A205E206K207C208I209M210N211K212R213T214L215N216Q217Y218G219A220K221A222K223Q224240
A225F226N227E228G229C230A231K232G233A234K235Q236A237E238K239C240I241M242N243K244R245T246L247N248Q249Y250G251A252K253A254K255Q256250
T257T258S259S260T261L262A263P264A265H266P267A268I269R270I271N272R273A274K275A276L277A278K279A280K281250
T282T283S284S285T286L287A288P289A290H291P292A293I294R295I296N297R298A299K300A301L302A303K304A305K306250

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SEQ ID NO: 304 moltype = DNA length = 902  
FEATURE Location/Qualifiers  
sig\_peptide 1..54  
mat\_peptide 55..899  
source 1..902  
mol\_type = genomic DNA  
organism = Ilyonectria rufa  
CDS 1..352  
CDS 418..548  
CDS 609..899

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CDS          809..899
SEQUENCE: 304
atgaagtctt ctctttgc tggctatgt cttgcagcat ccctgactag cgcctataag 60
atcacccggta acaatgtcaa ctggccaga ggtccaggca cttagctactc cgtaaaaggagg 120
tcccttcaaga agggactga ttgttaccca ttgttgc tccacccggaga aaatgttttgc 180
ggtaactgtt a tctgggacaa gaccatcat ggtgtctatg ttcggacta ctatgtcaag 240
acaggctcca gcggttttgtt cgttaaaaag tgccgttactt ggggtggcc gaagtcgaac 300
ggggctaccg tgaatctcat ctccgatttcc gagggttca gggcgaatat ctgttaagtgt 360
tctttgttct ttgaagacaa taccggaga tttagttatgc taatacgctg gcattagacaa 420
aggatgtctc tggctatccc actgtcgat atgggcacct ctgcagcaac tcggatgtca 480
ccgcacgtccc gtacttata ccaactgtca aggccaaatc aaaaaactc ctgcacactc 540
acatgacagt aagtattctc ctcttagcatt caactttcc acactcatttgc acaccccttc 600
ttttacagaa attcgagaag tgcatcacag ccatggtcg cagtcctcg actctcaaca 660
agaaccaga tggcccttg gtcaagctggg cttcaacat gggttgcggc gccactaaga 720
cgtctacccat gatcaagcgc ctcaacccgg gccagaaacgt gaacacgttgc ttgttactcg 780
agtcgtccggaa gtgggtgtac gcaagggtggca aqaagctcaa tggttttgtt cggccggc 840
acgcggagat tgctttggct aagaagaaga ccacccggaaa ggcttcccg aacaagtgtc 900
ag

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SEQ ID NO: 305 moltype = AA length = 258  
FEATURE Location/Qualifiers  
source 1..258  
mol\_type = protein  
organism = *Ilyonectria rufa*

SEQUENCE: 305 Organism = *Myxobacteria fulva*  
MKFSLFAVAYA LAASLTSAYK ITGDNVNCRS GPGTTSYSVKR SFKKGTDVTL SCOTTGENVL 60

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GTTSIWDKTSY GCYVSDYYVK TGSSGFVVKK CGTCGAPKSN AATVNLISDF EGFRANIYKD	120
AAGYPTVGYG HLCSNSRCTD VPYSIPLSKA NGKNLLATDM TKFEKCITAM VSSSVTLNKN	180
QY GALVSWAF NMCGCATKTS TLIKRLNQQ NVNTVLSTEL PKWVYAGGKK LNGLVRRNA	240
EITALAKKTT EKALPNKC	258
 SEQ ID NO: 306	moltype = AA length = 240
FEATURE	Location/Qualifiers
source	1..240
	mol_type = protein
	organism = Ilyonectria rufa
 SEQUENCE: 306	
YKITGDNVNC RSGPGTYSV KRSPFKKGTDV TLSCQTTGEN VLGTSIWDKT SYGCYVSDYY	60
VKTGSSGFV KKCGTCGAPK SNAATVNLS DFEGRANIY KDAAGYPTVG YGHLCNSRC	120
TDVPYSIPLS KANGKNLLAT DMTKFEKCIT AMVSSVTLN KNQY GALVSW AFNMGCCATK	180
TSTLIKRLNQ QGNVNTVLST ELPKWVYAGG KKLNGLVRRA NAEIALAKKK TTEKALPNKC	240

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That which is claimed:

1. A recombinant host cell comprising a nucleic acid construct or expression vector comprising a polynucleotide encoding a polypeptide having lysozyme activity, wherein the polynucleotide is operably linked to one or more control sequences that direct the production of the polypeptide in a recombinant host cell and wherein the polypeptide has at least 80% sequence identity to SEQ ID NO: 264.
2. A method comprising cultivating the recombinant host cell of claim 1 under conditions conducive for production of said polypeptide.
3. An animal feed additive comprising a polypeptide having lysozyme activity and at least 80% sequence identity to SEQ ID NO: 264.
4. The animal feed additive of claim 3, wherein the polypeptide has at least 85% sequence identity to SEQ ID NO: 264.
5. The animal feed additive of claim 3, wherein the polypeptide has at least 90% sequence identity to SEQ ID NO: 264.
6. The animal feed additive of claim 3, wherein the polypeptide has at least 95% sequence identity to SEQ ID NO: 264.
7. The animal feed additive of claim 3, wherein the polypeptide has at least 97% sequence identity to SEQ ID NO: 264.
8. The animal feed additive of claim 3, wherein the polypeptide has at least 99% sequence identity to SEQ ID NO: 264.
9. The animal feed additive of claim 3, wherein the polypeptide comprises SEQ ID NO: 264.
10. The animal feed additive of claim 3, wherein the polypeptide comprises a Glycoside Hydrolase Family 24 (GH24) catalytic domain and a lysozyme enhancing domain.
11. The animal feed additive of claim 3, wherein the polypeptide comprises a GH24 catalytic domain comprising motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252)

12. The animal feed additive of claim 3, wherein the polypeptide comprises a GH24 catalytic domain comprising motif II: LNXN[QE][YFW][GA]ALXS[WFL]X[YF]N (SEQ ID NO: 283).

13. The animal feed additive of claim 3, wherein the polypeptide comprises a lysozyme enhancing domain comprising motif III: [CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN] (SEQ ID NO: 254).

14. The animal feed additive of claim 3, wherein the polypeptide comprises:

- (a) GH24 catalytic domain comprising motif I: [TAS][VIL][GAC][YFI]GHX[CAYIV] (SEQ ID NO: 252) and/or a GH24 catalytic domain comprising motif II: LNXN[QE][YFW][GA]ALXS[WFL]X[YF]N (SEQ ID NO: 283); and
- (b) a lysozyme enhancing domain comprising motif III:

(SEQ ID NO: 254)  
[CGY][YF][VIL][ASTP][DG]X[YF][VIT]X[TS][GAN].

15. The animal feed additive of claim 3, further comprising one or more components selected from additional enzymes, amino acids, antibiotics, forages, microbes, minerals, and vitamins.

16. A method comprising administering the animal feed additive of claim 3 to an animal.

17. The method of claim 3, wherein the animal is a ruminant.

18. The method of claim 3, wherein the animal is monogastric.

19. The method of claim 3, wherein the animal is a poultry.

20. The method of claim 3, wherein the animal is a swine.

\* \* \* \* \*