US009624270B2

(12) **United States Patent**
Smith et al.

(10) **Patent No.: US 9,624,270 B2**
(45) **Date of Patent: Apr. 18, 2017**

(54) **ENGINEERING THE PRODUCTION OF A CONFORMATIONAL VARIANT OF OCCIDIOFUNGIN THAT HAS ENHANCED INHIBITORY ACTIVITY AGAINST FUNGAL SPECIES**

(71) Applicants: **THE TEXAS A&M UNIVERSITY SYSTEM**, College Station, TX (US); **MISSISSIPPI STATE UNIVERSITY**, Starkville, MS (US)

(72) Inventors: **James Leif Smith**, College Station, TX (US); **Akshaya Ravichandran**, College Station, TX (US); **Shien Lu**, College Station, TX (US); **Ganyu Gu**, Painter, VA (US)

(73) Assignees: **MISSISSIPPI STATE UNIVERSITY**, Starkville, MS (US); **THE TEXAS A&M UNIVERSITY SYSTEM**, College Station, TX (US)

(*) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 0 days.

(21) Appl. No.: **14/090,679**

(22) Filed: **Nov. 26, 2013**

(65) **Prior Publication Data**

US 2014/0147416 A1 May 29, 2014

Related U.S. Application Data

(60) Provisional application No. 61/731,105, filed on Nov. 29, 2012.

(51) **Int. Cl.**

C07K 7/54	(2006.01)
A61K 38/12	(2006.01)
A01N 43/713	(2006.01)
A01N 63/00	(2006.01)
A01N 63/02	(2006.01)
C12N 9/16	(2006.01)
C07K 7/56	(2006.01)

(52) **U.S. Cl.**

CPC ***C07K 7/54*** (2013.01); ***A01N 43/713*** (2013.01); ***A01N 63/00*** (2013.01); ***A01N 63/02*** (2013.01); ***A61K 38/12*** (2013.01); ***C07K 7/56*** (2013.01); ***C12N 9/16*** (2013.01); ***C12Y 301/02*** (2013.01)

(58) **Field of Classification Search**

CPC C07K 7/54; A01N 43/713; A01N 63/00; A61K 38/12

See application file for complete search history.

(56) **References Cited**

U.S. PATENT DOCUMENTS

7,560,252 B2 * 7/2009 Salas et al. 435/76
2011/0136729 A1 6/2011 Lu et al.

OTHER PUBLICATIONS

Thomson, E.L., and Dennis J.J. "A Burkholderia cepacia complex non-ribosomal peptide-synthesized toxin is hemolytic and required for full virulence", Virulence, May 2012, vol. 3, pp. 286-298.*

Baysal, C. et al. "Free Energy Based Populations of Interconverting Microstates of a Cyclic Peptide Lead to the Experimental NMR Data," *Biopolymers*, Feb. 1999, pp. 329-344, vol. 50.

Boddy, C. N. "Sweetening Cyclic Peptide Libraries," *Chemistry & Biology*, Dec. 2004, pp. 1599-1606, vol. 11, No. 15.

Boguslavsky, V. et al. "Effect of peptide conformation on membrane permeability," *J. Peptide Res.*, 2003, pp. 287-297, vol. 61.

Delagio, F. et al. "NMRPipe: A multidimensional spectral processing system based on UNIX pipes," *Journal of Biomolecular NMR*, 1995, pp. 277-293, vol. 6.

Ellis, D. et al. "Occidiofungin's Chemical Stability and In Vitro Potency against *Candida* Species," *Antimicrobial Agents and Chemotherapy*, Nov. 2011, pp. 765-769, vol. 56, No. 2.

Fernandez-Lopez, S. et al. "Antibacterial agents based on the cyclic D,L-α-peptide architecture," *Nature*, Jul. 26, 2001, pp. 452-455, vol. 412.

Fischbach, M. A. et al. "Assembly-Line Enzymology for Polyketide and Nonribsomal Peptide Antibiotics: Logic, Machinery, and Mechanisms," *Chem. Rev.*, Jul. 7, 2006, pp. 3468-3496, vol. 106, No. 8.

Fridkin, G. et al. "Azo cyclization: peptide cyclization via azo bridge formation," *The Journal of Peptide Research*, 2002, pp. 104-111, vol. 60.

Gu, G. et al. "Biosynthesis of an antifungal oligopeptide in Burkholderia contaminans strain MS14," *Biochemical and Biophysical Research Communications*, 2009, pp. 328-332, vol. 380.

Gu, G. et al. "AmbR1 is a key transcriptional regulator for production of antifungal activity of *Burkholderia contaminans* strain MS14," *FEMS Microbiol Lett*, 2009, pp. 54-60, vol. 297.

Gu, G. et al. "Genetic and Biochemical Map for the Biosynthesis of Occidiofungin, an Anitfungal Produced by *Burkholderia contaminans* Strain MS14," *Applied and Environmental Microbiology*, Sep. 2011, pp. 6189-6198, vol. 77, No. 17.

Heikkinen, S. et al. "Quantitative 2D HSQC (Q-HSQC) via Suppression of J-Dependence of Polarization Transfer in NMR Spectroscopy: Application to Wood Lignin," *J. Am. Chem. Soc.*, 2003, pp. 4362-4367, vol. 125, No. 14.

Jelokhani-Niaraki, M. et al. "Conformation and other biophysical properties of cyclic antimicrobial peptides in aqueous solutions," *J. Peptide Res.*, 2001, pp. 293-306, vol. 58.

Jelokhani-Niaraki, M. et al. "Interaction of Gramicidin S and its Aromatic Amino-Acid Analog with Phospholipid Membranes," *Biophysical Journal*, Oct. 2008, pp. 3306-3321, vol. 95, No. 7.

Johnson, B. A. et al. "NMR View: A computer program for the visualization and analysis of NMR data," *Journal of Biomolecular NMR*, 1994, pp. 603-614, vol. 4.

Koglin, A. et al. "Conformational Switches Modulate Protein Interactions in Peptide Antibiotic Synthetases," *Science*, Apr. 14, 2006, pp. 273-276, vol. 312, No. 5571.

(Continued)

Primary Examiner — Paul Holland

(74) *Attorney, Agent, or Firm* — Butler Snow LLP

(57) **ABSTRACT**

Occidiofungin is a cyclic nonribosomally synthesized antifungal peptide with submicromolar activity. This invention is directed to compositions enriched for particular occidiofungin diastereomers/conformers, methods of making compositions enriched for particular diastereomers/conformers and microorganisms suitable for producing enriched compositions of particular diastereomers/conformers. Methods of treating fungal infections or plants infected by fungi are also provided.

1 Claim, 14 Drawing Sheets
(4 of 14 Drawing Sheet(s) Filed in Color)

(56) **References Cited**

OTHER PUBLICATIONS

Koglin, A. et al. "Structural basis for the selectivity of the external thioesterase of the surfactin synthetase," *Nature*, Aug. 14, 2008, pp. 907-912, vol. 454.

Kohli, R. M. et al. "The thioesterase domain from a nonribosomal peptide synthetase as a cyclization catalyst for integrin binding peptides," *PNAS*, Feb. 5, 2002, pp. 1247-1252, vol. 99, No. 3.

Kohli, R. M. et al. "Biomimetic synthesis and optimization of cyclic peptide antibiotics," *Nature*, Aug. 8, 2002, pp. 658-661, vol. 418.

Lautru, S. et al. "Substrate recognition by nonribosomal peptide synthetase multi-enzymes," *Microbiology*, 2004, pp. 1629-1636, vol. 150.

Un, Z. et al. "Burkholdines from *Burkholderia ambifaria*: Antifungal Agents and Possible Virulence Factors," *Journal of Natural Products*, Sep. 18, 2012, pp. 1518-1523, vol. 75, No. 9.

Liao, G. et al. "Regulation Mechanisms Underlying the Biosynthesis of Daptomycin and Related Lipopeptides," *Journal of Cellular Biochemistry*, 2012, pp. 735-741, vol. 113.

Lu, S. et al "Occidiofungin, a Unique Antifungal Glycopeptide Produced by a Strain of *Burkholderia contaminans," Biochemistry*, 2009, pp. 8312-8321, vol. 48, No. 35.

Lu, S. et al. "Characterization of the salA, syrF, and syrG Regulatory Genes Located at the Right Border of the Syringomycin Gene Cluster of *Pseudomonas syringae* pv. *syringae*," MPMI, 2002, pp. 43-53, vol. 15, No. 1.

NCBI, GenBank accession No. ADT64850.1, "putatitve thioesterase [Burkholderia contaminans]," Dec. 13, 2010.

NCBI, GenBank accession No. ACL81527.1, "putative nonribosomal peptide synthetase [Burkholderia contaminans]," Dec. 13, 2010.

Prentki, P. et al. "The Plasmid cloning vector pBR325 contains a 482 base-pair-long inverted duplication," *Gene*, 1981, pp. 289-299, vol. 14.

Rai, R. K. et al. "Quantification of Metabolites from Two-Dimensional Nuclear Magnetic Resonance Spectroscopy: Application to Human Urine Samples," *Analytical Chemistry*, Dec. 15, 2009, pp. 10232-10238, vol. 81, No. 24.

Rayan, A. et al. "Exploring the conformational space of cyclic peptides by a stochastic search method," *Journal of Molecular Graphics and Modeling*, 2004, pp. 319-333, vol. 22.

Ravichandran, A. et al. "The Presence of Two Cyclase Thioesterases Expands the Conformational Freedom of the Cyclic Peptide Occidiofungin," *Journal of Natural Products*, Feb. 8, 2013, pp. 150-156, vol. 76. No. 2.

Samel, S. A. et al. "The Thioesterase Domain of the Fengycin Biosynthesis Cluster: A Structural Base for the Macrocyclization of a Non-ribosomal Lipopeptide," *J. Mol. Biol.*, 2006, pp. 876-889, vol. 359.

Schwarzer, D. et al. "Exploring the impact of different thioesterase domains for the design of hybrid peptide synthetases," *Chemistry & Biology*, 2001, pp. 997-1010, vol. 8, No. 10.

Sieber, S. A. et al. "Learning from Nature's Drug Factories: Nonribosomal Synthesis of Macrocyclic Peptides," *Journal of Bacteriology*, Dec. 2003, pp. 7036-7043, vol. 185, No. 24.

Tan, W. et al. "Nonclinical Toxicological Evaluation of Occidiofungin, a Unique Glycolipopeptide Antifungal," *International Journal of Toxicology*, Jun. 11, 2012, pp. 326-336, vol. 31, No. 4.

Thomson, E. L. S. et al. "A *Burhholderia cepacia* complex nonribosomal peptide-synthesized toxin is hemolytic and required for full virulence," *Virulence*, May/Jun. 2012, pp. 286-298, vol. 3, No. 3.

Tseng, C. C. et al. "Characterization of the Surfactin Synthetase C-Terminal Thioesterase Domain as a Cyclic Depsipeptide Synthase," *Biochemistry*, 2002, pp. 13350-13359, vol. 41, No. 45.

Walsh, C. T. "Polyketide and Nonribosomal Peptide Antibiotics: Modularity and Versatility," *Science*, Mar. 19, 2004, pp. 1805-1810, vol. 303, No. 5665.

White, C. J. et al. "Contemporary strategies for peptide macrocyclization," *Nature Chemistry*, Jul. 23, 2011, pp. 509-524, vol. 3.

Yeh, E. et al. "Type II Thioesterase Restores Activity of a NRPS Module Stalled with an Aminoacyl-S-enzyme that Cannot Be Elongated," *ChemBioChem*, 2004, pp. 1290-1293, vol. 5.

Bonmatin, J.-M. et al. "Diversity Among Microbial Cyclic Lipopeptides: Iturins and Surfactins. Activity-Structure Relationships to Design New Bioactive Agents" *Combinatorial Chemistry & High Throughput Screening*, 2003, pp. 541-556, vol. 6, No. 6.

Alexeyev, M. F. et al. "Three Kanamycin Resistance Gene Cassettes with Different Polylinkers" *Biotechniques*, 1995, pp. 52 and 54, vol. 18, No. 1.

Vilhena, C. et al. "Daptomycin: A Review of Properties, Clinical Use, Drug Delivery and Resistance" *Mini-Reviews in Medicinal Chemistry*, 2012, pp. 202-209, vol. 12.

* cited by examiner

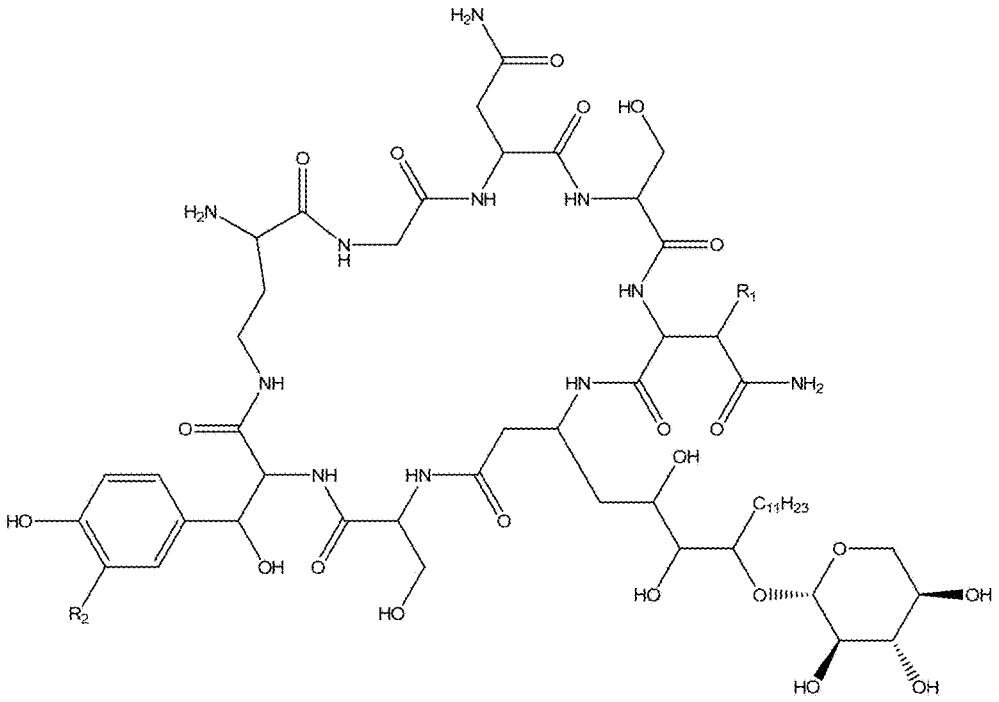

H2N
O
HO
O
O
NH
HN
H2N
N
H
O
HN
R1
NH
HN
NH2
O
O
O
OH
NH
HN
O
HO
C11H23
OH
O
HO
O
OH
R2
HO
HO
OH

FIGURE 1

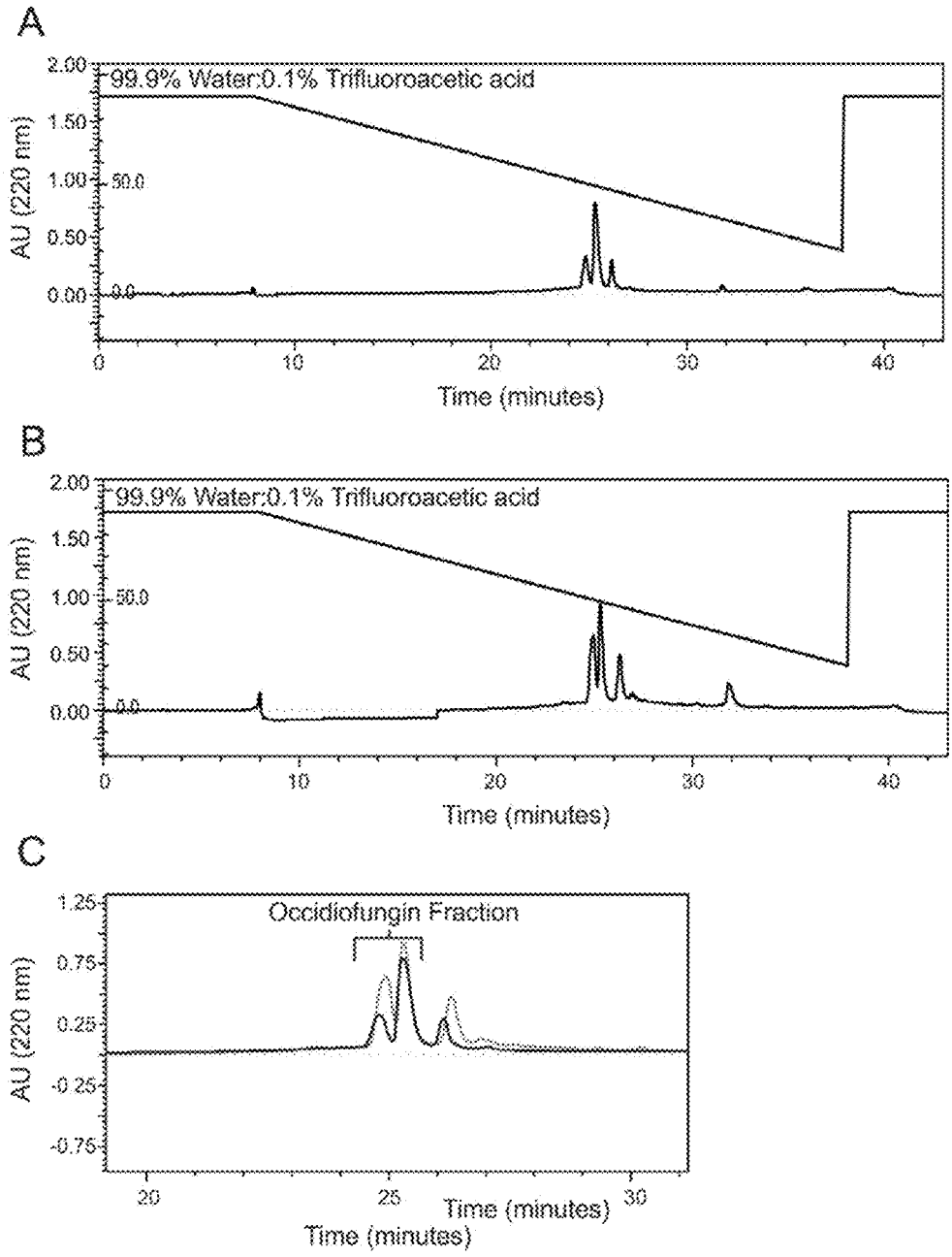

A
99.9% Water:0.1% Trifluoroacetic acid
AU (220 nm)
Time (minutes)
B
99.9% Water:0.1% Trifluoroacetic acid
AU (220 nm)
Time (minutes)
C
Occidiofungin Fraction
AU (220 nm)
Time (minutes)
Time (minutes)

FIGURE 2

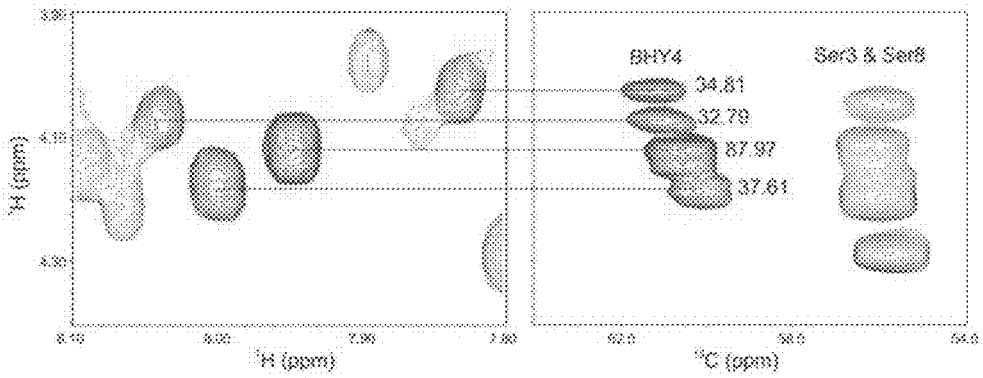


FIGURE 3

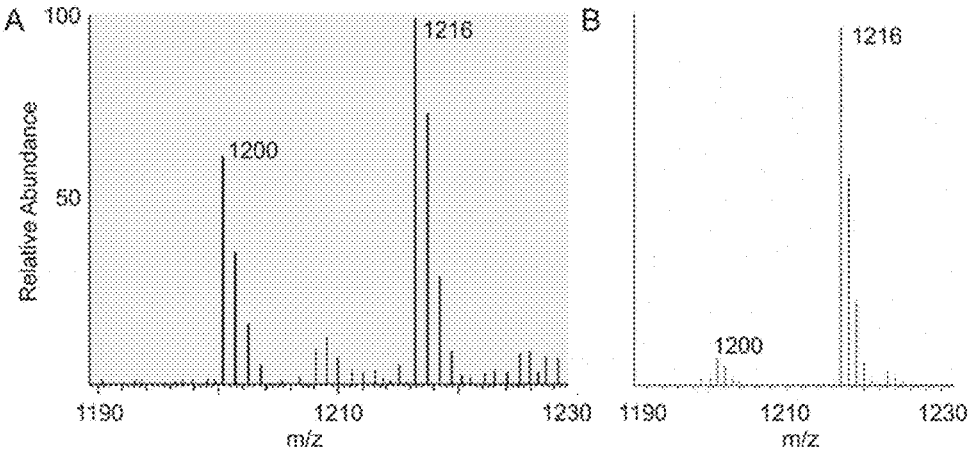


FIGURE 4

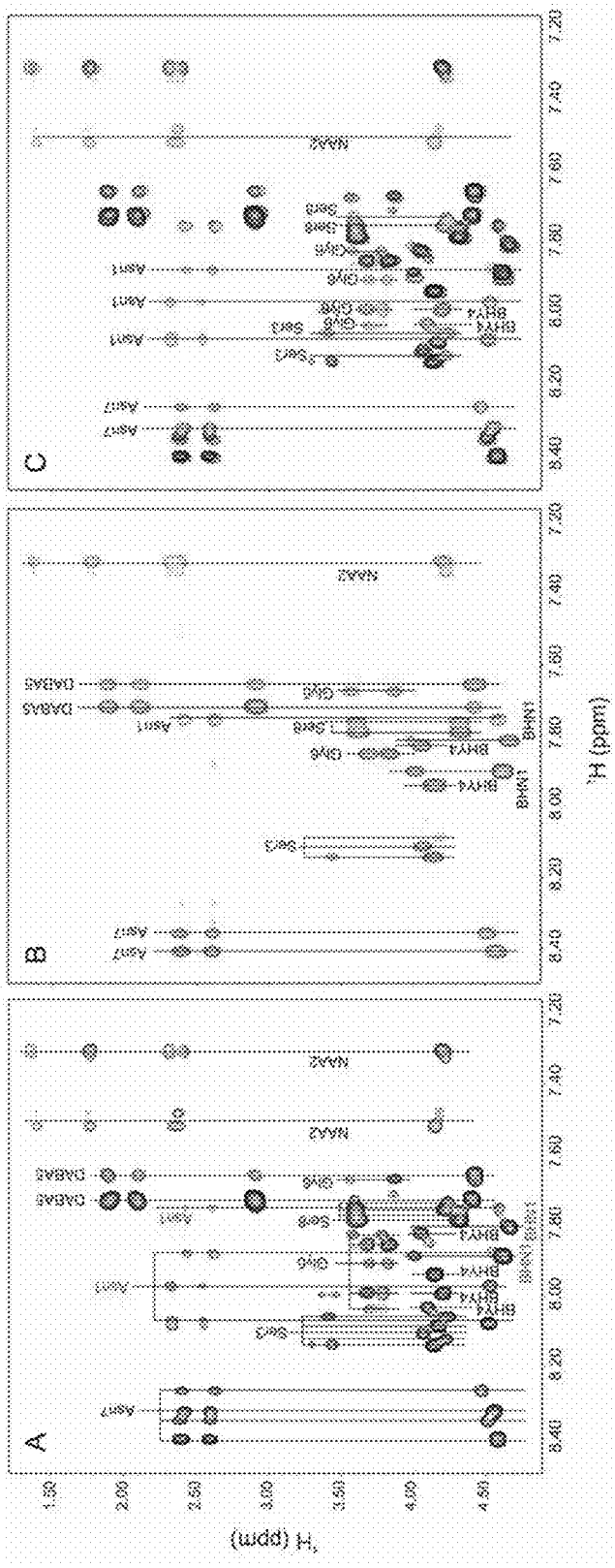


FIGURE 5

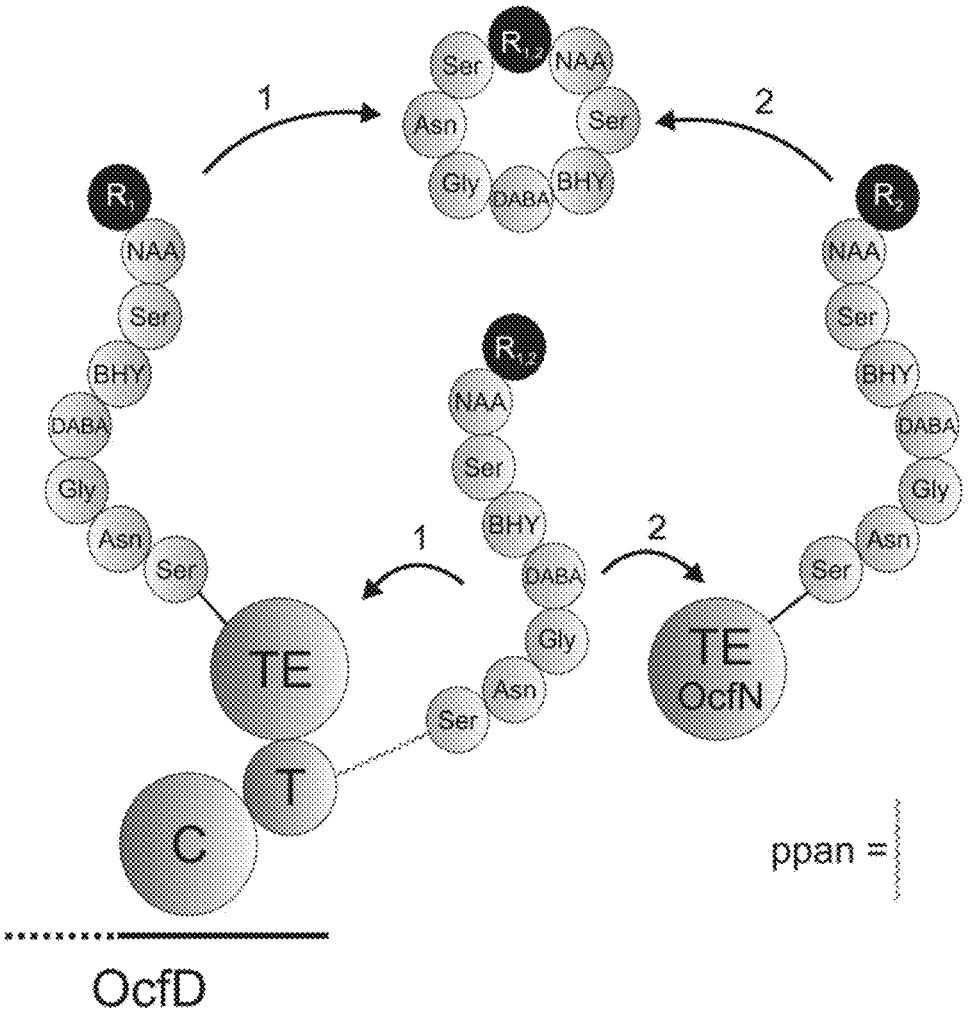

1
2
1
2
Ser
NAA
Asn
Ser
Gly
DABA
BHY
NAA
Ser
BHY
DABA
Gly
Asn
Ser
TE
T
C
TE
OcfN
ppan =
OcfD

FIGURE 6

A

Occidiofungin MICs

Isolate	Wild-Type MIC (μg/mL)	*ocfN* mutant MIC (μg/mL)
Candida albicans 66027	1.0	1.0
Candida albicans LL	0.5	1.0
Candida albicans TE	0.5	1.0
Candida glabrata 66032	0.5	1.0
Candida parapsilosis 90018	1.0	2.0
Candida tropicalis 66029	0.5	1.0

B

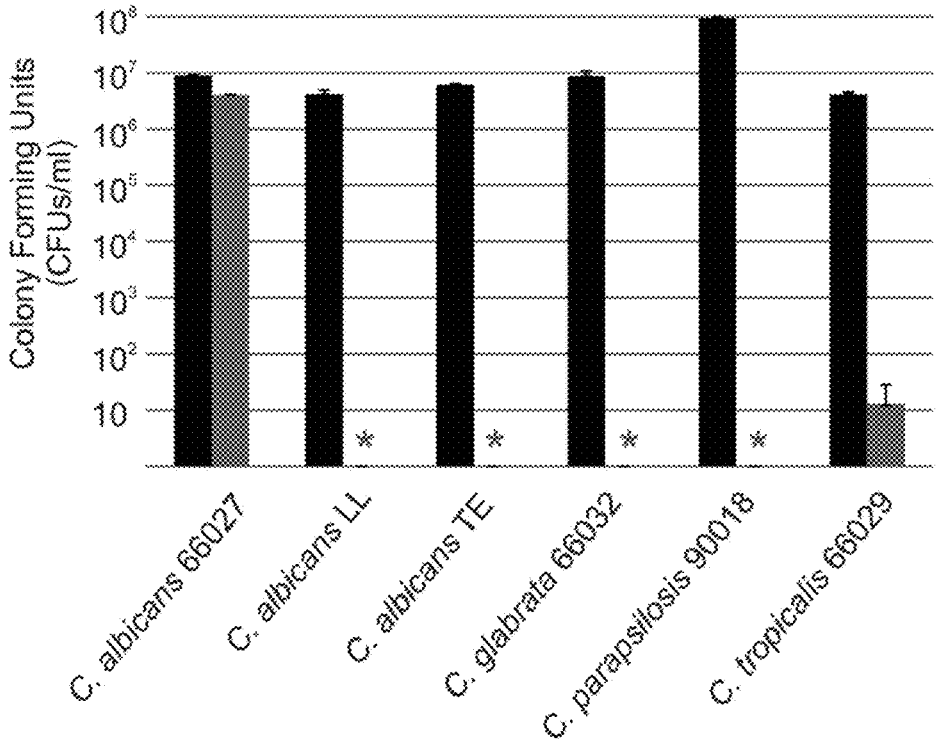


FIGURE 7

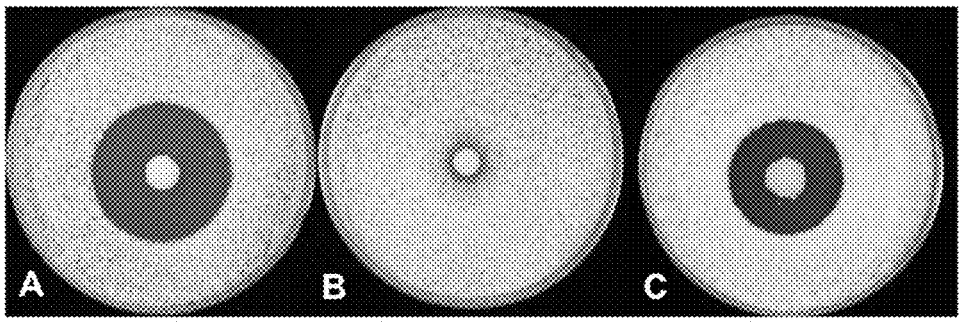
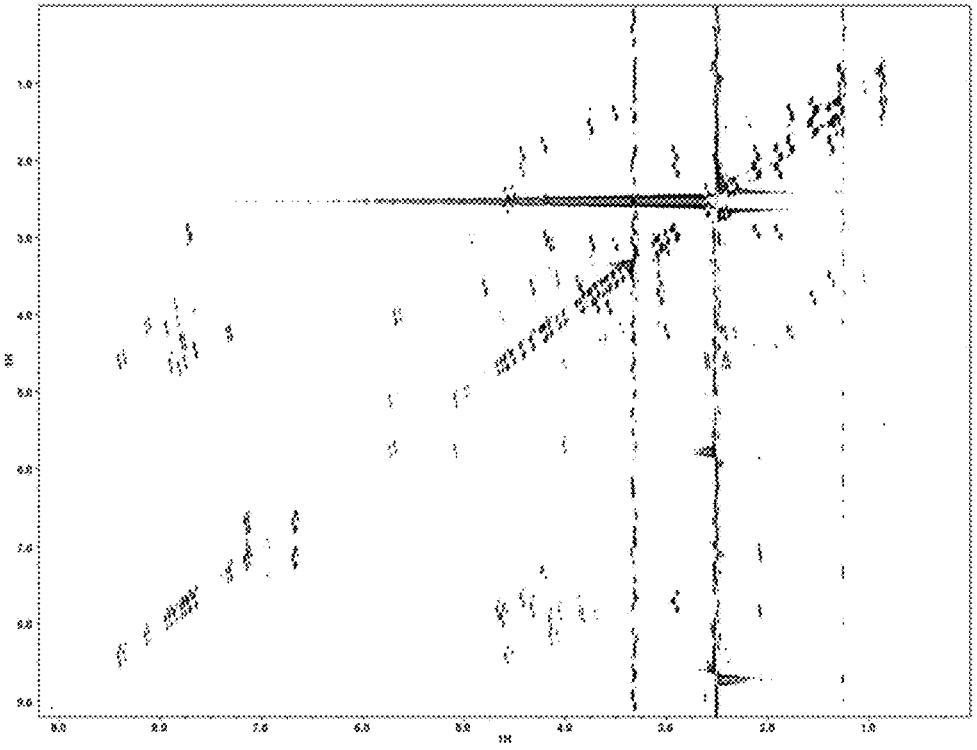
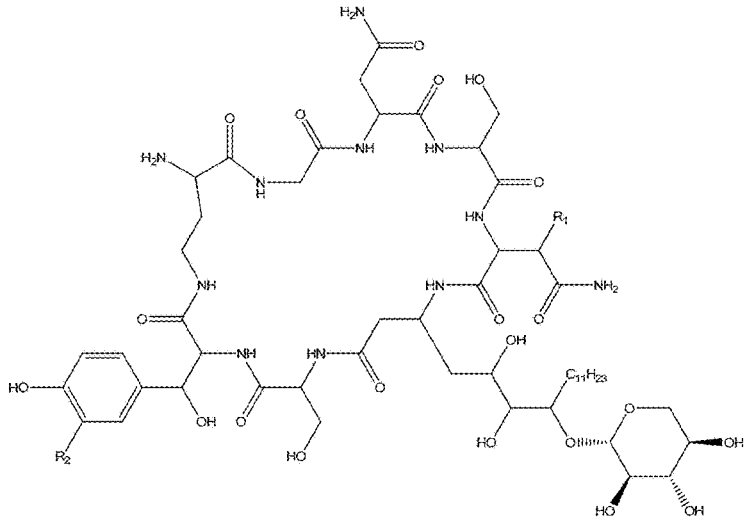


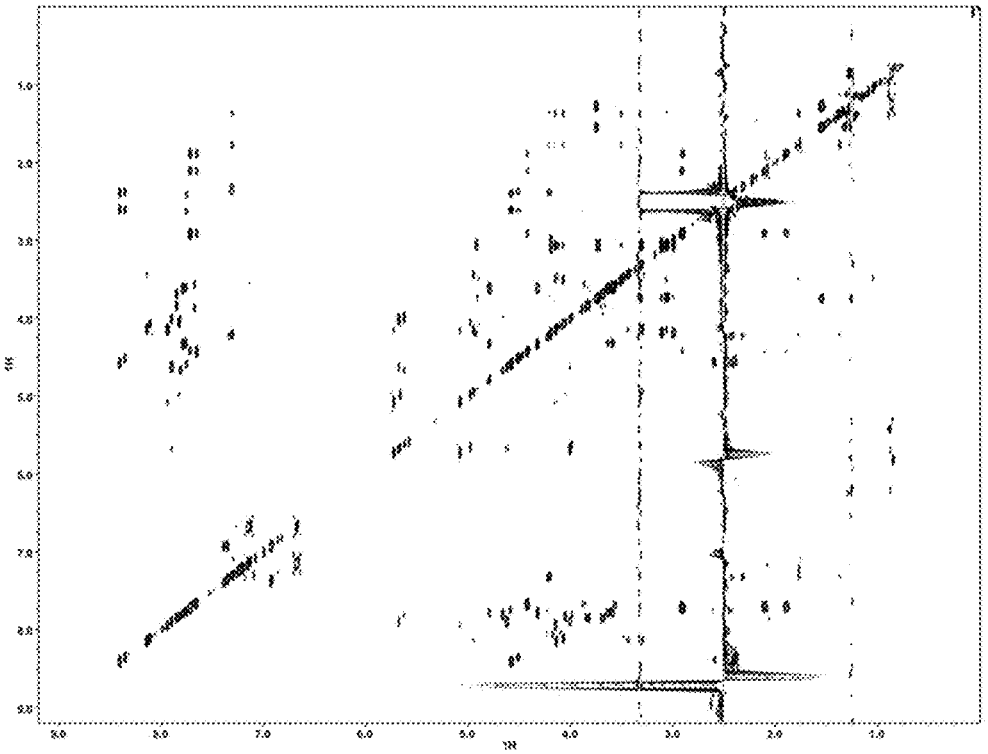
FIGURE 8

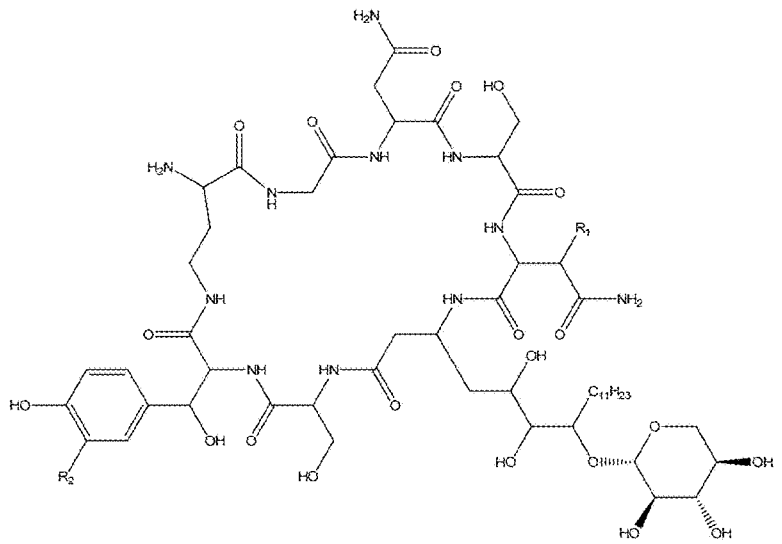




Occidiofungin: R1 (-H or -OH); R2 (-H or -Cl)

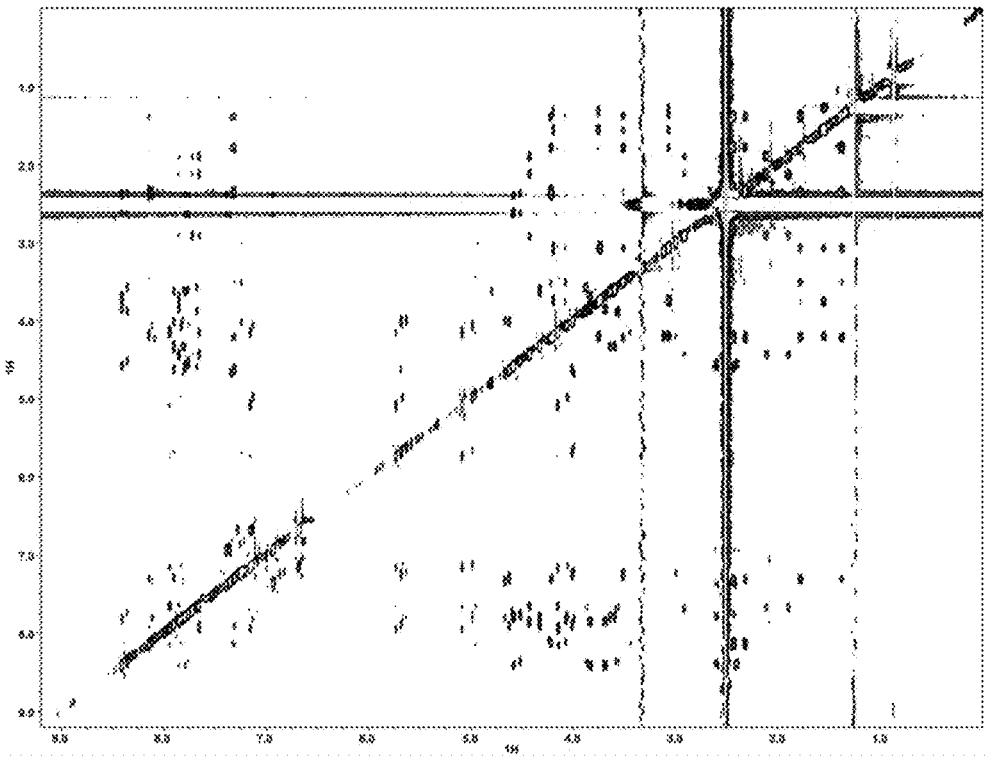
FIGURE 9

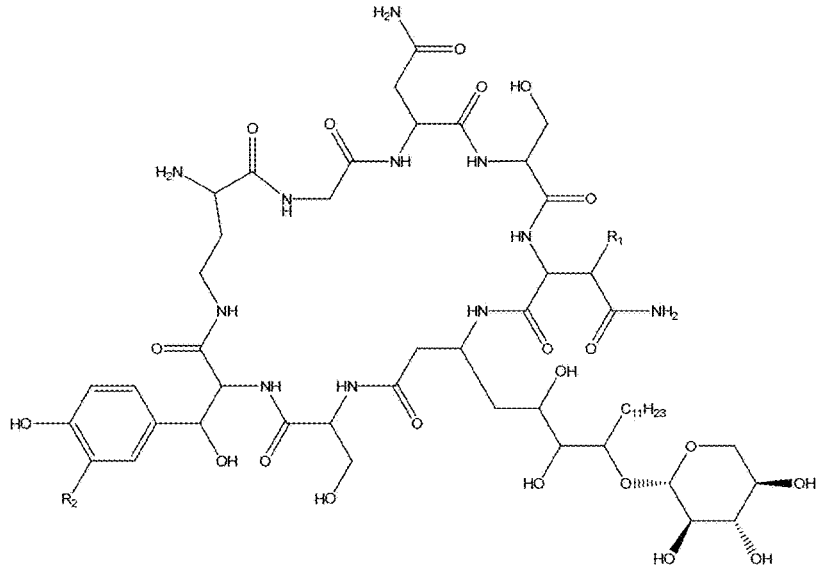




Occidiofungin: (R1,-H or -OH); (R2,-H or -Cl)

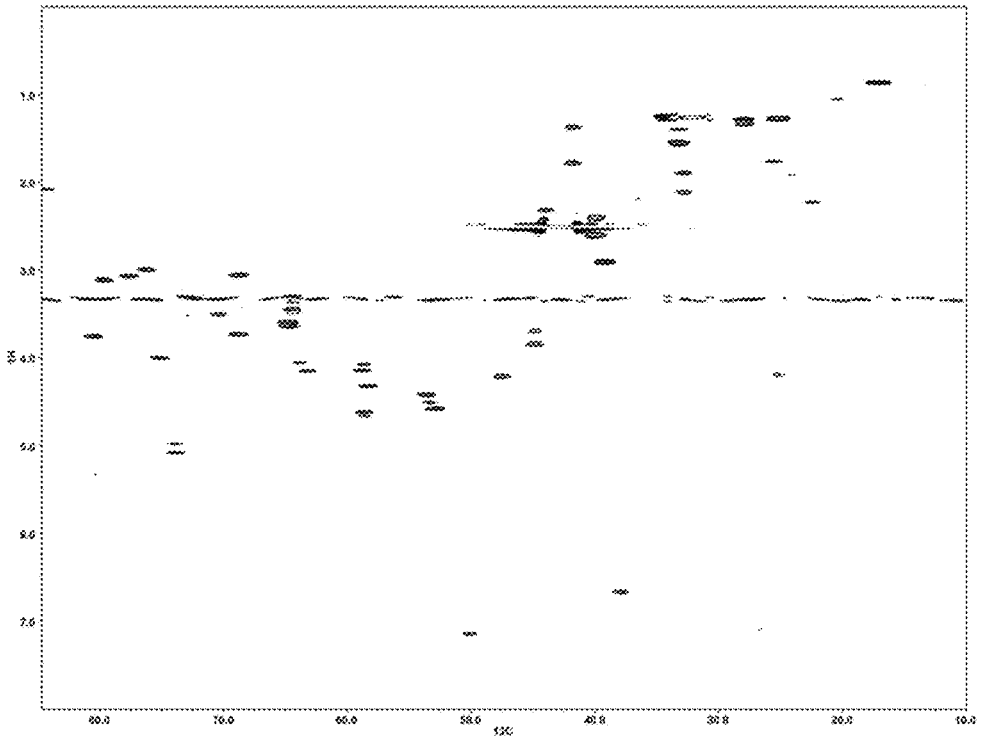
FIGURE 10

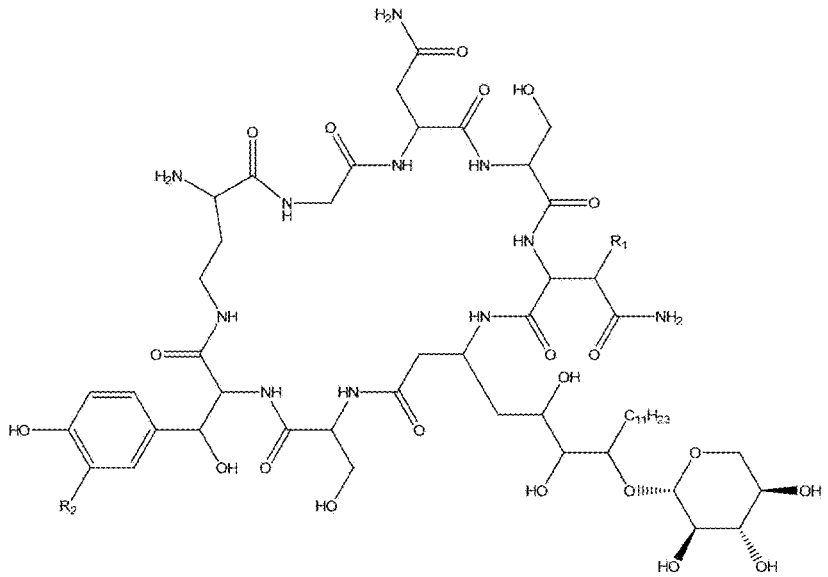




Occidiofungin: (R1,-H or -OH); (R2,-H or -Cl)

FIGURE 11





Occidiofungin: (R1,-H or -OH); (R2,-H or -Cl)

FIGURE 12

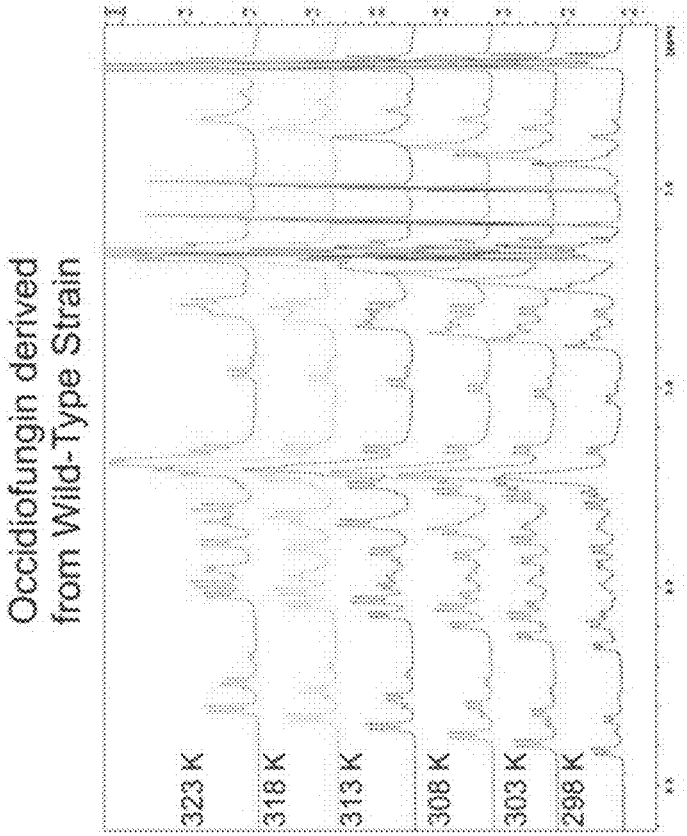


FIGURE 13B

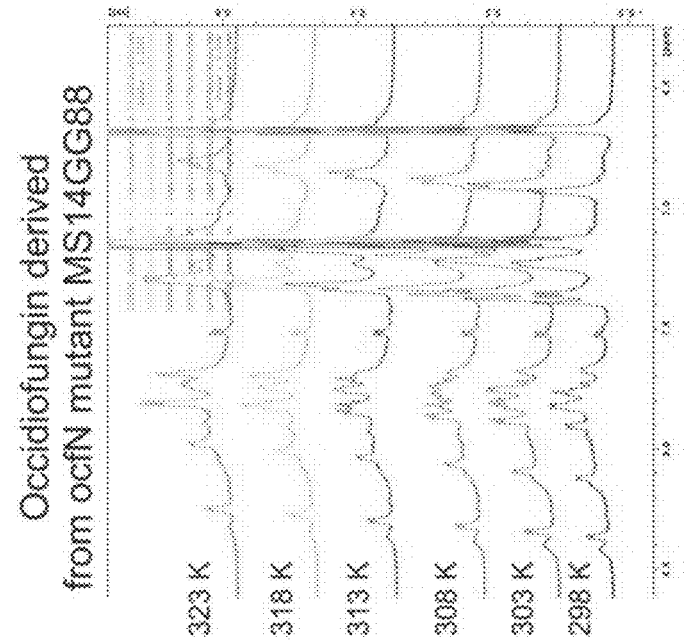


FIGURE 13A

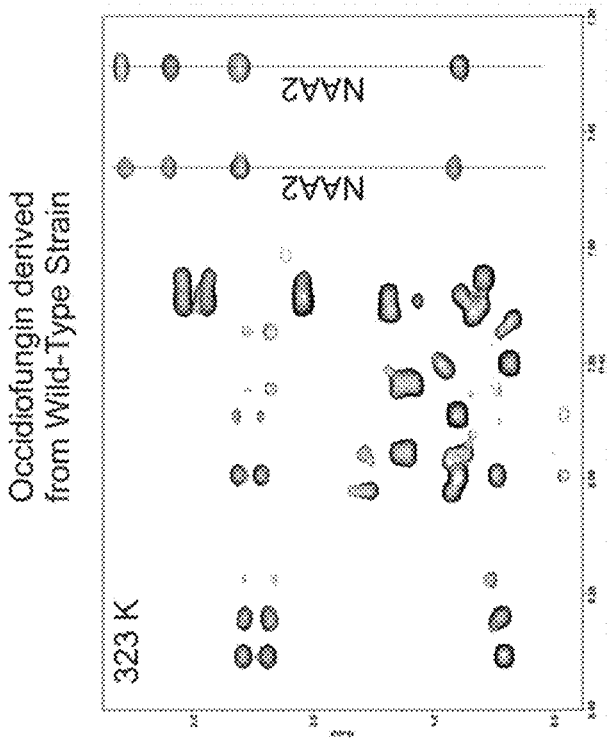


FIGURE 14B

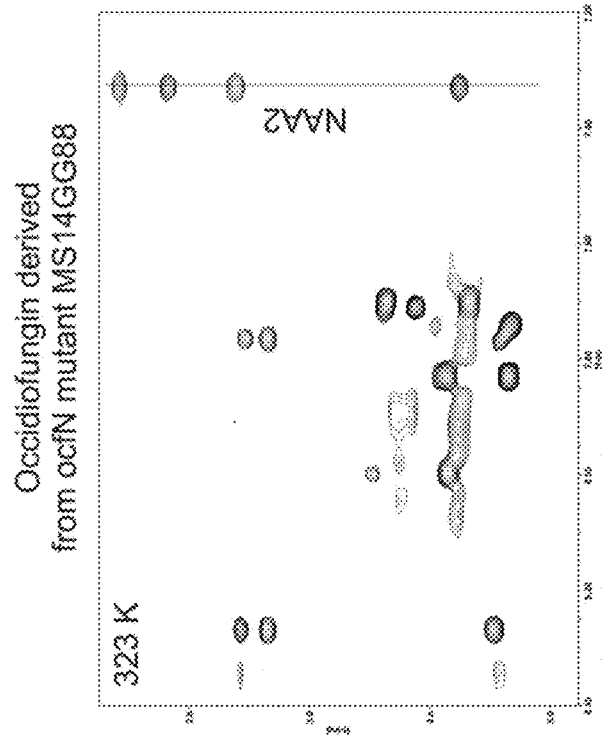


FIGURE 14A

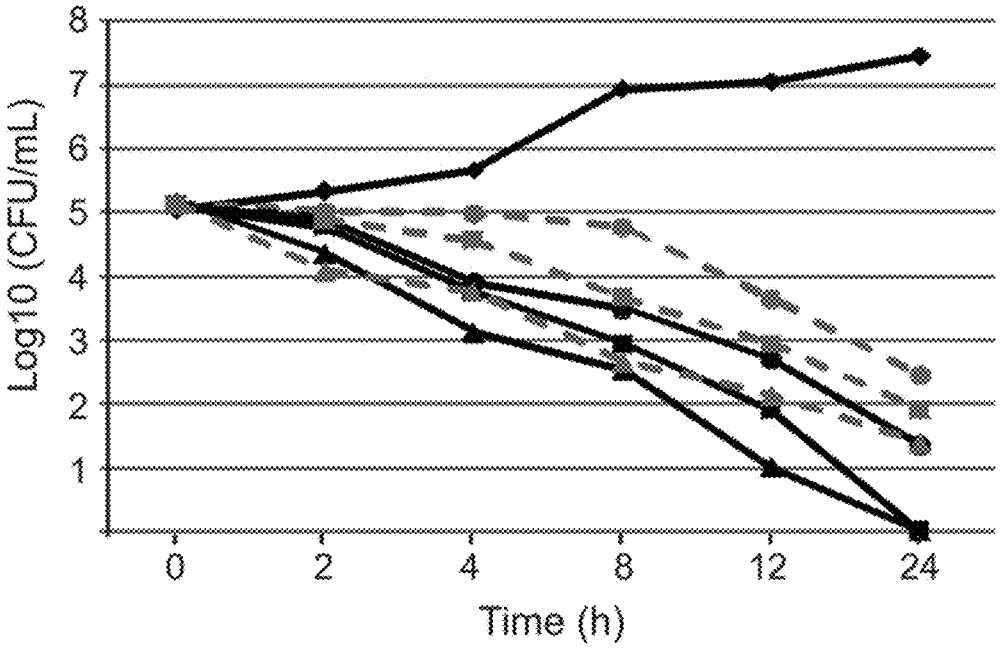


FIGURE 15

ENGINEERING THE PRODUCTION OF A CONFORMATIONAL VARIANT OF OCCIDIOFUNGIN THAT HAS ENHANCED INHIBITORY ACTIVITY AGAINST FUNGAL SPECIES

CROSS-REFERENCE TO RELATED APPLICATION

This application claims the benefit of U.S. Provisional Application Ser. No. 61/731,105, filed Nov. 29, 2012, the disclosure of which is hereby incorporated by reference in its entirety, including all figures, tables and amino acid or nucleic acid sequences.

The Sequence Listing for this application is labeled "Seq-List.txt" which was created on Nov. 26, 2013 and is 264 KB. The entire contents of the sequence listing is incorporated herein by reference in its entirety.

This invention was made with government support under 0204332 awarded by the National Institute of Food and Agriculture, USDA. The government has certain rights in the invention.

BACKGROUND OF THE INVENTION

Nonribosomal peptide synthetases (NRPSs) produce a wide array of small and structurally complex peptides that have therapeutic potential. The system enables the incorporation of nonproteinogenic amino acids into the polypeptide. Polyketide synthetases (PKSs) are a family of enzymes or enzyme complexes that produce polyketides. Integration of PKSs into the NRPSs system further increases the variety of polypeptides that can be produced by these systems. Recent studies are aimed at exploiting NRPSs for producing peptide libraries that can be screened for therapeutic applications.[1-9]

Unlike linear peptides, cyclic peptides are restrained to fewer conformations that facilitate their interaction with their molecular target.[10-18] These structural constraints provide resistance to proteases, extreme pH, and temperature.[10, 19] These attributes make them one of the most promising scaffolds for pharmacophores. Synthetic design of cyclic peptides is hindered by regioselectivity.

Classical total synthesis of peptides by solid phase or solution phase peptide synthesis followed by subsequent cyclization reactions requires the addition and removal of protecting groups at the right stages to drive the cyclization among the correct residues.[8] Even with these considerations, proper cyclization is hindered by intermolecular interactions and entropically disfavoured pre-cyclization conformations resulting in a vast mixture of compounds or low yields. Microorganisms ensure the formation of a functional cyclic peptide conformation by enzymatically catalyzing the cyclization and release of the peptide with regioselectivity using a cyclase thioesterase.[1, 7] The cyclase thioesterase is often located at the C-terminal end of the last NRPS involved in the synthesis of the peptide and is referred to as the TE (Thioesterase) domain.

The TE domain can hydrolyze the bound peptide as a linear peptide or it can catalyze an intramolecular reaction resulting in the formation of a cyclic peptide. At present, very little is known about the cyclization mechanism of peptides. The crystal structure of the surfactin peptide cyclase provided the first basic understanding of its mechanism of action.[20, 21] The peptidyl chain bound to 4-phosphopantetheine cofactor (ppan) that is attached to the thiolation (T)-domain is transferred to a serine in the adjacent TE domain. Ser80 is part of a catalytic triad of residues (His207 and Asp107) in the surfactin cyclase. His207 and Asp107 activate the Ser80, facilitating the transfer of the peptidyl chain to the TE domain. Once the peptide is transferred to the TE domain, the cyclase binding pocket enables proper orientation and cyclization of the peptide substrate. The enzyme was found to share structural homology to α,β-hydrolase family. The lack of water in the binding cleft of the cyclase, which prevents hydrolysis, is the significant alteration from the hydrolase family that gives the cyclase thioesterase its ability to form cyclic peptides.

Occidiofungin is a broad spectrum nonribosomally synthesized cyclic antifungal peptide that has submicro/nanomolar activity and low toxicity.[19, 22-26] An interesting feature in occidiofungin's biosynthetic pathway is the presence of two putative thioesterases. One is present as an independently expressed thioesterase, OcfN, and the other is a C-terminal TE domain of OcfD. There remains a need for the production of anti-fungal agents that have increased cidal activity against various fungi.

BRIEF SUMMARY OF THE INVENTION

This invention relates to antifungal compounds and their therapeutic use in the prevention or treatment of fungal infections and diseases. Particularly, various aspects of the invention provide compositions enriched for occidiofungin diastereomers/conformers that have higher activity against fungal infections or diseases (in mammals or plants).

Other aspects of the invention provide for compositions enriched for particular diastereomers/conformers produced by genetic modification of occidiofungin producing microorganisms such that the production of a particular occidiofungin diastereomer/conformer is favored. Thus, the invention relates to methods of making such occidiofungin diastereomers/conformers, compositions enriched for such diastereomers/conformers and methods of using compositions comprising occidiofungin diastereomers/conformers disclosed herein as fungicides for animals and plants. The invention further relates to the microorganisms that produce compositions enriched for occidiofungin enriched for occidiofungin diastereomers/conformers corresponding to diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations). Methods of increasing the production of occidiofungin diastereomers/conformers corresponding to diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations) in microorganisms and productions systems are also provided.

As discussed above, one aspect of the invention provides compositions enriched for occidiofungin diastereomers/conformers, in particular the occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations). Thus, the invention provides compositions enriched for such antifungal diastereomers/conformers for treating fungal infection. In certain embodiments of this aspect of the invention, pharmaceutical and agricultural compositions that contain a composition enriched for diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations) are provided. Compositions enriched for a particular occidiofungin diastereomer/conformer can also be produced by the genetically modified microorganisms discussed below (e.g., micororganisms in which the function of ocfD and/or ocfN has been altered in order to favor the production of a particular diastereomer/conformer).

Novel antifungals are needed because of the importance of fungal infections in immunocompromised patients, and the limitations of currently-available antifungal agents regarding their spectra of activity and toxicities. In addition, new antifungals are crucial for food preservation and production of a sufficient and affordable food supply. In this context, this application relates to the disclosure of a composition enriched for occidiofungin diastereomers/conformers having increased antifungal activity as compared to occidiofungin compositions produced by *Burkholderia contaminans* MS14 (disclosed in U.S. Patent Application Publication 2011/0136729, the disclosure of which is hereby incorporated by reference in its entirety). Diastereomers/conformers have been characterized by a number of techniques, including COSY, TOCSY, NOESY, ROESY, and HSQC 2D NMR spectroscopy experiments.

The antifungal activity of the disclosed occidiofungin diastereomers/conformers (diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations)) provides for compositions having greater antifungal activity as compared to as compared to occidiofungin compositions produced by *Burkholderia contaminans* MS 14 when cultured under the same conditions.

The phrase "enriched for the disclosed occidiofungin diastereomers/conformers" is intended to convey that the a composition contains the disclosed occidiofungin diastereomers/conformers (diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations)) in an amount higher/greater than that produced by *Burkholderia contaminans* MS14 as disclosed in the examples provided herein (in which approximately 36% of total amount of occidiofungin corresponds to occidiofungin diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations). Thus, the phrase indicates that at least 37% of the total amount of occidiofungin diastereomers/conformers present within an enriched composition are the disclosed diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations)). In various embodiments, compositions "enriched for the disclosed occidiofungin diastereomers/conformers" contain at least 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% of the disclosed diastereomers/conformers in relation to the total amount of occidiofungin diastereomers/conformers in the composition.

The phrase "enriched for a particular occidiofungin diastereomers/conformer" is intended to convey that a composition contains the an occidiofungin diastereomer/conformer that is produced by a microorganism in which the activity of the ocfD and/or ocfN thioesterase has been altered such that the production of a particular conformer is favored.

BRIEF DESCRIPTION OF THE DRAWINGS

The patent or application file contains at least one drawing executed in color. Copies of this patent or patent application publication, with color drawing(s), will be provided by the Office upon request and payment of the necessary fee.

FIG. **1**. Covalent structure of occidiofungin. R1 and R2 represent the locations where a hydroxyl or chlorine is added, respectively (R1, —H or —OH; R2, —H or —Cl).

FIGS. **2**A-**2**C. RP-HPLC Chromatograms. A. Chromatogram of the final purification step of the wild-type occidiofungin fraction at 220 nm using a 4.6×250 mm C18 column. B. Chromatogram of the final purification step of ocfN mutant occidiofungin fraction at 220 nm using a 4.6×250 mm C18 column. C. Overlay of the wild-type (black) and the mutant (grey) fractions of occidiofungin.

FIG. **3**. TOCSY (left panel) and HSQC (right panel) spectra of BHY4 in the wild-type sample. The proportions of Asn1 and BHN1 variants were determined by the measurement of the ^{13}C-HSQC Ha-Ca cross peak intensities of BHY4 in the HSQC spectra. These values are listed next to their corresponding peaks in the right panel. The peaks in red and green represent the BHY4 peaks associated with BHN1 and Asn1 variants, respectively. Based on the calculation of their relative proportions, i.e. (34.81+87.97 for the BHY4 peaks found in the BHN1 conformational variants) and (32.79+37.61 for the BHY4 peaks found in the Asn1 conformational variants), the approximate proportion of the Asn1 variants could be calculated as (32.79+37.61)/(34.81+87.97)+(32.79+37.61).

FIGS. **4**A-**4**B. ESI mass spectrometry. A. EST mass spectrometry data of purified wild-type occidiofungin fraction. B. ESI mass spectrometry data of purified ocfN mutant occidiofungin fraction.

FIGS. **5**A-**5**C. TOCSY fingerprint region (NH correlations). A. NH correlations in the wild-type sample. The two BHN1 and four Asn1 spin systems present in the wild-type sample are colored red. B. NH correlations in the ocfN mutant sample. C. Overlay of the NH correlations found in the wild-type and ocfN mutant samples. NH correlations that are not present in the ocfN mutant sample are colored green.

FIG. **6**. Schematic of occidiofungin ring closure. The completely synthesized eight amino acid linear peptide is bound by a 4-phosphopantetheine cofactor (ppan) linker to the thiolation (T) domain. The peptide varies by the presence or absence of a hydroxyl group on the beta carbon of Asn1. The TE domain of OcfD is capable of forming the cyclic peptide of both variants in the absence of a functional OcfN cyclase thioesterase. However, it is not as efficient at producing the Asn1 cyclic peptide variant as OcfN. In the presence of a functional OcfN cyclase thioesterase, a novel diastereomers of occidiofungin is formed by the selective ring closure of the Asn1 cyclic peptide. R1 and R2 are BHN1 and Asn1, respectively.

FIGS. **7**A-**7**B. Comparison of the bioactivity from the wild-type and ocfN mutant occidiofungin fractions. A. MICs of wild-type and ocfN mutant fraction determined by CLSI M27-A3 method in RPMI 1640. B. Comparison of the CFUs in the MIC wells of wild-type fraction to the corresponding well having the same concentration of the ocfN mutant occidiofungin fraction. Asterisks represent no detectable colonies in the MIC wells of the wild-type occidiofungin fraction. Black and grey bars are ocfN mutant and wild-type fractions, respectively. Standard deviations for the CFU measurements are presented.

FIGS. **8**A-**8**C. Potato dextrose agar plates were inoculated with each of the strains and incubated for 3 days at 28° C. The plates were oversprayed with the indicator fungus *Geotrichum candidum* and incubated overnight. A: The wild-type strain MS14; B: Negative control MS14GG78 (ocfJ::nptII); C: MS14GG88 (ocfN::nptII).

FIG. **9**. COSY60 NMR Spectrum of Occidiofungin from ocfN mutant MS14GG88 recorded at 600 MHz in DMSO-d6.

FIG. **10**. TOCSY60 NMR Spectrum of Occidiofungin from ocfN mutant MS14GG88 recorded at 600 MHz in DMSO-d6.

FIG. **11**. NOESY400 NMR Spectrum of Occidiofungin from ocfN mutant MS14GG88 recorded at 600 MHz in DMSO-d6.

FIG. **12**. ^{13}C-HSQC NMR Spectrum of Occidiofungin from ocfN mutant MS14GG88 recorded at 600 MHz in DMSO-d6.

FIGS. **13**A-**13**B. One-dimensional NMR temperature titration curves for occidiofungin derived from ocfN mutant MS14GG88 (FIG. **13**A) and wild-type strain MS14 (FIG. **13**B).

FIGS. **14**A-**14**B. TOCSY fingerprint region (NH correlations) for occidiofungin derived from ocfN mutant MS14GG88 (FIG. **14**A) and wild-type strain MS14 (FIG. **14**B) at 50° C.

FIG. **15**. Time-kill experiments performed against *Candida glabrata* ATCC66032. Solid black lines and dashed grey lines correspond to samples treated with occidiofungin derived from wild-type strain MS14 and ocfN mutant MS14GG88, respectively. Circles, squares, and triangles represent samples treated with 0.5, 1.0, and 2.0 μg/mL of occidiofungin, respectively. The diamond represents the sample treated with the blank control.

BRIEF DESCRIPTION OF THE SEQUENCES

SEQ ID NOs: 1-2: PCR primer sequences

SEQ ID NO: 3: amino acid sequence for OcfN (thioesterase; thioesterase motif of -G-X-S-X-G- underlined (X is any amino acid))

MRLICFPYAGGSAAVYRTLQASLPGIEVCRHELAGRGSRLSEPAVRDMA

TLVDTLLCDLDDCFDRPFALL**GHSMG**AAIAAELALRLPAHARPNLRHLF

VSARAAPGKERHDRRMQALDDRAFIDALREMGGTPKAVLDNSELMALL

MPALRADFTMIENHRPVPGPRLAVDITAFAGRADKEIPVDAVAGWGAAT

TGRFDFHVIEGDHFFLRNEMRTMAGIIAARMRRPEHAASSALQA

SEQ ID NO: 4: amino acid sequence for OcfD (thioesterase motif of -G-X-S-X-G-underlined (X is any amino acid))

MQDNNVLVTD RESLSRVAGV YGIAAYAPSQ QPGRPLTRSV RLTPASLDLL

RRIGDGELAE FAVAAAGIAF LLWKYFRIPV TVLGTPGLAG HPSARAAIVP

LIIEVRPDER IEDYLSRVAG IVEDSYAEPR FPLETLVRNE KDMALAQLTK

VALADDRVHH APTGRDDDLQ LHLRLARGEI ELRYSGAIEP FIIDGFAGSL

AAVLEAFEHL DGAVGDIEAA PPEQGPLLAA FNETATAGPS HPTVVAMFEA

QVARTPTAPA LVTDSSLMTY ADLNARANSL AHHLREHHGV GPESLVGIML

DRSEWMIVAI LGILKAGAAF VPLDPAYPAE RINHILGDTG LSLLVTQSSQ

LAQWYEFSGV TLLLDQELPG WQPLPDNPPH RAEPAHLAYV LYTSGSTGKP

KGCLLEHRNL AHYIAWAAGY YFPESTTGSF GLYSSLCFDF TLTNIFCPLV

RGKTLRIYPQ SESIDTILAR MFQPGSGVDT LKLTPTHIHL LEYMNLARSG

VRKVIVGGEE LTPQHIATLR KIDPAIEIYN EYGPTEATVG CIVERVEDAP

PTVLIGRPIA DTRVYMLDDA LRPVPLGVPG EICLAGAGLA RGYHQRPDVT

AAKFVEHPFP GEARIYRTGD IGRWLPDGRI QCYGRVDHQV KIRGHRVELG

EIEAAIAAHE DVVGAAVMLR ESAHGVRKLA AYVKGAASLS VPNLRAYLAG

KLPDYMVPSD IIPIAEFPLN ANGKLDRPAL LALEPAAAPE EAPLDATPIQ

RELVRIWRDV LDNPAVDLAG RFFDYGGDSL QAMQLVSRIW SSFSVEIGID

AIFELQTISA VSDLIEASSP HPGSTAGAIP PRSRANDLPL SFPQQRLWFL

AQLEGPSATY NISSALRFEG ELDVARLRFA VSEISRRHEI LRTTFPAVDG

RGVQRIAPPA PVALDVVDVA SESDTLALLA EEADRPFDLA AGPLYRVVLY

RVHERLHVFG IVMHHIVSDA WSSGILIGEL AALYAGESLP ELAVQYADYA

VWQHERLASA DTHRELALLS AALADAPDLI ELPTDRPRPA VQQFRGAVLP

FQLSAERADG LRAIARASGT STFMVVLAAY ALLLSRYSNQ QDLVIGSPIA

NRRSSMTEPL IGFFANMLAL RVDLSGNPTF GDLLARVKRV ALDGYSRQEI

PFEQVVDSLE LERNLGRTPV FQVVFAYEKA QPRAVSFPGL VATPVAVETH

TAKFDLTLHV QDADDGLAGS LEYNLDLFDA ATIDRMAEHF RTLVDAVIAD

PDRPLGALSL SNDAERNLLT VEWNRTDTDF GEDAAQPLHR LFEQQVERTP

-continued

DAVAIVFDDT ALTYAELNLR ANRLAHHLVA LGVGPDSLVG VAMERSLDMS

VALLAILKAG GAYVPVDPDY PAERVRFMID HAQLRWLLTQ QHLHDALPDT

DAHVIVVDRD SLDLDAAATS NPAPALNGDN LAYMIYTSGS TGRPKGALNT

HRAITNRILW MQHAYALDAD DAVLQKTPFS FDVSVWELFW PLVTGARLVF

ARPGGQRETD YLVELIERER ITTIHFVPSM LRAFLDHPDL DAHCASLRRV

VCSGEALPHD LQQRCLERLD VKLYNLYGPT EAAVDVTAWE CRRDDPHRIV

PIGRPIANTR LYIVDAQMQP TPIGVAGELL IGGTPVGRGY HGEPELSAEK

FIADPFSADP LARLYRTGDL ARYRPDGNIE FLGRIDHQIK LRGLRIEPGE

IEAALRAHPS VDDCVVIAKT EGARTFLIAY VATAAPDIAD LRGYLGGKLA

DYMVPSQFFA LESLPMLPNG KINRKALPLP ADRGDAAQPH APAVTPREIL

LASICIDVLQ LPSVGIHDNF FELGGDSILS IQVIARANQA GLRVTAKQLF

QYQTIAQLAA APEERAACAP TLSPLGDAPL TPVQHWFFEQ EIDAPSHYNQ

TVLIQVPADI DASRLADAFR QVYEHHDALR LRFSHDAGRW TQQVVAGGEM

PALFAKQVIA DDAGERLAAM RAAAADAERG IDITHGPLLA ARLFCLADEP

LARLFVSIHH LAVDGVSWRV LLEDLHAAYH GQPLPGKTTS FREWALHLQQ

LARSPAIGDE ARLWQALLAQ PVEPMPVDYP GTGAANNAVD DASSVSFELG

EADTTALLRR LPRAYDTRIN DVLLVALAQA CSMVTGNTRT RIDLESHGRH

VSDAPLDLTR TVGWFTSIYP VVLDADAMHA PEQALRAARQ QLRRIPADGL

GYSLLRYQSP DAAVRDSLAA LPKADILFNY HGQLDTVLRQ SDGWRPAAED

LGSLRAGRSQ RTHAFEIVAA VADGKLQVDW RYGERLHRRQ TVENLAAHFR

DRLLDFAASV PDTAADDIED SYPLSSLQQG ILFHSLYDLD PAAYFQQFSF

VVSGPLQVPA LRQAWANALA RHAVLRTAFA WADRDHPVQT VRHTVDLPWT

FLDWRHRDAS RRAQDFDAFL ADDRRRGFDL QRAPLFRCTL IQETDTRHRF

CWSAHHIILD GWSTATLMKE VFDDYLSLAR TGMPAVAASA PGYRAYIDWL

ARHPRSADET WWRAELAGFK AATPVAASPA RQATGDAPRQ DKRRTQQFLL

DEALAARLQT LTRTHRVTLN VLIRAVWALV LRRHAGTDDV VFGVTVSGRP

PMLDGVESIV GLFINTLPLR LRIAPERPFI EWLAEVHAAQ TAMEPHSYSS

LVDIQSWSEL PAGDSLFDSL LVFENFPVAA APDLGPDDIE ILDTRAFAES

NYPLTLTVHP NERIGFHISH DAHRIAPEVV RQMLDTLRTL LERFAENPGQ

LTGQLADPPA ADGRPSAPRS GAGPAIEAAA GAAAAARAVA HAADESTLLE

IWRRIFKRDD IAVSDNYFDL GGHSIIAIQL MAHVEKAFDR RLPISCLFEN

PTIEKLAAAL AAKEPSAPAG GLVPIRDGGP AAPLFLLPGA GGNVVYFRPL

ANHLSGAHAI HGLEALGLDG ACEPLTRVED IAARHIERIW PLVGAGPYYL

A**GHSFG**AHVA LEMSRQLVAK GADVKLLAIF DASAPIDSSA ATYWQDWDDT

EWLVAIAHEI GTFLGTDLQV TRADLVHLDP DGQAGLILER IGDRGSWFAD

AGSDRLRAYL RVYQANFKSH YAPHATPLPV PIALFRSTER DPGDYAPSSE

IAQLRLDATW GWSRFSAHPV AVTDVPGDHL TMLLDPHAGV LAAHVNSFLE KTPS

SEQ ID NOs: 5-23: polynucleotide and polypeptides associated with GenBank Accession No. EU938698.5.

DETAILED DESCRIPTION OF THE INVENTION

This invention relates to antifungal compounds and their therapeutic use in the prevention or treatment of fungal infections and diseases. Particularly, various aspects of the invention provide compositions enriched for occidiofungin diastereomers/conformers that have higher activity against fungal infections or diseases. Thus, the invention relates to methods of making such occidiofungin diastereomers/conformers, compositions enriched for such diastereomers/conformers and methods of using compositions comprising occidiofungin diastereomers/conformers disclosed herein as fungicides for animals and plants. The invention further relates to the microorganisms that produce compositions enriched for occidiofungin enriched for occidiofungin diastereomers/conformers corresponding to diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations). Methods of increasing the production of occidiofungin diastereomers/conformers corresponding to diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations) in microorganisms and productions systems are also provided.

As discussed above, one aspect of the invention provides compositions enriched for occidiofungin diastereomers/conformers, in particular the occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations observed under the following conditions: 2 mM samples of occidofungin diasteromers in dimethylsulfoxide (DMSO-d6, Cambridge Isotopes) subjected to 2-D TOCSY, spectra collected at 323 K with a mixing time of 60 milliseconds and data processing using NMRPipe with 45 degree sinebell squared shifts in both dimensions). Thus, the invention provides compositions enriched for such antifungal diastereomers/conformers for treating fungal infection. In certain embodiments of this aspect of the invention, pharmaceutical and agricultural compositions that contain a composition enriched for diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations) are provided.

Another aspect of the invention provides for compositions that are enriched for a particular occidofungin diasteromer/conformer. In this aspect of the invention, the activity of the ocfD and/or ocfN thioesterases is altered such that the activity of one of the thioesterases is decreased (or eliminated) and the activity of the second thioesterase remains functional or is increased. Thus, microorganisms can be genetically manipulated such that OcfD thioesterase activity is decreased or eliminated and the thioesterase activity of OcfN is increased or maintained at unaltered (e.g., levels of activity as observed in *Burkholderia contaminans* MS14 or microorganisms engineered with the biosynthetic pathway for the production of occidiofungin). Alternatively, microorganisms can be genetically manipulated such that OcfN activity is decreased or eliminated and the thioesterase activity of OcfD is increased or unaltered.

Compositions comprising occidiofungin diasteromers/conformers as disclosed herein may be formulated prior to administration in an agriculturally acceptable carrier, for example in an aqueous carrier, medium or suitable diluent, such as saline or other buffer. The formulated compositions may also be in the form of a dust or granular material, or a suspension in oil (vegetable or mineral), water or oil/water emulsions, a wettable powder, or in combination with any other carrier material suitable for agricultural application. Suitable agricultural carriers can be solid or liquid and are well known in the art. The term "agriculturally-acceptable carrier" covers all adjuvants, e.g. inert components, dispersants, surfactants, tackifiers, binders, etc. that are ordinarily used in the formulation of agricultural compositions; these are well known to those skilled in formulation of agricultural compositions.

A pharmaceutical composition contains a desired amount of an occidofungin diastereomers/conformers as disclosed herein. Thus, the pharmaceutical composition can comprise occidofungin diasteromers/conformers having the total correlation spectroscopy (TOCSY) fingerprint identified in FIG. **5**C as the green NH correlations or the pharmaceutical composition can comprise a particular occidiofungin diastereomer/conformer. Either of these pharmaceutical compositions can be in the form of, for example, a tablet, a caplet, a pill, a hard or soft capsule, a lozenge, a cachet, a dispensable powder, granules, a suspension, an elixir, a dispersion, a liquid, or any other form reasonably adapted for administration. If intended for parenteral administration, it can be in the form, for example, of a suspension or transdermal patch. Presently preferred are oral dosage forms that are discrete dose units each containing a predetermined amount of the disclosed occidiofungin diastereomers/con formers.

Pharmaceutically acceptable carriers that may be used in these compositions include, but are not limited to, ion exchangers, alumina, aluminum stearate, lecithin, serum proteins, such as human serum albumin, buffer substances such as phosphates, glycine, sorbic acid, potassium sorbate, partial glyceride mixtures of saturated vegetable fatty acids, water, salts or electrolytes, such as protamine sulfate, disodium hydrogen phosphate, potassium hydrogen phosphate, sodium chloride, zinc salts, colloidal silica, magnesium trisilicate, polyvinyl pyrrolidone, cellulose-based substances, polyethylene glycol, sodium carboxymethylcellulose, polyacrylates, waxes, polyethylene-polyoxypropylene-block polymers, polyethylene glycol and wool fat.

The compositions of the present invention may be administered orally, parenterally, by inhalation spray, topically, rectally, nasally, buccally, vaginally or via an implanted reservoir. The term "parenteral" as used herein includes subcutaneous, intravenous, intramuscular, intra-articular, intra-synovial, intrasternal, intrathecal, intrahepatic, intralesional and intracranial injection or infusion techniques. Preferably, the compositions are administered orally, intraperitoneally or intravenously.

Sterile injectable forms of the compositions of this invention may be aqueous or an oleaginous suspension. These suspensions may be formulated according to techniques known in the art using suitable dispersing or wetting agents and suspending agents. The sterile injectable preparation may also be a sterile injectable solution or suspension in a non-toxic parenterally acceptable diluent or solvent, for example as a solution in 1,3-butanediol. Among the acceptable vehicles and solvents that may be employed are water, Ringer's solution and isotonic sodium chloride solution. In addition, sterile, fixed oils are conventionally employed as a solvent or suspending medium. For this purpose, any bland fixed oil may be employed including synthetic mono- or diglycerides. Fatty acids, such as oleic acid and its glyceride derivatives are useful in the preparation of injectables, as are natural pharmaceutically-acceptable oils, such as olive oil or castor oil, especially in their polyoxyethylated versions. These oil solutions or suspensions may also contain a

long-chain alcohol diluent or dispersant, such as carboxymethyl cellulose or similar dispersing agents that are commonly used in the formulation of pharmaceutically acceptable dosage forms including emulsions and suspensions. Other commonly used surfactants, such as Tweens, Spans and other emulsifying agents or bioavailability enhancers which are commonly used in the manufacture of pharmaceutically acceptable solid, liquid, or other dosage forms may also be used for the purposes of formulation.

The compositions of this invention may be orally administered in any orally acceptable dosage form including, but not limited to, capsules, tablets, aqueous suspensions or solutions. In the case of tablets for oral use, carriers commonly used include lactose and corn starch. Lubricating agents, such as magnesium stearate, are also typically added. For oral administration in a capsule form, useful diluents include lactose and dried cornstarch. When aqueous suspensions are required for oral use, the active ingredient is combined with emulsifying and suspending agents. If desired, certain sweetening, flavoring or coloring agents may also be added.

Alternatively, the compositions of this invention may be administered in the form of suppositories for rectal administration. These can be prepared by mixing the agent with a suitable non-irritating excipient that is solid at room temperature but liquid at rectal temperature and therefore will melt in the rectum to release the drug. Such materials include cocoa butter, beeswax and polyethylene glycols. The compositions of this invention may also be administered topically, ophthalmically, by nasal aerosol or inhalation. Such compositions are prepared according to techniques well-known in the art of pharmaceutical formulation.

Compositions disclosed herein can be used to treat fungal infections in immunocompromised patients or patients having fungal infections. Thus, another aspect of the invention provides for administering compositions enriched for occidiofungin diastereomers/conformers (e.g., those corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations) having increased antifungal activity as compared to occidiofungin compositions produced by *Burkholderia contaminans* MS14 (disclosed in U.S. Patent Application Publication 2011/0136729, the disclosure of which is hereby incorporated by reference in its entirety). These diastereomers/conformers have been characterized by a number of techniques, including COSY, TOCSY, NOESY, ROESY, and HSQC 2D NMR spectroscopy experiments.

The antifungal activity of the disclosed occidiofungin diastereomers/conformers (diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations)) provides for compositions having greater antifungal activity as compared to as compared to occidiofungin compositions produced by *Burkholderia contaminans* MS 14 when cultured under the same conditions. The phrase "enriched for the disclosed occidiofungin diastereomers/conformers" is intended to convey that the composition contains disclosed occidiofungin diastereomers/conformers (diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations)) in amounts higher than that produced by a reference strain (e.g., *Burkholderia contaminans* MS14 as disclosed in the examples provided herein). Thus, the phrase indicates that at least 37% of the total amount of occidiofungin diastereomers/conformers present within an enriched composition are the disclosed diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations)). In various embodiments, compositions "enriched for the disclosed occidiofungin diastereomers/conformers" contain at least 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, 60%, 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, 70%, 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98% or 99% of the disclosed diastereomers/conformers in relation to the total amount of occidiofungin diastereomers/conformers in a composition.

As discussed above, one aspect of the invention provides microorganisms capable of producing compositions enriched for occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations). In this aspect of the invention, microorganisms are transformed with the genes associated with the biosynthesis of occidiofungin. These genes and open reading frames (ORFs) are disclosed in disclosed in U.S. Patent Application Publication 2011/0136729, the disclosure of which is hereby incorporated by reference in its entirety; Gu et al., *Appl. Environ. Microbiol.,* 2011, 77:(17):6189-6198 which is also incorporated by reference in its entirety and GenBank Accession No. EU938698.5, which is also hereby incorporated by reference in its entirety and is also provided on pages 29-72 (SEQ ID NOs: 5-23). These transformed microorganisms are further manipulated genetically such that the microorganisms exhibit an increase in the level of OcfN thioesterase (SEQ ID NO: 3) activity. An increase in the level of OcfN thioesterase activity can be achieved by means of expressing the ocfN gene in a multicopy plasmid with a native promoter or any other promoter sequence. Another way to increase the expression of the ocfN gene within the cell is to chromosomally integrate additional copies of the ocfN gene using transposons. Yet a further means to increase ocfN thioesterase activity is to substitute the native promoter associated with the ocfN gene with a promoter that increases expression of the gene (relative to the native promoter). In certain embodiments of this aspect of the invention, the thioesterase activity of OcfD can be decreased or eliminated by a point mutation of the catalytic serine at position 2954 of SEQ ID NO: 4, insertional mutation or point mutation of amino acids within the thioesterase motif (in addition to the substitution of the serine residue) found in ocfD to reduce or eliminate its activity, deletion of the catalytic serine or other portions of SEQ ID NO: 4 (e.g., portions or the entirety of the thioesterase motif in SEQ ID NO: 4) or truncation SEQ ID NO: 4 such that thioesterase activity is reduced or eliminated (in addition to increasing the level of OcfN thioesterase activity) within the genetically modified microorganisms.

Another aspect of the invention provides for compositions enriched for a particular Occidiofungin diastereomer/conformer. In this aspect of the invention, transformed microorganisms are manipulated genetically such that the microorganisms exhibit an increase in the level of OcfD thioesterase (SEQ ID NO: 4) activity. An increase in the level of OcfD thioesterase activity can be achieved by means of expressing the ocfD gene in a multicopy plasmid with a native promoter or any other promoter sequence. Another way to increase the expression of the ocfD gene within the cell is to chromosomally integrate additional copies of the ocfD gene using transposons. Yet a further means to increase ocfN thioesterase activity is to substitute the native promoter associated with the ocfD gene with a promoter that increases expression of the gene (relative to the native promoter). In certain embodiments of this aspect of the invention, the

thioesterase activity of OcfN can be decreased or eliminated by a point mutation of the catalytic serine at position **73** of SEQ ID NO: 3, insertional mutation or point mutations of other amino acids within the thioesterase motif (in addition to the substitution of the serine residue) of the thioesterase to reduce or eliminate its activity, deletion of the catalytic serine or other portions of SEQ ID NO: 3 (e.g., portions or the entirety of the thioesterase motif in SEQ ID NO: 3), truncation SEQ ID NO: 3 such that thioesterase activity is reduced or eliminated or deletion of ocfN in its entirety (in addition to increasing the level of OcfD thioesterase activity) within the genetically modified microorganisms. Where the biosynthetic pathway for occidiofungin biosynthesis is engineered into a microorganisms, once can, of course, omit ocfN to achieve the same effect as the mutation or deletion of ocfN as discussed above.

Thus, microorganisms such as bacterial cells, fungal cells and yeast can be transformed with genes encoding the occidiofungin biosynthetic pathway and genetically manipulated, as discussed above, such that the cells have increased OcfN activity and/or decreased OcfD activity as compared to reference bacterial, fungal or yeast cells. Alternatively, microorganisms such as bacterial cells, fungal cells and yeast can be transformed with genes encoding the occidiofungin biosynthetic pathway and genetically manipulated, as discussed above, such that the cells have increased OcfD activity and/or decreased OcfN activity as compared to reference bacterial, fungal or yeast cells. Such cells can then be used to produce compositions enriched for occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations) or to produce compositions enriched for a particular occidiofungin diasteromer/conformer. The phrase "reference bacterial, fungal or yeast cells" refers to bacterial, fungal or yeast cells containing the genes associated with the biosynthetic pathway for the production of occidiofungin and where the function/activity of OcfN and/or OcfD has not been altered as disclosed herein. Thus, the phrase "reference bacterial, fungal or yeast cells" refers to cells containing, for example, polynucleotide (SEQ ID NO: 23 encoding the open reading frames (ORFs; SEQ ID NOs: 5-22)) disclosed in GenBank Accession No. EU938698.5. For the comparison of compositions comprising particular occidofungin conformers (or compositions enriched for occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations)), compositions containing the diastereomers/conformers are obtained from cells genetically manipulated to have increased ocfN activity and/or decreased OcfD activity (or increased OcfD activity and/or decreased ocfN activity) and compared to compositions containing occidiofungin produced by reference bacterial, fungal or yeast cells cultured under similar or the same conditions (e.g., the same temperature and medium).

Bacterial cells can be selected Gram negative bacteria or Gram positive bacteria. In this aspect of the invention, the Gram-negative bacterial cell can be selected from the group consisting of *Escherichia, Zymomonas, Acinetobacter, Gluconobacter, Geobacter, Shewanella, Salmonella, Enterobacter* and *Klebsiella*. Gram-positive bacteria can be selected from the group consisting of *Bacillus, Clostridium, Corynebacterial, Lactobacillus, Lactococcus, Oenococcus, Streptococcus* and *Eubacterial* cells. Various thermophilic bacterial cells, such as *Thermoanaerobes* (e.g., *Thermoanaerobacterium saccharolvticum*). *Bacillus* spp., e.g., *Bacillus coagulans* strains, *Bacillus licheniformis* strains. *Bacillus subtilis* strains, *Bacillus amyloliquifaciens* strains, *Bacillus megaterium* strains, *Bacillus macerans* strains, *Paenibacillus* spp. strains or *Geobacillus* spp. such as *Geobacillus stearothermophilus.*

Yeast cells suitable for use in this aspect of the invention may be a *Candida, Hansenula, Kluveromyces, Pichia, Saccharomyces, Schizosaccharomyvces*, 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. In this aspect of the invention, the yeast cell must be resistant to the effects of occidiofungin to be a viable production system for compositions enriched for occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations).

In other embodiments of this aspect of the invention, fungal cells can be manipulated to produce compositions enriched for occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations). "Fungi" as used herein includes the phyla *Ascomycota, Basidiomycota, Chytridiomvcota*, and *Zygomycota, Oomycota* and all mitosporic fungi. A fungal cell may be a yeast cell. "Yeast" as used herein includes ascosporogenous yeast (*Endomycetales*), basidiosporogenous yeast, and yeast belonging to the Fungi Imperfecti (*Blastomycetes*). 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 is 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. The filamentous fungal host cell may be an *Acremonium, Aspergillus, Aureobasidium, Bjerkandera, Ceriporiopsis, Chrsosporium, Coprinus, Coriolus, Cryptococcus, Filibasidium, Fusarium, Humicola, Magnaporthe, Mucor, Myceliophthora, Neocallimastix. Neurospora, Paecilomyces, Penicillium, Phanerochaete, Phlebia, Piromyces, Pleurotus, Schizophillum, Talaromyces, Thermoascus, Thielavia, Tolypocladium, Trametes*, or *Trichoderma* cell. 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 caregiea, Ceriporiopsis gilvescens, Ceriporiopsis pannocinta, Ceriporiopsis rivulosa, Ceriporiopsis subrufa, Ceriporiopsis subvermispora, Chrysosporium inops, Chrysosporium keratinophilum, Chrysosporium lucknowense, Chrysosporium merdarium, Chrysosporium pannicola, Chrysosporium queenslandicum, Chrysosporium tropicum, Chrsosporium 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 trichothecioides, Fusarium venenatum, Humicola insolens, Humicola lanuginosa, Mucor miehei, Myceliophthora ther-*

mophila, 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.

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.

In another embodiment of the present invention, the native promoter of the ocfN gene within *Burkholderia contaminans* MS14 can be replaced by promoter elements known to enhance the level of gene expression, thereby increasing OcfN thioesterase activity within *Burkholderia contaminans* MS14. *Burkholderia contaminans* MS14 can also be genetically modified by other techniques to produce compositions enriched for occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations). Genetic modifications that ocfN thioesterase activity include the introduction of multicopy plasmids comprising a native promoter or any other promoter sequence operably liked to an ocfN gene into *Burkholderia contaminans* MS14, integration of additional copies of the ocfN gene operably linked to a promoter into the chromosome of *Burkholderia contaminans* MS14 using transposon mutagenesis or by replacement of the native ocfN promoter in *Burkholderia contaminans* MS14 with a promoter that increases the expression of ocfN transcripts relative to the native promoter sequence.

Another aspect of the invention provides for the introduction of a point mutation into the nucleotide sequence encoding OcfD, the truncation of ocfD (or introduction of a frameshift mutation) such that the thioesterase activity is reduced or eliminated or the deletion of the segment of the ocfD gene encoding the catalytic serine in order to increase the amounts of occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the TOCSY fingerprint identified in FIG. **5**C (the green NH correlations) produced by *Burkholderia contaminans* MS14 or by microorganisms genetically modified to produce occidiofungin (e.g., microorganisms into which the biosynthetic pathway for occidiofungin production have been introduced). In this aspect of the invention, a point mutation is introduced into the catalytic serine in the thioesterase domain of ocfD in order to reduce its activity. This amino acid is found at position 2954 of SEQ ID NO: 4. For example, the serine can be mutated into an alanine, glycine or proline residue (with glycine or alanine being preferred in this context). Certain embodiments of this aspect of the invention also provide for genetic modification of the microorganisms such that ocfN activity is increased as well (e.g., the level of OcfN thioesterase activity can be increased by means of expressing the ocfN gene in a multicopy plasmid with a native promoter or any other promoter sequence, chromosomal integration of additional copies of the ocfN gene using transposons or other means or substitution of the native promoter associated with the ocfN gene with a promoter that increases expression of the gene (relative to the native promoter)).

Another aspect of the invention provides for the introduction of a point mutation into the nucleotide sequence encoding OcfN, the truncation of ocfN (or introduction of a frameshift mutation) such that the thioesterase activity is reduced or eliminated, the deletion of the segment of the ocfN gene encoding the catalytic serine or chromosomal deletion of ocfN within a microorganism (e.g., Burkholderia contaminans MS14) in order to increase the amounts a particular occidiofungin diastereomer/conformer produced by a microorganism. As would be apparent to one skilled in the art, a similar effect can be obtained by transforming a microorganism with the genes encoding the occidiofungin biosynthetic pathway, with the exception of ocfN gene. In this aspect of the invention, a point mutation is introduced into the catalytic serine in the thioesterase domain of OcfN in order to reduce its activity. This amino acid is found at position **73** of SEQ ID NO: 3. For example, the serine can be mutated into an alanine, glycine or proline residue (with glycine or alanine being preferred in this context). Certain embodiments of this aspect of the invention also provide for genetic modification of the microorganisms such that OcfD activity is increased as well (e.g., the level of OcfD thioesterase activity can be increased by means of expressing the ocfD gene in a multicopy plasmid with a native promoter or any other promoter sequence, chromosomal integration of additional copies of the ocfD gene using transposons or other means or substitution of the native promoter associated with the ocfD gene with a promoter that increases expression of the gene (relative to the native promoter)).

Materials and Methods

Proportion of Occidiofungin Variants in the Sample. The C-terminal TE domain of OcfD and the OcfN cyclase thioesterase in the occidiofungin biosynthetic gene cluster are both predicted to be involved in the termination of synthesis and formation of the cyclic peptide. Given that the N-terminal end of the linear peptide is an Asn or BHN, we hypothesized that each thioesterase was required for cyclization of the Asn1 and BHN1 variants. The Asn1 and BHN1 variants of occidiofungin are not separable by RP-HPLC (reverse phase high performance liquid phase chromatography), thus, both variants are present in the purified fraction (FIG. **2**). The final RP-HPLC step in the purification process reveals the presence of three peaks. Occidiofungin samples elute as a doublet peak before the third peak. Both the wild type strain MS14 and the ocfN mutant MS14GG88 have the same chromatographic profile as observed in the last purification step. Occidiofungin peaks were confirmed by MALDI-TOF and bioassays. It is important to note that the presence of the doublet peak is not associated with the presence of Asn1 or BHN 1. Each peak of the doublet contains both the Asn1 and BHN 1 variants.

The relative proportion of the Asn1 and BHN1 variants could not be directly compared, because direct measurement of the Asn1 peak intensities could not be done due to the peaks overlapping with Asn7. The relative proportion of the Asn1 and BHN 1 variants in the wild-type fraction was determined by measuring the ^{13}C-HSQC Ha-Ca cross peak intensities of each BHY4 peak in the data set,[27, 28] given that each of the BHY4 peaks could be attributed to either the

Asn1 or BHN1 variant. Based on the Ha-Ca cross peak intensities for BHY4 in HSQC spectrum, the Asn1 and BHN 1 variants was determined by measuring the ^{13}C-HSQC Ha-Ca cross peak intensities of each BHY4 peak in the data set[27, 28], and was determined to be approximately 36% and 64% of the total amount of occidiofungin, respectively (FIG. **3**). The peaks in red and green represent the BHY4 peaks associated with BHN1 and Asn1 variants, respectively. A similar ratio was also observed in the relative abundance of each peak in the ESI-MS spectrum (FIG. **4**A). Furthermore, the ^{13}C-HSQC Ha-Ca cross peak intensities for the BHN1 peaks in the spectra were determined to be 90.50 and 38.65, which support the intensities measured for BHY4 peaks corresponding to the BHN1 conformational variants.

Mutagenesis of the ocfN gene was conducted via a marker exchange procedure as described previously[22], to generate the mutant MS14GG88. The percentage of Asn1 to BHN 1 variants in the ocfN mutant MS14GG88 fraction could be determined by measuring the proportion of each BHN1 variant using the HSQC data set and by the integration of the HN of Asn1 and BHN1 in the ^{1}H NMR spectra. Asn1 and BHN1 variants are approximately 20% and 80% of the total amount of occidiofungin, respectively. The ESI-MS spectrum also shows a lower relative abundance for the Asn1 variant (1200.39 Da) compared to the BHN 1 variant (1216.41 Da) (FIG. **4**B).

Comparison of Wild-Type and ocfN Mutant NMR Spectra. Occidiofungin has a complex spectrum for a peptide of only eight amino acids (FIG. **5**A and Table 1). The NMR spectrum represents an average of the conformers on the NMR time scale. Conformers in slow exchange on the NMR time scale may result in multiple spin systems for each amino acid. In some situations, multiple conformers are known to arise for cyclic peptides due to slow interconverting conformational families.[29, 30] Despite the conformation restrictions brought about by the ring closure, occidiofungin still has a significant amount of conformational freedom. Both Asn1 and BHN1 variants are visibly present in the wild-type fraction, which are colored red in FIG. **5**A. The TOCSY fingerprint region (NH correlations) is not as complex for the OcfN thioesterase MS14GG88 mutant spectra (FIG. **5**B). A significant number of spin systems found in the wild-type spectra are absent in the ocfN thioesterase mutant spectra. Our experiments show that the TE domain on the C-terminal region of OcfD is able to perform the peptide macrocyclization of both the Asn1 and BHN 1 variants. Although, there is only one amide spin system for Asn1 produced by OcfD. Whereas, the loss of OcfN results in the disappearance of the other three Asn1 amide spin systems.

An overlay of the wild-type and ocfN mutant NMR spectra shows the amino acid spin systems in green that are absent in the mutant spectra (FIG. **5**C). These spin systems are for Asn7, Ser8, Asn1, Novel Amino Acid 2 (NAA2), Ser3, BHY4, and Gly6. The loss of these spin systems suggests that the complex spin system observed for the wild-type occidiofungin fraction is not only due to interconverting conformational families, but is the result of distinct diastereomers formed by the regiospecific activity of the OcfN cyclase and OcfD TE domain. Dramatic chemical shifts observed, such as the 2 ppm shift for HN of the NAA2, support the formation of a structurally unique conformer of occidiofungin. A unique conformer is further supported by the subsequent loss of a NAA2 spin system in the ocfN mutant NMR spectra. Furthermore, the presence of both Asn1 and BHN1 spin systems in the mutant spectra along with the absence of the amide spin systems shown in green indicate that the additional spin systems are not due to the presence of the β-hydroxyl on Asn1. The additional spin systems are due to the formation of unique diastereomer produced by OcfN cyclase thioesterase. To further test for the formation of a configurational isomer versus an interchangeable conformational isomer, one dimensional NMR temperature titrations were performed. Amide and aromatic regions revealed little change in the complexity of peaks present with the occidiofungin derived from ocfN mutant MS14GG88 or wild-type strain MS14 (FIGS. **13**A-**13**B). Given that NAA2 spin systems are a good indicator for the presence of both diastereomers in the wild-type spectrum, we collected TOCSY spectra for occidiofungin derived from ocfN mutant MS14GG88 or wild-type strain at 50° C. (FIGS. **14**A-**14**B). There was no loss or addition of a spin system for NAA2 in the mutant spectrum. Furthermore, both spin systems for NAA2 remained in the wild-type spectrum. This data supports that the stereoisomers are non-interchangeable isomers, supporting their classification as a diastereomers (configurational isomers) rather than a conformational isomer.

Model for the Coordinated Function of Two Cyclase Thioesterases. There was no loss of an amide spin system for a BHN 1 in the ocfN mutant NMR spectra. This suggests that OcfN thioesterase has a substrate requirement for the peptide containing Asn1, since there is no concomitant loss of a BHN1 spin system with the observed loss of the Asn1 spin systems. The C-terminal TE domain of OcfD has a preference for the peptide containing the BHN1, but is capable, albeit at a lower efficiency of cyclizing the Asn1 variant. This provides an interesting scenario for the activity of the two thioesterases (FIG. **6**). Both thioesterases contain the GXSXG motif, which is important for the catalytic transfer of the peptide from the T domain to the cyclase. This suggests that substrate recognition occurs prior to the catalytic transfer of the peptide to the cyclase. Presumably, OcfN cyclase has a higher affinity or better access for the Asn1 peptide product given that the proportion of the Asn1 cyclic peptide product produced by OcfD compared to the BHN1 product is reduced in the wild-type fraction. Therefore the biosynthesis of occidiofungin utilizes the structural differences between Asn and BHN to increase the conformational biodiversity of occidiofungin. The increase in conformational diversity is accomplished by the regiospecific activity of each cyclase, presumably by differences in their binding clefts that helps orientate the peptide before cyclization.

Comparison of the Bioactivity of the Wild-Type and ocfN Mutant Product. To determine whether the increase in conformational diversity is important for bioactivity, minimum inhibitory concentrations were determined against medically relevant *Candida* species (FIG. **7**A). There was a 2-fold decrease in the minimum inhibitory concentration (MIC) with the purified ocfN mutant product with respect to the wild-type product against *Candida albicans* LL, *Candida albicans* TE, *Candida glabrata* ATCC66032, *Candida parapsilosis* ATCC90018, and *Candida tropicalis* ATCC66029. There was no difference in the MIC for *Candida albicans* ATCC66027. Colony forming units (CFUs/mL) were determined for the MIC wells of wild-type product for each *Candida* species and compared to the corresponding well containing the same concentration of the ocfN mutant product (FIG. **7**B). Following exposure to the same concentration of wild-type and ocfN mutant products, these results show a 5 to 7-log decrease in cell density of the *Candida* species treated with wild-type product. The differences in activity are also visualized by the rate of cell death. Time-kill experiments were performed against *Candida glabrata* ATCC66032. There was a ten-fold difference in

yeast present at 4 and 8 hours when cells were treated with 0.5 μg/mL of occidiofungin derived from ocfN mutant MS14GG88 or wild-type strain (FIG. **15**). Furthermore, a slower rate of cell death was also observed for yeast treated with occidiofungin derived from ocfN mutant MS14GG88 at 1.0 and 2.0 μg/mL. Given that the cyclic occidiofungin variants produced by OcfN constitute less than half of the total structural variants, a 2-fold loss in activity suggests that the configurational isomer made by OcfN are 4-fold more active than the stercoisomer produced by OcfD against five of the *Candida* species tested. Another possible explanation for the observed differences in activity could be attributed to possible synergism between the configurational isomers produced by each cyclase thioesterase. Furthermore, the antifungal activity of the ocfN mutant (MS14GG88: 8.79±0.38 mm) was also significantly reduced ($P<0.05$) compared to wild-type activity (inhibitory zone radius±SEM: 13.00±0.58 mm) in an overlay assay against *Geotrichum candidum* (FIG. **8**).

General Discussion. The findings from this study include experiments showing the following: the relative proportion of the Asn1 and BHN1 variants in the purified fraction; distinct differences in spin systems for the wild-type and ocfN mutant products: proposed model for the coordinated function of two cyclase thioesterases; and demonstrated differences in biological activity of wild-type and ocfN mutant products against therapeutically relevant *Candida* species. Expanding the conformational repertoire of cyclic peptide natural products can be beneficial to microorganisms. These data suggest that the bacterium *Burkholderia contaminans* MS14 is benefited by maintaining two distinct cyclase thioesterases that improves the spectrum of activity of occidiofungin.

Our data support the observation that cyclase thioesterase substrate recognition occurs prior to the catalytic transfer of the peptide. The presence or absence of a hydroxyl group on the beta carbon of the N-terminal amino acid (Asn1) appears to be important for the substrate recognition by the two cyclase thioesterases. It has also been shown that the N-terminal amino acid is important for substrate recognition for other thioesterases.[4, 8] It is possible that the presence of the hydroxyl group promotes a hydrogen bond with the ocfD cyclase thioesterase domain or more likely promotes an interaction within the T domain of the NRPS. Different bound orientations of the peptide to the T domain would establish a basis for the coordinated function of two cyclase thioesterases. It is also possible that the enzymatic conversion of one of the residues between L- and D-isomers is not completed by one of the epimerization domains. A combination of differences in the N-terminal amino acid and a possible difference in amino acid configuration (L or D), may contribute to the selective differences by the cyclase thioesterases that result in the formation of the observed configurational isomers.

The presence of the hydroxyl group on the beta carbon and the bound orientation of the peptide to the T domain may prevent the interaction of the OcfN cyclase, while enabling the continued substrate recognition by OcfD TE domain. There is evidence for the need of a bound orientation of the peptide to the T domain for the successful function of the cyclase thioesterase. Conformational diversity of the T domain has been shown to be important for the directed movement of the peptide substrate bound to the ppan cofactor and its interaction with externally acting enzymes.[3] More specifically, the active site serine of the cyclase thioesterase needs to attack the linear peptide attached by a thioester linkage to the ppan forming an acyl-O-TE intermediate. The position of the peptide bound to the ppan in the T domain will be important for bringing the peptide substrate in proximity of the appropriate cyclase thioesterase.

Furthermore, some cyclase thioesterases are capable of transacylation of the peptide to the active site serine, when the peptide is bound to a biomimetic prosthetic group.[4, 16] However, there are several cyclase thioesterases that will not function when the product is bound to a biomimetic group. These data suggest that the interaction of the peptide with the T domain is important for the enzymatic activity of some thioesterases and this interaction cannot be mimicked using a prosthetic group. It is conceivable that the coordinated function of the two cyclase thioesterases, involved in the synthesis of occidiofungin, utilize differences in the interaction of the ppan bound peptide within the T domain.

Presumably, ocfN was integrated into the occidiofungin biosynthetic gene cluster to improve its spectrum of activity against fungi. Given the broad spectrum of antifungal activity associated with occidiofungin, the molecular target is likely to be highly conserved. However, there must be some variation among fungal species to account for the differences in biological activity. Increasing the conformational repertoire must be a selective advantage to the bacterium for it to maintain the two functional cyclase thioesterases. The microbial environment is considerably different than how we intend to apply the natural products produced by microorganisms. For instance, the bacterium *Streptomyces roseosporus* is a soil saprotroph responsible for the production of daptomycin.[31, 32] The microbial community that this bacterium encounters is far more diverse than the group of bacteria that cause human infection. Thus, evolutionary pressures that selected for the current conformers of daptomycin may not necessarily be the best conformers for treating a *Staphylococcus aureus* infection. It is very likely that the therapeutic application of daptomycin or other cyclic peptide drugs could be improved by engineering novel conformational or configurational isomers.

Creating novel diastereomers of other cyclic peptide drugs using new or engineered cyclase thioesterases may lead to improvements in their therapeutic activity against clinically relevant pathogens. This is true for occidiofungin produced by the bacterium *Burkholderia contaminans* MS14, which accomplishes this goal by the evolutionary integration of an additional cyclase thioesterase into the occidiofungin biosynthetic gene cluster.

All patents, patent applications, provisional applications, and publications referred to or cited herein are incorporated by reference in their entirety, including all figures and tables, to the extent they are not inconsistent with the explicit teachings of this specification.

Following are examples which illustrate procedures for practicing the invention. These examples should not be construed as limiting. All percentages are by weight and all solvent mixture proportions are by volume unless otherwise noted.

EXAMPLE 1

Experimental Section

Materials. Occidiofungin produced by both the wild type strain MS14 and the ocfN mutant MS14GG88 were purified as previously described for the wild-type sample. Chemicals were purchased from Sigma-Aldrich (St. Louis, Mo.) and were the highest grade, unless otherwise stated. Media were purchased from Fisher Scientific, enzymes were purchased from New England BioLabs, and primers were purchased from Integrated DNA Technologies (IDT) unless otherwise

stated. *Candida* strains used were purchased from the ATCC biological resource center and were a gift from Thomas Edlind (Drexel University College of Medicine).

Site Directed Mutagenesis. A nonpolar mutation was constructed in the open reading frame of wild-type ocfN by the insertion of a kanamycin resistance gene, nptII.[33] To mutate ocfN, a 1-kb fragment containing ocfN was obtained by PCR using primers MocfNF (5'-CGCCACCCGTTAC-GAGGATTC, SEQ ID NO: 1) and MocfNR (5'-ACGCGTC-CCCTCTTCCTACG, SEQ ID NO: 2). The 1-kb PCR product was cloned into the pGEM-T Easy Vector System I (Promega Corporation, Madison. WI) resulting in plasmid pGG30. The nptII gene was inserted into the cloned ocfN at SmaI, generating plasmid pGG31. The ~2-kb EcoRI fragment of pGG31 harboring the ocfN gene disrupted by insertion of nptII was cloned into pBR325[34] at the EcoRI site to generate pGG32. Mutagenesis of the ocfN gene was conducted via a marker exchange procedure as described previously[35], to generate the mutant MS 14GG88. PCR analysis and sequencing were used to verify the double crossover mutants. Production and purification of the antifungal were done as previously described.[23]

NMR Spectroscopy. A 2 mM sample of ocfN thioesterase mutant fraction of occidiofungin was prepared in dimethyl sulfoxide (DMSO-d6, Cambridge Isotopes) and data were collected as previously described for the wild-type fraction.[22] The NMR data were collected on a Bruker Advance DRX spectrometer, equipped with a CryoProbe, operating at a proton frequency of 600 MHz. The ^{1}H resonances were assigned according to standard methods[36] using COSY (correlation spectroscopy), TOCSY (total correlation spectroscopy), NOESY (nuclear overhauser effect spectroscopy) and ^{13}C-HSQC (heteronuclear single quantum coherence) experiments. NMR experiments were collected at 25° C. The carrier frequency was centered on the residual water resonance (3.333 ppm), which was suppressed minimally using standard presaturation methods. A 2.0 s relaxation delay was used between scans. The TOCSY experiment was acquired with a 60 ms mixing time using the Bruker DIPSI-2 spinlock sequence. The NOESY experiment was acquired with 400 ms mixing time. The parameters for collecting the HSQC spectrum were optimized to observe aliphatic and aromatic CH groups. The spectral sweep width for the TOCSY and NOESY was 11.35 ppm in both dimensions. The spectral sweep widths for HSQC were 11.35 ppm in the proton dimensions and 0 and 85 ppm for the carbon dimension. All 2D data were collected with 2048 complex points in the acquisition dimension and 256 complex points for the indirect dimensions, except for the HSQC which was collected with 2048 and 128 complex points in the direct and indirect dimension, respectively. Phase sensitive indirect detection for NOESY, TOCSY, and COSY experiments was achieved using the standard Bruker pulse sequences. ^{1}H chemical shifts were referenced to the residual water peak (3.33 ppm). Data were processed with nmrPipe[37] by first removing the residual water signal by deconvolution, multiplying the data in both dimensions by a squared sinebell function with 45 or 60 degree shifts (for the ^{1}H dimension of HSQC), zerofilling once, Fourier transformation, and baseline correction. Data were analyzed with the interactive computer program NMRView.[38] One-dimensional NMR temperature titrations were collected on the wild type and mutant peptides, using a Bruker AVANCE III HD 600 MHz spectrometer equipped with a cryoprobe. Eight scans were collected in each 1-D experiment, using 32K points, at a temperature of 298 K. The experiments were repeated using higher temperatures for both samples in 5 degrees K increments, up to a temperature of 323 K. 2-D TOCSY spectra were collected at a temperature of 323 K, using a mixing time of 60 milliseconds. Eight scans and 256 indirect points were used for both the wild type and mutant peptides. The 2-D spectra were processed using NMRPipe, with 45 degree sinebell squared shifts in both dimensions.

Mass Spectrometry. The wild-type occidiofungin and the ocfN mutant sample (10 μg) were evaporated to dryness in a Speed Vac Concentrator (ThermoScientific, San Jose, Calif.) and the residue was taken up in 50 μl methanol and analyzed by direct infusion at 3 μl/minutes into an LCQ DecaXP (ThermoScientific. San Jose, Calif.). Data were acquired over a mass range of m/z 200 to 2000.

In Vitro Susceptibility Testing. Microdilution broth susceptibility testing was performed in triplicate according to the CLSI M27-A3 method in RPMI (Roswell Park Memorial Institute) 1640 [buffered to a pH of 7.0 with MOPS (morpholinepropanesulfonic acid)] growth medium. 100× stock solutions of occidiofungin were prepared in dimethyl sulfoxide (DMSO). MIC endpoints for occidiofungin were determined by visual inspection and were based on the wells that had no visible growth (an optically clear well) after 24 hours of incubation. DMSO containing no antifungal agent was used as a negative control. Colony forming units (CFUs) were determined in triplicate by plating 100 μl from the MIC wells onto a Yeast Peptone Dextrose (YPD) plate as well as plating 100 μl from 10-fold serial dilutions of the cell suspension in Yeast Peptone Dextrose (YPD) Broth. Colony counts were performed and reported as CFUs/ml. Time-kill experiments were performed as previously reported.[19] *Candida glabrata* (ATCC 66032) colonies on 24-h-old YPD plates were suspended in 9 ml of sterile water. The density was adjusted to a 0.5 McFarland standard and was diluted 10-fold with RPMI 1640 medium to a final volume of 10 ml containing a final concentration of 2, 1, 0.5 and 0 μg/ml of occidiofungin from wild type strain MS14 and the ocfN mutant MS14GG88. The cultures were incubated at 35° C. with agitation. Samples were drawn, serially diluted, and plated on YPD medium for colony counts.

It should be understood that the examples and embodiments described herein are for illustrative purposes only and that various modifications or changes in light thereof will be suggested to persons skilled in the art and are to be included within the spirit and purview of this application and the scope of the appended claims. In addition, any elements or limitations of any invention or embodiment thereof disclosed herein can be combined with any and/or all other elements or limitations (individually or in any combination) or any other invention or embodiment thereof disclosed herein, and all such combinations are contemplated with the scope of the invention without limitation thereto.

TABLE 1

Chemical Shift Values for Occidiofungin derived from the ocfN mutant MS14GG88[a]

Unit	No.	δ_C	δ_H
Asn1	2	52.71, CH	4.59
	2-NH		7.75
	3	39.91, CH2	2.62, 2.41
	4	—	
	4-NH2		7.39, 6.93
BHN1	2	58.47, CH	4.66, 4.61
	2-NH		7.81, 7.9
	3	75.01, C	3.98, 4.02
	3-OH		4.66
	4	—	
	4-NH2		7.24

TABLE 1-continued

Chemical Shift Values for Occidiofungin derived from the ocfN mutant MS14GG88[a]

Unit	No.	δ_C	δ_H
NAA2	2	43.88, CH2	2.34, 2.36
	3	47.25, CH	4.23
	3-NH		7.31, 7.34
	4	41.57, CH2	1.39, 1.76
	5	66.36, CH	3.50
	6	76.07, CH	3.08
	7	79.61, CH	3.72
	8	33.19, CH2	1.54
	9-17	25.14-28.02, CH2	1.27
	18	16.94, CH3	0.86
Ser3	2	58.59, CH	4.07, 4.15
	2-NH		8.11, 8.14
	3	70.23, 64.29	3.49, 3.45
	3-OH		4.95
BHY4	2	58.71, CH	4.06, 4.15
	2-NH		7.83, 7.94
	3	73.75, CH	4.98, 5.08
	3-OH		5.66, 5.73

TABLE 1-continued

Chemical Shift Values for Occidiofungin derived from the ocfN mutant MS14GG88[a]

Unit	No.	δ_C	δ_H
	4	—	
	5, 6	—	7.15
	8, 9	—	6.67
DABA5	2	53.49, CH	4.43
	2-NH		7.66
	3	32.68, CH2	1.88, 2.11
	4	39.17, CH2	2.92
	4, NH		7.71
Gly6	2	44.76, CH2	3.87, 3.58, 3.84, 3.70
	2-NH		7.68, 7.85
Asn7	2	53.25, CH	4.51, 4.58
	2-NH		8.35, 8.41
	3	40.03, CH2	2.61, 2.38
	4	—	
	4-NH2		7.39, 6.93
Ser8	2	58.11, CH	4.33, 4.32
	2-NH		7.76, 7.78
	3	64.59	3.61, 3.62
	3-OH		4.79

[a]Proton chemical shift values are from a TOCSY and NOESY experiments. Chemical shifts in brackets are ^{13}C values from the HSQC experiment.

GenBank: EU938698.5
Go to:
LOCUS EU938698 58101 by DNA linear BCT 13-DEC-2010
DEFINITION *Burkholderia contaminans* strain MS14 putative FAD linked oxidase
domain protein gene, partial cds; and putative LuxR-type egulator
(ambR1), putative LuxR-type regulator (ambR2), putative cyclic peptide transporter, hypothetical protein, putative glycosyl transferase, putative nonribosomal peptide synthetases, putative
beta-lactamase domain protein, putative beta-ketoacyl synthase nonribosomal peptide synthetase, putative short chain dehydrogenase/reductase SDR, putative beta-ketoacyl synthetase, putative taurine catabolism dioxygenase, putative transaminase, putative epemerase/dehydratase, putative thioesterase, and hypothetical protein genes, complete cds.
ACCESSION EU938698
VERSION EU938698.5 GI: 314950578
KEYWORDS .
SOURCE *Burkholderia contaminans*
ORGANISM *Burkholderia contaminans*
Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales; Burkholderiaceae; Burkholderia; Burkholderia cepacia complex.
REFERENCE 1 (bases 1 to 58101)
AUTHORS Gu, G., Smith, L., Wang, N., Wang, H. and Lu, S. E.
TITLE Biosynthesis of an antifungal oligopeptide in *Burkholderia contaminans strain* MS14
JOURNAL Biochem. Biophys. Res. Commun. 380 (2), 328-332 (2009)
PUBMED 19167363
REFERENCE 2 (bases 1 to 58101)
AUTHORS Gu, G., Wang, N., Chaney, N., Smith, L. and Lu, S. E.
TITLE AmbR1 is a key transcriptional regulator for production of antifungal activity of *Burkholderia contaminans* strain MS14
JOURNAL FEMS Microbiol. Lett. 297 (1), 54-60 (2009)
PUBMED 19500142
REFERENCE 3 (bases 1 to 58101)
AUTHORS Gu, G., Smith, L., Wang, N., Wang, H. and Lu, S.
TITLE Direct Submission
JOURNAL Submitted (01-AUG-2008) Entomology and Plant Pathology, Mississippi
State University, 32 Creelman St., Mississippi State, MS 39762, USA
REFERENCE 4 (bases 1 to 58101)
AUTHORS Gu, G., Smith, L., Wang, N., Wang, H. and Lu, S.
TITLE Direct Submission
JOURNAL Submitted (12-NOV-2008) Entomology and Plant Pathology, Mississippi
State University, 32 Creelman St., Mississippi State, MS 39762, USA
REMARK Sequence update by submitter

-continued

```
REFERENCE   5 (bases 1 to 58101)
AUTHORS     Gu, G., Smith, L., Wang, N., Wang, H. and Lu, S.
TITLE       Direct Submission
JOURNAL     Submitted (15-JAN-2009) Entomology and Plant Pathology,
            Mississippi
            State University, 32 Creelman St., Mississippi State, MS 39762,
            USA
REMARK      Sequence update by submitter
REFERENCE   6 (bases 1 to 58101)
AUTHORS     Gu, G., Smith, L., Wang, N., Wang, H. and Lu, S.
TITLE       Direct Submission
JOURNAL     Submitted (24-FEB-2009) Entomology and Plant Pathology,
            Mississippi
            State University, 32 Creelman St., Mississippi State, MS 39762,
            USA
REMARK      Sequence update by submitter
REFERENCE   7 (bases 1 to 58101)
AUTHORS     Gu, G., Smith, L., Wang, N., Wang, H. and Lu, S.
TITLE       Direct Submission
JOURNAL     Submitted (13-DEC-2010) Entomology and Plant Pathology,
            Mississippi
            State University, 32 Creelman St., Mississippi State, MS 39762,
            USA
REMARK      Sequence update by submitter
COMMENT     On Dec 13, 2010 this sequence version replaced gi: 224016442.
FEATURES    Location/Qualifiers
source 1 . . . 58101
       /organism = "Burkholderia contaminans"
       /mol_type = "genomic DNA"
       /strain = "MS14"
       /db_xref = "taxon: 488447"
CDS    complement(<1 . . . 1175)
       /note = "ORF1"
       /codon_start = 1
       /transl_table = 11
       /product = "putative FAD linked oxidase domain protein"
       /protein_id = "ACN32485.1"
       /db_xref = "GI: 224016443"
```

(SEQ ID NO: 5)

```
/translation = "MSHDFRDEPAPRRAFLADMAKLAAAGIVTGWTPLYQVAAHARTA

GETPPGFPADIQLYKQAFLNWSGEIAVQDVWTAAPRSADDVVATVNWARANGYRIRPR

GYTHNWSPLTLDPGAGAANLVLLDTTKSLTAVSVDTSARPARVTAQTGVSLESLLATL

EQVGLGVIAAPAPGDITLGGALIDAHGTAVPAAGETLQPGHTYGSLSNLVVALTAVV

FDPARQQYVLRRFERSDPEIGAFLAHIGRALVVEVTLTAGPNQRLRCQSYVDIPASEL

FAAPGTTGRTIASFLDGSGRVEAIWFPFTTKPWLKWTPTPSKPFLSRAVTQPYNYPF

SDSISQSISDLVKRIVIGGEGALTPLFGQTQLAITTAGLALTLSGDIWGWSRTVLQE"

gene 2480 . . . 3301
     /gene = "ambR1"
CDS  2480 . . . 3301
     /gene = "ambR1"
     /note = "AmbR1"
     /codon_start = 1
     /transl_table = 11
     /product = "putative LuxR-type regulator"
     /protein_id = "ACN32486.1"
     /db_xref = "GI: 224016444"
```

(SEQ ID NO: 6)

```
/translation = "MFAKLGKVISSAGSERFASDMHALLVESIPLTITRMTEWTLDEP

AGEVVRVQSLGADGAPGDDGRGAPAAHGEREPAAHPPLNRILAACDRQLIHINPLMRR

GNGGEVAPSRGPGGGFQCHLVSGKANRRYVISLHRTASHRDFSLREMSFLKNFADTLL

PLVEWHASTCRHGEREGATAPGATAGMPGVEALRHEFESRLARARVVLSARENEVCLG

LLAGKMLREMAGELGVKESTIETYIKPAAVKLGISGRHGLTKWMIDDSVPCASAA"

gene complement(3372 . . . 4262)
     /gene = "ambR2"
CDS  complement(3372 . . . 4262)
     /gene = "ambR2"
     /note = "AmbR2"
```

-continued

/codon_start = 1
/transl_table = 11
/product = "putative LuxR-type regulator"
/protein_id = "ACI01437.2"
/db_xref = "GI: 212381179"

(SEQ ID NO: 7)

/translation = "MEFSRLFAHVGEAISSSGSRRFPRMMYNLIAAAVPVDEIRISEL

AIDDVPDGPPEVRSLGAVGAALAKTGAAAVCCGPQMPPRPGTSPLHVDDTLAGHGPIH

AQLDRFILMQAAIVSPRYAQFHLVTRKRGHCYVISLYRTCTFDDFSPQERTFLKELSH

VLFPIVESHVAALDSAPPAARVTTAAPPATQSGRERVARRFADRLQQAGVKLSTREIE

ACTALLAGDTVPAIAMRFALRESTVETYLKRAAVKLGFSGRHGLTRWMLDETAGAATE

AAGGDMRSMRRDYASPRLGT"

CDS complement(4466 . . . 6169)
/note = "ORF2"
/codon_start = 1
/transl_table = 11
/product = "putative cyclic peptide transporter"
/protein_id = "ACJ24909.2"
/db_xref = "GI: 220898663"

(SEQ ID NO: 8)

/translation = "MDSAQSKSPPWHSAATLMWRSHPWLTLGTVVTGLVSGIASIAGV

GLISTVLHDQDDRQTLLLLFIAVNVVAVVCRSCAAVMPSYACMKVMTRLRVNLCKRIL

ATPLDEIDRRGAPNVLTMLTQDIPQLSQTLLTIPTIIVQSVVLICSIAYLAYLSWIVF

ASTIILTLVGLVLYLFFYRKAVNFTERVRDEFVQFNEYTHGLVFGIKELKLNRARRRW

FTRAAIELSSKRVAGFNYIERFWFMSGDSIGQITVAVLLGCLLFGVPSLGVVDPSVLT

ASILAVLYMMGPLTMLINVLPVVAEGKTALARLAEFGFLIDDTQASHEEPRPAGNVET

LSAKSWKVIELKDVTMNYRDNEASVDFVLGPIDMTIHAGELVYVIGGNGSGKSTLGKV

LSGLYAPTGGTISLDGKVVDDAARERYRNLFSAVFTDFHLFNRIIGPDRGNESIELAR

KYLATLKLADKIEISGRTYSTTRALSTGQRKRLALLCAYIEDRPIYILDEWAADQDPV

FKRFSYEVLVPDLKSRGKCVVIITHDDQYFKLADPVIRLDSGRIFSDTAMCAVRAEAA

G"

CDS complement(6186 . . . 6668)
/note = "ORF3"
/codon_start = 1
/transl_table = 11
/product = "hypothetical protein"
/protein_id = "ACL81525.1"
/db_xref = "GI: 220898664"

(SEQ ID NO: 9)

/translation = "MQLTTVDLEAAFVKAALDALHRDCKLGDAISLAYGKCESTAGVI

DLIFPLITKKLRIDYILMYSIESNPRTLLQFLRQIESGLARSEDWTAASVEAALRSVA

DSPDGVGWERAQRLLKCCILFSDSPLGIVESITFLGKHETSSRLRSAASNVELSHLIN"

CDS complement: (672 . . . 7378)
/note = "ORF4"
/codon_start = 1
/transl_table = 11
/product = "putative glycosyl transferase"
/protein_id = "ACL81526.1"
/db_xref = "GI: 220898665"

(SEQ ID NO: 10)

/translation = "MKSTPTIDNTFAPKVCINLDRRPDRWEAMQRKFAEQNILTVERL

PAVDARLVSVPESLSHMRAQDYGCTMSHLAAVKQAKAAGAREVLIFEDDAFFDADFAA

RFPEFIAQVPDDWHMLFLGAYHFTPPIPVAPNIVKAVETLTAHAYVVRNSLYDAFIAI

NENPPAINDRNNLVLQQTFNCYCFEPNLVGQESGYSDIMDEVMPEKPLTYSMPIPDGW"

-continued

CDS complement(7375 . . . 16869)
/note = "ORF5"
/codon_start = 1
/transl_table = 11
/product = "putative nonribosomal peptide synthetase"
/protein_id = "ACL81527.1"
/db_xref = "GI: 220898666"

(SEQ ID NO: 11)

/translation = "MQDNNVLVTDHRYAATARFWRESLSRVAGVYGIAAYAPSQQPGR

PLTRSVRLTPASLDLLRRIGDGELAEFAVAAAGIAFLLWKYFRIPVTVLGTPGLAGHP

SARAAIVPLIIEVRPDERIEDYLSRVAGIVEDSYAEPRFPLETLVRNEKDMALAQLTK

VALADDRVHHAPTGRDDDLQLHLRLARGEIELRYSGAIEPFIIDGFAGSLAAVLEAFE

HLDGAVGDIEAAPPEQGPLLAAFNETATAGPSHPTVVAMFEAQVARTPTAPALVTDSS

LMTYADLNARANSLAHHLREHHGVGPESLVGIMLDRSEWMIVAILGILKAGAAFVPLD

PAYPAERINHILGDTGLSLLVTQSSQLAQWYEFSGVTLLLDQELPGWQPLPDNPPHRA

EPAHLAYVLYTSGSTGKPKGCLLEHRNLAHYIAWAAGYYFPESTTGSFGLYSSLCFDF

TLTNIFCPLVRGKTLRIYPQSESIDTILARMFQPGSGVDTLKLTPTHIHLLEYMNLAR

SGVRKVIVGGEELTPQHIATLRKIDPAIEIYNEYGPTEATVGCIVERVEDAPPTVLIG

RPIADTRVYMLDDALRPVPLGVPGEICLAGAGLARGYHQRPDVTAAKFVEHPFPGEAR

IYRTGDIGRWLPDGRIQCYGRVDHQVKIRGHRVELGEIEAAIAAHEDVVGAAVMLRES

AHGVRKLAAYVKGAASLSVPNLRAYLAGKLPDYMVPSDIIPIAEFPLNANGKLDRPAL

LALEPAAAPEEAPLDATPIQRELVRIWRDVLDNPAVDLAGRFFDYGGDSLQAMQLVSR

IWSSFSVEIGIDAIFELQTISAVSDLIEASSPHPGSTAGAIPPRSRANDLPLSFPQQR

LWFLAQLEGPSATYNISSALRFEGELDVARLRFAVSEISRRHEILRTTFPAVDGRGVQ

RIAPPAPVALDVVDVASESDTLALLAEEADRPFDLAAGPLYRVVLYRVHERLHVFGIV

MHHIVSDAWSSGILIGELAALYAGESLPELAVQYADYAVWQHERLASADTHRELALLS

AALADAPDLIELPTDRPRPAVQQFRGAVLPFQLSAERADGLRAIARASGTSTFMVVLA

AYALLLSRYSNQQDLVIGSPIANRRSSMTEPLIGFFANMLALRVDLSGNPTFGDLLAR

VKRVALDGYSRQEIPFEQVVDSLELERNLGRTPVFQVVFAYEKAQPRAVSFPGLVATP

VAVETHTAKFDLTLHVQDADDGLAGSLEYNLDLFDAATIDRMAEHFRTLVDAVIADPD

RPLGALSLSNDAERNLLTVEWNRTDTDFGEDAAQPLHRLFEQQVERTPDAVAIVFDDT

ALTYAELNLRANRLAHHLVALGVGPDSLVGVAMERSLDMSVALLAILKAGGAYVPVDP

DYPAERVRFMIDHAQLRWLLTQQHLHDALPDTDAHVIVVDRDSLDLDAAATSNPAPAL

NGDNLAYMIYTSGSTGRPKGALNTHRAITNRILWMQHAYALDADDAVLQKTPFSFDVS

VWELFWPLVTGARLVFARPGGQRETDYLVELIERERITTIHFVPSMLRAFLDHPDLDA

HCASLRRVVCSGEALPHDLQQRCLERLDVKLYNLYGPTEAAVDVTAWECRRDDPHRIV

PIGRPIANTRLYIVDAQMQPTPIGVAGELLIGGTPVGRGYHGEPELSAEKFIADPFSA

DPLARLYRTGDLARYRFDGNIEFLGRIDHQIKLRGLRIEPGEIEAALRAHPSVDDCVV

IAKTEGARTFLIAYVATAAPDIADLRGYLGGKLADYMVPSQFFALESLPMLPNGKINR

KALPLPADRGDAAQPHAPAVTPREILLASICIDVLQLPSVGIHDNFFELGGDSILSIQ

VIARANQAGLRVTAKQLFQYQTIAQLAAAPEERAACAPTLSPLGDAPLTPVQHWFFEQ

EIDAPSHYNQTVLIQVPADIDASRLADAFRQVYEHHDALRLRFSHDAGRWTQQVVAGG

EMPALFAKQVIADDAGERLAAMRAAAADAERGIDITHGPLLAARLFCLADEPLARLFV

SIHHLAVDGVSWRVLLEDLHAAYHGQPLFGKTTSFREWALHLQQLARSPAIGDEARLW

-continued

QALLAQPVEPMPVDYPGTGAANNAVDDASSVSFELGEADTTALLRRLPRAYDTRINDV

LLVALAQACSMVTGNTRTRIDLESHGRHVSDAPLDLTRTVGWFTSIYPVVLDADAMHA

PEQALRAARQQLRRIPADGLGYSLLRYQSPDAAVRDSLAALPKADILFNYHGQLDTVL

RQSDGWRPAAEDLGSLRAGRSQRTHAFEIVAAVADGKLQVDWRYGERLHRRQTVENLA

AHFRDRLLDFAASVPDTAADDIEDSYPLSSLQQGILFHSLYDLDPAAYFQQFSFVVSG

PLQVPALRQAWANALARHAVLRTAFAWADRDHPVQTVRHTVDLPWTFLDWRHRDASRR

AQDFDAFLADDRRRGFDLQRAPLFRCTLIQETDTRHRFCWSAHHIILDGWSTATLMKE

VFDDYLSLARTGMPAVAASAPGYRAYIDWLARHPRSADETWWRAELAGFKAATPVAAS

PARQATGDAPRQDKRRTQQFLLDEALAARLQTLTRTHRVTLNVLIRAVWALVLRRHAG

TDDVVFGVTVSGRPPMLDGVESIVGLFINTLPLRLRIAPERPFIEWLAEVHAAQTAME

PHSYSSLVDIQSWSELPAGDSLFDSLLVFENFPVAAAPDLGPDDIEILDTRAFAESNY

PLTLTVHPNERIGFHISHDAHRIAPEVVRQMLDTLRTLLERFAENPGQLTGQLADPPA

ADGRPSAPRSGAGPAIEAAAGAAAAARAVAHAADESTLLEIWRRIFKRDDIAVSDNYF

DLGGHSIIAIQLMAHVEKAFDRRLPISCLFENPTIEKLAAALAAKEPSAPAGGLVPIR

DGGPAAPLFLLPGAGGNVVYFRPLANHLSGAHAIHGLEALGLDGACEPLTRVEDIAAR

HIERIWPLVGAGPYYLAGHSFGAHVALEMSRQLVAKGADVKLLAIFDASAPIDSSAAT

YWQDWDDTEWLVAIAHEIGTFLGTDLQVTRADLVHLDPDGQAGLILERIGDRGSWFAD

AGSDRLRAYLRVYQANFKSHYAQHATPLPVPIALFRSTERDPGDYAPSSEIAQLRLDA

TWGWSRFSAHPVAVTDVPGDHLTMLLDPHAGVLAAHVNSFLEKTPS"

CDS complement (16957 . . . 26022)
/note = "ORF6"
/codon_start = 1
/transl_table = 11
/product = "putative nonribosomal peptide synthetase"
/protein_id = "ACL81528.1"
/db_xref = "GI: 220898667"

(SEQ ID NO: 12)

/translation = "MQEGMLFHAVHEPGSRSSFNQLSCRITGSLDPALFHAAWQQLID

RHPVMRTSFHWEEFDKPMQVVHARATLPWVQDDWLDLPEHEQRSRWRAHLDNDLAEGF

ALDRAPLVRCRLVRVAADAYLFSWSHHHILADGWCLSLVIEEIFEVYGALARGVSPAL

PPVRPYRDYIQWLQQHEPQAAQQYWTRYLEGFRTPTPLPTAARAGADERFGQGLAQVQ

ADLSADLSARLRQFAARHHVTLNTLAQAAWALVLSRYSGETDVVFGAVVSGRGANLPG

IETMLGLFINTVPVRVRVDPRQPLVPWLKMIQARVAARAPFEHTPLPDIQRCSDVPPT

APLFESNITFMNYPLDASLTHGAHGLAVDEVQLYNRADIPLEFVVTARDDWKMELSFD

PRRFDEDTMQRMLGHVAATLDAFAADPNRLLGRVPILPDAERRQLLETFNDTAVPFDA

ALTVVHRLEQAAADHPERPAVEYEDGVLSAGELNARANBIAHRLLAAADLGPDALVAI

CMHRSAQLMEAILAVWKCGAAYIPVDPNYPVARIRTILEDSGAALVITCDGLLPPELA

GIALVVSLDAATDAVDDSNPGRPVSPDSLAYVIYTSGSTGKPKGAMVEHAGMLNHMLA

EIDEFSISASSVIAQTAPHCFDISVWQFFTAPLVGGKTVIVDDDCIRDPARFVAYLET

TRISILELVPSYLSAVLDRASERPALMRHLRHLLVTGEMVSPALVKQWFDVFPAIPLV

NAYGPAEASDDVAQHRMTGAPSTPYVPVGKPIRNVRLYVVDPQMNLCPIGIPGELCVS

GVAVGRGYLNNEAATQDAFVEDPFHPQRGVRLYRTRDIGCYLPDGTIVLHGRKDHQLK

IRGYRIELGEIDQRRLADHSRKLRQAAALDYRDEAGRAALCAYVAFRDGASLSDAGIA

AALSATLPDYMVPGIYVVLDALPLSGNGKIDRNALPPLDRARLAATAHAPTPPRTPTE

-continued

TLLCRIWGEALGIPSPGIHDNLFALGGDSILSMRIVSLAAKAGLKLTTRLIFQHPTVA

ELAAVATRGTVGAAAFVASSGPLPLTPIQKRFFAQGKHDPDQYNQAVLLDVPADLDPV

LLRQALRHAVKWHDALRLRFREGESGWTQEVVDDPEIPVVVSDIARDQLAQYVAQSHA

SLNLADGPVVRADLFRVDEGRSLRLLLVAHHLVVDGVSWGALLETVYDAYTRLRNGKA

PEFAGGSATWTAWTRAISTWAGSGAADADLAHWQALARAALPGLPLDRDAPADANTVS

SADTIVVELGHAATTALLGAAPRAYDAQVNDVLLAALAHAVSEWSGCADVLLDLEAHG

REELIDALDISRTVGWFTSVFPVLLTVDAGSHDPASLVASVRTRLRAVPNAGITYGLL

LDRLDGPLPQPRLQFNYLGQTDQLFTAAHDWKQAAHPSGDGRNANQLHEHLLDINAYV

TGNRLHVAWEFSRACHDTATILRVAQAYIAALETLVAGHAVPSASTRPATALPQAPAP

ASVSPDEIADVYPLTPTQQGMLFHSLYEFASDAYFSSLNFRIDGALDVERFRRAWETV

AHRHDILRTSFHWEDIESPVQVVHRRIDLPWHDEDLRAASAAEAEQRWEAYVAQDRAR

GFDFTRAPLMRLALFRVGEHAWRFHWSHHHILLDGWSSARLLSDVAAAYQAPPAEGAP

QRDAPPAFAGYVRWLARQDAAAAQRFWKTKLADFPATTPLVLGRPELDGTAAPGAYVE

EPLLLSESDTQRLVAFAQSRRLTLNTLAQGAWAQLLSRYSGESDVVFGTIVSGRPASL

PASDEMVGLFINTLPVRVRIDARPTSAWLAQLQMDLAQQEDYAHYPLADIQKFAGLPP

GVPLFESLLIFQNYPVEEALADALPGLRIGAFEVSDPNNYPLTLVVTPGKRLSLQVLY

DDGRFDRDTIVRLLRHVETLLTGLAGAEDRPNRSVPLLAAAERDAILLGWNDTFAPVP

SDRTLPELIEAVAAAHPERVAVRCGTEVRTYRDLVEGANRIAAHLLQTAFLQPDDRIA

VWMPRSPLMLETILAIWKCGAAYVPVDPAYPAQRVETILTLARPAVIVTTDCVPPPAL

ASIPLVDPARLPDRRGAEAPAPVTPRCRPADLAYVIFTSGSTGQPKGAMVEHRGMLNH

VLAMARRVGLGAQSAVAQTASHCSDISVWQCFAALASGGTTVIYPDAVILEPARLIDS

LHRDRITAMQFVPSYLATFLGELERHAAPAFPHLDTLLTIGETLQPATAQAWFRLNPA

VRLINAYGPTEASDSVAHYCLTRAPDGPAIPIGRPIENLRLYVVDADMNPCPAGVHGE

ICIGGVGVGRGYLFDEARTRAVFRDDPFSPEPGARLYRTGDIGCFGADGNLHFFGRRD

FQVKIRGYRIELGEIEAALTSLAGISHAVVVARETSDAEMTLCGYASGTGWTPQRVRD

ALRDTLPAHMVPDTVMLLPALPVMPNGKINRAALPLPDAASVPDGVRAEPRTPVEAAL

LRLFAEVLGRRENGVDDDFFEHGGQSLKAIQMVSRIPHAALNVAVADIFHAPTPRALA

QRLAAMPVDGAADDDAIIPALAAQPSYAVSRAQKRIWLASRGADPSTYNMAGALQLDG

AVDTARLVRAFDTLVDRHESLRTVFAMIEGELRQRVLSREASGFRVEQHDLADDAGFQ

AIDALIRAECEQPFDLASGPLFRVKLVRLSQEKHLLLLNMHHVISDAWSIRVLTDDLH

ALYAGRDLPPLSIQYRDYAAWHNASLAGPRAAAHRAYWLEQLAPPLPRLQLASDFPRP

ERLGHAGQTLEVELPQPHAAELATLARAHHTSLHAVLLASFCVLMHRYTGREDIVIGS

VSAGRDSEQLESQVGVYLNTVVLRVPVRKSATVAEVIDGVAKASAQALEHASYPFDVL

LEDLKIETPANHFPIFDIQVNHVSMPAPQPGLRITDISPADTTAKFDLSFQVVESEGR

HLIQFIYNTHLFRPSTIAAMRDRLLAIHDVFRRDPATPVDRIPLSDEAPAAGPRVRVG

LRLKRAPAVTADDALEEKT"

-continued

CDS complement(26061 . . . 29981)
/note = "ORF7"
/codon_start = 1
/transl_table = 11
/product = "putative nonribosomal peptide synthetase"
/protein_id = "ACN32478.1"
/db_xref = "GI: 224016445"

(SEQ ID NO: 13)

/translation = "MSELNLNALSTSGQYQEHVAFWNDALGRIDEDFRLQQAWQAYAL

PLGPEPALTFALDGDAAQVLERLAAGNELGAFVVLLAALFRVLGRYNGAAGLFVASPQ

LIVEPASGCAEPVPLLDAGEPGPTVRAYLNQLRDSVQRSYSYQDFPIAALAHKLHGER

RATNVGVRFDGLHEAWAAADYDLSIEIRHRERYEIVLTGRQTVFTLHYLQHVARHLRN

VVAGFGALDAPLDTVSLLDDEERARLRSHAAFVAVQGTFLEQFAQRVAAAPDSVAVVT

ADASLTYAELDDQASRLASFLLAEYAIERGDVVGVVADRSERWIVGMLGALKAGAVYL

PLDPEFPRERLRFMIEDAKVKALLTHSEHLPLLADFWAIPMFALDFQLDTLAPASASA

QVEVRPDDAAYIIYTSGSTGVPKGVVLEHAGLLNMAQYHVDAFGFDSADRFVQFYSPG

FDGSIMEIFVTLLAGARLVLAKTAVIRDVPRFVDYIAQQGVTTVNATPAYLAALDWHA

LGAVKRVISAGDSARVADLRELARTRTCHNSYGPTEATVCIADYVVDPAITYGARLPV

GRPIHNTHLYLLDEHGALAPEGCAGEICVSGIALARGYVGRDDLTAAAFVAHPFEAGE

RLYRTGDLGVWLPDGNLEVTGRRDTQVKIRGYRIEMGEIEAALRQHAGVADAIVFVRE

DTPQHKQLVACVATATASVASLREHLKERLPEFMVPASIVTLERLPLTPNGKPDRKAL

AALELAFAPSETAYVAPANDVEARLGRIWCDVLGREPIGVHDNFFELGGDSILIIQVM

SLAQQVGLKFTADQFFAHPTIAELAQVATEAPSIRIAQEPVVGPAPLTPIQHWFFAQD

VADPHHYNQSTMIEVPASLRPDTIERALAAVATHHDALRLSFACVAGVWQQSHAAPPL

AIPLGVTSLADAAPAARQAAMLATATGMQESFTLSAPPLLRAHLFQFGPDAPQRLLAV

AHHLVIDGVSWRILFEDLYTACRQLEAGDAVQLPARTTAWRDWSTRLSGLGATALDGL

GLDYWLQGNAGEPACFDDMPAGTVAEAGSTIVEFDAQQTLALLQDVPRAFNTQINEVL

LTALLLAFGDWTGNASLVVDLEGHGREDIFDGVDTSRTIGWFTTHYPVCLNAGDATVA

VDALRHVKEQLRAVPMRGLGYGIARYLGEDAGIAAALERQPPAPVRFNYLGQVDRVLP

DDTGWKPVLDFQSPEHSPRARRGHLFEIDGMVFDGRLRLTWHYNREACAPGVIEQLTQ

CYRSRLLSIVAAGGDGPRALSPSDFPAARISQEALDALVSRIKS"

CDS complement(29969 . . . 31585)
/note = "ORF8"
/codon_start = 1
/transl_table = 11
/product = "putative beta-lactamase domain protein"
/protein_id = "ACN32488.1"
/db_xref = "GI: 224016446"

(SEQ ID NO: 14)

/translation = "MTISSSAQVYLRQNIQFEPLINSWYAWYHTLPPLTAALNVAERF

LPLLKSYAASPMMHAAACKDPAMRGGPFLDLGGQRVDEIRTLIHQTTQRATRQLELAK

AYKAFSTLLLERATGMASDPLYPEIPEVLKGYVEIYYDLNHNPSFRVFESLLYASPFY

ARDAQSIALSAIEEHTPRPFILSTPRLRDERTVFSNMAFDDRALDTLFRMRDTFGSYA

KIVDLMRVEEKDEPLFRSFFVEEAPAPKPDRSFDGDDIRIRYYGHACVLIQSRGVSIL

IDPVISYGYDTALPRYTFADLPDQIDYVLITHSHHDHIVLETLLQLRHKVKTVVVGRN

LDGFPQDPSMELALRKLGFDDVLEVRDAQEIKVPGGAITAIPFMGEHNDLAIHSKQSF

MIRFGSRSVLCIADSCNLDPRLYEHVFRLAGKPDTLFVGMETEGAPPSWVYGPLFPKA

-continued

LPRDIDQSRRARGCQFGEAAALVDDFAFNAAYVYAMGQEPWLNHLLDNTFDENSPSHI

QSTQFVAHCKAKGIASEILYATREIVLCQN"

CDS complement(31596 . . . 45005)
/note = "ORF9"
/codon_start = 1
/transl_table = 11
/product = "putative beta-ketoacyl synthase nonribosomal peptide synthetase"
/protein_id = "ACN32489.1"
/dp_xref = "GI: 224016447"

(SEQ ID NO: 15)

/translation = "MNAKATHALKAALDELRLRRAEIAALRSDRNEPIAVIGMACRFP

GRSDTPDAFWQLLDGAHDAVTEVPGERWDIDRYYDPDPSTPGKMATRHGAFLERVDQF

DAAFFGIAPREATYLDPQQRLLLEVAWEALENAHLAPERFRQSATGVYVGITCFDHAI

QVSNASMPSSSYAGTGSALNMAAGRLSFVLGLTGPSMAIDTACSSSLVCLHLACESLR

SRESNMALAGGVNLMLSPEVMVSFSQARMLSPDGRCKTFDAAADGYVRGEGCGMVVLK

RLADALADGDRVLGIVRGTAVDQGGAGGGLTVPSRDSQERVIRRALNQAGLAPGDVSY

VEAHGTGTSLGDPIEVEALAGVYGPGRAANEPLVIGSVKTNIGHLESASGIAGLIKVL

LSFEHDRIPAHLHFTQPNPHTPWQDIPIRVAADPVAWRRGERRRIAGVSAFGFSGTNA

HAIVEEPPVAPAHAAQRALLLLSARSEAALAALVPRYERAIAGATPQELAAICRAAAT

GRSHYPFRAAYVSGARVASAAAPRTGKALRMGFGFGVPDTGVAHALHASEPLFRDAFA

RCSVPLDALETDAGRFAIQFAWAELWKGWGLRPAVVSGHGIGEYVAACVAGVVSVADA

LRLVAARSDAEALRAVLRDMPLARPSVRLISGYLGTDVTDEVTHPQYWLQLAGASDQA

DASHPPEGLADGWLPPPCAGDALERALAALYVQGAQFDWRALFPAPAQPATTLPNYPF

ERQRFSLEKIPSPIVGMDAGSIDAALRHLKSSGKYPEDMLNAFPDLLRTAFAAAETVA

SNAHPLYHVVWEQQAAMPAAPAAADASPWLIFADASGVGERLAALLRARGASCSLVRP

GIDYVTGAEAGWQVAPERPDDFVRLLNETAASGQRIVFLWALDEAVGETRMSAALLHL

VHALVGSEREWTPSTRPRISVVTRDAVEAGEAPHVSGLAQAALSGLARGAMIEHPEWF

GTAIDLDPAAPENETQALLQEMLGESREEQVALRHGARHVARLSPLAPAETAALPVDP

DAAYLITGGFGALGLHTARWLAARGAGTLILVGRQGAASDESQRAIAELRERNVTLRC

ERLDIADPAAVAAFFAALRRDGVPLKGIVHAAGIVGYKPIMQVERDELDAVLQPKVAG

AWLLHQQSEHFPLDFFLLFSSIASAWGSREQAHYSAANRFLDALAHHRRGQGLPALSV

NWGPWAEGGMTFPEAEALLRRVGIRSLAADRALDVLNRLPAVPQVAVVDIDLALFQGS

YEARGPKPFLDHVRVAKSAPSAPAMPALSDASPRERKRLLADSIDRAVAQVLGYDAGT

LDRDLGFFEMGMDSLMALDVRTHLENALGIPLSVALLFDHPTVNALADFLAEQASGTA

QAQTVPPQQQPRPIAPAIEARDAGTPEPIAIVGMSCRFPGAAHDLDAYWNLLNDGVDA

ISEVPRERWDVDAYYDPDPEAPGRMYSRFGGFLDDVDQFDPAFFRITPREAAAMDPQQ

RLLLEVSHEALEHAGIPVDSLKGSRTGVFVGITTNDYANLQLRNGGGSGIDGYFFTGN

PLNTAAGRISYGLGVQGPSMAIDTACSSSLTAIHTASQNLRSGECDLAIAGGVNLILS

PDNSIAVSRTRALAPDGRCKTFDAAADGFVRSEGCGALVLKRLSDALAAGDRVLAVLR

GSAVNHDGASSGFTAPNGRAQEAVIRQALGGLPAASIDYVEAHGTGTPLGDPVELQAL

ATVFGAGRDAGRRLRVGSVKTNIGHTESAAGIAGVIKVVLSLNHDRLPAHLHFRQPSP

LVQWDAMPVEICAEASAWPRGERPRRAGVSAFGASGTNAHLVLEEAPAPARQATPSRH

KVHPLVLSAKTPAALRELAGRYQRRLEAEPGLDIAAVAFSAATGRSHFAHRLAWPVTS

LDDAIDKLRAFHAKEPAGAAQPAPRVKMAFLFTGQGSQYAGMGRRLYDAYPVFRDAID

-continued

RCRAVADPLLDKPLLEVLSAQGEDIHQTGYSQPALFSLQYALTTLLASFGVVPDAVMG

HSVGEYAAACAAGVFSPEDGLRLIAERGRLMQALPRDGEMAAIFTDLATVERAIDAW

HEVAVAAVNGPASIVISGKRERIAMLVDAFAARDIRSVPLNTSHAFHSPLLEPMLDSF

QLAAKTVPVARPAIPFYSNLTGAVMDEAPTDTYWRRHCREPVQFASSVERLAEAGFNV

LVEIGPKPVLVNLARACCAPDAGIQFLALQRPQVEQQALIETLSSLYARGVDVDWAPT

ETPAPARIALPSYPFQRSRTWFQKADTSMTQTSASPIAAAPTHNRSGEILEWLRGKIG

ELIQADPATINIELPFLEMGADSIVLIEAIRHIEAEYGVKLAMRRFFEDLATVQALAE

YVADNLPAAAAPSGAEAVAVAVAAAEPSTPAVAVTPSAAGLAPLAAAPAEWVAAEGGS

TVERVLREQNQLLSHVMSQQMELLRTSLTGQPGVRPATAAVQAVASTASVAPKAASAA

PAAAPAAKPAPAAAAAPAADNPPPKPMMPWGSPVQQRARGLSAAQQEHLEALIVRYTT

RTRKSKDSVQASRPVLADSRATVGFRFSTKEMLYPIVGDRAAGSRLWDIDGNEYIDFT

MGFGVHLFGHTPDFIQQQVTREWQRPLELGARSSLVGEVAARFARVTGLDRVAFSNTG

TEAVMTAMRLARAVTGRDKIVMFTHSYHGHADGTLAAANAEGVTETIAPGVPFGSVEN

MILLDYGSDAALEAIRGMASTLAAVMVEPVQSRNPSLQPVAFLKELRRITEEAGVALI

FDEMITGFRVHPGGSQAMFGIRADLATYGKIIGGGLPLGVIAGTSRFMDAIDGGMWTY

GDHSFPAADRTAFGGTFCQYPLAMAAALAVLEKIEQEGPALQAALNERTAQIAGTLNA

FFAEAEAPIKVTWFGSMFRFEFTENLDLFFYHMLEKGIYIWEWRTCFLSTAHTDADID

RFIRAVKDSVADLRRGGFIRPHSKHGTVAALSEAQRQLWVLSEIDPEGSLAYNVNTTL

ELNGRLDEAAMRAAVQSLVDRHEALRTTVMADGSGQIVHPSLTLEIPLIDTDPNAWRE

QESRQPFDLVNGPLFRAALVRLGSERHLLVMTAHHIICDGSTFGVLLEDLARAYAGAA

PADAPLQFRAYLKQLDGQRHSPETKANREYWLAQCARQAAPLNLPVDYPRPAVKTFHG

ERVSLHLDAATAATLRTAARQNGCTLYMVLLAGFNLFLHRVAGQQEIVTGIPVTGRSV

AGSDRLAGYCTHLLPLHSTLPEQATVASFLAGTRQNLLDALEHQDYPFAELVREIGAQ

RDLNAAPLVSAVFNLEPVSALPELPGLTVGLVAPLIRHTAFDLNVNVLDAGQALLIDC

DYNTDLFDASTVQRFLDIYRTLLTHLADDASAAVARLPLSSDAERNLLTVEWNRTDTD

FGEDAAQPLHRLFEQQVERTPDAVAIVFDDTALTYAELNLRANRLAHHLVALGVGPDS

LVGVAMERSLDMSVALLAILKAGGAYVPVDPDYPAERVRFMIDHAQLRWLLTQQHLHD

ALPDTDAHVIVVDRDSLDLDAAATSNPAPALNGDNLAYMIYTSGSTGRPKGALNTHRA

ITNRILWMQHAYALGADDAVLQKTPFSFDVSVWELFWPLVTGARLVFARPGGQRETDY

LVELIERERITTIHFVPSMLRAFLDHPDLDAHCASLRRVVCSGEALPHDLQQRCLERL

DVELYNLYGPTEAAVDVTAWECRRDDPHRIVPIGRPIANTRLYIVDAQMQPTPIGVAG

ELLIGGTPVGRGYHGEPELSAEKFIADPFSADFLARLYRTGDLARYRPDGNIEFLGRI

DHQIKLRGLRIEPGEIEAALTSHPLVDAAVVALRGVDDGARLVGWLCSSHPEAELIEA

VRGHLRQRLPDYMVPSAFVVVSAFEHLPNGKLDRTRLPEPGDGLDHVAPVNALEAQLA

AIWQEVLGQARISTTGNFFDLGGNSLLATKVVARIRRDLHVKLEIRSLFALPTISSLA

KRIADTQPIDYAPVTPLPAQASYALSPAQTRLWVQDRLHAAQAEGPLPTSLLFEGVLD

VDALVRAFRALSERHEILRTRFVLEGNQPVQHVLPPGEAAFPVEIVDLQDAEDRDAQA

AAIQASERLVPMDLATGPLFRVKLLRLSEVRHVCLCTMHHIVSDGWSTEVLLDDLSAL

YDAFVQRRDDPLPALPIQYKDYAGWLNRLLAGPDGARMKDYWLTKLGGGLRALELPGD

VEQPAAPSWKSWRFDLPAAETAALESLGKRHGATLFIALLSAIKALFYRRSGQEDIVV

-continued

GTPVAGRELPELESQVGPYLNVLALRDRVAGDDRFDTLLTRVRDTTLEAFSHPLYPLD

RLLDELHIKRVAGRNPLFDIGLTLQNQRHGPVDRYAGQVHIAELPDHDPQRADTEAAT

DFWFLAEPHAEGLAIRVVYHAGRFSEALVQGLANELTSVIGEVLANPGVRIRNLTLGQ

RALHAEARQPTVELSAF"

CDS complement(45002 . . . 48325)
/note = "ORF10"
/codon_start = 1
/transl_table = 11
/product = "putative short chain dehydrogenase/reductase SDR"
/protein_id = "ACT64845.1"
/dp_xref = "GI: 314954101"

(SEQ ID NO: 16)

/translation = "MKFGLMFFASSEEALSGNKYQLVMESARFADANGFSSVWVPERH

FTEFGSLYPNPAVLHAALAAATQRVKLVAGSVVAALHNPIRIAEEWSMVDNLSNGRVG

VSFASGWNPDDFVFAPDKYATRQDDMLTTMRAVQHLWRGGTLDATNGVGKPVRLRVYP

TPVQPELPVWVTAASNPQTFVRAGEAGANLLTHVLDQDRDQLAHKIALYREARAKHGF

DPAAGTVSVMLHTFVGDDAAQAREQARVPFCNYIRSNIGLLNGLAQSRGQSVDVRAMG

ARELDEFVEFLYERFAQSRGLIGTPETCVELVRDLESIGVDEVACLLDFGPPVERILG

NLPQLRRLREMCAPRRSAAPTRFDAAEVQARCTETTSGADFNGEIRQHGVQIDGVFDA

IRQIWRTTGEALGKISLPADALASSPYQVHPAFLDACSRVLAAAIDPDALESGDLYLP

SSIGAVRVHQPPASTEAWSHATLRTPIGQGALEGDIRVHDLAGRLLIEIDALRLQQVR

AARAVERHDFAALLYQRVWRPSNVDAATGGSAHGEWLILADRGGVGAQLSALLEAHGD

TCTLRFADATPELPAADRPLKGVIHLWSLDLAPSDIAARRRASASVLHLVRALASRAP

SARQARLWLVTSGAMNVLDGESIAVAQAPLWGLGRAIAVEHAALWGGLVDLDPEQPSA

ADIMQAVQAGGREDMIAFRRDQHYVARIARDNREYVSHRPIRFHGDATYLVTGGLGGL

GLRLASWLADNGAGKIVLLGRGEPSAAAGKILRTLDARFIRADLSRREDVGQALGEIA

HSMPPLKGIFHLAGALDDALLTRQDDDFFHRAGSGKADGAWYLHELTAGLPLDHFVLF

SSMAALITMFGQGNYAAANSFLDALAQHRRAQGKPGLSVNWGFWAEIGHAATDYGRRA

HEQLGALGVGTLPPELAIATLERLMASGVAQSGVARIDWPTLFRVDAPAAGSALFSEL

TQPAAQPAQQETALLRQLHACAPRERVERITDTLAAMLAETLRLSGPDAIAPEQSLLD

LGLDSLVALELTDRLTKVFGRPFRATLFFSYPNLQTLAQYVLNELSPSLPAPVVDEAS

DDLDEDDLSELIAQEIGAQ"

CDS complement(48322 . . . 52749)
/note = "ORF11"
/codon_start = 1
/transl_table = 11
/product = "putative beta-ketoacyl synthetase"
/protein_id = "ADT64846.1"
/db_xref = "GI: 314954102"

(SEQ ID NO: 17)

/translation = "MLPDTKERTVTEILLFRGKVEPEKTAFIFLENGEAELTRLTFGD

LDKRARGIAARLQAIAQPGDRVLLVYPPGLEFICAWVGCLYAGLIGVPAYPPRRHRPA

DRLKAIVADATPVVALTDAATLDGIAHHADGYSDTLELKILATDQRFDAPAEQWRAPD

ITPQTLALLQYTSGSTGTPKGVMISHANILSNMAVIAEASDADASTVFVSWLPVFHDM

GFFGKVLLPIYLGVLSVLMAPAAFVQKPVRWLQAITKYRGTHCAAPDFAYDLCARKIA

DEARAQLDLSSWRVAFNGAEPVRAESVARFSRAFAACGFHAHTMRPVYGMAEATLFIS

GQPARSLPRVADYDADALAQGVATRNDSGKRHALVSCGRTWAEHRVRIVNPDTGERCA

-continued

PGRIGEIWLTGPSVGVGYWNRIDETERTFRAKLDGDDARYLRTGDLGFVDGEDLFVTG

RLKDLIIVAGRNHYPQDLEQSAEGSHPALAPNASAAFSIHVDNVERVVVACEVRREAL

NTLDAEAVAAEIRHTLAEVHDVDLYAAVLLKPATILRTSSGKIQRSRIRQAFLDEQGL

AIAGEWRRAFSAPPAPPQTAEPRDTQALVQWCIERVSRLSGIASGKIDPDAPFSVHGL

DSKDAIMLSGELQDWLGRPVSPTVVYDFPSISLLARHLSGTGSAMPDQAPGSAEARAD

IAIVGMGCRFPGAGNPDAFWQLLLEGRDAVGAATQRAADLPLAGLLDQVDQFDAAFFG

ISAREAESMDPQQRLLLEVAWETLEHAGIAPRSLAGGRTAVIVGISNSDYIRLAQDEV

ADVGPYVATGNALSVAANRISYALDLRGPSWAVDTACSSSLVAVHQACRALQRGESDA

ALAGGVNLILAPQLSASFTQAGMLSPDGRCKAFDAAANGYVRGEGVGMVLLKRLDDAL

ENGDTVFAVIRGSAVNQDGRSNGLTAPNGPAQQAVIHGALRDAGVRAQDIGFVETHGT

GTPLGDPIELNSLAAVLNESRRPDDLCWIGSVKTNIGHLESAAGIASLIKTALALHHR

AIPPNLHFRSINPQIALDGTPFRIPRQVTPWNSEHGPRLAGVSSFGFGGTNAHLILSE

APGLPEIEAEPVAPAARVVTLSARTPDALQALAASYAAYLDAHPEAGVRDVAFTANTG

RTHFTQRAAIVAPSRDSLRAQLDSVSSGEPAETPPAVTFHFCADDGASADAVRQLRAA

SPAFDALMQRQSDASGAPALAPDEAGFTRFQRALAQLWMSFGIAPDAVSSTGDGQRAA

AAWAGVPQAPDSGAAGHPGIVIDIGAHTAAWDAILHTLAALYVRGASIDWDAVEQGAP

HRRLALPTYPFERRGFWIRPHARRHPLLGRLMEQHAHAPATWIWQSRLDAPATNFLDG

HRVKGSPVLPYSAFVEMALSATSEIGAAGHTTLKDLALHAPLPLHPHESHTVQTVLSR

RSWGPFSFAVYHRIDDTRAAATWQMCASAEIHESDRSHA"

CDS complement(52936 . . . 53922)
/note = "ORF12"
/codon_start = 1
/transl_table = 11
/product = "putative taurine catabolism dioxygenase"
/protein_id = "ADT64847.1"
/db_xref = "GI: 314954103"

(SEQ ID NO: 18)

/translation = "MEGMTERKLLAEGSTPWLLEPVSNGRDLAQAVNDNRAALESRLL

EHGVLLFRGEDVSSVGGFEAFARAISAHQSDYVYRSTPRTSIGNGIFTATEYPPSETI

ALHCENAYQRSWPLRVAFCCLTPAATGGETPIADMREVSRRIGPRILDHFEARQVRYV

RHYRRHVDIPWETVFQTSDRNQVAAFCADNGIALEWLDDDTLRTAQINQGVAYHPVTG

ERVFFNQAHLFHISNLEASLASSIVSLFGEDRIPRNACHGDGSPFDLADLEQIRHAFR

ECAITFPWQRGDVLLVDNMRFAHGRNPFEGERKVVVSLLDPYTPDIEGIADR"

CDS complement (53999 . . . 55369)
/note = "ORF13"
/codon_start = 1
/transl_table = 11
/product = "putative transaminase"
/protein_id = "ADT64848.1"
/db_xref = "GI: 314954104"

(SEQ ID NO: 19)

/translation = "MKRFSCASVHQSALQAGSARMEKLEYLKQVESNARTYATSFPRL

FTHAKGIRVRDADGQEYIDCLSNAGTLALGHNHPEVNEAVMRFLSSDQMQQALDLATP

AKHAFVEQLFSLLPGKIAESGKIQFCSPSGADGVEAAIKLTRHYTGRPTIMAFHGAYH

GMTSGALAASGNLTPKSAGGNGRDVHFLPYPYAFRCPFGTDGSATDQLSINYIRTVLS

DPESGITKPAAIIVEVVQGEGGCIPAPDTWLIELRELTLRHEIPLIVDEVQTGLGRTG

ALFAIEHSGIRPDVLVLSKAFGGGYPLSVVVYDERLDTWPPGAHAGTFRGNQIAMVAG

LSTMRIVEREDLSAHADRVGKLLVAGLEELAERFPCLGQIRGRGLMIGAEVVVPGTHG

-continued

RAGPPHTERARAIKQNCLRNGLIVETGGRNGAVLRFLPPLIVSEADIHDILNRFEHAV

ETACRA"

CDS complement(55516 . . . 56466)
/note = "ORF14"
/codon_start = 1
/transl_table = 11
/product = "putative epemerase/dehydratase"
/protein_id = "ADT64849.1"
/db_xref = "GI: 314954105"

(SEQ ID NO: 20)

/translation = "MQRNRKRILVTGGAGFLGSHLCERLVELGHDVLCVDNYFTGTKQ

NVATLLGNPSFEALRHDVTFPLYVEVDEIYNLACPASPIHYQFDPVQTTKTSVMGAIN

MLGLAKRTHARVLQTSTSEVYGDPDVHPQPESYRGNVNPLGPRACYDEGKRCAETLFF

DYHRQQNVRIKVVRIFNTYGPRMHPNDGRVVSNFIVQALRGEDITLYGDGSQTRAFCY

VDDMVDGLIRMMATPAELTGPINLGNPHEIAVSELAQIILRLTGSKSRLVFRPLPKDD

PTQRCPDISLARTHLDWEPTIGLEAGLQRTIDYFCSTLAA"

CDS complement(56622 . . . 57341)
/note = "ORF15"
/codon_start = 1
/transl_table = 11
/product = "putative thioesterase"
/protein_id = "ADT64850.1"
/db_xref = "GI: 314954106"

(SEQ ID NO: 21)

/translation = "MRLICFPYAGGSAAVYRTLQASLPGIEVCRHELAGRGSRLSEPA

VRDMATLVDTLLCDLDDCFDRPFALLGHSMGAAIAAELALRLPAHARPNLRHLFVSAR

AAPGKERHDRRMQALDDRAFIDALREMGGTPKAVLDNSELMALLMPALRADFTMIENH

RPVPGPRLAVDITAFAGRADKEIPVDAVAGWGAATTGRFDFHVIEGDHFFLRNEMRTM

AGIIAARMRRPEHAASSALQA"

CDS 57710 . . . 57997
/note = "ORF16"
/codon_start = 1
/transl_table = 11
/product = "hypothetical protein"
/protein_id = "ADT64851.1"
/db_xref = "GI: 314954107"

(SEQ ID NO: 22)

/translation = "MQHRQKAVPTQQVANERVIVTEWRFAPGAETGWHVHRHDYVVVP
QTDGQLLLETAQGNRESQLHAGRSYAGLKGVEHNVVNATDHEVVFVEVEIL"

ORIGIN

(SEQ ID NO: 23)

```
    1  aattcctgca gcacggtgcg cgaccagccc cagatgtccc cgctgagcgt gagtgcgaga

   61  ccggccgtcg tgatggccag ctgcgtctgg ccgaacagcg gcgtcaatgc gccttcgccg

  121  ccgatcacga tccgcttgac gagatccgag atggactgcg agatcgaatc ggagaacgga

  181  tagttgtacg gctgcgtgac ggcgcgcgac aggaacggct tgctgggcgt cggcgtccag

  241  accttgagcc acggcttggt cgtgaacggg aaccagatgg cttccacccg gcccgagccg

  301  tcgagaaacg atgcgatcgt gcggcccgtc gtgccgggcg cggcgaacag ttcggaggcc

  361  ggaatatcga cgtagctctg gcagcgtagc cgctggttcg gccctgccgt cagcgtgact

  421  tcgacgacga gcgctcgccc gatgtgcgcg aggaacgcgc cgatctcggg atcgctgcgc

  481  tcgaaccggc gcagcacgta ttgctgccgg gccggatcga acacgaccgc cgtgagcgcg

  541  accacgagat tgctcagcga gccgtaggta tggcccggtt gcaaggtttc accggccgcg

  601  ggcacggcgg tgccgtgtgc atcgatcgcg agcgcgccgc cgagcgtgat gtcgcccggt
```

-continued

```
 661 gccggcgcgg caatcacgcc gaggccaacc tgctcgagcg tcgcgagcag cgactccagc
 721 gagacgcccg tttgggcggt gacgcgcgcc ggacgcgccg acgtgtcgac ggagacggcc
 781 gtcagcgact tcgtcgtatc gagcagcacg aggttcgcgg cgccggcgcc cgggtccagc
 841 gtcagcggcg accagttgtg cgtgtagccg cgcgggcgta tccgatagcc gtttgcgcgc
 901 gcccagttga cggttgcgac gacgtcgtcg gcggagcgcg gcgcggcggt ccatacgtcc
 961 tgcacggcga tctcgccgct ccagttcagg aacgcctgct tgtaaagctg gatgtcggcc
1021 gggaagccgg gcggtgtctc gccggccgtt cgcgcgtgcg ccgcaacctg gtagagcggt
1081 gtccagccgg tgacgatgcc ggccgccgcg agcttcgcca tgtcggccag gaaggcgcga
1141 cgcggcgcag gttcgtctct gaagtcgtga ctcatggtgt gctccaattt ttcggaattg
1201 ttttgcagat tggaaagacg acaaatgacg cgttgagact cgtgtggcaa ttcgagcagg
1261 tgcgacgcgc gggaagtgtt gcgcgtgggt gggccaggat tgaaaaaaga cggtgcgttc
1321 ggcaatgcgc ggccgcacat catcacggac gtctaatagg aaatcggaaa accgcctggc
1381 gattgcttta attggccgtc ggccggttct gtcggcaagc agatagggag attcgacgga
1441 atcgcgcgcg gcgaagcgct agccgtggcg atcgataaaa gatgatttca cgtgaatatt
1501 aatcttcatg tttcgatttt taaataaacc cggccgcagt tcaaggttga ttgacgatgc
1561 gtcatgcatt tcggtcgaaa gcgtagcaat ttatctatcg ggtgacaagc ggcggagttg
1621 acgaattccg agtcatttaa tatggaaatt ttatgacggg aaatggcttc gtccgttgtg
1681 ggtattttgc aacgcggctg ccggtgtcgc gccacgtggg cttggagcgc aaattatgct
1741 ttgccgtcgc gtatattgaa tcgattgttg agcgaatcga aataacgtcc ggaagacaat
1801 agctgaagcc gggtcgatga gcgggaggta gggtgaaatc cgataattcc tctctcgaat
1861 aacgctcctg gatgaaaatt cgtggtatgc gtcgcccggg tgattattac aaaagttcgt
1921 ggtaaacgga tgtcgattta tcggtgtatt cataataatg ccaatgagcg gctcgcgaat
1981 tgattgattt ccggttcgtg aaagatgtgt tttaaaaaaa tagatgtcgg gctgactgca
2041 aatgtctgaa tcgtcgctat catacgcggc tgggatatac atggatcaaa ttcaatggaa
2101 agaatcgttt cgctttttga tcgcgatttt tctttgaatt cgccgggaac gcgcccgctt
2161 cgagccggcg ccgggttttc cgattcaggt ttcaggcacg tccggcggcg gcgcgttttc
2221 atccggcaac gcgaatcggc cgaaatggac gtttcagcct tttgcggctt cgcgagtcgc
2281 ccgcatcggg ctgaactggg aacggcacgc cgtcgtctcg catgagccgg acgcatcggc
2341 gcgcgctggc ggcggcgcgt tgcccgcctg aaaaaggcgc gcgacgcagc gcgacccgac
2401 gcgcgccgcg caaaccgtgc cggttcgccg gcgcttgcgt tgtgccaggt cctcaagcac
2461 gcacaacaag gagagtcaga tgttcgcgaa gctcgggaag gtgatttcga gcgcaggcag
2521 tgagcggttc gcatccgaca tgcatgcatt gctggtcgag tcgattccgc tcacgatcac
2581 ccggatgact gaatggacgc tcgacgagcc ggcgggcgaa gtcgtccgcg tgcaatcgct
2641 cggcgcggac ggcgcgccgg gcgatgacgg gcgcggcgcg ccggccgcgc acggcgagcg
2701 ggaaccggca gcgcatccgc cgttgaaccg gatcctggcg gcctgcgacc ggcagctcat
2761 tcacatcaat ccgctgatgc ggcgcggcaa tggcggcgaa gtcgcgccgt cgcgcgggcc
2821 gggcggcgga tttcagtgcc atctcgtgtc gggcaaggcg aatcgccgtt acgtgatctc
2881 gctgcatcgc acggcatcgc atcgcgactt ctcgttgcgt gagatgtcgt tcctgaagaa
2941 tttcgccgat acgctgctgc cgctcgtcga gtggcatgcg tcgacgtgcc ggcacggcga
3001 gcgggaaggt gcgacggcac ccggtgcgac ggcaggcatg cccggcgtcg aggcgctgcg
```

-continued

3061 ccacgagttc gaatcgcggc tcgcgcgcgc gagggtcgtg ttgtcggcgc gtgaaaacga

3121 agtgtgcctc ggcctgctcg cgggcaagat gctgcgcgaa atggccggcg agctcggtgt

3181 gaaggagagc acgatcgaga cgtacatcaa gcgagccgcg gtgaagctcg gcatcagcgg

3241 ccggcacggg ctcacgaaat ggatgatcga cgattccgta ccgtgcgcgt cggcggcgtg

3301 acaccgtcac gccatcacgc cgcggacgcg cgacgcatgc cgccgggcat gcgcgttcgg

3361 gccgcgggcc ctcaggttcc gaggcgcggc gacgcgtagt cgcgccgcat gcttctcatg

3421 tcgcccccag cagcttccgt cgcggccccg gccgtctcgt cgagcatcca gcgcgtcagg

3481 ccatgacgcc cgctgaagcc cagcttgacg gccgcccgct tcaggtaggt ttcgacggtg

3541 ctttcgcgca gcgcgaagcg catggcgatg gcaggcaccg tgtcaccggc caggagtgcc

3601 gtgcatgcct cgatctcgcg cgtcgacagc ttgacgcccg cttgctgcag gcgatcggcg

3661 aatcgccgcg ccacgcgctc ccggcccgat tgcgtcgccg gcggcgcggc ggtcgtcaca

3721 cgagcggccg gcggagccga atcgagcgcc gcgacatggc tctcgacgat cggaaacagc

3781 acgtgcgaga gttccttgag gaaggtccgc tcctgcggcg agaaatcgtc gaacgtacag

3841 gtgcgataca acgagatcac gtaacagtgg ccccgcttgc gggtcacgag gtggaattgc

3901 gcgtagcgcg gcgacacgat cgccgcctgc atgaggatga agcggtcgag ctgcgcgtgg

3961 atcgggccgt ggccggcgag cgtgtcgtcg acgtgcaggg ggctcgtgcc cgggcgcggc

4021 ggcatctgcg gcccgcaaca gacagcggcc gcgccggtct tcgcgagcgc cgcgccgacc

4081 gcgccgaggc tgcgcacctc gggagggccg tccggcacgt cgtcgatcgc aagctccgaa

4141 atgcggatct cgtcgacggg gaccgccgcg gcgatcaggt tgtacatcat ccggggaaaa

4201 cgtcggctcc cgctgctcga gatcgcttcg ccgacgtgtg cgaacaatct gctgaactcc

4261 atgaagggat tcctgatgag acgttgaagc tgcgcttgtg cgcatgaatg ccgacatgat

4321 ttaaacaccc ggttgcgaac gcgtctgtaa cggattgccg ggacagacgc aacattgccg

4381 gccgtcgaag ccggtacggc gcacggcgac cgttgcgccc gtctgcgacg gatggcgcgc

4441 accttgtccg agtccggatc gctgctcatc cggctgcctc ggcccggacg gcacacatgg

4501 ccgtatcgga gaagatgcgg ccgctatcca ggcgaatgac ccgatccgcc agcttgaagt

4561 actgatcgtc gtgggtgatg atgacaacgc atttcccgcg tgatttcaga tcgggaacca

4621 gcacttcata ggaaaatcgc ttgaacaccg gatcctgatc ggcggcccat tcgtccagga

4681 tataaatcgg acgatcctcg atgtacgcgc aaagcagcgc caagcgcttg cgttgccctg

4741 tcgataacgc gcgggtggtc gagtaggtcc ggccggaaat ctcgatcttg tccgccagtt

4801 tcagggtggc gaggtatttc cgggcaagct cgatgctttc attgccccga tccggtccga

4861 tgatgcgatt gaacaaatgg aaatcggtga agacggcgga aaacaggttt cggtagcgtt

4921 ccctcgcagc gtcgtcaacg acttttccgt cgagggaaat cgtgccgccg gtaggcgcat

4981 agaggccgct gaggaccttg ccaagcgtgc tcttgccgct gccgtttccg ccgatcacgt

5041 agacgagttc tccggcatga atcgtcatgt cgatggggcc gagcacgaag tcgaccgatg

5101 cttcattgtc acggtagttc atcgtcacgt ctttcaactc gatgaccttc catgacttgg

5161 ccgacagggt ttccacgttg cccgcagggc gcggttcctc gtgtgaggcc tgcgtgtcgt

5221 cgatcagaaa gccgaattcc gccagccggg cgagcgcggt cttgccttcg gccaccaccg

5281 gcagaacatt gatcagcatg gtcaagggcc ccatcatgta gagcacggcc agaatgctcg

5341 ccgtgagtac ggagggatcc acgacgccca gagaaggtac gccgaacagc aggcatccga

5401 gcaggaccgc tacggtgatc tggccgatgc tgtcgccgct catgaaccag aagcgttcta

5461 tgtaattgaa tcccgccacg cgcttcgacg acaattcgat cgcggcgcgg gtaaaccagc

-continued

5521 gtcgcctggc ccggttgagc ttgagctcct tgatgccgaa cacgaggcca tgtgtgtatt

5581 cgttgaactg gacgaattca tcgcgaaccc gctccgtaaa attgaccgcc ttccgataga

5641 aaaacagata aagcaccagg ccgacgaggg tcaggatgat cgtcgacgcg aacacgatcc

5701 acgagagata ggcgagatag gcgatgctgc agatcaggac gactgattga acgatgatcg

5761 tcgggatggt cagcagggtc tggctcagtt gcggaatgtc ctgtgtcagc atggtcagca

5821 cattgggggc gccgcgtctg tcgatttcat ccagcggggt tgccaggatc cgtttgcaca

5881 ggttgacgcg caacctcgtc atgactttca tgcaggcata ggagggcatc acggcggcgc

5941 agctcctgca gaccaccgcg acgacattca ccgcgatgaa cagcagcaac agcgtctggc

6001 gatcatcctg gtcgtgcagc acggtgctga tcaacccgac gcccgcgatc gacgcgatgc

6061 cgctgacgag gcccgtcacg accgtgccca gcgtcagcca gggatgactg cgccacatca

6121 gggtggcggc ggaatgccat ggcggcgatt tgctttgagc ggaatccatg agtggccaat

6181 aggtctcagt tgatcaggtg gctgagttcg acattgcttg ccgctgatct caacctcgac

6241 gaggtttcgt gcttgcccag gaacgtgatg ctttccacga ttcccagcgg cgaatcggaa

6301 aacaggatgc agcacttcag caggcgctgc gcacgctccc agccgacgcc gtccggtgaa

6361 tcggccacgc ttcgcaacgc ggcctcgacc gaggcggccg tccagtcttc gctccgtgcc

6421 agccccgact cgatctgccg aagaaattgc aggagcgtgc ggggattgct ttcgatgctg

6481 tacatgagga tgtaatcgat ccgcagtttc ttcgtgatca gcggaaaaat caggtcgatc

6541 acgccggcgg tcgattcgca tttcccatat gccagtgaaa tcgcgtcgcc gagcttgcag

6601 tcccggtgaa gcgcatccag cgcggccttg acgaacgccg cttcgaggtc aacggtggtg

6661 agttgcatga tgttcagtgg cctgtcgagt gttggatcgc ggcgagcacg ggcggcaggc

6721 gttaccagcc gtccggaatg ggcatggaat aggtcagcgg cttctccggc atcacttcgt

6781 ccatgatgtc ggagtagccg gactcctgtc cgaccagatt cggctcgaag cagtagcaat

6841 tgaacgtctg ctgcaggacg aggttgttgc ggtcgttgat cgccggcggg ttttcgttga

6901 tcgcgatgaa tgcgtcgtaa agcgagttcc tgacgacgta cgcgtgcgcg gtgagcgtct

6961 ccacggcctt gacgatgttc ggcgcgacgg gaatcggcgg cgtgaagtga tacgcgccca

7021 ggaacagcat gtgccagtcg tccggcactt gcgcgatgaa ctcgggaaag cgcgcggcga

7081 aatcggcgtc gaagaacgcg tcgtcctcga agatcaggac ttctctcgca ccggcggcct

7141 tcgcctgttt caccgcggcg agatggctca tcgtgcagcc gtagtcctgc gcacgcatat

7201 ggctcaacga ttccggcacg ctcaccagcc ttgcatcgac ggcaggcagc cgttccaccg

7261 tgaggatgtt ctgctctgcg aattttcgtt gcatcgcttc ccagcggtcg gggcgccggt

7321 ccaggttgat gcagaccttg cgggcaaaag tattgtcgat cgtcggcgtt gatttcatga

7381 gggcgttttt tccagaaacg aattgacatg ggcggcgagg acaccggcat gcggatcgag

7441 cagcatggtc aggtggtcgc cggggacgtc cgtcaccgcg acggggtgcg ccgagaagcg

7501 agaccatccc caggtcgcgt ccaggcgaag ctgcgcgatc tcggacgacg gcgcgtagtc

7561 gccgggatcg cgctcggtgc tgcggaacaa cgcgatcggc acgggcagcg gggtggcgtg

7621 cggcgcgtag tgcgacttga agttggcctg atagacgcgc aggtaggcgc gcaggcggtc

7681 ggacccggcg tccgcgaacc agctgccgcg gtcgccgatc cgttcgagga tcaggccggc

7741 ctggccgtcg ggatcgagat ggacgaggtc cgctcgcgtc acctgaaggt cggtcccgag

7801 gaaggtgccg atttcgtggg cgatcgcgac cagccattcg gtgtcgtccc agtcctgcca

7861 gtaagtggcg gccgagctgt cgatgggcgc ggacgcgtcg aagatcgcca gcaatttcac

-continued

7921 gtcggcgccc ttggcgacca gttgcctgct catttcgagc gccacgtgcg cgccgaacga

7981 gtggcccgcc aggtagtacg gacccgcgcc caccagcggc cagatgcgtt cgatatgacg

8041 ggccgcgatg tcttccacgc gggtgagcgg ctcgcacgcg ccgtcgaggc cgagcgcttc

8101 cagcccgtga atcgcgtgag cgccgctcag gtggttcgcg agcgggcgga agtagaccac

8161 gttcccgccg gcgcccggca gcaggaagag cggcgcggcg gggccgccgt cgcgaatcgg

8221 cacgagcccg ccggcgggcg cggacggttc tttcgcggcc agcgccgccg ccagtttctc

8281 gatcgtcgga ttctcgaaga gacaggaaat cggcagcctg cgatcgaacg ccttctcgac

8341 atgggccatc agctggatcg cgatgatcga gtggccgccc aggtcgaaat agttgtcgct

8401 gaccgcgatg tcgtctcttt tgaagatccg ccgccagatc tccagcaacg tgctttcgtc

8461 cgccgcatgc gcgacggcgc gcgccgccgc ggccgcaccg gcagcggctt cgatggccgg

8521 cccggccccg ctgcgcggcg cgctcggccg gccgtcggcg gccggcggat cggcgagctg

8581 gccggtcaac tggcccgggt tctcggcgaa tcgctcgagc aacgtgcgga gggtatcgag

8641 catctgccgc acgacctccg gcgcgatgcg gtgggcatcg tgcgaaatat ggaagccgat

8701 gcgctcgttc gggtgcacgg tcagggtcag cgggtagttc gattccgcga acgcgcgggt

8761 gtcgaggatc tcgatgtcgt ccggcccgag atcgggggcg gcggcaaccg ggaagttctc

8821 gaagaccagc aggctgtcga acagactgtc gccggcgggc agttcgctcc acgactggat

8881 atcgaccagc gagctgtacg aatgcggctc catcgccgtc tgggctgcgt ggacctctgc

8941 cagccattcg atgaacgggc gctcgggcgc gatccgcagg cgcagcggca gcgtgttgat

9001 gaacagcccc acgatcgact cgacgccgtc gagcatcggc gggcgaccgg acacggtgac

9061 gccgaagacg acgtcgtccg ttccggcgtg gcgccgcagc accaacgccc agaccgcgcg

9121 gatcagcacg ttgagggtga cgcgatgcgt gcgcgtgagc gtttgcagcc gcgcggccag

9181 cgcctcgtcc agcaggaatt gctgggtccg gcgcttgtcc tgccgcgggg catcgccggt

9241 cgcctgccgg gccggactgg ccgcgaccgg cgtggcggcc ttgaagccgg ccagttcggc

9301 gcgccaccac gtttcgtcgg ccgagcgagg atgacgcgcg agccagtcga tgtacgcgcg

9361 gtatcccggc gccgacgccg cgaccgcggg catgccggtg cgggcgagcg acaggtagtc

9421 gtcgaacacc tccttcatca gggtcgcggt gctccagccg tcgaggatga tgtggtgcgc

9481 gctccagcag aagcgatggc gcgtgtccgt ttcctggatc agcgtgcagc ggaacaacgg

9541 cgcgcgctgc agatcgaagc cgcgccgccg gtcgtcggcg aggaacgcat cgaaatcctg

9601 cgcgcggcgg gacgcatcgc ggtgccgcca gtcaaggaac gtccatggca ggtcgaccgt

9661 gtgccgtacg gtctggacgg gatggtcgcg atcggcccac gcgaacgcgg tgcgcagcac

9721 ggcatggcgc gcgagcgcat tggcccacgc ctgccggagc gccggcacct ggagcgggcc

9781 gctgacgaca aagctgaact gctggaagta ggcggcagga tccaggtcgt acagcgaatg

9841 gaacaggatg ccctgttgca gcgacgagag cggatagctg tcctcgatat cgtccgctgc

9901 ggtgtcgggg accgacgccg cgaagtcgag caaccggtcc ctgaagtgcg cggccaggtt

9961 ctcgaccgtc tgccgccggt ggagccgctc gccgtagcgc cagtccacct ggagcttgcc

10021 gtcggcaacg gccgcgacga tctcgaaggc atgcgtgcgc tgcgaccgcc cggcgcgcag

10081 cgaaccgagg tcttcggccg ccgggcgcca gccatcggat tgccgcaata cggtatcgag

10141 ctgcccgtga tagttgaaga ggatatcggc cttcggcaac gcggcgagac tgtcgcgcac

10201 ggcggcgtcg gggctctggt agcggagcag cgaataaccg agaccgtcgg ccggaatccg

10261 gcgcagctgc tgccgtgcgg cacgcagcgc ttgctccggc gcgtgcatcg cgtcggcgtc

10321 gagcacgacg gggtagatgg acgtgaacca gcccaccgtc cgggtgaggt cgagcggcgc

-continued

10381 atccgacacg tggcggccgt gactctcgag atcgatccgc gtgcgggtgt tacccgtgac

10441 catgctgcag gcttgcgcga gcgcgacgag caggacgtcg ttgatgcggg tgtcgtaggc

10501 ccgcggcagc cggcgcagca acgcggtggt atcggcttcg cccagctcga atgaaacgga

10561 cgacgcgtcg tcgactgcgt tgttggccgc gcccgtgcct ggatagtcaa ccggcatcgg

10621 ctcgacgggc tgcgcgagga gggcttgcca cagccgtgct tcgtcgccga tggcgggcga

10681 ccgggccagt tgctgcagat gcaacgccca ttcgcggaac gaagtcgtct tcccgggcaa

10741 cggctggccg tggtaagcgg catgcaggtc ctcgagaagc acgcgccatg acacgccgtc

10801 caccgccagg tgatggatcg acacgaacag gcgggcgagc ggctcgtcgg ccaggcagaa

10861 gagccgggcc gccagcaacg ggccatgcgt gatgtcgatg ccgcgctccg cgtcagcggc

10921 ggcggcacgc atcgccgcca ggcgctcgcc tgcgtcgtcg gcgatcacct gtttcgcaaa

10981 gagcgccggc atctcgccgc cggcgacgac ctgctgggtc cagcggcccg catcgtgcga

11041 gaaacgcagt cgcaacgcat cgtgatgttc gtagacctgc cggaacgcgt cggccagcct

11101 cgatgcgtcg atatccgccg gcacctggat caggaccgtc tggttgtagt gcgacggcgc

11161 atcgatctcc tgttcgaaga accagtgctg caccggcgta agcggcgcat cgcccagcgg

11221 gctcaaggtc ggcgcgcagg ctgcccgctc ctcgggcgcg gcggccagct gcgcgatcgt

11281 ctgatactgg aacagctgct tcgccgtcac gcgcagccct gcctgattgg cgcgcgcgat

11341 cacctggatg ctcaggatcg agtcgccgcc gagttcgaag aaattgtcgt ggatgccgac

11401 ggaaggcaac tgcagcacgt ctatgcagat cgacgccagc aggatttccc gcggcgtgac

11461 ggcaggtgca tgcggctggg ccgcgtcgcc ccgatccgcc ggaagcggca gcgccttgcg

11521 gttgatcttg ccgttgggca gcatcggcaa ggattcaagg gcgaagaact gcgacggcac

11581 catgtagtcg gcgagcttgc cgcccagata gccgcgcaga tcggcgatgt ccggcgcggc

11641 ggtcgcgaca taggcgatca ggaacgttcg ggctccttcg gttttcgcga tcacgacgca

11701 gtcgtcgacc gacggatgcg cgcgcagcgc cgcctcgatt tcaccgggtt cgatgcgcag

11761 gccgcgcagc ttgatctggt gatcgatgcg gccgaggaac tcgatgttgc cgtcgggccg

11821 gtagcgcgcg aggtcgccgg tgcggtagag gcgcgcgagc gggtcggccg agaacggatc

11881 ggcgatgaac ttttcggcgc tcagttcggg ttcgccgtgg tagccgcgcc cgaccggtgt

11941 gccgccgatc agcaattcgc cggccacgcc gatcggcgtg ggctgcatct gcgcgtcgac

12001 gatgtagagg cgggtgttgg cgatgggccg gccgatcggc acgatgcggt gcggatcgtc

12061 gcgccggcat tcccacgcgg tcacgtcgac ggcggcctcg gtggggccgt agaggttgta

12121 gagcttgacg tccaggcgct cgaggcaacg ctgctgcagg tcatggggca aggcctcgcc

12181 gctgcacacg acgcggcgca gcgacgcgca gtgcgcgtcg aggtccggat gatcgaggaa

12241 cgcgcgcagc atcgacggca cgaaatggat cgtggtgatg cgttcgcgct cgatgagctc

12301 gaccaggtag tcggtctcgc gctggccgcc ggggcgggcg aacacgaggc gcgcgccggt

12361 gacgagcggc cagaagagtt cccagaccga gacgtcgaag ctgaacgggg tcttctgcag

12421 cacggcatcg tcggcgtcga gcgcataggc gtgctgcatc cagaggatgc ggttggtgat

12481 cgcgcgatgg gtgttgagcg cgcccttggg gcggccggtc gagccggacg tgtagatcat

12541 gtaggcgagg ttgtcgccgt tcagcgcggg tgcggggttg gacgtcgccg cggcgtcgag

12601 gtcgagcgag tcgcgatcga cgacgatcac gtgcgcgtcg gtgtcgggca gcgcgtcgtg

12661 cagatgctgc tgggtgagga gccagcgcaa ctgcgcgtgg tcgatcatga agcgcacgcg

12721 ctcggcgggg tagtcggggt cgacggggac gtaggcgccg ccggccttga ggatcgcgag

-continued

12781 cagggcaacg ctcatgtcga gcgaacgctc catggcgacg ccgacgagcg agtcggggcc

12841 gacgccgagc gcgacgaggt ggtgggcgag gcggttggcg cgcaggttga gttcggcgta

12901 ggtgagcgcg gtgtcatcga agacgatcgc gacggcatcg ggcgtgcgct cgacctgctg

12961 ctcgaacagg cggtgcagcg gttgcgcggc gtcctcgccg aaatccgtgt cggtgcggtt

13021 ccactcgacg gtcagcaggt tccgctccgc gtcattcgac aacgacagcg cgccgagcgg

13081 ccggtccgga tcggcgatca cggcatcgac gagcgtgcgg aagtgttccg ccatgcgatc

13141 gatcgtggcg gcgtcgaaca gatccaggtt gtattccagc gagcccgcga ggccgtcgtc

13201 ggcatcctga acatgaagcg tgaggtcgaa cttcgcggtg tgggtctcca ccgccaccgg

13261 cgtggccacg agaccgggga agctcactgc ccggggttgc gctttctcgt atgcgaacac

13321 gacctggaac accggcgtgc ggcccaggtt gcgttcgagc tcgagcgagt ccaccacctg

13381 ctcgaacgga atctcctggc ggctgtagcc gtccagcgcg acgcgcttca cgcgcgccag

13441 caggtcgccg aaggtcggat tgcccgacag gtccacgcgc agcgcgagca tgttcgcgaa

13501 gaagccgatc agcggctcgg tcatgctgga acgccgattg gcgatcgggg agccgatgac

13561 gaggtcctgc tggttgctgt atcgcgacag gagcagcgca tacgcggcga gcacgaccat

13621 gaacgtgctg gtgccggacg cacgggcaat cgcgcgcagg ccgtcggcgc gttcggcgct

13681 cagctggaac ggcaggaccg cgccgcggaa ctgctggacg gcgggccggg ggcggtcggt

13741 gggcagttcg atcaggtccg gcgcgtccgc cagcgcggcg ctcaggagcg ccagctcccg

13801 atgcgtgtcg gcggacgcca ggcgctcgtg ctgccacacg gcgtagtccg cgtactgcac

13861 ggccagttcc ggcagcgact cgccggcata gagcgcggcc agttcgccga tgaggatgcc

13921 tgacgaccat gcatcggaaa cgatgtgatg catcacgatg ccgaagacgt gcaggcgctc

13981 atggacgcga tacagcacga cgcgatagag cggcccggcg gcgagatcga acgggcggtc

14041 ggcttcctcc gcgagcagcg cgagcgtgtc ggattcgctg gcgacgtcga cgacgtcgag

14101 cgcgaccggc gccggcggcg caatgcgttg aaccccgcgg ccgtcgacgg cgggaaacgt

14161 cgtgcgcagg atctcgtgac gccggctgat ctcggacacg gcaaaccgca ggcgcgcgac

14221 gtcgagttcg ccttcgaagc gcagcgcgct cgagatgttg taggtggccg acgggccttc

14281 cagttgcgcg aggaaccaca gccgctgctg cggaaaggac agcggcaggt cgttcgcgcg

14341 cgagcggggc gggatggcgc cggccgtcga gccggggtgg ggcgacgacg cttcgatcag

14401 gtcggacacc gcgctgatgg tctggagttc gaagatcgcg tcgatgccga tctcgacgga

14461 gaagctgctc cagatccgcg agaccagttg catggcttgc agcgaatcgc cgccgtagtc

14521 gaagaagcgg ccggcgagat cgacggccgg attgtcgagc acgtcgcgcc agatgcgcac

14581 cagttcgcgc tgaatcggcg tggcgtcgag aggggcttcc tcgggcgcgg cggcaggctc

14641 cagggccagg agcgccgggc gatccagctt gccgttggcg ttgagcggga attcggcgat

14701 cgggatgatg tcggacggga ccatgtagtc cggcagcttc ccggccaggt aggcccgcag

14761 gttcggcacg ctcaggctcg cggcgccctt gacgtaggcc gccagcttgc gcaccccgtg

14821 ggcggattcg cgcagcatga ccgccgcgcc gacgacgtcc tcgtgcgcgg cgatcgcggc

14881 ctcgatctcg ccgagttcga cacggtgccc gcggatcttg acctggtggt cgacgcgtcc

14941 gtagcactgg atacgtccgt cgggcagcca ccggccgatg tcgccggtgc gatagatgcg

15001 cgcttcgccg ggaaacggat gctcgacgaa tttcgcggcg gtgacgtcgg gccgctggtg

15061 gtagccgcgt gcaaggccgg cgccggcgag gcagatttcc ccgggcacgc cgagcggaac

15121 cggccgcagc gcgtcgtcga gcatgtacac ccgggtgtcg gcgatgggac ggccgatcag

15181 caccgtgggc ggcgcgtcct cgacgcgctc gacgatgcag ccgaccgtcg cctcggtggg

-continued

15241 accgtactcg ttgtagattt cgatcgcggg atcgatcttg cgcagcgtgg cgatgtgctg

15301 gggcgtcagt tcctcgccgc ccacgatcac cttgcgcacg ccggagcgtg ccaggttcat

15361 gtattccagc aggtgaatgt gggtgggcgt gagcttgagg gtgtcgacgc cgctgccggg

15421 ctggaacatc cgggccagga tggtgtcgat gctttccgac tgcggataga tgcgcagcgt

15481 cttgccgcgc accagcgggc agaagatgtt ggtgagcgtg aagtcgaagc agagcgagct

15541 gtacaggccg aaactgccgg tcgtgctttc cggaaagtaa tacccggcgg cccacgcgat

15601 gtagtgggcc aggttccggt gttcgagcag gcagcctttg ggtttcccgg tcgagcccga

15661 cgtgtagagc acgtaggcca ggtgcgccgg ttcggcacgg tgcggcgggt tgtccggcag

15721 cggctgccag ccggggagtt cctggtccag cagcagcgtc acgccggaga attcatacca

15781 ctgcgcgagc tgactcgact gggtcaccag cagcgacagg cccgtgtcgc cgaggatgtg

15841 attgatccgc tcggccggat acgcggggtc cagcggaacg aacgccgccc ccgccttcag

15901 gatgccgaga atcgcgacga tcatccattc ggaacggtcg agcatgatgc cgaccagcga

15961 ttccggcccg acgccgtggt gttcgcgcaa gtgatgcgcg aggctgttgg cccgcgcgtt

16021 caggtcggcg taggtcatca gcgaactgtc ggtgaccagg gccggcgccg tcggcgtgcg

16081 tgcgacctgg gcttcgaaca tggcgacgac cgtcgggtgg ctggggccgg ccgtcgcggt

16141 ttcgttgaac gcggccagca gcgggccctg ttccggcggg gccgcttcga tgtcgccgac

16201 ggcgccgtcg aggtgttcga atgcctccag caccgcggcg aggctgccgg cgaaaccgtc

16261 gatgatgaaa ggctcgatgg ccccgctgta acgaagctcg atttcgccgc gcgcgagccg

16321 caggtgcaac tgcagatcgt cgtcccgacc ggtcggtgcg tggtgcacgc ggtcgtccgc

16381 cagcgcgact ttcgtgagct gcgcgagcgc catgtccttt tcgttgcgca cgagcgtttc

16441 cagcgggaat cgaggctcgg cgtagctgtc ttccacgatc ccggccacgc gcgacaggta

16501 gtcctcgatg cgctcgtcgg ggcggacctc gatgatcagc ggaacgatgg cggcccgggc

16561 cgacggatgc ccggccagcc ccggcgtgcc gagcaccgtg accggaatcc ggaagtattt

16621 ccagagcagg aacgcgatgc ccgccgccgc gacggcgaat tcggcaagct cgccgtcgcc

16681 gatgcgccgc aacaggtcga gcgacgcggg cgtgagccgc accgagcggg tcagcgggcg

16741 acccggctgc tggctcgggg cgtacgccgc gattccgtac acgccggcga cccgggaaag

16801 gctttcgcgc cagaaacgcg cggtggctgc atagcgatgg tcggtgacca gcacgttatt

16861 gtcttgcaca ggaaactcct tgagacgttt tgttcacctg aaacaacctg aagcagcacg

16921 cacggcgcgc gccgctcgaa ccccggcggg cgcgcatcac gtcttctcct cgagcgcgtc

16981 gtcggccgtg accgcgggcg cgcgcttcag gcgcaggccg acccggactc gcgggccggc

17041 ggcgggcgcc tcgtcggaga gcgggatgcg atcgaccggc gtggccggat cgcgacggaa

17101 gacgtcgtgg atcgcgagca gtcgatcgcg catcgcggcg atggtcgacg ggcggaacag

17161 gtgggtgttg tagatgaact ggatcaggtg ccggccttcg ctttccacga cctggaagga

17221 caggtcgaac ttggccgtcg tgtccgccgg cgagatgtcc gtgatgcgaa ggcctggctg

17281 cggcgccggc atcgacacgt ggttcacctg aatgtcgaag atcgggaaat ggttcgccgg

17341 cgtgcggatc ttcaggtctt ccagcaacac gtcgaacgga taggacgcat gctccagcgc

17401 ttgcgcggag gctttcgcca ccccgtcgat cacctccgcg accgtcgcgg atttccgcac

17461 cggcacgcgc agcacgacgg tgttgaggta cacgccgacc tgcgattcga gctgctcgct

17521 gtcgcgcccg gccgacacgc tgccgatgac gatgtcctca cgccccgtgt agcggtgcat

17581 cagcacgcag aacgacgcca gtagcaccgc gtggagcgac gtgtggtgag cgcgggccag

-continued

17641 cgtcgcgagt tccgccgcgt gcggctgcgg cagttcgact tcgagcgtct gcccggcatg

17701 accgagccgc tcgggacgcg ggaagtcgga tgccagttgc aggcggggca gcggcggcgc

17761 cagttgctcg agccagtacg cgcgatgcgc ggcggcgcgc ggacccgcga ggctcgcgtt

17821 gtgccacgcg gcgtagtcgc gatactggat cgacagcggc ggcaggtcgc gccccgcata

17881 cagcgcatgc aggtcgtcgg tcagcacgcg gatcgaccat gcatccgaga tcacgtggtg

17941 catgttcagc agcaacagat gcttctcctg cgacagccgg accagcttga cgcgaaagag

18001 cgggcccgac gcgagatcga acggctgctc gcattccgcg cgaatcagcg catcgatcgc

18061 ttgcggcccg gcatcgtccg cgagatcgcg ctgctcgacc cggaatccgg acgcttcgcg

18121 gctgaggacg cgttgccgca actcgccttc gatcatcgcg aacacggtgc gcaggctctc

18181 gtggcgatcg accagcgtgt cgaatgcacg gacgaggcgc gccgtatcga cggcgccgtc

18241 cagctgcagc gcgcccgcca tgttgtacgt ggacggatcc gcgccgcggc tggcgagcca

18301 gatccgcttc tgtgcacgag acaccgcgta ggacggttgc gcggccagcg ccgggatgat

18361 cgcgtcgtcg tcggcggcgc cgtcgacggg catggcagcc agcctttgtg cgagcgcgcg

18421 cggcgtcggc gcatggaaga tgtcggcgac cgcgacgttc agtgcagccc gggggatccg

18481 gctgaccatc tggatcgcct tgaggctttg gcctccgtgc tcgaagaaat cgtcgtcgac

18541 gccgttcggc cggcggccga gcacctcggc gaagaggcgc agcagcgccg cttcgaccgg

18601 cgtgcgcggt tcggcccgca cgccgtcggg cacggacgcg gcatccggca gcggcagcgc

18661 ggcgcggttg atcttgccgt tcggcatgac gggcagcgcc ggcagcagca tcacggtgtc

18721 gggcaccatg tgcgccggca gcgtgtcgcg cagtgcgtcg cgcacgcgct ggggcgtcca

18781 gccggttccc gacgcgtagc cgcacagggt catttcggca tccgacgttt cccgggcgac

18841 caccacggcg tgggaaatgc cggcaagact ggtcagcgcg gcttcgattt ccccgagctc

18901 gatgcggtag ccacggatct tgacctggaa gtcgcggcgg ccgaagaagt gcagattgcc

18961 gtccgccccg aagcagccga tgtcgccggt gcgatacagg cgcgcgcctg gttccggact

19021 gaacggatcg tcgcggaaca ccgcccgggt gcgggcttcg tcgaacaggt agccgcgccc

19081 gacgccgacg cccccgatgc agatctcgcc cttgacgccg gccgggcacg gattcatgtc

19141 ggcatccacg acgtagaggc gcaggttctc gatcggccgg ccgatcggaa tcgccggccc

19201 atccggcgcg cgcgtcaggc agtaatgcgc gacggagtcc gacgcttcgg tcggcccata

19261 ggcgttgatg agccggacgg ccggattcag gcggaaccac gcttgcgcgg tggcgggctg

19321 cagcgtttcg ccgatcgtca gcaacgtgtc gaggtgaggg aaggccggtg ccgcgtgccg

19381 ttccagttcg ccgagaaagg tcgcgagata ggacggtacg aattgcattg ccgtgatgcg

19441 gtcgcggtgc aggctgtcga tcaggcgcgc gggctcgagg atcacggcat cgggatagat

19501 caccgtcgtg ccgcccgacg ccagcgccgc gaagcattgc cagaccgaaa tatcggagca

19561 gtgcgaagcg gtctgggcga ccgcgctctg cgcgccgagc ccgacccggc gcgccatcgc

19621 gagcacgtga ttgagcatgc cgcgatgttc gaccatcgcg cccttcggct ggccggtcga

19681 acccgacgtg aagatcacgt aggcgaggtc cgcgggccgg cagcgcggcg tcaccggcgc

19741 cggcgcttcg gcgccgcgac ggtcgggcag gcgggccgga tcgaccagcg ggatcgacgc

19801 cagcgccggc ggcggcacgc agtccgtcgt gacgatgacg gccggccgcg ccagcgtcag

19861 gatggtctcg acccgctggg ccgggtaggc cggatcgacc ggaacgtacg ccgcgccgca

19921 cttccagatg gccaggatcg tttccagcat cagcggcgag cgcggcatcc agacggcgat

19981 ccggtcgtcc ggctgcagcg gcgccgtctg cagaagatgc gcggcgatcc ggttggcgcc

20041 ttcgacgagg tcacggtagg tgcgaacctc cgtgccgcag cgaaccgcca cgcgctcggg

-continued

20101 gtgcgctgcg gcgacggcct cgatcagttc gggcagcgtc cggtcggacg gaaccggcgc

20161 gaacgtgtcg ttccagccga gcaggatggc gtcccgctcg gcggcagcga gaagcggcac

20221 gctgcggttc gggcgatctt ccgcgccggc caggccggtg agcagggtct cgacatggcg

20281 cagcaggcgg acgatcgtgt cgcgatcgaa ccggccgtcg tcgtacagca cctgcagcga

20341 caggcgcttg cccggcgtca cgaccagcgt cagcgggtaa ttgttcggat cggacacctc

20401 gaatgcgccg atccgcaggc cgggcagcgc atcggccagc gcttcttcca ccggataatt

20461 ctggaagatg agcaggcttt cgaagagcgg cacgccgggt ggcaggccgg cgaatttctg

20521 gatgtcggcc agcggatagt gcgcatagtc ctcctgctgc gcgagatcca tctgcaattg

20581 cgccagccac gctgacgtcg ggcgtgcgtc gatgcgcacc cgcaccggca gcgtgttgat

20641 gaacagcccg accatttcgt cggatgccgg cagcgacgcc gggcggccgg aaacgatcgt

20701 gccgaacacg acgtccgatt cgccgctgta gcggctcagc aactgcgccc atgcgccctg

20761 cgcgagcgtg ttcagggtga ggcggcggga ttgcgcgaat gcgacgagcc gttgcgtgtc

20821 gctttcggag agcagcagcg gctcttccac gtaggcgccc ggcgcggccg tgccgtcgag

20881 ttcggggcgg cccagcacga gcggcgtcgt cgccgggaaa tccgccagct tcgtcttcca

20941 gaaacgttgc gcggcggcgg cgtcctggcg tgccagccag cgcacgtaac cggcgaaggc

21001 aggcggcgcg tcccgctgcg gcgcgccttc ggccggcggc gcctgatagg cggcggccac

21061 gtcgctcagc aaccgggcgg agctccaccc gtcgagcagg atgtggtgat ggctccaatg

21121 gaagcgccat gcgtgctcgc ccacgcggaa cagcgcgagc cgcatcagcg gcgcgcgggt

21181 aaagtcgaag ccgcgcgccc ggtcttgcgc cacgtaggct tcccagcgct gttcggcctc

21241 cgcggcggac gccgcgcgca gatcctcgtc gtgccacggc aagtcgatcc ggcgatgcac

21301 gacctgcacg gggctttcga tgtcttccca gtgaaacgac gtacgcagga tgtcgtgccg

21361 gtgcgccacg gtctcccacg cgcggcggaa ccgttcgacg tcgagcgccc cgtcgatacg

21421 gaaattcagg ctgctgaagt acgcatccga cgcgggttcg tacaggctgt ggaacagcat

21481 gccctgctgg gtcggcgtca gcgggtagac gtcggcgatc tcgtccggac tcaccgacgc

21541 cggcgccggc gcctgcggca acgcagtcgc gggccgggtc gatgcggacg ggacagcgtg

21601 gccggcgacc agggtttcga gcgccgcgat gtaggcttgc gcgacgcgca ggatggtggc

21661 cgtgtcgtgg caggcccggc tgaattccca cgcaacgtgc aggcgattac cggtcacgta

21721 cgcgttgatg tcgagcaggt gctcgcgcaa ctggttcgcg ttgcggccgt ccccgctcgg

21781 ctccgcggcc tgtttccagt cgcgtgcggc ggtgaacagc tggtcggtct gccccaggta

21841 gttgaactgc agtcgcggct gcggaagcgg gccgtcgagc cggtctagca gcaggccgta

21901 ggtgatgccc gcgttcggca ccgcgcgcag ccgcgtcctg accgatgcga cgaggctggc

21961 cggatcgtgc gaaccggcat cgaccgtcag caagaccggg aaaaccgacg taaaccagcc

22021 caccgtgcgc gagatgtcga gcgcgtcgat cagttcctcg cgcccgtgcg cttcgagatc

22081 cagcagcacg tcggcgcatc cgctccattc gctgacggca cgcgcgagcg cggcgagcag

22141 cacgtcgttg acctgcgcgt cgtaggcgcg gggcgcggcg cccagcaagg ccgtcgtcgc

22201 ggcttcgccc aactcgacga cgatcgtgtc ggcggacgac acggtattgg cgtcggcagg

22261 cgcatcgcga tcgagcggca ggccgggcag ggcggcacgc gcgagggcct gccaatgggc

22321 gaggtcggcg tcggcggcgc cggagccggc ccaggtcgag atcgcccggg tccatgcggt

22381 ccaggtcgcg ctgccgcctg cgaattcggg cgccttgccg ttgcgcagcc gggtataggc

22441 gtcgtacacg gtttcgagca gcgcgcccca cgacacgccg tcgacgacca gatgatgggc

-continued

22501 gaccagcagc aggcggagcg aacggccttc gtcgacgcgg aacaggtccg cgcgcacgac

22561 ggggccgtcc gcgagattca ggctcgcatg cgactgcgcg acgtactgcg cgagctgatc

22621 gcgcgcaatg tcggacacga cgacggggat ctccgggtcg tcgacgactt cctgggtcca

22681 gccgctctcg ccctcgcgaa agcgcagccg cagcgcgtca tgccatttga ccgcatgccg

22741 cagcgcctgg cgcagcaaga ccggatcgag gtcggccggc acgtcgagca ggaccgcctg

22801 gttgtactgg tccgggtcgt gcttgccctg cgcgaagaaa cgcttctgga tgggcgtcag

22861 cggcagcggg ccggacgatg cgacgaacgc cgccgcgccg accgtgccgc gcgtcgccac

22921 ggcggcgagt tcggccaccg tcggatgctg gaagatgagc cgggtggtga gcttcaggcc

22981 cgccttcgcg gccagcgaca cgatgcgcat gctcagaatc gaatcgccgc ccagcgcgaa

23041 gaggttgtcg tggatgccgg gcgacggaat gcccagcgct tcgccccaga tgcggcacag

23101 cagcgtctcg gtaggcgtgc ggggcggcgt cggcgcgtgt gccgtggcgg cgagtcgcgc

23161 gcggtccagc ggcggcagcg cgttgcggtc gatcttgccg ttgccgctca ggggcagcgc

23221 gtcgagcacc acgtagatgc cgggcaccat gtagtccggc agcgtggcgg acagcgcggc

23281 ggcgatcccg gcgtcgctca gcgacgcgcc gtcgcggaac gcgacgtacg cgcacagcgc

23341 ggcgcggccg gcctcgtcgc gatagtcgag cgcggcggcc tggcggagtt tccgcgaatg

23401 gtcggccagt cgtcgttggt cgatctcccc gagctcgatg cggtagccgc ggatcttcag

23461 ctggtggtcc ttgcggccgt gcagcacgat cgttccgtcg ggcaggtagc agccgatgtc

23521 gcgggtgcgg tacaggcgga cgccgcgctg aggatggaac ggatcctcga cgaacgcgtc

23581 ctgcgtggcg gcttcattgt tcagatagcc gcgaccgacg gcgacgccgg acacgcacag

23641 ctcgccggga atcccgatcg ggcacaggtt catctgcggg tcgacgacgt agaggcgaac

23701 gttgcggatc ggcttgccga ccggtacgta aggcgtggac ggcgcgcccg tcatgcggtg

23761 ctgtgcgacg tcgtcggacg cttcggccgg gccgtacgcg ttcaccagcg ggatcgccgg

23821 gaacacgtcg aaccactgtt tcaccagcgc cgggctgacc atctcgccgg tgacgagcag

23881 gtgccgcaga tgccgcatca gcgccggccg ttccgacgcg cggtcgagca cggcggacag

23941 ataggacggc accagttcga ggatgctgat ccgggtggtt tccaggtacg cgacgaaacg

24001 cgcgggatcg cgaatgcagt cgtcgtcgac gatcacggtc ttgccgccga cgagcggcgc

24061 cgtgaaaaat tgccagaccg aaatatcgaa gcaatgcggc gcggtttgcg cgatcaccga

24121 cgacgccgag atcgagaact cgtcgatctc ggcgagcatg tggttcagca tgccggcgtg

24181 ctcgaccatc gcgcctttgg gcttgccggt ggagccggac gtgtagatca cgtaggcgag

24241 gctgtcgggc gacacggggc ggccgggatt ggagtcgtcg acggcgtcgg tggcggcgtc

24301 gagcgacacg accagcgcga tcccggccag ctccgggggc aggagcccgt cgcaggtgat

24361 cacgagggcg gcgccggaat cctcgaggat ggtgcggatg cgggccaccg gataattcgg

24421 gtcgaccgga atataggcgg cgccgcactt ccagaccgcg aggatcgcct ccatcagctg

24481 ggcggaccgg tgcatgcaga ttgcgaccag cgcgtccggg cccaggtcgg cggcggcgag

24541 caggcggtgc gcgatgcggt tggcgcgcgc gttcagttcg cccgcgctca ggacgccatc

24601 ccggtactcg accgcgggcc gctcggggtg gtccgcggcg gcctgctcca ggcgatgcac

24661 cacggtgagc gcggcgtcga acggcacggc ggtgtcgttg aaggtctcca gcaactgccg

24721 gcgttccgcg tcgggcaaga tcggcacgcg gccgagcagc cggttcggat cggccgcgaa

24781 cgcgtcgagc gtcgcggcca cgtggcccag catccgctgc atcgtgtctt catcgaagcg

24841 ccgcgggtcg aacgacagtt ccatcttcca gtcgtcgcgc gccgtcacca cgaattcgag

24901 cggaatgtcg gcgcggttgt agagctgcac ctcgtcgacc gccagcccgt gcgcgccatg

-continued

24961 cgtgagcgac gcgtcgagcg ggtaattcat gaacgtgatg ttgctctcga acagcggcgc

25021 cgtcggcggc acgtcgctgc agcgctgaat gtcgggcaac ggggtgtgct cgaacggcgc

25081 gcgggcggcc acgcgcgcct ggatcatctt cagccacggc accagcggct gcctcgggtc

25141 gacccgcacc cgcaccggca ccgtattgat gaacaggccg agcatggttt cgatccccgg

25201 caggttggcg ccccgcccgg acacgacggc gccgaacacc acgtcggttt ccccgctgta

25261 acgcgacagc acgagcgccc acgccgcttg cgcgagggta ttgagggtga cgtgatggcg

25321 ggccgcgaat tgccgcaggc gcgcgctcag gtcggccgac aggtcggcct gcacttgcgc

25381 gaggccctgg ccgaagcgtt cgtccgcgcc cgcgcgcgcg gccgtgggca gcggggtcgg

25441 tgtgcggaac ccttcgagat agcgcgtcca gtattgctgc gcggcttgcg gctcgtgctg

25501 ctgcagccac tggatatagt cgcgataggg gcgcaccggc gggagcgccg gcgacacgcc

25561 gcgcgcgagc gcgccataga cctcgaagat ctcctcgatg acgagcgaca ggcaccagcc

25621 atcggccagg atgtgatggt ggctccagct gaacaggtag gcgtcggcgg cgacgcgcac

25681 caggcgacag cgcacgagcg gcgcgcgatc gagcgcgaag ccctcggcca ggtcgttgtc

25741 gagatgcgcg cgccaccgtg agcgctgttc gtgttccggc aggtcgagcc agtcgtcctg

25801 cacccacggc agcgtggcgc gcgcgtgcac gacctgcatc ggcttgtcga actcctccca

25861 atggaacgac gtgcgcatca ccggatgccg atcgatgagc tgctgccacg cggcatgaaa

25921 cagcgcggga tcgaggctgc cggtgatccg gcaactgagc tggttgaagc tgcttctcga

25981 gccgggctcg tgcacggcat gaaagagcat cccctcctgc atcggggaga gctcgtagat

26041 atcggcgatg gtgggggatg tcacgatttg atccttgaga caagggcgtc cagcgcttcc

26101 tggctgatgc gcgcggccgg aaagtccgac gggctcagcg cgcgcgggcc gtcgccgccg

26161 gccgcgacga tcgacagcag gcggctgcgg tagcactgcg tcagctgttc gatgacgccg

26221 ggtgcgcagg cctcgcggtt gtagtgccag gtcaggcgca gacggccgtc gaacaccatc

26281 ccgtcgatct cgaacagatg gccgcgacgt gcgcgcgggc tgtgctcggg gctctggaag

26341 tcgagtaccg gcttccagcc cgtgtcgtcg ggcagcacgc gatcgacctg gccgagatag

26401 ttgaagcgca ccggcgccgg cggctgccgt tcgagcgccg ccgcgatgcc ggcgtcgtgg

26461 ccgaggtagc gggcgatgcc gtagccgagc ccgcgcatcg gaaccgcgcg cagctgctcc

26521 ttgacgtggc gcagcgcgtc gaccgccacg gtggcgtcgc cggcgttcag gcacaccgga

26581 tagtgggtgg tgaaccagcc gatcgtgcgc gacgtatcga cgccgtcgaa aatgtcctcg

26641 cggccgtggc cttcgagatc gacgaccagc gacgcgttgc cggtccagtc gccgaacgcg

26701 agcagcaggg ccgtcagcag gacttcgttg atctgcgtgt tgaacgcacg cggcacgtcc

26761 tgcaacagcg cgagtgtctg ctgcgcatcg aactcgacga tcgtcgagcc cgcttcggcg

26821 acggtgccgg ccggcatgtc gtcgaagcac gccggctcgc cggcgttgcc ctggagccag

26881 tagtccagcc ccaggccgtc gagcgcggtc gcgccgagtc cggacaggcg cgtcgaccag

26941 tcgcgccagg ccgtcgtcct ggccgggagc tgtaccgcgt cgcccgcttc gagctggcga

27001 catgcggtgt acaggtcttc gaacaggatg cgccacgaca cgccgtcgat caccaggtga

27061 tgcgcgaccg cgagcaggcg ctgcggcgcg tcgggaccga actggaacag gtgcgcgcgc

27121 agcagcggcg gcgccgacag cgtgaagctt tcctgcatgc cggtggcggt cgcgagcatc

27181 gcggcctgcc gtgcggcagg cgccgcgtcc gccagcgacg tgacgccgag cggaatggcc

27241 agcggcggcg cggcatgcga ttgctgccac acgccggcga cgcacgcgaa actcagccgc

27301 agcgcgtcgt gatgcgtcgc gacggccgcc agcgcgcgct cgatcgtgtc cggccgcagc

-continued

27361 gatgcgggca cctcgatcat cgtcgactgg ttgtagtggt gcggatcggc gacgtcttgc

27421 gcgaagaacc agtgctggat cggcgtcagc ggggcggggc cgaccaccgg ctcctgcgcg

27481 atccggatcg acggcgcctc cgtcgcgacc tgggcgagct cggcgatggt cgggtgtgcg

27541 aagaactggt cggcggtgaa cttgagcccg acttgctggg ccagcgacat cacctggatg

27601 atcaggatcg agtcgccgcc cagttcgaag aaattgtcgt gcacgccgat cggctcgcgg

27661 cccagcacgt cgcaccagat cctgcccagg cgcgcctcga cgtcattggc cggtgcgacg

27721 taggcggttt cgctcggcgc gggcgccagt tccagcgcgg cgagcgcctt gcggtcgggc

27781 ttgccgttcg gcgtcagcgg caggcgttcg agcgtcacga tcgacgccgg caccatgaac

27841 tcgggcaggc gttccttcag gtgttcccgc aggctggcga cgctggccgt cgccgtcgcg

27901 acgcaggcca ccagctgctt gtgctgcggc gtgtcctcgc gcacgaacac gatcgcgtcg

27961 gcgacgccgg cgtgctgcct gagcgccgcc tcgatctcgc ccatttcgat ccggtagccg

28021 cgaatcttca cctgcgtgtc gcgccgcccg gtgacttcca ggttgccgtc cggcagccag

28081 acgccgaggt cgccggtgcg atagaggcgc tcgcccgcct cgaacgggtg ggcgacgaac

28141 gcggcggccg tcaggtcgtc gcggccgaca tagccgcgcg ccagcgcgat gccggacacg

28201 cagatctcgc ccgcgcaacc ctcgggggcc agcgccccgt gctcgtcgag caggtacagg

28261 tgcgtgttgt ggatcgggcg gcccaccggc agacgggcgc cgtaggtgat ggccgggtcg

28321 accacgtagt ccgcgatgca cacggttgcc tcggtcgggc cgtacgagtt gtggcacgtg

28381 cgggtccggg ccagctcgcg cagatccgcc acgcgggcgc tgtcgcccgc gctgatgacc

28441 cgtttcacgg cgccgagcgc atgccagtcg agcgcggcaa ggtaggccgg cgtcgcgttg

28501 acggtggtga cgccctgctg tgcgatgtag tcgacgaaac gcggcacgtc ccggatcacg

28561 gcggtctttg ccagcaccag gcgggcgccc gcgagcagcg tgacgaagat ttccatgatc

28621 gagccgtcga agcccgggga gtagaactgg acgaagcggt cggcggaatc gaaaccgaat

28681 gcgtccacgt ggtactgcgc catgttcagg agccctgcgt gttcgagcac gacgcccttg

28741 ggcacgcccg tggagccgga cgtgtagatg atgtatgccg cgtcgtccgg ccgcacctcg

28801 acctgcgccg atgccgacgc gggtgccagc gtgtcgagct ggaagtcgag ggcgaacatc

28861 gggatcgccc agaaatcggc gagcaacggc aggtgttccg agtgcgtcag cagcgccttg

28921 accttcgcgt cctcgatcat gaagcgcagg cgctcccgcg gaaattccgg gtcgagcggc

28981 agatacaccg cgcccgcctt gagggcgccg agcatgccga cgatccagcg ctcggaacgg

29041 tcggccacca cgcccaccac gtcgccgcgt tcgatcgcgt attccgcgag caggaagctc

29101 gccagccggg acgcctggtc gtcgagttcg gcataggtca gcgatgcgtc ggcggtcacc

29161 accgcgacgc tgtccggcgc ggccgcgacc cgttgcgcga actgctccag gaaggtgccc

29221 tgtaccgcga cgggcgccgc atgcgaacgc aggcgcgcgc gctcttcgtc gtcgagcagc

29281 gagacggtgt cgagcggcgc atccagtgcg ccgaagccgg ccacgacgtt gcgcaggtgc

29341 cgtgcgacat gctggagata gtgcagcgtg aacaccgtcg gccggcccgt cagcacgatc

29401 tcgtagcgct cccgatgccg gatctcgatc gacaggtcgt agtcggccgc tgcccaggct

29461 tcgtgaaggc cgtcgaagcg cacgccgacg ttggtcgcgc gccgttcgcc atgcagcttg

29521 tgcgcgaggg cggcgatcgg gaaatcctgg tacgaatagc tgcgctgcac gctgtcgcgc

29581 agctggttca ggtacgcgcg aaccgtgggg ccgggctcgc cggcgtcgag cagcgggaca

29641 ggctcggcgc agccgctcgc gggttcgacg atcagctgcg gcgacgccac gaacaggccg

29701 gccgcgccgt tgtagcgccc cagcacgcgg aacagcgcgg ccagcagcac gacgaacgcg

29761 cccagctcgt tgccggcggc gagccgctcc agcacctgcg ccgcgtcgcc gtcgagcgcg

-continued

29821 aacgtcagtg ccggctcggg gccgagcggc agcgcatacg cctgccacgc ctgctgaagg

29881 cggaaatctt catcgatgcg accgagcgcg tcgttccaga acgccacgtg ttcctggtat

29941 tgcccgctgg tcgagagcgc gttgagattc agttctgaca aagcacgatc tccctcgtcg

30001 cgtacaggat ttcggaagcg atgcccttgg ccttgcagtg cgcgacgaac tgggtggact

30061 ggatgtggct gggcgagttt tcgtcgaagg tgttgtcgag gaggtggttc agccagggct

30121 cctgacccat cgcatagaca tacgccgcgt tgaacgcgaa atcgtccacc agcgcggcgg

30181 cctcgccgaa ctggcagccg cgcgcccggc gtgattgatc gatgtcgcgc ggcagcgcct

30241 tgggaaacag cgggccgtag acccatgacg gcggcgcgcc ctcggtttcc atcccgacga

30301 acagggtgtc cggcttgccg gcgaggcgga agacatgctc gtagaggcgc gggtccaggt

30361 tgcacgaatc ggcgatgcac agcaccgagc gcgagccgaa gcggatcatg aagctctgct

30421 tgctgtggat cgccaggtcg ttgtgttcgc ccatgaacgg aatggcggtg atggcgccgc

30481 cgggcacctt gatttcctgc gcatcccgaa cttccagcac gtcgtcgaag ccgagcttgc

30541 gcaacgccag ctccatcgac ggatcttgcg gaaagccgtc gagattcctg ccgaccacca

30601 cggtcttgac cttgtggcga agctgcagca gcgtttcgag gacgatgtga tcgtgatggc

30661 tgtgcgtgat cagcacgtag tcgatctggt ccggcaggtc ggcgaacgta tagcgcggca

30721 gcgcggtgtc gtagccgtag ctgatcaccg gatcgatcag gatgctcacg ccccggctct

30781 ggatcagcac gcacgcgtgg ccgtagtagc ggatgcggat gtcgtcgccg tcgaacgaac

30841 gatccggttt cggcgccggc gcctcctcga cgaagaacga gcggaacagc ggctcgtcct

30901 tctcctccac gcgcatcagg tcgacgatct tcgcgtagct gccgggcgtg tcgcgcatgc

30961 ggaacagcgt gtcgagcgcg cggtcgtcga aggccatgtt gctgaacacc gtgcgctcgt

31021 cgcggagccg gggcgtgctg aggatgaacg gccgcggcgt gtgctcctcg atcgccgaca

31081 gcgcgatgct ctgcgcatcg cgcgcataga acgggctcgc gtacagcagg ctttcgaaca

31141 cccggaagga cgggttgtgg ttcaggtcgt agtagatctc gacatagccc ttcagcacct

31201 ccggaatctc ggggtagagc gggtccgacg ccatccccgt ggcccgttcc agcagcagcg

31261 tggagaacgc cttgtatgcc ttcgccagtt ccagttgccg ggtcgcgcgt tgggtggtct

31321 gctcgatcag cgtgcggatt tcgtcgacgc gctggccgcc caggtcgagg aacggcccgc

31381 cgcgcatcgc gggatccttg caggccgccg catgcatcat cggcgatgcg gcataggact

31441 tcagcagcgg caggaaccgc tccgccacgt tgagggcggc ggtcaacggc ggaagcgtgt

31501 gataccacgc gtaccagctg ttgatcagcg gttcgaactg gatgttttgg cgcaggtaga

31561 cctgcgcgct ggacgaaata gtcaacgaag gctccttaga atgcgctgag ttcgacggtg

31621 ggctggcggg cttcggcgtg cagcgcgcgt tgtcccaggg tcaggttccg gatgcgaacg

31681 cccggattgg cgagcacctc gccgatgacg gacgtcagct cgttggcgag gccttgcacc

31741 agggcttcgc tgaaccgccc cgcgtgatag acgacgcgga tcgcgagacc ctcggcgtgc

31801 ggctcggcca ggaaccagaa atcggttgcg gcttccgtgt ccgcgcgctg cgggtcgtgg

31861 tccggcagct cggcgatatg cacttgtccc gcgtagcgat cgacggggcc gtgtcgctgg

31921 ttctgcagcg tcaggccgat gtcgaagagc ggattgcgtc ccgccacgcg tttgatgtgc

31981 agctcgtcga gcaggcgatc cagcgggtac agcgggtgcg agaacgcttc gagcgtggtg

32041 tcccgcaccc gggtcagcag cgtgtcgaac cggtcgtcgc ccgcgacacg atcgcgcagc

32101 gccagcacgt tcaggtaggg gccgacctgc gactcgagtt cgggcagttc gcggcccgcg

32161 accggcgtgc cgacgacgat gtcctcctgg ccggagcggc ggtagaacag cgccttgatg

-continued

32221 gcggacagca gcgcgatgaa caaggtcgcg ccgtggcgct tgccgagcga ttccagcgcg

32281 gccgtctcgg cggcgggcag gtcgaatcgc caggatttcc agctcggcgc ggccggctgc

32341 tcgacgtcgc ccggcagttc cagtgcgcgc aggccgccgc ccagtttggt cagccagtag

32401 tccttcatgc gcgcgccgtc cggcccggcg agcaggcggt tcagccagcc ggcgtaatcc

32461 ttgtactgga tcgggagggc gggcagcgga tcgtcgcgac gctggacgaa tgcgtcatag

32521 agcgcggaca ggtcgtcgag cagtacctcc gtggaccagc cgtcgctcac gatgtgatgc

32581 atcgtgcaga ggcagacgtg acggacttcg gagagcctca gcagcttgac gcggaacagc

32641 gggccggtcg cgagatccat cggcacgagc cgttcgctcg cctggatcgc cgctgcctgg

32701 gcatcgcggt cctcggcatc ctgcagatcc acgatctcga ccgggaacgc ggcttcgccg

32761 ggcggcagca cgtgctggac cggctggttg ccttccagca cgaaacgcgt gcgcaggatc

32821 tcgtgacgct cgctcaacgc gcggaacgcc cgcacgagcg catccacgtc cagcacgccc

32881 tcgaacagca gcgacgtggg cagcggcccc tcggcttgcg ccgcatggag acgatcctgg

32941 acccacagcc gcgtctgtgc gggagagagc gcgtagcttg cctgcgccgg cagcggcgtc

33001 accggcgcgt aatcgatcgg ctgcgtatcg gcgatgcgct tcgcgaggct cgagatggtt

33061 gggagtgcga acaggctgcg gatttccagc ttcacatgca gatcgcgccg gatgcgcgcg

33121 acgaccttcg tcgccagcag cgaattgccg cccagatcga agaaattgcc ggtcgtgctg

33181 atccgcgcct ggccgagcac ttcctgccag atggcagcca actgcgcttc gagtgcgttg

33241 acgggcgcaa cgtggtccag gccgtcgccg ggttcgggca gcctggtgcg atcgagcttg

33301 ccgttgggca gatgctcgaa cgcgctcacg acgacgaacg cggagggcac catgtaatcc

33361 ggcagccgct gccgcaggtg gccgcgcacc gcttcgatca gttctgcttc ggggtgcgac

33421 gagcacagcc atccgaccag tctcgcgccg tcgtccacgc cgcgcagcgc gacgacggcg

33481 gcatcgacca gcgggtgcga cgtcagcgcc gcctcgattt caccgggttc gatgcgcagg

33541 ccgcgcagct tgatctggtg atcgatgcgg ccgaggaact cgatgttgcc gtcgggccgg

33601 tagcgcgcga ggtcgccggt gcggtagagg cgcgcgagcg ggtcggccga gaacggatcg

33661 gcgatgaact tttcggcgct cagttcgggt tcgccgtggt agccgcgccc gaccggtgtg

33721 ccgccgatca gcaattcgcc ggccacgccg atcggcgtgg gctgcatctg cgcgtcgacg

33781 atgtagaggc gggtgttggc gatgggccgg ccgatcggca cgatgcggtg cggatcgtcg

33841 cgccggcatt cccacgcggt cacgtcgacg gcggcctcgg tggggccgta gaggttgtag

33901 agctcgacgt ccaggcgctc gaggcaacgc tgctgcaggt catggggcaa ggcctcgccg

33961 ctgcacacga cgcggcgcag cgacgcgcag tgcgcgtcga ggtccggatg atcgaggaac

34021 gcgcgcagca tcgacggcac gaaatggatc gtggtgatgc gttcgcgctc gatgagctcg

34081 accaggtagt cggtctcgcg ctggccgccg gggcgggcga acacgaggcg cgcgccggtg

34141 acgagcggcc agaagagttc ccagaccgag acgtcgaagc tgaacggggt cttctgcagc

34201 acggcatcgt cggcgccgag ggcgtaggcg tgctgcatcc agaggatgcg gttggtgatc

34261 gcgcgatggg tgttgagcgc gcccttgggg cggccggtcg agccggacgt gtagatcatg

34321 taggcgaggt tgtcgccgtt cagcgcgggt gcggggttgg acgtcgccgc ggcgtcgagg

34381 tcgagcgagt cgcgatcgac gacgatcacg tgcgcgtcgg tgtcgggcag cgcgtcgtgc

34441 agatgctgct gggtgaggag ccagcgcaac tgcgcgtggt cgatcatgaa gcgcacgcgc

34501 tcggcggggt agtcggggtc gacggggacg taggcgccgc cggccttgag gatcgcgagc

34561 agggcaacgc tcatgtcgag cgaacgctcc atggcgacgc cgacgagcga gtcggggccg

34621 acgccgagcg cgacgaggtg gtgggcgagg cggttggcgc gcaggttgag ttcggcgtag

-continued

34681 gtgagcgcgg tgtcatcgaa gacgatcgcg acggcatcgg gcgtgcgctc gacctgctgc

34741 tcgaacaggc ggtgcagcgg ttgcgcggcg tcctcgccga aatccgtgtc ggtgcggttc

34801 cactcgacgg tcagcaggtt ccgctccgca tcgctcgaca acggcagacg ggcaacggcg

34861 gccgacgcat cgtccgcgag atgcgtcagt agggtccggt agatgtcgag gaaacgctgc

34921 accgtgctcg cgtcgaacag atcggtgttg tagtcgcaat cgatcaggag tgcttgcccc

34981 gcgtcgagca cgttgacgtt caggtcgaac gcggtatggc ggatcagcgg cgccacgagg

35041 ccgaccgtca ggccgggcag ttcgggcagc gccgacacgg gttcgaggtt gaagaccgcc

35101 gataccagcg gcgcggcgtt gagatcgcgc tgtgcgccga tttcgcggac cagttcggcg

35161 aacggataat cctggtgctc gagcgcgtcg agcaggttct gccgggtgcc ggccaggaaa

35221 ctggccacgg tggcctgctc cggcagcgtg gagtgcagcg gcagcagatg cgtgcagtag

35281 ccggcgaggc gatcgctgcc ggccaccgag cggccggtca ccggaatgcc ggtgacgatc

35341 tcctgctggc cggcgacgcg gtgcaggaac agattgaagc cggcgagcag caccatgtag

35401 agcgtgcagc cgttctgacg ggccgcggtg cgcagcgtcg cggccgtcgc cgcgtccaga

35461 tgcagggaca cgcgctcgcc gtgaaacgtc ttcaccgcgg gccgcgggta gtccaccgga

35521 agattcagcg gtgcggcctg acgcgcgcat tgcgccagcc agtactcgcg attcgccttc

35581 gtttccgggc tgtggcgctg gccgtcgagc tgcttcaggt acgcgcgaaa ctgcagcggc

35641 gcgtcggccg gcgccgcacc ggcatacgcg cgggccagat cctcgagcag cacgccgaac

35701 gtcgagccgt cacagatgat gtgatgggcc gtcatcacca gcaggtgacg ctcgctgccg

35761 aggcgcacga gcgcggcccg aaagagcggc ccgttcacca ggtcgaacgg ctggcggctt

35821 tcctgctccc gccacgcgtt cgggtccgtg tcgatcagcg gaatctcgag tgtcagcgac

35881 gggtgcacga tctggcccga cccgtccgcc atcaccgtgg tgcgcagtgc ctcgtgccga

35941 tcgacgaggc tctggacggc cgcgcgcatc gcggcttcgt cgagccggcc gttcagttcg

36001 agcgtggtgt tgacgttgta ggcgagcgat ccttcgggat cgatttccga caacacccac

36061 agctggcgtt gcgcttcgct cagcgcggcc accgtgccgt gtttcgagtg cggccggatg

36121 aagccgcccc ggcgcaggtc ggcgacgctg tccttcaccg cccggatgaa gcggtcgata

36181 tcggcatcgg tatgcgcggt ggacaggaag caggtgcgcc attcccagat gtagatgccc

36241 ttttcgagca tgtgatagaa gaacaggtcg aggttctcgg tgaattcgaa gcggaacatc

36301 gagccgaacc acgtgacctt gatcggcgcc tcggcctccg cgaagaatgc attcagcgtg

36361 ccggcgatct gcgcggtgcg ttcgttgagc gcggcctgca gcgccggccc ctcctgttcg

36421 atcttctcga gcacggccag cgccgccgcc atcgcgagcg gatactggca gaaggtgccg

36481 ccgaacgcgg tgcggtccgc cgcggggaac gagtggtcgc cgtaggtcca catgccgccg

36541 tcgatggcat ccatgaagcg gctggtgccg gcgatcacgc ccagcggcag gccgccgccg

36601 atgatcttgc cgtacgtcgc gagatcggcc ctgatgccga acatggcttg cgagccgccc

36661 ggatggacgc ggaaaccggt gatcatttcg tcgaagatca gtgcgacgcc ggcctcctcg

36721 gtgatgcgac gcagttcctt gaggaatgcg acgggctgca gggaagggtt gcggctctgc

36781 accggctcca ccatcacggc ggcgagggtc gacgccatcc cgcgaatggc ctcgagcgcg

36841 gcgtcgctgc cgtagtcgag caggatcatg ttctcgacgg agccgaacgg tacgcccggg

36901 gcgatggttt ccgtcacgcc ttccgcgttc gccgcggcga gcgtgccgtc ggcatggccg

36961 tgatacgaat gcgtgaacat cacgatcttg tcgcgcccgg tcacggcgcg cgcgagccgc

37021 atcgcggtca tgacggcctc ggtgccggtg ttcgagaacg ccacgcgatc gaggccggtc

-continued

37081 acgcgggcaa agcgcgcggc gacttcgccg acgaggctgg agcgcgcacc cagttcgagc

37141 gggcgctgcc attcccgcgt gacctgctgc tggatgaaat ccggcgtgtg gccgaacagg

37201 tgcacgccga agcccatcgt gaaatcgatg tactcgttgc cgtcgatgtc ccacagccgc

37261 gaaccggccg cgcgatcgcc gacgatcgga tacagcatct ccttggtcga aaagcggaag

37321 ccgaccgtgg cgcggctgtc ggccagcacc gggcgcgacg cctgcaccga gtccttcgat

37381 ttccgggtgc gcgtcgtgta gcgcacgatc agcgcctcga gatgctcctg ctgcgcggcg

37441 gacagcccgc gcgcccgctg ctggaccggg ctgccccacg gcatcatcgg cttgggcggc

37501 gggttgtcgg ccgcgggcgc ggcggcagct gcaggcgcgg gcttcgccgc gggtgcggcg

37561 gccggggccg cgctcgccgc tttgggtgcg acgctcgccg tgctcgcgac ggcttgcacg

37621 gcggccgtcg ccggccggac gccgggctgg ccggtcagcg acgtgcgcag cagttccatc

37681 tgctggctca tcacgtgcga cagcagctga ttctgctccc gcagcacgcg ctcgaccgtc

37741 gagccgcctt cggccgccac ccattccgcg ggggcggccg cgagcggcgc aagccccgcc

37801 gcggacggcg tgaccgcgac cgccggcgtg gacggttccg ccgcggccac ggctacggct

37861 acggcctcgg ccccggacgg tgcggcggct gccggcaggt tgtccgcgac atattcggcg

37921 agcgcctgca ccgtcgcgag gtcttcgaag aagcggcgca tggccagctt cacgccgtac

37981 tccgcctcga tgtgccggat ggcctcgatc agcacgatcg agtcggcgcc catctcgagg

38041 aagggcagtt cgatgttgat ggtggcggga tcggcctgga tcaattcgcc gatcttgccg

38101 cgaagccatt cgagaatctc gccgctgcga ttgtgcgtcg gtgctgcggc gatgggtgat

38161 gcgcttgtct gagtcatgga cgtgtccgct ttctggaacc aggtacggct gcgttggaag

38221 ggataggacg gcaatgcgat gcgcgcgggc gcgggtgttt cggtcggggc ccagtcgaca

38281 tcgacgccgc gggcatacag gctcgacagc gtttcgatca gcgcttgctg ctcgacttgc

38341 ggccgctgca gggcaaggaa ctggatcccg gcgtccggcg cacagcacgc gcgggccagg

38401 ttgacgagca ccggcttcgg gccgatttcg accagcacgt tgaaaccggc ttcggcgagg

38461 cgctcgacgc tgctcgcgaa ctgcactggc tcccggcagt ggcggcgcca gtacgtgtcg

38521 gtgggtgcct cgtccatcac ggcgcccgtg agattcgaat agaacgggat cgccgggcgt

38581 gcgacgggca cggttttcgc cgcgagctgg aagctgtcca gcatcggctc gagcagcggc

38641 gagtgaaacg cgtgcgacgt attgagcggc acggaccgga tgtcccgcgc ggcgaacgca

38701 tcgaccagca tcgcgatgcg ctcgcgcttg ccggaaatca cgatgctcgc cgggccgttg

38761 acggccgcca ccgcgacctc gtgcggccac gcgtcgatcg cgcgctcgac cgtggcgagg

38821 tcggtgaaaa tcgccgccat ctcgccgtcg cggggcaacg cctgcatcag ccggccgcgt

38881 tcggcgatca gccgcaggcc gtcttccggc gagaagacgc cggccgcgca agccgccgcg

38941 tactcgccga cgctgtggcc catcacggcg tcgggcacca cgccgaacga cgccagcaac

39001 gtggtgagcg cgtactgcag cgagaacagg gccggctggc tgtagccggt ctggtggatg

39061 tcctcgccct gggccgacag cacttcgagc aacggcttgt cgagcaacgg atcggccacc

39121 gcgcggcaac ggtcgatggc gtctcggaac accggatacg cgtcgtacag gcggcggccc

39181 atgccggcgt attgcgagcc ctggccggtg aacaggaagg ccatcttcac gcgggggcg

39241 ggctgcgccg cgccggccgg ttccttcgcg tggaaggcgc gcagcttgtc gatggcgtcg

39301 tcgagcgacg tcaccggcca tgccagccga tgcgcgaaat gcgagcggcc ggtcgccgcc

39361 gaaaaggcca cggccgcgat gtcgagaccg ggttcggctt cgagccgccg ctgatagcgc

39421 ccggccagct cgcgcaacgc cgcgggggtc ttggccgaca gcaccagcgg atgcaccttg

39481 tgtctcgacg gcgtcgcctg ccgcgccggc gccggcgctt cttccagcac caggtgggca

-continued

39541 ttggtgccgc tcgcgccgaa cgcgctgacg ccggctcgcc gtggccgttc gccacgcggc

39601 cacgcgctcg cctcggcgca gatctcgacg ggcattgcgt cccactgcac cagcgggctc

39661 ggctggcgga aatgcaggtg ggcgggcagg cggtcgtggt tcagcgacag cacgaccttg

39721 atgacgcccg cgatgccggc ggcggactcc gtgtggccga tgttggtttt caccgagccg

39781 acgcgcagcc gccggcccgc gtcgcggcct gcgccgaaca ccgtcgccag cgcctgcaac

39841 tcgacgggat cgcccagcgg ggtgccggtg ccgtgcgctt ccacgtaatc gatggacgcg

39901 gcgggcaacc cgcccagcgc ctggcggatc acggcttcct gcgcacgacc gttcggcgcg

39961 gtaaagccgc tcgacgcgcc gtcgtggttg accgccgaac cccgcagcac ggccagcacg

40021 cgatcgcccg cggcgagcgc atcggacagg cgcttgagca ccagcgcgcc gcagccttcg

40081 ctgcgtacga agccgtccgc cgccgcgtcg aaggtcttgc agcggccgtc cggcgccagc

40141 gcccgcgtgc gcgagacggc gatggagttg tccggcgaca ggatcaggtt gacgccgccc

40201 gcgatggcga gatcgcactc gccgctgcgc aggttctggc tggcggtatg gatcgccgtg

40261 agcgacgacg agcaggcggt gtcgatcgcc atgcttggcc cctgcacgcc gagtccgtag

40321 gagatgcggc cggccgccgt gttcagcggg ttgccggtga agaaatagcc gtcgatgccg

40381 ctgccgccgc cgttgcgaag ctgcaggttc gcgtaatcgt tggtggtgat gccgacgaac

40441 acgccggtgc ggctgccctt gagactgtcg accggaatgc cggcatgctc cagcgcttcg

40501 tgactgacct cgagcaacag gcgctgctgc gggtccatcg cggccgcttc gcgcggcgtg

40561 atgcggaaga acgccggatc gaactggtcg acgtcgtcga gaaaaccgcc gaagcggctg

40621 tacatacgcc ccggcgcttc cggatcggga tcgtagtacg cgtcgacatc ccagcgctcg

40681 cgcggcactt cggagatcgc atccacgccg tcgttcagca ggttccagta ggcgtcgaga

40741 tcgtgcgcgg cgcccggaaa ccggcagctc atgccgacga tcgcgatcgg ctccggcgtg

40801 ccggcgtcgc gggcctcgat ggccggcgcg atcggccgcg gctgctgctg cggcggcacg

40861 gtctgcgcct gcgccgtgcc ggacgcctgc tccgccagga aatccgcgag ggcgttgacc

40921 gtcggatgat cgaacaacag cgcgaccgac agcgggatgc ccagcgcatt ttcgaggtgc

40981 gtgcgcacgt ccagtgccat cagcgaatcc atgcccatct cgaagaagcc gagatcgcga

41041 tccagcgtcc ccgcgtcgta gcccagcacc tgggccaccg cgcgatcgat gctgtccgcc

41101 agcagccgct ttcgctcgcg cggcgatgcg tcgctcagcg ccggcattgc cggcgcgctc

41161 ggcgcgcttt tggccacccg cacgtggtcg aggaacggct tgggtccgcg cgcctcgtag

41221 gagccctgga acagcgccag gtcgatatcg acgaccgcga cctggggcac ggcggggaga

41281 cgattcagca cgtcgagcgc gcgatccgcc gccagcgacc ggatgccgac acgccgcagc

41341 agcgcttccg cctcggggaa cgtcatgccg ccttccgccc agggccccca gttcacgctc

41401 agcgccggca ggccctggcc gcggcgatga tgcgcgagcg cgtcgaggaa acggttcgct

41461 gcactgtagt gcgcctgctc acgcgagccc cacgcggacg cgatcgacga aaacaggagg

41521 aagaaatcga gcgggaagtg ctcgctctgc tgatggagca gccacgcgcc ggcgaccttc

41581 ggttgcagga ccgcgtccag ttcgtcgcgc tcgacctgca tgatcggctt gtagccgacg

41641 atgccggccg cgtgcacgat gcctttcagc ggcacgccgt cgcgccgcag cgcggcgaag

41701 aaagcggcga ccgctgcggg gtcggcgata tcgaggcgct cgcagcgcag cgtgacgttc

41761 cgctcacgca gctcggcgat cgcccgctgg ctctcgtcgc tcgcggcccc ttgccggccg

41821 accaggatca gcgtgcccgc accgcgcgcc gccagccatc gggcggtgtg cagcccgagc

41881 gcgccgaacc cgccggtgat caggtaggcc gcgtccgggt cgaccggcag cgcggccgtt

-continued

41941 tcggctggcg cgagcgggct caggcgcgcg acatggcgcg cgccgtgccg caacgccacc

42001 tgctcctcgc ggctctcgcc gagcatctcc tgaagcagtg cctgcgtctc gttctccggc

42061 gcggccggat cgagatcgat cgcggtgccg aaccattccg gatgctcgat cattgccccg

42121 cgtgcgaggc ccgacagcgc agcctgggcg agcccggata cgtgcggcgc ttcgccggct

42181 tccaccgcgt cgcgcgtgac caccgagatc ctgggccggg tcgaaggcgt ccactcgcgc

42241 tcgctgccga ccagcgcgtg cacgagatgc agcagggcgg cggacatgcg cgtttcgccg

42301 acggcttcgt ccagcgccca taaaaagacg atgcgctggc cggaagcggc ggtttcgttc

42361 agcaagcgga cgaaatcgtc cggccgctcg ggcgcgacct gccagcccgc ttccgcgccg

42421 gtgacatagt cgatgccggg gcggaccagc gagcaggatg cgccgcgcgc gcgcagcagc

42481 gctgcaagcc gctcgccgac accgctcgca tccgcgaaga tcagccacgg ggacgcgtcg

42541 gcggcggccg gtgccgccgg catcgcggcc tgctgctccc acaccacgtg atagagcggg

42601 tgtgcgttcg acgcgacggt ctcggcggcg gcgaatgcag tcctgagcag gtccggaaac

42661 gcgttcagca tgtcctccgg gtacttgccg gacgacttga ggtgccgcaa cgctgcgtcg

42721 atgctgccgg catccatgcc gacgatcggc gacggaatct tctccaggct gaagcgctgc

42781 cgctcgaacg ggtagttcgg cagggtcgtg gcgggctggg cgggcgccgg aaacagcgcg

42841 cgccagtcga actgcgcgcc ctgcacgtac agcgccgcga gtgcgcgctc cagtgcatcg

42901 cccgcgcagg gcggcggcag ccagccgtcg gcgagcccct ccggcgggtg cgatgcgtcg

42961 gcctgatccg acgcgccagc cagttgcaac cagtactgcg ggtgcgtcac ctcgtcggtc

43021 acgtcggtgc cgagatagcc cgaaatcagg cggaccgacg gccgtgcgag cggcatgtcc

43081 cgaagcacgg cgcgcaacgc ttcggcatcc gaacgggcgg ccacgaggcg cagcgcgtcg

43141 gccacgctca cgacgcccgc cacgcaggcc gcgacatatt cgccgatgcc atggcccgac

43201 acgacggccg ggcggaggcc ccatcccttc cacagttccg cccacgcgaa ctggatcgcg

43261 aaccggcccg cgtcggtctc gagtgcgtcc agcggcaccg agcaacgcgc gaacgcgtcg

43321 cggaacagcg gttccgacgc gtggagcgcg tgcgcgacgc cggtgtccgg cacaccgaac

43381 ccgaagccca tgcgcaacgc cttgcccgtg cgcggcgcgg ccgccgacgc taccctcgcg

43441 cccgatacat aggcggcgcg aaacggatag tgactccgcc cggtggcggc ggcacggcag

43501 atcgcggcta gctcctgcgg cgtcgcgccg gcgatcgcgc gctcgtagcg tggcacgagc

43561 gccgccagcg ccgcttcgga ccttgccgac agcagcagca acgcgcgctg cgcggcgtgt

43621 gccggcgcga cgggcggttc ctcgacgatg gcgtgggcat tggtgccgct gaatccgaac

43681 gcgctcaccc cggcgatgcg cctgcgttcc ccgcgccgcc acgcgaccgg atcggccgcg

43741 acgcggatcg ggatgtcctg ccacggcgta tgcggattgg gttgcgtgaa atgcaggtgc

43801 gccggaatcc ggtcgtgctc gaacgacagc agcaccttga tcaggccggc gatgccggag

43861 gccgactcca gatgcccgat attggtcttg accgaaccga tcacgagcgg ctcgttcgcc

43921 gcgcgcccgg ggccatagac gccggccagc gcttcgacct cgatcgggtc gccgagggac

43981 gtgccggtgc cgtgggcctc gacgtaggac acgtcgccgg gcgcgaggcc ggcctggttc

44041 agtgcgcggc ggatcacccg ttcctgcgaa tcgcggctcg gcacggtcag cccgccgccc

44101 gcgccgccct ggtcgaccgc cgtgccgcgc acgatgccga gcacccggtc gccgtcggcg

44161 agcgcgtcgg cgaggcgctt gagcaccacc atgccgcacc cttcgccgcg cacatagccg

44221 tccgccgccg cgtcgaaggt cttgcagcgt ccgtccggcg acagcatgcg cgcctgcgag

44281 aagctgacca tgacctcggg cgacagcatc aggttgacgc cgcccgcgag cgccatgttg

44341 ctttcgcgcg agcgcaggct ttcgcaggcg aggtgcaggc acaccagcga agacgagcag

-continued

44401 gcggtgtcga tcgccatgct cgggccggtg aggcccagca cgaacgacag ccggcccgcg

44461 gccatgttca gcgcgctgcc cgtgccggca tagctgctcg acggcatcga cgcattggac

44521 acctggatcg cgtggtcgaa gcaggtgatg ccgacgtaca cgcccgtggc ggactgccgg

44581 aagcgttcgg gcgcgagatg ggcgttctcg agcgcctccc acgccacttc gagcaggagc

44641 cgttgttgcg gatcgaggta ggtcgcttcg cgcggcgcga tcccgaagaa cgccgcgtcg

44701 aattgatcca cgcgttcgag aaaggcgccg tggcgggtcg ccatcttgcc gggcgtggac

44761 ggatcggggt cgtagtagcg atcgatgtcc cagcgttcgc cgggcacttc ggtgacggca

44821 tcgtgcgcgc cgtcgagcaa ttgccagaac gcgtccggcg tatcgctgcg tccggggaag

44881 cggcaagcca tgccgatgac ggcgatcggc tcgttgcggt cagaacgcag cgccgcgatt

44941 tccgcgcgcc gcaggcgcag ttcgtcgagc gcggctttca gtgcatgcgt ggccttggcg

45001 ttcattgggc gccgatctcc tgggcgatca gttcggaaag gtcgtcctcg tcgaggtcgt

45061 cggatgcttc gtcgacgacc ggcgcgggga gcgacggcga cagttcgttg agcacgtact

45121 gggcgagcgt ctgcaggttc ggataggaaa agaacaacgt cgcgcgaaac ggtcttccga

45181 ataccttggt gaggcggtcc gtcagttcga gcgcgaccag cgaatccagg ccgagatcga

45241 gcagcgattg ctcgggcgcg atggcatcgg ggccggaaag gcgcaaggtt tcagccagca

45301 tcgccgcgag cgtgtcggtg atgcgctcga cccgttcgcg cggcgcgcac gcatgcagct

45361 ggcgcagcaa cgccgtctcc tgctgcgccg gctgcgcggc cggttgcgtc agctcggaaa

45421 acagcgcgga cccggcggcc ggcgcatcga cccggaacag ggtcggccag tcgatccgcg

45481 cgactccgga ctgggcgacg ccggacgcca tcagccgttc cagcgtcgcg atggccagtt

45541 cgggcggcag cgtgccgacg ccgagcgcgc cgagttgttc gtgcgcgcgc cgtccgtagt

45601 cggtggcggc gtggccgatc tccgcccacg gcccccaatt gacgctgagc cccggtttcc

45661 cctgcgcgcg ccgatgctgg gcgagcgcgt cgaggaagct gttcgccgcc gcgtagttgc

45721 cctggcccgg catggtgatc agcgcggcca tcgacgagaa caggacgaaa tggtccagcg

45781 gcaagccggc cgtcagctcg tgcagatacc acgcgccgtc ggccttgccg ctgccggcgc

45841 gatggaagaa gtcgtcgtcc tggcgtgtca gcagcgcatc gtcgagcgcg ccggcgaggt

45901 gaaagatccc tttgagcggc ggcatcgaat gcgcgatttc accgagcgcc tgcccgacgt

45961 cctcgcgacg cgacaagtcg gcgcgaatga accgtgcgtc gagcgtgcgc aggattttcc

46021 cggctgcggc ggaaggttcg ccgcgcccca gcagcacgat tttcccggcg ccgttgtcgg

46081 caagccagga cgcgagccgc aggccgagcc cgccgagccc gccggtcaca agataggtcg

46141 cgtcaccgtg gaaccggatc ggccggtggc tgacgtattc gcgattgtcg cgggcgatgc

46201 gcgcgacgta gcgctggtcg cggcgaaacg cgatcatgtc ttcacggccg ccagcctgta

46261 ccgcttgcat gatgtccgct gccgacggct gctcgggatc gaggtcgacg agcccgcccc

46321 acagcgccgc atgctccacc gcgatcgcgc ggcccaatcc ccacagcggc gcctgtgcca

46381 ccgcgatcga ttcgccatcc agaacattca tcgcacccga cgtcaccagc cacaggcgag

46441 cctgccgggc cgacggcgcg cgtgacgcaa gcgccctgac caggtgcagc acgctcgcgc

46501 tggcacgccg tctcgccgcg atgtcagagg gtgcgagatc gagactccac aggtggatga

46561 cgcccttcag cgggcggtcg gccgcgggca gttccggcgt cgcgtcggcg aagcgcagcg

46621 tgcacgtatc gccgtgggct tccagcagag ctgacagctg ggcgcccacg ccgccgcggt

46681 ccgcgagaat cagccactcg ccgtgcgccg aaccgccggt tgccgcgtcg acgttcgacg

46741 gtctccagac gcgttgataa agcagcgcgg cgaagtcgtg ccgctcgacg gcgcgcgccg

-continued

46801 cgcgaacctg ttgcaaccgc agtgcatcga tctcgatcag cagtcggcca gcaaggtcat

46861 ggacgcggat gtcgccctcc agcgcgccct gtccgatcgg cgtgcgcagc gtggcgtgac

46921 tccatgcctc ggtcgacgcc ggcggctgat ggacccgtac cgcgccgatc gagctgggca

46981 ggtacaggtc gcccgactcc agcgcgtccg gatcgatggc ggcggcgagc acgcggctgc

47041 atgcgtcgag aaaggcgggg tgtacctggt acggcgacga cgccagcgca tctgccggca

47101 ggctgatttt ccccagcgcc tcgccggtcg tgcgccagat ctgccggatc gcgtcgaaca

47161 cgccgtcgat ctgcacgccg tgctgccgaa tttcgccgtt gaagtccgcg cccgacgtcg

47221 tttcggtgca gcgggcctgc acctcggcgg catcgaatcg cgtcggcgcg gcggatcgcc

47281 ggggggcaca catttcccgg agccggcgca gctgcggaag attgccgagg atccgctcga

47341 ccggcggacc gaaatcgagc aggcaggcca cttcatccac gccgatcgac tcgagatccc

47401 gcaccagttc gacgcaggtt tccggcgtgc cgatgagccc gcgcgattgc gcgaagcgtt

47461 catagagaaa ctcgacgaac tcgtccagct cgcgtgcgcc catcgcgcgc acgtcgaccg

47521 actggccgcg actctgcgcc agcccgttca atagcccgat attgctgcgg atgtagttgc

47581 agaacggcac acgcgcctgt tcgcgcgcct gcgccgcatc gtcgccgacg aacgtatgca

47641 gcatcacgga aacggtgccg gccgccggat cgaagccatg cttcgcacgc gcctcgcggt

47701 agagcgcgat cttgtgcgcg agctggtcac gatcctggtc gagcacgtgg gtcagcaggt

47761 tggcgccggc ttcgccggca cgcacgaatg tctgcggatt gctcgcggcg gtcacccaga

47821 cgggcagctc cggctgcacc ggcgtcggat agacacgcaa ccgcaccggc ttgccgacac

47881 cgttcgtcgc atccagcgtg ccgccgcgcc acagatgctg gacggcgcgc atcgtggtca

47941 gcatgtcgtc ctgccgggtc gcatatttgt ccggggcaaa cacgaagtcg tcaggattcc

48001 atccggaggc gaacgacacg cccacgcggc cgttcgacag gttgtccacc atcgaccatt

48061 cttccgcgat ccggatcggg ttgtgcagcg ccgcgaccac gctgcccgcg accagcttca

48121 cgcgctgggt ggccgcggcg agcgcggcgt gcaggacggc gggattcggg taaagcgagc

48181 cgaattcggt gaaatggcgc tccggcaccc agacgctgga gaacccgttc gcatcggcga

48241 aacgcgcgct ctccatcacg agctggtact tgttgccgga cagcgcctct tcactgctgg

48301 cgaagaacat cagtccgaat ttcatgcgtg gctccgatcc gattcgtgaa tttcggcact

48361 cgcgcacatc tgccacgtcg cggcggcgcg ggtgtcgtcg atccggtgat agacggcaaa

48421 cgaaaacggt ccccaggacc ggcggctcag cacggtctgc acggtgtgcg attcgtgcgg

48481 atgcagcggc aacggcgcat gcagtgcgag gtccttcaac gtcgtatggc cggctgcgcc

48541 gatttccgac gttgccgaca gcgccatttc cacgaaggcg gaatagggca ggacgggcga

48601 ccccttgacg cgatgaccgt cgagaaagtt ggttgccggc gcatcgagac gcgattgcca

48661 gatccacgtg gccggcgcat gcgcgtgctg ctccatgagg cgcccgagca acggatgccg

48721 acgcgcatgt ggcctgatcc agaagccgcg ccgctcgaac gggtaggtcg gcagggcgag

48781 ccggcggtgc ggtgcacctt gctccacggc atcccagtcg atggatgcgc cgcgtacgta

48841 gagcgcggcg agcgtgtgca ggatcgcgtc ccacgcggcc gtgtgcgcgc cgatgtcgat

48901 cacgatgccg gggtgtcctg ccgcaccgct gtccggcgcc tgcggcacgc cggcccacgc

48961 ggctgcggcg cgctgcccgt cgccggtgct gctgaccgca tccggtgcga tgccgaagga

49021 catccacagt tgcgcgagcg cgcgctggaa tctcgtgaac ccggcttcgt cgggggcgag

49081 cgcgggcgcg ccggatgcgt cggactgccg ctgcatcagc gcgtcgaaag cggggctggc

49141 cgcgcgcaat tgccgaaccg cgtcggcgct ggcgccgtcg tcggcgcaaa agtggaacgt

49201 caccgcgggc ggtgtttcgg caggctcccc ggacgaaacg gaatcaagtt gcgcacgcaa

-continued

49261 cgaatcgcga ctcggtgcga cgatggccgc gcgctgcgtg aagtgggtgc gcccggtatt

49321 ggccgtgaac gcgacatccc gcacaccggc ctcgggatgg gcgtcgagat aggccgcata

49381 ggacgcagcg agcgcttgca acgcgtccgg cgtgcgcgcg gagagcgtca cgacgcgcgc

49441 cgcgggtgca accggttcgg cttcgatctc cgggagcccg ggtgcttctg acaggatcag

49501 gtgcgcgttg gtgccgccga agccgaacga gctcaccccct gccaggcgcg gcccgtgttc

49561 cgaatgccag ggcgtgacct gccgaggaat ccggaagggc gtgccgtcga gcgcgatttg

49621 cggattgatc gaccggaaat ggaggttcgg cggaatcgcg cgatggtgta gtgcaagggc

49681 ggtcttgatc aggctggcga tgcccgcggc cgattccagg tggccgatgt tggtcttgac

49741 cgacccgatc cagcagagat cgtccgggcg gcgggattcg ttcaggacgg ccgccagcga

49801 gttcaactcg atcgggtcgc cgagcggcgt gcccgtcccg tgcgtctcga cgaagccgat

49861 gtcctgcgcg cgtacaccgg catcgcgcag cgcgccgtga atcacggcct gctgggccgg

49921 gccattcggc gcggtcaggc cgttgctgcg cccatcctga ttcaccgcgg agccgcggat

49981 cacggcgaac acggtgtcgc cgttctcgag cgcatcgtcg agccgcttga gcagcaccat

50041 gcccacgcct tcgccgcgaa cataaccgtt cgctgccgcg tcgaacgcct tgcatcggcc

50101 gtccggcgac agcatgcccg cttgcgtgaa ggacgcgctc aattgcggcg ccagaatcag

50161 gttgaccccg ccggccagcg ccgcatcgga ctcgccgcgc tgcagcgcgc ggcacgcctg

50221 gtgaaccgcg acgagcgagg acgaacacgc ggtgtcgacc gcccagctcg ggccgcgcaa

50281 atcgagcgcg taggaaatgc ggttggcggc gacgctgagc gcattgcccg tcgcgacata

50341 agggccgacg tccgcgactt cgtcctgcgc cagacggatg tagtccgaat tgctgatgcc

50401 gacgatgacc gcggtgcgtc cgccggcgag gctgcggggt gcgatccccg catgctcgag

50461 cgtctcccag gccacctcca gcagcaggcg ctgttgcgga tccatcgatt cggcttcgcg

50521 ggcgctgatg ccgaagaaag ccgcatcgaa ttgatcgacc tgatccagca gtccggcgag

50581 cggaaggtcg gccgcgcgct gcgtcgccgc accgaccgcg tcccggccct ccagcagaag

50641 ctgccagaat gcgtcgggat tgccggcgcc ggggaagcgg catcccatcc cgacgatcgc

50701 gatatccgcg cgtgcttcgg ccgagcccgg cgcctggtcc ggcatggcac tcccggtgcc

50761 gctcaaatgg cgcgccagca gggaaatact cggaaaatca tagacgacgg tcggggaaac

50821 cggccgcccg agccagtcct gcagctcgcc cgagagcatg atggcgtcct tcgaatcgag

50881 cccgtggacg ctgaacggcg cgtcggggtc gatcttgccg gaagcgattc ccgacagacg

50941 cgagacacgc tcgatgcacc attgcaccag cgcttgcgtg tcgcgtggct cggcagtctg

51001 cgggggggct ggcggcgcgg agaacgcacg ccgccattcg cccgcgatcg cgagcccctg

51061 ttcatcgagg aatgcctgcc tgatccggct ccgctggatt tttccgctgg acgtgcgcag

51121 gatcgtggca ggtttcaaca ggactgccgc atacagatcg acgtcgtgca cttcggcgag

51181 cgtgtgccgg atctcggcgg ccacggcttc cgcgtccagc gtgttgagcg cttcccggcg

51241 cacttcacag gcgacgacga cccgctccac gttatcgacg tggatcgaga aagccgccga

51301 tgcgttcggc gccagcgcgg ggtggctgcc ctccgcggat tgctcgagat cctgcgggta

51361 gtgattgcgg ccggcgacga tgatgaggtc tttcaagcgg ccggtaacga agagatcctc

51421 gccatcgacg aagccgagat cgcccgtgcg caggtaacgc gcgtcatcgc cgtccagctt

51481 cgcgcggaag gtgcgctccg tttcgtcgat acggttccag tagccgacgc cgacactcgg

51541 gccggtcagc cagatttcgc cgatccggcc gggcgcgcag cgctcaccgg tatccggatt

51601 cacgatgcgc acgcggtgct cagcccaggt ccggccgcat gagaccagcg cgtggcgctt

-continued

51661 gccggagtcg tttctcgtcg ccacgccttg tgccagcgcg tcggcatcgt agtccgccac

51721 gcgcggcagc gagcgtgccg gctggccgga gatgaacaag gtcgcctcgg ccatcccgta

51781 gacggggcgc atggtgtgcg cgtggaagcc gcacgcggcg aatgcgcgcg aaaaacgcgc

51841 caccgactcc gcgcgcaccg gttccgcgcc gttgaatgca acccgccagc tgctcaggtc

51901 cagctgcgcg cgcgcttcat cggcgatttt gcgagcacac aggtcatacg cgaaatccgg

51961 cgcggcacaa tgcgtgccgc gatacttcgt gatggcctgc agccagcgca cgggtttctg

52021 cacgaatgcc gcgggcgcca tcagcaccga cagcacgccg agatagatcg gcagcaacac

52081 cttcccgaag aaacccatgt cgtgaaacac cgggagccag ctgacgaaca ccgtcgacgc

52141 atcggcatcg ctcgcctcgg cgatgaccgc catattgctc aggatgttcg cgtggctgat

52201 catcacgcct ttgggcgtac cggtggagcc tgacgtgtat tgcagaagcg ccagcgtctg

52261 cggcgtgatg tccggtgcgc gccattgttc ggccggggcg tcgaagcgct ggtccgtcgc

52321 caggatcttc agttccagcg tgtcggaata accgtccgcg tgatgcgcga tgccgtcgag

52381 cgtcgcggcg tccgtcagcg cgacgaccgg cgtggcgtcg gcgacgatgg ccttgagacg

52441 atcggcggga cgatgcctgc gcggtggata cgcgggtacg ccgatcaggc cggcgtacag

52501 gcatcccacc catgcgcaga tgaattccag cccgggcgga taaaccagaa ggacgcgatc

52561 gcccggttga gcgatggctt gcagcctggc ggcgatgccg cgagcccgct tgtccaggtc

52621 gccgaacgtg aggcgggtca gctccgcttc gccgttctcg agaaaaatga atgcggtctt

52681 ctccggttcg accttgccgc gaaacaacaa aatttctgta acagtcctga attttgtatc

52741 gggaagcatg ctcaaccttc gttgtcttct aaacgttgaa tatctcagga ccggttgtgg

52801 cgatcccgcc aagcgtgctt catcggacgg tatcgaaatt agagcattgc tctaatccgg

52861 cgtctgcccc gtaatccaag gacacggcgt ttcgcgcact ggatcaatac ggcttgtcat

52921 tgatgtgcac gctcgctaac gatcggcgat tccttcgatg tcgggcgtgt acgggtccag

52981 cagcgacacg acgaccttgc gctcgccttc gaacgggttg cggccatgcg cgaagcgcat

53041 gttgtcgacc agcaggacgt cgcctcgttg ccacggaaac gtgatcgcgc attcgcggaa

53101 cgcgtggcgg atctgctcga ggtcggcgag atcgaacgga ctcccgtcgc catggcaggc

53161 attgcgcgga atgcgatcct cgccgaacag gctgacgatc gaactggcga gcgatgcttc

53221 caggttcgag atatggaaca gatgggcctg attgaagaac acccgctcgc cggtgaccgg

53281 atggtaggcc acgccctggt tgatctgcgc ggtgcgcaac gtgtcgtcgt cgagccattc

53341 gagcgcgatg ccgttatccg cgcagaaggc tgcaacctgg ttgcggtcgc tggtctggaa

53401 cacggtctcc cacggaatgt cgacgtgccg ccggtagtgc ctgacatagc ggacctgtct

53461 cgcctcgaag tgatccagga tgcgcggtcc gatcctgcgg ctcacctccc gcatgtcggc

53521 aatcggcgtt tcgccgccgg tcgcggccgg cgtcaggcaa cagaaggcca ctcgcagcgg

53581 ccagcttcgt tgatacgcgt tttcgcaatg aagggcgatc gtctcgctcg gcggatactc

53641 ggttgcggtg aagatgccgt tgccgatcga ggtgcgcggc gtggaacggt aaacgtagtc

53701 ggactgatgg gccgaaatcg cgcgagcaaa cgcttcgaag ccgcccacgg atgaaacgtc

53761 gaagccacga aacaggagta cgccgtgttc cagaagccgg gattcgagtg ccgcccggtt

53821 gtcgttcacc gcctgcgcca gatcgcgtcc attcgataca ggctccagca gccacggcgt

53881 gcttccctcg gcaagcaact tgcgttccgt catgcccagc atcgtcaata gtcctttcct

53941 gtacgtggat cacggcgaag ccgaacgggt cggcccgcgt ggtcgcgccg cggtgcggct

54001 atgcgcggca ggccgtttcc acggcatgct cgaagcgatt gagaatgtcg tggatgtccg

54061 cttccgaaac gatcagcggc ggcaggaacc ggagcaccgc gccgttgcgg ccgccggttt

-continued

54121 cgacgatgag cccgtttcgc aggcagttct gcttgatggc tcttgcccgt tccgtgtggg

54181 gcgggccggc tcggccgtgg gtgccgggca cgacgacttc ggcgccgatc atcaggccgc

54241 ggccgcgtat ctggcccagg caggggaagc gttcggcaag ctcctcgagg ccggcaacca

54301 ggagtttgcc gaccctgtcc gcgtgcgccg acagatcttc tctctcgacg atgcgcatgg

54361 tcgacaagcc ggccaccatc gcaatctggt tgcctcgaaa ggtgccggca tgcgcgccgg

54421 gcggccaggt gtccaggcgc tcgtcataga ccaccaccga taacggatag ccgccgccga

54481 atgccttcga cagcaccagt acgtccggcc ggatgccgga atgttcgatc gcgaacaggg

54541 cgccggtgcg accgagtccg gtctgcactt catcgacgat caacgggatt tcatgccgca

54601 gcgtcagctc gcgcaactcg atcaaccagg tgtcgggagc ggggatgcag cctccttcgc

54661 cttgcacgac ttcgacgatg atggccgccg gcttcgtgat cccgctctcg ggatcggaca

54721 ggacggtccg gatgtagttg atgctgagtt gatcggtcgc cgagccgtcg gtgccgaacg

54781 ggcagcgaaa ggcgtaggga tagggcagga aatgaacgtc gcgtccgttg ccgccggccg

54841 acttgggcgt gaggtttccc gacgcggcga gtgcgccgga cgtcatgccg tggtaggcgc

54901 cgtggaacgc catgatcgtc ggccggccgg tatagtgccg ggtcagcttg atcgccgctt

54961 cgacgccatc cgcgccactg gggctgcaaa actggatctt gccggattcg gcgatcttcc

55021 cgggcagaag cgagaaaagc tgctcgacga atgcgtgctt ggccggcgtc gccagatcga

55081 gtgcctgttg catctgatcg gacgacagaa accgcatcac ggcttcattg acttccgggt

55141 gattgtgtcc gagcgcgagc gtgcccgcat tcgacaggca gtcgatgtat tcctgcccgt

55201 cggcgtcgcg tacgcgtatg cctttcgcat gggtaaacag ccgcgggaag gaggttgcgt

55261 aggttcgcgc gttcgattcg acctgcttca gatactcgag tttttccatg cgcgcagatc

55321 cggcttgcaa ggcggattga tggacactgg cgcacgagaa tcgcttcatc ctggccaatg

55381 gtgtttaacg gtacgaccgg attggagcat ggtctccgta tcgcgtctgt cacgtaaaaa

55441 tgggacatcg gccatgcgac gtcaccacgt catgccgttg ccttccgatc atcgaagcgg

55501 tttccgggcg cgacgtcagg cagcgagggt cgagcagaaa taatcgatgg tccgttggag

55561 acccgcttcg agcccgatcg tcggctccca gtcgaggtgg gtgcgtgcga ggctgatgtc

55621 ggggcaacgt tgcgtcggat cgtccttcgg cagcggacgg aatacgagcc gcgacttcga

55681 gccggtcagg cgcaagatga tctgcgccag ttcgctgacc gcgatctcgt gcggattgcc

55741 gaggttgatc gggccggtga gctccgcggg cgtggccatc atccggatca aaccgtcgac

55801 catgtcgtcg acatagcaga atgcccgggt ctggctgccg tcgccataca gcgtgatgtc

55861 ctcgccccgc agcgcctgca cgatgaagtt ggacacgacg cggccgtcgt tgggatgcat

55921 gcgcggcccg tacgtgttga agatgcgtac caccttgatt cgtacgttct gctggcggtg

55981 atagtcgaag aacagggtct ccgcgcaacg cttgccttcg tcgtagcagg cgcgcggccc

56041 gagcgggttg acgttgcccc ggtaactctc cggttgcgga tgcacatcgg ggtcgccgta

56101 cacctcgctc gtcgacgttt gcagaacgcg tgcatgcgtg cgcttggcga gcccgagcat

56161 gttgatcgcg cccatcacac tggtcttggt ggtctgcacg ggatcgaatt gatagtggat

56221 gggcgaagcc gggcaggcga ggttgtagat ctcgtccacc tccacgtaca acggaaaagt

56281 gacgtcgtgg cgcagcgcct cgaagctcgg gttgccgagc agcgtagcca cgttctgctt

56341 cgtgccggtg aaatagttgt cgacgcacaa tacgtcgtga ccgagttcga cgagacgctc

56401 gcaaagatgc gaaccgagga aacccgcgcc acccgttacg aggattcgct ttcgattacg

56461 ttgcacaatt gcactccaag tatcgcgcgc tgggaagcga cgcggcctcc ccgcacgctt

-continued

```
56521 gaccggcccg cggcaccggc aggggagcgg atcaggcgcg cgggcgtttg cattcgacga

56581 tcacggcgcc ggccggcacg ccgatcgcga ggatcggccc gtcatgcctg cagtgcgctc

56641 gacgcggcgt gctccgggcg ccgcatgcgc gccgcgatga tgccggccat cgttcgcatt

56701 tcgtttctca aaaagaaatg atccccttcg atgacgtgaa aatcgaagcg cccggtcgtc

56761 gcggcgcccc agcctgcaac ggcatcgacg gggatctctt tatccgcccg gcccgcgaac

56821 gcggtgatgt ccaccgccag cctgggcccg ggcacgggcc ggtggttttc gatcatcgtg

56881 aaatccgcac gcagcgccgg catcagcagc gccatcagtt cgctgttgtc cagcaccgcc

56941 ttcggtgtgc cgcccatttc gcgcagcgca tcgatgaagg cgcggtcgtc cagcgcctgc

57001 atgcgccgat cgtggcgctc cttgcccggt gcggcacgcg cgctcacgaa cagatgccgc

57061 aggttcggtc gtgcgtgggc gggaagccgc agggccagtt cggccgcaat ggccgcgccc

57121 atgctgtgtc cgagcagtgc gaagggacga tcgaagcagt cgtccaggtc gcacagcaac

57181 gtgtcgacca gcgtcgccat gtctcggacg gcaggctcgg acaggcggct gcctcggcct

57241 gcaagttcat gacggcacac ttcgatgccc ggtaacgacg cttgcagcgt gcgatagacg

57301 gcggccgagc cgcccgcata gggaaaacag atcagacgca tgcgggcggg tactcgagcg

57361 gctcatctgc tgccggcgcg caggcgatgg cgctgtggaa attcatgtgt tcggcgtttt

57421 tcaccattca ggttccagat ccggttgggc gtgagttaaa cacgaggctg cgtggatgta

57481 tgtcgtagga agaggggacg cgttgtcggc catgtcgaag cggttcgtct ctgaatggat

57541 cccggcgcgg acacggtatc ggcgaaaaca gatgcgcggg aaatcgcgac gcatctgagt

57601 gtgtcgaacg atgcgcttcg tctttagaat gggcagcgag catggcgagc catcagaatt

57661 gcggcatccg atggtgccgc cgcgctaccc gataagttgg agacatacta tgcaacaccg

57721 tcagaaagcc gtcccgaccc agcaagtcgc gaacgagcgc gtgatcgtca ccgaatggcg

57781 attcgcgccc ggcgccgaga ccggctggca tgttcaccgg catgactatg tcgtggtgcc

57841 gcaaacggac ggtcagcttc tcctcgaaac cgcacaaggc aaccgcgagt cgcaattgca

57901 cgccgggcgc agctatgcgg ggctgaaggg cgtcgagcat aacgtcgtca acgcgacgga

57961 ccacgaagtg gtgttcgtcg aagtcgagat tctctaaggg gcgtcaggcc ccgcgagcaa

58021 ggccacgaca gggagcagca ggatgaaaat gaccgacatc ccgtttggca cgaccgactg

58081 gcgcaccgtt gaaccgaccg a
```

REFERENCES

(1) Fischbach, M. A.; Walsh, C. T. *Chem. Rev.* 2006, 106, 3468-3496.

(2) Koglin, A.; Löhr, F.; Bernhard, F.; Rogov, V. V.; Frueh, D. P.; Stricter, E. R.; Mofid, M. R.; Güntert, P.; Wagner, G.; Walsh. C. T.; Marahiel, M. A.; Dötsch, V. *Nature* 2008, 454, 907-911.

(3) Koglin, A.; Mofid, M. R.; Löhr, F.; Schäfer. B.; Rogov, V. V.; Blum, M.-M.; Mittag, T.; Marahiel, M. A.; Bernhard, F.; Dötsch, V. *Science* 2006, 312, 273-276.

(4) Kohli, R. M.; Takagi, J.; Walsh, C. T. *PNAS* 2002, 99, 1247-1252.

(5) Lautru, S.; Challis, G. L. *Microbiology* 2004, 150, 1629-1636.

(6) Samel, S. A.; Wagner, B.; Marahiel, M. A.; Essen, L.-O. *J. Mol. Biol.* 2006, 359, 876-889.

(7) Walsh, C. T. *Science* 2004, 303, 1805-1810.

(8) White, C. J.; Yudin, A. K. *Nat. Chem.* 2011, 3, 509-524.

(9) Yeh, E.; Kohli. R. M.; Bruner. S. D.: Walsh, C. T. *Chembiochem* 2004, 5, 1290-1293.

(10) Boddy, C. N. *Chem. Biol.* 2004, 11, 1599-1600.

(11) Boguslavsky, V.; Hruby, V. J.; O'Brien. D. F.: Misicka, A.; Lipkowski, A. W. *J. Pept. Res.* 2003, 61, 287-297.

(12) Fernandez-Lopez, S.; Kim, H. S.; Choi, E. C.; Delgado, M.; Granja, J. R.; Khasanov, A.; Kraehenbuehl. K.; Long, G.: Weinberger, D. A.; Wilcoxen, K. M.; Ghadiri, M. R. *Nature* 2001, 412, 452-455.

(13) Fridkin, G.; Gilon, C. *J. Pept. Res.* 2002, 60, 104-111.

(14) Jelokhani-Niaraki, M.; Hodges, R. S.; Meissner, J. E.; Hassenstein, U. E.; Wheaton. L. *Biophys. J.* 2008, 95, 3306-3321.

(15) Jelokhani-Niaraki, M.; Prenner, E. J.; Kondejewski, L. H.; Kay, C. M.; McElhaney, R. N.; Hodges, R. S. *J. Pept. Res.* 2001, 58, 293-306.

(16) Kohli, R. M.; Walsh. C. T.; Burkart. M. D. *Nature* 2002, 418, 658-661.

(17) Rayan, A.; Senderowitz, H.; Goldblum, A. *J. Mol. Graph. Model.* 2004, 22, 319-333.

(18) Schwarzer. D.; Mootz, H. D.: Marahiel, M. A., *Chem. Biol.* 2001, 8, 997-1010.

(19) Ellis, D.; Gosai, J.; Emrick, C.; Heintz, R.; Romans, L.; Gordon, D.; Lu, S.-E.; Austin. F.; Smith, L. *Antimicrob. Agents Ch.* 2012, 56, 765-769.

(20) Sieber, S. A.; Marahiel, M. A. *J. Bacteriol.* 2003, 185, 7036-7043.
(21) Tseng, C. C.; Bruner, S. D.; Kohli, R. M.; Marahici, M. A.; Walsh, C. T.; Sieber, S. A. *Biochemistry* 2002, 41, 13350-13359.
(22) Gu, G.; Smith, L.; Liu, A.; Lu, S.-E. *Appl. Environ. Microbiol.* 2011, 77, 6189-6198.
(23) Gu, G.; Smith. L.; Wang, N.; Wang. H.; Lu. S.-E. *Biochem. Bioph. Res. Co.* 2009, 380, 328-332.
(24) Gu, G.; Wang, N.; Chancy, N.; Smith, L.; Lu, S.-E. *FEMS Microbiol. Lett.* 2009, 297, 54-60.
(25) Lu. S.-E.; Novak. J.; Austin, F. W.; Gu, G.; Ellis, D.; Kirk. M.; Wilson-Stanford, S.; Tonelli. M.; Smith, L. *Biochemistry* 2009, 48, 8312-8321.
(26) Tan, W.; Cooley, J.; Austin. F.; Lu, S.-E.; Smith, L.; Pruett, S. *Int. J. Toxicol.* 2012, 31, 326-336.
(27) Heikkinen, S.; Toikka, M. M.; Karhunen, P. T.; Kilpeläinen, I. A. *JACS* 2003, 125, 4362-4367.
(28) Rai, R. K.; Tripathi, P.; Sinha, N. *Anal. Chem.* 2009, 81, 10232-10238.
(29) Baysal, C.; Meirovitch, H. *Biopolymers* 1999, 50, 329-344.
(30) Bonmatin, J.-M.; Laprévote. O.; Peypoux, F. *Com. Chem. High T. Scr.* 2003, 6, 541-556.
(31) Liao. G.; Shi, T.; Xie. J. *J. Cell. Biochem.* 2012, 113, 735-741.
(32) Vilhena, C.; Bettencourt. A. *Mini Rev. Med. Chem.* 2012, 12, 202-209.
(33) Alexeyev, M. F. *Biotechniques* 1995, 18, 52.
(34) Prentki, P.; Karch, F.; Iida, S.; Meyer, J. *Gene* 1981, 14, 289-299.
(35) Lu, S.-E.; Scholz-Schroeder, B. K.; Gross, D. C. *MPMI* 2002, 15, 43-53.
(36) Wüthrich, K., *NMR of Proteins and Nucleic Acids*; Wiley. New York, 1986.
(37) Delaglio, F.; Grzesiek, S.; Vuister, G. W.; Zhu, G.; Pfeifer, J.; Bax, A. *J. Biomol. NMR* 1995, 6, 277-293.
(38) Johnson, B. A.; Blevins, R. A. *J. Biomol. NMR* 1994, 4, 603-614.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 23

<210> SEQ ID NO 1
<211> LENGTH: 21
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 1

cgccacccgt tacgaggatt c 21

<210> SEQ ID NO 2
<211> LENGTH: 20
<212> TYPE: DNA
<213> ORGANISM: Artificial sequence
<220> FEATURE:
<223> OTHER INFORMATION: primer

<400> SEQUENCE: 2

acgcgtcccc tcttcctacg 20

<210> SEQ ID NO 3
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans MS14

<400> SEQUENCE: 3

Met Arg Leu Ile Cys Phe Pro Tyr Ala Gly Gly Ser Ala Ala Val Tyr
1 5 10 15

Arg Thr Leu Gln Ala Ser Leu Pro Gly Ile Glu Val Cys Arg His Glu
20 25 30

Leu Ala Gly Arg Gly Ser Arg Leu Ser Glu Pro Ala Val Arg Asp Met
35 40 45

Ala Thr Leu Val Asp Thr Leu Leu Cys Asp Leu Asp Asp Cys Phe Asp
50 55 60

Arg Pro Phe Ala Leu Leu Gly His Ser Met Gly Ala Ala Ile Ala Ala
65 70 75 80

Glu Leu Ala Leu Arg Leu Pro Ala His Ala Arg Pro Asn Leu Arg His
85 90 95

Leu Phe Val Ser Ala Arg Ala Ala Pro Gly Lys Glu Arg His Asp Arg

-continued

```
            100                 105                 110

Arg Met Gln Ala Leu Asp Asp Arg Ala Phe Ile Asp Ala Leu Arg Glu
        115                 120                 125

Met Gly Gly Thr Pro Lys Ala Val Leu Asp Asn Ser Glu Leu Met Ala
    130                 135                 140

Leu Leu Met Pro Ala Leu Arg Ala Asp Phe Thr Met Ile Glu Asn His
145                 150                 155                 160

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

Gly Arg Ala Asp Lys Glu Ile Pro Val Asp Ala Val Ala Gly Trp Gly
            180                 185                 190

Ala Ala Thr Thr Gly Arg Phe Asp Phe His Val Ile Glu Gly Asp His
        195                 200                 205

Phe Phe Leu Arg Asn Glu Met Arg Thr Met Ala Gly Ile Ile Ala Ala
    210                 215                 220

Arg Met Arg Arg Pro Glu His Ala Ala Ser Ser Ala Leu Gln Ala
225                 230                 235


<210> SEQ ID NO 4
<211> LENGTH: 3154
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans MS14

<400> SEQUENCE: 4

Met Gln Asp Asn Asn Val Leu Val Thr Asp Arg Glu Ser Leu Ser Arg
1               5                   10                  15

Val Ala Gly Val Tyr Gly Ile Ala Ala Tyr Ala Pro Ser Gln Gln Pro
            20                  25                  30

Gly Arg Pro Leu Thr Arg Ser Val Arg Leu Thr Pro Ala Ser Leu Asp
        35                  40                  45

Leu Leu Arg Arg Ile Gly Asp Gly Glu Leu Ala Glu Phe Ala Val Ala
    50                  55                  60

Ala Ala Gly Ile Ala Phe Leu Leu Trp Lys Tyr Phe Arg Ile Pro Val
65                  70                  75                  80

Thr Val Leu Gly Thr Pro Gly Leu Ala Gly His Pro Ser Ala Arg Ala
                85                  90                  95

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

Asp Tyr Leu Ser Arg Val Ala Gly Ile Val Glu Asp Ser Tyr Ala Glu
        115                 120                 125

Pro Arg Phe Pro Leu Glu Thr Leu Val Arg Asn Glu Lys Asp Met Ala
    130                 135                 140

Leu Ala Gln Leu Thr Lys Val Ala Leu Ala Asp Asp Arg Val His His
145                 150                 155                 160

Ala Pro Thr Gly Arg Asp Asp Asp Leu Gln Leu His Leu Arg Leu Ala
                165                 170                 175

Arg Gly Glu Ile Glu Leu Arg Tyr Ser Gly Ala Ile Glu Pro Phe Ile
            180                 185                 190

Ile Asp Gly Phe Ala Gly Ser Leu Ala Ala Val Leu Glu Ala Phe Glu
        195                 200                 205

His Leu Asp Gly Ala Val Gly Asp Ile Glu Ala Ala Pro Pro Glu Gln
    210                 215                 220

Gly Pro Leu Leu Ala Ala Phe Asn Glu Thr Ala Thr Ala Gly Pro Ser
225                 230                 235                 240
```

-continued

```
His Pro Thr Val Val Ala Met Phe Glu Ala Gln Val Ala Arg Thr Pro
               245                 250                 255

Thr Ala Pro Ala Leu Val Thr Asp Ser Ser Leu Met Thr Tyr Ala Asp
            260                 265                 270

Leu Asn Ala Arg Ala Asn Ser Leu Ala His His Leu Arg Glu His His
        275                 280                 285

Gly Val Gly Pro Glu Ser Leu Val Gly Ile Met Leu Asp Arg Ser Glu
    290                 295                 300

Trp Met Ile Val Ala Ile Leu Gly Ile Leu Lys Ala Gly Ala Ala Phe
305                 310                 315                 320

Val Pro Leu Asp Pro Ala Tyr Pro Ala Glu Arg Ile Asn His Ile Leu
                325                 330                 335

Gly Asp Thr Gly Leu Ser Leu Leu Val Thr Gln Ser Ser Gln Leu Ala
            340                 345                 350

Gln Trp Tyr Glu Phe Ser Gly Val Thr Leu Leu Leu Asp Gln Glu Leu
        355                 360                 365

Pro Gly Trp Gln Pro Leu Pro Asp Asn Pro Pro His Arg Ala Glu Pro
    370                 375                 380

Ala His Leu Ala Tyr Val Leu Tyr Thr Ser Gly Ser Thr Gly Lys Pro
385                 390                 395                 400

Lys Gly Cys Leu Leu Glu His Arg Asn Leu Ala His Tyr Ile Ala Trp
                405                 410                 415

Ala Ala Gly Tyr Tyr Phe Pro Glu Ser Thr Thr Gly Ser Phe Gly Leu
            420                 425                 430

Tyr Ser Ser Leu Cys Phe Asp Phe Thr Leu Thr Asn Ile Phe Cys Pro
        435                 440                 445

Leu Val Arg Gly Lys Thr Leu Arg Ile Tyr Pro Gln Ser Glu Ser Ile
    450                 455                 460

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

Leu Lys Leu Thr Pro Thr His Ile His Leu Leu Glu Tyr Met Asn Leu
                485                 490                 495

Ala Arg Ser Gly Val Arg Lys Val Ile Val Gly Gly Glu Glu Leu Thr
            500                 505                 510

Pro Gln His Ile Ala Thr Leu Arg Lys Ile Asp Pro Ala Ile Glu Ile
        515                 520                 525

Tyr Asn Glu Tyr Gly Pro Thr Glu Ala Thr Val Gly Cys Ile Val Glu
    530                 535                 540

Arg Val Glu Asp Ala Pro Pro Thr Val Leu Ile Gly Arg Pro Ile Ala
545                 550                 555                 560

Asp Thr Arg Val Tyr Met Leu Asp Asp Ala Leu Arg Pro Val Pro Leu
                565                 570                 575

Gly Val Pro Gly Glu Ile Cys Leu Ala Gly Ala Gly Leu Ala Arg Gly
            580                 585                 590

Tyr His Gln Arg Pro Asp Val Thr Ala Ala Lys Phe Val Glu His Pro
        595                 600                 605

Phe Pro Gly Glu Ala Arg Ile Tyr Arg Thr Gly Asp Ile Gly Arg Trp
    610                 615                 620

Leu Pro Asp Gly Arg Ile Gln Cys Tyr Gly Arg Val Asp His Gln Val
625                 630                 635                 640

Lys Ile Arg Gly His Arg Val Glu Leu Gly Glu Ile Glu Ala Ala Ile
                645                 650                 655

Ala Ala His Glu Asp Val Val Gly Ala Ala Val Met Leu Arg Glu Ser
```

-continued

```
           660                 665                 670

Ala His Gly Val Arg Lys Leu Ala Ala Tyr Val Lys Gly Ala Ala Ser
        675                 680                 685

Leu Ser Val Pro Asn Leu Arg Ala Tyr Leu Ala Gly Lys Leu Pro Asp
    690                 695                 700

Tyr Met Val Pro Ser Asp Ile Ile Pro Ile Ala Glu Phe Pro Leu Asn
705                 710                 715                 720

Ala Asn Gly Lys Leu Asp Arg Pro Ala Leu Leu Ala Leu Glu Pro Ala
                725                 730                 735

Ala Ala Pro Glu Glu Ala Pro Leu Asp Ala Thr Pro Ile Gln Arg Glu
            740                 745                 750

Leu Val Arg Ile Trp Arg Asp Val Leu Asp Asn Pro Ala Val Asp Leu
        755                 760                 765

Ala Gly Arg Phe Phe Asp Tyr Gly Gly Asp Ser Leu Gln Ala Met Gln
    770                 775                 780

Leu Val Ser Arg Ile Trp Ser Ser Phe Ser Val Glu Ile Gly Ile Asp
785                 790                 795                 800

Ala Ile Phe Glu Leu Gln Thr Ile Ser Ala Val Ser Asp Leu Ile Glu
                805                 810                 815

Ala Ser Ser Pro His Pro Gly Ser Thr Ala Gly Ala Ile Pro Pro Arg
            820                 825                 830

Ser Arg Ala Asn Asp Leu Pro Leu Ser Phe Pro Gln Gln Arg Leu Trp
        835                 840                 845

Phe Leu Ala Gln Leu Glu Gly Pro Ser Ala Thr Tyr Asn Ile Ser Ser
    850                 855                 860

Ala Leu Arg Phe Glu Gly Glu Leu Asp Val Ala Arg Leu Arg Phe Ala
865                 870                 875                 880

Val Ser Glu Ile Ser Arg Arg His Glu Ile Leu Arg Thr Thr Phe Pro
                885                 890                 895

Ala Val Asp Gly Arg Gly Val Gln Arg Ile Ala Pro Pro Ala Pro Val
            900                 905                 910

Ala Leu Asp Val Val Asp Val Ala Ser Glu Ser Asp Thr Leu Ala Leu
        915                 920                 925

Leu Ala Glu Glu Ala Asp Arg Pro Phe Asp Leu Ala Ala Gly Pro Leu
    930                 935                 940

Tyr Arg Val Val Leu Tyr Arg Val His Glu Arg Leu His Val Phe Gly
945                 950                 955                 960

Ile Val Met His His Ile Val Ser Asp Ala Trp Ser Ser Gly Ile Leu
                965                 970                 975

Ile Gly Glu Leu Ala Ala Leu Tyr Ala Gly Glu Ser Leu Pro Glu Leu
            980                 985                 990

Ala Val Gln Tyr Ala Asp Tyr Ala  Val Trp Gln His Glu  Arg Leu Ala
        995                 1000                1005

Ser Ala  Asp Thr His Arg Glu  Leu Ala Leu Leu Ser  Ala Ala Leu
    1010                1015                1020

Ala Asp  Ala Pro Asp Leu Ile  Glu Leu Pro Thr Asp  Arg Pro Arg
    1025                1030                1035

Pro Ala  Val Gln Gln Phe Arg  Gly Ala Val Leu Pro  Phe Gln Leu
    1040                1045                1050

Ser Ala  Glu Arg Ala Asp Gly  Leu Arg Ala Ile Ala  Arg Ala Ser
    1055                1060                1065

Gly Thr  Ser Thr Phe Met Val  Val Leu Ala Ala Tyr  Ala Leu Leu
    1070                1075                1080
```

-continued

```
Leu Ser  Arg Tyr Ser Asn Gln  Gln Asp Leu Val Ile  Gly Ser Pro
    1085                1090                1095

Ile Ala  Asn Arg Arg Ser Ser  Met Thr Glu Pro Leu  Ile Gly Phe
    1100                1105                1110

Phe Ala  Asn Met Leu Ala Leu  Arg Val Asp Leu Ser  Gly Asn Pro
    1115                1120                1125

Thr Phe  Gly Asp Leu Leu Ala  Arg Val Lys Arg Val  Ala Leu Asp
    1130                1135                1140

Gly Tyr  Ser Arg Gln Glu Ile  Pro Phe Glu Gln Val  Val Asp Ser
    1145                1150                1155

Leu Glu  Leu Glu Arg Asn Leu  Gly Arg Thr Pro Val  Phe Gln Val
    1160                1165                1170

Val Phe  Ala Tyr Glu Lys Ala  Gln Pro Arg Ala Val  Ser Phe Pro
    1175                1180                1185

Gly Leu  Val Ala Thr Pro Val  Ala Val Glu Thr His  Thr Ala Lys
    1190                1195                1200

Phe Asp  Leu Thr Leu His Val  Gln Asp Ala Asp Asp  Gly Leu Ala
    1205                1210                1215

Gly Ser  Leu Glu Tyr Asn Leu  Asp Leu Phe Asp Ala  Ala Thr Ile
    1220                1225                1230

Asp Arg  Met Ala Glu His Phe  Arg Thr Leu Val Asp  Ala Val Ile
    1235                1240                1245

Ala Asp  Pro Asp Arg Pro Leu  Gly Ala Leu Ser Leu  Ser Asn Asp
    1250                1255                1260

Ala Glu  Arg Asn Leu Leu Thr  Val Glu Trp Asn Arg  Thr Asp Thr
    1265                1270                1275

Asp Phe  Gly Glu Asp Ala Ala  Gln Pro Leu His Arg  Leu Phe Glu
    1280                1285                1290

Gln Gln  Val Glu Arg Thr Pro  Asp Ala Val Ala Ile  Val Phe Asp
    1295                1300                1305

Asp Thr  Ala Leu Thr Tyr Ala  Glu Leu Asn Leu Arg  Ala Asn Arg
    1310                1315                1320

Leu Ala  His His Leu Val Ala  Leu Gly Val Gly Pro  Asp Ser Leu
    1325                1330                1335

Val Gly  Val Ala Met Glu Arg  Ser Leu Asp Met Ser  Val Ala Leu
    1340                1345                1350

Leu Ala  Ile Leu Lys Ala Gly  Gly Ala Tyr Val Pro  Val Asp Pro
    1355                1360                1365

Asp Tyr  Pro Ala Glu Arg Val  Arg Phe Met Ile Asp  His Ala Gln
    1370                1375                1380

Leu Arg  Trp Leu Leu Thr Gln  Gln His Leu His Asp  Ala Leu Pro
    1385                1390                1395

Asp Thr  Asp Ala His Val Ile  Val Val Asp Arg Asp  Ser Leu Asp
    1400                1405                1410

Leu Asp  Ala Ala Ala Thr Ser  Asn Pro Ala Pro Ala  Leu Asn Gly
    1415                1420                1425

Asp Asn  Leu Ala Tyr Met Ile  Tyr Thr Ser Gly Ser  Thr Gly Arg
    1430                1435                1440

Pro Lys  Gly Ala Leu Asn Thr  His Arg Ala Ile Thr  Asn Arg Ile
    1445                1450                1455

Leu Trp  Met Gln His Ala Tyr  Ala Leu Asp Ala Asp  Asp Ala Val
    1460                1465                1470
```

-continued

```
Leu Gln  Lys Thr Pro Phe Ser  Phe Asp Val Ser Val  Trp Glu Leu
    1475                 1480                 1485

Phe Trp  Pro Leu Val Thr Gly  Ala Arg Leu Val Phe  Ala Arg Pro
    1490                 1495                 1500

Gly Gly  Gln Arg Glu Thr Asp  Tyr Leu Val Glu Leu  Ile Glu Arg
    1505                 1510                 1515

Glu Arg  Ile Thr Thr Ile His  Phe Val Pro Ser Met  Leu Arg Ala
    1520                 1525                 1530

Phe Leu  Asp His Pro Asp Leu  Asp Ala His Cys Ala  Ser Leu Arg
    1535                 1540                 1545

Arg Val  Val Cys Ser Gly Glu  Ala Leu Pro His Asp  Leu Gln Gln
    1550                 1555                 1560

Arg Cys  Leu Glu Arg Leu Asp  Val Lys Leu Tyr Asn  Leu Tyr Gly
    1565                 1570                 1575

Pro Thr  Glu Ala Ala Val Asp  Val Thr Ala Trp Glu  Cys Arg Arg
    1580                 1585                 1590

Asp Asp  Pro His Arg Ile Val  Pro Ile Gly Arg Pro  Ile Ala Asn
    1595                 1600                 1605

Thr Arg  Leu Tyr Ile Val Asp  Ala Gln Met Gln Pro  Thr Pro Ile
    1610                 1615                 1620

Gly Val  Ala Gly Glu Leu Leu  Ile Gly Gly Thr Pro  Val Gly Arg
    1625                 1630                 1635

Gly Tyr  His Gly Glu Pro Glu  Leu Ser Ala Glu Lys  Phe Ile Ala
    1640                 1645                 1650

Asp Pro  Phe Ser Ala Asp Pro  Leu Ala Arg Leu Tyr  Arg Thr Gly
    1655                 1660                 1665

Asp Leu  Ala Arg Tyr Arg Pro  Asp Gly Asn Ile Glu  Phe Leu Gly
    1670                 1675                 1680

Arg Ile  Asp His Gln Ile Lys  Leu Arg Gly Leu Arg  Ile Glu Pro
    1685                 1690                 1695

Gly Glu  Ile Glu Ala Ala Leu  Arg Ala His Pro Ser  Val Asp Asp
    1700                 1705                 1710

Cys Val  Val Ile Ala Lys Thr  Glu Gly Ala Arg Thr  Phe Leu Ile
    1715                 1720                 1725

Ala Tyr  Val Ala Thr Ala Ala  Pro Asp Ile Ala Asp  Leu Arg Gly
    1730                 1735                 1740

Tyr Leu  Gly Gly Lys Leu Ala  Asp Tyr Met Val Pro  Ser Gln Phe
    1745                 1750                 1755

Phe Ala  Leu Glu Ser Leu Pro  Met Leu Pro Asn Gly  Lys Ile Asn
    1760                 1765                 1770

Arg Lys  Ala Leu Pro Leu Pro  Ala Asp Arg Gly Asp  Ala Ala Gln
    1775                 1780                 1785

Pro His  Ala Pro Ala Val Thr  Pro Arg Glu Ile Leu  Leu Ala Ser
    1790                 1795                 1800

Ile Cys  Ile Asp Val Leu Gln  Leu Pro Ser Val Gly  Ile His Asp
    1805                 1810                 1815

Asn Phe  Phe Glu Leu Gly Gly  Asp Ser Ile Leu Ser  Ile Gln Val
    1820                 1825                 1830

Ile Ala  Arg Ala Asn Gln Ala  Gly Leu Arg Val Thr  Ala Lys Gln
    1835                 1840                 1845

Leu Phe  Gln Tyr Gln Thr Ile  Ala Gln Leu Ala Ala  Ala Pro Glu
    1850                 1855                 1860

Glu Arg  Ala Ala Cys Ala Pro  Thr Leu Ser Pro Leu  Gly Asp Ala
```

-continued

```
    1865                1870                1875

Pro Leu  Thr Pro Val Gln His  Trp Phe Phe Glu Gln  Glu Ile Asp
    1880                1885                1890

Ala Pro  Ser His Tyr Asn Gln  Thr Val Leu Ile Gln  Val Pro Ala
    1895                1900                1905

Asp Ile  Asp Ala Ser Arg Leu  Ala Asp Ala Phe Arg  Gln Val Tyr
    1910                1915                1920

Glu His  His Asp Ala Leu Arg  Leu Arg Phe Ser His  Asp Ala Gly
    1925                1930                1935

Arg Trp  Thr Gln Gln Val Val  Ala Gly Gly Glu Met  Pro Ala Leu
    1940                1945                1950

Phe Ala  Lys Gln Val Ile Ala  Asp Asp Ala Gly Glu  Arg Leu Ala
    1955                1960                1965

Ala Met  Arg Ala Ala Ala Ala  Asp Ala Glu Arg Gly  Ile Asp Ile
    1970                1975                1980

Thr His  Gly Pro Leu Leu Ala  Ala Arg Leu Phe Cys  Leu Ala Asp
    1985                1990                1995

Glu Pro  Leu Ala Arg Leu Phe  Val Ser Ile His His  Leu Ala Val
    2000                2005                2010

Asp Gly  Val Ser Trp Arg Val  Leu Leu Glu Asp Leu  His Ala Ala
    2015                2020                2025

Tyr His  Gly Gln Pro Leu Pro  Gly Lys Thr Thr Ser  Phe Arg Glu
    2030                2035                2040

Trp Ala  Leu His Leu Gln Gln  Leu Ala Arg Ser Pro  Ala Ile Gly
    2045                2050                2055

Asp Glu  Ala Arg Leu Trp Gln  Ala Leu Leu Ala Gln  Pro Val Glu
    2060                2065                2070

Pro Met  Pro Val Asp Tyr Pro  Gly Thr Gly Ala Ala  Asn Asn Ala
    2075                2080                2085

Val Asp  Asp Ala Ser Ser Val  Ser Phe Glu Leu Gly  Glu Ala Asp
    2090                2095                2100

Thr Thr  Ala Leu Leu Arg Arg  Leu Pro Arg Ala Tyr  Asp Thr Arg
    2105                2110                2115

Ile Asn  Asp Val Leu Leu Val  Ala Leu Ala Gln Ala  Cys Ser Met
    2120                2125                2130

Val Thr  Gly Asn Thr Arg Thr  Arg Ile Asp Leu Glu  Ser His Gly
    2135                2140                2145

Arg His  Val Ser Asp Ala Pro  Leu Asp Leu Thr Arg  Thr Val Gly
    2150                2155                2160

Trp Phe  Thr Ser Ile Tyr Pro  Val Val Leu Asp Ala  Asp Ala Met
    2165                2170                2175

His Ala  Pro Glu Gln Ala Leu  Arg Ala Ala Arg Gln  Gln Leu Arg
    2180                2185                2190

Arg Ile  Pro Ala Asp Gly Leu  Gly Tyr Ser Leu Leu  Arg Tyr Gln
    2195                2200                2205

Ser Pro  Asp Ala Ala Val Arg  Asp Ser Leu Ala Ala  Leu Pro Lys
    2210                2215                2220

Ala Asp  Ile Leu Phe Asn Tyr  His Gly Gln Leu Asp  Thr Val Leu
    2225                2230                2235

Arg Gln  Ser Asp Gly Trp Arg  Pro Ala Ala Glu Asp  Leu Gly Ser
    2240                2245                2250

Leu Arg  Ala Gly Arg Ser Gln  Arg Thr His Ala Phe  Glu Ile Val
    2255                2260                2265
```

-continued

```
Ala Ala  Val Ala Asp Gly Lys  Leu Gln Val Asp Trp  Arg Tyr Gly
    2270                 2275                 2280

Glu Arg  Leu His Arg Arg Gln  Thr Val Glu Asn Leu  Ala Ala His
    2285                 2290                 2295

Phe Arg  Asp Arg Leu Leu Asp  Phe Ala Ala Ser Val  Pro Asp Thr
    2300                 2305                 2310

Ala Ala  Asp Asp Ile Glu Asp  Ser Tyr Pro Leu Ser  Ser Leu Gln
    2315                 2320                 2325

Gln Gly  Ile Leu Phe His Ser  Leu Tyr Asp Leu Asp  Pro Ala Ala
    2330                 2335                 2340

Tyr Phe  Gln Gln Phe Ser Phe  Val Val Ser Gly Pro  Leu Gln Val
    2345                 2350                 2355

Pro Ala  Leu Arg Gln Ala Trp  Ala Asn Ala Leu Ala  Arg His Ala
    2360                 2365                 2370

Val Leu  Arg Thr Ala Phe Ala  Trp Ala Asp Arg Asp  His Pro Val
    2375                 2380                 2385

Gln Thr  Val Arg His Thr Val  Asp Leu Pro Trp Thr  Phe Leu Asp
    2390                 2395                 2400

Trp Arg  His Arg Asp Ala Ser  Arg Arg Ala Gln Asp  Phe Asp Ala
    2405                 2410                 2415

Phe Leu  Ala Asp Asp Arg Arg  Arg Gly Phe Asp Leu  Gln Arg Ala
    2420                 2425                 2430

Pro Leu  Phe Arg Cys Thr Leu  Ile Gln Glu Thr Asp  Thr Arg His
    2435                 2440                 2445

Arg Phe  Cys Trp Ser Ala His  His Ile Ile Leu Asp  Gly Trp Ser
    2450                 2455                 2460

Thr Ala  Thr Leu Met Lys Glu  Val Phe Asp Asp Tyr  Leu Ser Leu
    2465                 2470                 2475

Ala Arg  Thr Gly Met Pro Ala  Val Ala Ala Ser Ala  Pro Gly Tyr
    2480                 2485                 2490

Arg Ala  Tyr Ile Asp Trp Leu  Ala Arg His Pro Arg  Ser Ala Asp
    2495                 2500                 2505

Glu Thr  Trp Trp Arg Ala Glu  Leu Ala Gly Phe Lys  Ala Ala Thr
    2510                 2515                 2520

Pro Val  Ala Ala Ser Pro Ala  Arg Gln Ala Thr Gly  Asp Ala Pro
    2525                 2530                 2535

Arg Gln  Asp Lys Arg Arg Thr  Gln Gln Phe Leu Leu  Asp Glu Ala
    2540                 2545                 2550

Leu Ala  Ala Arg Leu Gln Thr  Leu Thr Arg Thr His  Arg Val Thr
    2555                 2560                 2565

Leu Asn  Val Leu Ile Arg Ala  Val Trp Ala Leu Val  Leu Arg Arg
    2570                 2575                 2580

His Ala  Gly Thr Asp Asp Val  Val Phe Gly Val Thr  Val Ser Gly
    2585                 2590                 2595

Arg Pro  Pro Met Leu Asp Gly  Val Glu Ser Ile Val  Gly Leu Phe
    2600                 2605                 2610

Ile Asn  Thr Leu Pro Leu Arg  Leu Arg Ile Ala Pro  Glu Arg Pro
    2615                 2620                 2625

Phe Ile  Glu Trp Leu Ala Glu  Val His Ala Ala Gln  Thr Ala Met
    2630                 2635                 2640

Glu Pro  His Ser Tyr Ser Ser  Leu Val Asp Ile Gln  Ser Trp Ser
    2645                 2650                 2655
```

-continued

```
Glu Leu  Pro Ala Gly Asp Ser  Leu Phe Asp Ser Leu  Leu Val Phe
    2660                 2665                 2670

Glu Asn  Phe Pro Val Ala Ala  Ala Pro Asp Leu Gly  Pro Asp Asp
    2675                 2680                 2685

Ile Glu  Ile Leu Asp Thr Arg  Ala Phe Ala Glu Ser  Asn Tyr Pro
    2690                 2695                 2700

Leu Thr  Leu Thr Val His Pro  Asn Glu Arg Ile Gly  Phe His Ile
    2705                 2710                 2715

Ser His  Asp Ala His Arg Ile  Ala Pro Glu Val Val  Arg Gln Met
    2720                 2725                 2730

Leu Asp  Thr Leu Arg Thr Leu  Leu Glu Arg Phe Ala  Glu Asn Pro
    2735                 2740                 2745

Gly Gln  Leu Thr Gly Gln Leu  Ala Asp Pro Pro Ala  Ala Asp Gly
    2750                 2755                 2760

Arg Pro  Ser Ala Pro Arg Ser  Gly Ala Gly Pro Ala  Ile Glu Ala
    2765                 2770                 2775

Ala Ala  Gly Ala Ala Ala Ala  Ala Arg Ala Val Ala  His Ala Ala
    2780                 2785                 2790

Asp Glu  Ser Thr Leu Leu Glu  Ile Trp Arg Arg Ile  Phe Lys Arg
    2795                 2800                 2805

Asp Asp  Ile Ala Val Ser Asp  Asn Tyr Phe Asp Leu  Gly Gly His
    2810                 2815                 2820

Ser Ile  Ile Ala Ile Gln Leu  Met Ala His Val Glu  Lys Ala Phe
    2825                 2830                 2835

Asp Arg  Arg Leu Pro Ile Ser  Cys Leu Phe Glu Asn  Pro Thr Ile
    2840                 2845                 2850

Glu Lys  Leu Ala Ala Ala Leu  Ala Ala Lys Glu Pro  Ser Ala Pro
    2855                 2860                 2865

Ala Gly  Gly Leu Val Pro Ile  Arg Asp Gly Gly Pro  Ala Ala Pro
    2870                 2875                 2880

Leu Phe  Leu Leu Pro Gly Ala  Gly Gly Asn Val Val  Tyr Phe Arg
    2885                 2890                 2895

Pro Leu  Ala Asn His Leu Ser  Gly Ala His Ala Ile  His Gly Leu
    2900                 2905                 2910

Glu Ala  Leu Gly Leu Asp Gly  Ala Cys Glu Pro Leu  Thr Arg Val
    2915                 2920                 2925

Glu Asp  Ile Ala Ala Arg His  Ile Glu Arg Ile Trp  Pro Leu Val
    2930                 2935                 2940

Gly Ala  Gly Pro Tyr Tyr Leu  Ala Gly His Ser Phe  Gly Ala His
    2945                 2950                 2955

Val Ala  Leu Glu Met Ser Arg  Gln Leu Val Ala Lys  Gly Ala Asp
    2960                 2965                 2970

Val Lys  Leu Leu Ala Ile Phe  Asp Ala Ser Ala Pro  Ile Asp Ser
    2975                 2980                 2985

Ser Ala  Ala Thr Tyr Trp Gln  Asp Trp Asp Asp Thr  Glu Trp Leu
    2990                 2995                 3000

Val Ala  Ile Ala His Glu Ile  Gly Thr Phe Leu Gly  Thr Asp Leu
    3005                 3010                 3015

Gln Val  Thr Arg Ala Asp Leu  Val His Leu Asp Pro  Asp Gly Gln
    3020                 3025                 3030

Ala Gly  Leu Ile Leu Glu Arg  Ile Gly Asp Arg Gly  Ser Trp Phe
    3035                 3040                 3045

Ala Asp  Ala Gly Ser Asp Arg  Leu Arg Ala Tyr Leu  Arg Val Tyr
```

-continued

```
    3050                3055                3060

Gln Ala  Asn Phe Lys Ser His  Tyr Ala Pro His Ala  Thr Pro Leu
    3065                3070                3075

Pro Val  Pro Ile Ala Leu Phe  Arg Ser Thr Glu Arg  Asp Pro Gly
    3080                3085                3090

Asp Tyr  Ala Pro Ser Ser Glu  Ile Ala Gln Leu Arg  Leu Asp Ala
    3095                3100                3105

Thr Trp  Gly Trp Ser Arg Phe  Ser Ala His Pro Val  Ala Val Thr
    3110                3115                3120

Asp Val  Pro Gly Asp His Leu  Thr Met Leu Leu Asp  Pro His Ala
    3125                3130                3135

Gly Val  Leu Ala Ala His Val  Asn Ser Phe Leu Glu  Lys Thr Pro
    3140                3145                3150

Ser


<210> SEQ ID NO 5
<211> LENGTH: 391
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(391)
<223> OTHER INFORMATION: putative FAD linked oxidase domain protein

<400> SEQUENCE: 5

Met Ser His Asp Phe Arg Asp Glu Pro Ala Pro Arg Arg Ala Phe Leu
1               5                   10                  15

Ala Asp Met Ala Lys Leu Ala Ala Ala Gly Ile Val Thr Gly Trp Thr
            20                  25                  30

Pro Leu Tyr Gln Val Ala Ala His Ala Arg Thr Ala Gly Glu Thr Pro
        35                  40                  45

Pro Gly Phe Pro Ala Asp Ile Gln Leu Tyr Lys Gln Ala Phe Leu Asn
    50                  55                  60

Trp Ser Gly Glu Ile Ala Val Gln Asp Val Trp Thr Ala Ala Pro Arg
65                  70                  75                  80

Ser Ala Asp Asp Val Val Ala Thr Val Asn Trp Ala Arg Ala Asn Gly
                85                  90                  95

Tyr Arg Ile Arg Pro Arg Gly Tyr Thr His Asn Trp Ser Pro Leu Thr
            100                 105                 110

Leu Asp Pro Gly Ala Gly Ala Ala Asn Leu Val Leu Leu Asp Thr Thr
        115                 120                 125

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

Val Thr Ala Gln Thr Gly Val Ser Leu Glu Ser Leu Leu Ala Thr Leu
145                 150                 155                 160

Glu Gln Val Gly Leu Gly Val Ile Ala Ala Pro Ala Pro Gly Asp Ile
                165                 170                 175

Thr Leu Gly Gly Ala Leu Ala Ile Asp Ala His Gly Thr Ala Val Pro
            180                 185                 190

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

Asn Leu Val Val Ala Leu Thr Ala Val Val Phe Asp Pro Ala Arg Gln
    210                 215                 220

Gln Tyr Val Leu Arg Arg Phe Glu Arg Ser Asp Pro Glu Ile Gly Ala
225                 230                 235                 240
```

-continued

```
Phe Leu Ala His Ile Gly Arg Ala Leu Val Val Glu Val Thr Leu Thr
                245                 250                 255

Ala Gly Pro Asn Gln Arg Leu Arg Cys Gln Ser Tyr Val Asp Ile Pro
            260                 265                 270

Ala Ser Glu Leu Phe Ala Ala Pro Gly Thr Thr Gly Arg Thr Ile Ala
        275                 280                 285

Ser Phe Leu Asp Gly Ser Gly Arg Val Glu Ala Ile Trp Phe Pro Phe
    290                 295                 300

Thr Thr Lys Pro Trp Leu Lys Val Trp Thr Pro Thr Pro Ser Lys Pro
305                 310                 315                 320

Phe Leu Ser Arg Ala Val Thr Gln Pro Tyr Asn Tyr Pro Phe Ser Asp
                325                 330                 335

Ser Ile Ser Gln Ser Ile Ser Asp Leu Val Lys Arg Ile Val Ile Gly
            340                 345                 350

Gly Glu Gly Ala Leu Thr Pro Leu Phe Gly Gln Thr Gln Leu Ala Ile
        355                 360                 365

Thr Thr Ala Gly Leu Ala Leu Thr Leu Ser Gly Asp Ile Trp Gly Trp
    370                 375                 380

Ser Arg Thr Val Leu Gln Glu
385                 390


<210> SEQ ID NO 6
<211> LENGTH: 273
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(273)
<223> OTHER INFORMATION: putative LuxR-type regulator

<400> SEQUENCE: 6

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

Phe Ala Ser Asp Met His Ala Leu Leu Val Glu Ser Ile Pro Leu Thr
            20                  25                  30

Ile Thr Arg Met Thr Glu Trp Thr Leu Asp Glu Pro Ala Gly Glu Val
        35                  40                  45

Val Arg Val Gln Ser Leu Gly Ala Asp Gly Ala Pro Gly Asp Asp Gly
    50                  55                  60

Arg Gly Ala Pro Ala Ala His Gly Glu Arg Glu Pro Ala Ala His Pro
65                  70                  75                  80

Pro Leu Asn Arg Ile Leu Ala Ala Cys Asp Arg Gln Leu Ile His Ile
                85                  90                  95

Asn Pro Leu Met Arg Arg Gly Asn Gly Gly Glu Val Ala Pro Ser Arg
            100                 105                 110

Gly Pro Gly Gly Gly Phe Gln Cys His Leu Val Ser Gly Lys Ala Asn
        115                 120                 125

Arg Arg Tyr Val Ile Ser Leu His Arg Thr Ala Ser His Arg Asp Phe
    130                 135                 140

Ser Leu Arg Glu Met Ser Phe Leu Lys Asn Phe Ala Asp Thr Leu Leu
145                 150                 155                 160

Pro Leu Val Glu Trp His Ala Ser Thr Cys Arg His Gly Glu Arg Glu
                165                 170                 175

Gly Ala Thr Ala Pro Gly Ala Thr Ala Gly Met Pro Gly Val Glu Ala
            180                 185                 190

Leu Arg His Glu Phe Glu Ser Arg Leu Ala Arg Ala Arg Val Val Leu
```

-continued

```
        195                 200                 205

Ser Ala Arg Glu Asn Glu Val Cys Leu Gly Leu Leu Ala Gly Lys Met
    210                 215                 220

Leu Arg Glu Met Ala Gly Glu Leu Gly Val Lys Glu Ser Thr Ile Glu
225                 230                 235                 240

Thr Tyr Ile Lys Arg Ala Ala Val Lys Leu Gly Ile Ser Gly Arg His
                245                 250                 255

Gly Leu Thr Lys Trp Met Ile Asp Asp Ser Val Pro Cys Ala Ser Ala
            260                 265                 270

Ala
```

<210> SEQ ID NO 7
<211> LENGTH: 296
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(296)
<223> OTHER INFORMATION: putative LuxR-type regulator

<400> SEQUENCE: 7

```
Met Glu Phe Ser Arg Leu Phe Ala His Val Gly Glu Ala Ile Ser Ser
1               5                   10                  15

Ser Gly Ser Arg Arg Phe Pro Arg Met Met Tyr Asn Leu Ile Ala Ala
            20                  25                  30

Ala Val Pro Val Asp Glu Ile Arg Ile Ser Glu Leu Ala Ile Asp Asp
        35                  40                  45

Val Pro Asp Gly Pro Pro Glu Val Arg Ser Leu Gly Ala Val Gly Ala
    50                  55                  60

Ala Leu Ala Lys Thr Gly Ala Ala Ala Val Cys Cys Gly Pro Gln Met
65                  70                  75                  80

Pro Pro Arg Pro Gly Thr Ser Pro Leu His Val Asp Asp Thr Leu Ala
                85                  90                  95

Gly His Gly Pro Ile His Ala Gln Leu Asp Arg Phe Ile Leu Met Gln
            100                 105                 110

Ala Ala Ile Val Ser Pro Arg Tyr Ala Gln Phe His Leu Val Thr Arg
        115                 120                 125

Lys Arg Gly His Cys Tyr Val Ile Ser Leu Tyr Arg Thr Cys Thr Phe
    130                 135                 140

Asp Asp Phe Ser Pro Gln Glu Arg Thr Phe Leu Lys Glu Leu Ser His
145                 150                 155                 160

Val Leu Phe Pro Ile Val Glu Ser His Val Ala Ala Leu Asp Ser Ala
                165                 170                 175

Pro Pro Ala Ala Arg Val Thr Thr Ala Ala Pro Pro Ala Thr Gln Ser
            180                 185                 190

Gly Arg Glu Arg Val Ala Arg Arg Phe Ala Asp Arg Leu Gln Gln Ala
        195                 200                 205

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

Ala Gly Asp Thr Val Pro Ala Ile Ala Met Arg Phe Ala Leu Arg Glu
225                 230                 235                 240

Ser Thr Val Glu Thr Tyr Leu Lys Arg Ala Ala Val Lys Leu Gly Phe
                245                 250                 255

Ser Gly Arg His Gly Leu Thr Arg Trp Met Leu Asp Glu Thr Ala Gly
            260                 265                 270
```

-continued

```
Ala Ala Thr Glu Ala Ala Gly Gly Asp Met Arg Ser Met Arg Arg Asp
        275                 280                 285

Tyr Ala Ser Pro Arg Leu Gly Thr
    290                 295


<210> SEQ ID NO 8
<211> LENGTH: 567
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(567)
<223> OTHER INFORMATION: putative cyclic peptide transporter

<400> SEQUENCE: 8

Met Asp Ser Ala Gln Ser Lys Ser Pro Pro Trp His Ser Ala Ala Thr
1               5                   10                  15

Leu Met Trp Arg Ser His Pro Trp Leu Thr Leu Gly Thr Val Val Thr
            20                  25                  30

Gly Leu Val Ser Gly Ile Ala Ser Ile Ala Gly Val Gly Leu Ile Ser
        35                  40                  45

Thr Val Leu His Asp Gln Asp Asp Arg Gln Thr Leu Leu Leu Leu Phe
    50                  55                  60

Ile Ala Val Asn Val Val Ala Val Val Cys Arg Ser Cys Ala Ala Val
65                  70                  75                  80

Met Pro Ser Tyr Ala Cys Met Lys Val Met Thr Arg Leu Arg Val Asn
                85                  90                  95

Leu Cys Lys Arg Ile Leu Ala Thr Pro Leu Asp Glu Ile Asp Arg Arg
            100                 105                 110

Gly Ala Pro Asn Val Leu Thr Met Leu Thr Gln Asp Ile Pro Gln Leu
        115                 120                 125

Ser Gln Thr Leu Leu Thr Ile Pro Thr Ile Ile Val Gln Ser Val Val
    130                 135                 140

Leu Ile Cys Ser Ile Ala Tyr Leu Ala Tyr Leu Ser Trp Ile Val Phe
145                 150                 155                 160

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

Phe Tyr Arg Lys Ala Val Asn Phe Thr Glu Arg Val Arg Asp Glu Phe
            180                 185                 190

Val Gln Phe Asn Glu Tyr Thr His Gly Leu Val Phe Gly Ile Lys Glu
        195                 200                 205

Leu Lys Leu Asn Arg Ala Arg Arg Arg Trp Phe Thr Arg Ala Ala Ile
    210                 215                 220

Glu Leu Ser Ser Lys Arg Val Ala Gly Phe Asn Tyr Ile Glu Arg Phe
225                 230                 235                 240

Trp Phe Met Ser Gly Asp Ser Ile Gly Gln Ile Thr Val Ala Val Leu
                245                 250                 255

Leu Gly Cys Leu Leu Phe Gly Val Pro Ser Leu Gly Val Val Asp Pro
            260                 265                 270

Ser Val Leu Thr Ala Ser Ile Leu Ala Val Leu Tyr Met Met Gly Pro
        275                 280                 285

Leu Thr Met Leu Ile Asn Val Leu Pro Val Val Ala Glu Gly Lys Thr
    290                 295                 300

Ala Leu Ala Arg Leu Ala Glu Phe Gly Phe Leu Ile Asp Asp Thr Gln
305                 310                 315                 320

Ala Ser His Glu Glu Pro Arg Pro Ala Gly Asn Val Glu Thr Leu Ser
```

-continued

```
                325                 330                 335

Ala Lys Ser Trp Lys Val Ile Glu Leu Lys Asp Val Thr Met Asn Tyr
            340                 345                 350

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

Thr Ile His Ala Gly Glu Leu Val Tyr Val Ile Gly Gly Asn Gly Ser
    370                 375                 380

Gly Lys Ser Thr Leu Gly Lys Val Leu Ser Gly Leu Tyr Ala Pro Thr
385                 390                 395                 400

Gly Gly Thr Ile Ser Leu Asp Gly Lys Val Val Asp Asp Ala Ala Arg
                405                 410                 415

Glu Arg Tyr Arg Asn Leu Phe Ser Ala Val Phe Thr Asp Phe His Leu
            420                 425                 430

Phe Asn Arg Ile Ile Gly Pro Asp Arg Gly Asn Glu Ser Ile Glu Leu
        435                 440                 445

Ala Arg Lys Tyr Leu Ala Thr Leu Lys Leu Ala Asp Lys Ile Glu Ile
    450                 455                 460

Ser Gly Arg Thr Tyr Ser Thr Thr Arg Ala Leu Ser Thr Gly Gln Arg
465                 470                 475                 480

Lys Arg Leu Ala Leu Leu Cys Ala Tyr Ile Glu Asp Arg Pro Ile Tyr
                485                 490                 495

Ile Leu Asp Glu Trp Ala Ala Asp Gln Asp Pro Val Phe Lys Arg Phe
            500                 505                 510

Ser Tyr Glu Val Leu Val Pro Asp Leu Lys Ser Arg Gly Lys Cys Val
        515                 520                 525

Val Ile Ile Thr His Asp Asp Gln Tyr Phe Lys Leu Ala Asp Arg Val
    530                 535                 540

Ile Arg Leu Asp Ser Gly Arg Ile Phe Ser Asp Thr Ala Met Cys Ala
545                 550                 555                 560

Val Arg Ala Glu Ala Ala Gly
                565


<210> SEQ ID NO 9
<211> LENGTH: 160
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(160)
<223> OTHER INFORMATION: hypothetical protein

<400> SEQUENCE: 9

Met Gln Leu Thr Thr Val Asp Leu Glu Ala Ala Phe Val Lys Ala Ala
1                   5                   10                  15

Leu Asp Ala Leu His Arg Asp Cys Lys Leu Gly Asp Ala Ile Ser Leu
            20                  25                  30

Ala Tyr Gly Lys Cys Glu Ser Thr Ala Gly Val Ile Asp Leu Ile Phe
        35                  40                  45

Pro Leu Ile Thr Lys Lys Leu Arg Ile Asp Tyr Ile Leu Met Tyr Ser
    50                  55                  60

Ile Glu Ser Asn Pro Arg Thr Leu Leu Gln Phe Leu Arg Gln Ile Glu
65                  70                  75                  80

Ser Gly Leu Ala Arg Ser Glu Asp Trp Thr Ala Ala Ser Val Glu Ala
                85                  90                  95

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

-continued

```
Ala Gln Arg Leu Leu Lys Cys Cys Ile Leu Phe Ser Asp Ser Pro Leu
        115                 120                 125

Gly Ile Val Glu Ser Ile Thr Phe Leu Gly Lys His Glu Thr Ser Ser
    130                 135                 140

Arg Leu Arg Ser Ala Ala Ser Asn Val Glu Leu Ser His Leu Ile Asn
145                 150                 155                 160


<210> SEQ ID NO 10
<211> LENGTH: 218
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(218)
<223> OTHER INFORMATION: putative glycosyl transferase

<400> SEQUENCE: 10

Met Lys Ser Thr Pro Thr Ile Asp Asn Thr Phe Ala Arg Lys Val Cys
1               5                   10                  15

Ile Asn Leu Asp Arg Arg Pro Asp Arg Trp Glu Ala Met Gln Arg Lys
            20                  25                  30

Phe Ala Glu Gln Asn Ile Leu Thr Val Glu Arg Leu Pro Ala Val Asp
        35                  40                  45

Ala Arg Leu Val Ser Val Pro Glu Ser Leu Ser His Met Arg Ala Gln
    50                  55                  60

Asp Tyr Gly Cys Thr Met Ser His Leu Ala Ala Val Lys Gln Ala Lys
65                  70                  75                  80

Ala Ala Gly Ala Arg Glu Val Leu Ile Phe Glu Asp Asp Ala Phe Phe
                85                  90                  95

Asp Ala Asp Phe Ala Ala Arg Phe Pro Glu Phe Ile Ala Gln Val Pro
            100                 105                 110

Asp Asp Trp His Met Leu Phe Leu Gly Ala Tyr His Phe Thr Pro Pro
        115                 120                 125

Ile Pro Val Ala Pro Asn Ile Val Lys Ala Val Glu Thr Leu Thr Ala
    130                 135                 140

His Ala Tyr Val Val Arg Asn Ser Leu Tyr Asp Ala Phe Ile Ala Ile
145                 150                 155                 160

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

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

Ser Gly Tyr Ser Asp Ile Met Asp Glu Val Met Pro Glu Lys Pro Leu
        195                 200                 205

Thr Tyr Ser Met Pro Ile Pro Asp Gly Trp
    210                 215


<210> SEQ ID NO 11
<211> LENGTH: 3164
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(3164)
<223> OTHER INFORMATION: putative nonribosomal peptide synthetase

<400> SEQUENCE: 11

Met Gln Asp Asn Asn Val Leu Val Thr Asp His Arg Tyr Ala Ala Thr
1               5                   10                  15
```

-continued

```
Ala Arg Phe Trp Arg Glu Ser Leu Ser Arg Val Ala Gly Val Tyr Gly
            20                  25                  30

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

Ser Val Arg Leu Thr Pro Ala Ser Leu Asp Leu Leu Arg Arg Ile Gly
    50                  55                  60

Asp Gly Glu Leu Ala Glu Phe Ala Val Ala Ala Ala Gly Ile Ala Phe
65                  70                  75                  80

Leu Leu Trp Lys Tyr Phe Arg Ile Pro Val Thr Val Leu Gly Thr Pro
                85                  90                  95

Gly Leu Ala Gly His Pro Ser Ala Arg Ala Ala Ile Val Pro Leu Ile
            100                 105                 110

Ile Glu Val Arg Pro Asp Glu Arg Ile Glu Asp Tyr Leu Ser Arg Val
        115                 120                 125

Ala Gly Ile Val Glu Asp Ser Tyr Ala Glu Pro Arg Phe Pro Leu Glu
    130                 135                 140

Thr Leu Val Arg Asn Glu Lys Asp Met Ala Leu Ala Gln Leu Thr Lys
145                 150                 155                 160

Val Ala Leu Ala Asp Asp Arg Val His His Ala Pro Thr Gly Arg Asp
                165                 170                 175

Asp Asp Leu Gln Leu His Leu Arg Leu Ala Arg Gly Glu Ile Glu Leu
            180                 185                 190

Arg Tyr Ser Gly Ala Ile Glu Pro Phe Ile Ile Asp Gly Phe Ala Gly
        195                 200                 205

Ser Leu Ala Ala Val Leu Glu Ala Phe Glu His Leu Asp Gly Ala Val
    210                 215                 220

Gly Asp Ile Glu Ala Ala Pro Pro Glu Gln Gly Pro Leu Leu Ala Ala
225                 230                 235                 240

Phe Asn Glu Thr Ala Thr Ala Gly Pro Ser His Pro Thr Val Val Ala
                245                 250                 255

Met Phe Glu Ala Gln Val Ala Arg Thr Pro Thr Ala Pro Ala Leu Val
            260                 265                 270

Thr Asp Ser Ser Leu Met Thr Tyr Ala Asp Leu Asn Ala Arg Ala Asn
        275                 280                 285

Ser Leu Ala His His Leu Arg Glu His His Gly Val Gly Pro Glu Ser
    290                 295                 300

Leu Val Gly Ile Met Leu Asp Arg Ser Glu Trp Met Ile Val Ala Ile
305                 310                 315                 320

Leu Gly Ile Leu Lys Ala Gly Ala Ala Phe Val Pro Leu Asp Pro Ala
                325                 330                 335

Tyr Pro Ala Glu Arg Ile Asn His Ile Leu Gly Asp Thr Gly Leu Ser
            340                 345                 350

Leu Leu Val Thr Gln Ser Ser Gln Leu Ala Gln Trp Tyr Glu Phe Ser
        355                 360                 365

Gly Val Thr Leu Leu Leu Asp Gln Glu Leu Pro Gly Trp Gln Pro Leu
    370                 375                 380

Pro Asp Asn Pro Pro His Arg Ala Glu Pro Ala His Leu Ala Tyr Val
385                 390                 395                 400

Leu Tyr Thr Ser Gly Ser Thr Gly Lys Pro Lys Gly Cys Leu Leu Glu
                405                 410                 415

His Arg Asn Leu Ala His Tyr Ile Ala Trp Ala Ala Gly Tyr Tyr Phe
            420                 425                 430

Pro Glu Ser Thr Thr Gly Ser Phe Gly Leu Tyr Ser Ser Leu Cys Phe
```

-continued

```
        435                 440                 445

Asp Phe Thr Leu Thr Asn Ile Phe Cys Pro Leu Val Arg Gly Lys Thr
    450                 455                 460

Leu Arg Ile Tyr Pro Gln Ser Glu Ser Ile Asp Thr Ile Leu Ala Arg
465                 470                 475                 480

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

His Ile His Leu Leu Glu Tyr Met Asn Leu Ala Arg Ser Gly Val Arg
            500                 505                 510

Lys Val Ile Val Gly Gly Glu Glu Leu Thr Pro Gln His Ile Ala Thr
        515                 520                 525

Leu Arg Lys Ile Asp Pro Ala Ile Glu Ile Tyr Asn Glu Tyr Gly Pro
    530                 535                 540

Thr Glu Ala Thr Val Gly Cys Ile Val Glu Arg Val Glu Asp Ala Pro
545                 550                 555                 560

Pro Thr Val Leu Ile Gly Arg Pro Ile Ala Asp Thr Arg Val Tyr Met
                565                 570                 575

Leu Asp Asp Ala Leu Arg Pro Val Pro Leu Gly Val Pro Gly Glu Ile
            580                 585                 590

Cys Leu Ala Gly Ala Gly Leu Ala Arg Gly Tyr His Gln Arg Pro Asp
        595                 600                 605

Val Thr Ala Ala Lys Phe Val Glu His Pro Phe Pro Gly Glu Ala Arg
    610                 615                 620

Ile Tyr Arg Thr Gly Asp Ile Gly Arg Trp Leu Pro Asp Gly Arg Ile
625                 630                 635                 640

Gln Cys Tyr Gly Arg Val Asp His Gln Val Lys Ile Arg Gly His Arg
                645                 650                 655

Val Glu Leu Gly Glu Ile Glu Ala Ala Ile Ala Ala His Glu Asp Val
            660                 665                 670

Val Gly Ala Ala Val Met Leu Arg Glu Ser Ala His Gly Val Arg Lys
        675                 680                 685

Leu Ala Ala Tyr Val Lys Gly Ala Ala Ser Leu Ser Val Pro Asn Leu
    690                 695                 700

Arg Ala Tyr Leu Ala Gly Lys Leu Pro Asp Tyr Met Val Pro Ser Asp
705                 710                 715                 720

Ile Ile Pro Ile Ala Glu Phe Pro Leu Asn Ala Asn Gly Lys Leu Asp
                725                 730                 735

Arg Pro Ala Leu Leu Ala Leu Glu Pro Ala Ala Ala Pro Glu Glu Ala
            740                 745                 750

Pro Leu Asp Ala Thr Pro Ile Gln Arg Glu Leu Val Arg Ile Trp Arg
        755                 760                 765

Asp Val Leu Asp Asn Pro Ala Val Asp Leu Ala Gly Arg Phe Phe Asp
    770                 775                 780

Tyr Gly Gly Asp Ser Leu Gln Ala Met Gln Leu Val Ser Arg Ile Trp
785                 790                 795                 800

Ser Ser Phe Ser Val Glu Ile Gly Ile Asp Ala Ile Phe Glu Leu Gln
                805                 810                 815

Thr Ile Ser Ala Val Ser Asp Leu Ile Glu Ala Ser Ser Pro His Pro
            820                 825                 830

Gly Ser Thr Ala Gly Ala Ile Pro Pro Arg Ser Arg Ala Asn Asp Leu
        835                 840                 845

Pro Leu Ser Phe Pro Gln Gln Arg Leu Trp Phe Leu Ala Gln Leu Glu
    850                 855                 860
```

-continued

```
Gly Pro Ser Ala Thr Tyr Asn Ile Ser Ser Ala Leu Arg Phe Glu Gly
865                 870                 875                 880

Glu Leu Asp Val Ala Arg Leu Arg Phe Ala Val Ser Glu Ile Ser Arg
                885                 890                 895

Arg His Glu Ile Leu Arg Thr Thr Phe Pro Ala Val Asp Gly Arg Gly
            900                 905                 910

Val Gln Arg Ile Ala Pro Pro Ala Pro Val Ala Leu Asp Val Val Asp
        915                 920                 925

Val Ala Ser Glu Ser Asp Thr Leu Ala Leu Leu Ala Glu Glu Ala Asp
    930                 935                 940

Arg Pro Phe Asp Leu Ala Ala Gly Pro Leu Tyr Arg Val Val Leu Tyr
945                 950                 955                 960

Arg Val His Glu Arg Leu His Val Phe Gly Ile Val Met His His Ile
                965                 970                 975

Val Ser Asp Ala Trp Ser Ser Gly Ile Leu Ile Gly Glu Leu Ala Ala
            980                 985                 990

Leu Tyr Ala Gly Glu Ser Leu Pro  Glu Leu Ala Val Gln  Tyr Ala Asp
        995                 1000                1005

Tyr Ala  Val Trp Gln His Glu  Arg Leu Ala Ser Ala  Asp Thr His
    1010                1015                1020

Arg Glu  Leu Ala Leu Leu Ser  Ala Ala Leu Ala Asp  Ala Pro Asp
    1025                1030                1035

Leu Ile  Glu Leu Pro Thr Asp  Arg Pro Arg Pro Ala  Val Gln Gln
    1040                1045                1050

Phe Arg  Gly Ala Val Leu Pro  Phe Gln Leu Ser Ala  Glu Arg Ala
    1055                1060                1065

Asp Gly  Leu Arg Ala Ile Ala  Arg Ala Ser Gly Thr  Ser Thr Phe
    1070                1075                1080

Met Val  Val Leu Ala Ala Tyr  Ala Leu Leu Leu Ser  Arg Tyr Ser
    1085                1090                1095

Asn Gln  Gln Asp Leu Val Ile  Gly Ser Pro Ile Ala  Asn Arg Arg
    1100                1105                1110

Ser Ser  Met Thr Glu Pro Leu  Ile Gly Phe Phe Ala  Asn Met Leu
    1115                1120                1125

Ala Leu  Arg Val Asp Leu Ser  Gly Asn Pro Thr Phe  Gly Asp Leu
    1130                1135                1140

Leu Ala  Arg Val Lys Arg Val  Ala Leu Asp Gly Tyr  Ser Arg Gln
    1145                1150                1155

Glu Ile  Pro Phe Glu Gln Val  Val Asp Ser Leu Glu  Leu Glu Arg
    1160                1165                1170

Asn Leu  Gly Arg Thr Pro Val  Phe Gln Val Val Phe  Ala Tyr Glu
    1175                1180                1185

Lys Ala  Gln Pro Arg Ala Val  Ser Phe Pro Gly Leu  Val Ala Thr
    1190                1195                1200

Pro Val  Ala Val Glu Thr His  Thr Ala Lys Phe Asp  Leu Thr Leu
    1205                1210                1215

His Val  Gln Asp Ala Asp Asp  Gly Leu Ala Gly Ser  Leu Glu Tyr
    1220                1225                1230

Asn Leu  Asp Leu Phe Asp Ala  Ala Thr Ile Asp Arg  Met Ala Glu
    1235                1240                1245

His Phe  Arg Thr Leu Val Asp  Ala Val Ile Ala Asp  Pro Asp Arg
    1250                1255                1260
```

-continued

```
Pro Leu  Gly Ala Leu Ser Leu  Ser Asn Asp Ala Glu  Arg Asn Leu
    1265                1270                1275

Leu Thr  Val Glu Trp Asn Arg  Thr Asp Thr Asp Phe  Gly Glu Asp
    1280                1285                1290

Ala Ala  Gln Pro Leu His Arg  Leu Phe Glu Gln Gln  Val Glu Arg
    1295                1300                1305

Thr Pro  Asp Ala Val Ala Ile  Val Phe Asp Asp Thr  Ala Leu Thr
    1310                1315                1320

Tyr Ala  Glu Leu Asn Leu Arg  Ala Asn Arg Leu Ala  His His Leu
    1325                1330                1335

Val Ala  Leu Gly Val Gly Pro  Asp Ser Leu Val Gly  Val Ala Met
    1340                1345                1350

Glu Arg  Ser Leu Asp Met Ser  Val Ala Leu Leu Ala  Ile Leu Lys
    1355                1360                1365

Ala Gly  Gly Ala Tyr Val Pro  Val Asp Pro Asp Tyr  Pro Ala Glu
    1370                1375                1380

Arg Val  Arg Phe Met Ile Asp  His Ala Gln Leu Arg  Trp Leu Leu
    1385                1390                1395

Thr Gln  Gln His Leu His Asp  Ala Leu Pro Asp Thr  Asp Ala His
    1400                1405                1410

Val Ile  Val Val Asp Arg Asp  Ser Leu Asp Leu Asp  Ala Ala Ala
    1415                1420                1425

Thr Ser  Asn Pro Ala Pro Ala  Leu Asn Gly Asp Asn  Leu Ala Tyr
    1430                1435                1440

Met Ile  Tyr Thr Ser Gly Ser  Thr Gly Arg Pro Lys  Gly Ala Leu
    1445                1450                1455

Asn Thr  His Arg Ala Ile Thr  Asn Arg Ile Leu Trp  Met Gln His
    1460                1465                1470

Ala Tyr  Ala Leu Asp Ala Asp  Asp Ala Val Leu Gln  Lys Thr Pro
    1475                1480                1485

Phe Ser  Phe Asp Val Ser Val  Trp Glu Leu Phe Trp  Pro Leu Val
    1490                1495                1500

Thr Gly  Ala Arg Leu Val Phe  Ala Arg Pro Gly Gly  Gln Arg Glu
    1505                1510                1515

Thr Asp  Tyr Leu Val Glu Leu  Ile Glu Arg Glu Arg  Ile Thr Thr
    1520                1525                1530

Ile His  Phe Val Pro Ser Met  Leu Arg Ala Phe Leu  Asp His Pro
    1535                1540                1545

Asp Leu  Asp Ala His Cys Ala  Ser Leu Arg Arg Val  Val Cys Ser
    1550                1555                1560

Gly Glu  Ala Leu Pro His Asp  Leu Gln Gln Arg Cys  Leu Glu Arg
    1565                1570                1575

Leu Asp  Val Lys Leu Tyr Asn  Leu Tyr Gly Pro Thr  Glu Ala Ala
    1580                1585                1590

Val Asp  Val Thr Ala Trp Glu  Cys Arg Arg Asp Asp  Pro His Arg
    1595                1600                1605

Ile Val  Pro Ile Gly Arg Pro  Ile Ala Asn Thr Arg  Leu Tyr Ile
    1610                1615                1620

Val Asp  Ala Gln Met Gln Pro  Thr Pro Ile Gly Val  Ala Gly Glu
    1625                1630                1635

Leu Leu  Ile Gly Gly Thr Pro  Val Gly Arg Gly Tyr  His Gly Glu
    1640                1645                1650

Pro Glu  Leu Ser Ala Glu Lys  Phe Ile Ala Asp Pro  Phe Ser Ala
```

-continued

```
    1655                1660                1665

Asp Pro  Leu Ala Arg Leu Tyr  Arg Thr Gly Asp Leu  Ala Arg Tyr
    1670                1675                1680

Arg Pro  Asp Gly Asn Ile Glu  Phe Leu Gly Arg Ile  Asp His Gln
    1685                1690                1695

Ile Lys  Leu Arg Gly Leu Arg  Ile Glu Pro Gly Glu  Ile Glu Ala
    1700                1705                1710

Ala Leu  Arg Ala His Pro Ser  Val Asp Asp Cys Val  Val Ile Ala
    1715                1720                1725

Lys Thr  Glu Gly Ala Arg Thr  Phe Leu Ile Ala Tyr  Val Ala Thr
    1730                1735                1740

Ala Ala  Pro Asp Ile Ala Asp  Leu Arg Gly Tyr Leu  Gly Gly Lys
    1745                1750                1755

Leu Ala  Asp Tyr Met Val Pro  Ser Gln Phe Phe Ala  Leu Glu Ser
    1760                1765                1770

Leu Pro  Met Leu Pro Asn Gly  Lys Ile Asn Arg Lys  Ala Leu Pro
    1775                1780                1785

Leu Pro  Ala Asp Arg Gly Asp  Ala Ala Gln Pro His  Ala Pro Ala
    1790                1795                1800

Val Thr  Pro Arg Glu Ile Leu  Leu Ala Ser Ile Cys  Ile Asp Val
    1805                1810                1815

Leu Gln  Leu Pro Ser Val Gly  Ile His Asp Asn Phe  Phe Glu Leu
    1820                1825                1830

Gly Gly  Asp Ser Ile Leu Ser  Ile Gln Val Ile Ala  Arg Ala Asn
    1835                1840                1845

Gln Ala  Gly Leu Arg Val Thr  Ala Lys Gln Leu Phe  Gln Tyr Gln
    1850                1855                1860

Thr Ile  Ala Gln Leu Ala Ala  Ala Pro Glu Glu Arg  Ala Ala Cys
    1865                1870                1875

Ala Pro  Thr Leu Ser Pro Leu  Gly Asp Ala Pro Leu  Thr Pro Val
    1880                1885                1890

Gln His  Trp Phe Phe Glu Gln  Glu Ile Asp Ala Pro  Ser His Tyr
    1895                1900                1905

Asn Gln  Thr Val Leu Ile Gln  Val Pro Ala Asp Ile  Asp Ala Ser
    1910                1915                1920

Arg Leu  Ala Asp Ala Phe Arg  Gln Val Tyr Glu His  His Asp Ala
    1925                1930                1935

Leu Arg  Leu Arg Phe Ser His  Asp Ala Gly Arg Trp  Thr Gln Gln
    1940                1945                1950

Val Val  Ala Gly Gly Glu Met  Pro Ala Leu Phe Ala  Lys Gln Val
    1955                1960                1965

Ile Ala  Asp Asp Ala Gly Glu  Arg Leu Ala Ala Met  Arg Ala Ala
    1970                1975                1980

Ala Ala  Asp Ala Glu Arg Gly  Ile Asp Ile Thr His  Gly Pro Leu
    1985                1990                1995

Leu Ala  Ala Arg Leu Phe Cys  Leu Ala Asp Glu Pro  Leu Ala Arg
    2000                2005                2010

Leu Phe  Val Ser Ile His His  Leu Ala Val Asp Gly  Val Ser Trp
    2015                2020                2025

Arg Val  Leu Leu Glu Asp Leu  His Ala Ala Tyr His  Gly Gln Pro
    2030                2035                2040

Leu Pro  Gly Lys Thr Thr Ser  Phe Arg Glu Trp Ala  Leu His Leu
    2045                2050                2055
```

-continued

```
Gln Gln  Leu Ala Arg Ser Pro  Ala Ile Gly Asp Glu  Ala Arg Leu
    2060                 2065                 2070

Trp Gln  Ala Leu Leu Ala Gln  Pro Val Glu Pro Met  Pro Val Asp
    2075                 2080                 2085

Tyr Pro  Gly Thr Gly Ala Ala  Asn Asn Ala Val Asp  Asp Ala Ser
    2090                 2095                 2100

Ser Val  Ser Phe Glu Leu Gly  Glu Ala Asp Thr Thr  Ala Leu Leu
    2105                 2110                 2115

Arg Arg  Leu Pro Arg Ala Tyr  Asp Thr Arg Ile Asn  Asp Val Leu
    2120                 2125                 2130

Leu Val  Ala Leu Ala Gln Ala  Cys Ser Met Val Thr  Gly Asn Thr
    2135                 2140                 2145

Arg Thr  Arg Ile Asp Leu Glu  Ser His Gly Arg His  Val Ser Asp
    2150                 2155                 2160

Ala Pro  Leu Asp Leu Thr Arg  Thr Val Gly Trp Phe  Thr Ser Ile
    2165                 2170                 2175

Tyr Pro  Val Val Leu Asp Ala  Asp Ala Met His Ala  Pro Glu Gln
    2180                 2185                 2190

Ala Leu  Arg Ala Ala Arg Gln  Gln Leu Arg Arg Ile  Pro Ala Asp
    2195                 2200                 2205

Gly Leu  Gly Tyr Ser Leu Leu  Arg Tyr Gln Ser Pro  Asp Ala Ala
    2210                 2215                 2220

Val Arg  Asp Ser Leu Ala Ala  Leu Pro Lys Ala Asp  Ile Leu Phe
    2225                 2230                 2235

Asn Tyr  His Gly Gln Leu Asp  Thr Val Leu Arg Gln  Ser Asp Gly
    2240                 2245                 2250

Trp Arg  Pro Ala Ala Glu Asp  Leu Gly Ser Leu Arg  Ala Gly Arg
    2255                 2260                 2265

Ser Gln  Arg Thr His Ala Phe  Glu Ile Val Ala Ala  Val Ala Asp
    2270                 2275                 2280

Gly Lys  Leu Gln Val Asp Trp  Arg Tyr Gly Glu Arg  Leu His Arg
    2285                 2290                 2295

Arg Gln  Thr Val Glu Asn Leu  Ala Ala His Phe Arg  Asp Arg Leu
    2300                 2305                 2310

Leu Asp  Phe Ala Ala Ser Val  Pro Asp Thr Ala Ala  Asp Asp Ile
    2315                 2320                 2325

Glu Asp  Ser Tyr Pro Leu Ser  Ser Leu Gln Gln Gly  Ile Leu Phe
    2330                 2335                 2340

His Ser  Leu Tyr Asp Leu Asp  Pro Ala Ala Tyr Phe  Gln Gln Phe
    2345                 2350                 2355

Ser Phe  Val Val Ser Gly Pro  Leu Gln Val Pro Ala  Leu Arg Gln
    2360                 2365                 2370

Ala Trp  Ala Asn Ala Leu Ala  Arg His Ala Val Leu  Arg Thr Ala
    2375                 2380                 2385

Phe Ala  Trp Ala Asp Arg Asp  His Pro Val Gln Thr  Val Arg His
    2390                 2395                 2400

Thr Val  Asp Leu Pro Trp Thr  Phe Leu Asp Trp Arg  His Arg Asp
    2405                 2410                 2415

Ala Ser  Arg Arg Ala Gln Asp  Phe Asp Ala Phe Leu  Ala Asp Asp
    2420                 2425                 2430

Arg Arg  Arg Gly Phe Asp Leu  Gln Arg Ala Pro Leu  Phe Arg Cys
    2435                 2440                 2445
```

-continued

```
Thr Leu  Ile Gln Glu Thr Asp  Thr Arg His Arg Phe  Cys Trp Ser
    2450                 2455                 2460

Ala His  His Ile Ile Leu Asp  Gly Trp Ser Thr Ala  Thr Leu Met
    2465                 2470                 2475

Lys Glu  Val Phe Asp Asp Tyr  Leu Ser Leu Ala Arg  Thr Gly Met
    2480                 2485                 2490

Pro Ala  Val Ala Ala Ser Ala  Pro Gly Tyr Arg Ala  Tyr Ile Asp
    2495                 2500                 2505

Trp Leu  Ala Arg His Pro Arg  Ser Ala Asp Glu Thr  Trp Trp Arg
    2510                 2515                 2520

Ala Glu  Leu Ala Gly Phe Lys  Ala Ala Thr Pro Val  Ala Ala Ser
    2525                 2530                 2535

Pro Ala  Arg Gln Ala Thr Gly  Asp Ala Pro Arg Gln  Asp Lys Arg
    2540                 2545                 2550

Arg Thr  Gln Gln Phe Leu Leu  Asp Glu Ala Leu Ala  Ala Arg Leu
    2555                 2560                 2565

Gln Thr  Leu Thr Arg Thr His  Arg Val Thr Leu Asn  Val Leu Ile
    2570                 2575                 2580

Arg Ala  Val Trp Ala Leu Val  Leu Arg Arg His Ala  Gly Thr Asp
    2585                 2590                 2595

Asp Val  Val Phe Gly Val Thr  Val Ser Gly Arg Pro  Pro Met Leu
    2600                 2605                 2610

Asp Gly  Val Glu Ser Ile Val  Gly Leu Phe Ile Asn  Thr Leu Pro
    2615                 2620                 2625

Leu Arg  Leu Arg Ile Ala Pro  Glu Arg Pro Phe Ile  Glu Trp Leu
    2630                 2635                 2640

Ala Glu  Val His Ala Ala Gln  Thr Ala Met Glu Pro  His Ser Tyr
    2645                 2650                 2655

Ser Ser  Leu Val Asp Ile Gln  Ser Trp Ser Glu Leu  Pro Ala Gly
    2660                 2665                 2670

Asp Ser  Leu Phe Asp Ser Leu  Leu Val Phe Glu Asn  Phe Pro Val
    2675                 2680                 2685

Ala Ala  Ala Pro Asp Leu Gly  Pro Asp Asp Ile Glu  Ile Leu Asp
    2690                 2695                 2700

Thr Arg  Ala Phe Ala Glu Ser  Asn Tyr Pro Leu Thr  Leu Thr Val
    2705                 2710                 2715

His Pro  Asn Glu Arg Ile Gly  Phe His Ile Ser His  Asp Ala His
    2720                 2725                 2730

Arg Ile  Ala Pro Glu Val Val  Arg Gln Met Leu Asp  Thr Leu Arg
    2735                 2740                 2745

Thr Leu  Leu Glu Arg Phe Ala  Glu Asn Pro Gly Gln  Leu Thr Gly
    2750                 2755                 2760

Gln Leu  Ala Asp Pro Pro Ala  Ala Asp Gly Arg Pro  Ser Ala Pro
    2765                 2770                 2775

Arg Ser  Gly Ala Gly Pro Ala  Ile Glu Ala Ala Ala  Gly Ala Ala
    2780                 2785                 2790

Ala Ala  Ala Arg Ala Val Ala  His Ala Ala Asp Glu  Ser Thr Leu
    2795                 2800                 2805

Leu Glu  Ile Trp Arg Arg Ile  Phe Lys Arg Asp Asp  Ile Ala Val
    2810                 2815                 2820

Ser Asp  Asn Tyr Phe Asp Leu  Gly Gly His Ser Ile  Ile Ala Ile
    2825                 2830                 2835

Gln Leu  Met Ala His Val Glu  Lys Ala Phe Asp Arg  Arg Leu Pro
```

-continued

```
    2840                2845                2850

Ile Ser  Cys Leu Phe Glu Asn  Pro Thr Ile Glu Lys  Leu Ala Ala
    2855                2860                2865

Ala Leu  Ala Ala Lys Glu Pro  Ser Ala Pro Ala Gly  Gly Leu Val
    2870                2875                2880

Pro Ile  Arg Asp Gly Gly Pro  Ala Ala Pro Leu Phe  Leu Leu Pro
    2885                2890                2895

Gly Ala  Gly Gly Asn Val Val  Tyr Phe Arg Pro Leu  Ala Asn His
    2900                2905                2910

Leu Ser  Gly Ala His Ala Ile  His Gly Leu Glu Ala  Leu Gly Leu
    2915                2920                2925

Asp Gly  Ala Cys Glu Pro Leu  Thr Arg Val Glu Asp  Ile Ala Ala
    2930                2935                2940

Arg His  Ile Glu Arg Ile Trp  Pro Leu Val Gly Ala  Gly Pro Tyr
    2945                2950                2955

Tyr Leu  Ala Gly His Ser Phe  Gly Ala His Val Ala  Leu Glu Met
    2960                2965                2970

Ser Arg  Gln Leu Val Ala Lys  Gly Ala Asp Val Lys  Leu Leu Ala
    2975                2980                2985

Ile Phe  Asp Ala Ser Ala Pro  Ile Asp Ser Ser Ala  Ala Thr Tyr
    2990                2995                3000

Trp Gln  Asp Trp Asp Asp Thr  Glu Trp Leu Val Ala  Ile Ala His
    3005                3010                3015

Glu Ile  Gly Thr Phe Leu Gly  Thr Asp Leu Gln Val  Thr Arg Ala
    3020                3025                3030

Asp Leu  Val His Leu Asp Pro  Asp Gly Gln Ala Gly  Leu Ile Leu
    3035                3040                3045

Glu Arg  Ile Gly Asp Arg Gly  Ser Trp Phe Ala Asp  Ala Gly Ser
    3050                3055                3060

Asp Arg  Leu Arg Ala Tyr Leu  Arg Val Tyr Gln Ala  Asn Phe Lys
    3065                3070                3075

Ser His  Tyr Ala Pro His Ala  Thr Pro Leu Pro Val  Pro Ile Ala
    3080                3085                3090

Leu Phe  Arg Ser Thr Glu Arg  Asp Pro Gly Asp Tyr  Ala Pro Ser
    3095                3100                3105

Ser Glu  Ile Ala Gln Leu Arg  Leu Asp Ala Thr Trp  Gly Trp Ser
    3110                3115                3120

Arg Phe  Ser Ala His Pro Val  Ala Val Thr Asp Val  Pro Gly Asp
    3125                3130                3135

His Leu  Thr Met Leu Leu Asp  Pro His Ala Gly Val  Leu Ala Ala
    3140                3145                3150

His Val  Asn Ser Phe Leu Glu  Lys Thr Pro Ser
    3155                3160


<210> SEQ ID NO 12
<211> LENGTH: 3021
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(3021)
<223> OTHER INFORMATION: putative nonribosomal peptide synthetase

<400> SEQUENCE: 12

Met Gln Glu Gly Met Leu Phe His Ala Val His Glu Pro Gly Ser Arg
1               5                   10                  15
```

-continued

```
Ser Ser Phe Asn Gln Leu Ser Cys Arg Ile Thr Gly Ser Leu Asp Pro
            20                  25                  30

Ala Leu Phe His Ala Ala Trp Gln Gln Leu Ile Asp Arg His Pro Val
        35                  40                  45

Met Arg Thr Ser Phe His Trp Glu Glu Phe Asp Lys Pro Met Gln Val
    50                  55                  60

Val His Ala Arg Ala Thr Leu Pro Trp Val Gln Asp Asp Trp Leu Asp
65                  70                  75                  80

Leu Pro Glu His Glu Gln Arg Ser Arg Trp Arg Ala His Leu Asp Asn
                85                  90                  95

Asp Leu Ala Glu Gly Phe Ala Leu Asp Arg Ala Pro Leu Val Arg Cys
            100                 105                 110

Arg Leu Val Arg Val Ala Ala Asp Ala Tyr Leu Phe Ser Trp Ser His
        115                 120                 125

His His Ile Leu Ala Asp Gly Trp Cys Leu Ser Leu Val Ile Glu Glu
    130                 135                 140

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

Pro Pro Val Arg Pro Tyr Arg Asp Tyr Ile Gln Trp Leu Gln Gln His
                165                 170                 175

Glu Pro Gln Ala Ala Gln Gln Tyr Trp Thr Arg Tyr Leu Glu Gly Phe
            180                 185                 190

Arg Thr Pro Thr Pro Leu Pro Thr Ala Ala Arg Ala Gly Ala Asp Glu
        195                 200                 205

Arg Phe Gly Gln Gly Leu Ala Gln Val Gln Ala Asp Leu Ser Ala Asp
    210                 215                 220

Leu Ser Ala Arg Leu Arg Gln Phe Ala Ala Arg His His Val Thr Leu
225                 230                 235                 240

Asn Thr Leu Ala Gln Ala Ala Trp Ala Leu Val Leu Ser Arg Tyr Ser
                245                 250                 255

Gly Glu Thr Asp Val Val Phe Gly Ala Val Val Ser Gly Arg Gly Ala
            260                 265                 270

Asn Leu Pro Gly Ile Glu Thr Met Leu Gly Leu Phe Ile Asn Thr Val
        275                 280                 285

Pro Val Arg Val Arg Val Asp Pro Arg Gln Pro Leu Val Pro Trp Leu
    290                 295                 300

Lys Met Ile Gln Ala Arg Val Ala Ala Arg Ala Pro Phe Glu His Thr
305                 310                 315                 320

Pro Leu Pro Asp Ile Gln Arg Cys Ser Asp Val Pro Pro Thr Ala Pro
                325                 330                 335

Leu Phe Glu Ser Asn Ile Thr Phe Met Asn Tyr Pro Leu Asp Ala Ser
            340                 345                 350

Leu Thr His Gly Ala His Gly Leu Ala Val Asp Glu Val Gln Leu Tyr
        355                 360                 365

Asn Arg Ala Asp Ile Pro Leu Glu Phe Val Val Thr Ala Arg Asp Asp
    370                 375                 380

Trp Lys Met Glu Leu Ser Phe Asp Pro Arg Arg Phe Asp Glu Asp Thr
385                 390                 395                 400

Met Gln Arg Met Leu Gly His Val Ala Ala Thr Leu Asp Ala Phe Ala
                405                 410                 415

Ala Asp Pro Asn Arg Leu Leu Gly Arg Val Pro Ile Leu Pro Asp Ala
            420                 425                 430
```

-continued

```
Glu Arg Arg Gln Leu Leu Glu Thr Phe Asn Asp Thr Ala Val Pro Phe
        435                 440                 445

Asp Ala Ala Leu Thr Val Val His Arg Leu Glu Gln Ala Ala Ala Asp
    450                 455                 460

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

Gly Glu Leu Asn Ala Arg Ala Asn Arg Ile Ala His Arg Leu Leu Ala
                485                 490                 495

Ala Ala Asp Leu Gly Pro Asp Ala Leu Val Ala Ile Cys Met His Arg
            500                 505                 510

Ser Ala Gln Leu Met Glu Ala Ile Leu Ala Val Trp Lys Cys Gly Ala
        515                 520                 525

Ala Tyr Ile Pro Val Asp Pro Asn Tyr Pro Val Ala Arg Ile Arg Thr
    530                 535                 540

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

Leu Pro Pro Glu Leu Ala Gly Ile Ala Leu Val Val Ser Leu Asp Ala
                565                 570                 575

Ala Thr Asp Ala Val Asp Asp Ser Asn Pro Gly Arg Pro Val Ser Pro
            580                 585                 590

Asp Ser Leu Ala Tyr Val Ile Tyr Thr Ser Gly Ser Thr Gly Lys Pro
        595                 600                 605

Lys Gly Ala Met Val Glu His Ala Gly Met Leu Asn His Met Leu Ala
    610                 615                 620

Glu Ile Asp Glu Phe Ser Ile Ser Ala Ser Ser Val Ile Ala Gln Thr
625                 630                 635                 640

Ala Pro His Cys Phe Asp Ile Ser Val Trp Gln Phe Phe Thr Ala Pro
                645                 650                 655

Leu Val Gly Gly Lys Thr Val Ile Val Asp Asp Asp Cys Ile Arg Asp
            660                 665                 670

Pro Ala Arg Phe Val Ala Tyr Leu Glu Thr Thr Arg Ile Ser Ile Leu
        675                 680                 685

Glu Leu Val Pro Ser Tyr Leu Ser Ala Val Leu Asp Arg Ala Ser Glu
    690                 695                 700

Arg Pro Ala Leu Met Arg His Leu Arg His Leu Leu Val Thr Gly Glu
705                 710                 715                 720

Met Val Ser Pro Ala Leu Val Lys Gln Trp Phe Asp Val Phe Pro Ala
                725                 730                 735

Ile Pro Leu Val Asn Ala Tyr Gly Pro Ala Glu Ala Ser Asp Asp Val
            740                 745                 750

Ala Gln His Arg Met Thr Gly Ala Pro Ser Thr Pro Tyr Val Pro Val
        755                 760                 765

Gly Lys Pro Ile Arg Asn Val Arg Leu Tyr Val Val Asp Pro Gln Met
    770                 775                 780

Asn Leu Cys Pro Ile Gly Ile Pro Gly Glu Leu Cys Val Ser Gly Val
785                 790                 795                 800

Ala Val Gly Arg Gly Tyr Leu Asn Asn Glu Ala Ala Thr Gln Asp Ala
                805                 810                 815

Phe Val Glu Asp Pro Phe His Pro Gln Arg Gly Val Arg Leu Tyr Arg
            820                 825                 830

Thr Arg Asp Ile Gly Cys Tyr Leu Pro Asp Gly Thr Ile Val Leu His
        835                 840                 845

Gly Arg Lys Asp His Gln Leu Lys Ile Arg Gly Tyr Arg Ile Glu Leu
```

-continued

```
    850                 855                 860

Gly Glu Ile Asp Gln Arg Arg Leu Ala Asp His Ser Arg Lys Leu Arg
865                 870                 875                 880

Gln Ala Ala Ala Leu Asp Tyr Arg Asp Glu Ala Gly Arg Ala Ala Leu
                885                 890                 895

Cys Ala Tyr Val Ala Phe Arg Asp Gly Ala Ser Leu Ser Asp Ala Gly
            900                 905                 910

Ile Ala Ala Ala Leu Ser Ala Thr Leu Pro Asp Tyr Met Val Pro Gly
        915                 920                 925

Ile Tyr Val Val Leu Asp Ala Leu Pro Leu Ser Gly Asn Gly Lys Ile
    930                 935                 940

Asp Arg Asn Ala Leu Pro Pro Leu Asp Arg Ala Arg Leu Ala Ala Thr
945                 950                 955                 960

Ala His Ala Pro Thr Pro Pro Arg Thr Pro Thr Glu Thr Leu Leu Cys
                965                 970                 975

Arg Ile Trp Gly Glu Ala Leu Gly Ile Pro Ser Pro Gly Ile His Asp
            980                 985                 990

Asn Leu Phe Ala Leu Gly Gly Asp  Ser Ile Leu Ser Met  Arg Ile Val
        995                 1000                1005

Ser Leu  Ala Ala Lys Ala Gly  Leu Lys Leu Thr Thr  Arg Leu Ile
    1010                1015                1020

Phe Gln  His Pro Thr Val Ala  Glu Leu Ala Ala Val  Ala Thr Arg
    1025                1030                1035

Gly Thr  Val Gly Ala Ala Ala  Phe Val Ala Ser Ser  Gly Pro Leu
    1040                1045                1050

Pro Leu  Thr Pro Ile Gln Lys  Arg Phe Phe Ala Gln  Gly Lys His
    1055                1060                1065

Asp Pro  Asp Gln Tyr Asn Gln  Ala Val Leu Leu Asp  Val Pro Ala
    1070                1075                1080

Asp Leu  Asp Pro Val Leu Leu  Arg Gln Ala Leu Arg  His Ala Val
    1085                1090                1095

Lys Trp  His Asp Ala Leu Arg  Leu Arg Phe Arg Glu  Gly Glu Ser
    1100                1105                1110

Gly Trp  Thr Gln Glu Val Val  Asp Asp Pro Glu Ile  Pro Val Val
    1115                1120                1125

Val Ser  Asp Ile Ala Arg Asp  Gln Leu Ala Gln Tyr  Val Ala Gln
    1130                1135                1140

Ser His  Ala Ser Leu Asn Leu  Ala Asp Gly Pro Val  Val Arg Ala
    1145                1150                1155

Asp Leu  Phe Arg Val Asp Glu  Gly Arg Ser Leu Arg  Leu Leu Leu
    1160                1165                1170

Val Ala  His His Leu Val Val  Asp Gly Val Ser Trp  Gly Ala Leu
    1175                1180                1185

Leu Glu  Thr Val Tyr Asp Ala  Tyr Thr Arg Leu Arg  Asn Gly Lys
    1190                1195                1200

Ala Pro  Glu Phe Ala Gly Gly  Ser Ala Thr Trp Thr  Ala Trp Thr
    1205                1210                1215

Arg Ala  Ile Ser Thr Trp Ala  Gly Ser Gly Ala Ala  Asp Ala Asp
    1220                1225                1230

Leu Ala  His Trp Gln Ala Leu  Ala Arg Ala Ala Leu  Pro Gly Leu
    1235                1240                1245

Pro Leu  Asp Arg Asp Ala Pro  Ala Asp Ala Asn Thr  Val Ser Ser
    1250                1255                1260
```

-continued

```
Ala Asp  Thr Ile Val Val Glu  Leu Gly Glu Ala Ala  Thr Thr Ala
    1265                 1270                 1275

Leu Leu  Gly Ala Ala Pro Arg  Ala Tyr Asp Ala Gln  Val Asn Asp
    1280                 1285                 1290

Val Leu  Leu Ala Ala Leu Ala  Arg Ala Val Ser Glu  Trp Ser Gly
    1295                 1300                 1305

Cys Ala  Asp Val Leu Leu Asp  Leu Glu Ala His Gly  Arg Glu Glu
    1310                 1315                 1320

Leu Ile  Asp Ala Leu Asp Ile  Ser Arg Thr Val Gly  Trp Phe Thr
    1325                 1330                 1335

Ser Val  Phe Pro Val Leu Leu  Thr Val Asp Ala Gly  Ser His Asp
    1340                 1345                 1350

Pro Ala  Ser Leu Val Ala Ser  Val Arg Thr Arg Leu  Arg Ala Val
    1355                 1360                 1365

Pro Asn  Ala Gly Ile Thr Tyr  Gly Leu Leu Leu Asp  Arg Leu Asp
    1370                 1375                 1380

Gly Pro  Leu Pro Gln Pro Arg  Leu Gln Phe Asn Tyr  Leu Gly Gln
    1385                 1390                 1395

Thr Asp  Gln Leu Phe Thr Ala  Ala Arg Asp Trp Lys  Gln Ala Ala
    1400                 1405                 1410

Glu Pro  Ser Gly Asp Gly Arg  Asn Ala Asn Gln Leu  Arg Glu His
    1415                 1420                 1425

Leu Leu  Asp Ile Asn Ala Tyr  Val Thr Gly Asn Arg  Leu His Val
    1430                 1435                 1440

Ala Trp  Glu Phe Ser Arg Ala  Cys His Asp Thr Ala  Thr Ile Leu
    1445                 1450                 1455

Arg Val  Ala Gln Ala Tyr Ile  Ala Ala Leu Glu Thr  Leu Val Ala
    1460                 1465                 1470

Gly His  Ala Val Pro Ser Ala  Ser Thr Arg Pro Ala  Thr Ala Leu
    1475                 1480                 1485

Pro Gln  Ala Pro Ala Pro Ala  Ser Val Ser Pro Asp  Glu Ile Ala
    1490                 1495                 1500

Asp Val  Tyr Pro Leu Thr Pro  Thr Gln Gln Gly Met  Leu Phe His
    1505                 1510                 1515

Ser Leu  Tyr Glu Pro Ala Ser  Asp Ala Tyr Phe Ser  Ser Leu Asn
    1520                 1525                 1530

Phe Arg  Ile Asp Gly Ala Leu  Asp Val Glu Arg Phe  Arg Arg Ala
    1535                 1540                 1545

Trp Glu  Thr Val Ala His Arg  His Asp Ile Leu Arg  Thr Ser Phe
    1550                 1555                 1560

His Trp  Glu Asp Ile Glu Ser  Pro Val Gln Val Val  His Arg Arg
    1565                 1570                 1575

Ile Asp  Leu Pro Trp His Asp  Glu Asp Leu Arg Ala  Ala Ser Ala
    1580                 1585                 1590

Ala Glu  Ala Glu Gln Arg Trp  Glu Ala Tyr Val Ala  Gln Asp Arg
    1595                 1600                 1605

Ala Arg  Gly Phe Asp Phe Thr  Arg Ala Pro Leu Met  Arg Leu Ala
    1610                 1615                 1620

Leu Phe  Arg Val Gly Glu His  Ala Trp Arg Phe His  Trp Ser His
    1625                 1630                 1635

His His  Ile Leu Leu Asp Gly  Trp Ser Ser Ala Arg  Leu Leu Ser
    1640                 1645                 1650
```

-continued

```
Asp Val  Ala Ala Ala Tyr Gln  Ala Pro Pro Ala Glu  Gly Ala Pro
    1655                1660                1665

Gln Arg  Asp Ala Pro Pro Ala  Phe Ala Gly Tyr Val  Arg Trp Leu
    1670                1675                1680

Ala Arg  Gln Asp Ala Ala Ala  Ala Gln Arg Phe Trp  Lys Thr Lys
    1685                1690                1695

Leu Ala  Asp Phe Pro Ala Thr  Thr Pro Leu Val Leu  Gly Arg Pro
    1700                1705                1710

Glu Leu  Asp Gly Thr Ala Ala  Pro Gly Ala Tyr Val  Glu Glu Pro
    1715                1720                1725

Leu Leu  Leu Ser Glu Ser Asp  Thr Gln Arg Leu Val  Ala Phe Ala
    1730                1735                1740

Gln Ser  Arg Arg Leu Thr Leu  Asn Thr Leu Ala Gln  Gly Ala Trp
    1745                1750                1755

Ala Gln  Leu Leu Ser Arg Tyr  Ser Gly Glu Ser Asp  Val Val Phe
    1760                1765                1770

Gly Thr  Ile Val Ser Gly Arg  Pro Ala Ser Leu Pro  Ala Ser Asp
    1775                1780                1785

Glu Met  Val Gly Leu Phe Ile  Asn Thr Leu Pro Val  Arg Val Arg
    1790                1795                1800

Ile Asp  Ala Arg Pro Thr Ser  Ala Trp Leu Ala Gln  Leu Gln Met
    1805                1810                1815

Asp Leu  Ala Gln Gln Glu Asp  Tyr Ala His Tyr Pro  Leu Ala Asp
    1820                1825                1830

Ile Gln  Lys Phe Ala Gly Leu  Pro Pro Gly Val Pro  Leu Phe Glu
    1835                1840                1845

Ser Leu  Leu Ile Phe Gln Asn  Tyr Pro Val Glu Glu  Ala Leu Ala
    1850                1855                1860

Asp Ala  Leu Pro Gly Leu Arg  Ile Gly Ala Phe Glu  Val Ser Asp
    1865                1870                1875

Pro Asn  Asn Tyr Pro Leu Thr  Leu Val Val Thr Pro  Gly Lys Arg
    1880                1885                1890

Leu Ser  Leu Gln Val Leu Tyr  Asp Asp Gly Arg Phe  Asp Arg Asp
    1895                1900                1905

Thr Ile  Val Arg Leu Leu Arg  His Val Glu Thr Leu  Leu Thr Gly
    1910                1915                1920

Leu Ala  Gly Ala Glu Asp Arg  Pro Asn Arg Ser Val  Pro Leu Leu
    1925                1930                1935

Ala Ala  Ala Glu Arg Asp Ala  Ile Leu Leu Gly Trp  Asn Asp Thr
    1940                1945                1950

Phe Ala  Pro Val Pro Ser Asp  Arg Thr Leu Pro Glu  Leu Ile Glu
    1955                1960                1965

Ala Val  Ala Ala Ala His Pro  Glu Arg Val Ala Val  Arg Cys Gly
    1970                1975                1980

Thr Glu  Val Arg Thr Tyr Arg  Asp Leu Val Glu Gly  Ala Asn Arg
    1985                1990                1995

Ile Ala  Ala His Leu Leu Gln  Thr Ala Pro Leu Gln  Pro Asp Asp
    2000                2005                2010

Arg Ile  Ala Val Trp Met Pro  Arg Ser Pro Leu Met  Leu Glu Thr
    2015                2020                2025

Ile Leu  Ala Ile Trp Lys Cys  Gly Ala Ala Tyr Val  Pro Val Asp
    2030                2035                2040

Pro Ala  Tyr Pro Ala Gln Arg  Val Glu Thr Ile Leu  Thr Leu Ala
```

-continued

```
    2045                2050                2055

Arg Pro  Ala Val Ile Val Thr  Thr Asp Cys Val Pro  Pro Pro Ala
    2060                2065                2070

Leu Ala  Ser Ile Pro Leu Val  Asp Pro Ala Arg Leu  Pro Asp Arg
    2075                2080                2085

Arg Gly  Ala Glu Ala Pro Ala  Pro Val Thr Pro Arg  Cys Arg Pro
    2090                2095                2100

Ala Asp  Leu Ala Tyr Val Ile  Phe Thr Ser Gly Ser  Thr Gly Gln
    2105                2110                2115

Pro Lys  Gly Ala Met Val Glu  His Arg Gly Met Leu  Asn His Val
    2120                2125                2130

Leu Ala  Met Ala Arg Arg Val  Gly Leu Gly Ala Gln  Ser Ala Val
    2135                2140                2145

Ala Gln  Thr Ala Ser His Cys  Ser Asp Ile Ser Val  Trp Gln Cys
    2150                2155                2160

Phe Ala  Ala Leu Ala Ser Gly  Gly Thr Thr Val Ile  Tyr Pro Asp
    2165                2170                2175

Ala Val  Ile Leu Glu Pro Ala  Arg Leu Ile Asp Ser  Leu His Arg
    2180                2185                2190

Asp Arg  Ile Thr Ala Met Gln  Phe Val Pro Ser Tyr  Leu Ala Thr
    2195                2200                2205

Phe Leu  Gly Glu Leu Glu Arg  His Ala Ala Pro Ala  Phe Pro His
    2210                2215                2220

Leu Asp  Thr Leu Leu Thr Ile  Gly Glu Thr Leu Gln  Pro Ala Thr
    2225                2230                2235

Ala Gln  Ala Trp Phe Arg Leu  Asn Pro Ala Val Arg  Leu Ile Asn
    2240                2245                2250

Ala Tyr  Gly Pro Thr Glu Ala  Ser Asp Ser Val Ala  His Tyr Cys
    2255                2260                2265

Leu Thr  Arg Ala Pro Asp Gly  Pro Ala Ile Pro Ile  Gly Arg Pro
    2270                2275                2280

Ile Glu  Asn Leu Arg Leu Tyr  Val Val Asp Ala Asp  Met Asn Pro
    2285                2290                2295

Cys Pro  Ala Gly Val Lys Gly  Glu Ile Cys Ile Gly  Gly Val Gly
    2300                2305                2310

Val Gly  Arg Gly Tyr Leu Phe  Asp Glu Ala Arg Thr  Arg Ala Val
    2315                2320                2325

Phe Arg  Asp Asp Pro Phe Ser  Pro Glu Pro Gly Ala  Arg Leu Tyr
    2330                2335                2340

Arg Thr  Gly Asp Ile Gly Cys  Phe Gly Ala Asp Gly  Asn Leu His
    2345                2350                2355

Phe Phe  Gly Arg Arg Asp Phe  Gln Val Lys Ile Arg  Gly Tyr Arg
    2360                2365                2370

Ile Glu  Leu Gly Glu Ile Glu  Ala Ala Leu Thr Ser  Leu Ala Gly
    2375                2380                2385

Ile Ser  His Ala Val Val Val  Ala Arg Glu Thr Ser  Asp Ala Glu
    2390                2395                2400

Met Thr  Leu Cys Gly Tyr Ala  Ser Gly Thr Gly Trp  Thr Pro Gln
    2405                2410                2415

Arg Val  Arg Asp Ala Leu Arg  Asp Thr Leu Pro Ala  His Met Val
    2420                2425                2430

Pro Asp  Thr Val Met Leu Leu  Pro Ala Leu Pro Val  Met Pro Asn
    2435                2440                2445
```

-continued

```
Gly Lys  Ile Asn Arg Ala Ala  Leu Pro Leu Pro Asp  Ala Ala Ser
    2450                 2455                 2460

Val Pro  Asp Gly Val Arg Ala  Glu Pro Arg Thr Pro  Val Glu Ala
    2465                 2470                 2475

Ala Leu  Leu Arg Leu Phe Ala  Glu Val Leu Gly Arg  Arg Pro Asn
    2480                 2485                 2490

Gly Val  Asp Asp Asp Phe Phe  Glu His Gly Gly Gln  Ser Leu Lys
    2495                 2500                 2505

Ala Ile  Gln Met Val Ser Arg  Ile Pro Arg Ala Ala  Leu Asn Val
    2510                 2515                 2520

Ala Val  Ala Asp Ile Phe His  Ala Pro Thr Pro Arg  Ala Leu Ala
    2525                 2530                 2535

Gln Arg  Leu Ala Ala Met Pro  Val Asp Gly Ala Ala  Asp Asp Asp
    2540                 2545                 2550

Ala Ile  Ile Pro Ala Leu Ala  Ala Gln Pro Ser Tyr  Ala Val Ser
    2555                 2560                 2565

Arg Ala  Gln Lys Arg Ile Trp  Leu Ala Ser Arg Gly  Ala Asp Pro
    2570                 2575                 2580

Ser Thr  Tyr Asn Met Ala Gly  Ala Leu Gln Leu Asp  Gly Ala Val
    2585                 2590                 2595

Asp Thr  Ala Arg Leu Val Arg  Ala Phe Asp Thr Leu  Val Asp Arg
    2600                 2605                 2610

His Glu  Ser Leu Arg Thr Val  Phe Ala Met Ile Glu  Gly Glu Leu
    2615                 2620                 2625

Arg Gln  Arg Val Leu Ser Arg  Glu Ala Ser Gly Phe  Arg Val Glu
    2630                 2635                 2640

Gln Arg  Asp Leu Ala Asp Asp  Ala Gly Pro Gln Ala  Ile Asp Ala
    2645                 2650                 2655

Leu Ile  Arg Ala Glu Cys Glu  Gln Pro Phe Asp Leu  Ala Ser Gly
    2660                 2665                 2670

Pro Leu  Phe Arg Val Lys Leu  Val Arg Leu Ser Gln  Glu Lys His
    2675                 2680                 2685

Leu Leu  Leu Leu Asn Met His  His Val Ile Ser Asp  Ala Trp Ser
    2690                 2695                 2700

Ile Arg  Val Leu Thr Asp Asp  Leu His Ala Leu Tyr  Ala Gly Arg
    2705                 2710                 2715

Asp Leu  Pro Pro Leu Ser Ile  Gln Tyr Arg Asp Tyr  Ala Ala Trp
    2720                 2725                 2730

His Asn  Ala Ser Leu Ala Gly  Pro Arg Ala Ala Ala  His Arg Ala
    2735                 2740                 2745

Tyr Trp  Leu Glu Gln Leu Ala  Pro Pro Leu Pro Arg  Leu Gln Leu
    2750                 2755                 2760

Ala Ser  Asp Phe Pro Arg Pro  Glu Arg Leu Gly His  Ala Gly Gln
    2765                 2770                 2775

Thr Leu  Glu Val Glu Leu Pro  Gln Pro His Ala Ala  Glu Leu Ala
    2780                 2785                 2790

Thr Leu  Ala Arg Ala His His  Thr Ser Leu His Ala  Val Leu Leu
    2795                 2800                 2805

Ala Ser  Phe Cys Val Leu Met  His Arg Tyr Thr Gly  Arg Glu Asp
    2810                 2815                 2820

Ile Val  Ile Gly Ser Val Ser  Ala Gly Arg Asp Ser  Glu Gln Leu
    2825                 2830                 2835
```

-continued

```
Glu Ser  Gln Val Gly Val Tyr  Leu Asn Thr Val Val  Leu Arg Val
    2840                 2845                 2850

Pro Val  Arg Lys Ser Ala Thr  Val Ala Glu Val Ile  Asp Gly Val
    2855                 2860                 2865

Ala Lys  Ala Ser Ala Gln Ala  Leu Glu His Ala Ser  Tyr Pro Phe
    2870                 2875                 2880

Asp Val  Leu Leu Glu Asp Leu  Lys Ile Arg Thr Pro  Ala Asn His
    2885                 2890                 2895

Phe Pro  Ile Phe Asp Ile Gln  Val Asn His Val Ser  Met Pro Ala
    2900                 2905                 2910

Pro Gln  Pro Gly Leu Arg Ile  Thr Asp Ile Ser Pro  Ala Asp Thr
    2915                 2920                 2925

Thr Ala  Lys Phe Asp Leu Ser  Phe Gln Val Val Glu  Ser Glu Gly
    2930                 2935                 2940

Arg His  Leu Ile Gln Phe Ile  Tyr Asn Thr His Leu  Phe Arg Pro
    2945                 2950                 2955

Ser Thr  Ile Ala Ala Met Arg  Asp Arg Leu Leu Ala  Ile His Asp
    2960                 2965                 2970

Val Phe  Arg Arg Asp Pro Ala  Thr Pro Val Asp Arg  Ile Pro Leu
    2975                 2980                 2985

Ser Asp  Glu Ala Pro Ala Ala  Gly Pro Arg Val Arg  Val Gly Leu
    2990                 2995                 3000

Arg Leu  Lys Arg Ala Pro Ala  Val Thr Ala Asp Asp  Ala Leu Glu
    3005                 3010                 3015

Glu Lys  Thr
    3020


<210> SEQ ID NO 13
<211> LENGTH: 1306
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1306)
<223> OTHER INFORMATION: putative nonribosomal peptide synthetase

<400> SEQUENCE: 13

Met Ser Glu Leu Asn Leu Asn Ala Leu Ser Thr Ser Gly Gln Tyr Gln
1               5                   10                  15

Glu His Val Ala Phe Trp Asn Asp Ala Leu Gly Arg Ile Asp Glu Asp
            20                  25                  30

Phe Arg Leu Gln Gln Ala Trp Gln Ala Tyr Ala Leu Pro Leu Gly Pro
        35                  40                  45

Glu Pro Ala Leu Thr Phe Ala Leu Asp Gly Asp Ala Ala Gln Val Leu
    50                  55                  60

Glu Arg Leu Ala Ala Gly Asn Glu Leu Gly Ala Phe Val Val Leu Leu
65                  70                  75                  80

Ala Ala Leu Phe Arg Val Leu Gly Arg Tyr Asn Gly Ala Ala Gly Leu
                85                  90                  95

Phe Val Ala Ser Pro Gln Leu Ile Val Glu Pro Ala Ser Gly Cys Ala
            100                 105                 110

Glu Pro Val Pro Leu Leu Asp Ala Gly Glu Pro Gly Pro Thr Val Arg
        115                 120                 125

Ala Tyr Leu Asn Gln Leu Arg Asp Ser Val Gln Arg Ser Tyr Ser Tyr
    130                 135                 140

Gln Asp Phe Pro Ile Ala Ala Leu Ala His Lys Leu His Gly Glu Arg
```

-continued

```
145                 150                 155                 160

Arg Ala Thr Asn Val Gly Val Arg Phe Asp Gly Leu His Glu Ala Trp
                165                 170                 175

Ala Ala Ala Asp Tyr Asp Leu Ser Ile Glu Ile Arg His Arg Glu Arg
            180                 185                 190

Tyr Glu Ile Val Leu Thr Gly Arg Pro Thr Val Phe Thr Leu His Tyr
        195                 200                 205

Leu Gln His Val Ala Arg His Leu Arg Asn Val Val Ala Gly Phe Gly
    210                 215                 220

Ala Leu Asp Ala Pro Leu Asp Thr Val Ser Leu Leu Asp Asp Glu Glu
225                 230                 235                 240

Arg Ala Arg Leu Arg Ser His Ala Ala Pro Val Ala Val Gln Gly Thr
                245                 250                 255

Phe Leu Glu Gln Phe Ala Gln Arg Val Ala Ala Ala Pro Asp Ser Val
            260                 265                 270

Ala Val Val Thr Ala Asp Ala Ser Leu Thr Tyr Ala Glu Leu Asp Asp
        275                 280                 285

Gln Ala Ser Arg Leu Ala Ser Phe Leu Leu Ala Glu Tyr Ala Ile Glu
    290                 295                 300

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

Val Gly Met Leu Gly Ala Leu Lys Ala Gly Ala Val Tyr Leu Pro Leu
                325                 330                 335

Asp Pro Glu Phe Pro Arg Glu Arg Leu Arg Phe Met Ile Glu Asp Ala
            340                 345                 350

Lys Val Lys Ala Leu Leu Thr His Ser Glu His Leu Pro Leu Leu Ala
        355                 360                 365

Asp Phe Trp Ala Ile Pro Met Phe Ala Leu Asp Phe Gln Leu Asp Thr
    370                 375                 380

Leu Ala Pro Ala Ser Ala Ser Ala Gln Val Glu Val Arg Pro Asp Asp
385                 390                 395                 400

Ala Ala Tyr Ile Ile Tyr Thr Ser Gly Ser Thr Gly Val Pro Lys Gly
                405                 410                 415

Val Val Leu Glu His Ala Gly Leu Leu Asn Met Ala Gln Tyr His Val
            420                 425                 430

Asp Ala Phe Gly Phe Asp Ser Ala Asp Arg Phe Val Gln Phe Tyr Ser
        435                 440                 445

Pro Gly Phe Asp Gly Ser Ile Met Glu Ile Phe Val Thr Leu Leu Ala
    450                 455                 460

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

Arg Phe Val Asp Tyr Ile Ala Gln Gln Gly Val Thr Thr Val Asn Ala
                485                 490                 495

Thr Pro Ala Tyr Leu Ala Ala Leu Asp Trp His Ala Leu Gly Ala Val
            500                 505                 510

Lys Arg Val Ile Ser Ala Gly Asp Ser Ala Arg Val Ala Asp Leu Arg
        515                 520                 525

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

Ala Thr Val Cys Ile Ala Asp Tyr Val Val Asp Pro Ala Ile Thr Tyr
545                 550                 555                 560

Gly Ala Arg Leu Pro Val Gly Arg Pro Ile His Asn Thr His Leu Tyr
                565                 570                 575
```

-continued

```
Leu Leu Asp Glu His Gly Ala Leu Ala Pro Glu Gly Cys Ala Gly Glu
            580                 585                 590

Ile Cys Val Ser Gly Ile Ala Leu Ala Arg Gly Tyr Val Gly Arg Asp
        595                 600                 605

Asp Leu Thr Ala Ala Ala Phe Val Ala His Pro Phe Glu Ala Gly Glu
    610                 615                 620

Arg Leu Tyr Arg Thr Gly Asp Leu Gly Val Trp Leu Pro Asp Gly Asn
625                 630                 635                 640

Leu Glu Val Thr Gly Arg Arg Asp Thr Gln Val Lys Ile Arg Gly Tyr
                645                 650                 655

Arg Ile Glu Met Gly Glu Ile Glu Ala Ala Leu Arg Gln His Ala Gly
            660                 665                 670

Val Ala Asp Ala Ile Val Phe Val Arg Glu Asp Thr Pro Gln His Lys
        675                 680                 685

Gln Leu Val Ala Cys Val Ala Thr Ala Thr Ala Ser Val Ala Ser Leu
    690                 695                 700

Arg Glu His Leu Lys Glu Arg Leu Pro Glu Phe Met Val Pro Ala Ser
705                 710                 715                 720

Ile Val Thr Leu Glu Arg Leu Pro Leu Thr Pro Asn Gly Lys Pro Asp
                725                 730                 735

Arg Lys Ala Leu Ala Ala Leu Glu Leu Ala Pro Ala Pro Ser Glu Thr
            740                 745                 750

Ala Tyr Val Ala Pro Ala Asn Asp Val Glu Ala Arg Leu Gly Arg Ile
        755                 760                 765

Trp Cys Asp Val Leu Gly Arg Glu Pro Ile Gly Val His Asp Asn Phe
    770                 775                 780

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

Ala Gln Gln Val Gly Leu Lys Phe Thr Ala Asp Gln Phe Phe Ala His
                805                 810                 815

Pro Thr Ile Ala Glu Leu Ala Gln Val Ala Thr Glu Ala Pro Ser Ile
            820                 825                 830

Arg Ile Ala Gln Glu Pro Val Val Gly Pro Ala Pro Leu Thr Pro Ile
        835                 840                 845

Gln His Trp Phe Phe Ala Gln Asp Val Ala Asp Pro His His Tyr Asn
    850                 855                 860

Gln Ser Thr Met Ile Glu Val Pro Ala Ser Leu Arg Pro Asp Thr Ile
865                 870                 875                 880

Glu Arg Ala Leu Ala Ala Val Ala Thr His His Asp Ala Leu Arg Leu
                885                 890                 895

Ser Phe Ala Cys Val Ala Gly Val Trp Gln Gln Ser His Ala Ala Pro
            900                 905                 910

Pro Leu Ala Ile Pro Leu Gly Val Thr Ser Leu Ala Asp Ala Ala Pro
        915                 920                 925

Ala Ala Arg Gln Ala Ala Met Leu Ala Thr Ala Thr Gly Met Gln Glu
    930                 935                 940

Ser Phe Thr Leu Ser Ala Pro Pro Leu Leu Arg Ala His Leu Phe Gln
945                 950                 955                 960

Phe Gly Pro Asp Ala Pro Gln Arg Leu Leu Ala Val Ala His His Leu
                965                 970                 975

Val Ile Asp Gly Val Ser Trp Arg Ile Leu Phe Glu Asp Leu Tyr Thr
            980                 985                 990
```

-continued

```
Ala Cys Arg Gln Leu Glu Ala Gly  Asp Ala Val Gln Leu  Pro Ala Arg
       995                1000                1005

Thr Thr  Ala Trp Arg Asp Trp  Ser Thr Arg Leu Ser  Gly Leu Gly
    1010                1015                1020

Ala Thr  Ala Leu Asp Gly Leu  Gly Leu Asp Tyr Trp  Leu Gln Gly
    1025                1030                1035

Asn Ala  Gly Glu Pro Ala Cys  Phe Asp Asp Met Pro  Ala Gly Thr
    1040                1045                1050

Val Ala  Glu Ala Gly Ser Thr  Ile Val Glu Phe Asp  Ala Gln Gln
    1055                1060                1065

Thr Leu  Ala Leu Leu Gln Asp  Val Pro Arg Ala Phe  Asn Thr Gln
    1070                1075                1080

Ile Asn  Glu Val Leu Leu Thr  Ala Leu Leu Leu Ala  Phe Gly Asp
    1085                1090                1095

Trp Thr  Gly Asn Ala Ser Leu  Val Val Asp Leu Glu  Gly His Gly
    1100                1105                1110

Arg Glu  Asp Ile Phe Asp Gly  Val Asp Thr Ser Arg  Thr Ile Gly
    1115                1120                1125

Trp Phe  Thr Thr His Tyr Pro  Val Cys Leu Asn Ala  Gly Asp Ala
    1130                1135                1140

Thr Val  Ala Val Asp Ala Leu  Arg His Val Lys Glu  Gln Leu Arg
    1145                1150                1155

Ala Val  Pro Met Arg Gly Leu  Gly Tyr Gly Ile Ala  Arg Tyr Leu
    1160                1165                1170

Gly His  Asp Ala Gly Ile Ala  Ala Ala Leu Glu Arg  Gln Pro Pro
    1175                1180                1185

Ala Pro  Val Arg Phe Asn Tyr  Leu Gly Gln Val Asp  Arg Val Leu
    1190                1195                1200

Pro Asp  Asp Thr Gly Trp Lys  Pro Val Leu Asp Phe  Gln Ser Pro
    1205                1210                1215

Glu His  Ser Pro Arg Ala Arg  Arg Gly His Leu Phe  Glu Ile Asp
    1220                1225                1230

Gly Met  Val Phe Asp Gly Arg  Leu Arg Leu Thr Trp  His Tyr Asn
    1235                1240                1245

Arg Glu  Ala Cys Ala Pro Gly  Val Ile Glu Gln Leu  Thr Gln Cys
    1250                1255                1260

Tyr Arg  Ser Arg Leu Leu Ser  Ile Val Ala Ala Gly  Gly Asp Gly
    1265                1270                1275

Pro Arg  Ala Leu Ser Pro Ser  Asp Phe Pro Ala Ala  Arg Ile Ser
    1280                1285                1290

Gln Glu  Ala Leu Asp Ala Leu  Val Ser Arg Ile Lys  Ser
    1295                1300                1305


<210> SEQ ID NO 14
<211> LENGTH: 538
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(538)
<223> OTHER INFORMATION: putative beta-lactamase domain protein

<400> SEQUENCE: 14

Met Thr Ile Ser Ser Ser Ala Gln Val Tyr Leu Arg Gln Asn Ile Gln
1               5                  10                  15

Phe Glu Pro Leu Ile Asn Ser Trp Tyr Ala Trp Tyr His Thr Leu Pro
```

-continued

```
           20                  25                  30

Pro Leu Thr Ala Ala Leu Asn Val Ala Glu Arg Phe Leu Pro Leu Leu
        35                  40                  45

Lys Ser Tyr Ala Ala Ser Pro Met Met His Ala Ala Ala Cys Lys Asp
    50                  55                  60

Pro Ala Met Arg Gly Gly Pro Phe Leu Asp Leu Gly Gly Gln Arg Val
65                  70                  75                  80

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

Gln Leu Glu Leu Ala Lys Ala Tyr Lys Ala Phe Ser Thr Leu Leu Leu
            100                 105                 110

Glu Arg Ala Thr Gly Met Ala Ser Asp Pro Leu Tyr Pro Glu Ile Pro
        115                 120                 125

Glu Val Leu Lys Gly Tyr Val Glu Ile Tyr Tyr Asp Leu Asn His Asn
    130                 135                 140

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

Ala Arg Asp Ala Gln Ser Ile Ala Leu Ser Ala Ile Glu Glu His Thr
                165                 170                 175

Pro Arg Pro Phe Ile Leu Ser Thr Pro Arg Leu Arg Asp Glu Arg Thr
            180                 185                 190

Val Phe Ser Asn Met Ala Phe Asp Asp Arg Ala Leu Asp Thr Leu Phe
        195                 200                 205

Arg Met Arg Asp Thr Pro Gly Ser Tyr Ala Lys Ile Val Asp Leu Met
    210                 215                 220

Arg Val Glu Glu Lys Asp Glu Pro Leu Phe Arg Ser Phe Phe Val Glu
225                 230                 235                 240

Glu Ala Pro Ala Pro Lys Pro Asp Arg Ser Phe Asp Gly Asp Asp Ile
                245                 250                 255

Arg Ile Arg Tyr Tyr Gly His Ala Cys Val Leu Ile Gln Ser Arg Gly
            260                 265                 270

Val Ser Ile Leu Ile Asp Pro Val Ile Ser Tyr Gly Tyr Asp Thr Ala
        275                 280                 285

Leu Pro Arg Tyr Thr Phe Ala Asp Leu Pro Asp Gln Ile Asp Tyr Val
    290                 295                 300

Leu Ile Thr His Ser His His Asp His Ile Val Leu Glu Thr Leu Leu
305                 310                 315                 320

Gln Leu Arg His Lys Val Lys Thr Val Val Val Gly Arg Asn Leu Asp
                325                 330                 335

Gly Phe Pro Gln Asp Pro Ser Met Glu Leu Ala Leu Arg Lys Leu Gly
            340                 345                 350

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

Gly Gly Ala Ile Thr Ala Ile Pro Phe Met Gly Glu His Asn Asp Leu
    370                 375                 380

Ala Ile His Ser Lys Gln Ser Phe Met Ile Arg Phe Gly Ser Arg Ser
385                 390                 395                 400

Val Leu Cys Ile Ala Asp Ser Cys Asn Leu Asp Pro Arg Leu Tyr Glu
                405                 410                 415

His Val Phe Arg Leu Ala Gly Lys Pro Asp Thr Leu Phe Val Gly Met
            420                 425                 430

Glu Thr Glu Gly Ala Pro Pro Ser Trp Val Tyr Gly Pro Leu Phe Pro
        435                 440                 445
```

-continued

```
Lys Ala Leu Pro Arg Asp Ile Asp Gln Ser Arg Arg Ala Arg Gly Cys
    450                 455                 460

Gln Phe Gly Glu Ala Ala Ala Leu Val Asp Asp Phe Ala Phe Asn Ala
465                 470                 475                 480

Ala Tyr Val Tyr Ala Met Gly Gln Glu Pro Trp Leu Asn His Leu Leu
                485                 490                 495

Asp Asn Thr Phe Asp Glu Asn Ser Pro Ser His Ile Gln Ser Thr Gln
            500                 505                 510

Phe Val Ala His Cys Lys Ala Lys Gly Ile Ala Ser Glu Ile Leu Tyr
        515                 520                 525

Ala Thr Arg Glu Ile Val Leu Cys Gln Asn
    530                 535


<210> SEQ ID NO 15
<211> LENGTH: 4469
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(4469)
<223> OTHER INFORMATION: putative beta-ketoacyl synthase nonribosomal
      peptide synthetase

<400> SEQUENCE: 15

Met Asn Ala Lys Ala Thr His Ala Leu Lys Ala Ala Leu Asp Glu Leu
1               5                   10                  15

Arg Leu Arg Arg Ala Glu Ile Ala Ala Leu Arg Ser Asp Arg Asn Glu
            20                  25                  30

Pro Ile Ala Val Ile Gly Met Ala Cys Arg Phe Pro Gly Arg Ser Asp
        35                  40                  45

Thr Pro Asp Ala Phe Trp Gln Leu Leu Asp Gly Ala His Asp Ala Val
    50                  55                  60

Thr Glu Val Pro Gly Glu Arg Trp Asp Ile Asp Arg Tyr Tyr Asp Pro
65                  70                  75                  80

Asp Pro Ser Thr Pro Gly Lys Met Ala Thr Arg His Gly Ala Phe Leu
                85                  90                  95

Glu Arg Val Asp Gln Phe Asp Ala Ala Phe Phe Gly Ile Ala Pro Arg
            100                 105                 110

Glu Ala Thr Tyr Leu Asp Pro Gln Gln Arg Leu Leu Leu Glu Val Ala
        115                 120                 125

Trp Glu Ala Leu Glu Asn Ala His Leu Ala Pro Glu Arg Phe Arg Gln
    130                 135                 140

Ser Ala Thr Gly Val Tyr Val Gly Ile Thr Cys Phe Asp His Ala Ile
145                 150                 155                 160

Gln Val Ser Asn Ala Ser Met Pro Ser Ser Ser Tyr Ala Gly Thr Gly
                165                 170                 175

Ser Ala Leu Asn Met Ala Ala Gly Arg Leu Ser Phe Val Leu Gly Leu
            180                 185                 190

Thr Gly Pro Ser Met Ala Ile Asp Thr Ala Cys Ser Ser Ser Leu Val
        195                 200                 205

Cys Leu His Leu Ala Cys Glu Ser Leu Arg Ser Arg Glu Ser Asn Met
    210                 215                 220

Ala Leu Ala Gly Gly Val Asn Leu Met Leu Ser Pro Glu Val Met Val
225                 230                 235                 240

Ser Phe Ser Gln Ala Arg Met Leu Ser Pro Asp Gly Arg Cys Lys Thr
                245                 250                 255
```

-continued

```
Phe Asp Ala Ala Ala Asp Gly Tyr Val Arg Gly Glu Gly Cys Gly Met
            260                 265                 270

Val Val Leu Lys Arg Leu Ala Asp Ala Leu Ala Asp Gly Asp Arg Val
        275                 280                 285

Leu Gly Ile Val Arg Gly Thr Ala Val Asp Gln Gly Gly Ala Gly Gly
    290                 295                 300

Gly Leu Thr Val Pro Ser Arg Asp Ser Gln Glu Arg Val Ile Arg Arg
305                 310                 315                 320

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

Ala His Gly Thr Gly Thr Ser Leu Gly Asp Pro Ile Glu Val Glu Ala
            340                 345                 350

Leu Ala Gly Val Tyr Gly Pro Gly Arg Ala Ala Asn Glu Pro Leu Val
        355                 360                 365

Ile Gly Ser Val Lys Thr Asn Ile Gly His Leu Glu Ser Ala Ser Gly
    370                 375                 380

Ile Ala Gly Leu Ile Lys Val Leu Leu Ser Phe Glu His Asp Arg Ile
385                 390                 395                 400

Pro Ala His Leu His Phe Thr Gln Pro Asn Pro His Thr Pro Trp Gln
                405                 410                 415

Asp Ile Pro Ile Arg Val Ala Ala Asp Pro Val Ala Trp Arg Arg Gly
            420                 425                 430

Glu Arg Arg Arg Ile Ala Gly Val Ser Ala Phe Gly Phe Ser Gly Thr
        435                 440                 445

Asn Ala His Ala Ile Val Glu Glu Pro Pro Val Ala Pro Ala His Ala
    450                 455                 460

Ala Gln Arg Ala Leu Leu Leu Leu Ser Ala Arg Ser Glu Ala Ala Leu
465                 470                 475                 480

Ala Ala Leu Val Pro Arg Tyr Glu Arg Ala Ile Ala Gly Ala Thr Pro
                485                 490                 495

Gln Glu Leu Ala Ala Ile Cys Arg Ala Ala Ala Thr Gly Arg Ser His
            500                 505                 510

Tyr Pro Phe Arg Ala Ala Tyr Val Ser Gly Ala Arg Val Ala Ser Ala
        515                 520                 525

Ala Ala Pro Arg Thr Gly Lys Ala Leu Arg Met Gly Phe Gly Phe Gly
    530                 535                 540

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

Phe Arg Asp Ala Phe Ala Arg Cys Ser Val Pro Leu Asp Ala Leu Glu
                565                 570                 575

Thr Asp Ala Gly Arg Phe Ala Ile Gln Phe Ala Trp Ala Glu Leu Trp
            580                 585                 590

Lys Gly Trp Gly Leu Arg Pro Ala Val Val Ser Gly His Gly Ile Gly
        595                 600                 605

Glu Tyr Val Ala Ala Cys Val Ala Gly Val Val Ser Val Ala Asp Ala
    610                 615                 620

Leu Arg Leu Val Ala Ala Arg Ser Asp Ala Glu Ala Leu Arg Ala Val
625                 630                 635                 640

Leu Arg Asp Met Pro Leu Ala Arg Pro Ser Val Arg Leu Ile Ser Gly
                645                 650                 655

Tyr Leu Gly Thr Asp Val Thr Asp Glu Val Thr His Pro Gln Tyr Trp
            660                 665                 670
```

-continued

```
Leu Gln Leu Ala Gly Ala Ser Asp Gln Ala Asp Ala Ser His Pro Pro
        675                 680                 685

Glu Gly Leu Ala Asp Gly Trp Leu Pro Pro Pro Cys Ala Gly Asp Ala
    690                 695                 700

Leu Glu Arg Ala Leu Ala Ala Leu Tyr Val Gln Gly Ala Gln Phe Asp
705                 710                 715                 720

Trp Arg Ala Leu Phe Pro Ala Pro Ala Gln Pro Ala Thr Thr Leu Pro
                725                 730                 735

Asn Tyr Pro Phe Glu Arg Gln Arg Phe Ser Leu Glu Lys Ile Pro Ser
            740                 745                 750

Pro Ile Val Gly Met Asp Ala Gly Ser Ile Asp Ala Ala Leu Arg His
        755                 760                 765

Leu Lys Ser Ser Gly Lys Tyr Pro Glu Asp Met Leu Asn Ala Phe Pro
    770                 775                 780

Asp Leu Leu Arg Thr Ala Phe Ala Ala Ala Glu Thr Val Ala Ser Asn
785                 790                 795                 800

Ala His Pro Leu Tyr His Val Val Trp Glu Gln Gln Ala Ala Met Pro
                805                 810                 815

Ala Ala Pro Ala Ala Ala Asp Ala Ser Pro Trp Leu Ile Phe Ala Asp
            820                 825                 830

Ala Ser Gly Val Gly Glu Arg Leu Ala Ala Leu Leu Arg Ala Arg Gly
        835                 840                 845

Ala Ser Cys Ser Leu Val Arg Pro Gly Ile Asp Tyr Val Thr Gly Ala
    850                 855                 860

Glu Ala Gly Trp Gln Val Ala Pro Glu Arg Pro Asp Asp Phe Val Arg
865                 870                 875                 880

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

Ala Leu Asp Glu Ala Val Gly Glu Thr Arg Met Ser Ala Ala Leu Leu
            900                 905                 910

His Leu Val His Ala Leu Val Gly Ser Glu Arg Glu Trp Thr Pro Ser
        915                 920                 925

Thr Arg Pro Arg Ile Ser Val Val Thr Arg Asp Ala Val Glu Ala Gly
    930                 935                 940

Glu Ala Pro His Val Ser Gly Leu Ala Gln Ala Ala Leu Ser Gly Leu
945                 950                 955                 960

Ala Arg Gly Ala Met Ile Glu His Pro Glu Trp Phe Gly Thr Ala Ile
                965                 970                 975

Asp Leu Asp Pro Ala Ala Pro Glu Asn Glu Thr Gln Ala Leu Leu Gln
            980                 985                 990

Glu Met Leu Gly Glu Ser Arg Glu  Glu Gln Val Ala Leu  Arg His Gly
        995                 1000                1005

Ala Arg  His Val Ala Arg Leu  Ser Pro Leu Ala Pro  Ala Glu Thr
    1010                1015                1020

Ala Ala  Leu Pro Val Asp Pro  Asp Ala Ala Tyr Leu  Ile Thr Gly
    1025                1030                1035

Gly Phe  Gly Ala Leu Gly Leu  His Thr Ala Arg Trp  Leu Ala Ala
    1040                1045                1050

Arg Gly  Ala Gly Thr Leu Ile  Leu Val Gly Arg Gln  Gly Ala Ala
    1055                1060                1065

Ser Asp  Glu Ser Gln Arg Ala  Ile Ala Glu Leu Arg  Glu Arg Asn
    1070                1075                1080

Val Thr  Leu Arg Cys Glu Arg  Leu Asp Ile Ala Asp  Pro Ala Ala
```

-continued

```
    1085                1090                1095

Val Ala  Ala Phe Phe Ala Ala  Leu Arg Arg Asp Gly  Val Pro Leu
    1100                1105                1110

Lys Gly  Ile Val His Ala Ala  Gly Ile Val Gly Tyr  Lys Pro Ile
    1115                1120                1125

Met Gln  Val Glu Arg Asp Glu  Leu Asp Ala Val Leu  Gln Pro Lys
    1130                1135                1140

Val Ala  Gly Ala Trp Leu Leu  His Gln Gln Ser Glu  His Phe Pro
    1145                1150                1155

Leu Asp  Phe Phe Leu Leu Phe  Ser Ser Ile Ala Ser  Ala Trp Gly
    1160                1165                1170

Ser Arg  Glu Gln Ala His Tyr  Ser Ala Ala Asn Arg  Phe Leu Asp
    1175                1180                1185

Ala Leu  Ala His His Arg Arg  Gly Gln Gly Leu Pro  Ala Leu Ser
    1190                1195                1200

Val Asn  Trp Gly Pro Trp Ala  Glu Gly Gly Met Thr  Phe Pro Glu
    1205                1210                1215

Ala Glu  Ala Leu Leu Arg Arg  Val Gly Ile Arg Ser  Leu Ala Ala
    1220                1225                1230

Asp Arg  Ala Leu Asp Val Leu  Asn Arg Leu Pro Ala  Val Pro Gln
    1235                1240                1245

Val Ala  Val Val Asp Ile Asp  Leu Ala Leu Phe Gln  Gly Ser Tyr
    1250                1255                1260

Glu Ala  Arg Gly Pro Lys Pro  Phe Leu Asp His Val  Arg Val Ala
    1265                1270                1275

Lys Ser  Ala Pro Ser Ala Pro  Ala Met Pro Ala Leu  Ser Asp Ala
    1280                1285                1290

Ser Pro  Arg Glu Arg Lys Arg  Leu Leu Ala Asp Ser  Ile Asp Arg
    1295                1300                1305

Ala Val  Ala Gln Val Leu Gly  Tyr Asp Ala Gly Thr  Leu Asp Arg
    1310                1315                1320

Asp Leu  Gly Phe Phe Glu Met  Gly Met Asp Ser Leu  Met Ala Leu
    1325                1330                1335

Asp Val  Arg Thr His Leu Glu  Asn Ala Leu Gly Ile  Pro Leu Ser
    1340                1345                1350

Val Ala  Leu Leu Phe Asp His  Pro Thr Val Asn Ala  Leu Ala Asp
    1355                1360                1365

Phe Leu  Ala Glu Gln Ala Ser  Gly Thr Ala Gln Ala  Gln Thr Val
    1370                1375                1380

Pro Pro  Gln Gln Gln Pro Arg  Pro Ile Ala Pro Ala  Ile Glu Ala
    1385                1390                1395

Arg Asp  Ala Gly Thr Pro Glu  Pro Ile Ala Ile Val  Gly Met Ser
    1400                1405                1410

Cys Arg  Phe Pro Gly Ala Ala  His Asp Leu Asp Ala  Tyr Trp Asn
    1415                1420                1425

Leu Leu  Asn Asp Gly Val Asp  Ala Ile Ser Glu Val  Pro Arg Glu
    1430                1435                1440

Arg Trp  Asp Val Asp Ala Tyr  Tyr Asp Pro Asp Pro  Glu Ala Pro
    1445                1450                1455

Gly Arg  Met Tyr Ser Arg Phe  Gly Gly Phe Leu Asp  Asp Val Asp
    1460                1465                1470

Gln Phe  Asp Pro Ala Phe Phe  Arg Ile Thr Pro Arg  Glu Ala Ala
    1475                1480                1485
```

-continued

```
Ala Met  Asp Pro Gln Gln Arg  Leu Leu Leu Glu Val  Ser His Glu
    1490                 1495                 1500

Ala Leu  Glu His Ala Gly Ile  Pro Val Asp Ser Leu  Lys Gly Ser
    1505                 1510                 1515

Arg Thr  Gly Val Phe Val Gly  Ile Thr Thr Asn Asp  Tyr Ala Asn
    1520                 1525                 1530

Leu Gln  Leu Arg Asn Gly Gly  Gly Ser Gly Ile Asp  Gly Tyr Phe
    1535                 1540                 1545

Phe Thr  Gly Asn Pro Leu Asn  Thr Ala Ala Gly Arg  Ile Ser Tyr
    1550                 1555                 1560

Gly Leu  Gly Val Gln Gly Pro  Ser Met Ala Ile Asp  Thr Ala Cys
    1565                 1570                 1575

Ser Ser  Ser Leu Thr Ala Ile  His Thr Ala Ser Gln  Asn Leu Arg
    1580                 1585                 1590

Ser Gly  Glu Cys Asp Leu Ala  Ile Ala Gly Gly Val  Asn Leu Ile
    1595                 1600                 1605

Leu Ser  Pro Asp Asn Ser Ile  Ala Val Ser Arg Thr  Arg Ala Leu
    1610                 1615                 1620

Ala Pro  Asp Gly Arg Cys Lys  Thr Phe Asp Ala Ala  Ala Asp Gly
    1625                 1630                 1635

Phe Val  Arg Ser Glu Gly Cys  Gly Ala Leu Val Leu  Lys Arg Leu
    1640                 1645                 1650

Ser Asp  Ala Leu Ala Ala Gly  Asp Arg Val Leu Ala  Val Leu Arg
    1655                 1660                 1665

Gly Ser  Ala Val Asn His Asp  Gly Ala Ser Ser Gly  Phe Thr Ala
    1670                 1675                 1680

Pro Asn  Gly Arg Ala Gln Glu  Ala Val Ile Arg Gln  Ala Leu Gly
    1685                 1690                 1695

Gly Leu  Pro Ala Ala Ser Ile  Asp Tyr Val Glu Ala  His Gly Thr
    1700                 1705                 1710

Gly Thr  Pro Leu Gly Asp Pro  Val Glu Leu Gln Ala  Leu Ala Thr
    1715                 1720                 1725

Val Phe  Gly Ala Gly Arg Asp  Ala Gly Arg Arg Leu  Arg Val Gly
    1730                 1735                 1740

Ser Val  Lys Thr Asn Ile Gly  His Thr Glu Ser Ala  Ala Gly Ile
    1745                 1750                 1755

Ala Gly  Val Ile Lys Val Val  Leu Ser Leu Asn His  Asp Arg Leu
    1760                 1765                 1770

Pro Ala  His Leu His Phe Arg  Gln Pro Ser Pro Leu  Val Gln Trp
    1775                 1780                 1785

Asp Ala  Met Pro Val Glu Ile  Cys Ala Glu Ala Ser  Ala Trp Pro
    1790                 1795                 1800

Arg Gly  Glu Arg Pro Arg Arg  Ala Gly Val Ser Ala  Phe Gly Ala
    1805                 1810                 1815

Ser Gly  Thr Asn Ala His Leu  Val Leu Glu Glu Ala  Pro Ala Pro
    1820                 1825                 1830

Ala Arg  Gln Ala Thr Pro Ser  Arg His Lys Val His  Pro Leu Val
    1835                 1840                 1845

Leu Ser  Ala Lys Thr Pro Ala  Ala Leu Arg Glu Leu  Ala Gly Arg
    1850                 1855                 1860

Tyr Gln  Arg Arg Leu Glu Ala  Glu Pro Gly Leu Asp  Ile Ala Ala
    1865                 1870                 1875
```

-continued

```
Val Ala  Phe Ser Ala Ala Thr  Gly Arg Ser His Phe  Ala His Arg
    1880                 1885                 1890

Leu Ala  Trp Pro Val Thr Ser  Leu Asp Asp Ala Ile  Asp Lys Leu
    1895                 1900                 1905

Arg Ala  Phe His Ala Lys Glu  Pro Ala Gly Ala Ala  Gln Pro Ala
    1910                 1915                 1920

Pro Arg  Val Lys Met Ala Phe  Leu Phe Thr Gly Gln  Gly Ser Gln
    1925                 1930                 1935

Tyr Ala  Gly Met Gly Arg Arg  Leu Tyr Asp Ala Tyr  Pro Val Phe
    1940                 1945                 1950

Arg Asp  Ala Ile Asp Arg Cys  Arg Ala Val Ala Asp  Pro Leu Leu
    1955                 1960                 1965

Asp Lys  Pro Leu Leu Glu Val  Leu Ser Ala Gln Gly  Glu Asp Ile
    1970                 1975                 1980

His Gln  Thr Gly Tyr Ser Gln  Pro Ala Leu Phe Ser  Leu Gln Tyr
    1985                 1990                 1995

Ala Leu  Thr Thr Leu Leu Ala  Ser Phe Gly Val Val  Pro Asp Ala
    2000                 2005                 2010

Val Met  Gly His Ser Val Gly  Glu Tyr Ala Ala Ala  Cys Ala Ala
    2015                 2020                 2025

Gly Val  Phe Ser Pro Glu Asp  Gly Leu Arg Leu Ile  Ala Glu Arg
    2030                 2035                 2040

Gly Arg  Leu Met Gln Ala Leu  Pro Arg Asp Gly Glu  Met Ala Ala
    2045                 2050                 2055

Ile Phe  Thr Asp Leu Ala Thr  Val Glu Arg Ala Ile  Asp Ala Trp
    2060                 2065                 2070

Pro His  Glu Val Ala Val Ala  Ala Val Asn Gly Pro  Ala Ser Ile
    2075                 2080                 2085

Val Ile  Ser Gly Lys Arg Glu  Arg Ile Ala Met Leu  Val Asp Ala
    2090                 2095                 2100

Phe Ala  Ala Arg Asp Ile Arg  Ser Val Pro Leu Asn  Thr Ser His
    2105                 2110                 2115

Ala Phe  His Ser Pro Leu Leu  Glu Pro Met Leu Asp  Ser Phe Gln
    2120                 2125                 2130

Leu Ala  Ala Lys Thr Val Pro  Val Ala Arg Pro Ala  Ile Pro Phe
    2135                 2140                 2145

Tyr Ser  Asn Leu Thr Gly Ala  Val Met Asp Glu Ala  Pro Thr Asp
    2150                 2155                 2160

Thr Tyr  Trp Arg Arg His Cys  Arg Glu Pro Val Gln  Phe Ala Ser
    2165                 2170                 2175

Ser Val  Glu Arg Leu Ala Glu  Ala Gly Phe Asn Val  Leu Val Glu
    2180                 2185                 2190

Ile Gly  Pro Lys Pro Val Leu  Val Asn Leu Ala Arg  Ala Cys Cys
    2195                 2200                 2205

Ala Pro  Asp Ala Gly Ile Gln  Phe Leu Ala Leu Gln  Arg Pro Gln
    2210                 2215                 2220

Val Glu  Gln Gln Ala Leu Ile  Glu Thr Leu Ser Ser  Leu Tyr Ala
    2225                 2230                 2235

Arg Gly  Val Asp Val Asp Trp  Ala Pro Thr Glu Thr  Pro Ala Pro
    2240                 2245                 2250

Ala Arg  Ile Ala Leu Pro Ser  Tyr Pro Phe Gln Arg  Ser Arg Thr
    2255                 2260                 2265

Trp Phe  Gln Lys Ala Asp Thr  Ser Met Thr Gln Thr  Ser Ala Ser
```

-continued

```
    2270                2275                2280

Pro Ile  Ala Ala Ala Pro Thr  His Asn Arg Ser Gly  Glu Ile Leu
    2285                2290                2295

Glu Trp  Leu Arg Gly Lys Ile  Gly Glu Leu Ile Gln  Ala Asp Pro
    2300                2305                2310

Ala Thr  Ile Asn Ile Glu Leu  Pro Phe Leu Glu Met  Gly Ala Asp
    2315                2320                2325

Ser Ile  Val Leu Ile Glu Ala  Ile Arg His Ile Glu  Ala Glu Tyr
    2330                2335                2340

Gly Val  Lys Leu Ala Met Arg  Arg Phe Phe Glu Asp  Leu Ala Thr
    2345                2350                2355

Val Gln  Ala Leu Ala Glu Tyr  Val Ala Asp Asn Leu  Pro Ala Ala
    2360                2365                2370

Ala Ala  Pro Ser Gly Ala Glu  Ala Val Ala Val Ala  Val Ala Ala
    2375                2380                2385

Ala Glu  Pro Ser Thr Pro Ala  Val Ala Val Thr Pro  Ser Ala Ala
    2390                2395                2400

Gly Leu  Ala Pro Leu Ala Ala  Ala Pro Ala Glu Trp  Val Ala Ala
    2405                2410                2415

Glu Gly  Gly Ser Thr Val Glu  Arg Val Leu Arg Glu  Gln Asn Gln
    2420                2425                2430

Leu Leu  Ser His Val Met Ser  Gln Gln Met Glu Leu  Leu Arg Thr
    2435                2440                2445

Ser Leu  Thr Gly Gln Pro Gly  Val Arg Pro Ala Thr  Ala Ala Val
    2450                2455                2460

Gln Ala  Val Ala Ser Thr Ala  Ser Val Ala Pro Lys  Ala Ala Ser
    2465                2470                2475

Ala Ala  Pro Ala Ala Ala Pro  Ala Ala Lys Pro Ala  Pro Ala Ala
    2480                2485                2490

Ala Ala  Ala Pro Ala Ala Asp  Asn Pro Pro Pro Lys  Pro Met Met
    2495                2500                2505

Pro Trp  Gly Ser Pro Val Gln  Gln Arg Ala Arg Gly  Leu Ser Ala
    2510                2515                2520

Ala Gln  Gln Glu His Leu Glu  Ala Leu Ile Val Arg  Tyr Thr Thr
    2525                2530                2535

Arg Thr  Arg Lys Ser Lys Asp  Ser Val Gln Ala Ser  Arg Pro Val
    2540                2545                2550

Leu Ala  Asp Ser Arg Ala Thr  Val Gly Phe Arg Phe  Ser Thr Lys
    2555                2560                2565

Glu Met  Leu Tyr Pro Ile Val  Gly Asp Arg Ala Ala  Gly Ser Arg
    2570                2575                2580

Leu Trp  Asp Ile Asp Gly Asn  Glu Tyr Ile Asp Phe  Thr Met Gly
    2585                2590                2595

Phe Gly  Val His Leu Phe Gly  His Thr Pro Asp Phe  Ile Gln Gln
    2600                2605                2610

Gln Val  Thr Arg Glu Trp Gln  Arg Pro Leu Glu Leu  Gly Ala Arg
    2615                2620                2625

Ser Ser  Leu Val Gly Glu Val  Ala Ala Arg Phe Ala  Arg Val Thr
    2630                2635                2640

Gly Leu  Asp Arg Val Ala Phe  Ser Asn Thr Gly Thr  Glu Ala Val
    2645                2650                2655

Met Thr  Ala Met Arg Leu Ala  Arg Ala Val Thr Gly  Arg Asp Lys
    2660                2665                2670
```

-continued

```
Ile Val  Met Phe Thr His Ser  Tyr His Gly His Ala  Asp Gly Thr
    2675                 2680                 2685

Leu Ala  Ala Ala Asn Ala Glu  Gly Val Thr Glu Thr  Ile Ala Pro
    2690                 2695                 2700

Gly Val  Pro Phe Gly Ser Val  Glu Asn Met Ile Leu  Leu Asp Tyr
    2705                 2710                 2715

Gly Ser  Asp Ala Ala Leu Glu  Ala Ile Arg Gly Met  Ala Ser Thr
    2720                 2725                 2730

Leu Ala  Ala Val Met Val Glu  Pro Val Gln Ser Arg  Asn Pro Ser
    2735                 2740                 2745

Leu Gln  Pro Val Ala Phe Leu  Lys Glu Leu Arg Arg  Ile Thr Glu
    2750                 2755                 2760

Glu Ala  Gly Val Ala Leu Ile  Phe Asp Glu Met Ile  Thr Gly Phe
    2765                 2770                 2775

Arg Val  His Pro Gly Gly Ser  Gln Ala Met Phe Gly  Ile Arg Ala
    2780                 2785                 2790

Asp Leu  Ala Thr Tyr Gly Lys  Ile Ile Gly Gly Gly  Leu Pro Leu
    2795                 2800                 2805

Gly Val  Ile Ala Gly Thr Ser  Arg Phe Met Asp Ala  Ile Asp Gly
    2810                 2815                 2820

Gly Met  Trp Thr Tyr Gly Asp  His Ser Phe Pro Ala  Ala Asp Arg
    2825                 2830                 2835

Thr Ala  Phe Gly Gly Thr Phe  Cys Gln Tyr Pro Leu  Ala Met Ala
    2840                 2845                 2850

Ala Ala  Leu Ala Val Leu Glu  Lys Ile Glu Gln Glu  Gly Pro Ala
    2855                 2860                 2865

Leu Gln  Ala Ala Leu Asn Glu  Arg Thr Ala Gln Ile  Ala Gly Thr
    2870                 2875                 2880

Leu Asn  Ala Phe Phe Ala Glu  Ala Glu Ala Pro Ile  Lys Val Thr
    2885                 2890                 2895

Trp Phe  Gly Ser Met Phe Arg  Phe Glu Phe Thr Glu  Asn Leu Asp
    2900                 2905                 2910

Leu Phe  Phe Tyr His Met Leu  Glu Lys Gly Ile Tyr  Ile Trp Glu
    2915                 2920                 2925

Trp Arg  Thr Cys Phe Leu Ser  Thr Ala His Thr Asp  Ala Asp Ile
    2930                 2935                 2940

Asp Arg  Phe Ile Arg Ala Val  Lys Asp Ser Val Ala  Asp Leu Arg
    2945                 2950                 2955

Arg Gly  Gly Phe Ile Arg Pro  His Ser Lys His Gly  Thr Val Ala
    2960                 2965                 2970

Ala Leu  Ser Glu Ala Gln Arg  Gln Leu Trp Val Leu  Ser Glu Ile
    2975                 2980                 2985

Asp Pro  Glu Gly Ser Leu Ala  Tyr Asn Val Asn Thr  Thr Leu Glu
    2990                 2995                 3000

Leu Asn  Gly Arg Leu Asp Glu  Ala Ala Met Arg Ala  Ala Val Gln
    3005                 3010                 3015

Ser Leu  Val Asp Arg His Glu  Ala Leu Arg Thr Thr  Val Met Ala
    3020                 3025                 3030

Asp Gly  Ser Gly Gln Ile Val  His Pro Ser Leu Thr  Leu Glu Ile
    3035                 3040                 3045

Pro Leu  Ile Asp Thr Asp Pro  Asn Ala Trp Arg Glu  Gln Glu Ser
    3050                 3055                 3060
```

-continued

```
Arg Gln  Pro Phe Asp Leu Val  Asn Gly Pro Leu Phe  Arg Ala Ala
    3065                3070                3075

Leu Val  Arg Leu Gly Ser Glu  Arg His Leu Leu Val  Met Thr Ala
    3080                3085                3090

His His  Ile Ile Cys Asp Gly  Ser Thr Phe Gly Val  Leu Leu Glu
    3095                3100                3105

Asp Leu  Ala Arg Ala Tyr Ala  Gly Ala Ala Pro Ala  Asp Ala Pro
    3110                3115                3120

Leu Gln  Phe Arg Ala Tyr Leu  Lys Gln Leu Asp Gly  Gln Arg His
    3125                3130                3135

Ser Pro  Glu Thr Lys Ala Asn  Arg Glu Tyr Trp Leu  Ala Gln Cys
    3140                3145                3150

Ala Arg  Gln Ala Ala Pro Leu  Asn Leu Pro Val Asp  Tyr Pro Arg
    3155                3160                3165

Pro Ala  Val Lys Thr Phe His  Gly Glu Arg Val Ser  Leu His Leu
    3170                3175                3180

Asp Ala  Ala Thr Ala Ala Thr  Leu Arg Thr Ala Ala  Arg Gln Asn
    3185                3190                3195

Gly Cys  Thr Leu Tyr Met Val  Leu Leu Ala Gly Phe  Asn Leu Phe
    3200                3205                3210

Leu His  Arg Val Ala Gly Gln  Gln Glu Ile Val Thr  Gly Ile Pro
    3215                3220                3225

Val Thr  Gly Arg Ser Val Ala  Gly Ser Asp Arg Leu  Ala Gly Tyr
    3230                3235                3240

Cys Thr  His Leu Leu Pro Leu  His Ser Thr Leu Pro  Glu Gln Ala
    3245                3250                3255

Thr Val  Ala Ser Phe Leu Ala  Gly Thr Arg Gln Asn  Leu Leu Asp
    3260                3265                3270

Ala Leu  Glu His Gln Asp Tyr  Pro Phe Ala Glu Leu  Val Arg Glu
    3275                3280                3285

Ile Gly  Ala Gln Arg Asp Leu  Asn Ala Ala Pro Leu  Val Ser Ala
    3290                3295                3300

Val Phe  Asn Leu Glu Pro Val  Ser Ala Leu Pro Glu  Leu Pro Gly
    3305                3310                3315

Leu Thr  Val Gly Leu Val Ala  Pro Leu Ile Arg His  Thr Ala Phe
    3320                3325                3330

Asp Leu  Asn Val Asn Val Leu  Asp Ala Gly Gln Ala  Leu Leu Ile
    3335                3340                3345

Asp Cys  Asp Tyr Asn Thr Asp  Leu Phe Asp Ala Ser  Thr Val Gln
    3350                3355                3360

Arg Phe  Leu Asp Ile Tyr Arg  Thr Leu Leu Thr His  Leu Ala Asp
    3365                3370                3375

Asp Ala  Ser Ala Ala Val Ala  Arg Leu Pro Leu Ser  Ser Asp Ala
    3380                3385                3390

Glu Arg  Asn Leu Leu Thr Val  Glu Trp Asn Arg Thr  Asp Thr Asp
    3395                3400                3405

Phe Gly  Glu Asp Ala Ala Gln  Pro Leu His Arg Leu  Phe Glu Gln
    3410                3415                3420

Gln Val  Glu Arg Thr Pro Asp  Ala Val Ala Ile Val  Phe Asp Asp
    3425                3430                3435

Thr Ala  Leu Thr Tyr Ala Glu  Leu Asn Leu Arg Ala  Asn Arg Leu
    3440                3445                3450

Ala His  His Leu Val Ala Leu  Gly Val Gly Pro Asp  Ser Leu Val
```

-continued

```
    3455                3460                3465

Gly Val  Ala Met Glu Arg Ser  Leu Asp Met Ser Val  Ala Leu Leu
    3470                3475                3480

Ala Ile  Leu Lys Ala Gly Gly  Ala Tyr Val Pro Val  Asp Pro Asp
    3485                3490                3495

Tyr Pro  Ala Glu Arg Val Arg  Phe Met Ile Asp His  Ala Gln Leu
    3500                3505                3510

Arg Trp  Leu Leu Thr Gln Gln  His Leu His Asp Ala  Leu Pro Asp
    3515                3520                3525

Thr Asp  Ala His Val Ile Val  Val Asp Arg Asp Ser  Leu Asp Leu
    3530                3535                3540

Asp Ala  Ala Ala Thr Ser Asn  Pro Ala Pro Ala Leu  Asn Gly Asp
    3545                3550                3555

Asn Leu  Ala Tyr Met Ile Tyr  Thr Ser Gly Ser Thr  Gly Arg Pro
    3560                3565                3570

Lys Gly  Ala Leu Asn Thr His  Arg Ala Ile Thr Asn  Arg Ile Leu
    3575                3580                3585

Trp Met  Gln His Ala Tyr Ala  Leu Gly Ala Asp Asp  Ala Val Leu
    3590                3595                3600

Gln Lys  Thr Pro Phe Ser Phe  Asp Val Ser Val Trp  Glu Leu Phe
    3605                3610                3615

Trp Pro  Leu Val Thr Gly Ala  Arg Leu Val Phe Ala  Arg Pro Gly
    3620                3625                3630

Gly Gln  Arg Glu Thr Asp Tyr  Leu Val Glu Leu Ile  Glu Arg Glu
    3635                3640                3645

Arg Ile  Thr Thr Ile His Phe  Val Pro Ser Met Leu  Arg Ala Phe
    3650                3655                3660

Leu Asp  His Pro Asp Leu Asp  Ala His Cys Ala Ser  Leu Arg Arg
    3665                3670                3675

Val Val  Cys Ser Gly Glu Ala  Leu Pro His Asp Leu  Gln Gln Arg
    3680                3685                3690

Cys Leu  Glu Arg Leu Asp Val  Glu Leu Tyr Asn Leu  Tyr Gly Pro
    3695                3700                3705

Thr Glu  Ala Ala Val Asp Val  Thr Ala Trp Glu Cys  Arg Arg Asp
    3710                3715                3720

Asp Pro  His Arg Ile Val Pro  Ile Gly Arg Pro Ile  Ala Asn Thr
    3725                3730                3735

Arg Leu  Tyr Ile Val Asp Ala  Gln Met Gln Pro Thr  Pro Ile Gly
    3740                3745                3750

Val Ala  Gly Glu Leu Leu Ile  Gly Gly Thr Pro Val  Gly Arg Gly
    3755                3760                3765

Tyr His  Gly Glu Pro Glu Leu  Ser Ala Glu Lys Phe  Ile Ala Asp
    3770                3775                3780

Pro Phe  Ser Ala Asp Pro Leu  Ala Arg Leu Tyr Arg  Thr Gly Asp
    3785                3790                3795

Leu Ala  Arg Tyr Arg Pro Asp  Gly Asn Ile Glu Phe  Leu Gly Arg
    3800                3805                3810

Ile Asp  His Gln Ile Lys Leu  Arg Gly Leu Arg Ile  Glu Pro Gly
    3815                3820                3825

Glu Ile  Glu Ala Ala Leu Thr  Ser His Pro Leu Val  Asp Ala Ala
    3830                3835                3840

Val Val  Ala Leu Arg Gly Val  Asp Asp Gly Ala Arg  Leu Val Gly
    3845                3850                3855
```

-continued

```
Trp Leu  Cys Ser Ser His Pro  Glu Ala Glu Leu Ile  Glu Ala Val
    3860                 3865                 3870

Arg Gly  His Leu Arg Gln Arg  Leu Pro Asp Tyr Met  Val Pro Ser
    3875                 3880                 3885

Ala Phe  Val Val Val Ser Ala  Phe Glu His Leu Pro  Asn Gly Lys
    3890                 3895                 3900

Leu Asp  Arg Thr Arg Leu Pro  Glu Pro Gly Asp Gly  Leu Asp His
    3905                 3910                 3915

Val Ala  Pro Val Asn Ala Leu  Glu Ala Gln Leu Ala  Ala Ile Trp
    3920                 3925                 3930

Gln Glu  Val Leu Gly Gln Ala  Arg Ile Ser Thr Thr  Gly Asn Phe
    3935                 3940                 3945

Phe Asp  Leu Gly Gly Asn Ser  Leu Leu Ala Thr Lys  Val Val Ala
    3950                 3955                 3960

Arg Ile  Arg Arg Asp Leu His  Val Lys Leu Glu Ile  Arg Ser Leu
    3965                 3970                 3975

Phe Ala  Leu Pro Thr Ile Ser  Ser Leu Ala Lys Arg  Ile Ala Asp
    3980                 3985                 3990

Thr Gln  Pro Ile Asp Tyr Ala  Pro Val Thr Pro Leu  Pro Ala Gln
    3995                 4000                 4005

Ala Ser  Tyr Ala Leu Ser Pro  Ala Gln Thr Arg Leu  Trp Val Gln
    4010                 4015                 4020

Asp Arg  Leu His Ala Ala Gln  Ala Glu Gly Pro Leu  Pro Thr Ser
    4025                 4030                 4035

Leu Leu  Phe Glu Gly Val Leu  Asp Val Asp Ala Leu  Val Arg Ala
    4040                 4045                 4050

Phe Arg  Ala Leu Ser Glu Arg  His Glu Ile Leu Arg  Thr Arg Phe
    4055                 4060                 4065

Val Leu  Glu Gly Asn Gln Pro  Val Gln His Val Leu  Pro Pro Gly
    4070                 4075                 4080

Glu Ala  Ala Phe Pro Val Glu  Ile Val Asp Leu Gln  Asp Ala Glu
    4085                 4090                 4095

Asp Arg  Asp Ala Gln Ala Ala  Ala Ile Gln Ala Ser  Glu Arg Leu
    4100                 4105                 4110

Val Pro  Met Asp Leu Ala Thr  Gly Pro Leu Phe Arg  Val Lys Leu
    4115                 4120                 4125

Leu Arg  Leu Ser Glu Val Arg  His Val Cys Leu Cys  Thr Met His
    4130                 4135                 4140

His Ile  Val Ser Asp Gly Trp  Ser Thr Glu Val Leu  Leu Asp Asp
    4145                 4150                 4155

Leu Ser  Ala Leu Tyr Asp Ala  Phe Val Gln Arg Arg  Asp Asp Pro
    4160                 4165                 4170

Leu Pro  Ala Leu Pro Ile Gln  Tyr Lys Asp Tyr Ala  Gly Trp Leu
    4175                 4180                 4185

Asn Arg  Leu Leu Ala Gly Pro  Asp Gly Ala Arg Met  Lys Asp Tyr
    4190                 4195                 4200

Trp Leu  Thr Lys Leu Gly Gly  Gly Leu Arg Ala Leu  Glu Leu Pro
    4205                 4210                 4215

Gly Asp  Val Glu Gln Pro Ala  Ala Pro Ser Trp Lys  Ser Trp Arg
    4220                 4225                 4230

Phe Asp  Leu Pro Ala Ala Glu  Thr Ala Ala Leu Glu  Ser Leu Gly
    4235                 4240                 4245
```

-continued

```
Lys Arg  His Gly Ala Thr Leu  Phe Ile Ala Leu Leu  Ser Ala Ile
    4250                4255                4260

Lys Ala  Leu Phe Tyr Arg Arg  Ser Gly Gln Glu Asp  Ile Val Val
    4265                4270                4275

Gly Thr  Pro Val Ala Gly Arg  Glu Leu Pro Glu Leu  Glu Ser Gln
    4280                4285                4290

Val Gly  Pro Tyr Leu Asn Val  Leu Ala Leu Arg Asp  Arg Val Ala
    4295                4300                4305

Gly Asp  Asp Arg Phe Asp Thr  Leu Leu Thr Arg Val  Arg Asp Thr
    4310                4315                4320

Thr Leu  Glu Ala Phe Ser His  Pro Leu Tyr Pro Leu  Asp Arg Leu
    4325                4330                4335

Leu Asp  Glu Leu His Ile Lys  Arg Val Ala Gly Arg  Asn Pro Leu
    4340                4345                4350

Phe Asp  Ile Gly Leu Thr Leu  Gln Asn Gln Arg His  Gly Pro Val
    4355                4360                4365

Asp Arg  Tyr Ala Gly Gln Val  His Ile Ala Glu Leu  Pro Asp His
    4370                4375                4380

Asp Pro  Gln Arg Ala Asp Thr  Glu Ala Ala Thr Asp  Phe Trp Phe
    4385                4390                4395

Leu Ala  Glu Pro His Ala Glu  Gly Leu Ala Ile Arg  Val Val Tyr
    4400                4405                4410

His Ala  Gly Arg Phe Ser Glu  Ala Leu Val Gln Gly  Leu Ala Asn
    4415                4420                4425

Glu Leu  Thr Ser Val Ile Gly  Glu Val Leu Ala Asn  Pro Gly Val
    4430                4435                4440

Arg Ile  Arg Asn Leu Thr Leu  Gly Gln Arg Ala Leu  His Ala Glu
    4445                4450                4455

Ala Arg  Gln Pro Thr Val Glu  Leu Ser Ala Phe
    4460                4465


<210> SEQ ID NO 16
<211> LENGTH: 1107
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1107)
<223> OTHER INFORMATION: putative short chain dehydrogenase/reductase
      SDR

<400> SEQUENCE: 16

Met Lys Phe Gly Leu Met Phe Phe Ala Ser Ser Glu Glu Ala Leu Ser
1               5                  10                  15

Gly Asn Lys Tyr Gln Leu Val Met Glu Ser Ala Arg Phe Ala Asp Ala
            20                  25                  30

Asn Gly Phe Ser Ser Val Trp Val Pro Glu Arg His Phe Thr Glu Phe
        35                  40                  45

Gly Ser Leu Tyr Pro Asn Pro Ala Val Leu His Ala Ala Leu Ala Ala
    50                  55                  60

Ala Thr Gln Arg Val Lys Leu Val Ala Gly Ser Val Val Ala Ala Leu
65                  70                  75                  80

His Asn Pro Ile Arg Ile Ala Glu Glu Trp Ser Met Val Asp Asn Leu
                85                  90                  95

Ser Asn Gly Arg Val Gly Val Ser Phe Ala Ser Gly Trp Asn Pro Asp
            100                 105                 110
```

-continued

```
Asp Phe Val Phe Ala Pro Asp Lys Tyr Ala Thr Arg Gln Asp Asp Met
        115                 120                 125

Leu Thr Thr Met Arg Ala Val Gln His Leu Trp Arg Gly Gly Thr Leu
    130                 135                 140

Asp Ala Thr Asn Gly Val Gly Lys Pro Val Arg Leu Arg Val Tyr Pro
145                 150                 155                 160

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

Pro Gln Thr Phe Val Arg Ala Gly Glu Ala Gly Ala Asn Leu Leu Thr
            180                 185                 190

His Val Leu Asp Gln Asp Arg Asp Gln Leu Ala His Lys Ile Ala Leu
        195                 200                 205

Tyr Arg Glu Ala Arg Ala Lys His Gly Phe Asp Pro Ala Ala Gly Thr
    210                 215                 220

Val Ser Val Met Leu His Thr Phe Val Gly Asp Asp Ala Ala Gln Ala
225                 230                 235                 240

Arg Glu Gln Ala Arg Val Pro Phe Cys Asn Tyr Ile Arg Ser Asn Ile
                245                 250                 255

Gly Leu Leu Asn Gly Leu Ala Gln Ser Arg Gly Gln Ser Val Asp Val
            260                 265                 270

Arg Ala Met Gly Ala Arg Glu Leu Asp Glu Phe Val Glu Phe Leu Tyr
        275                 280                 285

Glu Arg Phe Ala Gln Ser Arg Gly Leu Ile Gly Thr Pro Glu Thr Cys
    290                 295                 300

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

Cys Leu Leu Asp Phe Gly Pro Pro Val Glu Arg Ile Leu Gly Asn Leu
                325                 330                 335

Pro Gln Leu Arg Arg Leu Arg Glu Met Cys Ala Pro Arg Arg Ser Ala
            340                 345                 350

Ala Pro Thr Arg Phe Asp Ala Ala Glu Val Gln Ala Arg Cys Thr Glu
        355                 360                 365

Thr Thr Ser Gly Ala Asp Phe Asn Gly Glu Ile Arg Gln His Gly Val
    370                 375                 380

Gln Ile Asp Gly Val Phe Asp Ala Ile Arg Gln Ile Trp Arg Thr Thr
385                 390                 395                 400

Gly Glu Ala Leu Gly Lys Ile Ser Leu Pro Ala Asp Ala Leu Ala Ser
                405                 410                 415

Ser Pro Tyr Gln Val His Pro Ala Phe Leu Asp Ala Cys Ser Arg Val
            420                 425                 430

Leu Ala Ala Ala Ile Asp Pro Asp Ala Leu Glu Ser Gly Asp Leu Tyr
        435                 440                 445

Leu Pro Ser Ser Ile Gly Ala Val Arg Val His Gln Pro Pro Ala Ser
    450                 455                 460

Thr Glu Ala Trp Ser His Ala Thr Leu Arg Thr Pro Ile Gly Gln Gly
465                 470                 475                 480

Ala Leu Glu Gly Asp Ile Arg Val His Asp Leu Ala Gly Arg Leu Leu
                485                 490                 495

Ile Glu Ile Asp Ala Leu Arg Leu Gln Gln Val Arg Ala Ala Arg Ala
            500                 505                 510

Val Glu Arg His Asp Phe Ala Ala Leu Leu Tyr Gln Arg Val Trp Arg
        515                 520                 525

Pro Ser Asn Val Asp Ala Ala Thr Gly Gly Ser Ala His Gly Glu Trp
```

-continued

```
    530                 535                 540

Leu Ile Leu Ala Asp Arg Gly Gly Val Gly Ala Gln Leu Ser Ala Leu
545                 550                 555                 560

Leu Glu Ala His Gly Asp Thr Cys Thr Leu Arg Phe Ala Asp Ala Thr
                565                 570                 575

Pro Glu Leu Pro Ala Ala Asp Arg Pro Leu Lys Gly Val Ile His Leu
            580                 585                 590

Trp Ser Leu Asp Leu Ala Pro Ser Asp Ile Ala Ala Arg Arg Arg Ala
        595                 600                 605

Ser Ala Ser Val Leu His Leu Val Arg Ala Leu Ala Ser Arg Ala Pro
    610                 615                 620

Ser Ala Arg Gln Ala Arg Leu Trp Leu Val Thr Ser Gly Ala Met Asn
625                 630                 635                 640

Val Leu Asp Gly Glu Ser Ile Ala Val Ala Gln Ala Pro Leu Trp Gly
                645                 650                 655

Leu Gly Arg Ala Ile Ala Val Glu His Ala Ala Leu Trp Gly Gly Leu
            660                 665                 670

Val Asp Leu Asp Pro Glu Gln Pro Ser Ala Ala Asp Ile Met Gln Ala
        675                 680                 685

Val Gln Ala Gly Gly Arg Glu Asp Met Ile Ala Phe Arg Arg Asp Gln
    690                 695                 700

Arg Tyr Val Ala Arg Ile Ala Arg Asp Asn Arg Glu Tyr Val Ser His
705                 710                 715                 720

Arg Pro Ile Arg Phe His Gly Asp Ala Thr Tyr Leu Val Thr Gly Gly
                725                 730                 735

Leu Gly Gly Leu Gly Leu Arg Leu Ala Ser Trp Leu Ala Asp Asn Gly
            740                 745                 750

Ala Gly Lys Ile Val Leu Leu Gly Arg Gly Glu Pro Ser Ala Ala Ala
        755                 760                 765

Gly Lys Ile Leu Arg Thr Leu Asp Ala Arg Phe Ile Arg Ala Asp Leu
    770                 775                 780

Ser Arg Arg Glu Asp Val Gly Gln Ala Leu Gly Glu Ile Ala His Ser
785                 790                 795                 800

Met Pro Pro Leu Lys Gly Ile Phe His Leu Ala Gly Ala Leu Asp Asp
                805                 810                 815

Ala Leu Leu Thr Arg Gln Asp Asp Asp Phe Phe His Arg Ala Gly Ser
            820                 825                 830

Gly Lys Ala Asp Gly Ala Trp Tyr Leu His Glu Leu Thr Ala Gly Leu
        835                 840                 845

Pro Leu Asp His Phe Val Leu Phe Ser Ser Met Ala Ala Leu Ile Thr
    850                 855                 860

Met Pro Gly Gln Gly Asn Tyr Ala Ala Ala Asn Ser Phe Leu Asp Ala
865                 870                 875                 880

Leu Ala Gln His Arg Arg Ala Gln Gly Lys Pro Gly Leu Ser Val Asn
                885                 890                 895

Trp Gly Pro Trp Ala Glu Ile Gly His Ala Ala Thr Asp Tyr Gly Arg
            900                 905                 910

Arg Ala His Glu Gln Leu Gly Ala Leu Gly Val Gly Thr Leu Pro Pro
        915                 920                 925

Glu Leu Ala Ile Ala Thr Leu Glu Arg Leu Met Ala Ser Gly Val Ala
    930                 935                 940

Gln Ser Gly Val Ala Arg Ile Asp Trp Pro Thr Leu Phe Arg Val Asp
945                 950                 955                 960
```

-continued

```
Ala Pro Ala Ala Gly Ser Ala Leu Phe Ser Glu Leu Thr Gln Pro Ala
                965                 970                 975

Ala Gln Pro Ala Gln Gln Glu Thr Ala Leu Leu Arg Gln Leu His Ala
            980                 985                 990

Cys Ala Pro Arg Glu Arg Val Glu  Arg Ile Thr Asp Thr  Leu Ala Ala
        995                 1000                1005

Met Leu  Ala Glu Thr Leu Arg  Leu Ser Gly Pro Asp  Ala Ile Ala
    1010                1015                1020

Pro Glu  Gln Ser Leu Leu Asp  Leu Gly Leu Asp Ser  Leu Val Ala
    1025                1030                1035

Leu Glu  Leu Thr Asp Arg Leu  Thr Lys Val Phe Gly  Arg Pro Phe
    1040                1045                1050

Arg Ala  Thr Leu Phe Phe Ser  Tyr Pro Asn Leu Gln  Thr Leu Ala
    1055                1060                1065

Gln Tyr  Val Leu Asn Glu Leu  Ser Pro Ser Leu Pro  Ala Pro Val
    1070                1075                1080

Val Asp  Glu Ala Ser Asp Asp  Leu Asp Glu Asp Asp  Leu Ser Glu
    1085                1090                1095

Leu Ile  Ala Gln Glu Ile Gly  Ala Gln
    1100                1105


<210> SEQ ID NO 17
<211> LENGTH: 1475
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(1475)
<223> OTHER INFORMATION: putative beta-ketoacyl synthetase

<400> SEQUENCE: 17

Met Leu Pro Asp Thr Lys Phe Arg Thr Val Thr Glu Ile Leu Leu Phe
1               5                   10                  15

Arg Gly Lys Val Glu Pro Glu Lys Thr Ala Phe Ile Phe Leu Glu Asn
            20                  25                  30

Gly Glu Ala Glu Leu Thr Arg Leu Thr Phe Gly Asp Leu Asp Lys Arg
        35                  40                  45

Ala Arg Gly Ile Ala Ala Arg Leu Gln Ala Ile Ala Gln Pro Gly Asp
    50                  55                  60

Arg Val Leu Leu Val Tyr Pro Pro Gly Leu Glu Phe Ile Cys Ala Trp
65                  70                  75                  80

Val Gly Cys Leu Tyr Ala Gly Leu Ile Gly Val Pro Ala Tyr Pro Pro
                85                  90                  95

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

Thr Pro Val Val Ala Leu Thr Asp Ala Ala Thr Leu Asp Gly Ile Ala
        115                 120                 125

His His Ala Asp Gly Tyr Ser Asp Thr Leu Glu Leu Lys Ile Leu Ala
    130                 135                 140

Thr Asp Gln Arg Phe Asp Ala Pro Ala Glu Gln Trp Arg Ala Pro Asp
145                 150                 155                 160

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

Gly Thr Pro Lys Gly Val Met Ile Ser His Ala Asn Ile Leu Ser Asn
            180                 185                 190
```

-continued

```
Met Ala Val Ile Ala Glu Ala Ser Asp Ala Asp Ala Ser Thr Val Phe
        195                 200                 205

Val Ser Trp Leu Pro Val Phe His Asp Met Gly Phe Phe Gly Lys Val
    210                 215                 220

Leu Leu Pro Ile Tyr Leu Gly Val Leu Ser Val Leu Met Ala Pro Ala
225                 230                 235                 240

Ala Phe Val Gln Lys Pro Val Arg Trp Leu Gln Ala Ile Thr Lys Tyr
                245                 250                 255

Arg Gly Thr His Cys Ala Ala Pro Asp Phe Ala Tyr Asp Leu Cys Ala
            260                 265                 270

Arg Lys Ile Ala Asp Glu Ala Arg Ala Gln Leu Asp Leu Ser Ser Trp
        275                 280                 285

Arg Val Ala Phe Asn Gly Ala Glu Pro Val Arg Ala Glu Ser Val Ala
    290                 295                 300

Arg Phe Ser Arg Ala Phe Ala Ala Cys Gly Phe His Ala His Thr Met
305                 310                 315                 320

Arg Pro Val Tyr Gly Met Ala Glu Ala Thr Leu Phe Ile Ser Gly Gln
                325                 330                 335

Pro Ala Arg Ser Leu Pro Arg Val Ala Asp Tyr Asp Ala Asp Ala Leu
            340                 345                 350

Ala Gln Gly Val Ala Thr Arg Asn Asp Ser Gly Lys Arg His Ala Leu
        355                 360                 365

Val Ser Cys Gly Arg Thr Trp Ala Glu His Arg Val Arg Ile Val Asn
    370                 375                 380

Pro Asp Thr Gly Glu Arg Cys Ala Pro Gly Arg Ile Gly Glu Ile Trp
385                 390                 395                 400

Leu Thr Gly Pro Ser Val Gly Val Gly Tyr Trp Asn Arg Ile Asp Glu
                405                 410                 415

Thr Glu Arg Thr Phe Arg Ala Lys Leu Asp Gly Asp Asp Ala Arg Tyr
            420                 425                 430

Leu Arg Thr Gly Asp Leu Gly Phe Val Asp Gly Glu Asp Leu Phe Val
        435                 440                 445

Thr Gly Arg Leu Lys Asp Leu Ile Ile Val Ala Gly Arg Asn His Tyr
    450                 455                 460

Pro Gln Asp Leu Glu Gln Ser Ala Glu Gly Ser His Pro Ala Leu Ala
465                 470                 475                 480

Pro Asn Ala Ser Ala Ala Phe Ser Ile His Val Asp Asn Val Glu Arg
                485                 490                 495

Val Val Val Ala Cys Glu Val Arg Arg Glu Ala Leu Asn Thr Leu Asp
            500                 505                 510

Ala Glu Ala Val Ala Ala Glu Ile Arg His Thr Leu Ala Glu Val His
        515                 520                 525

Asp Val Asp Leu Tyr Ala Ala Val Leu Leu Lys Pro Ala Thr Ile Leu
    530                 535                 540

Arg Thr Ser Ser Gly Lys Ile Gln Arg Ser Arg Ile Arg Gln Ala Phe
545                 550                 555                 560

Leu Asp Glu Gln Gly Leu Ala Ile Ala Gly Glu Trp Arg Arg Ala Phe
                565                 570                 575

Ser Ala Pro Pro Ala Pro Pro Gln Thr Ala Glu Pro Arg Asp Thr Gln
            580                 585                 590

Ala Leu Val Gln Trp Cys Ile Glu Arg Val Ser Arg Leu Ser Gly Ile
        595                 600                 605

Ala Ser Gly Lys Ile Asp Pro Asp Ala Pro Phe Ser Val His Gly Leu
```

-continued

```
    610                 615                 620

Asp Ser Lys Asp Ala Ile Met Leu Ser Gly Glu Leu Gln Asp Trp Leu
625                 630                 635                 640

Gly Arg Pro Val Ser Pro Thr Val Val Tyr Asp Phe Pro Ser Ile Ser
                645                 650                 655

Leu Leu Ala Arg His Leu Ser Gly Thr Gly Ser Ala Met Pro Asp Gln
            660                 665                 670

Ala Pro Gly Ser Ala Glu Ala Arg Ala Asp Ile Ala Ile Val Gly Met
        675                 680                 685

Gly Cys Arg Phe Pro Gly Ala Gly Asn Pro Asp Ala Phe Trp Gln Leu
    690                 695                 700

Leu Leu Glu Gly Arg Asp Ala Val Gly Ala Ala Thr Gln Arg Ala Ala
705                 710                 715                 720

Asp Leu Pro Leu Ala Gly Leu Leu Asp Gln Val Asp Gln Phe Asp Ala
                725                 730                 735

Ala Phe Phe Gly Ile Ser Ala Arg Glu Ala Glu Ser Met Asp Pro Gln
            740                 745                 750

Gln Arg Leu Leu Leu Glu Val Ala Trp Glu Thr Leu Glu His Ala Gly
        755                 760                 765

Ile Ala Pro Arg Ser Leu Ala Gly Gly Arg Thr Ala Val Ile Val Gly
    770                 775                 780

Ile Ser Asn Ser Asp Tyr Ile Arg Leu Ala Gln Asp Glu Val Ala Asp
785                 790                 795                 800

Val Gly Pro Tyr Val Ala Thr Gly Asn Ala Leu Ser Val Ala Ala Asn
                805                 810                 815

Arg Ile Ser Tyr Ala Leu Asp Leu Arg Gly Pro Ser Trp Ala Val Asp
            820                 825                 830

Thr Ala Cys Ser Ser Ser Leu Val Ala Val His Gln Ala Cys Arg Ala
        835                 840                 845

Leu Gln Arg Gly Glu Ser Asp Ala Ala Leu Ala Gly Gly Val Asn Leu
    850                 855                 860

Ile Leu Ala Pro Gln Leu Ser Ala Ser Phe Thr Gln Ala Gly Met Leu
865                 870                 875                 880

Ser Pro Asp Gly Arg Cys Lys Ala Phe Asp Ala Ala Ala Asn Gly Tyr
                885                 890                 895

Val Arg Gly Glu Gly Val Gly Met Val Leu Leu Lys Arg Leu Asp Asp
            900                 905                 910

Ala Leu Glu Asn Gly Asp Thr Val Phe Ala Val Ile Arg Gly Ser Ala
        915                 920                 925

Val Asn Gln Asp Gly Arg Ser Asn Gly Leu Thr Ala Pro Asn Gly Pro
    930                 935                 940

Ala Gln Gln Ala Val Ile His Gly Ala Leu Arg Asp Ala Gly Val Arg
945                 950                 955                 960

Ala Gln Asp Ile Gly Phe Val Glu Thr His Gly Thr Gly Thr Pro Leu
                965                 970                 975

Gly Asp Pro Ile Glu Leu Asn Ser Leu Ala Ala Val Leu Asn Glu Ser
            980                 985                 990

Arg Arg Pro Asp Asp Leu Cys Trp  Ile Gly Ser Val Lys  Thr Asn Ile
        995                 1000                1005

Gly His  Leu Glu Ser Ala Ala  Gly Ile Ala Ser Leu  Ile Lys Thr
    1010                1015                1020

Ala Leu  Ala Leu His His Arg  Ala Ile Pro Pro Asn  Leu His Phe
    1025                1030                1035
```

-continued

```
Arg Ser  Ile Asn Pro Gln Ile  Ala Leu Asp Gly Thr  Pro Phe Arg
    1040                1045                1050

Ile Pro  Arg Gln Val Thr Pro  Trp His Ser Glu His  Gly Pro Arg
    1055                1060                1065

Leu Ala  Gly Val Ser Ser Phe  Gly Phe Gly Gly Thr  Asn Ala His
    1070                1075                1080

Leu Ile  Leu Ser Glu Ala Pro  Gly Leu Pro Glu Ile  Glu Ala Glu
    1085                1090                1095

Pro Val  Ala Pro Ala Ala Arg  Val Val Thr Leu Ser  Ala Arg Thr
    1100                1105                1110

Pro Asp  Ala Leu Gln Ala Leu  Ala Ala Ser Tyr Ala  Ala Tyr Leu
    1115                1120                1125

Asp Ala  His Pro Glu Ala Gly  Val Arg Asp Val Ala  Phe Thr Ala
    1130                1135                1140

Asn Thr  Gly Arg Thr His Phe  Thr Gln Arg Ala Ala  Ile Val Ala
    1145                1150                1155

Pro Ser  Arg Asp Ser Leu Arg  Ala Gln Leu Asp Ser  Val Ser Ser
    1160                1165                1170

Gly Glu  Pro Ala Glu Thr Pro  Pro Ala Val Thr Phe  His Phe Cys
    1175                1180                1185

Ala Asp  Asp Gly Ala Ser Ala  Asp Ala Val Arg Gln  Leu Arg Ala
    1190                1195                1200

Ala Ser  Pro Ala Phe Asp Ala  Leu Met Gln Arg Gln  Ser Asp Ala
    1205                1210                1215

Ser Gly  Ala Pro Ala Leu Ala  Pro Asp Glu Ala Gly  Phe Thr Arg
    1220                1225                1230

Phe Gln  Arg Ala Leu Ala Gln  Leu Trp Met Ser Phe  Gly Ile Ala
    1235                1240                1245

Pro Asp  Ala Val Ser Ser Thr  Gly Asp Gly Gln Arg  Ala Ala Ala
    1250                1255                1260

Ala Trp  Ala Gly Val Pro Gln  Ala Pro Asp Ser Gly  Ala Ala Gly
    1265                1270                1275

His Pro  Gly Ile Val Ile Asp  Ile Gly Ala His Thr  Ala Ala Trp
    1280                1285                1290

Asp Ala  Ile Leu His Thr Leu  Ala Ala Leu Tyr Val  Arg Gly Ala
    1295                1300                1305

Ser Ile  Asp Trp Asp Ala Val  Glu Gln Gly Ala Pro  His Arg Arg
    1310                1315                1320

Leu Ala  Leu Pro Thr Tyr Pro  Phe Glu Arg Arg Gly  Phe Trp Ile
    1325                1330                1335

Arg Pro  His Ala Arg Arg His  Pro Leu Leu Gly Arg  Leu Met Glu
    1340                1345                1350

Gln His  Ala His Ala Pro Ala  Thr Trp Ile Trp Gln  Ser Arg Leu
    1355                1360                1365

Asp Ala  Pro Ala Thr Asn Phe  Leu Asp Gly His Arg  Val Lys Gly
    1370                1375                1380

Ser Pro  Val Leu Pro Tyr Ser  Ala Phe Val Glu Met  Ala Leu Ser
    1385                1390                1395

Ala Thr  Ser Glu Ile Gly Ala  Ala Gly His Thr Thr  Leu Lys Asp
    1400                1405                1410

Leu Ala  Leu His Ala Pro Leu  Pro Leu His Pro His  Glu Ser His
    1415                1420                1425
```

-continued

```
Thr Val  Gln Thr Val Leu Ser  Arg Arg Ser Trp Gly  Pro Phe Ser
    1430                1435                1440

Phe Ala  Val Tyr His Arg Ile  Asp Asp Thr Arg Ala  Ala Ala Thr
    1445                1450                1455

Trp Gln  Met Cys Ala Ser Ala  Glu Ile His Glu Ser  Asp Arg Ser
    1460                1465                1470

His Ala
    1475


<210> SEQ ID NO 18
<211> LENGTH: 328
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(328)
<223> OTHER INFORMATION: putative taurine catabolism dioxygenase

<400> SEQUENCE: 18

Met Leu Gly Met Thr Glu Arg Lys Leu Leu Ala Glu Gly Ser Thr Pro
1               5                   10                  15

Trp Leu Leu Glu Pro Val Ser Asn Gly Arg Asp Leu Ala Gln Ala Val
            20                  25                  30

Asn Asp Asn Arg Ala Ala Leu Glu Ser Arg Leu Leu Glu His Gly Val
        35                  40                  45

Leu Leu Phe Arg Gly Phe Asp Val Ser Ser Val Gly Gly Phe Glu Ala
    50                  55                  60

Phe Ala Arg Ala Ile Ser Ala His Gln Ser Asp Tyr Val Tyr Arg Ser
65                  70                  75                  80

Thr Pro Arg Thr Ser Ile Gly Asn Gly Ile Phe Thr Ala Thr Glu Tyr
                85                  90                  95

Pro Pro Ser Glu Thr Ile Ala Leu His Cys Glu Asn Ala Tyr Gln Arg
            100                 105                 110

Ser Trp Pro Leu Arg Val Ala Phe Cys Cys Leu Thr Pro Ala Ala Thr
        115                 120                 125

Gly Gly Glu Thr Pro Ile Ala Asp Met Arg Glu Val Ser Arg Arg Ile
    130                 135                 140

Gly Pro Arg Ile Leu Asp His Phe Glu Ala Arg Gln Val Arg Tyr Val
145                 150                 155                 160

Arg His Tyr Arg Arg His Val Asp Ile Pro Trp Glu Thr Val Phe Gln
                165                 170                 175

Thr Ser Asp Arg Asn Gln Val Ala Ala Phe Cys Ala Asp Asn Gly Ile
            180                 185                 190

Ala Leu Glu Trp Leu Asp Asp Asp Thr Leu Arg Thr Ala Gln Ile Asn
        195                 200                 205

Gln Gly Val Ala Tyr His Pro Val Thr Gly Glu Arg Val Phe Phe Asn
    210                 215                 220

Gln Ala His Leu Phe His Ile Ser Asn Leu Glu Ala Ser Leu Ala Ser
225                 230                 235                 240

Ser Ile Val Ser Leu Phe Gly Glu Asp Arg Ile Pro Arg Asn Ala Cys
                245                 250                 255

His Gly Asp Gly Ser Pro Phe Asp Leu Ala Asp Leu Glu Gln Ile Arg
            260                 265                 270

His Ala Phe Arg Glu Cys Ala Ile Thr Phe Pro Trp Gln Arg Gly Asp
        275                 280                 285

Val Leu Leu Val Asp Asn Met Arg Phe Ala His Gly Arg Asn Pro Phe
```

-continued

```
    290                 295                 300

Glu Gly Glu Arg Lys Val Val Val Ser Leu Leu Asp Pro Tyr Thr Pro
305                 310                 315                 320

Asp Ile Glu Gly Ile Ala Asp Arg
                325
```

<210> SEQ ID NO 19
<211> LENGTH: 456
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(456)
<223> OTHER INFORMATION: putative transaminase

<400> SEQUENCE: 19

```
Met Lys Arg Phe Ser Cys Ala Ser Val His Gln Ser Ala Leu Gln Ala
1               5                   10                  15

Gly Ser Ala Arg Met Glu Lys Leu Glu Tyr Leu Lys Gln Val Glu Ser
            20                  25                  30

Asn Ala Arg Thr Tyr Ala Thr Ser Phe Pro Arg Leu Phe Thr His Ala
        35                  40                  45

Lys Gly Ile Arg Val Arg Asp Ala Asp Gly Gln Glu Tyr Ile Asp Cys
    50                  55                  60

Leu Ser Asn Ala Gly Thr Leu Ala Leu Gly His Asn His Pro Glu Val
65                  70                  75                  80

Asn Glu Ala Val Met Arg Phe Leu Ser Ser Asp Gln Met Gln Gln Ala
                85                  90                  95

Leu Asp Leu Ala Thr Pro Ala Lys His Ala Phe Val Glu Gln Leu Phe
            100                 105                 110

Ser Leu Leu Pro Gly Lys Ile Ala Glu Ser Gly Lys Ile Gln Phe Cys
        115                 120                 125

Ser Pro Ser Gly Ala Asp Gly Val Glu Ala Ala Ile Lys Leu Thr Arg
    130                 135                 140

His Tyr Thr Gly Arg Pro Thr Ile Met Ala Phe His Gly Ala Tyr His
145                 150                 155                 160

Gly Met Thr Ser Gly Ala Leu Ala Ala Ser Gly Asn Leu Thr Pro Lys
                165                 170                 175

Ser Ala Gly Gly Asn Gly Arg Asp Val His Phe Leu Pro Tyr Pro Tyr
            180                 185                 190

Ala Phe Arg Cys Pro Phe Gly Thr Asp Gly Ser Ala Thr Asp Gln Leu
        195                 200                 205

Ser Ile Asn Tyr Ile Arg Thr Val Leu Ser Asp Pro Glu Ser Gly Ile
    210                 215                 220

Thr Lys Pro Ala Ala Ile Ile Val Glu Val Val Gln Gly Glu Gly Gly
225                 230                 235                 240

Cys Ile Pro Ala Pro Asp Thr Trp Leu Ile Glu Leu Arg Glu Leu Thr
                245                 250                 255

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

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

Asp Val Leu Val Leu Ser Lys Ala Phe Gly Gly Gly Tyr Pro Leu Ser
    290                 295                 300

Val Val Val Tyr Asp Glu Arg Leu Asp Thr Trp Pro Pro Gly Ala His
305                 310                 315                 320
```

-continued

```
Ala Gly Thr Phe Arg Gly Asn Gln Ile Ala Met Val Ala Gly Leu Ser
                325                 330                 335

Thr Met Arg Ile Val Glu Arg Glu Asp Leu Ser Ala His Ala Asp Arg
            340                 345                 350

Val Gly Lys Leu Leu Val Ala Gly Leu Glu Glu Leu Ala Glu Arg Phe
        355                 360                 365

Pro Cys Leu Gly Gln Ile Arg Gly Arg Gly Leu Met Ile Gly Ala Glu
    370                 375                 380

Val Val Val Pro Gly Thr His Gly Arg Ala Gly Pro Pro His Thr Glu
385                 390                 395                 400

Arg Ala Arg Ala Ile Lys Gln Asn Cys Leu Arg Asn Gly Leu Ile Val
                405                 410                 415

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

Ile Val Ser Glu Ala Asp Ile His Asp Ile Leu Asn Arg Phe Glu His
        435                 440                 445

Ala Val Glu Thr Ala Cys Arg Ala
    450                 455


<210> SEQ ID NO 20
<211> LENGTH: 316
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(316)
<223> OTHER INFORMATION: putative epemerase/dehydratase

<400> SEQUENCE: 20

Met Gln Arg Asn Arg Lys Arg Ile Leu Val Thr Gly Gly Ala Gly Phe
1               5                   10                  15

Leu Gly Ser His Leu Cys Glu Arg Leu Val Glu Leu Gly His Asp Val
            20                  25                  30

Leu Cys Val Asp Asn Tyr Phe Thr Gly Thr Lys Gln Asn Val Ala Thr
        35                  40                  45

Leu Leu Gly Asn Pro Ser Phe Glu Ala Leu Arg His Asp Val Thr Phe
    50                  55                  60

Pro Leu Tyr Val Glu Val Asp Glu Ile Tyr Asn Leu Ala Cys Pro Ala
65                  70                  75                  80

Ser Pro Ile His Tyr Gln Phe Asp Pro Val Gln Thr Thr Lys Thr Ser
                85                  90                  95

Val Met Gly Ala Ile Asn Met Leu Gly Leu Ala Lys Arg Thr His Ala
            100                 105                 110

Arg Val Leu Gln Thr Ser Thr Ser Glu Val Tyr Gly Asp Pro Asp Val
        115                 120                 125

His Pro Gln Pro Glu Ser Tyr Arg Gly Asn Val Asn Pro Leu Gly Pro
    130                 135                 140

Arg Ala Cys Tyr Asp Glu Gly Lys Arg Cys Ala Glu Thr Leu Phe Phe
145                 150                 155                 160

Asp Tyr His Arg Gln Gln Asn Val Arg Ile Lys Val Val Arg Ile Phe
                165                 170                 175

Asn Thr Tyr Gly Pro Arg Met His Pro Asn Asp Gly Arg Val Val Ser
            180                 185                 190

Asn Phe Ile Val Gln Ala Leu Arg Gly Glu Asp Ile Thr Leu Tyr Gly
        195                 200                 205
```

-continued

```
Asp Gly Ser Gln Thr Arg Ala Phe Cys Tyr Val Asp Asp Met Val Asp
    210                 215                 220

Gly Leu Ile Arg Met Met Ala Thr Pro Ala Glu Leu Thr Gly Pro Ile
225                 230                 235                 240

Asn Leu Gly Asn Pro His Glu Ile Ala Val Ser Glu Leu Ala Gln Ile
                245                 250                 255

Ile Leu Arg Leu Thr Gly Ser Lys Ser Arg Leu Val Phe Arg Pro Leu
            260                 265                 270

Pro Lys Asp Asp Pro Thr Gln Arg Cys Pro Asp Ile Ser Leu Ala Arg
        275                 280                 285

Thr His Leu Asp Trp Glu Pro Thr Ile Gly Leu Glu Ala Gly Leu Gln
    290                 295                 300

Arg Thr Ile Asp Tyr Phe Cys Ser Thr Leu Ala Ala
305                 310                 315


<210> SEQ ID NO 21
<211> LENGTH: 239
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(239)
<223> OTHER INFORMATION: putative thioesterase

<400> SEQUENCE: 21

Met Arg Leu Ile Cys Phe Pro Tyr Ala Gly Gly Ser Ala Ala Val Tyr
1               5                   10                  15

Arg Thr Leu Gln Ala Ser Leu Pro Gly Ile Glu Val Cys Arg His Glu
            20                  25                  30

Leu Ala Gly Arg Gly Ser Arg Leu Ser Glu Pro Ala Val Arg Asp Met
        35                  40                  45

Ala Thr Leu Val Asp Thr Leu Leu Cys Asp Leu Asp Asp Cys Phe Asp
    50                  55                  60

Arg Pro Phe Ala Leu Leu Gly His Ser Met Gly Ala Ala Ile Ala Ala
65                  70                  75                  80

Glu Leu Ala Leu Arg Leu Pro Ala His Ala Arg Pro Asn Leu Arg His
                85                  90                  95

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

Arg Met Gln Ala Leu Asp Asp Arg Ala Phe Ile Asp Ala Leu Arg Glu
        115                 120                 125

Met Gly Gly Thr Pro Lys Ala Val Leu Asp Asn Ser Glu Leu Met Ala
    130                 135                 140

Leu Leu Met Pro Ala Leu Arg Ala Asp Phe Thr Met Ile Glu Asn His
145                 150                 155                 160

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

Gly Arg Ala Asp Lys Glu Ile Pro Val Asp Ala Val Ala Gly Trp Gly
            180                 185                 190

Ala Ala Thr Thr Gly Arg Phe Asp Phe His Val Ile Glu Gly Asp His
        195                 200                 205

Phe Phe Leu Arg Asn Glu Met Arg Thr Met Ala Gly Ile Ile Ala Ala
    210                 215                 220

Arg Met Arg Arg Pro Glu His Ala Ala Ser Ser Ala Leu Gln Ala
225                 230                 235
```

-continued

<210> SEQ ID NO 22
<211> LENGTH: 95
<212> TYPE: PRT
<213> ORGANISM: Burkholderia contaminans
<220> FEATURE:
<221> NAME/KEY: MISC_FEATURE
<222> LOCATION: (1)..(95)
<223> OTHER INFORMATION: hypothetical protein

<400> SEQUENCE: 22

Met Gln His Arg Gln Lys Ala Val Pro Thr Gln Gln Val Ala Asn Glu
1 5 10 15

Arg Val Ile Val Thr Glu Trp Arg Phe Ala Pro Gly Ala Glu Thr Gly
20 25 30

Trp His Val His Arg His Asp Tyr Val Val Val Pro Gln Thr Asp Gly
35 40 45

Gln Leu Leu Leu Glu Thr Ala Gln Gly Asn Arg Glu Ser Gln Leu His
50 55 60

Ala Gly Arg Ser Tyr Ala Gly Leu Lys Gly Val Glu His Asn Val Val
65 70 75 80

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

<210> SEQ ID NO 23
<211> LENGTH: 58101
<212> TYPE: DNA
<213> ORGANISM: Burkholderia contaminans

<400> SEQUENCE: 23

aattcctgca gcacggtgcg cgaccagccc cagatgtccc cgctgagcgt gagtgcgaga 60

ccggccgtcg tgatggccag ctgcgtctgg ccgaacagcg gcgtcaatgc gccttcgccg 120

ccgatcacga tccgcttgac gagatccgag atggactgcg agatcgaatc ggagaacgga 180

tagttgtacg gctgcgtgac ggcgcgcgac aggaacggct tgctgggcgt cggcgtccag 240

accttgagcc acggcttggt cgtgaacggg aaccagatgg cttccacccg gcccgagccg 300

tcgagaaacg atgcgatcgt gcggcccgtc gtgccgggcg cggcgaacag ttcggaggcc 360

ggaatatcga cgtagctctg gcagcgtagc cgctggttcg gccctgccgt cagcgtgact 420

tcgacgacga gcgctcgccc gatgtgcgcg aggaacgcgc cgatctcggg atcgctgcgc 480

tcgaaccggc gcagcacgta ttgctgccgg gccggatcga acacgaccgc cgtgagcgcg 540

accacgagat tgctcagcga gccgtaggta tggcccggtt gcaaggtttc accggccgcg 600

ggcacggcgg tgccgtgtgc atcgatcgcg agcgcgccgc cgagcgtgat gtcgcccggt 660

gccggcgcgg caatcacgcc gaggccaacc tgctcgagcg tcgcgagcag cgactccagc 720

gagacgcccg tttgggcggt gacgcgcgcc ggacgcgccg acgtgtcgac ggagacggcc 780

gtcagcgact tcgtcgtatc gagcagcacg aggttcgcgg cgccggcgcc cgggtccagc 840

gtcagcggcg accagttgtg cgtgtagccg cgcgggcgta tccgatagcc gtttgcgcgc 900

gcccagttga cggttgcgac gacgtcgtcg gcggagcgcg gcgcggcggt ccatacgtcc 960

tgcacggcga tctcgccgct ccagttcagg aacgcctgct tgtaaagctg gatgtcggcc 1020

gggaagccgg gcggtgtctc gccggccgtt cgcgcgtgcg ccgcaacctg gtagagcggt 1080

gtccagccgg tgacgatgcc ggccgccgcg agcttcgcca tgtcggccag gaaggcgcga 1140

cgcggcgcag gttcgtctct gaagtcgtga ctcatggtgt gctccaattt ttcggaattg 1200

ttttgcagat tggaaagacg acaaatgacg cgttgagact cgtgtggcaa ttcgagcagg 1260

-continued

tgcgacgcgc gggaagtgtt gcgcgtgggt gggccaggat tgaaaaaaga cggtgcgttc 1320

ggcaatgcgc ggccgcacat catcacggac gtctaatagg aaatcggaaa accgcctggc 1380

gattgcttta attggccgtc ggccggttct gtcggcaagc agatagggag attcgacgga 1440

atcgcgcgcg gcgaagcgct agccgtggcg atcgataaaa gatgatttca cgtgaatatt 1500

aatcttcatg tttcgatttt taaataaacc cggccgcagt tcaaggttga ttgacgatgc 1560

gtcatgcatt tcggtcgaaa gcgtagcaat ttatctatcg ggtgacaagc ggcggagttg 1620

acgaattccg agtcatttaa tatggaaatt ttatgacggg aaatggcttc gtccgttgtg 1680

ggtattttgc aacgcggctg ccggtgtcgc gccacgtggg cttggagcgc aaattatgct 1740

ttgccgtcgc gtatattgaa tcgattgttg agcgaatcga aataacgtcc ggaagacaat 1800

agctgaagcc gggtcgatga gcgggaggta gggtgaaatc cgataattcc tctctcgaat 1860

aacgctcctg gatgaaaatt cgtggtatgc gtcgcccggg tgattattac aaaagttcgt 1920

ggtaaacgga tgtcgattta tcggtgtatt cataataatg ccaatgagcg gctcgcgaat 1980

tgattgattt ccggttcgtg aaagatgtgt tttaaaaaaa tagatgtcgg gctgactgca 2040

aatgtctgaa tcgtcgctat catacgcggc tgggatatac atggatcaaa ttcaatggaa 2100

agaatcgttt cgctttttga tcgcgatttt tctttgaatt cgccgggaac gcgcccgctt 2160

cgagccggcg ccgggttttc cgattcaggt ttcaggcacg tccggcggcg gcgcgttttc 2220

atccggcaac gcgaatcggc cgaaatggac gtttcagcct tttgcggctt cgcgagtcgc 2280

ccgcatcggg ctgaactggg aacggcacgc cgtcgtctcg catgagccgg acgcatcggc 2340

gcgcgctggc ggcggcgcgt tgcccgcctg aaaaaggcgc gcgacgcagc gcgacccgac 2400

gcgcgccgcg caaaccgtgc cggttcgccg gcgcttgcgt tgtgccaggt cctcaagcac 2460

gcacaacaag gagagtcaga tgttcgcgaa gctcgggaag gtgatttcga gcgcaggcag 2520

tgagcggttc gcatccgaca tgcatgcatt gctggtcgag tcgattccgc tcacgatcac 2580

ccggatgact gaatggacgc tcgacgagcc ggcgggcgaa gtcgtccgcg tgcaatcgct 2640

cggcgcggac ggcgcgccgg gcgatgacgg gcgcggcgcg ccggccgcgc acggcgagcg 2700

ggaaccggca gcgcatccgc cgttgaaccg gatcctggcg gcctgcgacc ggcagctcat 2760

tcacatcaat ccgctgatgc ggcgcggcaa tggcggcgaa gtcgcgccgt cgcgcgggcc 2820

gggcggcgga tttcagtgcc atctcgtgtc gggcaaggcg aatcgccgtt acgtgatctc 2880

gctgcatcgc acggcatcgc atcgcgactt ctcgttgcgt gagatgtcgt tcctgaagaa 2940

tttcgccgat acgctgctgc cgctcgtcga gtggcatgcg tcgacgtgcc ggcacggcga 3000

gcgggaaggt gcgacggcac ccggtgcgac ggcaggcatg cccggcgtcg aggcgctgcg 3060

ccacgagttc gaatcgcggc tcgcgcgcgc gagggtcgtg ttgtcggcgc gtgaaaacga 3120

agtgtgcctc ggcctgctcg cgggcaagat gctgcgcgaa atggccggcg agctcggtgt 3180

gaaggagagc acgatcgaga cgtacatcaa gcgagccgcg gtgaagctcg gcatcagcgg 3240

ccggcacggg ctcacgaaat ggatgatcga cgattccgta ccgtgcgcgt cggcggcgtg 3300

acaccgtcac gccatcacgc cgcggacgcg cgacgcatgc cgccgggcat gcgcgttcgg 3360

gccgcgggcc ctcaggttcc gaggcgcggc gacgcgtagt cgcgccgcat gcttctcatg 3420

tcgcccccag cagcttccgt cgcggccccg gccgtctcgt cgagcatcca gcgcgtcagg 3480

ccatgacgcc cgctgaagcc cagcttgacg gccgcccgct tcaggtaggt ttcgacggtg 3540

ctttcgcgca gcgcgaagcg catggcgatg gcaggcaccg tgtcaccggc caggagtgcc 3600

gtgcatgcct cgatctcgcg cgtcgacagc ttgacgcccg cttgctgcag gcgatcggcg 3660

-continued

aatcgccgcg ccacgcgctc ccggcccgat tgcgtcgccg gcggcgcggc ggtcgtcaca 3720

cgagcggccg gcggagccga atcgagcgcc gcgacatggc tctcgacgat cggaaacagc 3780

acgtgcgaga gttccttgag gaaggtccgc tcctgcggcg agaaatcgtc gaacgtacag 3840

gtgcgataca acgagatcac gtaacagtgg ccccgcttgc gggtcacgag gtggaattgc 3900

gcgtagcgcg gcgacacgat cgccgcctgc atgaggatga agcggtcgag ctgcgcgtgg 3960

atcgggccgt ggccggcgag cgtgtcgtcg acgtgcaggg ggctcgtgcc cgggcgcggc 4020

ggcatctgcg gcccgcaaca gacagcggcc gcgccggtct tcgcgagcgc cgcgccgacc 4080

gcgccgaggc tgcgcacctc gggagggccg tccggcacgt cgtcgatcgc aagctccgaa 4140

atgcggatct cgtcgacggg gaccgccgcg gcgatcaggt tgtacatcat ccggggaaaa 4200

cgtcggctcc cgctgctcga gatcgcttcg ccgacgtgtg cgaacaatct gctgaactcc 4260

atgaagggat tcctgatgag acgttgaagc tgcgcttgtg cgcatgaatg ccgacatgat 4320

ttaaacaccc ggttgcgaac gcgtctgtaa cggattgccg ggacagacgc aacattgccg 4380

gccgtcgaag ccggtacggc gcacggcgac cgttgcgccc gtctgcgacg gatggcgcgc 4440

accttgtccg agtccggatc gctgctcatc cggctgcctc ggcccggacg gcacacatgg 4500

ccgtatcgga gaagatgcgg ccgctatcca ggcgaatgac ccgatccgcc agcttgaagt 4560

actgatcgtc gtgggtgatg atgacaacgc atttcccgcg tgatttcaga tcgggaacca 4620

gcacttcata ggaaaatcgc ttgaacaccg gatcctgatc ggcggcccat tcgtccagga 4680

tataaatcgg acgatcctcg atgtacgcgc aaagcagcgc caagcgcttg cgttgccctg 4740

tcgataacgc gcgggtggtc gagtaggtcc ggccggaaat ctcgatcttg tccgccagtt 4800

tcagggtggc gaggtatttc cgggcaagct cgatgctttc attgccccga tccggtccga 4860

tgatgcgatt gaacaaatgg aaatcggtga agacggcgga aaacaggttt cggtagcgtt 4920

ccctcgcagc gtcgtcaacg acttttccgt cgagggaaat cgtgccgccg gtaggcgcat 4980

agaggccgct gaggaccttg ccaagcgtgc tcttgccgct gccgtttccg ccgatcacgt 5040

agacgagttc tccggcatga atcgtcatgt cgatggggcc gagcacgaag tcgaccgatg 5100

cttcattgtc acggtagttc atcgtcacgt ctttcaactc gatgaccttc catgacttgg 5160

ccgacagggt ttccacgttg cccgcagggc gcggttcctc gtgtgaggcc tgcgtgtcgt 5220

cgatcagaaa gccgaattcc gccagccggg cgagcgcggt cttgccttcg gccaccaccg 5280

gcagaacatt gatcagcatg gtcaagggcc ccatcatgta gagcacggcc agaatgctcg 5340

ccgtgagtac ggagggatcc acgacgccca gagaaggtac gccgaacagc aggcatccga 5400

gcaggaccgc tacggtgatc tggccgatgc tgtcgccgct catgaaccag aagcgttcta 5460

tgtaattgaa tcccgccacg cgcttcgacg acaattcgat cgcggcgcgg gtaaaccagc 5520

gtcgcctggc ccggttgagc ttgagctcct tgatgccgaa cacgaggcca tgtgtgtatt 5580

cgttgaactg gacgaattca tcgcgaaccc gctccgtaaa attgaccgcc ttccgataga 5640

aaaacagata aagcaccagg ccgacgaggg tcaggatgat cgtcgacgcg aacacgatcc 5700

acgagagata ggcgagatag gcgatgctgc agatcaggac gactgattga acgatgatcg 5760

tcgggatggt cagcagggtc tggctcagtt gcggaatgtc ctgtgtcagc atggtcagca 5820

cattgggggc gccgcgtctg tcgatttcat ccagcggggt tgccaggatc cgtttgcaca 5880

ggttgacgcg caacctcgtc atgactttca tgcaggcata ggagggcatc acggcggcgc 5940

agctcctgca gaccaccgcg acgacattca ccgcgatgaa cagcagcaac agcgtctggc 6000

-continued

gatcatcctg gtcgtgcagc acggtgctga tcaacccgac gcccgcgatc gacgcgatgc 6060

cgctgacgag gcccgtcacg accgtgccca gcgtcagcca gggatgactg cgccacatca 6120

gggtggcggc ggaatgccat ggcggcgatt tgctttgagc ggaatccatg agtggccaat 6180

aggtctcagt tgatcaggtg gctgagttcg acattgcttg ccgctgatct caacctcgac 6240

gaggtttcgt gcttgcccag gaacgtgatg ctttccacga ttcccagcgg cgaatcggaa 6300

aacaggatgc agcacttcag caggcgctgc gcacgctccc agccgacgcc gtccggtgaa 6360

tcggccacgc ttcgcaacgc ggcctcgacc gaggcggccg tccagtcttc gctccgtgcc 6420

agccccgact cgatctgccg aagaaattgc aggagcgtgc ggggattgct ttcgatgctg 6480

tacatgagga tgtaatcgat ccgcagtttc ttcgtgatca gcggaaaaat caggtcgatc 6540

acgccggcgg tcgattcgca tttcccatat gccagtgaaa tcgcgtcgcc gagcttgcag 6600

tcccggtgaa gcgcatccag cgcggccttg acgaacgccg cttcgaggtc aacggtggtg 6660

agttgcatga tgttcagtgg cctgtcgagt gttggatcgc ggcgagcacg ggcggcaggc 6720

gttaccagcc gtccggaatg ggcatggaat aggtcagcgg cttctccggc atcacttcgt 6780

ccatgatgtc ggagtagccg gactcctgtc cgaccagatt cggctcgaag cagtagcaat 6840

tgaacgtctg ctgcaggacg aggttgttgc ggtcgttgat cgccggcggg ttttcgttga 6900

tcgcgatgaa tgcgtcgtaa agcgagttcc tgacgacgta cgcgtgcgcg gtgagcgtct 6960

ccacggcctt gacgatgttc ggcgcgacgg gaatcggcgg cgtgaagtga tacgcgccca 7020

ggaacagcat gtgccagtcg tccggcactt gcgcgatgaa ctcgggaaag cgcgcggcga 7080

aatcggcgtc gaagaacgcg tcgtcctcga agatcaggac ttctctcgca ccggcggcct 7140

tcgcctgttt caccgcggcg agatggctca tcgtgcagcc gtagtcctgc gcacgcatat 7200

ggctcaacga ttccggcacg ctcaccagcc ttgcatcgac ggcaggcagc cgttccaccg 7260

tgaggatgtt ctgctctgcg aattttcgtt gcatcgcttc ccagcggtcg gggcgccggt 7320

ccaggttgat gcagaccttg cgggcaaaag tattgtcgat cgtcggcgtt gatttcatga 7380

gggcgttttt tccagaaacg aattgacatg ggcggcgagg acaccggcat gcggatcgag 7440

cagcatggtc aggtggtcgc cggggacgtc cgtcaccgcg acggggtgcg ccgagaagcg 7500

agaccatccc caggtcgcgt ccaggcgaag ctgcgcgatc tcggacgacg gcgcgtagtc 7560

gccgggatcg cgctcggtgc tgcggaacaa cgcgatcggc acgggcagcg gggtggcgtg 7620

cggcgcgtag tgcgacttga agttggcctg atagacgcgc aggtaggcgc gcaggcggtc 7680

ggacccggcg tccgcgaacc agctgccgcg gtcgccgatc cgttcgagga tcaggccggc 7740

ctggccgtcg ggatcgagat ggacgaggtc cgctcgcgtc acctgaaggt cggtcccgag 7800

gaaggtgccg atttcgtggg cgatcgcgac cagccattcg gtgtcgtccc agtcctgcca 7860

gtaagtggcg gccgagctgt cgatgggcgc ggacgcgtcg aagatcgcca gcaatttcac 7920

gtcggcgccc ttggcgacca gttgcctgct catttcgagc gccacgtgcg cgccgaacga 7980

gtggcccgcc aggtagtacg gacccgcgcc caccagcggc cagatgcgtt cgatatgacg 8040

ggccgcgatg tcttccacgc gggtgagcgg ctcgcacgcg ccgtcgaggc cgagcgcttc 8100

cagcccgtga atcgcgtgag cgccgctcag gtggttcgcg agcgggcgga agtagaccac 8160

gttcccgccg gcgcccggca gcaggaagag cggcgcggcg gggccgccgt cgcgaatcgg 8220

cacgagcccg ccggcgggcg cggacggttc tttcgcggcc agcgccgccg ccagtttctc 8280

gatcgtcgga ttctcgaaga gacaggaaat cggcagcctg cgatcgaacg ccttctcgac 8340

atgggccatc agctggatcg cgatgatcga gtggccgccc aggtcgaaat agttgtcgct 8400

-continued

gaccgcgatg tcgtctcttt tgaagatccg ccgccagatc tccagcaacg tgctttcgtc 8460

cgccgcatgc gcgacggcgc gcgccgccgc ggccgcaccg gcagcggctt cgatggccgg 8520

cccggccccg ctgcgcggcg cgctcggccg gccgtcggcg gccggcggat cggcgagctg 8580

gccggtcaac tggcccgggt tctcggcgaa tcgctcgagc aacgtgcgga gggtatcgag 8640

catctgccgc acgacctccg gcgcgatgcg gtgggcatcg tgcgaaatat ggaagccgat 8700

gcgctcgttc gggtgcacgg tcagggtcag cgggtagttc gattccgcga acgcgcgggt 8760

gtcgaggatc tcgatgtcgt ccggcccgag atcgggggcg gcggcaaccg ggaagttctc 8820

gaagaccagc aggctgtcga acagactgtc gccggcgggc agttcgctcc acgactggat 8880

atcgaccagc gagctgtacg aatgcggctc catcgccgtc tgggctgcgt ggacctctgc 8940

cagccattcg atgaacgggc gctcgggcgc gatccgcagg cgcagcggca gcgtgttgat 9000

gaacagcccc acgatcgact cgacgccgtc gagcatcggc gggcgaccgg acacggtgac 9060

gccgaagacg acgtcgtccg ttccggcgtg gcgccgcagc accaacgccc agaccgcgcg 9120

gatcagcacg ttgagggtga cgcgatgcgt gcgcgtgagc gtttgcagcc gcgcggccag 9180

cgcctcgtcc agcaggaatt gctgggtccg gcgcttgtcc tgccgcgggg catcgccggt 9240

cgcctgccgg gccggactgg ccgcgaccgg cgtggcggcc ttgaagccgg ccagttcggc 9300

gcgccaccac gtttcgtcgg ccgagcgagg atgacgcgcg agccagtcga tgtacgcgcg 9360

gtatcccggc gccgacgccg cgaccgcggg catgccggtg cgggcgagcg acaggtagtc 9420

gtcgaacacc tccttcatca gggtcgcggt gctccagccg tcgaggatga tgtggtgcgc 9480

gctccagcag aagcgatggc gcgtgtccgt ttcctggatc agcgtgcagc ggaacaacgg 9540

cgcgcgctgc agatcgaagc cgcgccgccg gtcgtcggcg aggaacgcat cgaaatcctg 9600

cgcgcggcgg gacgcatcgc ggtgccgcca gtcaaggaac gtccatggca ggtcgaccgt 9660

gtgccgtacg gtctggacgg gatggtcgcg atcggcccac gcgaacgcgg tgcgcagcac 9720

ggcatggcgc gcgagcgcat tggcccacgc ctgccggagc gccggcacct ggagcgggcc 9780

gctgacgaca aagctgaact gctggaagta ggcggcagga tccaggtcgt acagcgaatg 9840

gaacaggatg ccctgttgca gcgacgagag cggatagctg tcctcgatat cgtccgctgc 9900

ggtgtcgggg accgacgccg cgaagtcgag caaccggtcc ctgaagtgcg cggccaggtt 9960

ctcgaccgtc tgccgccggt ggagccgctc gccgtagcgc cagtccacct ggagcttgcc 10020

gtcggcaacg gccgcgacga tctcgaaggc atgcgtgcgc tgcgaccgcc cggcgcgcag 10080

cgaaccgagg tcttcggccg ccgggcgcca gccatcggat tgccgcaata cggtatcgag 10140

ctgcccgtga tagttgaaga ggatatcggc cttcggcaac gcggcgagac tgtcgcgcac 10200

ggcggcgtcg gggctctggt agcggagcag cgaataaccg agaccgtcgg ccggaatccg 10260

gcgcagctgc tgccgtgcgg cacgcagcgc ttgctccggc gcgtgcatcg cgtcggcgtc 10320

gagcacgacg gggtagatgg acgtgaacca gcccaccgtc cgggtgaggt cgagcggcgc 10380

atccgacacg tggcggccgt gactctcgag atcgatccgc gtgcgggtgt tacccgtgac 10440

catgctgcag gcttgcgcga gcgcgacgag caggacgtcg ttgatgcggg tgtcgtaggc 10500

ccgcggcagc cggcgcagca acgcggtggt atcggcttcg cccagctcga atgaaacgga 10560

cgacgcgtcg tcgactgcgt tgttggccgc gcccgtgcct ggatagtcaa ccggcatcgg 10620

ctcgacgggc tgcgcgagga gggcttgcca cagccgtgct tcgtcgccga tggcgggcga 10680

ccgggccagt tgctgcagat gcaacgccca ttcgcggaac gaagtcgtct tcccgggcaa 10740

-continued

cggctggccg tggtaagcgg catgcaggtc ctcgagaagc acgcgccatg acacgccgtc 10800

caccgccagg tgatggatcg acacgaacag gcgggcgagc ggctcgtcgg ccaggcagaa 10860

gagccgggcc gccagcaacg ggccatgcgt gatgtcgatg ccgcgctccg cgtcagcggc 10920

ggcggcacgc atcgccgcca ggcgctcgcc tgcgtcgtcg gcgatcacct gtttcgcaaa 10980

gagcgccggc atctcgccgc cggcgacgac ctgctgggtc cagcggcccg catcgtgcga 11040

gaaacgcagt cgcaacgcat cgtgatgttc gtagacctgc cggaacgcgt cggccagcct 11100

cgatgcgtcg atatccgccg gcacctggat caggaccgtc tggttgtagt gcgacggcgc 11160

atcgatctcc tgttcgaaga accagtgctg caccggcgta agcggcgcat cgcccagcgg 11220

gctcaaggtc ggcgcgcagg ctgcccgctc ctcgggcgcg gcggccagct gcgcgatcgt 11280

ctgatactgg aacagctgct tcgccgtcac gcgcagccct gcctgattgg cgcgcgcgat 11340

cacctggatg ctcaggatcg agtcgccgcc gagttcgaag aaattgtcgt ggatgccgac 11400

ggaaggcaac tgcagcacgt ctatgcagat cgacgccagc aggatttccc gcggcgtgac 11460

ggcaggtgca tgcggctggg ccgcgtcgcc ccgatccgcc ggaagcggca gcgccttgcg 11520

gttgatcttg ccgttgggca gcatcggcaa ggattcaagg gcgaagaact gcgacggcac 11580

catgtagtcg gcgagcttgc cgcccagata gccgcgcaga tcggcgatgt ccggcgcggc 11640

ggtcgcgaca taggcgatca ggaacgttcg ggctccttcg gttttcgcga tcacgacgca 11700

gtcgtcgacc gacggatgcg cgcgcagcgc cgcctcgatt tcaccgggtt cgatgcgcag 11760

gccgcgcagc ttgatctggt gatcgatgcg gccgaggaac tcgatgttgc cgtcgggccg 11820

gtagcgcgcg aggtcgccgg tgcggtagag gcgcgcgagc gggtcggccg agaacggatc 11880

ggcgatgaac ttttcggcgc tcagttcggg ttcgccgtgg tagccgcgcc cgaccggtgt 11940

gccgccgatc agcaattcgc cggccacgcc gatcggcgtg ggctgcatct gcgcgtcgac 12000

gatgtagagg cgggtgttgg cgatgggccg gccgatcggc acgatgcggt gcggatcgtc 12060

gcgccggcat tcccacgcgg tcacgtcgac ggcggcctcg gtggggccgt agaggttgta 12120

gagcttgacg tccaggcgct cgaggcaacg ctgctgcagg tcatggggca aggcctcgcc 12180

gctgcacacg acgcggcgca gcgacgcgca gtgcgcgtcg aggtccggat gatcgaggaa 12240

cgcgcgcagc atcgacggca cgaaatggat cgtggtgatg cgttcgcgct cgatgagctc 12300

gaccaggtag tcggtctcgc gctggccgcc ggggcgggcg aacacgaggc gcgcgccggt 12360

gacgagcggc cagaagagtt cccagaccga gacgtcgaag ctgaacgggg tcttctgcag 12420

cacggcatcg tcggcgtcga gcgcataggc gtgctgcatc cagaggatgc ggttggtgat 12480

cgcgcgatgg gtgttgagcg cgcccttggg gcggccggtc gagccggacg tgtagatcat 12540

gtaggcgagg ttgtcgccgt tcagcgcggg tgcggggttg gacgtcgccg cggcgtcgag 12600

gtcgagcgag tcgcgatcga cgacgatcac gtgcgcgtcg gtgtcgggca gcgcgtcgtg 12660

cagatgctgc tgggtgagga gccagcgcaa ctgcgcgtgg tcgatcatga agcgcacgcg 12720

ctcggcgggg tagtcggggt cgacggggac gtaggcgccg ccggccttga ggatcgcgag 12780

cagggcaacg ctcatgtcga gcgaacgctc catggcgacg ccgacgagcg agtcggggcc 12840

gacgccgagc gcgacgaggt ggtgggcgag gcggttggcg cgcaggttga gttcggcgta 12900

ggtgagcgcg gtgtcatcga agacgatcgc gacggcatcg ggcgtgcgct cgacctgctg 12960

ctcgaacagg cggtgcagcg gttgcgcggc gtcctcgccg aaatccgtgt cggtgcggtt 13020

ccactcgacg gtcagcaggt tccgctccgc gtcattcgac aacgacagcg cgccgagcgg 13080

ccggtccgga tcggcgatca cggcatcgac gagcgtgcgg aagtgttccg ccatgcgatc 13140

-continued

gatcgtggcg gcgtcgaaca gatccaggtt gtattccagc gagcccgcga ggccgtcgtc 13200

ggcatcctga acatgaagcg tgaggtcgaa cttcgcggtg tgggtctcca ccgccaccgg 13260

cgtggccacg agaccgggga agctcactgc ccggggttgc gctttctcgt atgcgaacac 13320

gacctggaac accggcgtgc ggcccaggtt gcgttcgagc tcgagcgagt ccaccacctg 13380

ctcgaacgga atctcctggc ggctgtagcc gtccagcgcg acgcgcttca cgcgcgccag 13440

caggtcgccg aaggtcggat tgcccgacag gtccacgcgc agcgcgagca tgttcgcgaa 13500

gaagccgatc agcggctcgg tcatgctgga acgccgattg gcgatcgggg agccgatgac 13560

gaggtcctgc tggttgctgt atcgcgacag gagcagcgca tacgcggcga gcacgaccat 13620

gaacgtgctg gtgccggacg cacgggcaat cgcgcgcagg ccgtcggcgc gttcggcgct 13680

cagctggaac ggcaggaccg cgccgcggaa ctgctggacg gcgggccggg ggcggtcggt 13740

gggcagttcg atcaggtccg gcgcgtccgc cagcgcggcg ctcaggagcg ccagctcccg 13800

atgcgtgtcg gcggacgcca ggcgctcgtg ctgccacacg gcgtagtccg cgtactgcac 13860

ggccagttcc ggcagcgact cgccggcata gagcgcggcc agttcgccga tgaggatgcc 13920

tgacgaccat gcatcggaaa cgatgtgatg catcacgatg ccgaagacgt gcaggcgctc 13980

atggacgcga tacagcacga cgcgatagag cggcccggcg gcgagatcga acgggcggtc 14040

ggcttcctcc gcgagcagcg cgagcgtgtc ggattcgctg gcgacgtcga cgacgtcgag 14100

cgcgaccggc gccggcggcg caatgcgttg aaccccgcgg ccgtcgacgg cgggaaacgt 14160

cgtgcgcagg atctcgtgac gccggctgat ctcggacacg gcaaaccgca ggcgcgcgac 14220

gtcgagttcg ccttcgaagc gcagcgcgct cgagatgttg taggtggccg acgggccttc 14280

cagttgcgcg aggaaccaca gccgctgctg cggaaaggac agcggcaggt cgttcgcgcg 14340

cgagcggggc gggatggcgc cggccgtcga gccggggtgg ggcgacgacg cttcgatcag 14400

gtcggacacc gcgctgatgg tctggagttc gaagatcgcg tcgatgccga tctcgacgga 14460

gaagctgctc cagatccgcg agaccagttg catggcttgc agcgaatcgc cgccgtagtc 14520

gaagaagcgg ccggcgagat cgacggccgg attgtcgagc acgtcgcgcc agatgcgcac 14580

cagttcgcgc tgaatcggcg tggcgtcgag aggggcttcc tcgggcgcgg cggcaggctc 14640

cagggccagg agcgccgggc gatccagctt gccgttggcg ttgagcggga attcggcgat 14700

cgggatgatg tcggacggga ccatgtagtc cggcagcttc ccggccaggt aggcccgcag 14760

gttcggcacg ctcaggctcg cggcgccctt gacgtaggcc gccagcttgc gcaccccgtg 14820

ggcggattcg cgcagcatga ccgccgcgcc gacgacgtcc tcgtgcgcgg cgatcgcggc 14880

ctcgatctcg ccgagttcga cacggtgccc gcggatcttg acctggtggt cgacgcgtcc 14940

gtagcactgg atacgtccgt cgggcagcca ccggccgatg tcgccggtgc gatagatgcg 15000

cgcttcgccg ggaaacggat gctcgacgaa tttcgcggcg gtgacgtcgg gccgctggtg 15060

gtagccgcgt gcaaggccgg cgccggcgag gcagatttcc ccgggcacgc cgagcggaac 15120

cggccgcagc gcgtcgtcga gcatgtacac ccgggtgtcg gcgatgggac ggccgatcag 15180

caccgtgggc ggcgcgtcct cgacgcgctc gacgatgcag ccgaccgtcg cctcggtggg 15240

accgtactcg ttgtagattt cgatcgcggg atcgatcttg cgcagcgtgg cgatgtgctg 15300

gggcgtcagt tcctcgccgc ccacgatcac cttgcgcacg ccggagcgtg ccaggttcat 15360

gtattccagc aggtgaatgt gggtgggcgt gagcttgagg gtgtcgacgc cgctgccggg 15420

ctggaacatc cgggccagga tggtgtcgat gctttccgac tgcggataga tgcgcagcgt 15480

-continued

cttgccgcgc accagcgggc agaagatgtt ggtgagcgtg aagtcgaagc agagcgagct 15540

gtacaggccg aaactgccgg tcgtgctttc cggaaagtaa tacccggcgg cccacgcgat 15600

gtagtgggcc aggttccggt gttcgagcag gcagcctttg ggtttcccgg tcgagcccga 15660

cgtgtagagc acgtaggcca ggtgcgccgg ttcggcacgg tgcggcgggt tgtccggcag 15720

cggctgccag ccggggagtt cctggtccag cagcagcgtc acgccggaga attcatacca 15780

ctgcgcgagc tgactcgact gggtcaccag cagcgacagg cccgtgtcgc cgaggatgtg 15840

attgatccgc tcggccggat acgcggggtc cagcggaacg aacgccgccc ccgccttcag 15900

gatgccgaga atcgcgacga tcatccattc ggaacggtcg agcatgatgc cgaccagcga 15960

ttccggcccg acgccgtggt gttcgcgcaa gtgatgcgcg aggctgttgg cccgcgcgtt 16020

caggtcggcg taggtcatca gcgaactgtc ggtgaccagg gccggcgccg tcggcgtgcg 16080

tgcgacctgg gcttcgaaca tggcgacgac cgtcgggtgg ctggggccgg ccgtcgcggt 16140

ttcgttgaac gcggccagca gcgggccctg ttccggcggg gccgcttcga tgtcgccgac 16200

ggcgccgtcg aggtgttcga atgcctccag caccgcggcg aggctgccgg cgaaaccgtc 16260

gatgatgaaa ggctcgatgg ccccgctgta acgaagctcg atttcgccgc gcgcgagccg 16320

caggtgcaac tgcagatcgt cgtcccgacc ggtcggtgcg tggtgcacgc ggtcgtccgc 16380

cagcgcgact ttcgtgagct gcgcgagcgc catgtccttt tcgttgcgca cgagcgtttc 16440

cagcgggaat cgaggctcgg cgtagctgtc ttccacgatc ccggccacgc gcgacaggta 16500

gtcctcgatg cgctcgtcgg ggcggacctc gatgatcagc ggaacgatgg cggcccgggc 16560

cgacggatgc ccggccagcc ccggcgtgcc gagcaccgtg accggaatcc ggaagtattt 16620

ccagagcagg aacgcgatgc ccgccgccgc gacggcgaat tcggcaagct cgccgtcgcc 16680

gatgcgccgc aacaggtcga gcgacgcggg cgtgagccgc accgagcggg tcagcgggcg 16740

acccggctgc tggctcgggg cgtacgccgc gattccgtac acgccggcga cccgggaaag 16800

gctttcgcgc cagaaacgcg cggtggctgc atagcgatgg tcggtgacca gcacgttatt 16860

gtcttgcaca ggaaactcct tgagacgttt tgttcacctg aaacaacctg aagcagcacg 16920

cacggcgcgc gccgctcgaa ccccggcggg cgcgcatcac gtcttctcct cgagcgcgtc 16980

gtcggccgtg accgcgggcg cgcgcttcag gcgcaggccg acccggactc gcgggccggc 17040

ggcgggcgcc tcgtcggaga gcgggatgcg atcgaccggc gtggccggat cgcgacggaa 17100

gacgtcgtgg atcgcgagca gtcgatcgcg catcgcggcg atggtcgacg ggcggaacag 17160

gtgggtgttg tagatgaact ggatcaggtg ccggccttcg ctttccacga cctggaagga 17220

caggtcgaac ttggccgtcg tgtccgccgg cgagatgtcc gtgatgcgaa ggcctggctg 17280

cggcgccggc atcgacacgt ggttcacctg aatgtcgaag atcgggaaat ggttcgccgg 17340

cgtgcggatc ttcaggtctt ccagcaacac gtcgaacgga taggacgcat gctccagcgc 17400

ttgcgcggag gctttcgcca ccccgtcgat cacctccgcg accgtcgcgg atttccgcac 17460

cggcacgcgc agcacgacgg tgttgaggta cacgccgacc tgcgattcga gctgctcgct 17520

gtcgcgcccg gccgacacgc tgccgatgac gatgtcctca cgccccgtgt agcggtgcat 17580

cagcacgcag aacgacgcca gtagcaccgc gtggagcgac gtgtggtgag cgcgggccag 17640

cgtcgcgagt tccgccgcgt gcggctgcgg cagttcgact tcgagcgtct gcccggcatg 17700

accgagccgc tcgggacgcg ggaagtcgga tgccagttgc aggcggggca gcggcggcgc 17760

cagttgctcg agccagtacg cgcgatgcgc ggcggcgcgc ggacccgcga ggctcgcgtt 17820

gtgccacgcg gcgtagtcgc gatactggat cgacagcggc ggcaggtcgc gccccgcata 17880

-continued

cagcgcatgc aggtcgtcgg tcagcacgcg gatcgaccat gcatccgaga tcacgtggtg 17940

catgttcagc agcaacagat gcttctcctg cgacagccgg accagcttga cgcgaaagag 18000

cgggcccgac gcgagatcga acggctgctc gcattccgcg cgaatcagcg catcgatcgc 18060

ttgcggcccg gcatcgtccg cgagatcgcg ctgctcgacc cggaatccgg acgcttcgcg 18120

gctgaggacg cgttgccgca actcgccttc gatcatcgcg aacacggtgc gcaggctctc 18180

gtggcgatcg accagcgtgt cgaatgcacg gacgaggcgc gccgtatcga cggcgccgtc 18240

cagctgcagc gcgcccgcca tgttgtacgt ggacggatcc gcgccgcggc tggcgagcca 18300

gatccgcttc tgtgcacgag acaccgcgta ggacggttgc gcggccagcg ccgggatgat 18360

cgcgtcgtcg tcggcggcgc cgtcgacggg catggcagcc agcctttgtg cgagcgcgcg 18420

cggcgtcggc gcatggaaga tgtcggcgac cgcgacgttc agtgcagccc gggggatccg 18480

gctgaccatc tggatcgcct tgaggctttg gcctccgtgc tcgaagaaat cgtcgtcgac 18540

gccgttcggc cggcggccga gcacctcggc gaagaggcgc agcagcgccg cttcgaccgg 18600

cgtgcgcggt tcggcccgca cgccgtcggg cacggacgcg gcatccggca gcggcagcgc 18660

ggcgcggttg atcttgccgt tcggcatgac gggcagcgcc ggcagcagca tcacggtgtc 18720

gggcaccatg tgcgccggca gcgtgtcgcg cagtgcgtcg cgcacgcgct ggggcgtcca 18780

gccggttccc gacgcgtagc cgcacagggt catttcggca tccgacgttt cccgggcgac 18840

caccacggcg tgggaaatgc cggcaagact ggtcagcgcg gcttcgattt ccccgagctc 18900

gatgcggtag ccacggatct tgacctggaa gtcgcggcgg ccgaagaagt gcagattgcc 18960

gtccgccccg aagcagccga tgtcgccggt gcgatacagg cgcgcgcctg gttccggact 19020

gaacggatcg tcgcggaaca ccgcccgggt gcgggcttcg tcgaacaggt agccgcgccc 19080

gacgccgacg cccccgatgc agatctcgcc cttgacgccg gccgggcacg gattcatgtc 19140

ggcatccacg acgtagaggc gcaggttctc gatcggccgg ccgatcggaa tcgccggccc 19200

atccggcgcg cgcgtcaggc agtaatgcgc gacggagtcc gacgcttcgg tcggcccata 19260

ggcgttgatg agccggacgg ccggattcag gcggaaccac gcttgcgcgg tggcgggctg 19320

cagcgtttcg ccgatcgtca gcaacgtgtc gaggtgaggg aaggccggtg ccgcgtgccg 19380

ttccagttcg ccgagaaagg tcgcgagata ggacggtacg aattgcattg ccgtgatgcg 19440

gtcgcggtgc aggctgtcga tcaggcgcgc gggctcgagg atcacggcat cgggatagat 19500

caccgtcgtg ccgcccgacg ccagcgccgc gaagcattgc cagaccgaaa tatcggagca 19560

gtgcgaagcg gtctgggcga ccgcgctctg cgcgccgagc ccgacccggc gcgccatcgc 19620

gagcacgtga ttgagcatgc cgcgatgttc gaccatcgcg cccttcggct ggccggtcga 19680

acccgacgtg aagatcacgt aggcgaggtc cgcgggccgg cagcgcggcg tcaccggcgc 19740

cggcgcttcg gcgccgcgac ggtcgggcag gcgggccgga tcgaccagcg ggatcgacgc 19800

cagcgccggc ggcggcacgc agtccgtcgt gacgatgacg gccggccgcg ccagcgtcag 19860

gatggtctcg acccgctggg ccgggtaggc cggatcgacc ggaacgtacg ccgcgccgca 19920

cttccagatg gccaggatcg tttccagcat cagcggcgag cgcggcatcc agacggcgat 19980

ccggtcgtcc ggctgcagcg gcgccgtctg cagaagatgc gcggcgatcc ggttggcgcc 20040

ttcgacgagg tcacggtagg tgcgaacctc cgtgccgcag cgaaccgcca cgcgctcggg 20100

gtgcgctgcg gcgacggcct cgatcagttc gggcagcgtc cggtcggacg gaaccggcgc 20160

gaacgtgtcg ttccagccga gcaggatggc gtcccgctcg gcggcagcga gaagcggcac 20220

-continued

gctgcggttc gggcgatctt ccgcgccggc caggccggtg agcagggtct cgacatggcg 20280

cagcaggcgg acgatcgtgt cgcgatcgaa ccggccgtcg tcgtacagca cctgcagcga 20340

caggcgcttg cccggcgtca cgaccagcgt cagcgggtaa ttgttcggat cggacacctc 20400

gaatgcgccg atccgcaggc cgggcagcgc atcggccagc gcttcttcca ccggataatt 20460

ctggaagatg agcaggcttt cgaagagcgg cacgccgggt ggcaggccgg cgaatttctg 20520

gatgtcggcc agcggatagt gcgcatagtc ctcctgctgc gcgagatcca tctgcaattg 20580

cgccagccac gctgacgtcg ggcgtgcgtc gatgcgcacc cgcaccggca gcgtgttgat 20640

gaacagcccg accatttcgt cggatgccgg cagcgacgcc gggcggccgg aaacgatcgt 20700

gccgaacacg acgtccgatt cgccgctgta gcggctcagc aactgcgccc atgcgccctg 20760

cgcgagcgtg ttcagggtga ggcggcggga ttgcgcgaat gcgacgagcc gttgcgtgtc 20820

gctttcggag agcagcagcg gctcttccac gtaggcgccc ggcgcggccg tgccgtcgag 20880

ttcggggcgg cccagcacga gcggcgtcgt cgccgggaaa tccgccagct tcgtcttcca 20940

gaaacgttgc gcggcggcgg cgtcctggcg tgccagccag cgcacgtaac cggcgaaggc 21000

aggcggcgcg tcccgctgcg gcgcgccttc ggccggcggc gcctgatagg cggcggccac 21060

gtcgctcagc aaccgggcgg agctccaccc gtcgagcagg atgtggtgat ggctccaatg 21120

gaagcgccat gcgtgctcgc ccacgcggaa cagcgcgagc cgcatcagcg gcgcgcgggt 21180

aaagtcgaag ccgcgcgccc ggtcttgcgc cacgtaggct tcccagcgct gttcggcctc 21240

cgcggcggac gccgcgcgca gatcctcgtc gtgccacggc aagtcgatcc ggcgatgcac 21300

gacctgcacg gggctttcga tgtcttccca gtgaaacgac gtacgcagga tgtcgtgccg 21360

gtgcgccacg gtctcccacg cgcggcggaa ccgttcgacg tcgagcgccc cgtcgatacg 21420

gaaattcagg ctgctgaagt acgcatccga cgcgggttcg tacaggctgt ggaacagcat 21480

gccctgctgg gtcggcgtca gcgggtagac gtcggcgatc tcgtccggac tcaccgacgc 21540

cggcgccggc gcctgcggca acgcagtcgc gggccgggtc gatgcggacg ggacagcgtg 21600

gccggcgacc agggtttcga gcgccgcgat gtaggcttgc gcgacgcgca ggatggtggc 21660

cgtgtcgtgg caggcccggc tgaattccca cgcaacgtgc aggcgattac cggtcacgta 21720

cgcgttgatg tcgagcaggt gctcgcgcaa ctggttcgcg ttgcggccgt ccccgctcgg 21780

ctccgcggcc tgtttccagt cgcgtgcggc ggtgaacagc tggtcggtct gccccaggta 21840

gttgaactgc agtcgcggct gcggaagcgg gccgtcgagc cggtctagca gcaggccgta 21900

ggtgatgccc gcgttcggca ccgcgcgcag ccgcgtcctg accgatgcga cgaggctggc 21960

cggatcgtgc gaaccggcat cgaccgtcag caagaccggg aaaaccgacg taaaccagcc 22020

caccgtgcgc gagatgtcga gcgcgtcgat cagttcctcg cgcccgtgcg cttcgagatc 22080

cagcagcacg tcggcgcatc cgctccattc gctgacggca cgcgcgagcg cggcgagcag 22140

cacgtcgttg acctgcgcgt cgtaggcgcg gggcgcggcg cccagcaagg ccgtcgtcgc 22200

ggcttcgccc aactcgacga cgatcgtgtc ggcggacgac acggtattgg cgtcggcagg 22260

cgcatcgcga tcgagcggca ggccgggcag ggcggcacgc gcgagggcct gccaatgggc 22320

gaggtcggcg tcggcggcgc cggagccggc ccaggtcgag atcgcccggg tccatgcggt 22380

ccaggtcgcg ctgccgcctg cgaattcggg cgccttgccg ttgcgcagcc gggtataggc 22440

gtcgtacacg gtttcgagca gcgcgcccca cgacacgccg tcgacgacca gatgatgggc 22500

gaccagcagc aggcggagcg aacggccttc gtcgacgcgg aacaggtccg cgcgcacgac 22560

ggggccgtcc gcgagattca ggctcgcatg cgactgcgcg acgtactgcg cgagctgatc 22620

-continued

gcgcgcaatg tcggacacga cgacggggat ctccgggtcg tcgacgactt cctgggtcca 22680

gccgctctcg ccctcgcgaa agcgcagccg cagcgcgtca tgccatttga ccgcatgccg 22740

cagcgcctgg cgcagcaaga ccggatcgag gtcggccggc acgtcgagca ggaccgcctg 22800

gttgtactgg tccgggtcgt gcttgccctg cgcgaagaaa cgcttctgga tgggcgtcag 22860

cggcagcggg ccggacgatg cgacgaacgc cgccgcgccg accgtgccgc gcgtcgccac 22920

ggcggcgagt tcggccaccg tcggatgctg gaagatgagc cgggtggtga gcttcaggcc 22980

cgccttcgcg gccagcgaca cgatgcgcat gctcagaatc gaatcgccgc ccagcgcgaa 23040

gaggttgtcg tggatgccgg gcgacggaat gcccagcgct tcgccccaga tgcggcacag 23100

cagcgtctcg gtaggcgtgc ggggcggcgt cggcgcgtgt gccgtggcgg cgagtcgcgc 23160

gcggtccagc ggcggcagcg cgttgcggtc gatcttgccg ttgccgctca ggggcagcgc 23220

gtcgagcacc acgtagatgc cgggcaccat gtagtccggc agcgtggcgg acagcgcggc 23280

ggcgatcccg gcgtcgctca gcgacgcgcc gtcgcggaac gcgacgtacg cgcacagcgc 23340

ggcgcggccg gcctcgtcgc gatagtcgag cgcggcggcc tggcggagtt tccgcgaatg 23400

gtcggccagt cgtcgttggt cgatctcccc gagctcgatg cggtagccgc ggatcttcag 23460

ctggtggtcc ttgcggccgt gcagcacgat cgttccgtcg ggcaggtagc agccgatgtc 23520

gcgggtgcgg tacaggcgga cgccgcgctg aggatggaac ggatcctcga cgaacgcgtc 23580

ctgcgtggcg gcttcattgt tcagatagcc gcgaccgacg gcgacgccgg acacgcacag 23640

ctcgccggga atcccgatcg ggcacaggtt catctgcggg tcgacgacgt agaggcgaac 23700

gttgcggatc ggcttgccga ccggtacgta aggcgtggac ggcgcgcccg tcatgcggtg 23760

ctgtgcgacg tcgtcggacg cttcggccgg gccgtacgcg ttcaccagcg ggatcgccgg 23820

gaacacgtcg aaccactgtt tcaccagcgc cgggctgacc atctcgccgg tgacgagcag 23880

gtgccgcaga tgccgcatca gcgccggccg ttccgacgcg cggtcgagca cggcggacag 23940

ataggacggc accagttcga ggatgctgat ccgggtggtt tccaggtacg cgacgaaacg 24000

cgcgggatcg cgaatgcagt cgtcgtcgac gatcacggtc ttgccgccga cgagcggcgc 24060

cgtgaaaaat tgccagaccg aaatatcgaa gcaatgcggc gcggtttgcg cgatcaccga 24120

cgacgccgag atcgagaact cgtcgatctc ggcgagcatg tggttcagca tgccggcgtg 24180

ctcgaccatc gcgcctttgg gcttgccggt ggagccggac gtgtagatca cgtaggcgag 24240

gctgtcgggc gacacggggc ggccgggatt ggagtcgtcg acggcgtcgg tggcggcgtc 24300

gagcgacacg accagcgcga tcccggccag ctccgggggc aggagcccgt cgcaggtgat 24360

cacgagggcg gcgccggaat cctcgaggat ggtgcggatg cgggccaccg gataattcgg 24420

gtcgaccgga atataggcgg cgccgcactt ccagaccgcg aggatcgcct ccatcagctg 24480

ggcggaccgg tgcatgcaga ttgcgaccag cgcgtccggg cccaggtcgg cggcggcgag 24540

caggcggtgc gcgatgcggt tggcgcgcgc gttcagttcg cccgcgctca ggacgccatc 24600

ccggtactcg accgcgggcc gctcggggtg gtccgcggcg gcctgctcca ggcgatgcac 24660

cacggtgagc gcggcgtcga acggcacggc ggtgtcgttg aaggtctcca gcaactgccg 24720

gcgttccgcg tcgggcaaga tcggcacgcg gccgagcagc cggttcggat cggccgcgaa 24780

cgcgtcgagc gtcgcggcca cgtggcccag catccgctgc atcgtgtctt catcgaagcg 24840

ccgcgggtcg aacgacagtt ccatcttcca gtcgtcgcgc gccgtcacca cgaattcgag 24900

cggaatgtcg gcgcggttgt agagctgcac ctcgtcgacc gccagcccgt gcgcgccatg 24960

-continued

cgtgagcgac gcgtcgagcg ggtaattcat gaacgtgatg ttgctctcga acagcggcgc 25020

cgtcggcggc acgtcgctgc agcgctgaat gtcgggcaac ggggtgtgct cgaacggcgc 25080

gcgggcggcc acgcgcgcct ggatcatctt cagccacggc accagcggct gcctcgggtc 25140

gacccgcacc cgcaccggca ccgtattgat gaacaggccg agcatggttt cgatccccgg 25200

caggttggcg ccccgcccgg acacgacggc gccgaacacc acgtcggttt ccccgctgta 25260

acgcgacagc acgagcgccc acgccgcttg cgcgagggta ttgagggtga cgtgatggcg 25320

ggccgcgaat tgccgcaggc gcgcgctcag gtcggccgac aggtcggcct gcacttgcgc 25380

gaggccctgg ccgaagcgtt cgtccgcgcc cgcgcgcgcg gccgtgggca gcggggtcgg 25440

tgtgcggaac ccttcgagat agcgcgtcca gtattgctgc gcggcttgcg gctcgtgctg 25500

ctgcagccac tggatatagt cgcgataggg gcgcaccggc gggagcgccg gcgacacgcc 25560

gcgcgcgagc gcgccataga cctcgaagat ctcctcgatg acgagcgaca ggcaccagcc 25620

atcggccagg atgtgatggt ggctccagct gaacaggtag gcgtcggcgg cgacgcgcac 25680

caggcgacag cgcacgagcg gcgcgcgatc gagcgcgaag ccctcggcca ggtcgttgtc 25740

gagatgcgcg cgccaccgtg agcgctgttc gtgttccggc aggtcgagcc agtcgtcctg 25800

cacccacggc agcgtggcgc gcgcgtgcac gacctgcatc ggcttgtcga actcctccca 25860

atggaacgac gtgcgcatca ccggatgccg atcgatgagc tgctgccacg cggcatgaaa 25920

cagcgcggga tcgaggctgc cggtgatccg gcaactgagc tggttgaagc tgcttctcga 25980

gccgggctcg tgcacggcat gaaagagcat cccctcctgc atcggggaga gctcgtagat 26040

atcggcgatg gtgggggatg tcacgatttg atccttgaga caagggcgtc cagcgcttcc 26100

tggctgatgc gcgcggccgg aaagtccgac gggctcagcg cgcgcgggcc gtcgccgccg 26160

gccgcgacga tcgacagcag gcggctgcgg tagcactgcg tcagctgttc gatgacgccg 26220

ggtgcgcagg cctcgcggtt gtagtgccag gtcaggcgca gacggccgtc gaacaccatc 26280

ccgtcgatct cgaacagatg gccgcgacgt gcgcgcgggc tgtgctcggg gctctggaag 26340

tcgagtaccg gcttccagcc cgtgtcgtcg ggcagcacgc gatcgacctg gccgagatag 26400

ttgaagcgca ccggcgccgg cggctgccgt tcgagcgccg ccgcgatgcc ggcgtcgtgg 26460

ccgaggtagc gggcgatgcc gtagccgagc ccgcgcatcg gaaccgcgcg cagctgctcc 26520

ttgacgtggc gcagcgcgtc gaccgccacg gtggcgtcgc cggcgttcag gcacaccgga 26580

tagtgggtgg tgaaccagcc gatcgtgcgc gacgtatcga cgccgtcgaa aatgtcctcg 26640

cggccgtggc cttcgagatc gacgaccagc gacgcgttgc cggtccagtc gccgaacgcg 26700

agcagcaggg ccgtcagcag gacttcgttg atctgcgtgt tgaacgcacg cggcacgtcc 26760

tgcaacagcg cgagtgtctg ctgcgcatcg aactcgacga tcgtcgagcc cgcttcggcg 26820

acggtgccgg ccggcatgtc gtcgaagcac gccggctcgc cggcgttgcc ctggagccag 26880

tagtccagcc ccaggccgtc gagcgcggtc gcgccgagtc cggacaggcg cgtcgaccag 26940

tcgcgccagg ccgtcgtcct ggccgggagc tgtaccgcgt cgcccgcttc gagctggcga 27000

catgcggtgt acaggtcttc gaacaggatg cgccacgaca cgccgtcgat caccaggtga 27060

tgcgcgaccg cgagcaggcg ctgcggcgcg tcgggaccga actggaacag gtgcgcgcgc 27120

agcagcggcg gcgccgacag cgtgaagctt tcctgcatgc cggtggcggt cgcgagcatc 27180

gcggcctgcc gtgcggcagg cgccgcgtcc gccagcgacg tgacgccgag cggaatggcc 27240

agcggcggcg cggcatgcga ttgctgccac acgccggcga cgcacgcgaa actcagccgc 27300

agcgcgtcgt gatgcgtcgc gacggccgcc agcgcgcgct cgatcgtgtc cggccgcagc 27360

-continued

gatgcgggca cctcgatcat cgtcgactgg ttgtagtggt gcggatcggc gacgtcttgc 27420

gcgaagaacc agtgctggat cggcgtcagc ggggcggggc cgaccaccgg ctcctgcgcg 27480

atccggatcg acggcgcctc cgtcgcgacc tgggcgagct cggcgatggt cgggtgtgcg 27540

aagaactggt cggcggtgaa cttgagcccg acttgctggg ccagcgacat cacctggatg 27600

atcaggatcg agtcgccgcc cagttcgaag aaattgtcgt gcacgccgat cggctcgcgg 27660

cccagcacgt cgcaccagat cctgcccagg cgcgcctcga cgtcattggc cggtgcgacg 27720

taggcggttt cgctcggcgc gggcgccagt tccagcgcgg cgagcgcctt gcggtcgggc 27780

ttgccgttcg gcgtcagcgg caggcgttcg agcgtcacga tcgacgccgg caccatgaac 27840

tcgggcaggc gttccttcag gtgttcccgc aggctggcga cgctggccgt cgccgtcgcg 27900

acgcaggcca ccagctgctt gtgctgcggc gtgtcctcgc gcacgaacac gatcgcgtcg 27960

gcgacgccgg cgtgctgcct gagcgccgcc tcgatctcgc ccatttcgat ccggtagccg 28020

cgaatcttca cctgcgtgtc gcgccgcccg gtgacttcca ggttgccgtc cggcagccag 28080

acgccgaggt cgccggtgcg atagaggcgc tcgcccgcct cgaacgggtg ggcgacgaac 28140

gcggcggccg tcaggtcgtc gcggccgaca tagccgcgcg ccagcgcgat gccggacacg 28200

cagatctcgc ccgcgcaacc ctcgggggcc agcgccccgt gctcgtcgag caggtacagg 28260

tgcgtgttgt ggatcgggcg gcccaccggc agacgggcgc cgtaggtgat ggccgggtcg 28320

accacgtagt ccgcgatgca cacggttgcc tcggtcgggc cgtacgagtt gtggcacgtg 28380

cgggtccggg ccagctcgcg cagatccgcc acgcgggcgc tgtcgcccgc gctgatgacc 28440

cgtttcacgg cgccgagcgc atgccagtcg agcgcggcaa ggtaggccgg cgtcgcgttg 28500

acggtggtga cgccctgctg tgcgatgtag tcgacgaaac gcggcacgtc ccggatcacg 28560

gcggtctttg ccagcaccag gcgggcgccc gcgagcagcg tgacgaagat ttccatgatc 28620

gagccgtcga agcccgggga gtagaactgg acgaagcggt cggcggaatc gaaaccgaat 28680

gcgtccacgt ggtactgcgc catgttcagg agccctgcgt gttcgagcac gacgcccttg 28740

ggcacgcccg tggagccgga cgtgtagatg atgtatgccg cgtcgtccgg ccgcacctcg 28800

acctgcgccg atgccgacgc gggtgccagc gtgtcgagct ggaagtcgag ggcgaacatc 28860

gggatcgccc agaaatcggc gagcaacggc aggtgttccg agtgcgtcag cagcgccttg 28920

accttcgcgt cctcgatcat gaagcgcagg cgctcccgcg gaaattccgg gtcgagcggc 28980

agatacaccg cgcccgcctt gagggcgccg agcatgccga cgatccagcg ctcggaacgg 29040

tcggccacca cgcccaccac gtcgccgcgt tcgatcgcgt attccgcgag caggaagctc 29100

gccagccggg acgcctggtc gtcgagttcg gcataggtca gcgatgcgtc ggcggtcacc 29160

accgcgacgc tgtccggcgc ggccgcgacc cgttgcgcga actgctccag gaaggtgccc 29220

tgtaccgcga cgggcgccgc atgcgaacgc aggcgcgcgc gctcttcgtc gtcgagcagc 29280

gagacggtgt cgagcggcgc atccagtgcg ccgaagccgg ccacgacgtt gcgcaggtgc 29340

cgtgcgacat gctggagata gtgcagcgtg aacaccgtcg gccggcccgt cagcacgatc 29400

tcgtagcgct cccgatgccg gatctcgatc gacaggtcgt agtcggccgc tgcccaggct 29460

tcgtgaaggc cgtcgaagcg cacgccgacg ttggtcgcgc gccgttcgcc atgcagcttg 29520

tgcgcgaggg cggcgatcgg gaaatcctgg tacgaatagc tgcgctgcac gctgtcgcgc 29580

agctggttca ggtacgcgcg aaccgtgggg ccgggctcgc cggcgtcgag cagcgggaca 29640

ggctcggcgc agccgctcgc gggttcgacg atcagctgcg gcgacgccac gaacaggccg 29700

-continued

gccgcgccgt tgtagcgccc cagcacgcgg aacagcgcgg ccagcagcac gacgaacgcg 29760

cccagctcgt tgccggcggc gagccgctcc agcacctgcg ccgcgtcgcc gtcgagcgcg 29820

aacgtcagtg ccggctcggg gccgagcggc agcgcatacg cctgccacgc ctgctgaagg 29880

cggaaatctt catcgatgcg accgagcgcg tcgttccaga acgccacgtg ttcctggtat 29940

tgcccgctgg tcgagagcgc gttgagattc agttctgaca aagcacgatc tccctcgtcg 30000

cgtacaggat ttcggaagcg atgcccttgg ccttgcagtg cgcgacgaac tgggtggact 30060

ggatgtggct gggcgagttt tcgtcgaagg tgttgtcgag gaggtggttc agccagggct 30120

cctgacccat cgcatagaca tacgccgcgt tgaacgcgaa atcgtccacc agcgcggcgg 30180

cctcgccgaa ctggcagccg cgcgcccggc gtgattgatc gatgtcgcgc ggcagcgcct 30240

tgggaaacag cgggccgtag acccatgacg gcggcgcgcc ctcggtttcc atcccgacga 30300

acagggtgtc cggcttgccg gcgaggcgga agacatgctc gtagaggcgc gggtccaggt 30360

tgcacgaatc ggcgatgcac agcaccgagc gcgagccgaa gcggatcatg aagctctgct 30420

tgctgtggat cgccaggtcg ttgtgttcgc ccatgaacgg aatggcggtg atggcgccgc 30480

cgggcacctt gatttcctgc gcatcccgaa cttccagcac gtcgtcgaag ccgagcttgc 30540

gcaacgccag ctccatcgac ggatcttgcg gaaagccgtc gagattcctg ccgaccacca 30600

cggtcttgac cttgtggcga agctgcagca gcgtttcgag gacgatgtga tcgtgatggc 30660

tgtgcgtgat cagcacgtag tcgatctggt ccggcaggtc ggcgaacgta tagcgcggca 30720

gcgcggtgtc gtagccgtag ctgatcaccg gatcgatcag gatgctcacg ccccggctct 30780

ggatcagcac gcacgcgtgg ccgtagtagc ggatgcggat gtcgtcgccg tcgaacgaac 30840

gatccggttt cggcgccggc gcctcctcga cgaagaacga gcggaacagc ggctcgtcct 30900

tctcctccac gcgcatcagg tcgacgatct tcgcgtagct gccgggcgtg tcgcgcatgc 30960

ggaacagcgt gtcgagcgcg cggtcgtcga aggccatgtt gctgaacacc gtgcgctcgt 31020

cgcggagccg gggcgtgctg aggatgaacg gccgcggcgt gtgctcctcg atcgccgaca 31080

gcgcgatgct ctgcgcatcg cgcgcataga acgggctcgc gtacagcagg ctttcgaaca 31140

cccggaagga cgggttgtgg ttcaggtcgt agtagatctc gacatagccc ttcagcacct 31200

ccggaatctc ggggtagagc gggtccgacg ccatccccgt ggcccgttcc agcagcagcg 31260

tggagaacgc cttgtatgcc ttcgccagtt ccagttgccg ggtcgcgcgt tgggtggtct 31320

gctcgatcag cgtgcggatt tcgtcgacgc gctggccgcc caggtcgagg aacggcccgc 31380

cgcgcatcgc gggatccttg caggccgccg catgcatcat cggcgatgcg gcataggact 31440

tcagcagcgg caggaaccgc tccgccacgt tgagggcggc ggtcaacggc ggaagcgtgt 31500

gataccacgc gtaccagctg ttgatcagcg gttcgaactg gatgttttgg cgcaggtaga 31560

cctgcgcgct ggacgaaata gtcaacgaag gctccttaga atgcgctgag ttcgacggtg 31620

ggctggcggg cttcggcgtg cagcgcgcgt tgtcccaggg tcaggttccg gatgcgaacg 31680

cccggattgg cgagcacctc gccgatgacg gacgtcagct cgttggcgag gccttgcacc 31740

agggcttcgc tgaaccgccc cgcgtgatag acgacgcgga tcgcgagacc ctcggcgtgc 31800

ggctcggcca ggaaccagaa atcggttgcg gcttccgtgt ccgcgcgctg cgggtcgtgg 31860

tccggcagct cggcgatatg cacttgtccc gcgtagcgat cgacggggcc gtgtcgctgg 31920

ttctgcagcg tcaggccgat gtcgaagagc ggattgcgtc ccgccacgcg tttgatgtgc 31980

agctcgtcga gcaggcgatc cagcgggtac agcgggtgcg agaacgcttc gagcgtggtg 32040

tcccgcaccc gggtcagcag cgtgtcgaac cggtcgtcgc ccgcgacacg atcgcgcagc 32100

-continued

gccagcacgt tcaggtaggg gccgacctgc gactcgagtt cgggcagttc gcggcccgcg 32160

accggcgtgc cgacgacgat gtcctcctgg ccggagcggc ggtagaacag cgccttgatg 32220

gcggacagca gcgcgatgaa caaggtcgcg ccgtggcgct tgccgagcga ttccagcgcg 32280

gccgtctcgg cggcgggcag gtcgaatcgc caggatttcc agctcggcgc ggccggctgc 32340

tcgacgtcgc ccggcagttc cagtgcgcgc aggccgccgc ccagtttggt cagccagtag 32400

tccttcatgc gcgcgccgtc cggcccggcg agcaggcggt tcagccagcc ggcgtaatcc 32460

ttgtactgga tcgggagggc gggcagcgga tcgtcgcgac gctggacgaa tgcgtcatag 32520

agcgcggaca ggtcgtcgag cagtacctcc gtggaccagc cgtcgctcac gatgtgatgc 32580

atcgtgcaga ggcagacgtg acggacttcg gagagcctca gcagcttgac gcggaacagc 32640

gggccggtcg cgagatccat cggcacgagc cgttcgctcg cctggatcgc cgctgcctgg 32700

gcatcgcggt cctcggcatc ctgcagatcc acgatctcga ccgggaacgc ggcttcgccg 32760

ggcggcagca cgtgctggac cggctggttg ccttccagca cgaaacgcgt gcgcaggatc 32820

tcgtgacgct cgctcaacgc gcggaacgcc cgcacgagcg catccacgtc cagcacgccc 32880

tcgaacagca gcgacgtggg cagcggcccc tcggcttgcg ccgcatggag acgatcctgg 32940

acccacagcc gcgtctgtgc gggagagagc gcgtagcttg cctgcgccgg cagcggcgtc 33000

accggcgcgt aatcgatcgg ctgcgtatcg gcgatgcgct tcgcgaggct cgagatggtt 33060

gggagtgcga acaggctgcg gatttccagc ttcacatgca gatcgcgccg gatgcgcgcg 33120

acgaccttcg tcgccagcag cgaattgccg cccagatcga agaaattgcc ggtcgtgctg 33180

atccgcgcct ggccgagcac ttcctgccag atggcagcca actgcgcttc gagtgcgttg 33240

acgggcgcaa cgtggtccag gccgtcgccg ggttcgggca gcctggtgcg atcgagcttg 33300

ccgttgggca gatgctcgaa cgcgctcacg acgacgaacg cggagggcac catgtaatcc 33360

ggcagccgct gccgcaggtg gccgcgcacc gcttcgatca gttctgcttc ggggtgcgac 33420

gagcacagcc atccgaccag tctcgcgccg tcgtccacgc cgcgcagcgc gacgacggcg 33480

gcatcgacca gcgggtgcga cgtcagcgcc gcctcgattt caccgggttc gatgcgcagg 33540

ccgcgcagct tgatctggtg atcgatgcgg ccgaggaact cgatgttgcc gtcgggccgg 33600

tagcgcgcga ggtcgccggt gcggtagagg cgcgcgagcg ggtcggccga gaacggatcg 33660

gcgatgaact tttcggcgct cagttcgggt tcgccgtggt agccgcgccc gaccggtgtg 33720

ccgccgatca gcaattcgcc ggccacgccg atcggcgtgg gctgcatctg cgcgtcgacg 33780

atgtagaggc gggtgttggc gatgggccgg ccgatcggca cgatgcggtg cggatcgtcg 33840

cgccggcatt cccacgcggt cacgtcgacg gcggcctcgg tggggccgta gaggttgtag 33900

agctcgacgt ccaggcgctc gaggcaacgc tgctgcaggt catggggcaa ggcctcgccg 33960

ctgcacacga cgcggcgcag cgacgcgcag tgcgcgtcga ggtccggatg atcgaggaac 34020

gcgcgcagca tcgacggcac gaaatggatc gtggtgatgc gttcgcgctc gatgagctcg 34080

accaggtagt cggtctcgcg ctggccgccg gggcgggcga acacgaggcg cgcgccggtg 34140

acgagcggcc agaagagttc ccagaccgag acgtcgaagc tgaacggggt cttctgcagc 34200

acggcatcgt cggcgccgag ggcgtaggcg tgctgcatcc agaggatgcg gttggtgatc 34260

gcgcgatggg tgttgagcgc gcccttgggg cggccggtcg agccggacgt gtagatcatg 34320

taggcgaggt tgtcgccgtt cagcgcgggt gcggggttgg acgtcgccgc ggcgtcgagg 34380

tcgagcgagt cgcgatcgac gacgatcacg tgcgcgtcgg tgtcgggcag cgcgtcgtgc 34440

-continued

agatgctgct gggtgaggag ccagcgcaac tgcgcgtggt cgatcatgaa gcgcacgcgc 34500

tcggcggggt agtcggggtc gacggggacg taggcgccgc cggccttgag gatcgcgagc 34560

agggcaacgc tcatgtcgag cgaacgctcc atggcgacgc cgacgagcga gtcggggccg 34620

acgccgagcg cgacgaggtg gtgggcgagg cggttggcgc gcaggttgag ttcggcgtag 34680

gtgagcgcgg tgtcatcgaa gacgatcgcg acggcatcgg gcgtgcgctc gacctgctgc 34740

tcgaacaggc ggtgcagcgg ttgcgcggcg tcctcgccga aatccgtgtc ggtgcggttc 34800

cactcgacgg tcagcaggtt ccgctccgca tcgctcgaca acggcagacg ggcaacggcg 34860

gccgacgcat cgtccgcgag atgcgtcagt agggtccggt agatgtcgag gaaacgctgc 34920

accgtgctcg cgtcgaacag atcggtgttg tagtcgcaat cgatcaggag tgcttgcccc 34980

gcgtcgagca cgttgacgtt caggtcgaac gcggtatggc ggatcagcgg cgccacgagg 35040

ccgaccgtca ggccgggcag ttcgggcagc gccgacacgg gttcgaggtt gaagaccgcc 35100

gataccagcg gcgcggcgtt gagatcgcgc tgtgcgccga tttcgcggac cagttcggcg 35160

aacggataat cctggtgctc gagcgcgtcg agcaggttct gccgggtgcc ggccaggaaa 35220

ctggccacgg tggcctgctc cggcagcgtg gagtgcagcg gcagcagatg cgtgcagtag 35280

ccggcgaggc gatcgctgcc ggccaccgag cggccggtca ccggaatgcc ggtgacgatc 35340

tcctgctggc cggcgacgcg gtgcaggaac agattgaagc cggcgagcag caccatgtag 35400

agcgtgcagc cgttctgacg ggccgcggtg cgcagcgtcg cggccgtcgc cgcgtccaga 35460

tgcagggaca cgcgctcgcc gtgaaacgtc ttcaccgcgg gccgcgggta gtccaccgga 35520

agattcagcg gtgcggcctg acgcgcgcat tgcgccagcc agtactcgcg attcgccttc 35580

gtttccgggc tgtggcgctg gccgtcgagc tgcttcaggt acgcgcgaaa ctgcagcggc 35640

gcgtcggccg gcgccgcacc ggcatacgcg cgggccagat cctcgagcag cacgccgaac 35700

gtcgagccgt cacagatgat gtgatgggcc gtcatcacca gcaggtgacg ctcgctgccg 35760

aggcgcacga gcgcggcccg aaagagcggc ccgttcacca ggtcgaacgg ctggcggctt 35820

tcctgctccc gccacgcgtt cgggtccgtg tcgatcagcg gaatctcgag tgtcagcgac 35880

gggtgcacga tctggcccga cccgtccgcc atcaccgtgg tgcgcagtgc ctcgtgccga 35940

tcgacgaggc tctggacggc cgcgcgcatc gcggcttcgt cgagccggcc gttcagttcg 36000

agcgtggtgt tgacgttgta ggcgagcgat ccttcgggat cgatttccga caacacccac 36060

agctggcgtt gcgcttcgct cagcgcggcc accgtgccgt gtttcgagtg cggccggatg 36120

aagccgcccc ggcgcaggtc ggcgacgctg tccttcaccg cccggatgaa gcggtcgata 36180

tcggcatcgg tatgcgcggt ggacaggaag caggtgcgcc attcccagat gtagatgccc 36240

ttttcgagca tgtgatagaa gaacaggtcg aggttctcgg tgaattcgaa gcggaacatc 36300

gagccgaacc acgtgacctt gatcggcgcc tcggcctccg cgaagaatgc attcagcgtg 36360

ccggcgatct gcgcggtgcg ttcgttgagc gcggcctgca gcgccggccc ctcctgttcg 36420

atcttctcga gcacggccag cgccgccgcc atcgcgagcg gatactggca gaaggtgccg 36480

ccgaacgcgg tgcggtccgc cgcggggaac gagtggtcgc cgtaggtcca catgccgccg 36540

tcgatggcat ccatgaagcg gctggtgccg gcgatcacgc ccagcggcag gccgccgccg 36600

atgatcttgc cgtacgtcgc gagatcggcc ctgatgccga acatggcttg cgagccgccc 36660

ggatggacgc ggaaaccggt gatcatttcg tcgaagatca gtgcgacgcc ggcctcctcg 36720

gtgatgcgac gcagttcctt gaggaatgcg acgggctgca gggaagggtt gcggctctgc 36780

accggctcca ccatcacggc ggcgagggtc gacgccatcc cgcgaatggc ctcgagcgcg 36840

-continued

gcgtcgctgc cgtagtcgag caggatcatg ttctcgacgg agccgaacgg tacgcccggg 36900

gcgatggttt ccgtcacgcc ttccgcgttc gccgcggcga gcgtgccgtc ggcatggccg 36960

tgatacgaat gcgtgaacat cacgatcttg tcgcgcccgg tcacggcgcg cgcgagccgc 37020

atcgcggtca tgacggcctc ggtgccggtg ttcgagaacg ccacgcgatc gaggccggtc 37080

acgcgggcaa agcgcgcggc gacttcgccg acgaggctgg agcgcgcacc cagttcgagc 37140

gggcgctgcc attcccgcgt gacctgctgc tggatgaaat ccggcgtgtg gccgaacagg 37200

tgcacgccga agcccatcgt gaaatcgatg tactcgttgc cgtcgatgtc ccacagccgc 37260

gaaccggccg cgcgatcgcc gacgatcgga tacagcatct ccttggtcga aaagcggaag 37320

ccgaccgtgg cgcggctgtc ggccagcacc gggcgcgacg cctgcaccga gtccttcgat 37380

ttccgggtgc gcgtcgtgta gcgcacgatc agcgcctcga gatgctcctg ctgcgcggcg 37440

gacagcccgc gcgcccgctg ctggaccggg ctgccccacg gcatcatcgg cttgggcggc 37500

gggttgtcgg ccgcgggcgc ggcggcagct gcaggcgcgg gcttcgccgc gggtgcggcg 37560

gccggggccg cgctcgccgc tttgggtgcg acgctcgccg tgctcgcgac ggcttgcacg 37620

gcggccgtcg ccggccggac gccgggctgg ccggtcagcg acgtgcgcag cagttccatc 37680

tgctggctca tcacgtgcga cagcagctga ttctgctccc gcagcacgcg ctcgaccgtc 37740

gagccgcctt cggccgccac ccattccgcg ggggcggccg cgagcggcgc aagccccgcc 37800

gcggacggcg tgaccgcgac cgccggcgtg gacggttccg ccgcggccac ggctacggct 37860

acggcctcgg ccccggacgg tgcggcggct gccggcaggt tgtccgcgac atattcggcg 37920

agcgcctgca ccgtcgcgag gtcttcgaag aagcggcgca tggccagctt cacgccgtac 37980

tccgcctcga tgtgccggat ggcctcgatc agcacgatcg agtcggcgcc catctcgagg 38040

aagggcagtt cgatgttgat ggtggcggga tcggcctgga tcaattcgcc gatcttgccg 38100

cgaagccatt cgagaatctc gccgctgcga ttgtgcgtcg gtgctgcggc gatgggtgat 38160

gcgcttgtct gagtcatgga cgtgtccgct ttctggaacc aggtacggct gcgttggaag 38220

ggataggacg gcaatgcgat gcgcgcgggc gcgggtgttt cggtcggggc ccagtcgaca 38280

tcgacgccgc gggcatacag gctcgacagc gtttcgatca gcgcttgctg ctcgacttgc 38340

ggccgctgca gggcaaggaa ctggatcccg gcgtccggcg cacagcacgc gcgggccagg 38400

ttgacgagca ccggcttcgg gccgatttcg accagcacgt tgaaaccggc ttcggcgagg 38460

cgctcgacgc tgctcgcgaa ctgcactggc tcccggcagt ggcggcgcca gtacgtgtcg 38520

gtgggtgcct cgtccatcac ggcgcccgtg agattcgaat agaacgggat cgccgggcgt 38580

gcgacgggca cggttttcgc cgcgagctgg aagctgtcca gcatcggctc gagcagcggc 38640

gagtgaaacg cgtgcgacgt attgagcggc acggaccgga tgtcccgcgc ggcgaacgca 38700

tcgaccagca tcgcgatgcg ctcgcgcttg ccggaaatca cgatgctcgc cgggccgttg 38760

acggccgcca ccgcgacctc gtgcggccac gcgtcgatcg cgcgctcgac cgtggcgagg 38820

tcggtgaaaa tcgccgccat ctcgccgtcg cggggcaacg cctgcatcag ccggccgcgt 38880

tcggcgatca gccgcaggcc gtcttccggc gagaagacgc cggccgcgca agccgccgcg 38940

tactcgccga cgctgtggcc catcacggcg tcgggcacca cgccgaacga cgccagcaac 39000

gtggtgagcg cgtactgcag cgagaacagg gccggctggc tgtagccggt ctggtggatg 39060

tcctcgccct gggccgacag cacttcgagc aacggcttgt cgagcaacgg atcggccacc 39120

gcgcggcaac ggtcgatggc gtctcggaac accggatacg cgtcgtacag gcggcggccc 39180

-continued

atgccggcgt attgcgagcc ctggccggtg aacaggaagg ccatcttcac gcgggggcg 39240

ggctgcgccg cgccggccgg ttccttcgcg tggaaggcgc gcagcttgtc gatggcgtcg 39300

tcgagcgacg tcaccggcca tgccagccga tgcgcgaaat gcgagcggcc ggtcgccgcc 39360

gaaaaggcca cggccgcgat gtcgagaccg ggttcggctt cgagccgccg ctgatagcgc 39420

ccggccagct cgcgcaacgc cgcgggggtc ttggccgaca gcaccagcgg atgcaccttg 39480

tgtctcgacg gcgtcgcctg ccgcgccggc gccggcgctt cttccagcac caggtgggca 39540

ttggtgccgc tcgcgccgaa cgcgctgacg ccggctcgcc gtggccgttc gccacgcggc 39600

cacgcgctcg cctcggcgca gatctcgacg ggcattgcgt cccactgcac cagcgggctc 39660

ggctggcgga aatgcaggtg ggcgggcagg cggtcgtggt tcagcgacag cacgaccttg 39720

atgacgcccg cgatgccggc ggcggactcc gtgtggccga tgttggtttt caccgagccg 39780

acgcgcagcc gccggcccgc gtcgcggcct gcgccgaaca ccgtcgccag cgcctgcaac 39840

tcgacgggat cgcccagcgg ggtgccggtg ccgtgcgctt ccacgtaatc gatggacgcg 39900

gcgggcaacc cgcccagcgc ctggcggatc acggcttcct gcgcacgacc gttcggcgcg 39960

gtaaagccgc tcgacgcgcc gtcgtggttg accgccgaac cccgcagcac ggccagcacg 40020

cgatcgcccg cggcgagcgc atcggacagg cgcttgagca ccagcgcgcc gcagccttcg 40080

ctgcgtacga agccgtccgc cgccgcgtcg aaggtcttgc agcggccgtc cggcgccagc 40140

gcccgcgtgc gcgagacggc gatggagttg tccggcgaca ggatcaggtt gacgccgccc 40200

gcgatggcga gatcgcactc gccgctgcgc aggttctggc tggcggtatg gatcgccgtg 40260

agcgacgacg agcaggcggt gtcgatcgcc atgcttggcc cctgcacgcc gagtccgtag 40320

gagatgcggc cggccgccgt gttcagcggg ttgccggtga agaaatagcc gtcgatgccg 40380

ctgccgccgc cgttgcgaag ctgcaggttc gcgtaatcgt tggtggtgat gccgacgaac 40440

acgccggtgc ggctgccctt gagactgtcg accggaatgc cggcatgctc cagcgcttcg 40500

tgactgacct cgagcaacag gcgctgctgc gggtccatcg cggccgcttc gcgcggcgtg 40560

atgcggaaga acgccggatc gaactggtcg acgtcgtcga gaaaaccgcc gaagcggctg 40620

tacatacgcc ccggcgcttc cggatcggga tcgtagtacg cgtcgacatc ccagcgctcg 40680

cgcggcactt cggagatcgc atccacgccg tcgttcagca ggttccagta ggcgtcgaga 40740

tcgtgcgcgg cgcccggaaa ccggcagctc atgccgacga tcgcgatcgg ctccggcgtg 40800

ccggcgtcgc gggcctcgat ggccggcgcg atcggccgcg gctgctgctg cggcggcacg 40860

gtctgcgcct gcgccgtgcc ggacgcctgc tccgccagga aatccgcgag ggcgttgacc 40920

gtcggatgat cgaacaacag cgcgaccgac agcgggatgc ccagcgcatt ttcgaggtgc 40980

gtgcgcacgt ccagtgccat cagcgaatcc atgcccatct cgaagaagcc gagatcgcga 41040

tccagcgtcc ccgcgtcgta gcccagcacc tgggccaccg cgcgatcgat gctgtccgcc 41100

agcagccgct ttcgctcgcg cggcgatgcg tcgctcagcg ccggcattgc cggcgcgctc 41160

ggcgcgcttt tggccacccg cacgtggtcg aggaacggct tgggtccgcg cgcctcgtag 41220

gagccctgga acagcgccag gtcgatatcg acgaccgcga cctggggcac ggcggggaga 41280

cgattcagca cgtcgagcgc gcgatccgcc gccagcgacc ggatgccgac acgccgcagc 41340

agcgcttccg cctcggggaa cgtcatgccg ccttccgccc agggccccca gttcacgctc 41400

agcgccggca ggccctggcc gcggcgatga tgcgcgagcg cgtcgaggaa acggttcgct 41460

gcactgtagt gcgcctgctc acgcgagccc cacgcggacg cgatcgacga aaacaggagg 41520

aagaaatcga gcgggaagtg ctcgctctgc tgatggagca gccacgcgcc ggcgaccttc 41580

-continued

ggttgcagga ccgcgtccag ttcgtcgcgc tcgacctgca tgatcggctt gtagccgacg 41640

atgccggccg cgtgcacgat gcctttcagc ggcacgccgt cgcgccgcag cgcggcgaag 41700

aaagcggcga ccgctgcggg gtcggcgata tcgaggcgct cgcagcgcag cgtgacgttc 41760

cgctcacgca gctcggcgat cgcccgctgg ctctcgtcgc tcgcggcccc ttgccggccg 41820

accaggatca gcgtgcccgc accgcgcgcc gccagccatc gggcggtgtg cagcccgagc 41880

gcgccgaacc cgccggtgat caggtaggcc gcgtccgggt cgaccggcag cgcggccgtt 41940

tcggctggcg cgagcgggct caggcgcgcg acatggcgcg cgccgtgccg caacgccacc 42000

tgctcctcgc ggctctcgcc gagcatctcc tgaagcagtg cctgcgtctc gttctccggc 42060

gcggccggat cgagatcgat cgcggtgccg aaccattccg gatgctcgat cattgccccg 42120

cgtgcgaggc ccgacagcgc agcctgggcg agcccggata cgtgcggcgc ttcgccggct 42180

tccaccgcgt cgcgcgtgac caccgagatc ctgggccggg tcgaaggcgt ccactcgcgc 42240

tcgctgccga ccagcgcgtg cacgagatgc agcagggcgg cggacatgcg cgtttcgccg 42300

acggcttcgt ccagcgccca taaaaagacg atgcgctggc cggaagcggc ggtttcgttc 42360

agcaagcgga cgaaatcgtc cggccgctcg ggcgcgacct gccagcccgc ttccgcgccg 42420

gtgacatagt cgatgccggg gcggaccagc gagcaggatg cgccgcgcgc gcgcagcagc 42480

gctgcaagcc gctcgccgac accgctcgca tccgcgaaga tcagccacgg ggacgcgtcg 42540

gcggcggccg gtgccgccgg catcgcggcc tgctgctccc acaccacgtg atagagcggg 42600

tgtgcgttcg acgcgacggt ctcggcggcg gcgaatgcag tcctgagcag gtccggaaac 42660

gcgttcagca tgtcctccgg gtacttgccg gacgacttga ggtgccgcaa cgctgcgtcg 42720

atgctgccgg catccatgcc gacgatcggc gacggaatct tctccaggct gaagcgctgc 42780

cgctcgaacg ggtagttcgg cagggtcgtg gcgggctggg cgggcgccgg aaacagcgcg 42840

cgccagtcga actgcgcgcc ctgcacgtac agcgccgcga gtgcgcgctc cagtgcatcg 42900

cccgcgcagg gcggcggcag ccagccgtcg gcgagcccct ccggcgggtg cgatgcgtcg 42960

gcctgatccg acgcgccagc cagttgcaac cagtactgcg ggtgcgtcac ctcgtcggtc 43020

acgtcggtgc cgagatagcc cgaaatcagg cggaccgacg gccgtgcgag cggcatgtcc 43080

cgaagcacgg cgcgcaacgc ttcggcatcc gaacgggcgg ccacgaggcg cagcgcgtcg 43140

gccacgctca cgacgcccgc cacgcaggcc gcgacatatt cgccgatgcc atggcccgac 43200

acgacggccg ggcggaggcc ccatcccttc cacagttccg cccacgcgaa ctggatcgcg 43260

aaccggcccg cgtcggtctc gagtgcgtcc agcggcaccg agcaacgcgc gaacgcgtcg 43320

cggaacagcg gttccgacgc gtggagcgcg tgcgcgacgc cggtgtccgg cacaccgaac 43380

ccgaagccca tgcgcaacgc cttgcccgtg cgcggcgcgg ccgccgacgc taccctcgcg 43440

cccgatacat aggcggcgcg aaacggatag tgactccgcc cggtggcggc ggcacggcag 43500

atcgcggcta gctcctgcgg cgtcgcgccg gcgatcgcgc gctcgtagcg tggcacgagc 43560

gccgccagcg ccgcttcgga ccttgccgac agcagcagca acgcgcgctg cgcggcgtgt 43620

gccggcgcga cgggcggttc ctcgacgatg gcgtgggcat tggtgccgct gaatccgaac 43680

gcgctcaccc cggcgatgcg cctgcgttcc ccgcgccgcc acgcgaccgg atcggccgcg 43740

acgcggatcg ggatgtcctg ccacggcgta tgcggattgg gttgcgtgaa atgcaggtgc 43800

gccggaatcc ggtcgtgctc gaacgacagc agcaccttga tcaggccggc gatgccggag 43860

gccgactcca gatgcccgat attggtcttg accgaaccga tcacgagcgg ctcgttcgcc 43920

-continued

gcgcgcccgg ggccatagac gccggccagc gcttcgacct cgatcgggtc gccgagggac 43980

gtgccggtgc cgtgggcctc gacgtaggac acgtcgccgg gcgcgaggcc ggcctggttc 44040

agtgcgcggc ggatcacccg ttcctgcgaa tcgcggctcg gcacggtcag cccgccgccc 44100

gcgccgccct ggtcgaccgc cgtgccgcgc acgatgccga gcacccggtc gccgtcggcg 44160

agcgcgtcgg cgaggcgctt gagcaccacc atgccgcacc cttcgccgcg cacatagccg 44220

tccgccgccg cgtcgaaggt cttgcagcgt ccgtccggcg acagcatgcg cgcctgcgag 44280

aagctgacca tgacctcggg cgacagcatc aggttgacgc cgcccgcgag cgccatgttg 44340

ctttcgcgcg agcgcaggct ttcgcaggcg aggtgcaggc acaccagcga agacgagcag 44400

gcggtgtcga tcgccatgct cgggccggtg aggcccagca cgaacgacag ccggcccgcg 44460

gccatgttca gcgcgctgcc cgtgccggca tagctgctcg acggcatcga cgcattggac 44520

acctggatcg cgtggtcgaa gcaggtgatg ccgacgtaca cgcccgtggc ggactgccgg 44580

aagcgttcgg gcgcgagatg ggcgttctcg agcgcctccc acgccacttc gagcaggagc 44640

cgttgttgcg gatcgaggta ggtcgcttcg cgcggcgcga tcccgaagaa cgccgcgtcg 44700

aattgatcca cgcgttcgag aaaggcgccg tggcgggtcg ccatcttgcc gggcgtggac 44760

ggatcggggt cgtagtagcg atcgatgtcc cagcgttcgc cgggcacttc ggtgacggca 44820

tcgtgcgcgc cgtcgagcaa ttgccagaac gcgtccggcg tatcgctgcg tccggggaag 44880

cggcaagcca tgccgatgac ggcgatcggc tcgttgcggt cagaacgcag cgccgcgatt 44940

tccgcgcgcc gcaggcgcag ttcgtcgagc gcggctttca gtgcatgcgt ggccttggcg 45000

ttcattgggc gccgatctcc tgggcgatca gttcggaaag gtcgtcctcg tcgaggtcgt 45060

cggatgcttc gtcgacgacc ggcgcgggga gcgacggcga cagttcgttg agcacgtact 45120

gggcgagcgt ctgcaggttc ggataggaaa agaacaacgt cgcgcgaaac ggtcttccga 45180

ataccttggt gaggcggtcc gtcagttcga gcgcgaccag cgaatccagg ccgagatcga 45240

gcagcgattg ctcgggcgcg atggcatcgg ggccggaaag gcgcaaggtt tcagccagca 45300

tcgccgcgag cgtgtcggtg atgcgctcga cccgttcgcg cggcgcgcac gcatgcagct 45360

ggcgcagcaa cgccgtctcc tgctgcgccg gctgcgcggc cggttgcgtc agctcggaaa 45420

acagcgcgga cccggcggcc ggcgcatcga cccggaacag ggtcggccag tcgatccgcg 45480

cgactccgga ctgggcgacg ccggacgcca tcagccgttc cagcgtcgcg atggccagtt 45540

cgggcggcag cgtgccgacg ccgagcgcgc cgagttgttc gtgcgcgcgc cgtccgtagt 45600

cggtggcggc gtggccgatc tccgcccacg gcccccaatt gacgctgagc cccggtttcc 45660

cctgcgcgcg ccgatgctgg gcgagcgcgt cgaggaagct gttcgccgcc gcgtagttgc 45720

cctggcccgg catggtgatc agcgcggcca tcgacgagaa caggacgaaa tggtccagcg 45780

gcaagccggc cgtcagctcg tgcagatacc acgcgccgtc ggccttgccg ctgccggcgc 45840

gatggaagaa gtcgtcgtcc tggcgtgtca gcagcgcatc gtcgagcgcg ccggcgaggt 45900

gaaagatccc tttgagcggc ggcatcgaat gcgcgatttc accgagcgcc tgcccgacgt 45960

cctcgcgacg cgacaagtcg gcgcgaatga accgtgcgtc gagcgtgcgc aggattttcc 46020

cggctgcggc ggaaggttcg ccgcgcccca gcagcacgat tttcccggcg ccgttgtcgg 46080

caagccagga cgcgagccgc aggccgagcc cgccgagccc gccggtcaca agataggtcg 46140

cgtcaccgtg gaaccggatc ggccggtggc tgacgtattc gcgattgtcg cgggcgatgc 46200

gcgcgacgta gcgctggtcg cggcgaaacg cgatcatgtc ttcacggccg ccagcctgta 46260

ccgcttgcat gatgtccgct gccgacggct gctcgggatc gaggtcgacg agcccgcccc 46320

-continued

acagcgccgc atgctccacc gcgatcgcgc ggcccaatcc ccacagcggc gcctgtgcca 46380

ccgcgatcga ttcgccatcc agaacattca tcgcacccga cgtcaccagc cacaggcgag 46440

cctgccgggc cgacggcgcg cgtgacgcaa gcgccctgac caggtgcagc acgctcgcgc 46500

tggcacgccg tctcgccgcg atgtcagagg gtgcgagatc gagactccac aggtggatga 46560

cgcccttcag cgggcggtcg gccgcgggca gttccggcgt cgcgtcggcg aagcgcagcg 46620

tgcacgtatc gccgtgggct tccagcagag ctgacagctg ggcgcccacg ccgccgcggt 46680

ccgcgagaat cagccactcg ccgtgcgccg aaccgccggt tgccgcgtcg acgttcgacg 46740

gtctccagac gcgttgataa agcagcgcgg cgaagtcgtg ccgctcgacg gcgcgcgccg 46800

cgcgaacctg ttgcaaccgc agtgcatcga tctcgatcag cagtcggcca gcaaggtcat 46860

ggacgcggat gtcgccctcc agcgcgccct gtccgatcgg cgtgcgcagc gtggcgtgac 46920

tccatgcctc ggtcgacgcc ggcggctgat ggacccgtac cgcgccgatc gagctgggca 46980

ggtacaggtc gcccgactcc agcgcgtccg gatcgatggc ggcggcgagc acgcggctgc 47040

atgcgtcgag aaaggcgggg tgtacctggt acggcgacga cgccagcgca tctgccggca 47100

ggctgatttt ccccagcgcc tcgccggtcg tgcgccagat ctgccggatc gcgtcgaaca 47160

cgccgtcgat ctgcacgccg tgctgccgaa tttcgccgtt gaagtccgcg cccgacgtcg 47220

tttcggtgca gcgggcctgc acctcggcgg catcgaatcg cgtcggcgcg gcggatcgcc 47280

gggggggcaca catttcccgg agccggcgca gctgcggaag attgccgagg atccgctcga 47340

ccggcggacc gaaatcgagc aggcaggcca cttcatccac gccgatcgac tcgagatccc 47400

gcaccagttc gacgcaggtt tccggcgtgc cgatgagccc gcgcgattgc gcgaagcgtt 47460

catagagaaa ctcgacgaac tcgtccagct cgcgtgcgcc catcgcgcgc acgtcgaccg 47520

actggccgcg actctgcgcc agcccgttca atagcccgat attgctgcgg atgtagttgc 47580

agaacggcac acgcgcctgt tcgcgcgcct gcgccgcatc gtcgccgacg aacgtatgca 47640

gcatcacgga aacggtgccg gccgccggat cgaagccatg cttcgcacgc gcctcgcggt 47700

agagcgcgat cttgtgcgcg agctggtcac gatcctggtc gagcacgtgg gtcagcaggt 47760

tggcgccggc ttcgccggca cgcacgaatg tctgcggatt gctcgcggcg gtcacccaga 47820

cgggcagctc cggctgcacc ggcgtcggat agacacgcaa ccgcaccggc ttgccgacac 47880

cgttcgtcgc atccagcgtg ccgccgcgcc acagatgctg gacggcgcgc atcgtggtca 47940

gcatgtcgtc ctgccgggtc gcatatttgt ccggggcaaa cacgaagtcg tcaggattcc 48000

atccggaggc gaacgacacg cccacgcggc cgttcgacag gttgtccacc atcgaccatt 48060

cttccgcgat ccggatcggg ttgtgcagcg ccgcgaccac gctgcccgcg accagcttca 48120

cgcgctgggt ggccgcggcg agcgcggcgt gcaggacggc gggattcggg taaagcgagc 48180

cgaattcggt gaaatggcgc tccggcaccc agacgctgga gaacccgttc gcatcggcga 48240

aacgcgcgct ctccatcacg agctggtact tgttgccgga cagcgcctct tcactgctgg 48300

cgaagaacat cagtccgaat ttcatgcgtg gctccgatcc gattcgtgaa tttcggcact 48360

cgcgcacatc tgccacgtcg cggcggcgcg ggtgtcgtcg atccggtgat agacggcaaa 48420

cgaaaacggt ccccaggacc ggcggctcag cacggtctgc acggtgtgcg attcgtgcgg 48480

atgcagcggc aacggcgcat gcagtgcgag gtccttcaac gtcgtatggc cggctgcgcc 48540

gatttccgac gttgccgaca gcgccatttc cacgaaggcg gaatagggca ggacgggcga 48600

ccccttgacg cgatgaccgt cgagaaagtt ggttgccggc gcatcgagac gcgattgcca 48660

-continued

gatccacgtg gccggcgcat gcgcgtgctg ctccatgagg cgcccgagca acggatgccg 48720

acgcgcatgt ggcctgatcc agaagccgcg ccgctcgaac gggtaggtcg gcagggcgag 48780

ccggcggtgc ggtgcacctt gctccacggc atcccagtcg atggatgcgc cgcgtacgta 48840

gagcgcggcg agcgtgtgca ggatcgcgtc ccacgcggcc gtgtgcgcgc cgatgtcgat 48900

cacgatgccg gggtgtcctg ccgcaccgct gtccggcgcc tgcggcacgc cggcccacgc 48960

ggctgcggcg cgctgcccgt cgccggtgct gctgaccgca tccggtgcga tgccgaagga 49020

catccacagt tgcgcgagcg cgcgctggaa tctcgtgaac ccggcttcgt cgggggcgag 49080

cgcgggcgcg ccggatgcgt cggactgccg ctgcatcagc gcgtcgaaag cggggctggc 49140

cgcgcgcaat tgccgaaccg cgtcggcgct ggcgccgtcg tcggcgcaaa agtggaacgt 49200

caccgcgggc ggtgtttcgg caggctcccc ggacgaaacg gaatcaagtt gcgcacgcaa 49260

cgaatcgcga ctcggtgcga cgatggccgc gcgctgcgtg aagtgggtgc gcccggtatt 49320

ggccgtgaac gcgacatccc gcacaccggc ctcgggatgg gcgtcgagat aggccgcata 49380

ggacgcagcg agcgcttgca acgcgtccgg cgtgcgcgcg gagagcgtca cgacgcgcgc 49440

cgcgggtgca accggttcgg cttcgatctc cgggagcccg ggtgcttctg acaggatcag 49500

gtgcgcgttg gtgccgccga agccgaacga gctcacccct gccaggcgcg gcccgtgttc 49560

cgaatgccag ggcgtgacct gccgaggaat ccggaagggc gtgccgtcga gcgcgatttg 49620

cggattgatc gaccggaaat ggaggttcgg cggaatcgcg cgatggtgta gtgcaagggc 49680

ggtcttgatc aggctggcga tgcccgcggc cgattccagg tggccgatgt tggtcttgac 49740

cgacccgatc cagcagagat cgtccgggcg gcgggattcg ttcaggacgg ccgccagcga 49800

gttcaactcg atcgggtcgc cgagcggcgt gcccgtcccg tgcgtctcga cgaagccgat 49860

gtcctgcgcg cgtacaccgg catcgcgcag cgcgccgtga atcacggcct gctgggccgg 49920

gccattcggc gcggtcaggc cgttgctgcg cccatcctga ttcaccgcgg agccgcggat 49980

cacggcgaac acggtgtcgc cgttctcgag cgcatcgtcg agccgcttga gcagcaccat 50040

gcccacgcct tcgccgcgaa cataaccgtt cgctgccgcg tcgaacgcct tgcatcggcc 50100

gtccggcgac agcatgcccg cttgcgtgaa ggacgcgctc aattgcggcg ccagaatcag 50160

gttgaccccg ccggccagcg ccgcatcgga ctcgccgcgc tgcagcgcgc ggcacgcctg 50220

gtgaaccgcg acgagcgagg acgaacacgc ggtgtcgacc gcccagctcg ggccgcgcaa 50280

atcgagcgcg taggaaatgc ggttggcggc gacgctgagc gcattgcccg tcgcgacata 50340

agggccgacg tccgcgactt cgtcctgcgc cagacggatg tagtccgaat tgctgatgcc 50400

gacgatgacc gcggtgcgtc cgccggcgag gctgcggggt gcgatccccg catgctcgag 50460

cgtctcccag gccacctcca gcagcaggcg ctgttgcgga tccatcgatt cggcttcgcg 50520

ggcgctgatg ccgaagaaag ccgcatcgaa ttgatcgacc tgatccagca gtccggcgag 50580

cggaaggtcg gccgcgcgct gcgtcgccgc accgaccgcg tcccggccct ccagcagaag 50640

ctgccagaat gcgtcgggat tgccggcgcc ggggaagcgg catcccatcc cgacgatcgc 50700

gatatccgcg cgtgcttcgg ccgagcccgg cgcctggtcc ggcatggcac tcccggtgcc 50760

gctcaaatgg cgcgccagca gggaaatact cggaaaatca tagacgacgg tcggggaaac 50820

cggccgcccg agccagtcct gcagctcgcc cgagagcatg atggcgtcct tcgaatcgag 50880

cccgtggacg ctgaacggcg cgtcggggtc gatcttgccg gaagcgattc ccgacagacg 50940

cgagacacgc tcgatgcacc attgcaccag cgcttgcgtg tcgcgtggct cggcagtctg 51000

cgggggggct ggcggcgcgg agaacgcacg ccgccattcg cccgcgatcg cgagcccctg 51060

-continued

ttcatcgagg aatgcctgcc tgatccggct ccgctggatt tttccgctgg acgtgcgcag 51120

gatcgtggca ggtttcaaca ggactgccgc atacagatcg acgtcgtgca cttcggcgag 51180

cgtgtgccgg atctcggcgg ccacggcttc cgcgtccagc gtgttgagcg cttcccggcg 51240

cacttcacag gcgacgacga cccgctccac gttatcgacg tggatcgaga aagccgccga 51300

tgcgttcggc gccagcgcgg ggtggctgcc ctccgcggat tgctcgagat cctgcgggta 51360

gtgattgcgg ccggcgacga tgatgaggtc tttcaagcgg ccggtaacga agagatcctc 51420

gccatcgacg aagccgagat cgcccgtgcg caggtaacgc gcgtcatcgc cgtccagctt 51480

cgcgcggaag gtgcgctccg tttcgtcgat acggttccag tagccgacgc cgacactcgg 51540

gccggtcagc cagatttcgc cgatccggcc gggcgcgcag cgctcaccgg tatccggatt 51600

cacgatgcgc acgcggtgct cagcccaggt ccggccgcat gagaccagcg cgtggcgctt 51660

gccggagtcg tttctcgtcg ccacgccttg tgccagcgcg tcggcatcgt agtccgccac 51720

gcgcggcagc gagcgtgccg gctggccgga gatgaacaag gtcgcctcgg ccatcccgta 51780

gacggggcgc atggtgtgcg cgtggaagcc gcacgcggcg aatgcgcgcg aaaaacgcgc 51840

caccgactcc gcgcgcaccg gttccgcgcc gttgaatgca acccgccagc tgctcaggtc 51900

cagctgcgcg cgcgcttcat cggcgatttt gcgagcacac aggtcatacg cgaaatccgg 51960

cgcggcacaa tgcgtgccgc gatacttcgt gatggcctgc agccagcgca cgggtttctg 52020

cacgaatgcc gcgggcgcca tcagcaccga cagcacgccg agatagatcg gcagcaacac 52080

cttcccgaag aaacccatgt cgtgaaacac cgggagccag ctgacgaaca ccgtcgacgc 52140

atcggcatcg ctcgcctcgg cgatgaccgc catattgctc aggatgttcg cgtggctgat 52200

catcacgcct ttgggcgtac cggtggagcc tgacgtgtat tgcagaagcg ccagcgtctg 52260

cggcgtgatg tccggtgcgc gccattgttc ggccggggcg tcgaagcgct ggtccgtcgc 52320

caggatcttc agttccagcg tgtcggaata accgtccgcg tgatgcgcga tgccgtcgag 52380

cgtcgcggcg tccgtcagcg cgacgaccgg cgtggcgtcg gcgacgatgg ccttgagacg 52440

atcggcggga cgatgcctgc gcggtggata cgcgggtacg ccgatcaggc cggcgtacag 52500

gcatcccacc catgcgcaga tgaattccag cccgggcgga taaaccagaa ggacgcgatc 52560

gcccggttga gcgatggctt gcagcctggc ggcgatgccg cgagcccgct tgtccaggtc 52620

gccgaacgtg aggcgggtca gctccgcttc gccgttctcg agaaaaatga atgcggtctt 52680

ctccggttcg accttgccgc gaaacaacaa aatttctgta acagtcctga attttgtatc 52740

gggaagcatg ctcaaccttc gttgtcttct aaacgttgaa tatctcagga ccggttgtgg 52800

cgatcccgcc aagcgtgctt catcggacgg tatcgaaatt agagcattgc tctaatccgg 52860

cgtctgcccc gtaatccaag gacacggcgt ttcgcgcact ggatcaatac ggcttgtcat 52920

tgatgtgcac gctcgctaac gatcggcgat tccttcgatg tcgggcgtgt acgggtccag 52980

cagcgacacg acgaccttgc gctcgccttc gaacgggttg cggccatgcg cgaagcgcat 53040

gttgtcgacc agcaggacgt cgcctcgttg ccacggaaac gtgatcgcgc attcgcggaa 53100

cgcgtggcgg atctgctcga ggtcggcgag atcgaacgga ctcccgtcgc catggcaggc 53160

attgcgcgga atgcgatcct cgccgaacag gctgacgatc gaactggcga gcgatgcttc 53220

caggttcgag atatggaaca gatgggcctg attgaagaac acccgctcgc cggtgaccgg 53280

atggtaggcc acgccctggt tgatctgcgc ggtgcgcaac gtgtcgtcgt cgagccattc 53340

gagcgcgatg ccgttatccg cgcagaaggc tgcaacctgg ttgcggtcgc tggtctggaa 53400

-continued

cacggtctcc cacggaatgt cgacgtgccg ccggtagtgc ctgacatagc ggacctgtct 53460

cgcctcgaag tgatccagga tgcgcggtcc gatcctgcgg ctcacctccc gcatgtcggc 53520

aatcggcgtt tcgccgccgg tcgcggccgg cgtcaggcaa cagaaggcca ctcgcagcgg 53580

ccagcttcgt tgatacgcgt tttcgcaatg aagggcgatc gtctcgctcg gcggatactc 53640

ggttgcggtg aagatgccgt tgccgatcga ggtgcgcggc gtggaacggt aaacgtagtc 53700

ggactgatgg gccgaaatcg cgcgagcaaa cgcttcgaag ccgcccacgg atgaaacgtc 53760

gaagccacga aacaggagta cgccgtgttc cagaagccgg gattcgagtg ccgcccggtt 53820

gtcgttcacc gcctgcgcca gatcgcgtcc attcgataca ggctccagca gccacggcgt 53880

gcttccctcg gcaagcaact tgcgttccgt catgcccagc atcgtcaata gtcctttcct 53940

gtacgtggat cacggcgaag ccgaacgggt cggcccgcgt ggtcgcgccg cggtgcggct 54000

atgcgcggca ggccgtttcc acggcatgct cgaagcgatt gagaatgtcg tggatgtccg 54060

cttccgaaac gatcagcggc ggcaggaacc ggagcaccgc gccgttgcgg ccgccggttt 54120

cgacgatgag cccgtttcgc aggcagttct gcttgatggc tcttgcccgt tccgtgtggg 54180

gcgggccggc tcggccgtgg gtgccgggca cgacgacttc ggcgccgatc atcaggccgc 54240

ggccgcgtat ctggcccagg caggggaagc gttcggcaag ctcctcgagg ccggcaacca 54300

ggagtttgcc gaccctgtcc gcgtgcgccg acagatcttc tctctcgacg atgcgcatgg 54360

tcgacaagcc ggccaccatc gcaatctggt tgcctcgaaa ggtgccggca tgcgcgccgg 54420

gcggccaggt gtccaggcgc tcgtcataga ccaccaccga taacggatag ccgccgccga 54480

atgccttcga cagcaccagt acgtccggcc ggatgccgga atgttcgatc gcgaacaggg 54540

cgccggtgcg accgagtccg gtctgcactt catcgacgat caacgggatt tcatgccgca 54600

gcgtcagctc gcgcaactcg atcaaccagg tgtcgggagc ggggatgcag cctccttcgc 54660

cttgcacgac ttcgacgatg atggccgccg gcttcgtgat cccgctctcg ggatcggaca 54720

ggacggtccg gatgtagttg atgctgagtt gatcggtcgc cgagccgtcg gtgccgaacg 54780

ggcagcgaaa ggcgtaggga tagggcagga aatgaacgtc gcgtccgttg ccgccggccg 54840

acttgggcgt gaggtttccc gacgcggcga gtgcgccgga cgtcatgccg tggtaggcgc 54900

cgtggaacgc catgatcgtc ggccggccgg tatagtgccg ggtcagcttg atcgccgctt 54960

cgacgccatc cgcgccactg gggctgcaaa actggatctt gccggattcg gcgatcttcc 55020

cgggcagaag cgagaaaagc tgctcgacga atgcgtgctt ggccggcgtc gccagatcga 55080

gtgcctgttg catctgatcg gacgacagaa accgcatcac ggcttcattg acttccgggt 55140

gattgtgtcc gagcgcgagc gtgcccgcat tcgacaggca gtcgatgtat tcctgcccgt 55200

cggcgtcgcg tacgcgtatg cctttcgcat gggtaaacag ccgcgggaag gaggttgcgt 55260

aggttcgcgc gttcgattcg acctgcttca gatactcgag tttttccatg cgcgcagatc 55320

cggcttgcaa ggcggattga tggacactgg cgcacgagaa tcgcttcatc ctggccaatg 55380

gtgtttaacg gtacgaccgg attggagcat ggtctccgta tcgcgtctgt cacgtaaaaa 55440

tgggacatcg gccatgcgac gtcaccacgt catgccgttg ccttccgatc atcgaagcgg 55500

tttccgggcg cgacgtcagg cagcgagggt cgagcagaaa taatcgatgg tccgttggag 55560

acccgcttcg agcccgatcg tcggctccca gtcgaggtgg gtgcgtgcga ggctgatgtc 55620

ggggcaacgt tgcgtcggat cgtccttcgg cagcggacgg aatacgagcc gcgacttcga 55680

gccggtcagg cgcaagatga tctgcgccag ttcgctgacc gcgatctcgt gcggattgcc 55740

gaggttgatc gggccggtga gctccgcggg cgtggccatc atccggatca aaccgtcgac 55800

-continued

catgtcgtcg acatagcaga atgcccgggt ctggctgccg tcgccataca gcgtgatgtc 55860

ctcgccccgc agcgcctgca cgatgaagtt ggacacgacg cggccgtcgt tgggatgcat 55920

gcgcggcccg tacgtgttga agatgcgtac caccttgatt cgtacgttct gctggcggtg 55980

atagtcgaag aacagggtct ccgcgcaacg cttgccttcg tcgtagcagg cgcgcggccc 56040

gagcgggttg acgttgcccc ggtaactctc cggttgcgga tgcacatcgg ggtcgccgta 56100

cacctcgctc gtcgacgttt gcagaacgcg tgcatgcgtg cgcttggcga gcccgagcat 56160

gttgatcgcg cccatcacac tggtcttggt ggtctgcacg ggatcgaatt gatagtggat 56220

gggcgaagcc gggcaggcga ggttgtagat ctcgtccacc tccacgtaca acggaaaagt 56280

gacgtcgtgg cgcagcgcct cgaagctcgg gttgccgagc agcgtagcca cgttctgctt 56340

cgtgccggtg aaatagttgt cgacgcacaa tacgtcgtga ccgagttcga cgagacgctc 56400

gcaaagatgc gaaccgagga aacccgcgcc acccgttacg aggattcgct ttcgattacg 56460

ttgcacaatt gcactccaag tatcgcgcgc tgggaagcga cgcggcctcc ccgcacgctt 56520

gaccggcccg cggcaccggc aggggagcgg atcaggcgcg cgggcgtttg cattcgacga 56580

tcacggcgcc ggccggcacg ccgatcgcga ggatcggccc gtcatgcctg cagtgcgctc 56640

gacgcggcgt gctccgggcg ccgcatgcgc gccgcgatga tgccggccat cgttcgcatt 56700

tcgtttctca aaaagaaatg atccccttcg atgacgtgaa aatcgaagcg cccggtcgtc 56760

gcggcgcccc agcctgcaac ggcatcgacg gggatctctt tatccgcccg gcccgcgaac 56820

gcggtgatgt ccaccgccag cctgggcccg ggcacgggcc ggtggttttc gatcatcgtg 56880

aaatccgcac gcagcgccgg catcagcagc gccatcagtt cgctgttgtc cagcaccgcc 56940

ttcggtgtgc cgcccatttc gcgcagcgca tcgatgaagg cgcggtcgtc cagcgcctgc 57000

atgcgccgat cgtggcgctc cttgcccggt gcggcacgcg cgctcacgaa cagatgccgc 57060

aggttcggtc gtgcgtgggc gggaagccgc agggccagtt cggccgcaat ggccgcgccc 57120

atgctgtgtc cgagcagtgc gaagggacga tcgaagcagt cgtccaggtc gcacagcaac 57180

gtgtcgacca gcgtcgccat gtctcggacg gcaggctcgg acaggcggct gcctcggcct 57240

gcaagttcat gacggcacac ttcgatgccc ggtaacgacg cttgcagcgt gcgatagacg 57300

gcggccgagc cgcccgcata gggaaaacag atcagacgca tgcgggcggg tactcgagcg 57360

gctcatctgc tgccggcgcg caggcgatgg cgctgtggaa attcatgtgt tcggcgtttt 57420

tcaccattca ggttccagat ccggttgggc gtgagttaaa cacgaggctg cgtggatgta 57480

tgtcgtagga agaggggacg cgttgtcggc catgtcgaag cggttcgtct ctgaatggat 57540

cccggcgcgg acacggtatc ggcgaaaaca gatgcgcggg aaatcgcgac gcatctgagt 57600

gtgtcgaacg atgcgcttcg tctttagaat gggcagcgag catggcgagc catcagaatt 57660

gcggcatccg atggtgccgc cgcgctaccc gataagttgg agacatacta tgcaacaccg 57720

tcagaaagcc gtcccgaccc agcaagtcgc gaacgagcgc gtgatcgtca ccgaatggcg 57780

attcgcgccc ggcgccgaga ccggctggca tgttcaccgg catgactatg tcgtggtgcc 57840

gcaaacggac ggtcagcttc tcctcgaaac cgcacaaggc aaccgcgagt cgcaattgca 57900

cgccgggcgc agctatgcgg ggctgaaggg cgtcgagcat aacgtcgtca acgcgacgga 57960

ccacgaagtg gtgttcgtcg aagtcgagat tctctaaggg gcgtcaggcc ccgcgagcaa 58020

ggccacgaca gggagcagca ggatgaaaat gaccgacatc ccgtttggca cgaccgactg 58080

gcgcaccgtt gaaccgaccg a 58101

We claim:

1. A method of increasing production of occidiofungin diastereomers/conformers corresponding to the diastereomers/conformers having the total correlation spectroscopy (TOCSY) fingerprint set forth in FIG. **5**C as the green NH correlations in a microorganism producing occidiofungin comprising:

decreasing the thioesterase activity of an occidiofungin gene D (ocfD) product (OcfD) in said microorganism, wherein said OcfD thioesterase activity is decreased by the introduction of a point mutation at the serine in position 2954 of the amino acid sequence of SEQ ID NO: 4, said point mutation replaces said serine with an alanine, glycine or proline, and culturing said microorganism under conditions to produce said occidiofungin diastereomers/conformers,

wherein said increase in production of occidiofungin diastereomers/conformers is as compared to a reference microorganism without said decrease in OcfD thioesterase activity cultured under the same conditions.

* * * * *