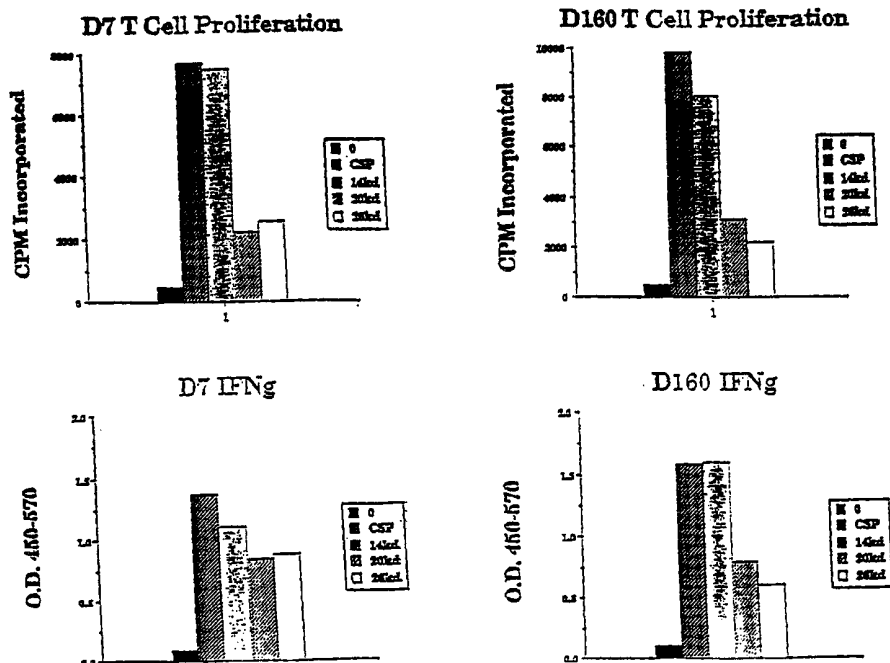




INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification ⁶ : A61K	A2	(11) International Publication Number: WO 99/42076 (43) International Publication Date: 26 August 1999 (26.08.99)
(21) International Application Number: PCT/US99/03268 (22) International Filing Date: 17 February 1999 (17.02.99) (30) Priority Data: 09/025,197 18 February 1998 (18.02.98) US 09/072,967 5 May 1998 (05.05.98) US (71) Applicant: CORIXA CORPORATION [US/US]; 1124 Columbia Street, Seattle, WA 98104 (US). (72) Inventors: REED, Steven, G.; 2843 - 122nd Place, N.E., Bellevue, WA 98005 (US). SKEIKY, Yasir, A., W.; 8327 25th Street, Seattle, WA 98107 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US). CAMPOS-NETO, Antonio; 9308 Midship Court, N.E., Bainbridge Island, WA 98110 (US). HOUGHTON, Raymond; 2636 - 242nd Place, S.E., Bothell, WA 98021 (US). VEDVICK, Thomas, S.; 124 South 300th Place, Federal Way, WA 98003 (US). TWARDZIK, Daniel, R.; 10195 South Beach Drive, Bainbridge Island, WA 98110 (US). LODES, Michael, J.; 9223 - 36th Avenue S.W., Seattle, WA 98126 (US). HENDRICKSON, Ronald, C.; 4114 S.W. Charlestown Street, Seattle, WA 98116 (US).		(74) Agents: CORUZZI, Laura, A. et al.; Pennie & Edmonds LLP, 1155 Avenue of the Americas, New York, NY 10036 (US). (81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG). Published <i>Without international search report and to be republished upon receipt of that report.</i>

(54) Title: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY AND DIAGNOSIS OF TUBERCULOSIS



(57) Abstract

Compounds and methods for inducing protective immunity against tuberculosis are disclosed. The compounds provided include polypeptides that contain at least one immunogenic portion of one or more *M. tuberculosis* proteins and DNA molecules encoding such polypeptides. Such compounds may be formulated into vaccines and/or pharmaceutical compositions for immunization against *M. tuberculosis* infection, or may be used for the diagnosis of tuberculosis.

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COMPOUNDS AND METHODS FOR IMMUNOTHERAPY
AND DIAGNOSIS OF TUBERCULOSIS

5 CROSS-REFERENCE TO RELATED APPLICATIONS

This application is a continuation-in-part of U.S. Application No. 9/025,197, filed February 18, 1998; which is a continuation-in-part of U.S. Application No. 08/942,578, filed October 1, 1997; which is a continuation-in-part of U.S. Application No. 08/818,112, filed March 13, 1997; which is a continuation-in-
10 part of U.S. Application No. 08/730,510, filed October 11, 1996; which claims priority from PCT Application No. PCT/US 96/14674, filed August 30, 1996; and is a continuation-in-part of U.S. Application No. 08/680,574, filed July 12, 1996; which is a continuation-in-part of U.S. Application No. 08/659,683, filed June 5, 1996; which is a continuation-in-part of U.S. Application No. 08/620,874, filed March 22, 1996, now
15 abandoned; which is a continuation-in-part of U.S. Application No. 08/533,634, filed September 22, 1995, now abandoned; which is a continuation-in-part of U.S. Application No. 08/523,436, filed September 1, 1995, now abandoned.

TECHNICAL FIELD

20 The present invention relates generally to detecting, treating and preventing *Mycobacterium tuberculosis* infection. The invention is more particularly related to polypeptides comprising a *Mycobacterium tuberculosis* antigen, or a portion or other variant thereof, and the use of such polypeptides for diagnosing and vaccinating against *Mycobacterium tuberculosis* infection.

25

BACKGROUND OF THE INVENTION

Tuberculosis is a chronic, infectious disease, that is generally caused by infection with *Mycobacterium tuberculosis*. It is a major disease in developing countries, as well as an increasing problem in developed areas of the world, with about
30 8 million new cases and 3 million deaths each year. Although the infection may be asymptomatic for a considerable period of time, the disease is most commonly

manifested as an acute inflammation of the lungs, resulting in fever and a nonproductive cough. If left untreated, serious complications and death typically result.

Although tuberculosis can generally be controlled using extended antibiotic therapy, such treatment is not sufficient to prevent the spread of the disease. 5 Infected individuals may be asymptomatic, but contagious, for some time. In addition, although compliance with the treatment regimen is critical, patient behavior is difficult to monitor. Some patients do not complete the course of treatment, which can lead to ineffective treatment and the development of drug resistance.

Inhibiting the spread of tuberculosis requires effective vaccination and 10 accurate, early diagnosis of the disease. Currently, vaccination with live bacteria is the most efficient method for inducing protective immunity. The most common Mycobacterium employed for this purpose is *Bacillus Calmette-Guerin* (BCG), an avirulent strain of *Mycobacterium bovis*. However, the safety and efficacy of BCG is a source of controversy and some countries, such as the United States, do not vaccinate 15 the general public. Diagnosis is commonly achieved using a skin test, which involves intradermal exposure to tuberculin PPD (protein-purified derivative). Antigen-specific T cell responses result in measurable induration at the injection site by 48-72 hours after injection, which indicates exposure to Mycobacterial antigens. Sensitivity and specificity have, however, been a problem with this test, and individuals vaccinated 20 with BCG cannot be distinguished from infected individuals.

While macrophages have been shown to act as the principal effectors of *M. tuberculosis* immunity, T cells are the predominant inducers of such immunity. The essential role of T cells in protection against *M. tuberculosis* infection is illustrated by the frequent occurrence of *M. tuberculosis* in AIDS patients, due to the depletion of 25 CD4 T cells associated with human immunodeficiency virus (HIV) infection. Mycobacterium-reactive CD4 T cells have been shown to be potent producers of gamma-interferon (IFN- γ), which, in turn, has been shown to trigger the anti-mycobacterial effects of macrophages in mice. While the role of IFN- γ in humans is less clear, studies have shown that 1,25-dihydroxy-vitamin D₃, either alone or in 30 combination with IFN- γ or tumor necrosis factor-alpha, activates human macrophages

to inhibit *M. tuberculosis* infection. Furthermore, it is known that IFN- γ stimulates human macrophages to make 1,25-dihydroxy-vitamin D3. Similarly, IL-12 has been shown to play a role in stimulating resistance to *M. tuberculosis* infection. For a review of the immunology of *M. tuberculosis* infection see Chan and Kaufmann in
5 *Tuberculosis: Pathogenesis, Protection and Control*, Bloom (ed.), ASM Press, Washington, DC, 1994.

Accordingly, there is a need in the art for improved vaccines and methods for preventing, treating and detecting tuberculosis. The present invention fulfills these needs and further provides other related advantages.

10

SUMMARY OF THE INVENTION

Briefly stated, this invention provides compounds and methods for preventing and diagnosing tuberculosis. In one aspect, polypeptides are provided comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of
15 such an antigen that differs only in conservative substitutions and/or modifications. In one embodiment of this aspect, the soluble antigen has one of the following N-terminal sequences:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- 20 (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 121)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 123)
25
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 124)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 125)
- 30 (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser; (SEQ ID No. 126)

- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 127)
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn; (SEQ ID No. 128)
- (j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-Ser; (SEQ ID No. 134)
- (k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-Asp; (SEQ ID No. 135) or
- (l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid.

In a related aspect, polypeptides are provided comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of such an antigen that differs only in conservative substitutions and/or modifications, the antigen having one of the following N-terminal sequences:

- (m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137) or
- (n) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129)

wherein Xaa may be any amino acid.

In another embodiment, the soluble *M. tuberculosis* antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101 or a complement thereof under moderately stringent conditions.

In a related aspect, the polypeptides comprise an immunogenic portion of a *M. tuberculosis* antigen, or a variant of such an antigen that differs only in conservative substitutions and/or modifications, wherein the antigen comprises an

amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 339, 333, 335, 337, 339 and 341, the complements of said sequences, and DNA sequences that hybridize to a sequence
5 recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341 or a complement thereof under moderately stringent conditions.

In related aspects, DNA sequences encoding the above polypeptides, expression vectors comprising these DNA sequences and host cells transformed or
10 transfected with such expression vectors are also provided.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known *M. tuberculosis* antigen.

Within other aspects, the present invention provides pharmaceutical
15 compositions that comprise one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier. The invention also provides vaccines comprising one or more of the polypeptides as described above and a non-specific immune response enhancer, together with vaccines comprising one or more DNA sequences encoding such polypeptides and a non-specific immune
20 response enhancer.

In yet another aspect, methods are provided for inducing protective immunity in a patient, comprising administering to a patient an effective amount of one or more of the above polypeptides.

In further aspects of this invention, methods and diagnostic kits are
25 provided for detecting tuberculosis in a patient. The methods comprise contacting dermal cells of a patient with one or more of the above polypeptides and detecting an immune response on the patient's skin. The diagnostic kits comprise one or more of the above polypeptides in combination with an apparatus sufficient to contact the polypeptide with the dermal cells of a patient.

In yet other aspects, methods are provided for detecting tuberculosis in a patient, such methods comprising contacting dermal cells of a patient with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-
5 276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and detecting an immune response on the
10 patient's skin. Diagnostic kits for use in such methods are also provided.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if
15 each was incorporated individually.

BRIEF DESCRIPTION OF THE DRAWINGS AND SEQUENCE IDENTIFIERS

Figure 1A and B illustrate the stimulation of proliferation and interferon- γ production in T cells derived from a first and a second *M. tuberculosis*-immune donor, respectively, by the 14 Kd, 20 Kd and 26 Kd antigens described in Example 1.
20

Figure 2 illustrates the stimulation of proliferation and interferon- γ production in T cells derived from an *M. tuberculosis*-immune individual by the two representative polypeptides TbRa3 and TbRa9.

Figures 3A-D illustrate the reactivity of antisera raised against secretory
25 *M. tuberculosis* proteins, the known *M. tuberculosis* antigen 85b and the inventive antigens Tb38-1 and TbH-9, respectively, with *M. tuberculosis* lysate (lane 2), *M. tuberculosis* secretory proteins (lane 3), recombinant Tb38-1 (lane 4), recombinant TbH-9 (lane 5) and recombinant 85b (lane 5).

Figure 4A illustrates the stimulation of proliferation in a TbH-9-specific
30 T cell clone by secretory *M. tuberculosis* proteins, recombinant TbH-9 and a control antigen, TbRa11.

Figure 4B illustrates the stimulation of interferon- γ production in a TbH-9-specific T cell clone by secretory *M. tuberculosis* proteins, PPD and recombinant TbH-9.

Figures 5A and B illustrate the stimulation of proliferation and interferon- γ production in TbH9-specific T cells by the fusion protein TbH9-Tb38-1.

Figures 6A and B illustrate the stimulation of proliferation and interferon- γ production in Tb38-1-specific T cells by the fusion protein TbH9-Tb38-1.

Figures 7A and B illustrate the stimulation of proliferation and interferon- γ production in T cells previously shown to respond to both TbH-9 and Tb38-1 by the fusion protein TbH9-Tb38-1.

Figures 8A and B illustrate the stimulation of proliferation and interferon- γ production in T cells derived from a first *M. tuberculosis*-immune individual by the representative polypeptides XP-1, RDIF6, RDIF8, RDIF10 and RDIF11.

Figures 9A and B illustrate the stimulation of proliferation and interferon- γ production in T cells derived from a second *M. tuberculosis*-immune individual by the representative polypeptides XP-1, RDIF6, RDIF8, RDIF10 and RDIF11.

SEQ. ID NO. 1 is the DNA sequence of TbRa1.

SEQ. ID NO. 2 is the DNA sequence of TbRa10.

SEQ. ID NO. 3 is the DNA sequence of TbRa11.

SEQ. ID NO. 4 is the DNA sequence of TbRa12.

SEQ. ID NO. 5 is the DNA sequence of TbRa13.

SEQ. ID NO. 6 is the DNA sequence of TbRa16.

SEQ. ID NO. 7 is the DNA sequence of TbRa17.

SEQ. ID NO. 8 is the DNA sequence of TbRa18.

SEQ. ID NO. 9 is the DNA sequence of TbRa19.

SEQ. ID NO. 10 is the DNA sequence of TbRa24.

SEQ. ID NO. 11 is the DNA sequence of TbRa26.

SEQ. ID NO. 12 is the DNA sequence of TbRa28.

- SEQ. ID NO. 13 is the DNA sequence of TbRa29.
SEQ. ID NO. 14 is the DNA sequence of TbRa2A.
SEQ. ID NO. 15 is the DNA sequence of TbRa3.
SEQ. ID NO. 16 is the DNA sequence of TbRa32.
5 SEQ. ID NO. 17 is the DNA sequence of TbRa35.
SEQ. ID NO. 18 is the DNA sequence of TbRa36.
SEQ. ID NO. 19 is the DNA sequence of TbRa4.
SEQ. ID NO. 20 is the DNA sequence of TbRa9.
SEQ. ID NO. 21 is the DNA sequence of TbRaB.
10 SEQ. ID NO. 22 is the DNA sequence of TbRaC.
SEQ. ID NO. 23 is the DNA sequence of TbRaD.
SEQ. ID NO. 24 is the DNA sequence of YYWCPCG.
SEQ. ID NO. 25 is the DNA sequence of AAMK.
SEQ. ID NO. 26 is the DNA sequence of TbL-23.
15 SEQ. ID NO. 27 is the DNA sequence of TbL-24.
SEQ. ID NO. 28 is the DNA sequence of TbL-25.
SEQ. ID NO. 29 is the DNA sequence of TbL-28.
SEQ. ID NO. 30 is the DNA sequence of TbL-29.
SEQ. ID NO. 31 is the DNA sequence of TbH-5.
20 SEQ. ID NO. 32 is the DNA sequence of TbH-8.
SEQ. ID NO. 33 is the DNA sequence of TbH-9.
SEQ. ID NO. 34 is the DNA sequence of TbM-1.
SEQ. ID NO. 35 is the DNA sequence of TbM-3.
SEQ. ID NO. 36 is the DNA sequence of TbM-6.
25 SEQ. ID NO. 37 is the DNA sequence of TbM-7.
SEQ. ID NO. 38 is the DNA sequence of TbM-9.
SEQ. ID NO. 39 is the DNA sequence of TbM-12.
SEQ. ID NO. 40 is the DNA sequence of TbM-13.
SEQ. ID NO. 41 is the DNA sequence of TbM-14.
30 SEQ. ID NO. 42 is the DNA sequence of TbM-15.

- SEQ. ID NO. 43 is the DNA sequence of TbH-4.
- SEQ. ID NO. 44 is the DNA sequence of TbH-4-FWD.
- SEQ. ID NO. 45 is the DNA sequence of TbH-12.
- SEQ. ID NO. 46 is the DNA sequence of Tb38-1.
- 5 SEQ. ID NO. 47 is the DNA sequence of Tb38-4.
- SEQ. ID NO. 48 is the DNA sequence of TbL-17.
- SEQ. ID NO. 49 is the DNA sequence of TbL-20.
- SEQ. ID NO. 50 is the DNA sequence of TbL-21.
- SEQ. ID NO. 51 is the DNA sequence of TbH-16.
- 10 SEQ. ID NO. 52 is the DNA sequence of DPEP.
- SEQ. ID NO. 53 is the deduced amino acid sequence of DPEP.
- SEQ. ID NO. 54 is the protein sequence of DPV N-terminal Antigen.
- SEQ. ID NO. 55 is the protein sequence of AVGS N-terminal Antigen.
- SEQ. ID NO. 56 is the protein sequence of AAMK N-terminal Antigen.
- 15 SEQ. ID NO. 57 is the protein sequence of YYWC N-terminal Antigen.
- SEQ. ID NO. 58 is the protein sequence of DIGS N-terminal Antigen.
- SEQ. ID NO. 59 is the protein sequence of AEES N-terminal Antigen.
- SEQ. ID NO. 60 is the protein sequence of DPEP N-terminal Antigen.
- SEQ. ID NO. 61 is the protein sequence of APKT N-terminal Antigen.
- 20 SEQ. ID NO. 62 is the protein sequence of DPAS N-terminal Antigen.
- SEQ. ID NO. 63 is the deduced amino acid sequence of TbRa1.
- SEQ. ID NO. 64 is the deduced amino acid sequence of TbRa10.
- SEQ. ID NO. 65 is the deduced amino acid sequence of TbRa11.
- SEQ. ID NO. 66 is the deduced amino acid sequence of TbRa12.
- 25 SEQ. ID NO. 67 is the deduced amino acid sequence of TbRa13.
- SEQ. ID NO. 68 is the deduced amino acid sequence of TbRa16.
- SEQ. ID NO. 69 is the deduced amino acid sequence of TbRa17.
- SEQ. ID NO. 70 is the deduced amino acid sequence of TbRa18.
- SEQ. ID NO. 71 is the deduced amino acid sequence of TbRa19.
- 30 SEQ. ID NO. 72 is the deduced amino acid sequence of TbRa24.

- SEQ. ID NO. 73 is the deduced amino acid sequence of TbRa26.
SEQ. ID NO. 74 is the deduced amino acid sequence of TbRa28.
SEQ. ID NO. 75 is the deduced amino acid sequence of TbRa29.
SEQ. ID NO. 76 is the deduced amino acid sequence of TbRa2A.
5 SEQ. ID NO. 77 is the deduced amino acid sequence of TbRa3.
SEQ. ID NO. 78 is the deduced amino acid sequence of TbRa32.
SEQ. ID NO. 79 is the deduced amino acid sequence of TbRa35.
SEQ. ID NO. 80 is the deduced amino acid sequence of TbRa36.
SEQ. ID NO. 81 is the deduced amino acid sequence of TbRa4.
10 SEQ. ID NO. 82 is the deduced amino acid sequence of TbRa9.
SEQ. ID NO. 83 is the deduced amino acid sequence of TbRaB.
SEQ. ID NO. 84 is the deduced amino acid sequence of TbRaC.
SEQ. ID NO. 85 is the deduced amino acid sequence of TbRaD.
SEQ. ID NO. 86 is the deduced amino acid sequence of YYWCPG.
15 SEQ. ID NO. 87 is the deduced amino acid sequence of TbAAMK.
SEQ. ID NO. 88 is the deduced amino acid sequence of Tb38-1.
SEQ. ID NO. 89 is the deduced amino acid sequence of TbH-4.
SEQ. ID NO. 90 is the deduced amino acid sequence of TbH-8.
SEQ. ID NO. 91 is the deduced amino acid sequence of TbH-9.
20 SEQ. ID NO. 92 is the deduced amino acid sequence of TbH-12.
SEQ. ID NO. 93 is the amino acid sequence of Tb38-1 Peptide 1.
SEQ. ID NO. 94 is the amino acid sequence of Tb38-1 Peptide 2.
SEQ. ID NO. 95 is the amino acid sequence of Tb38-1 Peptide 3.
SEQ. ID NO. 96 is the amino acid sequence of Tb38-1 Peptide 4.
25 SEQ. ID NO. 97 is the amino acid sequence of Tb38-1 Peptide 5.
SEQ. ID NO. 98 is the amino acid sequence of Tb38-1 Peptide 6.
SEQ. ID NO. 99 is the DNA sequence of DPAS.
SEQ. ID NO. 100 is the deduced amino acid sequence of DPAS.
SEQ. ID NO. 101 is the DNA sequence of DPV.
30 SEQ. ID NO. 102 is the deduced amino acid sequence of DPV.

- SEQ. ID NO. 103 is the DNA sequence of ESAT-6.
- SEQ. ID NO. 104 is the deduced amino acid sequence of ESAT-6.
- SEQ. ID NO. 105 is the DNA sequence of TbH-8-2.
- SEQ. ID NO. 106 is the DNA sequence of TbH-9FL.
- 5 SEQ. ID NO. 107 is the deduced amino acid sequence of TbH-9FL.
- SEQ. ID NO. 108 is the DNA sequence of TbH-9-1.
- SEQ. ID NO. 109 is the deduced amino acid sequence of TbH-9-1.
- SEQ. ID NO. 110 is the DNA sequence of TbH-9-4.
- SEQ. ID NO. 111 is the deduced amino acid sequence of TbH-9-4.
- 10 SEQ. ID NO. 112 is the DNA sequence of Tb38-1F2 IN.
- SEQ. ID NO. 113 is the DNA sequence of Tb38-2F2 RP.
- SEQ. ID NO. 114 is the deduced amino acid sequence of Tb37-FL.
- SEQ. ID NO. 115 is the deduced amino acid sequence of Tb38-IN.
- SEQ. ID NO. 116 is the DNA sequence of Tb38-1F3.
- 15 SEQ. ID NO. 117 is the deduced amino acid sequence of Tb38-1F3.
- SEQ. ID NO. 118 is the DNA sequence of Tb38-1F5.
- SEQ. ID NO. 119 is the DNA sequence of Tb38-1F6.
- SEQ. ID NO. 120 is the deduced N-terminal amino acid sequence of DPV.
- SEQ. ID NO. 121 is the deduced N-terminal amino acid sequence of AVGS.
- 20 SEQ. ID NO. 122 is the deduced N-terminal amino acid sequence of AAMK.
- SEQ. ID NO. 123 is the deduced N-terminal amino acid sequence of YYWC.
- SEQ. ID NO. 124 is the deduced N-terminal amino acid sequence of DIGS.
- SEQ. ID NO. 125 is the deduced N-terminal amino acid sequence of AEES.
- SEQ. ID NO. 126 is the deduced N-terminal amino acid sequence of DPEP.
- 25 SEQ. ID NO. 127 is the deduced N-terminal amino acid sequence of APKT.
- SEQ. ID NO. 128 is the deduced amino acid sequence of DPAS.
- SEQ. ID NO. 129 is the protein sequence of DPPD N-terminal Antigen.
- SEQ ID NO. 130-133 are the protein sequences of four DPPD cyanogen bromide fragments.
- 30 SEQ ID NO. 134 is the N-terminal protein sequence of XDS antigen.

- SEQ ID NO. 135 is the N-terminal protein sequence of AGD antigen.
SEQ ID NO. 136 is the N-terminal protein sequence of APE antigen.
SEQ ID NO. 137 is the N-terminal protein sequence of XYI antigen.
SEQ ID NO. 138 is the DNA sequence of TbH-29.
5 SEQ ID NO. 139 is the DNA sequence of TbH-30.
SEQ ID NO. 140 is the DNA sequence of TbH-32.
SEQ ID NO. 141 is the DNA sequence of TbH-33.
SEQ ID NO. 142 is the predicted amino acid sequence of TbH-29.
SEQ ID NO. 143 is the predicted amino acid sequence of TbH-30.
10 SEQ ID NO. 144 is the predicted amino acid sequence of TbH-32.
SEQ ID NO. 145 is the predicted amino acid sequence of TbH-33.
SEQ ID NO: 146-151 are PCR primers used in the preparation of a fusion protein containing TbRa3, 38 kD and Tb38-1.
SEQ ID NO: 152 is the DNA sequence of the fusion protein containing TbRa3,
15 38 kD and Tb38-1.
SEQ ID NO: 153 is the amino acid sequence of the fusion protein containing TbRa3, 38 kD and Tb38-1.
SEQ ID NO: 154 is the DNA sequence of the *M. tuberculosis* antigen 38 kD.
SEQ ID NO: 155 is the amino acid sequence of the *M. tuberculosis* antigen 38
20 kD.
SEQ ID NO: 156 is the DNA sequence of XP14.
SEQ ID NO: 157 is the DNA sequence of XP24.
SEQ ID NO: 158 is the DNA sequence of XP31.
SEQ ID NO: 159 is the 5' DNA sequence of XP32.
25 SEQ ID NO: 160 is the 3' DNA sequence of XP32.
SEQ ID NO: 161 is the predicted amino acid sequence of XP14.
SEQ ID NO: 162 is the predicted amino acid sequence encoded by the reverse complement of XP14.
SEQ ID NO: 163 is the DNA sequence of XP27.
30 SEQ ID NO: 164 is the DNA sequence of XP36.

- SEQ ID NO: 165 is the 5' DNA sequence of XP4.
- SEQ ID NO: 166 is the 5' DNA sequence of XP5.
- SEQ ID NO: 167 is the 5' DNA sequence of XP17.
- SEQ ID NO: 168 is the 5' DNA sequence of XP30.
- 5 SEQ ID NO: 169 is the 5' DNA sequence of XP2.
- SEQ ID NO: 170 is the 3' DNA sequence of XP2.
- SEQ ID NO: 171 is the 5' DNA sequence of XP3.
- SEQ ID NO: 172 is the 3' DNA sequence of XP3.
- SEQ ID NO: 173 is the 5' DNA sequence of XP6.
- 10 SEQ ID NO: 174 is the 3' DNA sequence of XP6.
- SEQ ID NO: 175 is the 5' DNA sequence of XP18.
- SEQ ID NO: 176 is the 3' DNA sequence of XP18.
- SEQ ID NO: 177 is the 5' DNA sequence of XP19.
- SEQ ID NO: 178 is the 3' DNA sequence of XP19.
- 15 SEQ ID NO: 179 is the 5' DNA sequence of XP22.
- SEQ ID NO: 180 is the 3' DNA sequence of XP22.
- SEQ ID NO: 181 is the 5' DNA sequence of XP25.
- SEQ ID NO: 182 is the 3' DNA sequence of XP25.
- SEQ ID NO: 183 is the full-length DNA sequence of TbH4-XP1.
- 20 SEQ ID NO: 184 is the predicted amino acid sequence of TbH4-XP1.
- SEQ ID NO: 185 is the predicted amino acid sequence encoded by the reverse complement of TbH4-XP1.
- SEQ ID NO: 186 is a first predicted amino acid sequence encoded by XP36.
- SEQ ID NO: 187 is a second predicted amino acid sequence encoded by XP36.
- 25 SEQ ID NO: 188 is the predicted amino acid sequence encoded by the reverse complement of XP36.
- SEQ ID NO: 189 is the DNA sequence of RDIF2.
- SEQ ID NO: 190 is the DNA sequence of RDIF5.
- SEQ ID NO: 191 is the DNA sequence of RDIF8.
- 30 SEQ ID NO: 192 is the DNA sequence of RDIF10.

- SEQ ID NO: 193 is the DNA sequence of RDIF11.
- SEQ ID NO: 194 is the predicted amino acid sequence of RDIF2.
- SEQ ID NO: 195 is the predicted amino acid sequence of RDIF5.
- SEQ ID NO: 196 is the predicted amino acid sequence of RDIF8.
- 5 SEQ ID NO: 197 is the predicted amino acid sequence of RDIF10.
- SEQ ID NO: 198 is the predicted amino acid sequence of RDIF11.
- SEQ ID NO: 199 is the 5' DNA sequence of RDIF12.
- SEQ ID NO: 200 is the 3' DNA sequence of RDIF12.
- SEQ ID NO: 201 is the DNA sequence of RDIF7.
- 10 SEQ ID NO: 202 is the predicted amino acid sequence of RDIF7.
- SEQ ID NO: 203 is the DNA sequence of DIF2-1.
- SEQ ID NO: 204 is the predicted amino acid sequence of DIF2-1.
- SEQ ID NO: 205-212 are PCR primers used in the preparation of a fusion
protein containing TbRa3, 38 kD, Tb38-1 and DPEP (hereinafter referred to as
15 TbF-2).
- SEQ ID NO: 213 is the DNA sequence of the fusion protein TbF-2.
- SEQ ID NO: 214 is the amino acid sequence of the fusion protein TbF-2.
- SEQ ID NO: 215 is the 5' DNA sequence of MO-1.
- SEQ ID NO: 216 is the 5' DNA sequence for MO-2
- 20 SEQ ID NO: 217 is the 5' DNA sequence for MO-4.
- SEQ ID NO: 218 is the 5' DNA sequence for MO-8.
- SEQ ID NO: 219 is the 5' DNA sequence for MO-9.
- SEQ ID NO: 220 is the 5' DNA sequence for MO-26.
- SEQ ID NO: 221 is the 5' DNA sequence for MO-28.
- 25 SEQ ID NO: 222 is the 5' DNA sequence for MO-29.
- SEQ ID NO: 223 is the 5' DNA sequence for MO-30.
- SEQ ID NO: 224 is the 5' DNA sequence for MO-34.
- SEQ ID NO: 225 is the 5' DNA sequence for MO-35.
- SEQ ID NO: 226 is the predicted amino acid sequence for MO-1.
- 30 SEQ ID NO: 227 is the predicted amino acid sequence for MO-2.

SEQ ID NO: 228 is the predicted amino acid sequence for MO-4.
SEQ ID NO: 229 is the predicted amino acid sequence for MO-8.
SEQ ID NO: 230 is the predicted amino acid sequence for MO-9.
SEQ ID NO: 231 is the predicted amino acid sequence for MO-26.
5 SEQ ID NO: 232 is the predicted amino acid sequence for MO-28.
SEQ ID NO: 233 is the predicted amino acid sequence for MO-29.
SEQ ID NO: 234 is the predicted amino acid sequence for MO-30.
SEQ ID NO: 235 is the predicted amino acid sequence for MO-34.
SEQ ID NO: 236 is the predicted amino acid sequence for MO-35.
10 SEQ ID NO: 237 is the determined DNA sequence for MO-10.
SEQ ID NO: 238 is the predicted amino acid sequence for MO-10.
SEQ ID NO: 239 is the 3' DNA sequence for MO-27.
SEQ ID NO: 240 is the full-length DNA sequence for DPPD.
SEQ ID NO: 241 is the predicted full-length amino acid sequence for DPPD.
15 SEQ ID NO: 242 is the determined 5' cDNA sequence for LSER-10
SEQ ID NO: 243 is the determined 5' cDNA sequence for LSER-11
SEQ ID NO: 244 is the determined 5' cDNA sequence for LSER-12
SEQ ID NO: 245 is the determined 5' cDNA sequence for LSER-13
SEQ ID NO: 246 is the determined 5' cDNA sequence for LSER-16
20 SEQ ID NO: 247 is the determined 5' cDNA sequence for LSER-25
SEQ ID NO: 248 is the predicted amino acid sequence for LSER-10
SEQ ID NO: 249 is the predicted amino acid sequence for LSER-12
SEQ ID NO: 250 is the predicted amino acid sequence for LSER-13
SEQ ID NO: 251 is the predicted amino acid sequence for LSER-16
25 SEQ ID NO: 252 is the predicted amino acid sequence for LSER-25
SEQ ID NO: 253 is the determined cDNA sequence for LSER-18
SEQ ID NO: 254 is the determined cDNA sequence for LSER-23
SEQ ID NO: 255 is the determined cDNA sequence for LSER-24
SEQ ID NO: 256 is the determined cDNA sequence for LSER-27
30 SEQ ID NO: 257 is the predicted amino acid sequence for LSER-18

SEQ ID NO: 258 is the predicted amino acid sequence for LSER-23
SEQ ID NO: 259 is the predicted amino acid sequence for LSER-24
SEQ ID NO: 260 is the predicted amino acid sequence for LSER-27
SEQ ID NO: 261 is the determined 5' cDNA sequence for LSER-1
5 SEQ ID NO: 262 is the determined 5' cDNA sequence for LSER-3
SEQ ID NO: 263 is the determined 5' cDNA sequence for LSER-4
SEQ ID NO: 264 is the determined 5' cDNA sequence for LSER-5
SEQ ID NO: 265 is the determined 5' cDNA sequence for LSER-6
SEQ ID NO: 266 is the determined 5' cDNA sequence for LSER-8
10 SEQ ID NO: 267 is the determined 5' cDNA sequence for LSER-14
SEQ ID NO: 268 is the determined 5' cDNA sequence for LSER-15
SEQ ID NO: 269 is the determined 5' cDNA sequence for LSER-17
SEQ ID NO: 270 is the determined 5' cDNA sequence for LSER-19
SEQ ID NO: 271 is the determined 5' cDNA sequence for LSER-20
15 SEQ ID NO: 272 is the determined 5' cDNA sequence for LSER-22
SEQ ID NO: 273 is the determined 5' cDNA sequence for LSER-26
SEQ ID NO: 274 is the determined 5' cDNA sequence for LSER-28
SEQ ID NO: 275 is the determined 5' cDNA sequence for LSER-29
SEQ ID NO: 276 is the determined 5' cDNA sequence for LSER-30
20 SEQ ID NO: 277 is the predicted amino acid sequence for LSER-1
SEQ ID NO: 278 is the predicted amino acid sequence for LSER-3
SEQ ID NO: 279 is the predicted amino acid sequence for LSER-5
SEQ ID NO: 280 is the predicted amino acid sequence for LSER-6
SEQ ID NO: 281 is the predicted amino acid sequence for LSER-8
25 SEQ ID NO: 282 is the predicted amino acid sequence for LSER-14
SEQ ID NO: 283 is the predicted amino acid sequence for LSER-15
SEQ ID NO: 284 is the predicted amino acid sequence for LSER-17
SEQ ID NO: 285 is the predicted amino acid sequence for LSER-19
SEQ ID NO: 286 is the predicted amino acid sequence for LSER-20
30 SEQ ID NO: 287 is the predicted amino acid sequence for LSER-22

- SEQ ID NO: 288 is the predicted amino acid sequence for LSER-26
SEQ ID NO: 289 is the predicted amino acid sequence for LSER-28
SEQ ID NO: 290 is the predicted amino acid sequence for LSER-29
SEQ ID NO: 291 is the predicted amino acid sequence for LSER-30
5 SEQ ID NO: 292 is the determined cDNA sequence for LSER-9
SEQ ID NO: 293 is the determined cDNA sequence for the reverse complement
of LSER-6
SEQ ID NO: 294 is the predicted amino acid sequence for the reverse
complement of LSER-6
10 SEQ ID NO: 295 is the determined 5' cDNA sequence for MO-12
SEQ ID NO: 296 is the determined 5' cDNA sequence for MO-13
SEQ ID NO: 297 is the determined 5' cDNA sequence for MO-19
SEQ ID NO: 298 is the determined 5' cDNA sequence for MO-39
SEQ ID NO: 299 is the predicted amino acid sequence for MO-12
15 SEQ ID NO: 300 is the predicted amino acid sequence for MO-13
SEQ ID NO: 301 is the predicted amino acid sequence for MO-19
SEQ ID NO: 302 is the predicted amino acid sequence for MO-39
SEQ ID NO: 303 is the determined 5' cDNA sequence for Erdsn-1
SEQ ID NO: 304 is the determined 5' cDNA sequence for Erdsn-2
20 SEQ ID NO: 305 is the determined 5' cDNA sequence for Erdsn-4
SEQ ID NO: 306 is the determined 5' cDNA sequence for Erdsn-5
SEQ ID NO: 307 is the determined 5' cDNA sequence for Erdsn-6
SEQ ID NO: 308 is the determined 5' cDNA sequence for Erdsn-7
SEQ ID NO: 309 is the determined 5' cDNA sequence for Erdsn-8
25 SEQ ID NO: 310 is the determined 5' cDNA sequence for Erdsn-9
SEQ ID NO: 311 is the determined 5' cDNA sequence for Erdsn-10
SEQ ID NO: 312 is the determined 5' cDNA sequence for Erdsn-12
SEQ ID NO: 313 is the determined 5' cDNA sequence for Erdsn-13
SEQ ID NO: 314 is the determined 5' cDNA sequence for Erdsn-14
30 SEQ ID NO: 315 is the determined 5' cDNA sequence for Erdsn-15

- SEQ ID NO: 316 is the determined 5' cDNA sequence for Erdsn-16
SEQ ID NO: 317 is the determined 5' cDNA sequence for Erdsn-17
SEQ ID NO: 318 is the determined 5' cDNA sequence for Erdsn-18
SEQ ID NO: 319 is the determined 5' cDNA sequence for Erdsn-21
5 SEQ ID NO: 320 is the determined 5' cDNA sequence for Erdsn-22
SEQ ID NO: 321 is the determined 5' cDNA sequence for Erdsn-23
SEQ ID NO: 322 is the determined 5' cDNA sequence for Erdsn-25
SEQ ID NO: 323 is the determined 3' cDNA sequence for Erdsn-1
SEQ ID NO: 324 is the determined 3' cDNA sequence for Erdsn-2
10 SEQ ID NO: 325 is the determined 3' cDNA sequence for Erdsn-4
SEQ ID NO: 326 is the determined 3' cDNA sequence for Erdsn-5
SEQ ID NO: 327 is the determined 3' cDNA sequence for Erdsn-7
SEQ ID NO: 328 is the determined 3' cDNA sequence for Erdsn-8
SEQ ID NO: 329 is the determined 3' cDNA sequence for Erdsn-9
15 SEQ ID NO: 330 is the determined 3' cDNA sequence for Erdsn-10
SEQ ID NO: 331 is the determined 3' cDNA sequence for Erdsn-12
SEQ ID NO: 332 is the determined 3' cDNA sequence for Erdsn-13
SEQ ID NO: 333 is the determined 3' cDNA sequence for Erdsn-14
SEQ ID NO: 334 is the determined 3' cDNA sequence for Erdsn-15
20 SEQ ID NO: 335 is the determined 3' cDNA sequence for Erdsn-16
SEQ ID NO: 336 is the determined 3' cDNA sequence for Erdsn-17
SEQ ID NO: 337 is the determined 3' cDNA sequence for Erdsn-18
SEQ ID NO: 338 is the determined 3' cDNA sequence for Erdsn-21
SEQ ID NO: 339 is the determined 3' cDNA sequence for Erdsn-22
25 SEQ ID NO: 340 is the determined 3' cDNA sequence for Erdsn-23
SEQ ID NO: 341 is the determined 3' cDNA sequence for Erdsn-25
SEQ ID NO: 342 is the determined cDNA sequence for Erdsn-24
SEQ ID NO: 343 is the determined amino acid sequence for a *M. tuberculosis*
85b precursor homolog
30 SEQ ID NO: 344 is the determined amino acid sequence for spot 1

- SEQ ID NO: 345 is a determined amino acid sequence for spot 2
SEQ ID NO: 346 is a determined amino acid sequence for spot 2
SEQ ID NO: 347 is the determined amino acid seq for spot 4
SEQ ID NO: 348 is the sequence of primer PDM-157
5 SEQ ID NO: 349 is the sequence of primer PDM-160
SEQ ID NO: 350 is the DNA sequence of the fusion protein TbF-6
SEQ ID NO: 351 is the amino acid sequence of fusion protein TbF-6
SEQ ID NO: 352 is the sequence of primer PDM-176
SEQ ID NO: 353 is the sequence of primer PDM-175
10 SEQ ID NO: 354 is the DNA sequence of the fusion protein TbF-8
SEQ ID NO: 355 is the amino acid sequence of the fusion protein TbF-8

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to
15 compositions and methods for preventing, treating and diagnosing tuberculosis. The
compositions of the subject invention include polypeptides that comprise at least one
immunogenic portion of a *M. tuberculosis* antigen, or a variant of such an antigen that
differs only in conservative substitutions and/or modifications. Polypeptides within the
scope of the present invention include, but are not limited to, immunogenic soluble
20 *M. tuberculosis* antigens. A "soluble *M. tuberculosis* antigen" is a protein of
M. tuberculosis origin that is present in *M. tuberculosis* culture filtrate. As used herein,
the term "polypeptide" encompasses amino acid chains of any length, including full
length proteins (*i.e.*, antigens), wherein the amino acid residues are linked by covalent
peptide bonds. Thus, a polypeptide comprising an immunogenic portion of one of the
25 above antigens may consist entirely of the immunogenic portion, or may contain
additional sequences. The additional sequences may be derived from the native
M. tuberculosis antigen or may be heterologous, and such sequences may (but need not)
be immunogenic.

"Immunogenic," as used herein, refers to the ability to elicit an immune
30 response (*e.g.*, cellular) in a patient, such as a human, and/or in a biological sample. In
particular, antigens that are immunogenic (and immunogenic portions or other variants

of such antigens) are capable of stimulating cell proliferation, interleukin-12 production and/or interferon- γ production in biological samples comprising one or more cells selected from the group of T cells, NK cells, B cells and macrophages, where the cells are derived from an *M. tuberculosis*-immune individual. Polypeptides comprising at least an immunogenic portion of one or more *M. tuberculosis* antigens may generally be used to detect tuberculosis or to induce protective immunity against tuberculosis in a patient.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of tuberculosis. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the

antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other
5 sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or
10 additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and
15 most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recite nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two
20 washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

In a related aspect, combination polypeptides are disclosed. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic *M. tuberculosis* sequences, which are joined via a peptide linkage into a single amino acid chain. The
25 sequences may be joined directly (i.e., with no intervening amino acids) or may be joined by way of a linker sequence (e.g., Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

In general, *M. tuberculosis* antigens, and DNA sequences encoding such antigens, may be prepared using any of a variety of procedures. For example, soluble
30 antigens may be isolated from *M. tuberculosis* culture filtrate by procedures known to

those of ordinary skill in the art, including anion-exchange and reverse phase chromatography. Purified antigens are then evaluated for their ability to elicit an appropriate immune response (e.g., cellular) using, for example, the representative methods described herein. Immunogenic antigens may then be partially sequenced
5 using techniques such as traditional Edman chemistry. See Edman and Berg, *Eur. J. Biochem.* 80:116-132, 1967.

Immunogenic antigens may also be produced recombinantly using a DNA sequence that encodes the antigen, which has been inserted into an expression vector and expressed in an appropriate host. DNA molecules encoding soluble antigens
10 may be isolated by screening an appropriate *M. tuberculosis* expression library with anti-sera (e.g., rabbit) raised specifically against soluble *M. tuberculosis* antigens. DNA sequences encoding antigens that may or may not be soluble may be identified by screening an appropriate *M. tuberculosis* genomic or cDNA expression library with sera obtained from patients infected with *M. tuberculosis*. Such screens may generally be
15 performed using techniques well known to those of ordinary skill in the art, such as those described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories. Cold Spring Harbor, NY, 1989.

DNA sequences encoding soluble antigens may also be obtained by screening an appropriate *M. tuberculosis* cDNA or genomic DNA library for DNA
20 sequences that hybridize to degenerate oligonucleotides derived from partial amino acid sequences of isolated soluble antigens. Degenerate oligonucleotide sequences for use in such a screen may be designed and synthesized, and the screen may be performed, as described (for example) in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989 (and references cited
25 therein). Polymerase chain reaction (PCR) may also be employed, using the above oligonucleotides in methods well known in the art, to isolate a nucleic acid probe from a cDNA or genomic library. The library screen may then be performed using the isolated probe.

Alternatively, genomic or cDNA libraries derived from *M. tuberculosis*
30 may be screened directly using peripheral blood mononuclear cells (PBMCs) or T cell

lines or clones derived from one or more *M. tuberculosis*-immune individuals. In general, PBMCs and/or T cells for use in such screens may be prepared as described below. Direct library screens may generally be performed by assaying pools of expressed recombinant proteins for the ability to induce proliferation and/or interferon- γ production in T cells derived from an *M. tuberculosis*-immune individual. Alternatively, potential T cell antigens may be first selected based on antibody reactivity, as described above.

Regardless of the method of preparation, the antigens (and immunogenic portions thereof) described herein (which may or may not be soluble) have the ability to induce an immunogenic response. More specifically, the antigens have the ability to induce proliferation and/or cytokine production (*i.e.*, interferon- γ and/or interleukin-12 production) in T cells, NK cells, B cells and/or macrophages derived from an *M. tuberculosis*-immune individual. The selection of cell type for use in evaluating an immunogenic response to a antigen will, of course, depend on the desired response. For example, interleukin-12 production is most readily evaluated using preparations containing B cells and/or macrophages. An *M. tuberculosis*-immune individual is one who is considered to be resistant to the development of tuberculosis by virtue of having mounted an effective T cell response to *M. tuberculosis* (*i.e.*, substantially free of disease symptoms). Such individuals may be identified based on a strongly positive (*i.e.*, greater than about 10 mm diameter induration) intradermal skin test response to tuberculosis proteins (PPD) and an absence of any signs or symptoms of tuberculosis disease. T cells, NK cells, B cells and macrophages derived from *M. tuberculosis*-immune individuals may be prepared using methods known to those of ordinary skill in the art. For example, a preparation of PBMCs (*i.e.*, peripheral blood mononuclear cells) may be employed without further separation of component cells. PBMCs may generally be prepared, for example, using density centrifugation through Ficoll™ (Winthrop Laboratories, NY). T cells for use in the assays described herein may also be purified directly from PBMCs. Alternatively, an enriched T cell line reactive against mycobacterial proteins, or T cell clones reactive to individual mycobacterial proteins, may be employed. Such T cell clones may be generated by, for example, culturing

PBMCs from *M. tuberculosis*-immune individuals with mycobacterial proteins for a period of 2-4 weeks. This allows expansion of only the mycobacterial protein-specific T cells, resulting in a line composed solely of such cells. These cells may then be cloned and tested with individual proteins, using methods known to those of ordinary skill in the art, to more accurately define individual T cell specificity. In general, antigens that test positive in assays for proliferation and/or cytokine production (*i.e.*, interferon- γ and/or interleukin-12 production) performed using T cells, NK cells, B cells and/or macrophages derived from an *M. tuberculosis*-immune individual are considered immunogenic. Such assays may be performed, for example, using the representative procedures described below. Immunogenic portions of such antigens may be identified using similar assays, and may be present within the polypeptides described herein.

The ability of a polypeptide (*e.g.*, an immunogenic antigen, or a portion or other variant thereof) to induce cell proliferation is evaluated by contacting the cells (*e.g.*, T cells and/or NK cells) with the polypeptide and measuring the proliferation of the cells. In general, the amount of polypeptide that is sufficient for evaluation of about 10^5 cells ranges from about 10 ng/mL to about 100 μ g/mL and preferably is about 10 μ g/mL. The incubation of polypeptide with cells is typically performed at 37°C for about six days. Following incubation with polypeptide, the cells are assayed for a proliferative response, which may be evaluated by methods known to those of ordinary skill in the art, such as exposing cells to a pulse of radiolabeled thymidine and measuring the incorporation of label into cellular DNA. In general, a polypeptide that results in at least a three fold increase in proliferation above background (*i.e.*, the proliferation observed for cells cultured without polypeptide) is considered to be able to induce proliferation.

The ability of a polypeptide to stimulate the production of interferon- γ and/or interleukin-12 in cells may be evaluated by contacting the cells with the polypeptide and measuring the level of interferon- γ or interleukin-12 produced by the cells. In general, the amount of polypeptide that is sufficient for the evaluation of about 10^5 cells ranges from about 10 ng/mL to about 100 μ g/mL and preferably is about 10 μ g/mL. The polypeptide may, but need not, be immobilized on a solid support, such as a

bead or a biodegradable microsphere, such as those described in U.S. Patent Nos. 4,897,268 and 5,075,109. The incubation of polypeptide with the cells is typically performed at 37°C for about six days. Following incubation with polypeptide, the cells are assayed for interferon- γ and/or interleukin-12 (or one or more subunits thereof), which may be evaluated by methods known to those of ordinary skill in the art, such as an enzyme-linked immunosorbent assay (ELISA) or, in the case of IL-12 P70 subunit, a bioassay such as an assay measuring proliferation of T cells. In general, a polypeptide that results in the production of at least 50 pg of interferon- γ per mL of cultured supernatant (containing 10^4 - 10^5 T cells per mL) is considered able to stimulate the production of interferon- γ . A polypeptide that stimulates the production of at least 10 pg/mL of IL-12 P70 subunit, and/or at least 100 pg/mL of IL-12 P40 subunit, per 10^3 macrophages or B cells (or per 3×10^5 PBMC) is considered able to stimulate the production of IL-12.

In general, immunogenic antigens are those antigens that stimulate proliferation and/or cytokine production (*i.e.*, interferon- γ and/or interleukin-12 production) in T cells, NK cells, B cells and/or macrophages derived from at least about 25% of *M. tuberculosis*-immune individuals. Among these immunogenic antigens, polypeptides having superior therapeutic properties may be distinguished based on the magnitude of the responses in the above assays and based on the percentage of individuals for which a response is observed. In addition, antigens having superior therapeutic properties will not stimulate proliferation and/or cytokine production *in vitro* in cells derived from more than about 25% of individuals that are not *M. tuberculosis*-immune, thereby eliminating responses that are not specifically due to *M. tuberculosis*-responsive cells. Those antigens that induce a response in a high percentage of T cell, NK cell, B cell and/or macrophage preparations from *M. tuberculosis*-immune individuals (with a low incidence of responses in cell preparations from other individuals) have superior therapeutic properties.

Antigens with superior therapeutic properties may also be identified based on their ability to diminish the severity of *M. tuberculosis* infection in experimental animals, when administered as a vaccine. Suitable vaccine preparations

for use on experimental animals are described in detail below. Efficacy may be determined based on the ability of the antigen to provide at least about a 50% reduction in bacterial numbers and/or at least about a 40% decrease in mortality following experimental infection. Suitable experimental animals include mice, guinea pigs and
5 primates.

Antigens having superior diagnostic properties may generally be identified based on the ability to elicit a response in an intradermal skin test performed on an individual with active tuberculosis, but not in a test performed on an individual who is not infected with *M. tuberculosis*. Skin tests may generally be performed as
10 described below, with a response of at least 5 mm induration considered positive.

Immunogenic portions of the antigens described herein may be prepared and identified using well known techniques, such as those summarized in Paul, *Fundamental Immunology*, 3d ed., Raven Press, 1993, pp. 243-247 and references cited therein. Such techniques include screening polypeptide portions of the native antigen
15 for immunogenic properties. The representative proliferation and cytokine production assays described herein may generally be employed in these screens. An immunogenic portion of a polypeptide is a portion that, within such representative assays, generates an immune response (*e.g.*, proliferation, interferon- γ production and/or interleukin-12 production) that is substantially similar to that generated by the full length antigen. In
20 other words, an immunogenic portion of an antigen may generate at least about 20%, and preferably about 100%, of the proliferation induced by the full length antigen in the model proliferation assay described herein. An immunogenic portion may also, or alternatively, stimulate the production of at least about 20%, and preferably about 100%, of the interferon- γ and/or interleukin-12 induced by the full length antigen in the
25 model assay described herein.

Portions and other variants of *M. tuberculosis* antigens may be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such
30 polypeptides may be synthesized using any of the commercially available solid-phase

techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a growing amino acid chain. See Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963. Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Applied BioSystems, Inc., Foster City, CA, and may be operated according to the manufacturer's instructions. Variants of a native antigen may generally be prepared using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis. Sections of the DNA sequence may also be removed using standard techniques to permit preparation of truncated polypeptides.

Recombinant polypeptides containing portions and/or variants of a native antigen may be readily prepared from a DNA sequence encoding the polypeptide using a variety of techniques well known to those of ordinary skill in the art. For example, supernatants from suitable host/vector systems which secrete recombinant protein into culture media may be first concentrated using a commercially available filter. Following concentration, the concentrate may be applied to a suitable purification matrix such as an affinity matrix or an ion exchange resin. Finally, one or more reverse phase HPLC steps can be employed to further purify a recombinant protein.

Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line such as COS or CHO. The DNA sequences expressed in this manner may encode naturally occurring antigens, portions of naturally occurring antigens, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form. Preferably, the polypeptides are at least about 80% pure, more preferably at least about 90% pure and most

preferably at least about 99% pure. In certain preferred embodiments, described in detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In certain specific embodiments, the subject invention discloses
5 polypeptides comprising at least an immunogenic portion of a soluble *M. tuberculosis* antigen having one of the following N-terminal sequences, or a variant thereof that differs only in conservative substitutions and/or modifications:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-
Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- 10 (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-
Ser; (SEQ ID No. 121)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-
Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- 15 (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-
Pro; (SEQ ID No. 123)
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val;
(SEQ ID No. 124)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID
No. 125)
- 20 (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Ala-Ala-Ala-Ser-
Pro-Pro-Ser; (SEQ ID No. 126)
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-
Gly; (SEQ ID No. 127)
- 25 (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-
Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-
Ala-Asn; (SEQ ID No. 128)
- (j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-
Ser; (SEQ ID No. 134)
- 30 (k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-
Asp; (SEQ ID No. 135) or

- (l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid, preferably a cysteine residue. A DNA sequence encoding the antigen identified as (g) above is provided in SEQ ID No. 52, and the polypeptide encoded by SEQ ID No. 52 is provided in SEQ ID No. 53. A DNA sequence encoding the antigen defined as (a) above is provided in SEQ ID No. 101; its deduced amino acid sequence is provided in SEQ ID No. 102. A DNA sequence corresponding to antigen (d) above is provided in SEQ ID No. 24 a DNA sequence corresponding to antigen (c) is provided in SEQ ID No. 25 and a DNA sequence corresponding to antigen (i) is provided in SEQ ID No. 99; its deduced amino acid sequence is provided in SEQ ID No. 100.

In a further specific embodiment, the subject invention discloses polypeptides comprising at least an immunogenic portion of an *M. tuberculosis* antigen having one of the following N-terminal sequences, or a variant thereof that differs only in conservative substitutions and/or modifications:

- (m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No 137) or

- (n) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129)

wherein Xaa may be any amino acid, preferably a cysteine residue.

In other specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a soluble *M. tuberculosis* antigen (or a variant of such an antigen) that comprises one or more of the amino acid sequences encoded by (a) the DNA sequences of SEQ ID Nos.: 1, 2, 4-10, 13-25 and 52; (b) the complements of such DNA sequences, or (c) DNA sequences substantially homologous to a sequence in (a) or (b).

In further specific embodiments, the subject invention discloses polypeptides comprising at least an immunogenic portion of a *M. tuberculosis* antigen (or a variant of such an antigen), which may or may not be soluble, that comprises one or more of the amino acid sequences encoded by (a) the DNA sequences of SEQ ID

Nos.: 26-51, 138, 139, 163-183, 189-193, 199, 200, 201, 203, 215-225, 239, 240, 242-247, 253-256, 261-276, 292, 293, 295-298 and 303-342, (b) the complements of such DNA sequences or (c) DNA sequences substantially homologous to a sequence in (a) or (b).

5 In the specific embodiments discussed above, the *M. tuberculosis* antigens include variants that are encoded by DNA sequences which are substantially homologous to one or more of DNA sequences specifically recited herein. "Substantial homology," as used herein, refers to DNA sequences that are capable of hybridizing under moderately stringent conditions. Suitable moderately stringent conditions include
10 prewashing in a solution of 5X SSC, 0.5% SDS, 1.0 mM EDTA (pH 8.0); hybridizing at 50°C-65°C, 5X SSC, overnight or, in the case of cross-species homology at 45°C, 0.5X SSC; followed by washing twice at 65°C for 20 minutes with each of 2X, 0.5X and 0.2X SSC containing 0.1% SDS). Such hybridizing DNA sequences are also within the scope of this invention, as are nucleotide sequences that, due to code
15 degeneracy, encode an immunogenic polypeptide that is encoded by a hybridizing DNA sequence.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known *M. tuberculosis* antigen, such as the 38 kD antigen
20 described in Andersen and Hansen, *Infect. Immun.* 57:2481-2488, 1989, (Genbank Accession No. M30046) or ESAT-6 (SEQ ID Nos. 103 and 104), together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is
25 constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5'-end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA

translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

In another aspect, the present invention provides methods for using one or more of the above polypeptides or fusion proteins (or DNA molecules encoding such polypeptides) to induce protective immunity against tuberculosis in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient

may be afflicted with a disease, or may be free of detectable disease and/or infection. In other words, protective immunity may be induced to prevent or treat tuberculosis.

In this aspect, the polypeptide, fusion protein or DNA molecule is generally present within a pharmaceutical composition and/or a vaccine. 5 Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. Vaccines may comprise one or more of the above polypeptides and a non-specific immune response enhancer, such as an adjuvant or a liposome (into which the polypeptide is incorporated). Such pharmaceutical 10 compositions and vaccines may also contain other *M. tuberculosis* antigens, either incorporated into a combination polypeptide or present within a separate polypeptide.

Alternatively, a vaccine may contain DNA encoding one or more polypeptides as described above, such that the polypeptide is generated *in situ*. In such vaccines, the DNA may be present within any of a variety of delivery systems known to 15 those of ordinary skill in the art, including nucleic acid expression systems, bacterial and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter and terminating signal). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an immunogenic portion 20 of the polypeptide on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (*e.g.*, vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the use of a non-pathogenic (defective), replication competent virus. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as 25 described, for example, in Ulmer et al., *Science* 259:1745-1749, 1993 and reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

In a related aspect, a DNA vaccine as described above may be 30 administered simultaneously with or sequentially to either a polypeptide of the present

invention or a known *M. tuberculosis* antigen, such as the 38 kD antigen described above. For example, administration of DNA encoding a polypeptide of the present invention, either "naked" or in a delivery system as described above, may be followed by administration of an antigen in order to enhance the protective immune effect of the
5 vaccine.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunization using BCG. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or
10 subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 3 doses may be administered for a 1-36 week period. Preferably, 3 doses are administered, at intervals of 3-4 months, and booster vaccinations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that, when administered as described above, is capable
15 of raising an immune response in an immunized patient sufficient to protect the patient from *M. tuberculosis* infection for at least 1-2 years. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the
20 size of the patient, but will typically range from about 0.1 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a fat, a
25 wax or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and magnesium carbonate, may be employed. Biodegradable microspheres (*e.g.*, polylactic galactide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable
30 microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of adjuvants may be employed in the vaccines of this invention to nonspecifically enhance the immune response. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune responses, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Suitable adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Freund's Complete Adjuvant (Difco Laboratories) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ). Other suitable adjuvants include alum, biodegradable microspheres, monophosphoryl lipid A and quil A.

In another aspect, this invention provides methods for using one or more of the polypeptides described above to diagnose tuberculosis using a skin test. As used herein, a "skin test" is any assay performed directly on a patient in which a delayed-type hypersensitivity (DTH) reaction (such as swelling, reddening or dermatitis) is measured following intradermal injection of one or more polypeptides as described above. Such injection may be achieved using any suitable device sufficient to contact the polypeptide or polypeptides with dermal cells of the patient, such as a tuberculin syringe or 1 mL syringe. Preferably, the reaction is measured at least 48 hours after injection, more preferably 48-72 hours.

The DTH reaction is a cell-mediated immune response, which is greater in patients that have been exposed previously to the test antigen (*i.e.*, the immunogenic portion of the polypeptide employed, or a variant thereof). The response may be measured visually, using a ruler. In general, a response that is greater than about 0.5 cm in diameter, preferably greater than about 1.0 cm in diameter, is a positive response, indicative of tuberculosis infection, which may or may not be manifested as an active disease.

The polypeptides of this invention are preferably formulated, for use in a skin test, as pharmaceutical compositions containing a polypeptide and a physiologically acceptable carrier, as described above. Such compositions typically contain one or more of the above polypeptides in an amount ranging from about 1 μ g to about 100 μ g, preferably from about 10 μ g to about 50 μ g in a volume of 0.1 mL.

Preferably, the carrier employed in such pharmaceutical compositions is a saline solution with appropriate preservatives, such as phenol and/or Tween 80™.

In a preferred embodiment, a polypeptide employed in a skin test is of sufficient size such that it remains at the site of injection for the duration of the reaction period. In general, a polypeptide that is at least 9 amino acids in length is sufficient. The polypeptide is also preferably broken down by macrophages within hours of injection to allow presentation to T-cells. Such polypeptides may contain repeats of one or more of the above sequences and/or other immunogenic or nonimmunogenic sequences.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

EXAMPLE 1

PURIFICATION AND CHARACTERIZATION OF POLYPEPTIDES FROM *M. TUBERCULOSIS* CULTURE FILTRATE

This example illustrates the preparation of *M. tuberculosis* soluble polypeptides from culture filtrate. Unless otherwise noted, all percentages in the following example are weight per volume.

M. tuberculosis (either H37Ra, ATCC No. 25177, or H37Rv, ATCC No. 25618) was cultured in sterile GAS media at 37°C for fourteen days. The media was then vacuum filtered (leaving the bulk of the cells) through a 0.45 µ filter into a sterile 2.5 L bottle. The media was next filtered through a 0.2 µ filter into a sterile 4 L bottle and NaN₃ was added to the culture filtrate to a concentration of 0.04%. The bottles were then placed in a 4°C cold room.

The culture filtrate was concentrated by placing the filtrate in a 12 L reservoir that had been autoclaved and feeding the filtrate into a 400 ml Amicon stir cell

which had been rinsed with ethanol and contained a 10,000 kDa MWCO membrane. The pressure was maintained at 60 psi using nitrogen gas. This procedure reduced the 12 L volume to approximately 50 ml.

The culture filtrate was dialyzed into 0.1% ammonium bicarbonate using
5 a 8,000 kDa MWCO cellulose ester membrane, with two changes of ammonium bicarbonate solution. Protein concentration was then determined by a commercially available BCA assay (Pierce, Rockford, IL).

The dialyzed culture filtrate was then lyophilized, and the polypeptides resuspended in distilled water. The polypeptides were dialyzed against 0.01 mM 1.3
10 bis[tris(hydroxymethyl)-methylamino]propane. pH 7.5 (Bis-Tris propane buffer), the initial conditions for anion exchange chromatography. Fractionation was performed using gel perfusion chromatography on a POROS 146 II Q/M anion exchange column 4.6 mm x 100 mm (Perseptive BioSystems, Framingham, MA) equilibrated in 0.01 mM Bis-Tris propane buffer pH 7.5. Polypeptides were eluted with a linear 0-0.5 M NaCl
15 gradient in the above buffer system. The column eluent was monitored at a wavelength of 220 nm.

The pools of polypeptides eluting from the ion exchange column were dialyzed against distilled water and lyophilized. The resulting material was dissolved in 0.1% trifluoroacetic acid (TFA) pH 1.9 in water, and the polypeptides were purified on
20 a Delta-Pak C18 column (Waters, Milford, MA) 300 Angstrom pore size, 5 micron particle size (3.9 x 150 mm). The polypeptides were eluted from the column with a linear gradient from 0-60% dilution buffer (0.1% TFA in acetonitrile). The flow rate was 0.75 ml/minute and the HPLC eluent was monitored at 214 nm. Fractions containing the eluted polypeptides were collected to maximize the purity of the
25 individual samples. Approximately 200 purified polypeptides were obtained.

The purified polypeptides were then screened for the ability to induce T-cell proliferation in PBMC preparations. The PBMCs from donors known to be PPD skin test positive and whose T-cells were shown to proliferate in response to PPD and crude soluble proteins from MTB were cultured in medium comprising RPMI 1640
30 supplemented with 10% pooled human serum and 50 µg/ml gentamicin. Purified

polypeptides were added in duplicate at concentrations of 0.5 to 10 $\mu\text{g/mL}$. After six days of culture in 96-well round-bottom plates in a volume of 200 μl , 50 μl of medium was removed from each well for determination of IFN- γ levels, as described below. The plates were then pulsed with 1 $\mu\text{Ci/well}$ of tritiated thymidine for a further 18 hours, harvested and tritium uptake determined using a gas scintillation counter. Fractions that resulted in proliferation in both replicates three fold greater than the proliferation observed in cells cultured in medium alone were considered positive.

IFN- γ was measured using an enzyme-linked immunosorbent assay (ELISA). ELISA plates were coated with a mouse monoclonal antibody directed to human IFN- γ (PharMingen, San Diego, CA) in PBS for four hours at room temperature. Wells were then blocked with PBS containing 5% (W/V) non-fat dried milk for 1 hour at room temperature. The plates were then washed six times in PBS/0.2% TWEEN-20 and samples diluted 1:2 in culture medium in the ELISA plates were incubated overnight at room temperature. The plates were again washed and a polyclonal rabbit anti-human IFN- γ serum diluted 1:3000 in PBS/10% normal goat serum was added to each well. The plates were then incubated for two hours at room temperature, washed and horseradish peroxidase-coupled anti-rabbit IgG (Sigma Chemical So., St. Louis, MO) was added at a 1:2000 dilution in PBS/5% non-fat dried milk. After a further two hour incubation at room temperature, the plates were washed and TMB substrate added. The reaction was stopped after 20 min with 1 N sulfuric acid. Optical density was determined at 450 nm using 570 nm as a reference wavelength. Fractions that resulted in both replicates giving an OD two fold greater than the mean OD from cells cultured in medium alone, plus 3 standard deviations, were considered positive.

For sequencing, the polypeptides were individually dried onto Biobrene TM (Perkin Elmer/Applied BioSystems Division, Foster City, CA) treated glass fiber filters. The filters with polypeptide were loaded onto a Perkin Elmer/Applied BioSystems Division Procise 492 protein sequencer. The polypeptides were sequenced from the amino terminal and using traditional Edman chemistry. The amino acid sequence was determined for each polypeptide by comparing the retention time of the PTH amino acid derivative to the appropriate PTH derivative standards.

Using the procedure described above, antigens having the following N-terminal sequences were isolated:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Xaa-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 54)
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 55)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 56)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 57)
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 58)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 59)
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Ala-Ala-Ala-Ala-Pro-Pro-Ala; (SEQ ID No. 60) and
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 61)

wherein Xaa may be any amino acid.

An additional antigen was isolated employing a microbore HPLC purification step in addition to the procedure described above. Specifically, 20 μ l of a fraction comprising a mixture of antigens from the chromatographic purification step previously described, was purified on an Aquapore C18 column (Perkin Elmer/Applied Biosystems Division, Foster City, CA) with a 7 micron pore size. column size 1 mm x 100 mm, in a Perkin Elmer/Applied Biosystems Division Model 172 HPLC. Fractions were eluted from the column with a linear gradient of 1%/minute of acetonitrile (containing 0.05% TFA) in water (0.05% TFA) at a flow rate of 80 μ l/minute. The eluent was monitored at 250 nm. The original fraction was separated into 4 major peaks plus other smaller components and a polypeptide was obtained which was shown to

have a molecular weight of 12.054 Kd (by mass spectrometry) and the following N-terminal sequence:

- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Gln-
Thr-Ser-Leu-Leu-Asn-Asn-Leu-Ala-Asp-Pro-Asp-Val-Ser-Phe-
Ala-Asp (SEQ ID No. 62).

This polypeptide was shown to induce proliferation and IFN- γ production in PBMC preparations using the assays described above.

Additional soluble antigens were isolated from *M. tuberculosis* culture filtrate as follows. *M. tuberculosis* culture filtrate was prepared as described above. Following dialysis against Bis-Tris propane buffer, at pH 5.5, fractionation was performed using anion exchange chromatography on a Poros QE column 4.6 x 100 mm (Perseptive Biosystems) equilibrated in Bis-Tris propane buffer pH 5.5. Polypeptides were eluted with a linear 0-1.5 M NaCl gradient in the above buffer system at a flow rate of 10 ml/min. The column eluent was monitored at a wavelength of 214 nm.

The fractions eluting from the ion exchange column were pooled and subjected to reverse phase chromatography using a Poros R2 column 4.6 x 100 mm (Perseptive Biosystems). Polypeptides were eluted from the column with a linear gradient from 0-100% acetonitrile (0.1% TFA) at a flow rate of 5 ml/min. The eluent was monitored at 214 nm.

Fractions containing the eluted polypeptides were lyophilized and resuspended in 80 μ l of aqueous 0.1% TFA and further subjected to reverse phase chromatography on a Vydac C4 column 4.6 x 150 mm (Western Analytical, Temecula, CA) with a linear gradient of 0-100% acetonitrile (0.1% TFA) at a flow rate of 2 ml/min. Eluent was monitored at 214 nm.

The fraction with biological activity was separated into one major peak plus other smaller components. Western blot of this peak onto PVDF membrane revealed three major bands of molecular weights 14 Kd, 20 Kd and 26 Kd. These polypeptides were determined to have the following N-terminal sequences, respectively:

- (j) Xaa-Asp-Ser-Glu-Lys-Ser-Ala-Thr-Ile-Lys-Val-Thr-Asp-Ala-Ser; (SEQ ID No. 134)

(k) Ala-Gly-Asp-Thr-Xaa-Ile-Tyr-Ile-Val-Gly-Asn-Leu-Thr-Ala-Asp; (SEQ ID No. 135) and

(l) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136), wherein Xaa may be any amino acid.

5 Using the assays described above, these polypeptides were shown to induce proliferation and IFN- γ production in PBMC preparations. Figs. 1A and B show the results of such assays using PBMC preparations from a first and a second donor, respectively.

DNA sequences that encode the antigens designated as (a), (c), (d) and
10 (g) above were obtained by screening a genomic *M. tuberculosis* library using ³²P end labeled degenerate oligonucleotides corresponding to the N-terminal sequence and containing *M. tuberculosis* codon bias. The screen performed using a probe corresponding to antigen (a) above identified a clone having the sequence provided in SEQ ID No. 101. The polypeptide encoded by SEQ ID No. 101 is provided in SEQ ID
15 No. 102. The screen performed using a probe corresponding to antigen (g) above identified a clone having the sequence provided in SEQ ID No. 52. The polypeptide encoded by SEQ ID No. 52 is provided in SEQ ID No. 53. The screen performed using a probe corresponding to antigen (d) above identified a clone having the sequence provided in SEQ ID No. 24, and the screen performed with a probe corresponding to
20 antigen (c) identified a clone having the sequence provided in SEQ ID No. 25.

The above amino acid sequences were compared to known amino acid sequences in the gene bank using the DNA STAR system. The database searched contains some 173,000 proteins and is a combination of the Swiss, PIR databases along with translated protein sequences (Version 87). No significant homologies to the amino
25 acid sequences for antigens (a)-(h) and (l) were detected.

The amino acid sequence for antigen (i) was found to be homologous to a sequence from *M. leprae*. The full length *M. leprae* sequence was amplified from genomic DNA using the sequence obtained from GENBANK. This sequence was then used to screen the *M. tuberculosis* library described below in Example 2 and a full
30 length copy of the *M. tuberculosis* homologue was obtained (SEQ ID No. 99).

The amino acid sequence for antigen (j) was found to be homologous to a known *M. tuberculosis* protein translated from a DNA sequence. To the best of the inventors' knowledge, this protein has not been previously shown to possess T-cell stimulatory activity. The amino acid sequence for antigen (k) was found to be related to
 5 a sequence from *M. leprae*.

In the proliferation and IFN- γ assays described above, using three PPD positive donors, the results for representative antigens provided above are presented in Table 1:

10

TABLE 1
RESULTS OF PBMC PROLIFERATION AND IFN- γ ASSAYS

Sequence	Proliferation	IFN- γ
(a)	+	-
(c)	+++	+++
(d)	++	++
(g)	+++	+++
(h)	+++	+++

In Table 1, responses that gave a stimulation index (SI) of between 2 and
 15 4 (compared to cells cultured in medium alone) were scored as +, an SI of 4-8 or 2-4 at a concentration of 1 μ g or less was scored as ++ and an SI of greater than 8 was scored as +++. The antigen of sequence (i) was found to have a high SI (+++) for one donor and lower SI (++ and +) for the two other donors in both proliferation and IFN- γ assays. These results indicate that these antigens are capable of inducing proliferation and/or
 20 interferon- γ production.

EXAMPLE 2

USE OF PATIENT SERA TO ISOLATE *M. TUBERCULOSIS* ANTIGENS

This example illustrates the isolation of antigens from *M. tuberculosis* lysate by screening with serum from *M. tuberculosis*-infected individuals.

Dessicated *M. tuberculosis* H37Ra (Difco Laboratories) was added to a 2% NP40 solution, and alternately homogenized and sonicated three times. The resulting suspension was centrifuged at 13,000 rpm in microfuge tubes and the supernatant put through a 0.2 micron syringe filter. The filtrate was bound to Macro Prep DEAE beads (BioRad, Hercules, CA). The beads were extensively washed with 20 mM Tris pH 7.5 and bound proteins eluted with 1M NaCl. The 1M NaCl elute was dialyzed overnight against 10 mM Tris, pH 7.5. Dialyzed solution was treated with DNase and RNase at 0.05 mg/ml for 30 min. at room temperature and then with α -D-mannosidase, 0.5 U/mg at pH 4.5 for 3-4 hours at room temperature. After returning to pH 7.5, the material was fractionated via FPLC over a Bio Scale-Q-20 column (BioRad). Fractions were combined into nine pools, concentrated in a Centriprep 10 (Amicon, Beverley, MA) and then screened by Western blot for serological activity using a serum pool from *M. tuberculosis*-infected patients which was not immunoreactive with other antigens of the present invention.

The most reactive fraction was run in SDS-PAGE and transferred to PVDF. A band at approximately 85 Kd was cut out yielding the sequence:

(m) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137), wherein Xaa may be any amino acid.

Comparison of this sequence with those in the gene bank as described above, revealed no significant homologies to known sequences.

A DNA sequence that encodes the antigen designated as (m) above was obtained by screening a genomic *M. tuberculosis* Erdman strain library using labeled degenerate oligonucleotides corresponding to the N-terminal sequence of SEQ ID NO:137. A clone was identified having the DNA sequence provided in SEQ ID NO:

203. This sequence was found to encode the amino acid sequence provided in SEQ ID NO: 204. Comparison of these sequences with those in the genebank revealed some similarity to sequences previously identified in *M. tuberculosis* and *M. bovis*.

5

EXAMPLE 3

PREPARATION OF DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

This example illustrates the preparation of DNA sequences encoding *M. tuberculosis* antigens by screening a *M. tuberculosis* expression library with sera
10 obtained from patients infected with *M. tuberculosis*, or with anti-sera raised against soluble *M. tuberculosis* antigens.

A. PREPARATION OF *M. TUBERCULOSIS* SOLUBLE ANTIGENS USING RABBIT ANTI-SERA RAISED AGAINST *M. TUBERCULOSIS* SUPERNATANT

15 Genomic DNA was isolated from the *M. tuberculosis* strain H37Ra. The DNA was randomly sheared and used to construct an expression library using the Lambda ZAP expression system (Stratagene, La Jolla, CA). Rabbit anti-sera was generated against secretory proteins of the *M. tuberculosis* strains H37Ra, H37Rv and Erdman by immunizing a rabbit with concentrated supernatant of the *M. tuberculosis*
20 cultures. Specifically, the rabbit was first immunized subcutaneously with 200 µg of protein antigen in a total volume of 2 ml containing 10 µg muramyl dipeptide (Calbiochem, La Jolla, CA) and 1 ml of incomplete Freund's adjuvant. Four weeks later the rabbit was boosted subcutaneously with 100 µg antigen in incomplete Freund's adjuvant. Finally, the rabbit was immunized intravenously four weeks later with 50 µg
25 protein antigen. The anti-sera were used to screen the expression library as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. Bacteriophage plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones deduced.

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Thirty two clones were purified. Of these, 25 represent sequences that have not been previously identified in human *M. tuberculosis*. Recombinant antigens

were expressed and purified antigens used in the immunological analysis described in Example 1. Proteins were induced by IPTG and purified by gel elution, as described in Skeiky et al., *J. Exp. Med.* 181:1527-1537, 1995. Representative sequences of DNA molecules identified in this screen are provided in SEQ ID Nos.: 1-25. The
5 corresponding predicted amino acid sequences are shown in SEQ ID Nos. 63-87.

On comparison of these sequences with known sequences in the gene bank using the databases described above, it was found that the clones referred to hereinafter as TbRA2A, TbRA16, TbRA18, and TbRA29 (SEQ ID Nos. 76, 68, 70, 75) show some homology to sequences previously identified in *Mycobacterium leprae* but
10 not in *M. tuberculosis*. TbRA2A was found to be a lipoprotein, with a six residue lipidation sequence being located adjacent to a hydrophobic secretory sequence. TbRA11, TbRA26, TbRA28 and TbDPEP (SEQ ID Nos.: 65, 73, 74, 53) have been previously identified in *M. tuberculosis*. No significant homologies were found to TbRA1, TbRA3, TbRA4, TbRA9, TbRA10, TbRA13, TbRA17, TbRa19, TbRA29,
15 TbRA32, TbRA36 and the overlapping clones TbRA35 and TbRA12 (SEQ ID Nos. 63, 77, 81, 82, 64, 67, 69, 71, 75, 78, 80, 79, 66). The clone TbRa24 is overlapping with clone TbRa29.

The results of PBMC proliferation and interferon- γ assays performed on representative recombinant antigens, and using T-cell preparations from several
20 different *M. tuberculosis*-immune patients, are presented in Tables 2 and 3, respectively.

TABLE 2
RESULTS OF PBMC PROLIFERATION TO REPRESENTATIVE SOLUBLE ANTIGENS

Antigen	Patient												
	1	2	3	4	5	6	7	8	9	10	11	12	13
TbRa1	-	-	±	++	-	-	±	±	-	-	+	±	-
TbRa3	-	±	++	-	±	-	-	++	±	-	-	-	-
TbRa9	-	-	nt	nt	++	++	nt	nt	nt	nt	nt	nt	nt
TbRa10	-	-	±	±	±	+	nt	±	-	+	±	±	-
TbRa11	±	±	+	++	++	+	nt	-	++	++	++	±	nt
TbRa12	-	-	+	+	±	++	+	±	±	-	+	-	-
TbRa16	nt	nt	nt	nt	-	+	nt	nt	nt	nt	nt	nt	nt
TbRa24	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRa26	-	+	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRa29	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRa35	++	nt	++	++	++	++	nt	++	++	++	++	++	nt
TbRaB	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRaC	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
TbRaD	nt	nt	nt	nt	-	-	nt	nt	nt	nt	nt	nt	nt
AAMK	-	-	±	-	-	-	nt	-	-	-	nt	±	nt
YY	-	-	-	-	-	-	nt	-	-	-	nt	+	nt
DPEP	-	+	-	++	-	-	nt	++	±	+	±	±	nt
Control	-	-	-	-	-	-	-	-	-	-	-	-	-

nt = not tested

In Tables 2 and 3, responses that gave a stimulation index (SI) of between 1.2 and 2 (compared to cells cultured in medium alone) were scored as $\pm$, a SI of 2-4 was scored as +, as SI of 4-8 or 2-4 at a concentration of 1 μ g or less was scored as ++ and an SI of greater than 8 was scored as +++. In addition, the effect of concentration on proliferation and interferon- γ production is shown for two of the above antigens in the attached Figure. For both proliferation and interferon- γ production, TbRa3 was scored as ++ and TbRa9 as +.

These results indicate that these soluble antigens can induce proliferation and/or interferon- γ production in T-cells derived from an *M. tuberculosis*-immune individual.

B. USE OF SERA FROM PATIENTS HAVING PULMONARY OR PLEURAL TUBERCULOSIS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

The genomic DNA library described above, and an additional H37Rv library, were screened using pools of sera obtained from patients with active tuberculosis. To prepare the H37Rv library, *M. tuberculosis* strain H37Rv genomic DNA was isolated, subjected to partial *Sau*3A digestion and used to construct an expression library using the Lambda Zap expression system (Stratagene, La Jolla, Ca). Three different pools of sera, each containing sera obtained from three individuals with active pulmonary or pleural disease, were used in the expression screening. The pools were designated TbL, TbM and TbH, referring to relative reactivity with H37Ra lysate (i.e., TbL = low reactivity, TbM = medium reactivity and TbH = high reactivity) in both ELISA and immunoblot format. A fourth pool of sera from seven patients with active pulmonary tuberculosis was also employed. All of the sera lacked increased reactivity with the recombinant 38 kD *M. tuberculosis* H37Ra phosphate-binding protein.

All pools were pre-adsorbed with *E. coli* lysate and used to screen the H37Ra and H37Rv expression libraries, as described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratories, Cold Spring Harbor, NY, 1989. Bacteriophage plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones deduced.

Thirty two clones were purified. Of these, 31 represented sequences that had not been previously identified in human *M. tuberculosis*. Representative sequences of the DNA molecules identified are provided in SEQ ID Nos.: 26-51 and 105. Of these, TbH-8-2 (SEQ. ID NO. 105) is a partial clone of TbH-8, and TbH-4 (SEQ. ID NO. 43) and TbH-4-FWD (SEQ. ID NO. 44) are non-contiguous sequences from the same clone. Amino acid sequences for the antigens hereinafter identified as Tb38-1, TbH-4, TbH-8, TbH-9, and TbH-12 are shown in SEQ ID Nos.: 88-92. Comparison of these sequences with known sequences in the gene bank using the databases identified above revealed no significant homologies to TbH-4, TbH-8, TbH-9 and TbM-3, although weak homologies were found to TbH-9. TbH-12 was found to be homologous to a 34 kD antigenic protein previously identified in *M. paratuberculosis* (Acc. No. S28515). Tb38-1 was found to be located 34 base pairs upstream of the open reading frame for the antigen ESAT-6 previously identified in *M. bovis* (Acc. No. U34848) and in *M. tuberculosis* (Sorensen et al., *Infect. Immun.* 63:1710-1717, 1995).

Probes derived from Tb38-1 and TbH-9, both isolated from an H37Ra library, were used to identify clones in an H37Rv library. Tb38-1 hybridized to Tb38-1F2, Tb38-1F3, Tb38-1F5 and Tb38-1F6 (SEQ. ID NOS. 112, 113, 116, 118, and 119). (SEQ ID NOS. 112 and 113 are non-contiguous sequences from clone Tb38-1F2.) Two open reading frames were deduced in Tb38-1F2; one corresponds to Tb37FL (SEQ. ID. NO. 114), the second, a partial sequence, may be the homologue of Tb38-1 and is called Tb38-IN (SEQ. ID NO. 115). The deduced amino acid sequence of Tb38-1F3 is presented in SEQ. ID. NO. 117. A TbH-9 probe identified three clones in the H37Rv library: TbH-9-FL (SEQ. ID NO. 106), which may be the homologue of TbH-9 (R37Ra), TbH-9-1 (SEQ. ID NO. 108), and TbH-9-4 (SEQ. ID NO. 110), all of which are highly related sequences to TbH-9. The deduced amino acid sequences for these three clones are presented in SEQ ID NOS. 107, 109 and 111.

Further screening of the *M. tuberculosis* genomic DNA library, as described above, resulted in the recovery of ten additional reactive clones, representing seven different genes. One of these genes was identified as the 38 Kd antigen discussed

above, one was determined to be identical to the 14Kd alpha crystallin heat shock protein previously shown to be present in *M. tuberculosis*, and a third was determined to be identical to the antigen TbH-8 described above. The determined DNA sequences for the remaining five clones (hereinafter referred to as TbH-29, TbH-30, TbH-32 and TbH-33) are provided in SEQ ID NO: 138-141, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 142-145, respectively. The DNA and amino acid sequences for these antigens were compared with those in the gene bank as described above. No homologies were found to the 5' end of TbH-29 (which contains the reactive open reading frame), although the 3' end of TbH-29 was found to be identical to the *M. tuberculosis* cosmid Y227. TbH-32 and TbH-33 were found to be identical to the previously identified *M. tuberculosis* insertion element IS6110 and to the *M. tuberculosis* cosmid Y50, respectively. No significant homologies to TbH-30 were found.

Positive phagemid from this additional screening were used to infect *E. coli* XL-1 Blue MRF', as described in Sambrook et al., *supra*. Induction of recombinant protein was accomplished by the addition of IPTG. Induced and uninduced lysates were run in duplicate on SDS-PAGE and transferred to nitrocellulose filters. Filters were reacted with human *M. tuberculosis* sera (1:200 dilution) reactive with TbH and a rabbit sera (1:200 or 1:250 dilution) reactive with the N-terminal 4 Kd portion of lacZ. Sera incubations were performed for 2 hours at room temperature. Bound antibody was detected by addition of ¹²⁵I-labeled Protein A and subsequent exposure to film for variable times ranging from 16 hours to 11 days. The results of the immunoblots are summarized in Table 4.

TABLE 4

<u>Antigen</u>	<u>Human M. tb Sera</u>	<u>Anti-lacZ Sera</u>
TbH-29	45 Kd	45 Kd
TbH-30	No reactivity	29 Kd
TbH-32	12 Kd	12 Kd
TbH-33	16 Kd	16 Kd

Positive reaction of the recombinant human *M. tuberculosis* antigens with both the human *M. tuberculosis* sera and anti-lacZ sera indicate that reactivity of the human *M. tuberculosis* sera is directed towards the fusion protein. Antigens reactive with the anti-lacZ sera but not with the human *M. tuberculosis* sera may be the result of the human *M. tuberculosis* sera recognizing conformational epitopes, or the antigen-antibody binding kinetics may be such that the 2 hour sera exposure in the immunoblot is not sufficient.

The results of T-cell assays performed on Tb38-1, ESAT-6 and other representative recombinant antigens are presented in Tables 5A, B and 6, respectively, below:

TABLE 5A
RESULTS OF PBMC PROLIFERATION TO REPRESENTATIVE ANTIGENS

Antigen	Donor										
	1	2	3	4	5	6	7	8	9	10	11
Tb38.1	---	+	-	-	-	++	-	+	-	++	---
ESAT-6	+++	+	+	+	-	+	-	+	+	++	---
TbH-9	++	++	-	++	±	±	++	++	++	++	---

TABLE 5B
RESULTS OF PBMC INTERFERON- γ PRODUCTION TO REPRESENTATIVE ANTIGENS

Antigen	Donor										
	1	2	3	4	5	6	7	8	9	10	11
Tb38.1	+++	+	-	+	+	+++	-	++	-	+++	+++
ESAT-6	+++	+	+	+	+-	+	-	+	+	+++	+++
TbH-9	++	++	-	+++	$\pm$	$\pm$	+++	+++	++	+++	++

5

TABLE 6
SUMMARY OF T-CELL RESPONSES TO REPRESENTATIVE ANTIGENS

Antigen	Proliferation			Interferon- γ			total
	patient 4	patient 5	patient 6	patient 4	patient 5	patient 6	
TbH9	++	++	++	+++	++	++	13
TbM7	-	+	-	++	+	-	4
TbH5	-	+	+	++	++	++	8
TbL23	-	+	$\pm$	++	++	+	7.5
TbH4	-	++	$\pm$	++	++	$\pm$	7
- control	-	-	-	-	-	-	0

10 These results indicate that both the inventive *M. tuberculosis* antigens and ESAT-6 can induce proliferation and/or interferon- γ production in T-cells derived from an *M. tuberculosis*-immune individual. To the best of the inventors' knowledge, ESAT-6 has not been previously shown to stimulate human immune responses

15 A set of six overlapping peptides covering the amino acid sequence of the antigen Tb38-1 was constructed using the method described in Example 6. The sequences of these peptides, hereinafter referred to as pep1-6, are provided in SEQ ID Nos. 93-98, respectively. The results of T-cell assays using these peptides are shown in Tables 7 and 8. These results confirm the existence, and help to localize T-cell epitopes within Tb38-1 capable of inducing proliferation and interferon- γ production in T-cells
20 derived from an *M. tuberculosis* immune individual.

Studies were undertaken to determine whether the antigens TbH-9 and Tb38-1 represent cellular proteins or are secreted into *M. tuberculosis* culture media. In the first study, rabbit sera were raised against A) secretory proteins of *M. tuberculosis*, B) the known secretory recombinant *M. tuberculosis* antigen 85b, C) recombinant Tb38-1 and D) recombinant TbH-9, using protocols substantially the same as that as described in Example 3A. Total *M. tuberculosis* lysate, concentrated supernatant of *M. tuberculosis* cultures and the recombinant antigens 85b, TbH-9 and Tb38-1 were resolved on denaturing gels, immobilized on nitrocellulose membranes and duplicate blots were probed using the rabbit sera described above.

The results of this analysis using control sera (panel I) and antisera (panel II) against secretory proteins, recombinant 85b, recombinant Tb38-1 and recombinant TbH-9 are shown in Figures 3A-D, respectively, wherein the lane designations are as follows: 1) molecular weight protein standards; 2) 5 μ g of *M. tuberculosis* lysate; 3) 5 μ g secretory proteins; 4) 50 ng recombinant Tb38-1; 5) 50 ng recombinant TbH-9; and 6) 50 ng recombinant 85b. The recombinant antigens were engineered with six terminal histidine residues and would therefore be expected to migrate with a mobility approximately 1 kD larger than the native protein. In Figure 3D, recombinant TbH-9 is lacking approximately 10 kD of the full-length 42 kD antigen, hence the significant difference in the size of the immunoreactive native TbH-9 antigen in the lysate lane (indicated by an arrow). These results demonstrate that Tb38-1 and TbH-9 are intracellular antigens and are not actively secreted by *M. tuberculosis*.

The finding that TbH-9 is an intracellular antigen was confirmed by determining the reactivity of TbH-9-specific human T cell clones to recombinant TbH-9, secretory *M. tuberculosis* proteins and PPD. A TbH-9-specific T cell clone (designated 131TbH-9) was generated from PBMC of a healthy PPD-positive donor. The proliferative response of 131TbH-9 to secretory proteins, recombinant TbH-9 and a control *M. tuberculosis* antigen, TbRa11, was determined by measuring uptake of tritiated thymidine, as described in Example 1. As shown in Figure 4A, the clone 131TbH-9 responds specifically to TbH-9, showing that TbH-9 is not a significant component of *M. tuberculosis* secretory proteins. Figure 4B shows the production of IFN- γ by a second TbH-9-specific T cell clone

(designated PPD 800-10) prepared from PBMC from a healthy PPD-positive donor, following stimulation of the T cell clone with secretory proteins, PPD or recombinant TbH-9. These results further confirm that TbH-9 is not secreted by *M. tuberculosis*.

C. USE OF SERA FROM PATIENTS HAVING EXTRAPULMONARY TUBERCULOSIS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

Genomic DNA was isolated from *M. tuberculosis* Erdman strain, randomly sheared and used to construct an expression library employing the Lambda ZAP expression system (Stratagene, La Jolla, CA). The resulting library was screened using pools of sera obtained from individuals with extrapulmonary tuberculosis, as described above in Example 3B, with the secondary antibody being goat anti-human IgG + A + M (H+L) conjugated with alkaline phosphatase.

Eighteen clones were purified. Of these, 4 clones (hereinafter referred to as XP14, XP24, XP31 and XP32) were found to bear some similarity to known sequences. The determined DNA sequences for XP14, XP24 and XP31 are provided in SEQ ID Nos.: 156-158, respectively, with the 5' and 3' DNA sequences for XP32 being provided in SEQ ID Nos.: 159 and 160, respectively. The predicted amino acid sequence for XP14 is provided in SEQ ID No: 161. The reverse complement of XP14 was found to encode the amino acid sequence provided in SEQ ID No.: 162.

Comparison of the sequences for the remaining 14 clones (hereinafter referred to as XP1-XP6, XP17-XP19, XP22, XP25, XP27, XP30 and XP36) with those in the genebank as described above, revealed no homologies with the exception of the 3' ends of XP2 and XP6 which were found to bear some homology to known *M. tuberculosis* cosmids. The DNA sequences for XP27 and XP36 are shown in SEQ ID Nos.: 163 and 164, respectively, with the 5' sequences for XP4, XP5, XP17 and XP30 being shown in SEQ ID Nos: 165-168, respectively, and the 5' and 3' sequences for XP2, XP3, XP6, XP18, XP19, XP22 and XP25 being shown in SEQ ID Nos: 169 and 170; 171 and 172; 173 and 174; 175 and 176; 177 and 178; 179 and 180; and 181 and 182, respectively. XP1 was found to overlap with the DNA sequences for TbH4, disclosed above. The full-length DNA sequence for TbH4-XP1 is provided in SEQ ID No.: 183. This DNA sequence was found to contain an

open reading frame encoding the amino acid sequence shown in SEQ ID No: 184. The reverse complement of TbH4-XP1 was found to contain an open reading frame encoding the amino acid sequence shown in SEQ ID No.: 185. The DNA sequence for XP36 was found to contain two open reading frames encoding the amino acid sequence shown in SEQ ID Nos.: 186 and 187, with the reverse complement containing an open reading frame encoding the amino acid sequence shown in SEQ ID No.: 188.

Recombinant XP1 protein was prepared as described above in Example 3B, with a metal ion affinity chromatography column being employed for purification. As illustrated in Figures 8A-B and 9A-B, using the assays described herein, recombinant XP1 was found to stimulate cell proliferation and IFN- γ production in T cells isolated from an *M. tuberculosis*-immune donors.

D. USE OF A LYSATE POSITIVE SERUM POOL FROM PATIENTS HAVING TUBERCULOSIS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

Genomic DNA was isolated from *M. tuberculosis* Erdman strain, randomly sheared and used to construct an expression library employing the Lambda Screen expression system (Novagen, Madison, WI), as described below in Example 6. Pooled serum obtained from *M. tuberculosis*-infected patients and that was shown to react with *M. tuberculosis* lysate but not with the previously expressed proteins 38kD, Tb38-1, TbRa3, TbH4, DPEP and TbRa11, was used to screen the expression library as described above in Example 3B, with the secondary antibody being goat anti-human IgG + A + M (H+L) conjugated with alkaline phosphatase.

Twenty-seven clones were purified. Comparison of the determined cDNA sequences for these clones revealed no significant homologies to 10 of the clones (hereinafter referred to as LSER-10, LSER-11, LSER-12, LSER-13, LSER-16, LSER-18, LSER-23, LSER-24, LSER-25 and LSER-27). The determined 5' cDNA sequences for LSER-10, LSER-11, LSER-12, LSER-13, LSER-16 and LSER-25 are provided in SEQ ID NO: 242-247, respectively, with the corresponding predicted amino acid sequences for LSER-10, LSER-12, LSER-13, LSER-16 and LSER-25 being provided in SEQ ID NO: 248-252, respectively. The determined full-length cDNA sequences for LSER-18, LSER-23, LSER-24

and LSER-27 are shown in SEQ ID NO: 253-256, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 257-260. The remaining seventeen clones were found to show similarities to unknown sequences previously identified in *M. tuberculosis*. The determined 5' cDNA sequences for sixteen of these clones (hereinafter referred to as LSER-1, LSER-3, LSER-4, LSER-5, LSER-6, LSER-8, LSER-14, LSER-15, LSER-17, LSER-19, LSER-20, LSER-22, LSER-26, LSER-28, LSER-29 and LSER-30) are provided in SEQ ID NO: 261-276, respectively, with the corresponding predicted amino acid sequences for LSER-1, LSER-3, LSER-5, LSER-6, LSER-8, LSER-14, LSER-15, LSER-17, LSER-19, LSER-20, LSER-22, LSER-26, LSER-28, LSER-29 and LSER-30 being provided in SEQ ID NO: 277-291, respectively. The determined full-length cDNA sequence for the clone LSER-9 is provided in SEQ ID NO: 292. The reverse complement of LSER-6 (SEQ ID NO: 293) was found to encode the predicted amino acid sequence of SEQ ID NO: 294.

E. PREPARATION OF *M. TUBERCULOSIS* SOLUBLE ANTIGENS USING RABBIT ANTI-SERA RAISED AGAINST *M. TUBERCULOSIS* FRACTIONATED PROTEINS

M. tuberculosis lysate was prepared as described above in Example 2. The resulting material was fractionated by HPLC and the fractions screened by Western blot for serological activity with a serum pool from *M. tuberculosis*-infected patients which showed little or no immunoreactivity with other antigens of the present invention. Rabbit anti-sera was generated against the most reactive fraction using the method described in Example 3A. The anti-sera was used to screen an *M. tuberculosis* Erdman strain genomic DNA expression library prepared as described above. Bacteriophage plaques expressing immunoreactive antigens were purified. Phagemid from the plaques was rescued and the nucleotide sequences of the *M. tuberculosis* clones determined.

Ten different clones were purified. Of these, one was found to be TbRa35, described above, and one was found to be the previously identified *M. tuberculosis* antigen, HSP60. Of the remaining eight clones, seven (hereinafter referred to as RDIF2, RDIF5, RDIF8, RDIF10, RDIF11 and RDIF 12) were found to bear some similarity to previously identified *M. tuberculosis* sequences. The determined DNA sequences for RDIF2, RDIF5, RDIF8, RDIF10 and RDIF11 are provided in SEQ ID Nos.: 189-193, respectively, with the

corresponding predicted amino acid sequences being provided in SEQ ID Nos: 194-198, respectively. The 5' and 3' DNA sequences for RDIF12 are provided in SEQ ID Nos.: 199 and 200, respectively. No significant homologies were found to the antigen RDIF-7. The determined DNA and predicted amino acid sequences for RDIF7 are provided in SEQ ID Nos.: 201 and 202, respectively. One additional clone, referred to as RDIF6 was isolated, however, this was found to be identical to RDIF5.

Recombinant RDIF6, RDIF8, RDIF10 and RDIF11 were prepared as described above. As shown in Figures 8A-B and 9A-B, these antigens were found to stimulate cell proliferation and IFN- γ production in T cells isolated from *M. tuberculosis*-immune donors.

EXAMPLE 4

PURIFICATION AND CHARACTERIZATION OF A POLYPEPTIDE FROM TUBERCULIN PURIFIED PROTEIN DERIVATIVE

An *M. tuberculosis* polypeptide was isolated from tuberculin purified protein derivative (PPD) as follows.

PPD was prepared as published with some modification (Seibert, F. et al., Tuberculin purified protein derivative. Preparation and analyses of a large quantity for standard. The American Review of Tuberculosis 44:9-25, 1941).

M. tuberculosis Rv strain was grown for 6 weeks in synthetic medium in roller bottles at 37°C. Bottles containing the bacterial growth were then heated to 100° C in water vapor for 3 hours. Cultures were sterile filtered using a 0.22 μ filter and the liquid phase was concentrated 20 times using a 3 kD cut-off membrane. Proteins were precipitated once with 50% ammonium sulfate solution and eight times with 25% ammonium sulfate solution. The resulting proteins (PPD) were fractionated by reverse phase liquid chromatography (RP-HPLC) using a C18 column (7.8 x 300 mM; Waters, Milford, MA) in a Biocad HPLC system (Perseptive Biosystems, Framingham, MA). Fractions were eluted from the column with a linear gradient from 0-100% buffer (0.1% TFA in acetonitrile). The flow rate was 10 ml/minute and eluent was monitored at 214 nm and 280 nm.

Six fractions were collected, dried, suspended in PBS and tested individually in *M. tuberculosis*-infected guinea pigs for induction of delayed type hypersensitivity (DTH) reaction. One fraction was found to induce a strong DTH reaction and was subsequently fractionated further by RP-HPLC on a microbore Vydac C18 column (Cat. No. 218TP5115) in a Perkin Elmer/Applied Biosystems Division Model 172 HPLC. Fractions were eluted with a linear gradient from 5-100% buffer (0.05% TFA in acetonitrile) with a flow rate of 80 μ l/minute. Eluent was monitored at 215 nm. Eight fractions were collected and tested for induction of DTH in *M. tuberculosis*-infected guinea pigs. One fraction was found to induce strong DTH of about 16 mm induration. The other fractions did not induce detectable DTH. The positive fraction was submitted to SDS-PAGE gel electrophoresis and found to contain a single protein band of approximately 12 kD molecular weight.

This polypeptide, herein after referred to as DPPD, was sequenced from the amino terminal using a Perkin Elmer/Applied Biosystems Division Procise 492 protein sequencer as described above and found to have the N-terminal sequence shown in SEQ ID No.: 129. Comparison of this sequence with known sequences in the gene bank as described above revealed no known homologies. Four cyanogen bromide fragments of DPPD were isolated and found to have the sequences shown in SEQ ID Nos.: 130-133. A subsequent search of the *M. tuberculosis* genome database released by the Institute for Genomic Research revealed a match of the DPPD partial amino acid sequence with a sequence present within the *M. tuberculosis* cosmid MTY21C12. An open reading frame of 336 bp was identified. The full-length DNA sequence for DPPD is provided in SEQ ID NO: 240. with the corresponding full-length amino acid sequence being provided in SEQ ID NO: 241.

The ability of the antigen DPPD to stimulate human PBMC to proliferate and to produce IFN- γ was assayed as described in Example 1. As shown in Table 9, DPPD was found to stimulate proliferation and elicit production of large quantities of IFN- γ ; more than that elicited by commercial PPD.

TABLE 9
RESULTS OF PROLIFERATION AND INTERFERON- γ ASSAYS TO DPPD

PBMC Donor	Stimulator	Proliferation (CPM)	IFN- γ (OD ₄₅₀)
A	Medium	1,089	0.17
	PPD (commercial)	8,394	1.29
	DPPD	13,451	2.21
B	Medium	450	0.09
	PPD (commercial)	3,929	1.26
	DPPD	6,184	1.49
C	Medium	541	0.11
	PPD (commercial)	8,907	0.76
	DPPD	23,024	>2.70

EXAMPLE 5

USE OF SERA FROM TUBERCULOSIS-INFECTED MONKEYS TO IDENTIFY DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

Genomic DNA was isolated from *M. tuberculosis* Erdman strain, randomly sheared and used to construct an expression library employing the Lambda ZAP expression system (Stratagene, La Jolla, CA). Serum samples were obtained from a cynomolgous monkey 18, 33, 51 and 56 days following infection with *M. tuberculosis* Erdman strain. These samples were pooled and used to screen the *M. tuberculosis* genomic DNA expression library using the procedure described above in Example 3C.

Twenty clones were purified. The determined 5' DNA sequences for the clones referred to as MO-1, MO-2, MO-4, MO-8, MO-9, MO-26, MO-28, MO-29, MO-30, MO-34 and MO-35 are provided in SEQ ID NO: 215-225, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 226-236. The full-length DNA sequence of the clone MO-10 is provided in SEQ ID NO: 237, with the corresponding

predicted amino acid sequence being provided in SEQ ID NO: 238. The 3' DNA sequence for the clone MO-27 is provided in SEQ ID NO: 239.

Clones MO-1, MO-30 and MO-35 were found to show a high degree of relatedness and showed some homology to a previously identified unknown *M. tuberculosis* sequence and to cosmid MTCI237. MO-2 was found to show some homology to aspartokinase from *M. tuberculosis*. Clones MO-3, MO-7 and MO-27 were found to be identical and to show a high degree of relatedness to MO-5. All four of these clones showed some homology to *M. tuberculosis* heat shock protein 70. MO-27 was found to show some homology to *M. tuberculosis* cosmid MTCY339. MO-4 and MO-34 were found to show some homology to cosmid SCY21B4 and *M. smegmatis* integration host factor, and were both found to show some homology to a previously identified, unknown *M. tuberculosis* sequence. MO-6 was found to show some homology to *M. tuberculosis* heat shock protein 65. MO-8, MO-9, MO-10, MO-26 and MO-29 were found to be highly related to each other and to show some homology to *M. tuberculosis* dihydrolipamide succinyltransferase. MO-28, MO-31 and MO-32 were found to be identical and to show some homology to a previously identified *M. tuberculosis* protein. MO-33 was found to show some homology to a previously identified 14 kDa *M. tuberculosis* heat shock protein.

Further studies using the above protocol resulted in the isolation of an additional four clones, hereinafter referred to as MO-12, MO-13, MO-19 and MO-39. The determined 5' cDNA sequences for these clones are provided in SEQ ID NO: 295-298, respectively, with the corresponding predicted protein sequences being provided in SEQ ID NO: 299-302, respectively. Comparison of these sequences with those in the gene bank as described above revealed no significant homologies to MO-39. MO-12, MO-13 and MO-19 were found to show some homologies to unknown sequences previously isolated from *M. tuberculosis*.

EXAMPLE 6

ISOLATION OF DNA SEQUENCES ENCODING *M. TUBERCULOSIS* ANTIGENS

BY SCREENING OF A NOVEL EXPRESSION LIBRARY

This example illustrates isolation of DNA sequences encoding *M. tuberculosis* antigens by screening of a novel expression library with sera from *M. tuberculosis*-infected patients that were shown to be unreactive with a panel of the recombinant *M. tuberculosis* antigens TbRa11, TbRa3, Tb38-1, TbH4, TbF and 38 kD.

Genomic DNA from *M. tuberculosis* Erdman strain was randomly sheared to an average size of 2 kb, and blunt ended with Klenow polymerase, followed by the addition of EcoRI adaptors. The insert was subsequently ligated into the Screen phage vector (Novagen, Madison, WI) and packaged *in vitro* using the PhageMaker extract (Novagen). The resulting library was screened with sera from several *M. tuberculosis* donors that had been shown to be negative on a panel of previously identified *M. tuberculosis* antigens as described above in Example 3B.

A total of 22 different clones were isolated. By comparison, screening of the λ Zap library described above using the same sera did not result in any positive hits. One of the clones was found to represent TbRa11, described above. The determined 5' cDNA sequences for 19 of the remaining 21 clones (hereinafter referred to as Erdsn1, Erdsn2, Erdsn4-Erdsn10, Erdsn12-18, Erdsn21-Erdsn23 and Erdsn25) are provided in SEQ ID NO: 303-322, respectively, with the determined 3' cDNA sequences for Erdsn1, Erdsn2, Erdsn4, Erdsn-5, Erdsn-7-Erdsn10, Erdsn12-18, Erdsn21-Erdsn23 and Erdsn25 being provided in SEQ ID NO: 323-341, respectively. The complete cDNA insert sequence for the clone Erdsn24 is provided in SEQ ID NO: 342. Comparison of the determined cDNA sequences with those in the gene bank revealed no significant homologies to the sequences provided in SEQ ID NO: 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341. The sequences of SEQ ID NO: 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342 were found to show some homology to unknown sequences previously identified in *M. tuberculosis*.

EXAMPLE 7

ISOLATION OF SOLUBLE *M. TUBERCULOSIS* ANTIGENS

USING MASS SPECTROMETRY

This example illustrates the use of mass spectrometry to identify soluble *M. tuberculosis* antigens.

In a first approach, *M. tuberculosis* culture filtrate was screened by Western analysis using serum from a tuberculosis-infected individual. The reactive bands were excised from a silver stained gel and the amino acid sequences determined by mass spectrometry. The determined amino acid sequence for one of the isolated antigens is provided in SEQ ID NO: 343. Comparison of this sequence with those in the gene bank revealed homology to the 85b precursor antigen previously identified in *M. tuberculosis*.

In a second approach, the high molecular weight region of *M. tuberculosis* culture supernatant was studied. This area may contain immunodominant antigens which may be useful in the diagnosis of *M. tuberculosis* infection. Two known monoclonal antibodies, IT42 and IT57 (available from the Center for Disease Control, Atlanta, GA), show reactivity by Western analysis to antigens in this vicinity, although the identity of the antigens remains unknown. In addition, unknown high-molecular weight proteins have been described as containing a surrogate marker for *M. tuberculosis* infection in HIV-positive individuals (*Jnl. Infect. Dis.*, 176:133-143, 1997). To determine the identity of these antigens, two-dimensional gel electrophoresis and two-dimensional Western analysis were performed using the antibodies IT57 and IT42. Five protein spots in the high molecular weight region were identified, individually excised, enzymatically digested and subjected to mass spectrometric analysis.

The determined amino acid sequences for three of these spots (referred to as spots 1, 2 and 4) are provided in SEQ ID NO: 344, 345-346 and 347, respectively. Comparison of these sequences with those in the gene bank revealed that spot 1 is the previously identified PcK-1, a phosphoenolpyruvate kinase. The two sequences isolated from spot 2 were determined to be from two DNAs, previously identified in *M. tuberculosis* as heat shock proteins. Spot 4 was determined to be the previously identified *M. tuberculosis* protein Kat G. To the best of the inventors' knowledge, neither PcK-1 nor the two DNAs have previously been shown to have utility in the diagnosis of *M. tuberculosis* infection.

EXAMPLE 8

USE OF REPRESENTATIVE ANTIGENS FOR DIAGNOSIS OF TUBERCULOSIS

This example illustrates the effectiveness of several representative polypeptides in skin tests for the diagnosis of *M. tuberculosis* infection.

Individuals were injected intradermally with 100 μ l of either PBS or PBS plus Tween 20TM containing either 0.1 μ g of protein (for TbH-9 and TbRa35) or 1.0 μ g of protein (for TbRa38-1). Induration was measured between 5-7 days after injection, with a response of 5 mm or greater being considered positive. Of the 20 individuals tested, 2 were PPD negative and 18 were PPD positive. Of the PPD positive individuals, 3 had active tuberculosis, 3 had been previously infected with tuberculosis and 9 were healthy. In a second study, 13 PPD positive individuals were tested with 0.1 μ g TbRa11 in either PBS or PBS plus Tween 20TM as described above. The results of both studies are shown in Table 10.

TABLE 10
RESULTS OF DTH TESTING WITH REPRESENTATIVE ANTIGENS

	TbH-9 Pos/Total	Tb38-1 Pos/Total	TbRa35 Pos/Total	Cumulative Pos/Total	TbRa11 Pos/Total
PPD negative	0/2	0/2	0/2	0/2	
PPD positive					
healthy	5/9	4/9	4/9	6/9	1/4
prior TB	3/5	2/5	2/5	4/5	3/5
active	3/4	3/4	0/4	4/4	1/4
TOTAL	11/18	9/18	6/18	14/18	5/13

EXAMPLE 9

SYNTHESIS OF SYNTHETIC POLYPEPTIDES

Polypeptides may be synthesized on a Millipore 9050 peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium

hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following lyophilization of the pure fractions, the peptides may be characterized using electrospray mass spectrometry and by amino acid analysis.

EXAMPLE 10

PREPARATION AND CHARACTERIZATION OF *M. TUBERCULOSIS* FUSION PROTEINS

A fusion protein containing TbRa3, the 38 kD antigen and Tb38-1 was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR in order to facilitate their fusion and the subsequent expression of the fusion protein TbRa3-38 kD-Tb38-1. TbRa3, 38 kD and Tb38-1 DNA was used to perform PCR using the primers PDM-64 and PDM-65 (SEQ ID NO: 146 and 147), PDM-57 and PDM-58 (SEQ ID NO: 148 and 149), and PDM-69 and PDM-60 (SEQ ID NO: 150 and 151), respectively. In each case, the DNA amplification was performed using 10 µl 10X Pfu buffer, 2 µl 10 mM dNTPs, 2 µl each of the PCR primers at 10 µM concentration, 81.5 µl water, 1.5 µl Pfu DNA polymerase (Stratagene, La Jolla, CA) and 1 µl DNA at either 70 ng/µl (for TbRa3) or 50 ng/µl (for 38 kD and Tb38-1). For TbRa3, denaturation at 94°C was performed for 2 min, followed by 40 cycles of 96°C for 15 sec and 72°C for 1 min, and lastly by 72°C for 4 min. For 38 kD, denaturation at 96°C was performed for 2 min, followed by 40 cycles of 96°C for 30 sec, 68°C for 15 sec and 72°C for 3 min, and finally by 72°C for 4 min. For Tb38-1 denaturation at 94°C for 2 min was followed by 10 cycles of 96°C for 15 sec, 68°C for 15 sec and 72°C for

1.5 min, 30 cycles of 96°C for 15 sec, 64°C for 15 sec and 72°C for 1.5, and finally by 72°C for 4 min.

The TbRa3 PCR fragment was digested with NdeI and EcoRI and cloned directly into pT7⁺L2 IL 1 vector using NdeI and EcoRI sites. The 38 kD PCR fragment was digested with Sse8387I, treated with T4 DNA polymerase to make blunt ends and then digested with EcoRI for direct cloning into the pT7⁺L2Ra3-1 vector which was digested with StuI and EcoRI. The 38-1 PCR fragment was digested with Eco47III and EcoRI and directly subcloned into pT7⁺L2Ra3/38kD-17 digested with the same enzymes. The whole fusion was then transferred to pET28b – using NdeI and EcoRI sites. The fusion construct was confirmed by DNA sequencing.

The expression construct was transformed into BLR pLys S *E. coli* (Novagen, Madison, WI) and grown overnight in LB broth with kanamycin (30 µg/ml) and chloramphenicol (34 µg/ml). This culture (12 ml) was used to inoculate 500 ml 2XYT with the same antibiotics and the culture was induced with IPTG at an OD₅₆₀ of 0.44 to a final concentration of 1.2 mM. Four hours post-induction, the bacteria were harvested and sonicated in 20 mM Tris (8.0), 100 mM NaCl, 0.1% DOC, 20 µg/ml Leupeptin, 20 mM PMSF followed by centrifugation at 26,000 X g. The resulting pellet was resuspended in 8 M urea, 20 mM Tris (8.0), 100 mM NaCl and bound to Pro-bond nickel resin (Invitrogen, Carlsbad, CA). The column was washed several times with the above buffer then eluted with an imidazole gradient (50 mM, 100 mM, 500 mM imidazole was added to 8 M urea, 20 mM Tris (8.0), 100 mM NaCl). The eluates containing the protein of interest were then dialyzed against 10 mM Tris (8.0).

The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbRa3-38 kD-Tb38-1) are provided in SEQ ID NO: 152 and 153, respectively.

A fusion protein containing the two antigens TbH-9 and Tb38-1 (hereinafter referred to as TbH9-Tb38-1) without a hinge sequence, was prepared using a similar procedure to that described above. The DNA sequence for the TbH9-Tb38-1 fusion protein is provided in SEQ ID NO: 156.

The ability of the fusion protein TbH9-Tb38-1 to induce T cell proliferation and IFN- γ production in PBMC preparations was examined using the protocol described above in Example 1. PBMC from three donors were employed: one who had been previously shown to respond to TbH9 but not Tb38-1 (donor 131); one who had been shown to respond to Tb38-1 but not TbH9 (donor 184); and one who had been shown to respond to both antigens (donor 201). The results of these studies (Figs. 5-7, respectively) demonstrate the functional activity of both the antigens in the fusion protein.

A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and DPEP was prepared as follows.

Each of the DNA constructs TbRa3, 38 kD and Tb38-1 were modified by PCR and cloned into vectors essentially as described above, with the primers PDM-69 (SEQ ID NO:150 and PDM-83 (SEQ ID NO: 205) being used for amplification of the Tb38-1A fragment. Tb38-1A differs from Tb38-1 by a DraI site at the 3' end of the coding region that keeps the final amino acid intact while creating a blunt restriction site that is in frame. The TbRa3/38kD/Tb38-1A fusion was then transferred to pET28b using NdeI and EcoRI sites.

DPEP DNA was used to perform PCR using the primers PDM-84 and PDM-85 (SEQ ID NO: 206 and 207, respectively) and 1 μ l DNA at 50 ng/ μ l. Denaturation at 94 °C was performed for 2 min, followed by 10 cycles of 96 °C for 15 sec, 68 °C for 15 sec and 72 °C for 1.5 min; 30 cycles of 96 °C for 15 sec, 64 °C for 15 sec and 72 °C for 1.5 min; and finally by 72 °C for 4 min. The DPEP PCR fragment was digested with EcoRI and Eco72I and clones directly into the pET28Ra3/38kD/38-1A construct which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-2) are provided in SEQ ID NO: 208 and 209, respectively.

The reactivity of the fusion protein TbF-2 with sera from *M. tuberculosis*-infected patients was examined by ELISA using the protocol described above. The results of these studies (Table 11) demonstrate that all four antigens function independently in the fusion protein.

TABLE 11
 REACTIVITY OF TbF-2 FUSION RECOMBINANT WITH TB AND NORMAL SERA

Serum ID	Status	TbF OD450	Status	TbF-2 OD450	Status	ELISA Reactivity			
						38 kD	TbRa3	Tb38-1	DPEP
B931-40	TB	0.57	+	0.321	+	-	+	-	+
B931-41	TB	0.601	+	0.396	+	+	+	+	-
B931-109	TB	0.494	+	0.404	+	+	+	±	-
B931-132	TB	1.502	-	1.292	+	+	+	+	±
5004	TB	1.806	+	1.666	-	±	±	+	-
15004	TB	2.862	+	2.468	+	+	+	+	-
39004	TB	2.443	+	1.722	+	-	-	-	-
68004	TB	2.871	-	2.575	+	+	-	-	-
99004	TB	0.691	-	0.971	-	-	-	-	-
107004	TB	0.875	+	0.732	-	-	±	-	-
92004	TB	1.632	-	1.394	-	+	±	±	-
97004	TB	1.491	+	1.979	+	+	±	-	+
118004	TB	3.182	+	3.045	+	+	±	-	-
173004	TB	3.644	-	3.578	+	+	-	+	-
175004	TB	3.332	-	2.916	-	-	+	-	-
274004	TB	3.696	-	3.716	+	-	+	-	-
276004	TB	3.243	-	2.56	-	-	-	-	-
282004	TB	1.249	-	1.234	-	-	-	-	-
289004	TB	1.373	+	1.17	-	-	-	-	-
308004	TB	3.708	-	3.355	-	-	+	-	-
314004	TB	1.663	-	1.399	-	-	-	+	-
317004	TB	1.163	-	0.92	-	-	-	-	-
312004	TB	1.709	-	1.453	-	-	-	-	-
380004	TB	0.238	-	0.461	-	-	±	-	-
451004	TB	0.18	-	0.2	-	-	-	-	-
478004	TB	0.188	-	0.469	-	-	-	-	±
410004	TB	0.384	-	2.392	+	±	-	-	-
411004	TB	0.306	-	0.874	-	-	-	-	-
421004	TB	0.357	-	1.456	+	-	-	-	-
528004	TB	0.047	-	0.196	-	-	-	-	-
A6-87	Normal	0.094	-	0.063	-	-	-	-	-
A6-88	Normal	0.214	-	0.19	-	-	-	-	-
A6-89	Normal	0.248	-	0.125	-	-	-	-	-
A6-90	Normal	0.179	-	0.206	-	-	-	-	-
A6-91	Normal	0.135	-	0.151	-	-	-	-	-
A6-92	Normal	0.064	-	0.097	-	-	-	-	-
A6-93	Normal	0.072	-	0.098	-	-	-	-	-
A6-94	Normal	0.072	-	0.064	-	-	-	-	-
A6-95	Normal	0.125	-	0.159	-	-	-	-	-
A6-96	Normal	0.121	-	0.12	-	-	-	-	-
Cut-off		0.284		0.266					

A fusion protein containing TbRa3, the antigen 38kD, Tb38-1 and TbH4 was prepared as follows.

Genomic *M. tuberculosis* DNA was used to PCR full-length TbH4 (FL TbH4) with the primers PDM-157 and PDM-160 (SEQ ID NO: 348 and 349, respectively) and 2 μ l DNA at 100 ng/ μ l. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 61 °C for 20 sec and 72 °C for 5 min; and finally by annealing at 72 °C for 10 min. The FL TbH4 PCR fragment was digested with EcoRI and Sca I (New England Biolabs.) and cloned directly into the pET28Ra3/38kD/38-1A construct described above which was digested with DraI and EcoRI. The fusion construct was confirmed to be correct by DNA sequencing. Recombinant protein was prepared as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-6) are provided in SEQ ID NO: 350 and 351, respectively.

A fusion protein containing the antigen 38kD and DPEP separated by a linker was prepared as follows.

38 kD DNA was used to perform PCR using the primers PDM-176 and PDM-175 (SEQ ID NO: 352 and 353, respectively), and 1 μ l PET28Ra3/38kD/38-1/Ra2A-12 DNA at 110 ng/ μ l. Denaturation at 96 °C was performed for 2 min, followed by 40 cycles of 96 °C for 30 sec, 71 °C for 15 sec and 72 °C for 5 min and 40 sec; and finally by annealing at 72 °C for 4 min. The two sets of primers PDM-171, PDM-172, and PDM-173, PDM-174 were annealed by heating to 95 °C for 2 min and then ramping down to 25 °C slowly at 0.1 °C/sec. DPEP DNA was used to perform PCR as described above. The 38 kD fragment was digested with Eco RI (New England Biolabs) and cloned into a modified pT7 Δ L2 vector which was cut with Eco 72 I (Promega) and Eco RI. The modified pT7 Δ L2 construct was designed to have a MGHHHHHH amino acid coding region in frame just 5' of the Eco 72 I site. The construct was digested with Kpn 2I (Gibco, BRL) and Pst I (New England Biolabs) and the annealed sets of phosphorylated primers (PDM-171, PDM-172 and PDM-173, PDM-174) were cloned in. The DPEP PCR fragment was digested with Eco RI and Eco 72 I and cloned into this second construct which was digested with Eco 47 III (New England Biolabs) and Eco RI. Ligations were done with a ligation kit from Panvera (Madison, WI). The resulting construct was digested with NdeI (New England Biolabs) and Eco RI, and transferred to a

modified pET28 vector. The fusion construct was confirmed to be correct by DNA sequencing.

Recombinant protein was prepared essentially as described above. The DNA and amino acid sequences for the resulting fusion protein (hereinafter referred to as TbF-8) are provided in SEQ ID NO: 354 and 355, respectively.

One of skill in the art will appreciate that the order of the individual antigens within the fusion protein may be changed and that comparable activity would be expected provided each of the epitopes is still functionally available. In addition, truncated forms of the proteins containing active epitopes may be used in the construction of fusion proteins.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purpose of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

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 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE: 05-MAY-1998
 - (C) CLASSIFICATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 766 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CGAGGCACCG	GTAGTTTGAA	CCAAACGCAC	AATCGACGGG	CAAACGAACG	GAAGAACACA	60
ACCATGAAGA	TGGTGAAATC	GATCGCCGCA	GGTCTGACCG	CCGCGGCTGC	AATCGGCGCC	120
GCTGCGGCCG	GTGTGACTTC	GATCATGGCT	GGCGGCCCGG	TCGTATACCA	GATGCAGCCG	180
GTCGTCTTCG	GCGCGCCACT	GCCGTTGGAC	CCGCGATCCG	CCCCTGACGT	CCCGACCGCC	240
GCCCAGTTGA	CCAGCCTGCT	CAACAGCCTC	GCCGATCCCA	ACGTGTCGTT	TGCGAACAAAG	300
GGCAGTCTGG	TCGAGGGCGG	CATCGGGGGC	ACCGAGGCGC	GCATCGCCGA	CCACAAGCTG	360
AAGAAGGCCG	CCGAGCACGG	GGATCTGCCG	CTGTCTTCA	GCGTGACGAA	CATCCAGCCG	420
GCGGCCCGCG	GTTCCGGCCAC	CGCCGACGTT	TCCGTCTCGG	GTCCGAAGCT	CTCGTCGCCG	480
GTCACGCAGA	ACGTACGTT	CGTGAATCAA	GGCGGCTGGA	TGCTGTCACG	CGCATCGGCG	540
ATGGAGTTGC	TGCAGGCCGC	AGGGNAACTG	ATTGGCGGGC	CGGNTTCAGC	CCGCTGTTCA	600
GCTACGCCGC	CCGCCTGGTG	ACGCGTCCAT	GTCGAACACT	CGCGCGTGTA	GCACGGTGCG	660
GTNTGCGCAG	GGNCGCACGC	ACCGCCCGGT	GCAAGCCGTC	CTCGAGATAG	GTGGTGNCTC	720
GNCACCAGNG	ANCACCCCN	NNTCGNCNNT	TCTCGNTGNT	GNATGA		766

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 752 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ATGCATCACC	ATCACCATCA	CGATGAAGTC	ACGGTAGAGA	CGACCTCCGT	CTTCCGCGCA	60
GACTTCCTCA	GCGAGCTGGA	CGTCCTGCG	CAAGCGGGTA	CGGAGAGCGC	GGTCTCCGGG	120
GTGGAAGGGC	TCCCGCCGGG	CTCGGCGTTG	CTGGTAGTCA	AACGAGGCC	CAACGCCGGG	180
TCCCGGTTCC	TACTCGACCA	AGCCATCACG	TCGGCTGGTC	GGCATCCCGA	CAGCGACATA	240
TTTCTCGACG	ACGTGACCGT	GAGCCGTCGC	CATGCTGAAT	TCCGGTTGGA	AAACAACGAA	300
TTCAATGTCT	TCGATGTCGG	GAGTCTCAAC	GGCACCTACG	TCAACCGCGA	GCCCCGTGGAT	360
TCGGCGGTGC	TGGCGAACGG	CGACGAGGTC	CAGATCGGCA	AGCTCCGGTT	GGTGTTCCTG	420
ACCGGACCCA	AGCAAGGCGA	GGATGACGGG	AGTACCGGGG	GCCCCGTGAGC	GCACCCGATA	480
GCCCCGCGCT	GGCCGGGATG	TCGATCGGGG	CGGTCTCTCC	ACCTGCTACG	ACCGGATTTT	540
CCCTGATGTC	CACCATCTCC	AAGATTCGAT	TCTTGGGAGG	CTTGAGGGTC	NGGGTGACCC	600
CCCCGCGGGC	CTCATTCTNG	GGTNTCGGCN	GGTTTCACCC	CNTACCNACT	GCCNCCCGGN	660
TTGCNAATTC	NTTCTTCNCT	GCCCNAAAG	GGACNNTTAN	CTTGCCGCTN	GAAANGGTNA	720
TCCNGGGCCC	NTCCTNGAAN	CCCCNTCCCC	CT			752

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 813 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATATGCATC	ACCATCACCA	TCACACTTCT	AACCGCCCCAG	CGCGTCGGGG	GCGTCGAGCA	60
CCACGCGACA	CCGGGCCCCGA	TCGATCTGCT	AGCTTGAGTC	TGGTCAGGCA	TCGTCTGTCAG	120
CAGCGCGATG	CCCTATGTTT	GTCGTGCACT	CAGATATCGC	GGCAATCCAA	TCTCCCGCCT	180

GCGGCCGGCG	GTGCTGCAAA	CTACTCCC	AGGAATTT	ACGTGCGCAT	CAAGATCTTC	240
ATGCTGGTCA	CGGCTGTCGT	TTTGCTCTGT	TGTTCCGGTG	TGGCCACGGC	CGCGCCCAAG	300
ACCTACTGCG	AGGAGTTGAA	AGGCACCGAT	ACCGGCCAGG	CGTGCCAGAT	TCAAATGTCC	360
GACCCGGCCT	ACAACATCAA	CATCAGCCTG	CCCAGTTACT	ACCCCGACCA	GAAGTCGCTG	420
GAAAATTACA	TCGCCCAGAC	GCGCGACAAG	TTCCTCAGCG	CGGCCACATC	GTCCACTCCA	480
CGCGAAGCCC	CCTACGAATT	GAATATCACC	TCGGCCACAT	ACCAGTCCGC	GATACCGCCG	540
CGTGGTACGC	AGGCCGTGGT	GCTCAMGGTC	TACCACAACG	CCGGCGGCAC	GCACCCAACG	600
ACCACGTACA	AGGCCTTCGA	TTGGGACCAG	GCCTATCGCA	AGCCAATCAC	CTATGACACG	660
CTGTGGCAGG	CTGACACCGA	TCCGCTGCCA	GTCGTCTTCC	CCATTGTTGC	AAGGTGAACT	720
GAGCAACGCA	GACCGGGACA	ACWGGTATCG	ATAGCCGCCN	AATGCCGGCT	TGGAACCCNG	780
TGAAATTATC	ACAACCTTCG	AGTCACNAAA	NAA			813

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 447 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGTATGAAC	ACGGCCGCGT	CCGATAACTT	CCAGCTGTCC	CAGGGTGGGC	AGGGATTTCG	60
CATTCCGATC	GGGCAGGCGA	TGGCGATCGC	GGGCCAGATC	CGATCGGGTG	GGGGGTCACC	120
CACCGTTTCAT	ATCGGGCCTA	CCGCCTTCCT	CGGCTTGGGT	GTTGTGCGACA	ACAACGGCAA	180
CGGCGCACGA	GTCCAACGCG	TGGTCGGGAG	CGTCCGGCG	GCAAGTCTCG	GCATCTCCAC	240
CGGCGACGTG	ATCACC	CGCG	TCGACGGCGC	TCCGATCAAC	TCGGCCACCG	300
CGCGCTTAAC	GGGCATCATC	CCGGTGACGT	CATCTCGGTG	AACTGGCAAA	CCAAGTCGGG	360
CGGCACGCGT	ACAGGGAACG	TGACATTGGC	CGAGGGACCC	CCGGCCTGAT	TTGTCGYGG	420
ATACCACCCG	CCGGCCGGCC	AATTGGA				447

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 604 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCCCACTGC	GGTCGCCGAG	TATGTCGCCC	AGCAAATGTC	TGGCAGCCGC	CCAACGGAAT	60
CCGGTGATCC	GACGTCGAG	GTTGTCGAAC	CCGCCGCCGC	GGAAGTATCG	GTCCATGCCT	120
AGCCCGGCGA	CGGCGAGCGC	CGGAATGGCG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGGGGC	180
CCGGCGACGG	NGAGCGCCGG	AATGGCGCGA	GTGAGGAGGT	GGNCAGTCAT	GCCCAGNGTG	240
ATCCAATCAA	CCTGNATTCG	GNCTGNNGGN	CCATTTGACA	ATCGAGGTAG	TGAGCGCAAA	300
TGAATGATGG	AAAACGGGNG	GNGACGTCCG	NTGTTCTGGT	GGTGNTAGGT	GNCTGNCTGG	360
NGTNGNGGNT	ATCAGGATGT	TCTTCGNCGA	AANCTGATGN	CGAGGAACAG	GGTGTNCCCG	420
NNANNCCNAN	GGNGTCCNAN	CCCNMNTCC	TCGNCGANAT	CANANAGNCG	NTTGATGNGA	480
NAAAAGGGTG	GANCAGNNVN	AANTNGNGGN	CCNAANAANC	NNNANNGNNG	NNAGNTNGNT	540
NNNTNTTNNC	ANNNNNNNTG	NNGNNGNNCN	NNNCAANCNN	NTNNNNNGNAA	NNGGNTTNTT	600
NAAT						604

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 633 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTGCANGTCG	AACCACCTCA	CTAAAGGGAA	CAAAAGCTNG	AGCTCCACCG	CGGTGGCGGC	60
CGCTCTAGAA	CTAGTGKATM	YYYCKGGCTG	CAGSAATYCG	GYACGAGCAT	TAGGACAGTC	120
TAACGGTCCT	GTTACGGTGA	TGGAATGACC	GACGACATCC	TGCTGATCGA	CACCGACGAA	180
CGGGTGCAGAA	CCCTCACCTT	CAACCGGCCG	CAGTCCCGYA	ACGCGCTCTC	GGCGGCGCTA	240
CGGGATCGGT	TTTTTCGCGY	GTTGGYCGAC	GCCGAGGYCG	ACGACGACAT	CGACGTCGTC	300
ATCCTCACCG	GYGCCGATCC	GGTGTCTGTC	GCCGGACTGG	ACCTCAAGGT	AGCTGGCCGG	360
GCAGACCGCG	CTGCCGGACA	TCTCACCGCG	GTGGGCGGCC	ATGACCAAGC	CGGTGATCGG	420
CGCGATCAAC	GGCGCCGCGG	TCACCGGCGG	GCTCGAACTG	GCGCTGTACT	GCGACATCCT	480
GATCGCCTCC	GAGCACGCCC	GCTTCGNCGA	CACCCACGCC	CGGGTGGGGC	TGCTGCCAC	540
CTGGGGACTC	AGTGTGTGCT	TGCCGCAAAA	GGTCGGCATC	GGNCTGGGCC	GGTGGATGAG	600
CCTGACCGGC	GACTACCTGT	CCGTGACCGA	CGC			633

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1362 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CGACGACGAC	GGCGCCGGAG	AGCGGGCGCG	AACGGCGATC	GACGCGGCCC	TGGCCAGAGT	60
CGGCACCACC	CAGGAGGGAG	TGGAATCATG	AAATTTGTCA	ACCATATTGA	GCCCCTCGCG	120
CCCCGCCGAG	CCGCGCGCGC	GGTCGCGGAG	GTCTATGCCG	AGGCCCGCCG	CGAGTTCGGC	180
CGGCTGCCCG	AGCCGCTCGC	CATGCTGTCC	CCGGACGAGG	GACTGCTCAC	CGCCGGCTGG	240
GCGACGTTGC	GCGAGACACT	GCTGGTGGGC	CAGGTGCCGC	GTGGCCGCAA	GGAAGCCGTC	300
GCCGCCCGCG	TGCGGGCCAG	CCTGCGCTGC	CCCTGGTGCG	TCGACGCACA	CACCACCATG	360
CTGTACGCGG	CAGGCCAAAC	CGACACCGCC	GCGGCGATCT	TGGCCGGCAC	AGCACCTGCC	420
GCCGGTGACC	CGAACGCGCC	GTATGTGGCG	TGGGCGGCAG	GAACCGGGAC	ACCGGCGGGA	480
CCGCCGGCAC	CGTTCGGCCC	GGATGTCGCC	GCCGAATACC	TGGGCACCGC	GGTGCAATTC	540
CACCTTCATC	CACGCCTGGT	CCTGGTGCTG	CTGGACGAAA	CCTTCCTGCC	GGGGGGCCCC	600
CGCGCCCAAC	AGCTCATGCG	CCGCGCCGGT	GGACTGGTGT	TCGCCCCGAA	GGTGCGCGCG	660
GAGCATCGGC	CGGGCCGCTC	CACCCGCCGG	CTCGAGCCGC	GAACGCTGCC	CGACGATCTG	720
GCATGGGCAA	CACCGTCCGA	GCCCATAGCA	ACCGCGTTCC	CCGCGCTCAG	CCACCACCTG	780
GACACCGCGC	CGCACCTGCC	GCCACCGACT	CGTCAGGTGG	TCAGGCGGGT	CGTGGGGTCG	840
TGGCACGGCG	AGCCAATGCC	GATGAGCAGT	CGCTGGACGA	ACGAGCACAC	CGCCGAGCTG	900
CCCGCCGACC	TGCACGCGCC	CACCCGTCTT	GCCCTGCTGA	CCGGCCTGGC	CCCGCATCAG	960
GTGACCGACG	ACGACGTCGC	CGCGGCCCGA	TCCCTGCTCG	ACACCGATGC	GGCGTGGTT	1020
GGCGCCCTGG	CCTGGGCCGC	CTTACCGGCC	GCGCGGCGCA	TCGGCACCTG	GATCGGCGCC	1080
GCCGCCGAGG	GCCAGGTGTC	GCGGCAAAAC	CCGACTGGGT	GAGTGTGCGC	GCCCTGTCCG	1140
TAGGGTGTCA	TCGCTGGCCC	GAGGGATCTC	GCGGCGGCGA	ACGGAGGTGG	CGACACAGGT	1200
GGAAGCTGCG	CCCACTGGCT	TGCGCCCCAA	CGCCGTCGTG	GGCGTTCCGT	TGGCCGCACT	1260
GGCCGATCAG	GTCGGCGCCG	GCCCTTGGCC	GAAGGTCCAG	CTCAACGTGC	CGTCACCGAA	1320
GGACCGGACG	GTCACCGGGG	GTCACCTGCG	GCGCCCAAGG	AA		1362

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1458 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GCGACGACCC	CGATATGCCG	GGCACCGTAG	CGAAAGCCGT	CGCCGACGCA	CTCGGGCGCG	60
GTATCGCTCC	CGTTGAGGAC	ATTCAGGACT	GCGTGGAGGC	CCGGCTGGGG	GAAGCCGGTC	120
TGGATGACGT	GGCCCGTGTT	TACATCATCT	ACCGGCAGCG	GCGCGCCGAG	CTGCGGACGG	180
CTAAGGCCTT	GCTCGGCGTG	CGGGACGAGT	TAAAGCTGAG	CTTGGCGGCC	GTGACGGTAC	240
TGCGCGAGCG	CTATCTGCTG	CACGACGAGC	AGGGCCGGCC	GGCCGAGTCG	ACCGGCGAGC	300
TGATGGACCG	ATCGGCGCGC	TGTGTCGCGG	CGGCGGAGGA	CCAGTATGAG	CCGGGCTCGT	360
CGAGGCGGTG	GGCCGAGCGG	TTCGCCACGC	TATTACGCAA	CCTGGAATTC	CTGCCGAATT	420
CGCCACGTT	GATGAACTCT	GGCACCGACC	TGGGACTGCT	CGCCGGCTGT	TTTGTTCCTG	480
CGATTGAGGA	TTCGCTGCAA	TCGATCTTTG	CGACGCTGGG	ACAGGCCGCC	GAGCTGCAGC	540
GGGCTGGAGG	CGGCACCGGA	TATGCGTTCA	GCCACCTGCG	ACCCGCCGGG	GATCGGGTGG	600
CCTCCACGGG	CGGCACGGCC	AGCGGACCGG	TGTCGTTTCT	ACGGCTGTAT	GACAGTGCCG	660
CGGGTGTGGT	CTCCATGGGC	GGTCGCGCGC	GTGGCGCCTG	TATGGCTGTG	CTTGATGTGT	720
CGCACCCGGA	TATCTGTGAT	TTCGTCACCG	CCAAGGCCGA	ATCCCCCAGC	GAGCTCCCGC	780
ATTTCAACCT	ATCGGTTGGT	GTGACCGACG	CGTTCCTGCG	GGCCGTCGAA	CGCAACGGCC	840
TACACCGGCT	GGTCAATCCG	CGAACCGGCA	AGATCGTCGC	GCGGATGCCC	GCCGCCGAGC	900
TGTTGACGCG	CATCTGCAAA	GCCGCGCAGC	CCGGTGGCGA	TCCCGGGCTG	GTGTTTCTCG	960
ACACGATCAA	TAGGGCAAAC	CCGGTGCCCG	GGAGAGGCCG	CATCGAGGCG	ACCAACCCGT	1020
GCGGGGAGGT	CCCACTGCTG	CCTTACGAGT	CATGTAATCT	CGGCTCGATC	AACCTCGCCC	1080
GGATGCTCGC	CGACGGTCGC	GTGACTGGG	ACCGGCTCGA	GGAGGTCGCC	GGTGTGGCGG	1140
TGCGGTTCCCT	TGATGACGTC	ATCGATGTCA	GCCGCTACCC	CTTCCCCGAA	CTGGGTGAGG	1200
CGGCCCCGCG	CACCCGCAAG	ATCGGGCTGG	GAGTCATGGG	TTTGGCGGAA	CTGCTTGCCG	1260
CACTGGGTAT	TCCGTACGAC	AGTGAAGAAG	CCGTGCGGTT	AGCCACCCGG	CTCATGCGTC	1320
GCATACAGCA	GGCGGCGCAC	ACGGCATCGC	GGAGGCTGGC	CGAAGAGCGG	GGCGCATTC	1380
CGGCGTTTAC	CGATAGCCGG	TTCGCGCGGT	CGGGCCCCGAG	GCGCAACGCA	CAGGTCACCT	1440
CCGTCGCTCC	GACGGGCA					1458

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 862 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGGTGTAAT	CGTGCTGGAT	CTGGAACCGC	GTGGCCCCGCT	ACCTACCGAG	ATCTACTGGC	60
GGCGCAGGGG	GCTGGCCCTG	GGCATCGCGG	TCGTCGTAAGT	CGGGATCGCG	GTGGCCATCG	120
TCATCGCCTT	CGTCGACAGC	AGCGCCGGTG	CCAAACCGGT	CAGCGCCGAC	AAGCCGGCCT	180
CCGCCCAGAG	CCATCCGGGC	TCGCGGGCAC	CCCAAGCACC	CCAGCCGGCC	GGGCAAACCG	240
AAGGTAACGC	CGCCGCGGCC	CCGCCGCGAG	GCCAAAACCC	CGAGACACCC	ACGCCACCCG	300
CCGCGGTGCA	GCCGCCGCCG	GTGCTCAAGG	AAGGGGACGA	TTGCCCCGAT	TCGACGCTGG	360
CCGTCAAAGG	TTTGACCAAC	GCGCCGCGAGT	ACTACGTCGG	CGACCAGCCG	AAGTTACCA	420
TGGTGGTCAC	CAACATCGGC	CTGGTGTCTT	GTAACGCGCA	CGTTGGGGCC	GCGGTGTTGG	480
CCGCCTACGT	TTACTCGCTG	GACAACAAGC	GGTTGTGGTC	CAACCTGGAC	TGCGCGCCCT	540
CGAATGAGAC	GCTGGTCAAG	ACGTTTTCCC	CCGGTGAGCA	GGTAACGACC	GCGGTGACCT	600

GGACCGGGAT GGGATCGGCG CCGCGCTGCC CATTGCCGCG GCCGGCGATC GGGCCGGGCA	660
CCTACAATCT CGTGGTACAA CTGGGCAATC TGCGCTCGCT GCCGGTTCCG TTCATCCTGA	720
ATCAGCCGCC GCCGCCGCC GGGCCGGTAC CCGCTCCGGG TCCAGCGCAG GCGCCTCCGC	780
CGGAGTCTCC CGCGCAAGGC GGATAATTAT TGATCGCTGA TGGTCGATTC CGCCAGCTGT	840
GACAACCCCT CGCCTCGTGC CG	862

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 622 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TTGATCAGCA CCGGCAAGGC GTCACATGCC TCCCTGGGTG TGCAGGTGAC CAATGACAAA	60
GACACCCCGG GCGCCAAGAT CGTCGAAGTA GTGGCCGGTG GTGCTGCCGC GAACGCTGGA	120
GTGCCGAAGG GCGTCGTTGT CACCAAGGTC GACGACCGCC CGATCAACAG CGCGGACGCG	180
TTGGTTGCCG CCGTGCGGTC CAAAGCGCCG GCGGCCACGG TGGCGCTAAC CTTTCAGGAT	240
CCCTCGGGCG GTAGCCGCAC AGTGCAAGTC ACCCTCGGCA AGGCGGAGCA GTGATGAAGG	300
TCGCCGCGCA GTGTTCAAAG CTCGGATATA CCGGTGGCACC CATGGAACAG CGTGCGGAGT	360
TGGTGGTTGG CCGGGCACTT GTCGTCGTCG TTGACGATCG CACGGCGCAC GGCGATGAAG	420
ACCACAGCGG GCCGCTTGTC ACCGAGCTGC TCACCGAGGC CGGGTTTGTT GTCGACGGCG	480
TGGTGGCGGT GTCGGCCGAC GAGGTCGAGA TCCGAAATGC GCTGAACACA GCGGTGATCG	540
GCGGGGTGGA CCTGGTGGTG TCGGTCGGCG GGACCGNGT GACGNCTCGC GATGTCACCC	600
CGGAAGCCAC CCGNGACATT CT	622

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1200 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GGCGCAGCGG TAAGCCTGTT GGCCGCCGGC ACACTGGTGT TGACAGCATG CGGCGGTGGC	60
ACCAACAGCT CGTCGTCAGG CGCAGGCGGA ACGTCTGGGT CGGTGCACCTG CGGCGGCAAG	120
AAGGAGCTCC ACTCCAGCGG CTCGACCGCA CAAGAAAATG CCATGGAGCA GTTCGTCTAT	180
GCCTACGTGC GATCGTGCCC GGGCTACACG TTGGACTACA ACGCCAACGG GTCCGGTGCC	240
GGGGTGACCC AGTTTCTCAA CAACGAAACC GATTTTCGCC GTCGCGATGT CCCGTTGAAT	300
CCGTCGACCG GTCAACCTGA CCGGTCGGCG GAGCGGTGCG GTTCCCCGGC ATGGGACCTG	360
CCGACGGTGT TCGGCCCCGAT CGCGATCACC TACAATATCA AGGGCGTGAG CACGCTGAAT	420
CTTGACGGAC CCACTACCGC CAAGATTTTC AACGGCACCA TCACCGTGTG GAATGATCCA	480
CAGATCCAAG CCCTCAACTC CGGCACCGAC CTGCCGCCAA CACCGATTAG CGTTATCTTC	540
CGCAGCGACA AGTCCGGTAC GTCGGACAAC TTCCAGAAAT ACCTCGACGG TGTATCCAAC	600
GGGGCGTGGG GCAAAGGCGC CAGCGAAACG TTCAGCGGGG GCGTCGGCGT CGGCGCCAGC	660
GGAACAACG GAACGTCGGC CCTACTGCAG ACGACCGACG GGTGCGATCAC CTACAACGAG	720
TGGTCGTTTG CCGTGGGTAA GCAGTTGAAC ATGGCCCAGA TCATCACGTC GGCGGGTCCG	780
GATCCAGTGG CGATCACCAC CGAGTCGGTC GGTAAGACAA TCGCCGGGGC CAAGATCATG	840
GGACAAGGCA ACGACCTGGT ATTGGACAG TCGTCGTTCT ACAGACCCAC CCAGCCTGGC	900
TCTTACCCGA TCGTGCTGGC GACCTATGAG ATCGTCTGCT CGAAATACCC GGATGCGACG	960
ACCGGTACTG CGGTAAGGGC GTTTATGCAA GCCGCGATTG GTCCAGGCCA AGAAGGCTG	1020

GACCAATACG GCTCCATTCC GTTGCCCAAA TCGTTCCAAG CAAAATTGGC GGCCGCGGTG	1080
AATGCTATTT CTTGACCTAG TGAAGGGAAT TCGACGGTGA GCGATGCCGT TCCGCGAGTA	1140
GGGTCGCAAT TTGGGCCGTA TCAGCTATTG CGGCTGCTGG GCCGAGGCGG GATGGGCGAG	1200

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1155 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCAAGCAGCT GCAGGTCGTG CTGTTTCGACG AACTGGGCAT GCCGAAGACC AAACGCACCA	60
AGACCGGCTA CACCACGGAT GCCGACGCGC TGCAGTCGTT GTTCGACAAG ACCGGGCATC	120
CGTTTCTGCA ACATCTGCTC GCCCACC GCG	180
GGTTGCTCCA AGCGGTGGCC GCCGACGGCC GCATCCACAC CACGTTCAAC CAGACGATCG	240
CCGCGACCGG CCGGCTCTCC TCGACCGAAC CCAACCTGCA GAACATCCCG ATCCGCACCG	300
ACGCGGGCCG GCGGATCCGG GACGCTTCG TGGTCGGGGA CGGTTACGCC GAGTTGATGA	360
CGGCCGACTA CAGCCAGATC GAGATGCGGA TCATGGGGCA CCTGTCCGGG GACGAGGGCC	420
TCATCGAGGC GTTCAACACC GGGGAGGACC TGTATTCTGT CGTCGCGTCC CGGGTGTTTCG	480
GTGTGCCCAT CGACGAGGTC ACCGGCGAGT TGCGGCGCCG GGTCAAGGCG ATGTCCTACG	540
GGCTGGTTTA CGGGTTGAGC GCCTACGGCC TGTGCGAGCA GTTGAAAATC TCCACCGAGG	600
AAGCCAACGA GCAGATGGAC GCGTATTTTCG CCCGATTCCG CGGGGTGCGC GACTACCTGC	660
GCGCCGTAGT CGAGCGGGCC CGCAAGGACG GTTACACCTC GACGGTGCTG GGCCGTCGCC	720
GCTACCTGCC CGAGCTGGAC AGCAGCAACC GTCAAGTGCG GGAGGCCGCC GAGCGGGCGG	780
CGCTGAACGC GCCGATCCAG GGCAGCGCGG CCGACATCAT CAAGGTGGCC ATGATCCAGG	840
TCGACAAGGC GCTCAACGAG GCACAGCTGG CGTCGCGCAT GCTGCTGCAG GTCCACGACG	900
AGCTGCTGTT CGAAATCGCC CCCGGTGAAC GCGAGCGGGT CGAGGCCCTG GTGCGCGACA	960
AGATGGGCGG CGCTTACCCG CTCGACGTCC CGTTGGAGGT GTCGGTGGGC TACGGCCGCA	1020
GCTGGGACGC GCGGCGCAC TGAGTGCCGA GCGTGCACTT GGGGCGGGAA TTCGGCGATT	1080
TTTCCGCCCT GAGTTCACGC TCGGCGCAAT CGGGACCGAG TTTGTCCAGC GTGTACCCGT	1140
CGAGTAGCCT CGTCA	1155

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1771 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCGCCGTC TGGTGTGTTGA ACGGTTTTTAC CGGTCGGCAT CGGCACGGGC GTTGCCGGGT	60
TCGGGCCTCG GGTGGGCGAT CGTCAAACAG GTGGTGCTCA ACCACGGCGG ATTGCTGCGC	120
ATCGAAGACA CCGACCCAGG CGGCCAGCCC CCTGGAACGT CGATTTACGT GCTGCTCCCC	180
GGCCGTCGGA TGCCGATTCC GCAGCTTCCC GGTGCGACGG CTGGCGCTCG GAGCACGGAC	240
ATCGAGAACT CTCGGGGTTC GGCGAACGTT ATCTCAGTGG AATCTCAGTC CACGCGCGCA	300
ACCTAGTTGT GCAGTTACTG TTGAAAGCCA CACCCATGCC AGTCCACGCA TGGCCAAGTT	360
GGCCCGAGTA GTGGGCCTAG TACAGGAAGA GCAACCTAGC GACATGACGA ATCACCACG	420
GTATTGCGCA CCGCCGACG AGCCGGGAAC CCCAGGTTAT GCTCAGGGGC AGCAGCAAAC	480
GTACAGCCAG CAGTTCGACT GGCGTTACCC ACCGTCCCCG CCCCCGACG CAACCCAGTA	540
CCGTCAACCC TACGAGGCGT TGGGTGGTAC CCGGCCGGGT CTGATACCTG GCGTGATTCC	600

GACCATGACG	CCCCCTCCTG	GGATGGTTCG	CCAACGCCCT	CGTGCAGGCA	TGTTGGCCAT	660
CGGCGCGGTG	ACGATAGCGG	TGGTGTCCGC	CGGCATCGGC	GGCGCGGCCG	CATCCCTGGT	720
CGGGTTCAAC	CGGGCACCCG	CCGGCCCCAG	CGGCGGCCCA	GTGGCTGCCA	GCGCGGCGCC	780
AAGCATCCCC	GCAGCAAACA	TGCCGCCGGG	GTCGGTCGAA	CAGGTGGCGG	CCAAGGTGGT	840
GCCCCAGTGC	GTCATGTTGG	AAACCGATCT	GGGCCGCCAG	TCGGAGGAGG	GCTCCGGCAT	900
CATTCTGTCT	GCCGAGGGGC	TGATCTTGAC	CAACAACCAC	GTGATCGCGG	CGGCCGCCAA	960
GCCTCCCCTG	GGCAGTCCGC	CGCCGAAAAC	GACGGTAACC	TTCTCTGACG	GGCGGACCGC	1020
ACCCTTCACG	GTGGTGGGGG	CTGACCCAC	CAGTGATATC	GCCGTCGTCC	GTGTTCAGGG	1080
CGTCTCCGGG	CTCACCCCGA	TCTCCCTGGG	TTCCTCCTCG	GACCTGAGGG	TCGGTCAGCC	1140
GGTGTGGCG	ATCGGGTCGC	CGCTCGGTTT	GGAGGGCACC	GTGACCACGG	GGATCGTCAG	1200
CGCTCTCAAC	CGTCCAGTGT	CGACGACCGG	CGAGGCCGGC	AACCAGAAAC	CCGTGCTGGA	1260
CGCCATTGAG	ACCGACGCCG	CGATCAACCC	CGGTAACCTC	GGGGGCGCGC	TGGTGAACAT	1320
GAACGCTCAA	CTCGTCGGAG	TCAACTCGGC	CATTGCCACG	CTGGGCGCGG	ACTCAGCCGA	1380
TGCGCAGAGC	GGCTCGATCG	GTCTCGGTTT	TGCGATTCCA	GTCGACCAGG	CCAAGCGCAT	1440
CGCCGACGAG	TTGATCAGCA	CCGGCAAGGC	GTCACATGCC	TCCCTGGGTG	TGCAGGTGAC	1500
CAATGACAAA	GACACCCCGG	GCGCCAAGAT	CGTCGAAGTA	GTGGCCGGTG	GTGCTGCCGC	1560
GAACGCTGGA	GTGCCGAAGG	GCGTCGTTGT	CACCAAGGTC	GACGACCGCC	CGATCAACAG	1620
CGCGGACGCG	TTGGTTGCCG	CCGTGCGGTC	CAAAGCGCCG	GGCGCCACGG	TGGCGCTAAC	1680
CTTTCAGGAT	CCCTCGGGCG	GTAGCCGCAC	AGTGCAAGTC	ACCCTCGGCA	AGGCGGAGCA	1740
GTGATGAAGG	TCGCCGCGCA	GTGTTCAAAG	C			1771

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCCACCGCG	GTGGCGGCCG	CTCTAGAACT	AGTGGATCCC	CCGGGCTGCA	GGAATTCGGC	60
ACGAGGATCC	GACGTGCGAG	GTTGTGCAAC	CCGCCGCCGC	GGAAGTATCG	GTCCATGCCT	120
AGCCCGGCGA	CGGCGAGCGC	CGGAATGGCG	CGAGTGAGGA	GGCGGGCAAT	TTGGCGGGGC	180
CCGGCGACGG	CGAGCGCCGG	AATGGCGCGA	GTGAGGAGGC	GGGCAGTCAT	GCCCAGCGTG	240
ATCCAATCAA	CCTGCATTCT	GCCTGCGGGC	CCATTTGACA	ATCGAGGTAG	TGAGCGCAAA	300
TGAATGATGG	AAAACGGGCG	GTGACGTCCG	CTGTTCTGGT	GGTGCTAGGT	GCCTGCCTGG	360
CGTTGTGGCT	ATCAGGATGT	TCTTCGCCGA	AACCTGATGC	CGAGGAACAG	GGTGTTCCTG	420
TGAGCCCGAC	GGCGTCCGAC	CCCGCGCTCC	TCGCCGAGAT	CAGGCAGTCG	CTTGATGCGA	480
CAAAAGGGTT	GACCAGCGTG	CACGTAGCGG	TCCGAACAAC	CGGGAAAGTC	GACAGCTTGC	540
TGGGTATTAC	CAGTGCCGAT	GTCGACGTCC	GGGCCAATCC	GCTCGCGGCA	AAGGGCGTAT	600
GCACCTACAA	CGACGAGCAG	GGTGTCCTGT	TTCGGGTACA	AGGCGACAAC	ATCTCGGTGA	660
AACTGTTTCA	CGACTGGAGC	AATCTCGGCT	CGATTTCTGA	ACTGTCAACT	TCACGCGTGC	720
TCGATCCTGC	CGCTGGGGTG	ACGCAGCTGC	TGTCCGGTGT	CACGAACCTC	CAAGCGCAAG	780
GTACCGAAGT	GATAGACGGA	ATTTCGACCA	CCAAAATCAC	CGGGACCATC	CCCAGGAGCT	840
CTGTCAAGAT	GCTTGATCCT	GGCGCCAAGA	GTGCAAGGCC	GGCGACCGTG	TGGATTGCCC	900
AGGACGGCTC	GCACCACCTC	GTCCGAGCGA	GCATCGACCT	CGGATCCGGG	TCGATTGAGC	960
TCACGCAGTC	GAAATGGAAC	GAACCCGTCA	ACGTCGACTA	GGCCGAAGTT	GCGTCGACGC	1020
GTTGNTCGAA	ACGCCCTTGT	GAACGGTGTC	AACGGNAC			1058

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 542 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAATTCGGCA	CGAGAGGTGA	TCGACATCAT	CGGGACCAGC	CCCACATCCT	GGGAACAGGC	60
GGCGGCGGAG	GCGGTCCAGC	GGGCGCGGGA	TAGCGTCGAT	GACATCCGCG	TCGCTCGGGT	120
CATTGAGCAG	GACATGGCCG	TGGACAGCGC	CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	180
AGTGTCGTTC	AAGATGAGGC	CGGCGCAACC	GCGCTAGCAC	GGGCCGGCGA	GCAAGACGCA	240
AAATCGCACG	GTTTGCGGTT	GATTCGTGCG	ATTTGTGTGC	TGCTCGCCGA	GGCCTACCAG	300
GCGCGGCCCA	GGTCCGCGTG	CTGCCGTATC	CAGGCGTGCA	TCGCGATTCC	GGCGGCCACG	360
CCGAGATTAA	TGCTTCGCGT	CGACCCGAAC	TGGGCGATCC	GCCGGNGAGC	TGATCGATGA	420
CCGTGGCCAG	CCCGTCGATG	CCCGAGTTGC	CCGAGGAAAC	GTGCTGCCAG	GCCGGTAGGA	480
AGCGTCCGTA	GGCGGCGGTG	CTGACCGGCT	CTGCCTGCGC	CCTCAGTGCG	GCCAGCGAGC	540
GG						542

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 913 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CGGTGCCGCC	CGCGCCTCCG	TTGCCCCCAT	TGCCGCCGTC	GCCGATCAGC	TGCGCATCGC	60
CACCATCACC	GCCTTTGCCG	CCGGCACC GC	CGGTGGCGCC	GGGGCCGCCG	ATGCCACCGC	120
TTGACCCCTG	CCGCCGGCGC	CGCCATTGCC	ATACAGCACC	CCGCCGGGGG	CACCGTTACC	180
GCCGTCGCCA	CCGTCGCCGC	CGCTGCCGTT	TCAGGCCGGG	GAGGCCGAAT	GAACCGCCGC	240
CAAGCCCCGC	GCCGGCACC	TTGCCGCCCT	TTCCGCCCGC	CCCGCCGGCG	CCGCCAATTG	300
CCGAACAGCC	AMGCACCGTT	GCCGCCAGCC	CCGCCGCCGT	TAACGGCGCT	GCCGGGCGCC	360
GCCGCCGGAC	CCGCCATTAC	CGCCGTTCCC	GTTCCGGTGCC	CCGCCGTTAC	CGGCGCCGCC	420
GTTTGCCGCC	AATATTCGGC	GGGCACCGCC	AGACCCGCCG	GGGCCACCAT	TGCCGCCGGG	480
CACCGAAACA	ACAGCCCAAC	GGTGCCGCCG	GCCCCGCCGT	TTGCCGCCAT	CACCGGCCAT	540
TCACCGCCAG	CACCGCCGTT	AATGTTTATG	AACCCGGTAC	CGCCAGCGCG	GCCCCATTG	600
CCGGGCGCCG	GAGNGCGTGC	CCGCCGGCGC	CGCCAACGCC	CAAAAGCCCG	GGGTTGCCAC	660
CGGCCCCGCC	GGACCCACCG	GTCCCCCGCA	TCCCCCGGTT	GCCGCCGGTG	CCGCCGCCAT	720
TGGTGCTGCT	GAAGCCGTTA	GCGCCGGTTC	CGCSGGTTCC	GGCGGTGGCG	CCNTGGCCGC	780
CGGCCCCGCC	GTTGCCGTAC	AGCCACCCCC	CGGTGGCGCC	GTTGCCGCCA	TTGCCGCCAT	840
TGCCGCCGTT	GCCGCCATTG	CCGCCGTTCC	CGCCGCCACC	GCCGGNTTGG	CCGCCGGCGC	900
CGCCGGCGGC	CGC					913

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1872 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GACTACGTTG	GTGTAGAAAA	ATCCTGCCGC	CCGGACCCCT	AAGGCTGGGA	CAATTTCTGA	60
TAGTACCCCC	GACACAGGAG	GTTACGGGAT	GAGCAATTCT	CGCCGCCGCT	CACTCAGGTG	120

GTCATGGTTG	CTGAGCGTGC	TGGCTGCCGT	CGGGCTGGGC	CTGGCCACGG	CGCCGGCCCA	180
GGCGGCCCCG	CCGGCCTTGT	CGCAGGACCG	GTTTCGCCGAC	TTCCCCGCGC	TGCCCCCTCGA	240
CCCGTCCGCG	ATGGTCGCCC	AAGTGGCGCC	ACAGGTGGTC	AACATCAACA	CCAAACTGGG	300
CTACAACAAC	GCCGTGGGCG	CCGGGACCGG	CATCGTCATC	GATCCCAACG	GTGTCTGTCT	360
GACCAACAAC	CACGTGATCG	CGGGCGCCAC	CGACATCAAT	GCGTTCAGCG	TCGGCTCCGG	420
CCAAACCTAC	GGCGTCGATG	TGGTCGGGTA	TGACCGCACC	CAGGATGTCT	CGGTGCTGCA	480
GCTGCGCGGT	GCCGGTGGCC	TGCCGTCCGC	GGCGATCGGT	GGCGGCGTCG	CGGTTGGTGA	540
GCCCCGTCGT	GCGATGGGCA	ACAGCGGTGG	GCAGGGCGGA	ACGCCCCGTG	CGGTGCCTGG	600
CAGGATTGGTC	GCGCTCGGCC	AAACCGTGCA	GGCGTCGGAT	TCGCTGACCG	GTGCCGAAGA	660
GACATTGAAC	GGGTTGATCC	AGTTCGATGC	CGCAATCCAG	CCCGGTGATT	CGGGCGGGCC	720
CGTCGTCAAC	GGCCTAGGAC	AGGTGGTCGG	TATGAACACG	GCCGCGTCCG	ATAACTTCCA	780
GCTGTCCCAG	GGTGGGCAGG	GATTCGCCAT	TCCGATCGGG	CAGGCGATGG	CGATCGCGGG	840
CCAAATCCGA	TCGGGTGGGG	GGTCACCCAC	CGTTCATATC	GGGCCTACCG	CCTTCTCTCG	900
CTTGGGTGTT	GTGACAACA	ACGGCAACGG	CGCACGAGTC	CAACGCGTGG	TCGGAAGCGC	960
TCCGGCGGCA	AGTCTCGGCA	TCTCCACCGG	CGACGTGATC	ACCGCGGTCT	ACGGCGCTCC	1020
GATCAACTCG	GCCACCGCGA	TGGCGGACGC	GCTTAACGGG	CATCATCCCG	GTGACGTCAT	1080
CTCGGTGAAC	TGGCAAACCA	AGTCGGGCGG	CACGCGTACA	GGGAACGTGA	CATTGGCCGA	1140
GGGACCCCCG	GCCTGATTTG	TCGCGGATAC	CACCCGCCCG	CCGGCCAATT	GGATTGGCGC	1200
CAGCCGTGAT	TGCCGCGTGA	GCCCCCGAGT	TCCGTCTCCC	GTGCGCGTGG	CATTGTGGAA	1260
GCAATGAACG	AGGCAGAACA	CAGCGTTGAG	CACCCCTCCG	TGCAGGGCAG	TTACGTCGAA	1320
GGCGGTGTGG	TCGAGCATCC	GGATGCCAAG	GACTTCGGCA	GCGCCGCCGC	CCTGCCCCGC	1380
GATCCGACCT	GGTTTAAGCA	CGCCGTCTTC	TACGAGGTGC	TGGTCCGGGC	GTTCTTCGAC	1440
GCCAGCGCGG	ACGGTTCGCG	CGATCTGCGT	GGACTCATCG	ATCGCCTCGA	CTACCTGCAG	1500
TGGCTTGCCA	TCGACTGCAT	CTGTTGCCGC	CGTTCCTACG	ACTCACCCTG	GCGCGACGGC	1560
GGTTACGACA	TTTCGCGACTT	CTACAAGGTG	CTGCCCCGAAT	TCGGCACCCT	CGACGATTTT	1620
GTGCGCCTGG	TCGACACCGC	TCACCGGCGA	GGTATCCGCA	TCATCACCCT	CCTGGTGATG	1680
AATCACACCT	CGGAGTCGCA	CCCCTGGTTT	CAGGAGTCCC	GCCGCGACCC	AGACGGACCG	1740
TACGGTGAAT	ATTACGTGTG	GAGCGACACC	AGCGAGCGCT	ACACCGACGC	CCGGATCATC	1800
TTCGTGCGAC	CCGAAGAGTC	GAAGTGGTCA	TTCGATCCTG	TCCGCCGACA	GTTNCTACTG	1860
GCACCGATTC	TT					1872

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCGCCGAA	ACCTGATGCC	GAGGAACAGG	GTGTTCCCGT	GAGCCCCGACG	GCGTCCGACC	60
CCGCGCTCCT	CGCCGAGATC	AGGCAGTCGC	TTGATGCGAC	AAAAGGGTTG	ACCAGCGTGC	120
ACGTAGCGGT	CCGAACAACC	GGGAAAGTCG	ACAGCTTGCT	GGGTATTACC	AGTGCCGATG	180
TCGACGTCCG	GGCCAATCCG	CTCGCGGCAA	AGGGCGTATG	CACCTACAAC	GACGAGCAGG	240
GTGTCCCCTT	TCGGGTACAA	GGCGACAACA	TCTCGGTGAA	ACTGTTTCGAC	GAATGGAGCA	300
ATCTCGGCTC	GATTTCTGAA	CTGTCAACTT	CACGCGTGCT	CGATCCTGCC	GCTGGGGTGA	360
CGCAGCTGCT	GTCCGGTGTC	ACGAACCTCC	AAGCGCAAGG	TACCGAAGTG	ATAGACGGAA	420
TTTCGACCAC	CAAAATCACC	GGGACCATCC	CCGCGAGCTC	TGTCAAGATG	CTTGATCCTG	480
GCGCCAAGAG	TGCAAGGCCG	GCGACCGTGT	GGATTGCCCA	GGACGGCTCG	CACCACCTCG	540
TCCGAGCGAG	CATCGACCTC	GGATCCGGGT	CGATTCAGCT	CACGCGATCG	AAATGGAACG	600
AACCCGTCAA	CGTCGACTAG	GCCGAAGTTG	CGTCGACGCG	TTGCTCGAAA	CGCCCTTGTG	660
AACGGTGTCA	ACGGCACCCG	AAAAGTGACC	CCCTGACGGC	ATCTGAAAAT	TGACCCCTTA	720
GACCGGGCGG	TTGGTGGTTA	TTCTTCGGTG	GTTCCGGCTG	GTGGGACGCG	GCCGAGGTCT	780
CGGTCTTTGA	GCCGGTAGCT	GTGCGCTTTG	AGGGCGACGA	CTTCAGCATG	GTGGACGAGG	840

CGGTCGATCA	TGGCGGCAGC	AACGACGTCG	TCGCCGCCGA	AAACCTCGCC	CCACCGGCCG	900
AAGGCCTTAT	TGGACGTGAC	GATCAAGCTG	GCCCCGTCAT	ACCGGGAGGA	CACCAGCTGG	960
AAGAAGAGGT	TGGCGGCCTC	GGGCTCAAAC	GGAATGTAAC	CGACTTCGTC	AACCACCAGG	1020
AGCGGATAGC	GGCCAAACCG	GGTGAGTTCG	GCGTAGATGC	GCCCCGGCGT	GTGAGCCTCG	1080
GCGAACCGTG	CTACCCATTC	GGCGGCGGTG	GCGAACAGCA	CCCGATGACC	GGCCTGACAC	1140
GCGCGTATCG	CCAGGCCGAC	CGCAAGATGA	GTCTTCCCCG	TGCCAGGCGG	GGCCCCAAAA	1200
CACGACGTTA	TCGCGGGCGG	TGATGAAATC	CAGGGTGCCC	AGATGTGCGA	TGGTGTGCGG	1260
TTTGAGGCCA	CGAGCATGCT	CAAAGTCGAA	CTCTTCCAAC	GACTTCCGAA	CCGGGAAGCG	1320
GGCGGCGCGG	ATGCGGCCCT	CACCACCATG	GGACTCCCCG	GCTGACACTT	CCCCGTGCAG	1380
GCAGGCGGCC	AGGTATTCTT	CGTGGCTCCA	GTTCTCGGCG	CGGGCGCGAT	CGGCCAGCCG	1440
GGACACTGAC	TCACGCAGGG	TGGGAGCTTT	CAATGCTCTT	GT		1482

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 876 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GAATTCGGCA	CGAGCCGGCG	ATAGCTTCTG	GGCCGCGGCC	GACCAGATGG	CTCGAGGGTT	60
CGTGCTCGGG	GCCACCGCCG	GGCGCACCAC	CCTGACCGGT	GAGGGCCTGC	AACACGCCGA	120
CGGTCACTCG	TTGCTGCTGG	ACGCCACCAA	CCCGGCGGTG	GTTGCCTACG	ACCCGGCCTT	180
CGCCTACGAA	ATCGGCTACA	TCGNGGAAAG	CGGACTGGCC	AGGATGTGCG	GGGAGAACCC	240
GGAGAACATC	TTCTTCTACA	TCACCGTCTA	CAACGAGCCG	TACGTGCAGC	CGCCGGAGCC	300
GGAGAACTTC	GATCCCGAGG	GCGTGCTGGG	GGGTATCTAC	CGNTATCACG	CGGCCACCGA	360
GCAACGCACC	AACAAGGNGC	AGATCCTGGC	CTCCGGGGTA	GCGATGCCCC	CGGCGCTGCG	420
GGCAGCACAG	ATGCTGGCCG	CCGAGTGGGA	TGTCGCCGCC	GACGTGTGGT	CGGTGACCAG	480
TTGGGGCGAG	CTAAACCGCG	ACGGGGTGGT	CATCGAGACC	GAGAAGCTCC	GCCACCCCGA	540
TCGGCCGGCG	GGCGTGCCCT	ACGTGACGAG	AGCGCTGGAG	AATGCTCGGG	GCCCCTGTAT	600
CGCGGTGTCT	GACTGGATGC	GCGCGGTCCC	CGAGCAGATC	CGACCGTGGG	TGCCGGGCAC	660
ATACCTCACG	TTGGGCACCG	ACGGGTTCCG	TTTTTCCGAC	ACTCGGCCCG	CCGGTCTGTC	720
TTACTTCAAC	ACCGACGCCG	AATCCCAGGT	TGGTCGCGGT	TTTGGGAGGG	GTTGGCCGGG	780
TCGACGGGTG	AATATCGACC	CATTGCGTGC	CGGTCGTGGG	CCGCCCCGCC	AGTTACCCCG	840
ATTCGACGAA	GGTGGGGGGT	TGCGCCCGAN	TAAGTT			876

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1021 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ATCCCCCGGG	GCTGCAGGAA	TTCGGCACGA	GAGACAAAAT	TCCACGCGTT	AATGCAGGAA	60
CAGATTGATA	ACGAATTAC	AGCGGCACAA	CAATATGTCG	CGATCGCGGT	TTATTTTCGAC	120
AGCGAAGACC	TGCCGCGAGT	GGCGAAGCAT	TTTTACAGCC	AAGCGGTCGA	GGAACGAAAC	180
CATGCAATGA	TGCTCGTGCA	ACACCTGCTC	GACCGCGACC	TTCGTGTGCA	AATTTCCCGGC	240
GTAGACACGG	TGCGAAACCA	GTTTCGACAGA	CCCCGCGAGG	CACTGGCGCT	GGCGCTCGAT	300
CAGGAACGCA	CAGTCACCGA	CCAGGTCGGT	CGGCTGACAG	CGGTGGCCCC	CGACGAGGGC	360
GATTTCCCTG	GCGAGCAGTT	CATGCAGTGG	TTCTTGACAG	AACAGATCGA	AGAGGTGGCC	420

TTGATGGCAA CCCTGGTGCG GGTGCGCGAT CGGGCCGGGG CCAACCTGTT CGAGCTAGAG	480
AACTTCGTCG CACGTGAAGT GGATGTGGCG CCGGCCGCAT CAGGCGCCCC GCACGCTGCC	540
GGGGGCCGCC TCTAGATCCC TGGGGGGGAT CAGCGAGTGG TCCCGTTCGC CCGCCCGTCT	600
TCCAGCCAGG CCTTGGTGCG GCCGGGGTGG TGAGTACCAA TCCAGGCCAC CCGACCTCC	660
CGGNAAAAGT CGATGTCCTC GTACTCATCG ACGTTCCAGG AGTACACCGC CCGGCCCTGA	720
GCTGCCGAGC GGTCAACGAG TTGCGGATAT TCCTTTAACG CAGGCAGTGA GGGTCCCACG	780
GCGGTTGGCC CGACCGCCGT GGCCGCACTG CTGGTCAGGT ATCGGGGGGT CTTGGCGAGC	840
AACAACGTCG GCAGGAGGGG TGGAGCCCGC CGGATCCGCA GACCGGGGGG GCGAAAACGA	900
CATCAACACC GCACGGGATC GATCTGCGGA GGGGGGTGCG GGAATACCGA ACCGGTGTAG	960
GAGCGCCAGC AGTTGTTTTT CCACCAGCGA AGCGTTTTTCG GGTCATCGGN GGCNNTTAAG	1020
T	1021

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CGTGCCGACG AACGGAAGAA CACAACCATG AAGATGGTGA AATCGATCGC CGCAGGTCTG	60
ACCGCCGCGG CTGCAATCGG CGCCGCTGCG GCCGGTGTGA CTTGATCAT GGCTGGCGGN	120
CCGGTCGTAT ACCAGATGCA GCCGGTCGTC TTCGGCGCGC CACTGCCGTT GGACCCGGNA	180
TCCGCCCCCTG ANGTCCCGAC CGCCGCCAG TGGACCAGNC TGCTCAACAG NCTCGNCGAT	240
CCCAACGTGT CGTTTNGAA CAAGGGNAGT CTGGTCGAGG GNGGNATCGG NGGNANCGAG	300
GGNGNGNATC GNCGANCA A	321

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TCTTATCGGT TCCGGTTGGC GACGGGTTTT GGGNGCGGGT GGTAAACCCG CTCGGCCAGC	60
CGATCGACGG GCGCGGAGAC GTCGACTCCG ATACTCGGCG CGCGCTGGAG CTCCAGGCGC	120
CCTCGGTGGT GNACCGGCAA GGCGTGAAGG AGCCGTTGNA GACCGGGATC AAGGCGATTG	180
ACGCGATGAC CCGATCGGC CGCGGGCAGC GCCAGCTGAT CATCGGGGAC CGCAAGACCG	240
GCAAAAACCG CCGTCTGTGT CGGACACCAT CCTCAAACCA GCGGGAAGAA CTGGGAGTCC	300
GGTGGATCCC AAGAAGCAGG TCGCCTTGTG TATACGTTGG CCATCGGGCA AGAAGGGGAA	360
CTTACCATCG CCG	373

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 352 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GTGACGCCGT GATGGGATTC CTGGGCGGGG CCGGTCCGCT GGCGGTGGTG GATCAGCAAC	60
TGGTTACCCG GGTGCCGCAA GGCTGGTCGT TTGCTCAGGC AGCCGCTGTG CCGGTGGTGT	120
TCTTGACGGC CTGGTACGGG TTGGCCGATT TAGCCGAGAT CAAGGCGGGC GAATCGGTGC	180
TGATCCATGC CCGTACCGGC GGTGTGGGCA TGGCGGCTGT GCAGCTGGCT CGCCAGTGGG	240
GCGTGGAGGT TTTCGTCACC GCCAGCCGTG GNAAGTGGGA CACGCTGCGC GCCATNGNGT	300
TTGACGACGA NCCATATCGG NGATTCCNC ACATNCGAAG TTCCGANGGA GA	352

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 726 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GAAATCCGCG TTCATTCCGT TCGACCAGCG GCTGGCGATA ATCGACGAAG TGATCAAGCC	60
GCGGTTCCGCG GCGCTCATGG GTCACAGCGA GTAATCAGCA AGTTCTCTGG TATATCGCAC	120
CTAGCGTCCA GTTGCTTGCC AGATCGCTTT CGTACCGTCA TCGCATGTAC CCGTTCCGCGT	180
GCCGCACGCT CATGCTGGCG GCGTGCATCC TGGCCACGGG TGTGGCGGGT CTCGGGGTCG	240
GCGCGCAGTC CGCAGCCCAA ACCGCGCCGG TGGCCGACTA CTAATGGTGC CCGGGGCAGC	300
CTTTCGACCC CGCATGGGGG CCCAATGGG ATCCCTACAC CTGCCATGAC GACTTCCACC	360
GCGACAGCGA CGGCCCCGAC CACAGCCGCG ACTACCCCGG ACCCATCCTC GAAGGTCCCC	420
TGCTTGACGA TCCCGGTGCT GCGCCGCCCG CCCCAGCTGC CCGTGGCGGC GCATAGCGCT	480
CGTTGACCGG GCCGCATCAG CGAATACGCG TATAAACCCG GCGGTGCCCC CCGCAAGCTA	540
CGACCCCCCG CCGGGCAGAT TTACGCTCCC GTGCCGATGG ATCGCGCCGT CCGATGACAG	600
AAAATAGGCG ACGGTTTTGG CAACCGCTT GAGGACGCTT GAAGGGAACC TGTCATGAAC	660
GGCGACAGCG CCTCCACCAT CGACATCGAC AAGGTTGTTA CCCGCACACC CGTTCCCGG	720
ATCGTG	726

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CGCGACGACG ACGAACGTCG GGCCACCAC CGCCTATGCG TTGATGCAGG CGACCGGGAT	60
GGTCGCCGAC CATATCCAAG CATGCTGGGT GCCCACTGAG CGACCTTTTG ACCAGCCGGG	120
CTGCCCCGATG GCGGCCCGGT GAAGTCATTG CGCCGGGGCT TGTGCACCTG ATGAACCCGA	180
ATAGGGAACA ATAGGGGGGT GATTGGCAG TTCAATGTCT GGTATGGCTG GAAATCCAAT	240
GGCGGGGCAT GCTCGGCGCC GACCAGGCTC GCGCAGGCGG GCCAGCCCGA ATCTGGAGGG	300
AGCACTCAAT GGCGGCGATG AAGCCCCGGA CCGGCGACGG TCCTTTGGAA GCAACTAAGG	360
AGGGGCGCGG CATTGTGATG CGAGTACCAC TTGAGGGTGG CCGTCCGCTG GTCGTCGAGC	420
TGACACCCGA CGAAGCCGCC GCACTGGGTG ACGAACTCAA AGGCGTTACT AGCTAAGACC	480
AGCCCAACGG CGAATGGTCG GCGTTACGCG CACACCTTCC GGTAGATGTC CAGTGTCTGC	540
TCGGCGATGT ATGCCAGGA GAACTCTTGG ATACAGCGCT	580

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 160 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

AACGGAGGCG CCGGGGGTTT TGGCGGGGCC GGGGCGGTCG GCGGCAACGG CGGGGCCGGC	60
GGTACCGCCG GGTGTTCCG TGTCGGCGGG GCCGGTGGGG CCGGAGGCAA CGGCATCGCC	120
GGTGTACCG GTACGTCGGC CAGCACACCG GGTGGATCCG	160

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

GACACCGATA CGATGGTGAT GTACGCCAAC GTTGTGACGA CGCTCGAGGC GTTCACGATC	60
CAGCGCACAC CCGACGGCGT GACCATCGGC GATGCGGCCC CGTTCGCGGA GGCGGCTGCC	120
AAGGCGATGG GAATCGACAA GCTGCGGGTA ATTCATACCG GAATGGACCC CGTCGTCGCT	180
GAACGCGAAC AGTGGGACGA CGGCAACAAC ACGTTGGCGT TGGCGCCCGG TGTCGTTGTC	240
GCCTACGAGC GCAACGTACA GACCAACGCC CG	272

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 317 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GCAGCCGGTG GTTCTCGGAC TATCTGCGCA CGGTGACGCA GCGCGACGTG CGCGAGCTGA	60
AGCGGATCGA GCAGACGGAT CGCCTGCCGC GGTTCATGCG CTACCTGGCC GCTATCACCG	120
CGCAGGAGCT GAACGTGGCC GAAGCGGCGC GGGTCATCGG GGTGACGCG GGGACGATCC	180
GTTCGGATCT GGCGTGGTTC GAGACGGTCT ATCTGGTACA TCGCCTGCCC GCCTGGTCGC	240
GGAATCTGAC CGCGAAGATC AAGAAGCGGT CAAAGATCCA CGTCGTCGAC AGTGGCTTCG	300
CGGCCTGGTT GCGCGGG	317

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCGTGGAG CTGTCGATGA ACAGCGTTGC CGGACGCGCG GCGGCCAGCA CGTCGGTGTA	60
GCAGCGCCGG ACCACCTCGC CGGTGGGCAG CATGGTGATG ACCACGTCGG CCTCGGCCAC	120
CGCTTCGGGC GCGCTACGAA ACACCGCGAC ACCGTGCGCG GCGGCGCCGG ACGCCGCCGT	180
GG	182

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 308 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GATCGCGAAG TTTGGTGAGC AGGTGGTCGA CGCGAAAGTC TGGGCGCCTG CGAAGCGGGT	60
CGGCGTTCAC GAGGCGAAGA CACGCCTGTC CGAGCTGCTG CGGCTCGTCT ACGGCGGGCA	120
GAGGTTGAGA TTGCCCCGCCG CGGCGAGCCG GTAGCAAAGC TTGTGCCGCT GCATCCTCAT	180
GAGACTCGGC GGTTAGGCAT TGACCATGGC GTGTACCGCG TGCCCCACGA TTTGGACGCT	240
CCGTTGTGAG ACGACGTGCT CGAACGCTTT CACCGGTGAA GCGCTACCTC ATCGACACCC	300
ACGTTTGG	308

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CCGACGACGA GCAACTCAGC TGGATGATGG TCGGCAGCGG CATTGAGGAC GGAGAGAATC	60
CGGCCGAAGC TGCCGCGCGG CAAGTGCTCA TAGTGACCGG CCGTAGAGGG CTCCCCCGAT	120
GGCACCAGGAC TATTCTGGTG TGCCGCTGGC CGGTAAGAGC GGGTAAAAGA ATGTGAGGGG	180
ACACGATGAG CAATCACACC TACCGAGTGA TCGAGATCGT CGGGACCTCG CCCGACGGCG	240
TCGACGCGGC AATCCAGGGC GGTCTGG	267

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1539 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

CTCGTGCCGA AAGAATGTGA GGGGACACGA TGAGCAATCA CACCTACCGA GTGATCGAGA	60
TCGTGCGGAC CTCGCCCCGAC GGCGTCGACG CGGCAATCCA GGGCGGTCTG GCCCCGAGCTG	120
CGCAGACCAT GCGCGCGCTG GACTGGTTTC AAGTACAGTC AATTCGAGGC CACCTGGTTCG	180
ACGGAGCGGT CGCGCACTTC CAGGTGACTA TGAAAGTCGG CTTCCGCTGG AGGATTCTCTG	240
AACCTTCAAG CGCGGCCGAT AACTGAGGTG CATCATTAAG CGACTTTTCC AGAACATCCT	300
GACGCGCTCG AAACGCGGTT CAGCCGACGG TGGCTCCGCC GAGGCGCTGC CTCCAAAATC	360
CCTGCGACAA TTCGTGCGCG GCGCCTACAA GGAAGTCGGT GCTGAATTCTG TCGGGTATCT	420

GGTCGACCTG	TGTGGGCTGC	AGCCGGACGA	AGCGGTGCTC	GACGTCGGCT	GCGGCTCGGG	480
GCGGATGGCG	TTGCCGCTCA	CCGGCTATCT	GAACAGCGAG	GGACGCTACG	CCGGCTTCGA	540
TATCTCGCAG	AAAGCCATCG	CGTGGTGCCA	GGAGCACATC	ACCTCGGCGC	ACCCCAACTT	600
CCAGTTCGAG	GTCTCCGACA	TCTACAATC	GCTGTACAAC	CCGAAAGGGA	AATACCAGTC	660
ACTAGACTTT	CGCTTTCCAT	ATCCGGATGC	GTCGTTTCGAT	GTGGTGTTTC	TTACCTCGGT	720
GTTCAACCCAC	ATGTTTCCGC	CGGACGTGGA	GCACTATCTG	GACGAGATCT	CCCCTCGTCT	780
GAAGCCCGGC	GGACGATGCC	TGTGCACGTA	CTTCTTGCTC	AATGACGAGT	CGTTAGCCCA	840
CATCGCGGAA	GGAAAGAGTG	CGCACAACTT	CCAGCATGAG	GGACCGGGTT	ATCGGACAAT	900
CCACAAGAAG	CGGCCCCAAG	AAGCAATCGG	CTTGCCGGAG	ACCTTCGTCA	GGGATGTCTA	960
TGGCAAGTTC	GGCCTCGCCG	TGCACGAACC	ATTGCACTAC	GGCTCATGGA	GTGGCCGGGA	1020
ACCACGCCTA	AGCTTCCAGG	ACATCGTCAT	CGCGACCAAA	ACCGCGAGCT	AGGTCGGCAT	1080
CCGGGAAGCA	TCGCGACACC	GTGGCGCCGA	GCGCCGCTGC	CGGCAGGCCG	ATTAGCGGGG	1140
CAGATTAGCC	CGCCGCGGCT	CCCGGCTCCG	AGTACGGCGC	CCCGAATGGC	GTCACCGGCT	1200
GGTAACCACG	CTTGCGCGCC	TGGGCGGCGG	CCTGCCGGAT	CAGGTGGTAG	ATGCCGACAA	1260
AGCCTGCGTG	ATCGGTCATC	ACCAACGGTG	ACAGCAGCCG	GTTGTGCACC	AGCCGAAACG	1320
CCACCCCGGT	CTCCGGGTCT	GTCCAGCCGA	TCGAGCCGCC	CAAGCCCACA	TGACCAAAACC	1380
CCGGCATCAC	GTTGCCGATC	GGCATACCGT	GATAGCCAAG	ATGAAAATTT	AAGGGCACCA	1440
ATAGATTTTCG	ATCCGGCAGA	ACTTGCCGTC	GGTTGCGGGT	CAGGCCCGTG	ACCAGCTCCC	1500
GCGACAAGAA	CCGTATGCCG	TCGATCTCGC	CTCGTGCCG			1539

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 851 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CTGCAGGGTG	GCGTGGATGA	GCGTCACCGC	GGGGCAGGCC	GAGCTGACCG	CCGCCCAGGT	60
CCGGGTGCT	GCGGCGGCCT	ACGAGACGGC	GTATGGGCTG	ACGGTGCCCC	CGCCGGTGAT	120
CGCCGAGAAC	CGTGCTGAAC	TGATGATTCT	GATAGCGACC	AACCTCTTGG	GGCAAAACAC	180
CCCGGCGATC	GCGGTCAACG	AGGCCGAATA	CGGCAGATG	TGGGCCCCAAG	ACGCCGCCGC	240
GATGTTTGGC	TACGCCGCGG	CGACGGCGAC	GGCGACGGCG	ACGTTGCTGC	CGTTCGAGGA	300
GGCGCCGGAG	ATGACCAGCG	CGGGTGGGCT	CCTCGAGCAG	GCCGCCGCGG	TCGAGGAGGC	360
CTCCGACACC	GCCGCGGCGA	ACCAGTTGAT	GAACAATGTG	CCCCAGGCGC	TGAAACAGTT	420
GGCCCAGCCC	ACGCAGGGCA	CCACGCCTTC	TTCCAAGCTG	GGTGGCCTGT	GGAAGACGGT	480
CTCGCCGCAT	CGGTCGCCGA	TCAGCAACAT	GGTGTGATG	GCCAACAACC	ACATGTCGAT	540
GACCAACTCG	GGTGTGTCGA	TGACCAACAC	CTTGAGCTCG	ATGTTGAAGG	GCTTTGCTCC	600
GGCGGCGGCC	GCCCAGGCCG	TGCAAACCGC	GGCGCAAAAC	GGGGTCCGGG	CGATGAGCTC	660
GCTGGGCGGC	TCGCTGGGTT	CTTCGGGTCT	GGGCGGTGGG	GTGGCCGCCA	ACTTGGGTCG	720
GGCGGCCTCG	GTACGGTATG	GTCACCGGGA	TGGCGGAAAA	TATGCANAGT	CTGGTCGGCG	780
GAACGGTGGT	CCGGCGTAAG	GTTTACCCCC	GTTTTCTGGA	TGCGGTGAAC	TTCGTCAACG	840
GAAACAGTTA	C					851

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 254 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GATCGATCGG	GCGGAAATTT	GGACCAGATT	CGCCTCCGGC	GATAACCCAA	TCAATCGAAC	60
CTAGATTTAT	TCCGTCCAGG	GGCCCAGTA	ATGGCTCGCA	GGAGAGGAAC	CTTACTGCTG	120
CGGGCACCTG	TCGTAGGTCC	TCGATACGGC	GGAAGGCGTC	GACATTTTCC	ACCGACACCC	180
CCATCCAAAC	GTTTCGAGGGC	CACTCCAGCT	TGTGAGCGAG	GCGACGCAGT	CGCAGGCTGC	240
GCTTGGTCAA	GATC					254

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1227 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GATCCTGACC	GAAGCGGCCG	CCGCCAAGGC	GAAGTCGCTG	TTGGACCAGG	AGGGACGGGA	60
CGATCTGGCG	CTGCGGATCG	CGGTTTCAGCC	GGGGGGGTGC	GCTGGATTGC	GCTATAACCT	120
TTTCTTCGAC	GACCGGACGC	TGGATGGTGA	CCAAACCGCG	GAGTTCGGTG	GTGTCAGGTT	180
GATCGTGGAC	CGGATGAGCG	CGCCGTATGT	GGAAGGCGCG	TCGATCGATT	TCGTCGACAC	240
TATTGAGAAG	CAAGGTTTAC	CATCGACAAT	CCCAACGCCA	CCGGCTCCTG	CGCGTGCGGG	300
GATTCGTTCA	ACTGATAAAA	CGTAGTACG	ACCCCGCGGT	GCGCAACACG	TACGAGCACA	360
CCAAGACCTG	ACCGCGCTGG	AAAAGCAACT	GAGCGATGCC	TTGCACCTGA	CCGCGTGGCG	420
GGCCGCCGGC	GGCAGGTGTC	ACCTGCATGG	TGAACAGCAC	CTGGGCGCTGA	TATTGCGACC	480
AGTACACGAT	TTTGTTCGATC	GAGGTCACTT	CGACCTGGGA	GAAGTGCCTG	CGGAACGCGT	540
CGCTGCTCAG	CTTGGCCAAG	GCCTGATCGG	AGCGCTTGTC	GCGCACGCCG	TCGTGGATAC	600
CGCACAGCGC	ATTGCGAACG	ATGGTGTCCA	CATCGCGGTT	CTCCAGCGCG	TTGAGGTATC	660
CCTGAATCGC	GGTTTTGGCC	GGTCCCTCCG	AGAATGTGCC	TGCCGTGTTG	GCTCCGTTGG	720
TGCGGACCCC	GTATATGATC	GCCGCCGTCA	TAGCCGACAC	CAGCGCGAGG	GCTACCACAA	780
TGCCGATCAG	CAGCCGCTTG	TGCCGTCGCT	TCGGGTAGGA	CACCTGCGGC	GGCACGCCGG	840
GATATGCGGC	GGGCGGCAGC	GCCGCGTCGT	CTGCCGGTCC	CGGGGCGAAG	GCCGGTTCGG	900
CGGCGCCGAG	STCSTGGGGG	TAGTCCAGGG	CTTGGGGTTC	GTGGGATGAG	GGCTCGGGGT	960
ACGGCGCCGG	TCCGTGGGTG	CCGACACCGG	GGTTCGGCGA	GTGGGGACCG	GGCATTGTGG	1020
TTCTCCTAGG	GTGGTGGACG	GGACCAGCTG	CTAGGGCGAC	AACCGCCCGT	CGCGTCAGCC	1080
GGCAGCATCG	GCAATCAGGT	GAGCTCCCTA	GGCAGGCTAG	CGCAACAGCT	GCCGTCAGCT	1140
CTCAACCGCA	CGGGGCGGGC	CGCGGCGCCG	ATAATGTTGA	AAGACTAGGC	AACCTTAGGA	1200
ACGAAGGACG	GAGATTTTGT	GACGATC				1227

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 181 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GCGGTGTGCG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGGGCCGGC	GGGGCCGGCG	60
GGACCGGCGC	TAACGGTGGT	GCCGGCGGCA	ACGCCTGGTT	GTTCCGGGGC	GGCGGGTCCG	120
GCGGNGCCGG	CACCAATGGT	GGNGTCGGCG	GGTCCGGCGG	ATTTGTCTAC	GGCAACGGCG	180
G						181

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 290 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCGGTGTCGG	CGGATCCGGC	GGGTGGTTGA	ACGGCAACGG	CGGTGTCGGC	GGCCGGGGCG	60
GCGACGGCGT	CTTTGCCGGT	GCCGGCGGCC	AGGGCGGCCT	CGGTGGGCAG	GGCGGCAATG	120
GCGGCGGCTC	CACCGGCGGC	AACGGCGGTC	TTGGCGGCGC	GGGCGGTGGC	GGAGGCAACG	180
CCCCGGACGG	CGGCTTCGGT	GGCAACGGCG	GTAAGGGTGG	CCAGGGCGGN	ATTGGCGGCG	240
GCACTCAGAG	CGCGACCGGC	CTCGNGGTG	ACGGCGGTGA	CGGCGGTGAC		290

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GATCCAGTGG	CATGGNGGGT	GTCAGTGGAA	GCAT	34
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(2) INFORMATION FOR SEQ ID NO:39:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 155 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GATCGCTGCT	CGTCCCCCCC	TTGCCGCCGA	CGCCACCGGT	CCCACCGTTA	CCGAACAAGC	60
TGGCGTGGTC	GCCAGACCCC	CCGGCACCGC	CGACGCCGGA	GTCGAACAAT	GGCACCGTCG	120
TATCCCCACC	ATTGCCGCCG	GNCCCACCGG	CACCG			155

(2) INFORMATION FOR SEQ ID NO:40:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

ATGGCGTTCA	CGGGGCGCCG	GGGACCGGGC	AGCCCGGNGG	GGCCGGGGGG	TGG	53
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(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GATCCACCGC GGGTGCAGAC GGTGCCCCGCG GCGCCACCCC GACCAGCGGC GGCAACGGCG	60
GCACCGGCGG CAACGGGCGG AACGCCACCG TCGTCGGNGG GGCCGGCGGG GCCGGCGGCA	120
AGGGCGGCAA CG	132

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GATCGGCGGC CGGNACGGNC GGGGACGGCG GCAAGGGCGG NAACGGGGGC GCCGNAGCCA	60
CCNGCCAAGA ATCCTCCGNG TCCNCCAATG GCGCGAATGG CGGACAGGGC GGCAACGGCG	120
GCANCGGCGG CA	132

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 702 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC	60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCC CGATGCCGGC	120
ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTTCAGT TTAGCGACGA TAATGGCTAT	180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG	240
AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCATGGC GGACCCACCG ACTGATGTCC	300
CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTTGTCCG	360
CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGCGT CTGGCGACCT	420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG	480
ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCCG GGCCGTCGGA GGGGACAGTT	540
CGGCCGAACT AACCGATACG CCGAGGGTGG CCACGGCCCG TGAACCCAAC TTCATGGATC	600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG	660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG	702

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

GAAGCCGCAG	CGCTGTCGGG	CGACGTGGCG	GTCAAAGCGG	CATCGCTCGG	TGGCGGTGGA	60
GGCGGCGGGG	TGCCGTCGGC	GCCGTTGGGA	TCCGCGATCG	GGGGCGCCGA	ATCGGTGCGG	120
CCCGCTGGCG	CTGGTGACAT	TGCCGGCTTA	GGCCAGGGAA	GGGCCGGCGG	CGGCGCCGCG	180
CTGGGCGGCG	GTGGCATGGG	AATGCCGATG	GGTGCCGCGC	ATCAGGGACA	AGGGGGCGCC	240
AAGTCCAAGG	GTTCTCAGCA	GGAAGACGAG	GCGCTCTACA	CCGAGGATCC	TCGTGCCG	298

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1058 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CGGCACGAGG	ATCGAATCGC	GTCGCCGGGA	GCACAGCGTC	GCACTGCACC	AGTGGAGGAG	60
CCATGACCTA	CTCGCCGGGT	AACCCCGGAT	ACCCGCAAGC	GCAGCCCGCA	GGCTCCTACG	120
GAGGCGTCAC	ACCCTCGTTC	GCCACGCCG	ATGAGGGTGC	GAGCAAGCTA	CCGATGTACC	180
TGAACATCGC	GGTGGCAGTG	CTCGGTCTGG	CTGCGTACTT	CGCCAGCTTC	GGCCCAATGT	240
TCACCCTCAG	TACCGAACTC	GGGGGGGGTG	ATGGCGCAGT	GTCCGGTGAC	ACTGGGCTGC	300
CGGTGCGGGT	GGCTCTGCTG	GCTGCGCTGC	TTGCCGGGGT	GGTTCTGGTG	CCTAAGGCCA	360
AGAGCCATGT	GACGCTAGTT	GCGGTGCTCG	GGGTACTCGG	CGTATTTCTG	ATGGTCTCGG	420
CGACGTTTTA	CAAGCCCAGC	GCCTATTCGA	CCGGTTGGGC	ATTGTGGGTT	GTGTTGGCTT	480
TCATCGTGTT	CCAGGCGGTT	GCGGCAGTCC	TGGCGCTCTT	GGTGGAGACC	GGCGCTATCA	540
CCGCGCCGGC	GCCGCGGCCC	AAGTTCGACC	CGTATGGACA	GTACGGGCGG	TACGGGCAGT	600
ACGGGCAGTA	CGGGGTGCAG	CCGGGTGGGT	ACTACGGTCA	GCAGGGTGCT	CAGCAGGCCG	660
CGGGACTGCA	GTCGCCCGGC	CCGCAGCAGT	CTCCGCAGCC	TCCCGGATAT	GGGTGCGAGT	720
ACGGCGGCTA	TTCGTCCAGT	CCGAGCCCAAT	CGGGCAGTGG	ATACACTGCT	CAGCCCCCGG	780
CCCAGCCGCC	GGCGCAGTCC	GGGTGCGAAC	AATCGCACCA	GGGCCCCATC	ACGCCACCTA	840
CCGGCTTTCC	GAGCTTCAGC	CCACCACCAC	CGGTCAGTGC	CGGGACGGGG	TCGCAGGCTG	900
GTTGCGCTCC	AGTCAACTAT	TCAAACCCCA	GCGGGGGCGA	GCAGTCGTCG	TCCCCCGGGG	960
GGGCGCCGGT	CTAACCAGGC	GTTCCCGCGT	CCGGTCGCGC	GTGTGCGCGA	AGAGTGAACA	1020
GGGTGTCAGC	AAGCGCGGAC	GATCCTCGTG	CCGAATTC			1058

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 327 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

CGGCACGAGA	GACCGATGCC	GCTACCCTCG	CGCAGGAGGC	AGGTAATTTT	GAGCGGATCT	60
CCGGCGACCT	GAAAACCCAG	ATCGACCAGG	TGGAGTCGAC	GGCAGGTTTC	TTGCAGGGCC	120
AGTGGCGCGG	CGCGGCGGGG	ACGGCCGCCC	AGGCCGCGGT	GGTGCCTTTC	CAAGAAGCAG	180
CCAATAAGCA	GAAGCAGGAA	CTCGACGAGA	TCTCGACGAA	TATTCGTCAG	GCCGGCGTCC	240
AATACTCGAG	GGCCGACGAG	GAGCAGCAGC	AGGCGCTGTC	CTCGCAAATG	GGCTTCTGAC	300
CCGCTAATAC	GAAAAGAAAC	GGAGCAA				327

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 170 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGTCGCGAT GATGGCGTTG TCGAACGTGA CCGATTCTGT ACCGCCGTCG TTGAGATCAA	60
CCAACAACGT GTTGGCGTCG GCAAATGTGC CGNACCCGTG GATCTCGGTG ATCTTGTTCT	120
TCTTCATCAG GAAGTGCACA CCGGCCACCC TGCCCTCGGN TACCTTTCGG	170

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 127 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

GATCCGGCGG CACGGGGGGT GCCGGCGGCA GCACCGCTGG CGCTGGCGGC AACGGCGGGG	60
CCGGGGGTGG CGGCGGAACC GGTGGGTTC TCTTCGGCAA CGGCGGTGCC GGCGGGCACG	120
GGGCCGT	127

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

CGGCGGCAAG GGCGGCACCG CCGGCAACGG GAGCGGCGCG GCCGGCGGCA ACGGCGGCAA	60
CGGCGGCTCC GGCCTCAACG G	81

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

GATCAGGGCT GGCCGGCTCC GGCCAGAAGG GCGGTAACGG AGGAGCTGCC GGATTGTTTG	60
GCAACGGCGG GGCCGGNGGT GCCGGCGCGT CCAACCAAGC CGGTAACGGC GGNGCCGGCG	120
GAAACGGTGG TGCCGGTGG CTGATCTGG	149

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

CGGCACGAGA TCACACCTAC CGAGTGATCG AGATCGTCGG GACCTCGCCC GACGGTGTCTG	60
ACGCGGNAAT CCAGGGCGGT CTGGCCCGAG CTGCGCAGAC CATGCGCGCG CTGGACTGGT	120
TCGAAGTACA GTCAATTCCA GGCCACCTGG TCGACGGAGC GGTGCGGCAC TTCCAGGTGA	180
CTATGAAAGT CGGCTTCCGC CTGGAGGATT CCTGAACCTT CAAGCGCGGC CGATAACTGA	240
GGTGCAATCAT TAAGCGACTT TTCCAGAACA TCCTGACGCG CTCGAAACGC GGTTCAGCCG	300
ACGGTGGCTC CGCCGAGGCG CTGCCTCCAA AATCCCTGCG ACAATTCGTC GGC	355

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 999 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA	60
CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG	120
CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCTCG	180
CCGCCGTCGA CCGCTGCAGC GCCACCCGCA CCGGCGACAC CTGTTGCCCC CCCACCACCG	240
GCCGCCGCCA ACACGCCGAA TGCCCAGCCG GGCATCCCA ACGCAGCACC TCCGCCGGCC	300
GACCCGAACG CACCGCCGCC ACCTGTCATT GCCCAAACG CACCCCAACC TGTCCGGATC	360
GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC	420
GCCCACTTCG ACTACGGTTC AGCACTCCTC AGCAAAACCA CCGGGGACCC GCCATTTCCC	480
GGACAGCCGC CGCCGGTGGC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAAG	540
CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG	600
GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC	660
GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG	720
CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCC CGGCGAACGC ACCGGACGCC	780
GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG	840
GGCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCCGGCGCCG	900
GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCGG CCGGGGAAGT CGCTCCTACC	960
CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCCTGA	999

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

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Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1      5      10      15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20      25      30
Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35      40      45
Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50      55      60
Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65      70      75      80
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85      90      95
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100     105     110
Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Gly Phe Ser
115     120     125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130     135     140
Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145     150     155     160
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165     170     175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180     185     190
Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195     200     205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210     215     220
Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225     230     235     240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
245     250     255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260     265     270
Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275     280     285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290     295     300
Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305     310     315     320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325     330

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(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Asp Pro Val Asp Ala Val Ile Asn Thr Thr Xaa Asn Tyr Gly Gln Val

1	5	10	15
Val Ala Ala Leu			
20			

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

Ala Val Glu Ser Gly Met Leu Ala Leu Gly Thr Pro Ala Pro Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala Ala Lys
1 5 10 15
Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
1 5 10

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
1 5 10

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Ala Ala Ala Ala Pro Pro
1 5 10 15
Ala

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Gln Thr Ser
1 5 10 15

Leu Leu Asn Asn Leu Ala Asp Pro Asp Val Ser Phe Ala Asp
 20 25 30

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 187 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

Thr Gly Ser Leu Asn Gln Thr His Asn Arg Arg Ala Asn Glu Arg Lys
 1 5 10 15
 Asn Thr Thr Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala
 20 25 30
 Ala Ala Ala Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala
 35 40 45
 Gly Gly Pro Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro
 50 55 60
 Leu Pro Leu Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln
 65 70 75 80
 Leu Thr Ser Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala
 85 90 95
 Asn Lys Gly Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg
 100 105 110
 Ile Ala Asp His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro
 115 120 125
 Leu Ser Phe Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala
 130 135 140
 Thr Ala Asp Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr
 145 150 155 160
 Gln Asn Val Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala
 165 170 175
 Ser Ala Met Glu Leu Leu Gln Ala Ala Gly Xaa
 180 185

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 148 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

Asp Glu Val Thr Val Glu Thr Thr Ser Val Phe Arg Ala Asp Phe Leu
 1 5 10 15
 Ser Glu Leu Asp Ala Pro Ala Gln Ala Gly Thr Glu Ser Ala Val Ser
 20 25 30
 Gly Val Glu Gly Leu Pro Pro Gly Ser Ala Leu Leu Val Val Lys Arg
 35 40 45
 Gly Pro Asn Ala Gly Ser Arg Phe Leu Leu Asp Gln Ala Ile Thr Ser

```

      50              55              60
Ala Gly Arg His Pro Asp Ser Asp Ile Phe Leu Asp Asp Val Thr Val
65              70              75              80
Ser Arg Arg His Ala Glu Phe Arg Leu Glu Asn Asn Glu Phe Asn Val
      85              90              95
Val Asp Val Gly Ser Leu Asn Gly Thr Tyr Val Asn Arg Glu Pro Val
      100             105             110
Asp Ser Ala Val Leu Ala Asn Gly Asp Glu Val Gln Ile Gly Lys Leu
      115             120             125
Arg Leu Val Phe Leu Thr Gly Pro Lys Gln Gly Glu Asp Asp Gly Ser
      130             135             140
Thr Gly Gly Pro
145

```

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 230 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```

Thr Ser Asn Arg Pro Ala Arg Arg Gly Arg Arg Ala Pro Arg Asp Thr
1              5              10              15
Gly Pro Asp Arg Ser Ala Ser Leu Ser Leu Val Arg His Arg Arg Gln
      20              25              30
Gln Arg Asp Ala Leu Cys Leu Ser Thr Gln Ile Ser Arg Gln Ser
      35              40              45
Asn Leu Pro Pro Ala Ala Gly Gly Ala Ala Asn Tyr Ser Arg Arg Asn
      50              55              60
Phe Asp Val Arg Ile Lys Ile Phe Met Leu Val Thr Ala Val Val Leu
65              70              75              80
Leu Cys Cys Ser Gly Val Ala Thr Ala Ala Pro Lys Thr Tyr Cys Glu
      85              90              95
Glu Leu Lys Gly Thr Asp Thr Gly Gln Ala Cys Gln Ile Gln Met Ser
      100             105             110
Asp Pro Ala Tyr Asn Ile Asn Ile Ser Leu Pro Ser Tyr Tyr Pro Asp
      115             120             125
Gln Lys Ser Leu Glu Asn Tyr Ile Ala Gln Thr Arg Asp Lys Phe Leu
      130             135             140
Ser Ala Ala Thr Ser Ser Thr Pro Arg Glu Ala Pro Tyr Glu Leu Asn
145             150             155             160
Ile Thr Ser Ala Thr Tyr Gln Ser Ala Ile Pro Pro Arg Gly Thr Gln
      165             170             175
Ala Val Val Leu Xaa Val Tyr His Asn Ala Gly Gly Thr His Pro Thr
      180             185             190
Thr Thr Tyr Lys Ala Phe Asp Trp Asp Gln Ala Tyr Arg Lys Pro Ile
      195             200             205
Thr Tyr Asp Thr Leu Trp Gln Ala Asp Thr Asp Pro Leu Pro Val Val
      210             215             220
Phe Pro Ile Val Ala Arg
225             230

```

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1           5           10           15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20           25           30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35           40           45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50           55           60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65           70           75           80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85           90           95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100          105          110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115          120          125
Gly Pro Pro Ala
130

```

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```

Val Pro Leu Arg Ser Pro Ser Met Ser Pro Ser Lys Cys Leu Ala Ala
1           5           10           15
Ala Gln Arg Asn Pro Val Ile Arg Arg Arg Arg Leu Ser Asn Pro Pro
20           25           30
Pro Arg Lys Tyr Arg Ser Met Pro Ser Pro Ala Thr Ala Ser Ala Gly
35           40           45
Met Ala Arg Val Arg Arg Arg Ala Ile Trp Arg Gly Pro Ala Thr Xaa
50           55           60
Ser Ala Gly Met Ala Arg Val Arg Arg Trp Xaa Val Met Pro Xaa Val
65           70           75           80
Ile Gln Ser Thr Xaa Ile Arg Xaa Xaa Gly Pro Phe Asp Asn Arg Gly
85           90           95
Ser Glu Arg Lys
100

```

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

```

Met Thr Asp Asp Ile Leu Leu Ile Asp Thr Asp Glu Arg Val Arg Thr
1           5           10           15
Leu Thr Leu Asn Arg Pro Gln Ser Arg Asn Ala Leu Ser Ala Ala Leu
20           25           30
Arg Asp Arg Phe Phe Ala Xaa Leu Xaa Asp Ala Glu Xaa Asp Asp Asp
35           40           45
Ile Asp Val Val Ile Leu Thr Gly Ala Asp Pro Val Phe Cys Ala Gly
50           55           60
Leu Asp Leu Lys Val Ala Gly Arg Ala Asp Arg Ala Ala Gly His Leu
65           70           75           80
Thr Ala Val Gly Gly His Asp Gln Ala Gly Asp Arg Arg Asp Gln Arg
85           90           95
Arg Arg Gly His Arg Arg Ala Arg Thr Gly Ala Val Leu Arg His Pro
100          105          110
Asp Arg Leu Arg Ala Arg Pro Leu Arg Arg His Pro Arg Pro Gly Gly
115          120          125
Ala Ala Ala His Leu Gly Thr Gln Cys Val Leu Ala Ala Lys Gly Arg
130          135          140
His Arg Xaa Gly Pro Val Asp Glu Pro Asp Arg Arg Leu Pro Val Arg
145          150          155          160
Asp Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 344 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

```

Met Lys Phe Val Asn His Ile Glu Pro Val Ala Pro Arg Arg Ala Gly
1           5           10           15
Gly Ala Val Ala Glu Val Tyr Ala Glu Ala Arg Arg Glu Phe Gly Arg
20           25           30
Leu Pro Glu Pro Leu Ala Met Leu Ser Pro Asp Glu Gly Leu Leu Thr
35           40           45
Ala Gly Trp Ala Thr Leu Arg Glu Thr Leu Leu Val Gly Gln Val Pro
50           55           60
Arg Gly Arg Lys Glu Ala Val Ala Ala Val Ala Ala Ser Leu Arg
65           70           75           80
Cys Pro Trp Cys Val Asp Ala His Thr Thr Met Leu Tyr Ala Ala Gly
85           90           95
Gln Thr Asp Thr Ala Ala Ala Ile Leu Ala Gly Thr Ala Pro Ala Ala
100          105          110

```

100

Gly Asp Pro Asn Ala Pro Tyr Val Ala Trp Ala Ala Gly Thr Gly Thr
 115 120 125
 Pro Ala Gly Pro Pro Ala Pro Phe Gly Pro Asp Val Ala Ala Glu Tyr
 130 135 140
 Leu Gly Thr Ala Val Gln Phe His Phe Ile Ala Arg Leu Val Leu Val
 145 150 155 160
 Leu Leu Asp Glu Thr Phe Leu Pro Gly Gly Pro Arg Ala Gln Gln Leu
 165 170 175
 Met Arg Arg Ala Gly Gly Leu Val Phe Ala Arg Lys Val Arg Ala Glu
 180 185 190
 His Arg Pro Gly Arg Ser Thr Arg Arg Leu Glu Pro Arg Thr Leu Pro
 195 200 205
 Asp Asp Leu Ala Trp Ala Thr Pro Ser Glu Pro Ile Ala Thr Ala Phe
 210 215 220
 Ala Ala Leu Ser His His Leu Asp Thr Ala Pro His Leu Pro Pro Pro
 225 230 235 240
 Thr Arg Gln Val Val Arg Arg Val Val Gly Ser Trp His Gly Glu Pro
 245 250 255
 Met Pro Met Ser Ser Arg Trp Thr Asn Glu His Thr Ala Glu Leu Pro
 260 265 270
 Ala Asp Leu His Ala Pro Thr Arg Leu Ala Leu Leu Thr Gly Leu Ala
 275 280 285
 Pro His Gln Val Thr Asp Asp Asp Val Ala Ala Ala Arg Ser Leu Leu
 290 295 300
 Asp Thr Asp Ala Ala Leu Val Gly Ala Leu Ala Trp Ala Ala Phe Thr
 305 310 315 320
 Ala Ala Arg Arg Ile Gly Thr Trp Ile Gly Ala Ala Ala Glu Gly Gln
 325 330 335
 Val Ser Arg Gln Asn Pro Thr Gly
 340

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 485 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Asp Asp Pro Asp Met Pro Gly Thr Val Ala Lys Ala Val Ala Asp Ala
 1 5 10 15
 Leu Gly Arg Gly Ile Ala Pro Val Glu Asp Ile Gln Asp Cys Val Glu
 20 25 30
 Ala Arg Leu Gly Glu Ala Gly Leu Asp Asp Val Ala Arg Val Tyr Ile
 35 40 45
 Ile Tyr Arg Gln Arg Arg Ala Glu Leu Arg Thr Ala Lys Ala Leu Leu
 50 55 60
 Gly Val Arg Asp Glu Leu Lys Leu Ser Leu Ala Ala Val Thr Val Leu
 65 70 75 80
 Arg Glu Arg Tyr Leu Leu His Asp Glu Gln Gly Arg Pro Ala Glu Ser
 85 90 95
 Thr Gly Glu Leu Met Asp Arg Ser Ala Arg Cys Val Ala Ala Ala Glu
 100 105 110

```

Asp Gln Tyr Glu Pro Gly Ser Ser Arg Arg Trp Ala Glu Arg Phe Ala
115                               120                               125
Thr Leu Leu Arg Asn Leu Glu Phe Leu Pro Asn Ser Pro Thr Leu Met
130                               135                               140
Asn Ser Gly Thr Asp Leu Gly Leu Leu Ala Gly Cys Phe Val Leu Pro
145                               150                               155                               160
Ile Glu Asp Ser Leu Gln Ser Ile Phe Ala Thr Leu Gly Gln Ala Ala
165                               170                               175
Glu Leu Gln Arg Ala Gly Gly Gly Thr Gly Tyr Ala Phe Ser His Leu
180                               185                               190
Arg Pro Ala Gly Asp Arg Val Ala Ser Thr Gly Gly Thr Ala Ser Gly
195                               200                               205
Pro Val Ser Phe Leu Arg Leu Tyr Asp Ser Ala Ala Gly Val Val Ser
210                               215                               220
Met Gly Gly Arg Arg Arg Gly Ala Cys Met Ala Val Leu Asp Val Ser
225                               230                               235                               240
His Pro Asp Ile Cys Asp Phe Val Thr Ala Lys Ala Glu Ser Pro Ser
245                               250                               255
Glu Leu Pro His Phe Asn Leu Ser Val Gly Val Thr Asp Ala Phe Leu
260                               265                               270
Arg Ala Val Glu Arg Asn Gly Leu His Arg Leu Val Asn Pro Arg Thr
275                               280                               285
Gly Lys Ile Val Ala Arg Met Pro Ala Ala Glu Leu Phe Asp Ala Ile
290                               295                               300
Cys Lys Ala Ala His Ala Gly Gly Asp Pro Gly Leu Val Phe Leu Asp
305                               310                               315                               320
Thr Ile Asn Arg Ala Asn Pro Val Pro Gly Arg Gly Arg Ile Glu Ala
325                               330                               335
Thr Asn Pro Cys Gly Glu Val Pro Leu Leu Pro Tyr Glu Ser Cys Asn
340                               345                               350
Leu Gly Ser Ile Asn Leu Ala Arg Met Leu Ala Asp Gly Arg Val Asp
355                               360                               365
Trp Asp Arg Leu Glu Glu Val Ala Gly Val Ala Val Arg Phe Leu Asp
370                               375                               380
Asp Val Ile Asp Val Ser Arg Tyr Pro Phe Pro Glu Leu Gly Glu Ala
385                               390                               395                               400
Ala Arg Ala Thr Arg Lys Ile Gly Leu Gly Val Met Gly Leu Ala Glu
405                               410                               415
Leu Leu Ala Ala Leu Gly Ile Pro Tyr Asp Ser Glu Glu Ala Val Arg
420                               425                               430
Leu Ala Thr Arg Leu Met Arg Arg Ile Gln Gln Ala Ala His Thr Ala
435                               440                               445
Ser Arg Arg Leu Ala Glu Glu Arg Gly Ala Phe Pro Ala Phe Thr Asp
450                               455                               460
Ser Arg Phe Ala Arg Ser Gly Pro Arg Arg Asn Ala Gln Val Thr Ser
465                               470                               475                               480
Val Ala Pro Thr Gly
485

```

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

```

Gly Val Ile Val Leu Asp Leu Glu Pro Arg Gly Pro Leu Pro Thr Glu
1      5      10      15
Ile Tyr Trp Arg Arg Arg Gly Leu Ala Leu Gly Ile Ala Val Val Val
20      25      30
Val Gly Ile Ala Val Ala Ile Val Ile Ala Phe Val Asp Ser Ser Ala
35      40      45
Gly Ala Lys Pro Val Ser Ala Asp Lys Pro Ala Ser Ala Gln Ser His
50      55      60
Pro Gly Ser Pro Ala Pro Gln Ala Pro Gln Pro Ala Gly Gln Thr Glu
65      70      75      80
Gly Asn Ala Ala Ala Pro Pro Gln Gly Gln Asn Pro Glu Thr Pro
85      90      95
Thr Pro Thr Ala Ala Val Gln Pro Pro Pro Val Leu Lys Glu Gly Asp
100     105     110
Asp Cys Pro Asp Ser Thr Leu Ala Val Lys Gly Leu Thr Asn Ala Pro
115     120     125
Gln Tyr Tyr Val Gly Asp Gln Pro Lys Phe Thr Met Val Val Thr Asn
130     135     140
Ile Gly Leu Val Ser Cys Lys Arg Asp Val Gly Ala Ala Val Leu Ala
145     150     155     160
Ala Tyr Val Tyr Ser Leu Asp Asn Lys Arg Leu Trp Ser Asn Leu Asp
165     170     175
Cys Ala Pro Ser Asn Glu Thr Leu Val Lys Thr Phe Ser Pro Gly Glu
180     185     190
Gln Val Thr Thr Ala Val Thr Trp Thr Gly Met Gly Ser Ala Pro Arg
195     200     205
Cys Pro Leu Pro Arg Pro Ala Ile Gly Pro Gly Thr Tyr Asn Leu Val
210     215     220
Val Gln Leu Gly Asn Leu Arg Ser Leu Pro Val Pro Phe Ile Leu Asn
225     230     235     240
Gln Pro Pro Pro Pro Gly Pro Val Pro Ala Pro Gly Pro Ala Gln
245     250     255
Ala Pro Pro Pro Glu Ser Pro Ala Gln Gly Gly
260     265

```

(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```

Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly Val Gln Val
1      5      10      15
Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu Val Val Ala
20      25      30
Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val Val Val Thr
35      40      45

```

Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu Val Ala Ala
 50 55 60
 Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr Phe Gln Asp
 65 70 75 80
 Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly Lys Ala Glu
 85 90 95
 Gln

(2) INFORMATION FOR SEQ ID NO:73:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

Gly Ala Ala Val Ser Leu Leu Ala Ala Gly Thr Leu Val Leu Thr Ala
 1 5 10 15
 Cys Gly Gly Gly Thr Asn Ser Ser Ser Gly Ala Gly Gly Thr Ser
 20 25 30
 Gly Ser Val His Cys Gly Gly Lys Lys Glu Leu His Ser Ser Gly Ser
 35 40 45
 Thr Ala Gln Glu Asn Ala Met Glu Gln Phe Val Tyr Ala Tyr Val Arg
 50 55 60
 Ser Cys Pro Gly Tyr Thr Leu Asp Tyr Asn Ala Asn Gly Ser Gly Ala
 65 70 75 80
 Gly Val Thr Gln Phe Leu Asn Asn Glu Thr Asp Phe Ala Gly Ser Asp
 85 90 95
 Val Pro Leu Asn Pro Ser Thr Gly Gln Pro Asp Arg Ser Ala Glu Arg
 100 105 110
 Cys Gly Ser Pro Ala Trp Asp Leu Pro Thr Val Phe Gly Pro Ile Ala
 115 120 125
 Ile Thr Tyr Asn Ile Lys Gly Val Ser Thr Leu Asn Leu Asp Gly Pro
 130 135 140
 Thr Thr Ala Lys Ile Phe Asn Gly Thr Ile Thr Val Trp Asn Asp Pro
 145 150 155 160
 Gln Ile Gln Ala Leu Asn Ser Gly Thr Asp Leu Pro Pro Thr Pro Ile
 165 170 175
 Ser Val Ile Phe Arg Ser Asp Lys Ser Gly Thr Ser Asp Asn Phe Gln
 180 185 190
 Lys Tyr Leu Asp Gly Val Ser Asn Gly Ala Trp Gly Lys Gly Ala Ser
 195 200 205
 Glu Thr Phe Ser Gly Gly Val Gly Val Gly Ala Ser Gly Asn Asn Gly
 210 215 220
 Thr Ser Ala Leu Leu Gln Thr Thr Asp Gly Ser Ile Thr Tyr Asn Glu
 225 230 235 240
 Trp Ser Phe Ala Val Gly Lys Gln Leu Asn Met Ala Gln Ile Ile Thr
 245 250 255
 Ser Ala Gly Pro Asp Pro Val Ala Ile Thr Thr Glu Ser Val Gly Lys
 260 265 270
 Thr Ile Ala Gly Ala Lys Ile Met Gly Gln Gly Asn Asp Leu Val Leu
 275 280 285
 Asp Thr Ser Ser Phe Tyr Arg Pro Thr Gln Pro Gly Ser Tyr Pro Ile

290	295	300
Val Leu Ala Thr Tyr Glu Ile Val Cys Ser Lys Tyr Pro Asp Ala Thr		
305	310	315
Thr Gly Thr Ala Val Arg Ala Phe Met Gln Ala Ala Ile Gly Pro Gly		320
	325	330
Gln Glu Gly Leu Asp Gln Tyr Gly Ser Ile Pro Leu Pro Lys Ser Phe		335
	340	345
Gln Ala Lys Leu Ala Ala Ala Val Asn Ala Ile Ser		350
355	360	

(2) INFORMATION FOR SEQ ID NO:74:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 309 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

Gln	Ala	Ala	Ala	Gly	Arg	Ala	Val	Arg	Arg	Thr	Gly	His	Ala	Glu	Asp	1	5	10	15
Gln	Thr	His	Gln	Asp	Arg	Leu	His	His	Gly	Cys	Arg	Arg	Ala	Ala	Val	20	25	30	
Val	Val	Arg	Gln	Asp	Arg	Ala	Ser	Val	Ser	Ala	Thr	Ser	Ala	Arg	Pro	35	40	45	
Pro	Arg	Arg	His	Pro	Ala	Gln	Gly	His	Arg	Arg	Arg	Val	Ala	Pro	Ser	50	55	60	
Gly	Gly	Arg	Arg	Arg	Pro	His	Pro	His	His	Val	Gln	Pro	Asp	Asp	Arg	65	70	75	80
Arg	Asp	Arg	Pro	Ala	Leu	Leu	Asp	Arg	Thr	Gln	Pro	Ala	Glu	His	Pro	85	90	95	
Asp	Pro	His	Arg	Arg	Gly	Pro	Ala	Asp	Pro	Gly	Arg	Val	Arg	Gly	Arg	100	105	110	
Gly	Arg	Leu	Arg	Arg	Val	Asp	Asp	Gly	Arg	Leu	Gln	Pro	Asp	Arg	Asp	115	120	125	
Ala	Asp	His	Gly	Ala	Pro	Val	Arg	Gly	Arg	Gly	Pro	His	Arg	Gly	Val	130	135	140	
Gln	His	Arg	Gly	Gly	Pro	Val	Phe	Val	Arg	Arg	Val	Pro	Gly	Val	Arg	145	150	155	160
Cys	Ala	His	Arg	Arg	Gly	His	Arg	Arg	Val	Ala	Ala	Pro	Gly	Gln	Gly	165	170	175	
Asp	Val	Leu	Arg	Ala	Gly	Leu	Arg	Val	Glu	Arg	Leu	Arg	Pro	Val	Ala	180	185	190	
Ala	Val	Glu	Asn	Leu	His	Arg	Gly	Ser	Gln	Arg	Ala	Asp	Gly	Arg	Val	195	200	205	
Phe	Arg	Pro	Ile	Arg	Arg	Gly	Ala	Arg	Leu	Pro	Ala	Arg	Arg	Ser	Arg	210	215	220	
Ala	Gly	Pro	Gln	Gly	Arg	Leu	His	Leu	Asp	Gly	Ala	Gly	Pro	Ser	Pro	225	230	235	240
Leu	Pro	Ala	Arg	Ala	Gly	Gln	Gln	Gln	Pro	Ser	Ser	Ala	Gly	Gly	Arg	245	250	255	
Arg	Ala	Gly	Gly	Ala	Glu	Arg	Ala	Asp	Pro	Gly	Gln	Arg	Gly	Arg	His	260	265	270	
His	Gln	Gly	Gly	His	Asp	Pro	Gly	Arg	Gln	Gly	Ala	Gln	Arg	Gly	Thr				

```

      275                      280                      285
Ala Gly Val Ala His Ala Ala Ala Gly Pro Arg Arg Ala Ala Val Arg
      290                      295                      300
Asn Arg Pro Arg Arg
    305

```

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 580 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

Ser	Ala	Val	Trp	Cys	Leu	Asn	Gly	Phe	Thr	Gly	Arg	His	Arg	His	Gly
1				5					10					15	
Arg	Cys	Arg	Val	Arg	Ala	Ser	Gly	Trp	Arg	Ser	Ser	Asn	Arg	Trp	Cys
			20					25					30		
Ser	Thr	Thr	Ala	Asp	Cys	Cys	Ala	Ser	Lys	Thr	Pro	Thr	Gln	Ala	Ala
			35				40					45			
Ser	Pro	Leu	Glu	Arg	Arg	Phe	Thr	Cys	Cys	Ser	Pro	Ala	Val	Gly	Cys
			50			55					60				
Arg	Phe	Arg	Ser	Phe	Pro	Val	Arg	Arg	Leu	Ala	Leu	Gly	Ala	Arg	Thr
65					70				75						80
Ser	Arg	Thr	Leu	Gly	Val	Arg	Arg	Thr	Leu	Ser	Gln	Trp	Asn	Leu	Ser
				85				90						95	
Pro	Arg	Ala	Gln	Pro	Ser	Cys	Ala	Val	Thr	Val	Glu	Ser	His	Thr	His
			100					105					110		
Ala	Ser	Pro	Arg	Met	Ala	Lys	Leu	Ala	Arg	Val	Val	Gly	Leu	Val	Gln
			115				120					125			
Glu	Glu	Gln	Pro	Ser	Asp	Met	Thr	Asn	His	Pro	Arg	Tyr	Ser	Pro	Pro
			130			135					140				
Pro	Gln	Gln	Pro	Gly	Thr	Pro	Gly	Tyr	Ala	Gln	Gly	Gln	Gln	Gln	Thr
145					150				155						160
Tyr	Ser	Gln	Gln	Phe	Asp	Trp	Arg	Tyr	Pro	Pro	Ser	Pro	Pro	Pro	Gln
				165				170						175	
Pro	Thr	Gln	Tyr	Arg	Gln	Pro	Tyr	Glu	Ala	Leu	Gly	Gly	Thr	Arg	Pro
			180					185					190		
Gly	Leu	Ile	Pro	Gly	Val	Ile	Pro	Thr	Met	Thr	Pro	Pro	Pro	Gly	Met
			195				200					205			
Val	Arg	Gln	Arg	Pro	Arg	Ala	Gly	Met	Leu	Ala	Ile	Gly	Ala	Val	Thr
			210			215					220				
Ile	Ala	Val	Val	Ser	Ala	Gly	Ile	Gly	Gly	Ala	Ala	Ala	Ser	Leu	Val
225					230					235					240
Gly	Phe	Asn	Arg	Ala	Pro	Ala	Gly	Pro	Ser	Gly	Gly	Pro	Val	Ala	Ala
				245				250						255	
Ser	Ala	Ala	Pro	Ser	Ile	Pro	Ala	Ala	Asn	Met	Pro	Pro	Gly	Ser	Val
			260				265						270		
Glu	Gln	Val	Ala	Ala	Lys	Val	Val	Pro	Ser	Val	Val	Met	Leu	Glu	Thr
			275				280					285			
Asp	Leu	Gly	Arg	Gln	Ser	Glu	Glu	Gly	Ser	Gly	Ile	Ile	Leu	Ser	Ala
			290			295					300				
Glu	Gly	Leu	Ile	Leu	Thr	Asn	Asn	His	Val	Ile	Ala	Ala	Ala	Ala	Lys

```

305          310          315          320
Pro Pro Leu Gly Ser Pro Pro Pro Lys Thr Thr Val Thr Phe Ser Asp
          325          330          335
Gly Arg Thr Ala Pro Phe Thr Val Val Gly Ala Asp Pro Thr Ser Asp
          340          345          350
Ile Ala Val Val Arg Val Gln Gly Val Ser Gly Leu Thr Pro Ile Ser
          355          360          365
Leu Gly Ser Ser Ser Asp Leu Arg Val Gly Gln Pro Val Leu Ala Ile
          370          375          380
Gly Ser Pro Leu Gly Leu Glu Gly Thr Val Thr Thr Gly Ile Val Ser
385          390          395          400
Ala Leu Asn Arg Pro Val Ser Thr Thr Gly Glu Ala Gly Asn Gln Asn
          405          410          415
Thr Val Leu Asp Ala Ile Gln Thr Asp Ala Ala Ile Asn Pro Gly Asn
          420          425          430
Ser Gly Gly Ala Leu Val Asn Met Asn Ala Gln Leu Val Gly Val Asn
          435          440          445
Ser Ala Ile Ala Thr Leu Gly Ala Asp Ser Ala Asp Ala Gln Ser Gly
          450          455          460
Ser Ile Gly Leu Gly Phe Ala Ile Pro Val Asp Gln Ala Lys Arg Ile
465          470          475          480
Ala Asp Glu Leu Ile Ser Thr Gly Lys Ala Ser His Ala Ser Leu Gly
          485          490          495
Val Gln Val Thr Asn Asp Lys Asp Thr Pro Gly Ala Lys Ile Val Glu
          500          505          510
Val Val Ala Gly Gly Ala Ala Ala Asn Ala Gly Val Pro Lys Gly Val
          515          520          525
Val Val Thr Lys Val Asp Asp Arg Pro Ile Asn Ser Ala Asp Ala Leu
530          535          540
Val Ala Ala Val Arg Ser Lys Ala Pro Gly Ala Thr Val Ala Leu Thr
545          550          555          560
Phe Gln Asp Pro Ser Gly Gly Ser Arg Thr Val Gln Val Thr Leu Gly
          565          570          575
Lys Ala Glu Gln
          580

```

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```

Met Asn Asp Gly Lys Arg Ala Val Thr Ser Ala Val Leu Val Val Leu
1          5          10          15
Gly Ala Cys Leu Ala Leu Trp Leu Ser Gly Cys Ser Ser Pro Lys Pro
          20          25          30
Asp Ala Glu Gln Gly Val Pro Val Ser Pro Thr Ala Ser Asp Pro
          35          40          45
Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala Thr Lys Gly Leu
50          55          60
Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys Val Asp Ser Leu

```

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65		70		75		80
Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala Asn Pro Leu Ala						
	85			90		95
Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly Val Pro Phe Arg						
	100			105		110
Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp Asp Trp Ser Asn						
	115			120		125
Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val Leu Asp Pro Ala						
	130			135		140
Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn Leu Gln Ala Gln						
	145			150		155
Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys Ile Thr Gly Thr						
	165			170		175
Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly Ala Lys Ser Ala						
	180			185		190
Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser His His Leu Val						
	195			200		205
Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln Leu Thr Gln Ser						
	210			215		220
Lys Trp Asn Glu Pro Val Asn Val Asp						
225				230		

(2) INFORMATION FOR SEQ ID NO:77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala														
1			5				10					15		
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val														
			20				25					30		
Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile														
			35				40					45		
Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln														
			50				55					60		
Pro Arg														
65														

(2) INFORMATION FOR SEQ ID NO:78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

Val Pro Pro Ala Pro Pro Leu Pro Pro Leu Pro Pro Ser Pro Ile Ser														
1				5				10					15	

[illegible]

(2) INFORMATION FOR SEQ ID NO:79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

Met	Ser	Asn	Ser	Arg	Arg	Arg	Ser	Leu	Arg	Trp	Ser	Trp	Leu	Leu	Ser
1			5						10					15	
Val	Leu	Ala	Ala	Val	Gly	Leu	Gly	Leu	Ala	Thr	Ala	Pro	Ala	Gln	Ala
		20						25					30		
Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe	Ala	Asp	Phe	Pro	Ala	Leu
		35					40					45			
Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln	Val	Ala	Pro	Gln	Val	Val
	50					55					60				
Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn	Ala	Val	Gly	Ala	Gly	Thr
65					70						75				80
Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val	Leu	Thr	Asn	Asn	His	Val
				85					90					95	
Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe	Ser	Val	Gly	Ser	Gly	Gln
			100					105					110		
Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp	Arg	Thr	Gln	Asp	Val	Ala
		115					120					125			
Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	Leu	Pro	Ser	Ala	Ala	Ile	Gly
	130					135					140				
Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	Val	Ala	Met	Gly	Asn	Ser	Gly
145					150					155					160
Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro	Gly	Arg	Val	Val	Ala	Leu
				165					170					175	
Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu	Thr	Gly	Ala	Glu	Glu	Thr
			180					185					190		
Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala	Ile	Gln	Pro	Gly	Asp	Ser
		195					200					205			
Gly	Gly	Pro	Val	Val	Asn	Gly	Leu	Gly	Gln	Val	Val	Gly	Met	Asn	Thr
		210				215					220				
Ala	Ala	Ser	Asp	Asn	Phe	Gln	Leu	Ser	Gln	Gly	Gln	Gly	Gly	Phe	Ala
225					230					235					240
Ile	Pro	Ile	Gly	Gln	Ala	Met	Ala	Ile	Ala	Gly	Gln	Ile	Arg	Ser	Gly
				245					250					255	
Gly	Gly	Ser	Pro	Thr	Val	His	Ile	Gly	Pro	Thr	Ala	Phe	Leu	Gly	Leu
			260					265					270		
Gly	Val	Val	Asp	Asn	Asn	Gly	Asn	Gly	Ala	Arg	Val	Gln	Arg	Val	Val
		275					280					285			

```

Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
290                               295                               300
Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
305                               310                               315                               320
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
                               325                               330                               335
Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
340                               345                               350
Pro Pro Ala
                               355

```

(2) INFORMATION FOR SEQ ID NO:80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```

Ser Pro Lys Pro Asp Ala Glu Glu Gln Gly Val Pro Val Ser Pro Thr
1                               5                               10                               15
Ala Ser Asp Pro Ala Leu Leu Ala Glu Ile Arg Gln Ser Leu Asp Ala
                               20                               25                               30
Thr Lys Gly Leu Thr Ser Val His Val Ala Val Arg Thr Thr Gly Lys
                               35                               40                               45
Val Asp Ser Leu Leu Gly Ile Thr Ser Ala Asp Val Asp Val Arg Ala
50                               55                               60
Asn Pro Leu Ala Ala Lys Gly Val Cys Thr Tyr Asn Asp Glu Gln Gly
65                               70                               75                               80
Val Pro Phe Arg Val Gln Gly Asp Asn Ile Ser Val Lys Leu Phe Asp
                               85                               90                               95
Asp Trp Ser Asn Leu Gly Ser Ile Ser Glu Leu Ser Thr Ser Arg Val
                               100                               105                               110
Leu Asp Pro Ala Ala Gly Val Thr Gln Leu Leu Ser Gly Val Thr Asn
                               115                               120                               125
Leu Gln Ala Gln Gly Thr Glu Val Ile Asp Gly Ile Ser Thr Thr Lys
130                               135                               140
Ile Thr Gly Thr Ile Pro Ala Ser Ser Val Lys Met Leu Asp Pro Gly
145                               150                               155                               160
Ala Lys Ser Ala Arg Pro Ala Thr Val Trp Ile Ala Gln Asp Gly Ser
                               165                               170                               175
His His Leu Val Arg Ala Ser Ile Asp Leu Gly Ser Gly Ser Ile Gln
180                               185                               190
Leu Thr Gln Ser Lys Trp Asn Glu Pro Val Asn Val Asp
195                               200                               205

```

(2) INFORMATION FOR SEQ ID NO:81:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 286 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
 1 5 10 15
 Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
 20 25 30
 His Ala Asp Gly His Ser Leu Leu Leu Asp Ala Thr Asn Pro Ala Val
 35 40 45
 Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
 50 55 60
 Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
 65 70 75 80
 Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
 85 90 95
 Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
 100 105 110
 Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
 115 120 125
 Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
 130 135 140
 Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
 145 150 155 160
 Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
 165 170 175
 Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
 180 185 190
 Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
 195 200 205
 Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
 210 215 220
 Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
 225 230 235 240
 Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
 245 250 255
 Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
 260 265 270
 Leu Pro Gly Phe Asp Glu Gly Gly Gly Leu Arg Pro Xaa Lys
 275 280 285

(2) INFORMATION FOR SEQ ID NO:82:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 173 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

Thr Lys Phe His Ala Leu Met Gln Glu Gln Ile His Asn Glu Phe Thr
 1 5 10 15
 Ala Ala Gln Gln Tyr Val Ala Ile Ala Val Tyr Phe Asp Ser Glu Asp
 20 25 30
 Leu Pro Gln Leu Ala Lys His Phe Tyr Ser Gln Ala Val Glu Glu Arg

111

```

      35              40              45
Asn His Ala Met Met Leu Val Gln His Leu Leu Asp Arg Asp Leu Arg
  50              55              60
Val Glu Ile Pro Gly Val Asp Thr Val Arg Asn Gln Phe Asp Arg Pro
  65              70              75              80
Arg Glu Ala Leu Ala Leu Ala Leu Asp Gln Glu Arg Thr Val Thr Asp
      85              90              95
Gln Val Gly Arg Leu Thr Ala Val Ala Arg Asp Glu Gly Asp Phe Leu
      100              105              110
Gly Glu Gln Phe Met Gln Trp Phe Leu Gln Glu Gln Ile Glu Glu Val
      115              120              125
Ala Leu Met Ala Thr Leu Val Arg Val Ala Asp Arg Ala Gly Ala Asn
      130              135              140
Leu Phe Glu Leu Glu Asn Phe Val Ala Arg Glu Val Asp Val Ala Pro
  145              150              155              160
Ala Ala Ser Gly Ala Pro His Ala Ala Gly Gly Arg Leu
      165              170

```

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```

Arg Ala Asp Glu Arg Lys Asn Thr Thr Met Lys Met Val Lys Ser Ile
  1              5              10              15
Ala Ala Gly Leu Thr Ala Ala Ala Ala Ile Gly Ala Ala Ala Gly
      20              25              30
Val Thr Ser Ile Met Ala Gly Gly Pro Val Val Tyr Gln Met Gln Pro
      35              40              45
Val Val Phe Gly Ala Pro Leu Pro Leu Asp Pro Xaa Ser Ala Pro Xaa
      50              55              60
Val Pro Thr Ala Ala Gln Trp Thr Xaa Leu Leu Asn Xaa Leu Xaa Asp
  65              70              75              80
Pro Asn Val Ser Phe Xaa Asn Lys Gly Ser Leu Val Glu Gly Gly Ile
      85              90              95
Gly Gly Xaa Glu Gly Xaa Xaa Arg Arg Xaa Gln
      100              105

```

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 125 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```

Val Leu Ser Val Pro Val Gly Asp Gly Phe Trp Xaa Arg Val Val Asn
  1              5              10              15
Pro Leu Gly Gln Pro Ile Asp Gly Arg Gly Asp Val Asp Ser Asp Thr

```

112

```

      20      25      30
Arg Arg Ala Leu Glu Leu Gln Ala Pro Ser Val Val Xaa Arg Gln Gly
      35      40      45
Val Lys Glu Pro Leu Xaa Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
      50      55      60
Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
      65      70      75      80
Gly Lys Asn Arg Arg Leu Cys Arg Thr Pro Ser Ser Asn Gln Arg Glu
      85      90      95
Glu Leu Gly Val Arg Trp Ile Pro Arg Ser Arg Cys Ala Cys Val Tyr
      100      105      110
Val Gly His Arg Ala Arg Arg Gly Thr Tyr His Arg Arg
      115      120      125

```

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```

Cys Asp Ala Val Met Gly Phe Leu Gly Gly Ala Gly Pro Leu Ala Val
1      5      10      15
Val Asp Gln Gln Leu Val Thr Arg Val Pro Gln Gly Trp Ser Phe Ala
      20      25      30
Gln Ala Ala Ala Val Pro Val Val Phe Leu Thr Ala Trp Tyr Gly Leu
      35      40      45
Ala Asp Leu Ala Glu Ile Lys Ala Gly Glu Ser Val Leu Ile His Ala
      50      55      60
Gly Thr Gly Gly Val Gly Met Ala Ala Val Gln Leu Ala Arg Gln Trp
      65      70      75      80
Gly Val Glu Val Phe Val Thr Ala Ser Arg Gly Lys Trp Asp Thr Leu
      85      90      95
Arg Ala Xaa Xaa Phe Asp Asp Xaa Pro Tyr Arg Xaa Phe Pro His Xaa
      100      105      110
Arg Ser Ser Xaa Gly
      115

```

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 103 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```

Met Tyr Arg Phe Ala Cys Arg Thr Leu Met Leu Ala Ala Cys Ile Leu
1      5      10      15
Ala Thr Gly Val Ala Gly Leu Gly Val Gly Ala Gln Ser Ala Ala Gln
      20      25      30

```

113

Thr Ala Pro Val Pro Asp Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp
 35 40 45
 Pro Ala Trp Gly Pro Asn Trp Asp Pro Tyr Thr Cys His Asp Asp Phe
 50 55 60
 His Arg Asp Ser Asp Gly Pro Asp His Ser Arg Asp Tyr Pro Gly Pro
 65 70 75 80
 Ile Leu Glu Gly Pro Val Leu Asp Asp Pro Gly Ala Ala Pro Pro Pro
 85 90 95
 Pro Ala Ala Gly Gly Gly Ala
 100

(2) INFORMATION FOR SEQ ID NO:87:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 88 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Val Gln Cys Arg Val Trp Leu Glu Ile Gln Trp Arg Gly Met Leu Gly
 1 5 10 15
 Ala Asp Gln Ala Arg Ala Gly Gly Pro Ala Arg Ile Trp Arg Glu His
 20 25 30
 Ser Met Ala Ala Met Lys Pro Arg Thr Gly Asp Gly Pro Leu Glu Ala
 35 40 45
 Thr Lys Glu Gly Arg Gly Ile Val Met Arg Val Pro Leu Glu Gly Gly
 50 55 60
 Gly Arg Leu Val Val Glu Leu Thr Pro Asp Glu Ala Ala Ala Leu Gly
 65 70 75 80
 Asp Glu Leu Lys Gly Val Thr Ser
 85

(2) INFORMATION FOR SEQ ID NO:88:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
 1 5 10 15
 Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
 20 25 30
 Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
 35 40 45
 Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
 50 55 60
 Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 65 70 75 80
 Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe

85

90

95

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

```

Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
1           5           10           15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
20           25           30
Pro Ile Thr Pro Cys Glu Leu Thr Xaa Xaa Lys Asn Ala Ala Gln Gln
35           40           45
Xaa Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
50           55           60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Xaa
65           70           75           80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
85           90           95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
100          105          110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
115          120          125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
130          135          140
Gln Gly Ala Ser Leu Ala His Xaa Gly Asp Gly Trp Asn Thr Xaa Thr
145          150          155          160
Leu Thr Leu Gln Gly Asp
165

```

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

```

Arg Ala Glu Arg Met
1           5

```

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

```

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
1      5      10      15
Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
20      25      30
Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
35      40      45
Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
50      55      60
Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
65      70      75      80
Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
85      90      95
Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
100     105     110
Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
115     120     125
Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
130     135     140
Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
145     150     155     160
His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
165     170     175
Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
180     185     190
Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
195     200     205
Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
210     215     220
Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
225     230     235     240
Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
245     250     255
Arg Arg Asn Gly Gly Pro Ala
260

```

(2) INFORMATION FOR SEQ ID NO:92:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 303 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

```

Met Thr Tyr Ser Pro Gly Asn Pro Gly Tyr Pro Gln Ala Gln Pro Ala
1      5      10      15
Gly Ser Tyr Gly Gly Val Thr Pro Ser Phe Ala His Ala Asp Glu Gly
20      25      30
Ala Ser Lys Leu Pro Met Tyr Leu Asn Ile Ala Val Ala Val Leu Gly
35      40      45
Leu Ala Ala Tyr Phe Ala Ser Phe Gly Pro Met Phe Thr Leu Ser Thr

```

116

```

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

```

(2) INFORMATION FOR SEQ ID NO:93:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

```

Gly Cys Gly Glu Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn
1           5           10           15
Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile
      20           25

```

(2) INFORMATION FOR SEQ ID NO:94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

Gly Cys Gly Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala
 1 5 10 15
 Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:96:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Gly Cys Gly Gly Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu
 1 5 10 15
 Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu
 20 25

(2) INFORMATION FOR SEQ ID NO:97:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

Gly Cys Gly Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr
 1 5 10 15
 Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
 20 25

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids

- (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

```

Gly Cys Gly Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu
1       5       10      15
Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
      20      25
  
```

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 507 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

```

ATGAAGATGG TGAAATCGAT CGCCGCAGGT CTGACCGCCG CGGCTGCAAT CGGCGCCGCT      60
GCGGCCGGTG TGACTTCGAT CATGGCTGGC GGCCCGGTTCG TATACCAGAT GCAGCCGGTC      120
GTCTTCGGCG CGCCACTGCC GTTGGACCCG GCATCCGCCC CTGACGTCCC GACCGCCGCC      180
CAGTTGACCA GCCTGCTCAA CAGCCTCGCC GATCCCAACG TGTCGTTTGC GAACAAGGGC      240
AGTCTGGTCG AGGGCGGCAT CGGGGGCACC GAGGCGCGCA TCGCCGACCA CAAGCTGAAG      300
AAGGCCGCGG AGCACGGGGA TCTGCCGCTG TCCTTCAGCG TGACGAACAT CCAGCCGGCG      360
GCCGCCGGTT CGGCCACCGC CGACGTTTCC GTCTCGGGTC CGAAGCTCTC GTCGCCGGTC      420
ACGCAGAACG TCACGTTCGT GAATCAAGGC GGCTGGATGC TGTCACGCGC ATCGGCGATG      480
GAGTTGCTGC AGGCCGCAGG GAACTGA                                     507
  
```

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 168 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

```

Met Lys Met Val Lys Ser Ile Ala Ala Gly Leu Thr Ala Ala Ala Ala
1       5       10      15
Ile Gly Ala Ala Ala Gly Val Thr Ser Ile Met Ala Gly Gly Pro
      20      25      30
Val Val Tyr Gln Met Gln Pro Val Val Phe Gly Ala Pro Leu Pro Leu
      35      40      45
Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
      50      55      60
Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn Lys Gly
      65      70      75      80
Ser Leu Val Glu Gly Gly Ile Gly Gly Thr Glu Ala Arg Ile Ala Asp
      85      90      95
His Lys Leu Lys Lys Ala Ala Glu His Gly Asp Leu Pro Leu Ser Phe
  
```

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```

          100              105              110
Ser Val Thr Asn Ile Gln Pro Ala Ala Ala Gly Ser Ala Thr Ala Asp
          115              120              125
Val Ser Val Ser Gly Pro Lys Leu Ser Ser Pro Val Thr Gln Asn Val
          130              135              140
Thr Phe Val Asn Gln Gly Gly Trp Met Leu Ser Arg Ala Ser Ala Met
          145              150              155              160
Glu Leu Leu Gln Ala Ala Gly Asn
          165

```

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 500 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

```

CGTGGCAATG TCGTTGACCG TCGGGGCCGG GGTGCGCTCC GCAGATCCCG TGGACGCGGT      60
CATTAACACC ACCTGCAATT ACGGGCAGGT AGTAGCTGCG CTCAACGCGA CGGATCCGGG      120
GGCTGCCGCA CAGTTCAACG CCTCACCAGT GCGCGAGTCC TATTTGCGCA ATTTCTCTCG      180
CGCACCGCCA CCTCAGCGCG CTGCCATGGC CGCGCAATTG CAAGCTGTGC CGGGGGCGGC      240
ACAGTACATC GGCCTTGTCG AGTCGGTTGC CGGCTCCTGC AACAACTATT AAGCCCATGC      300
GGGCCCCATC CCGCGACCCG GCATCGTCGC CGGGGCTAGG CCAGATTGCC CCGCTCCTCA      360
ACGGGCCGCA TCCCGCGACC CGGCATCGTC GCGGGGGCTA GGCCAGATTG CCCCCTCCT      420
CAACGGGCCG CATCTCGTGC CGAATTCCTG CAGCCCGGGG GATCCACTAG TTCTAGAGCG      480
CGCGCCACCG CGGTGGAGCT

```

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

```

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1              5              10              15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
          20              25              30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
          35              40              45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
          50              55              60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65              70              75              80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
          85              90              95

```

(2) INFORMATION FOR SEQ ID NO:103:

120

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

```

ATGACAGAGC AGCAGTGGAA TTTCGCGGGT ATCGAGGCCG CGGCAAGCGC AATCCAGGGA      60
AATGTCACGT CCATTCAATC CCTCCTTGAC GAGGGGAAGC AGTCCCTGAC CAAGCTCGCA      120
GCGGCCTGGG GCGGTAGCGG TTCGGAAGCG TACC                                154

```

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 51 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

```

Met Thr Glu Gln Gln Trp Asn Phe Ala Gly Ile Glu Ala Ala Ala Ser
1           5           10           15
Ala Ile Gln Gly Asn Val Thr Ser Ile His Ser Leu Leu Asp Glu Gly
          20           25           30
Lys Gln Ser Leu Thr Lys Leu Ala Ala Ala Trp Gly Gly Ser Gly Ser
          35           40           45
Glu Ala Tyr
          50

```

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

```

CGGTGCGCGCA CTTCCAGGTG ACTATGAAAG TCGGCTTCCG NCTGGAGGAT TCCTGAACCT      60
TCAAGCGCGG CCGATAACTG AGGTGCATCA TTAAGCGACT TTTCCAGAAC ATCCTGACGC      120
GCTCGAAACG CGGCACAGCC GACGGTGGCT CCGNCGAGGC GCTGNCTCCA AAATCCCTGA      180
GACAATTTCGN CGGGGGCGCC TACAAGGAAG TCGGTGCTGA ATTCGNCNG TATCTGGTTCG      240
ACCTGTGTGG TCTGNAGCCG GACGAAGCGG TGCTCGACGT CG                                282

```

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3058 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT	60
GGCATAACCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC	120
TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA	180
TGAGGTGTCT GCGCTGACTG CGGCGCACTT CGCCGCACAT GCGGCGATGT ATCAGTCCGT	240
GAGCGCTCGG GCTGCTGCGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG	300
CTCGTATGCG GCCACTGAAG TCGCCAATGC GCGGCGGGCC AGCTAAGCCA GGAACAGTCG	360
GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGGA TTTCGGGGCG TTACCACCGG	420
AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC CTCGCTGGTG GCCGCGGCTC	480
AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC GTCGGCGTTT CAGTCGGTGG	540
TCTGGGGTCT GACGGTGGGG TCGTGATAG GTTCGTCCGC GGGTCTGATG GTGGCGGCGG	600
CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA GGCCGAGCTG ACCGCCGCCC	660
AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG GCTGACGGTG CCCCCGCGG	720
TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA	780
ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGCGA GATGTGGGCC CAAGACGCCG	840
CCGCGATGTT TGGCTACGCC GCGGCGACGG CGACGGCGAC GGCGACGTTG CTGCCGTTG	900
AGGAGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC GCGGTCGAGG	960
AGGCCTCCGA CACCGCCGCG GCGAACCAGT TGATGAACAA TGTGCCCCAG GCGCTGCAAC	1020
AGCTGGCCCA GCCACGCAG GGCACCACGC CTTCTTCCAA GCTGGGTGGC CTGTGGAAGA	1080
CGGTCTCGCC GCATCGGTCT CCGATCAGCA ACATGGTGTC GATGGCCAAC AACCACATGT	1140
CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGGCTTTG	1200
CTCCGGCGGC GGCCGCCGAG GCCGTGCAAA CCGCGGCGCA AAACGGGGTC CGGGCGATGA	1260
GCTCGCTGGG CAGCTCGCTG GGTCTTCGG GTCTGGGCGG TGGGTGGCC GCCAACTTGG	1320
GTCGGGCGGC CTCGGTCGGT TCGTTGTCGG TGCCGCAGGC CTGGGCCGCG GCCAACCAGG	1380
CAGTACCCCC GGCGGCGCGG GCGCTGCCGC TGACCAGCCT GACCAGCGCC GCGGAAAGAG	1440
GGCCCGGGCA GATGCTGGGC GGGCTGCCGG TGGGGCAGAT GGGCGCCAGG GCCGGTGGTG	1500
GGCTCAGTGG TGTGCTGCGT GTTCCGCCGC GACCCTATGT GATGCCGCAT TCTCCGGCGG	1560
CCGGCTAGGA GAGGGGGCGC AGACTGTCTG TATTTGACCA GTGATCGGCG GTCTCGGTGT	1620

TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG	1680
GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTTATG ACGGATCCGC ACGCGATGCG	1740
GGACATGGCG GGCCGTTTTG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGGAT	1800
GTGGGCGTCC GCGCAAAACA TTTCCGGTGC GGGCTGGAGT GGCATGGCCG AGGCGACCTC	1860
GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGCTGCACGG	1920
GGTGCGTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA	1980
GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAAT ACTTTTACAA GCGAAGGAGA	2040
ACAGGTTTGA TGACCATCAA CTATCAATTC GGGGATGTCT ACGCTCACGG CGCCATGATC	2100
CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTCTGTA TGTGTTGACC	2160
GCGAGTGACT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTTCAT TACCCAGTTG	2220
GGCCGTAACT TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT	2280
GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGGC CTGACACCAG	2340
GCCAAGGCCA GGGACGTGGT GTACGAGTGA AGTTCCTCGC GTGATCCTTC GGGTGGCAGT	2400
CTAAGTGGTC AGTGCTGGGG TGTGTTGGT TTGCTGCTTG GCGGGTTCTT CGGTGCTGGT	2460
CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCCAGG TAGCGCCGTC CTTCGATCCA	2520
TTCGTCGTGT TGTTCGGCGA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCTGGG	2580
GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT	2640
GTTGGACCAG ATTTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT	2700
GCGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC	2760
CCGATCATAT TGGGCAACAA CTGATTCGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG	2820
GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG	2880
GTTTCTGCAG CGCTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCGG CCACCAGGCC	2940
GGCGTGGGCG TCGCTGGTGA CCAGCGCGAC CCCGGACAGG CCGCGGGCGA CCAGGTCGCG	3000
GAAGAACGCC AGCCAGCCGG CCCCCTCCTC GGCGGAGGTG ACCTGGATGC CCAGGATC	3058

(2) INFORMATION FOR SEQ ID NO:107:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160
 Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
 165 170 175
 Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270

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Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285

Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300

Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320

Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335

Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350

Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365

Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380

Pro His Ser Pro Ala Ala Gly
 385 390

(2) INFORMATION FOR SEQ ID NO:108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1725 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

GACGTCAGCA CCCGCCGTGC AGGGCTGGAG CGTGGTCGGT TTTGATCTGC GGTCAAGGTG 60

ACGTCCCTCG GCGTGTCGCC GGCCTGGATG CAGACTCGAT GCCGCTCTTT AGTGCAACTA 120

ATTTCGTTGA AGTGCTGCG AGGTATAGGA CTTACGATT GGTAAATGTA GCGTTCACCC 180

CGTGTGGGG TCGATTTGGC CGGACCAGTC GTCACCAACG CTTGGCGTGC GCGCCAGGCG 240

GGCGATCAGA TCGCTTGACT ACCAATCAAT CTTGAGCTCC CGGGCCGATG CTCGGGCTAA 300

ATGAGGAGGA GCACGCGTGT CTTTCACTGC GCAACCGGAG ATGTTGGCGG CCGCGGCTGG 360

CGAACTTCGT TCCCTGGGGG CAACGCTGAA GGCTAGCAAT GCCGCCGCAG CCGTGCCGAC 420

GACTGGGGTG GTGCCCCCGG CTGCCGACGA GGTGTCGCTG CTGCTTGCCA CACAATTCCG 480

TACGCATGCG GCGACGTATC AGACGGCCAG CGCCAAGGCC GCGGTGATCC ATGAGCAGTT 540

TGTGACCACG CTGGCCACCA GCGCTAGTTC ATATGCGGAC ACCGAGGCCG CCAACGCTGT 600

GGTCACCGGC TAGCTGACCT GACGGTATTC GAGCGGAAGG ATTATCGAAG TGGTGGATTT 660

CGGGGCGTTA CCACCGGAGA TCAACTCCGC GAGGATGTAC GCCGGCCCCG GTTCGGCCTC 720
 GCTGGTGGCC GCCGCGAAGA TGTGGGACAG CGTGGCGAGT GACCTGTTTT CGGCCGCGTC 780
 GGCGTTTCAG TCGGTGGTCT GGGGTCTGAC GGTGGGGTCG TGGATAGGTT CGTCGGCGGG 840
 TCTGATGGCG GCGGCGGCCT CGCCGTATGT GCGGTGGATG AGCGTCACCG CGGGGCAGGC 900
 CCAGCTGACC GCCGCCCAGG TCCGGGTTGC TCGGCGGCC TACGAGACAG CGTATAGGCT 960
 GACGGTGCCC CCGCCGGTGA TCGCCGAGAA CCGTACCGAA CTGATGACGC TGACCGCGAC 1020
 CAACCTCTTG GGGCAAAACA CGCCGGCGAT CGAGGCCAAT CAGGCCGCAT ACAGCCAGAT 1080
 GTGGGGCCAA GACGCGGAGG CGATGTATGG CTACGCCGCC ACGGCGGCGA CGGCGACCGA 1140
 GGCGTTGCTG CCGTTCGAGG ACGCCCCACT GATCACCAAC CCCGGCGGGC TCCTTGAGCA 1200
 GGCCGTCGCG GTCGAGGAGG CCATCGACAC CGCCGCGGCG AACCAGTTGA TGAACAATGT 1260
 GCCCCAAGCG CTGCAACAGC TGGCCCAGCC AGCGCAGGGC GTCGTACCTT CTTCCAAGCT 1320
 GGGTGGGCTG TGGACGGCGG TCTCGCCGCA TCTGTGCGCG CTCAGCAACG TCAGTTGAT 1380
 AGCCAACAAC CACATGTGCA TGATGGGCAC GGGTGTGTCG ATGACCAACA CCTTGCACTC 1440
 GATGTTGAAG GGCTTAGCTC CGGCGGCGGC TCAGGCCGTG GAAACCGCGG CGGAAAACGG 1500
 GGTCTGGGCG ATGAGCTCGC TGGGCAGCCA GCTGGGTTG TCGCTGGGTT CTTGCGGTCT 1560
 GGGCGCTGGG GTGGCCGCCA ACTTGGGTCG GGCGGCCTCG GTCGGTTCGT TGTCGGTGCC 1620
 GCCAGCATGG GCCGCGGCCA ACCAGGCGGT CACCCCGGCG GCGCGGGCGC TGCCGCTGAC 1680
 CAGCCTGACC AGCGCCGCCC AAACCGCCCC CGGACACATG CTGGG 1725

(2) INFORMATION FOR SEQ ID NO:109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 359 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45

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

Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Gln Thr
 340 345 350

Ala Pro Gly His Met Leu Gly
 355

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3027 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

AGTTCAGTCG AGAATGATAC TGACGGGCTG TATCCACGAT GGCTGAGACA ACCGAACCAC	60
CGTCGGACGC GGGGACATCG CAAGCCGACG CGATGGCGTT GGCCGCCGAA GCCGAAGCCG	120
CCGAAGCCGA AGCGCTGGCC GCCGCGGCGC GGGCCCGTGC CCGTGCCGCC CGGTTGAAGC	180
GTGAGGCGCT GGCGATGGCC CCAGCCGAGG ACGAGAACGT CCCCAGGAT ATGCAGACTG	240
GGAAGACGCC GAAGACTATG ACGACTATGA CGACTATGAG GCCGCAGACC AGGAGGCCGC	300
ACGGTCGGCA TCCTGGCGAC GGCGGTTGCG GGTGCGGTTA CCAAGACTGT CCACGATTGC	360
CATGGCGGCC GCAGTCGTCA TCATCTGCGG CTTACCCGGG CTCAGCGGAT ACATTGTGTG	420
GCAACACCAT GAGGCCACCG AACGCCAGCA GCGCGCCGCG GCGTTCGCCG CCGGAGCCAA	480
GCAAGGTGTC ATCAACATGA CCTCGCTGGA CTTCAACAAG GCCAAAGAAG ACGTCGCGCG	540
TGTGATCGAC AGTCCACCG GCGAATTCAG GGATGACTTC CAGCAGCGGG CAGCCGATTT	600
CACCAAGGTT GTCGAACAGT CCAAAGTGGT CACCGAAGGC ACGGTGAACG CGACAGCCGT	660
CGAATCCATG AACGAGCATT CCGCCCTGGT GCTCGTCGCG GCGACTTCAC GGGTCACCAA	720
TTCCGCTGGG GCGAAAGACG AACCACGTGC GTGGCGGCTC AAAGTGACCG TGACCGAAGA	780
GGGGGGACAG TACAAGATGT CGAAAGTTGA GTTCGTACCG TGACCGATGA CGTACGCGAC	840
GTCAACACCG AAACCACTGA CGCCACCGAA GTCGCTGAGA TCGACTCAGC CGCAGGCGAA	900
GCCGGTGATT CGGCGACCGA GGCATTTGAC ACCGACTCTG CAACGGAATC TACCGCGCAG	960
AAGGGTCAGC GGCACCGTGA CCTGTGGCGA ATGCAGGTTA CTTGAAACC CGTTCCGGTG	1020
ATTCTCATCC TGCTCATGTT GATCTCTGGG GGCGCGACGG GATGGCTATA CCTTGAGCAA	1080
TACGACCCGA TCAGCAGACG GACTCCGGCG CCGCCCGTGC TGCCGTCGCC GCGGCGTCTG	1140
ACGGGACAAT CGCGCTGTTG TGTATTCACC CGACACGTGC ACCAAGACTT CGCTACCGCC	1200

AGGTCGCACC TCGCCGGCGA TTTCTGTCC TATACGACCA GTTCACGCAG CAGATCGTGG 1260
CTCCGGCGGC CAAACAGAAG TCACTGAAAA CCACCGCCAA GGTGGTGCGC GCGGCCGTGT 1320
CGGAGCTACA TCCGGATTCTG GCCGTCGTTC TGGTTTTTGT CGACCAGAGC ACTACCAGTA 1380
AGGACAGCCC CAATCCGTCG ATGGCGGCCA GCAGCGTGAT GGTGACCCTA GCCAAGGTCTG 1440
ACGGCAATTG GCTGATCACC AAGTTCACCC CGGTTTAGGT TGCCGTAGGC GGTGCGCAAG 1500
TCTGACGGGG GCGCGGGTGG CTGCTCGTGC GAGATACCGG CCGTTCTCCG GACAATCAGC 1560
GCCCCACCTC AAACAGATCT CGGCCGCTGT CTAATCGGCC GGGTTATTTA AGATTAGTTG 1620
CCACTGTATT TACCTGATGT TCAGATTGTT CAGCTGGATT TAGCTTCGCG GCAGGGCGGC 1680
TGGTGCACTT TGCATCTGGG GTTGTGACTA CTTGAGAGAA TTTGACCTGT TGCCGACGTT 1740
GTTTGCTGTC CATCATTTGGT GCTAGTTATG GCCGAGCGGA AGGATTATCG AAGTGGTGA 1800
CTTCGGGGCG TTACCACCGG AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC 1860
CTCGCTGGTG GCCGCCGCGA AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC 1920
GTCGGCGTTT CAGTCGGTGG TCTGGGGTCT GACGACGGGA TCGTGATAG GTTCGTCGGC 1980
GGGTCTGATG GTGGCGGCGG CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA 2040
GGCCGAGCTG ACCGCCGCC AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG 2100
GCTGACGGTG CCCCCGCCG TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC 2160
GACCAACCTC TTGGGGCAAA ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGGGA 2220
GATGTGGGCC CAAGACGCCG CCGCATGTT TGGCTACGCC GCCACGGCGG CGACGGCGAC 2280
CGAGGCGTTG CTGCCGTTCTG AGGACGCCCC ACTGATCACC AACCCCGGCG GGCTCCTTGA 2340
GCAGGCCGTC GCGGTCGAGG AGGCCATCGA CACCGCCGCG GCGAACCAGT TGATGAACAA 2400
TGTGCCCCAA GCGCTGCAAC AACTGGCCCA GCCCAGGAAA AGCATCTGGC CGTTCGACCA 2460
ACTGAGTGAA CTCTGGAAAG CCATCTCGCC GCATCTGTCTG CCGCTCAGCA ACATCGTGTC 2520
GATGCTCAAC AACCACGTGT CGATGACCAA CTCGGGTGTG TCGATGGCCA GCACCTTGCA 2580
CTCAATGTTG AAGGGCTTTG CTCCGGCGGC GGCTCAGGCC GTGGAAACCG CGGCGCAAAA 2640
CGGGGTCCAG GCGATGAGCT CGCTGGGCAG CCAGCTGGGT TCGTCGCTGG GTTCTTCGGG 2700
TCTGGGCGCT GGGGTGGCCG CCAACTTGGG TCGGGCGGCC TCGGTCGGTT CGTTGTCTGGT 2760
GCCGCAGGCC TGGGCCGCGG CCAACCAGGC GGTCACCCCG GCGGCGCGGG CGCTGCCGCT 2820

GACCAGCCTG ACCAGCGCCG CCCAAACCGC CCCC GGACAC ATGCTGGGCG GGCTACCGCT 2880
 GGGGCAACTG ACCAATAGCG GCGGCGGGTT CGGCGGGGTT AGCAATGCGT TCGGATGCC 2940
 GCCGCGGGCG TACGTAATGC CCCGTGTGCC CGCCGCCGGG TAACGCCGAT CCGCACGCAA 3000
 TCGGGGCCCT CTATGCGGGC AGCGATC 3027

(2) INFORMATION FOR SEQ ID NO:111:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

Val Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Lys Met Trp
 20 25 30
 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Thr Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110
 Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125
 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Thr Ala Ala
 145 150 155 160
 Thr Ala Thr Glu Ala Leu Leu Pro Phe Glu Asp Ala Pro Leu Ile Thr
 165 170 175
 Asn Pro Gly Gly Leu Leu Glu Gln Ala Val Ala Val Glu Glu Ala Ile
 180 185 190
 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu

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

(2) INFORMATION FOR SEQ ID NO:112:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1616 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

CATCGGAGGG AGTGATCACC ATGCTGTGGC ⁻ ACGCAATGCC ACCGGAGTAA ATACCGCACG	60
GCTGATGGCC GGCGCGGGTC CGGCTCCAAT GCTTGCGGCG GCCGCGGGAT GGCAGACGCT	120
TTCGGCGGCT CTGGACGCTC AGGCCGTCGA GTTGACCGCG CGCCTGAACT CTCTGGGAGA	180
AGCCTGGACT GGAGGTGGCA GCGACAAGGC GCTTGCGGCT GCAACGCCGA TGGTGGTCTG	240

GCTACAAACC GCGTCAACAC AGGCCAAGAC CCGTGCGATG CAGGCGACGG CGCAAGCCGC	300
GGCATAACACC CAGGCCATGG CCACGACGCC GTCGCTGCCG GAGATCGCCG CCAACCACAT	360
CACCCAGGCC GTCCTTACGG CCACCAACTT CTTCGGTATC AACACGATCC CGATCGCGTT	420
GACCGAGATG GATTATTTCA TCCGTATGTG GAACCAGGCA GCCCTGGCAA TGGAGGTCTA	480
CCAGGCCGAG ACCGCGGTTA ACACGCTTTT CGAGAAGCTC GAGCCGATGG CGTCGATCCT	540
TGATCCCGGC GCGAGCCAGA GCACGACGAA CCCGATCTTC GGAATGCCCT CCCCTGGCAG	600
CTCAACACCG GTTGGCCAGT TGCCGCCGGC GGCTACCCAG ACCCTCGGCC AACTGGGTGA	660
GATGAGCGGC CCGATGCAGC AGCTGACCCA GCCGCTGCAG CAGGTGACGT CGTTGTTTCA	720
CCAGGTGGGC GGCACCGGCG GCGGCAACCC AGCCGACGAG GAAGCCGCGC AGATGGGCCT	780
GCTCGGCACC AGTCCGCTGT CGAACCATCC GCTGGCTGGT GGATCAGGCC CCAGCGCGGG	840
CGCGGGCCTG CTGCGCGCGG AGTCGCTACC TGGCGCAGGT GGGTCGTTGA CCCGCACGCC	900
GCTGATGTCT CAGCTGATCG AAAAGCCGGT TGCCCCCTCG GTGATGCCGG CGGCTGCTGC	960
CGGATCGTCG GCGACGGGTG GCGCCGCTCC GGTGGGTGCG GGAGCGATGG GCCAGGGTGC	1020
GCAATCCGGC GGCTCCACCA GGCCGGGTCT GGTGCGCGCG GCACCGCTCG CGCAGGAGCG	1080
TGAAGAAGAC GACGAGGACG ACTGGGACGA AGAGGACGAC TGGTGAGCTC CCGTAATGAC	1140
AACAGACTTC CCGGCCACCC GGGCCGGAAG ACTTGCCAAC ATTTTGGCGA GGAAGGTAAA	1200
GAGAGAAAGT AGTCCAGCAT GGCAGAGATG AAGACCGATG CCGCTACCCT CGCGCAGGAG	1260
GCAGGTAATT TCGAGCGGAT CTCCGGCGAC CTGAAAACCC AGATCGACCA GGTGGAGTCG	1320
ACGGCAGGTT CGTTGCAGGG CCAGTGGCGC GGC CGCGCGG GGACGGCCGC CCAGGCCGCG	1380
GTGGTGCGCT TCCAAGAAGC AGCCAATAAG CAGAAGCAGG AACTCGACGA GATCTCGACG	1440
AATATTCGTC AGGCCGGCGT CCAATACTCG AGGGCCGACG AGGAGCAGCA GCAGGCGCTG	1500
TCCTCGCAA TGGGCTTCTG ACCCGCTAAT ACGAAAAGAA ACGGAGCAA AACATGACAG	1560
AGCAGCAGTG GAATTCGCG GGTATCGAGG CCGCGGCAAG CGCAATCCAG GGAAAT	1616

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

CTAGTGGATG GGACCATGGC CATTTTCTGC AGTCTCACTG CCTTCTGTGT TGACATTTTG	60
GCACGCCGGC GGAAACGAAG CACTGGGGTC GAAGAACGGC TGCGCTGCCA TATCGTCCGG	120
AGCTTCCATA CCTTCGTGCG GCCGGAAGAG CTTGTCGTAG TCGGCCGCCA TGACAACCTC	180
TCAGAGTGCG CTCAAACGTA TAAACACGAG AAAGGGCGAG ACCGACGGAA GGTGGAATC	240
GCCCCATCCC GTGTTTCGCT ATTCTACGCG AACTCGGCGT TGCCCTATGC GAACATCCCA	300
GTGACGTTGC CTTCCGGTCGA AGCCATTGCC TGACCGGCTT CGCTGATCGT CCGCGCCAGG	360
TTCTGCAGCG CGTTGTTCAG CTCGGTAGCC GTGGCGTCCC ATTTTGTCTG GACACCCTGG	420
TACGCCTCCG AA	432

(2) INFORMATION FOR SEQ ID NO:114:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:

Met	Leu	Trp	His	Ala	Met	Pro	Pro	Glu	Xaa	Asn	Thr	Ala	Arg	Leu	Met	1	5	10	15
Ala	Gly	Ala	Gly	Pro	Ala	Pro	Met	Leu	Ala	Ala	Ala	Ala	Gly	Trp	Gln	20	25	30	
Thr	Leu	Ser	Ala	Ala	Leu	Asp	Ala	Gln	Ala	Val	Glu	Leu	Thr	Ala	Arg	35	40	45	
Leu	Asn	Ser	Leu	Gly	Glu	Ala	Trp	Thr	Gly	Gly	Gly	Ser	Asp	Lys	Ala	50	55	60	
Leu	Ala	Ala	Ala	Thr	Pro	Met	Val	Val	Trp	Leu	Gln	Thr	Ala	Ser	Thr	65	70	75	80
Gln	Ala	Lys	Thr	Arg	Ala	Met	Gln	Ala	Thr	Ala	Gln	Ala	Ala	Ala	Tyr	85	90	95	
Thr	Gln	Ala	Met	Ala	Thr	Thr	Pro	Ser	Leu	Pro	Glu	Ile	Ala	Ala	Asn	100	105	110	
His	Ile	Thr	Gln	Ala	Val	Leu	Thr	Ala	Thr	Asn	Phe	Phe	Gly	Ile	Asn	115	120	125	
Thr	Ile	Pro	Ile	Ala	Leu	Thr	Glu	Met	Asp	Tyr	Phe	Ile	Arg	Met	Trp	130	135	140	

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

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

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

134

Asn Phe Glu Arg Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val
 20 25 30
 Glu Ser Thr Ala Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly
 35 40 45
 Thr Ala Ala Gln Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys
 50 55 60
 Gln Lys Gln Glu Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly
 65 70 75 80
 Val Gln Tyr Ser Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser
 85 90 95
 Gln Met Gly Phe
 100

(2) INFORMATION FOR SEQ ID NO:116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

GATCTCCGGC GACCTGAAAA CCCAGATCGA CCAGGTGGAG TCGACGGCAG GTTCGTTGCA 60
 GGGCCAGTGG CGCGGCGCGG CGGGGACGGC CGCCCAGGCC GCGGTGGTGC GCTTCCAAGA 120
 AGCAGCCAAT AAGCAGAAGC AGGAACTCGA CGAGATCTCG ACGAATATTC GTCAGGCCGG 180
 CGTCCAATAC TCGAGGGCCG ACGAGGAGCA GCAGCAGGCG CTGTCCTCGC AAATGGGCTT 240
 CTGACCCGCT AATACGAAAA GAAACGGAGC AAAACATGA CAGAGCAGCA GTGGAATTTT 300
 GCGGGTATCG AGGCCGCGGC AAGCGCAATC CAGGGAAATG TCACGTCCAT TCATTCCTC 360
 CTTGACGAGG GGAAGCAGTC CCTGACCAAG CTCGCA 396

(2) INFORMATION FOR SEQ ID NO:117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

Ile Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala
 1 5 10 15

135

Gly Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln
 20 25 30
 Ala Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu
 35 40 45
 Leu Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser
 50 55 60
 Arg Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
 65 70 75 80

(2) INFORMATION FOR SEQ ID NO:118:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 387 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

GTGGATCCCG ATCCCGTGTT TCGCTATTCT ACGCGAACTC GGC GTTGCCC TATGCGAACA 60
 TCCCAGTGAC GTTGCCCTTCG GTCGAAGCCA TTGCCTGACC GGCTTCGCTG ATCGTCCGCG 120
 CCAGGTTCTG CAGCGCGTTG TTCAGCTCGG TAGCCGTGGC GTCCCATTTT TGCTGGACAC 180
 CCTGGTACGC CTCCGAACCG CTACCGCCCC AGGCCGCTGC GAGCTTGGTC AGGGACTGCT 240
 TCCCCTCGTC AAGGAGGGAA TGAATGGACG TGACATTTCC CTGGATTGCG CTTGCCGCGG 300
 CCTCGATACC CGCGAAATTC CACTGCTGCT CTGTCTGTT TTTGCTCCGT TTCTTTTCGT 360
 ATTAGCGGGT CAGAAGCCCA TTTGCGA 387

(2) INFORMATION FOR SEQ ID NO:119:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 272 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

CGGCACGAGG ATCTCGGTTG GCCCAACGGG GCTGGCGAGG GCTCCGTTCC GGGGGCGAGC 60
 TGCGCGCCCG ATGCTTCCTC TGCCCGCAGC CGCGCCTGGA TGGATGGACC AGTTGCTACC 120
 TTCCCACGCT TTCGTTCCGT GTCTGTGCGA TAGCGGTGAC CCCGGCGCGC ACGTCTGGGAG 180
 TGTGTTTTGGG CAGGCCGGGT CGGTGGTTTC GCCGGGGGAC CAGACGGTCT GGACGGAACG 240

GGCGGGGGTT CGCCGATTGG CATCTTTGCC CA

272

(2) INFORMATION FOR SEQ ID NO:120:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val
1				5					10					15	
Val Ala Ala Leu															
20															

(2) INFORMATION FOR SEQ ID NO:121:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

Ala	Val	Glu	Ser	Gly	Met	Leu	Ala	Leu	Gly	Thr	Pro	Ala	Pro	Ser
1				5					10				15	

(2) INFORMATION FOR SEQ ID NO:122:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

Ala	Ala	Met	Lys	Pro	Arg	Thr	Gly	Asp	Gly	Pro	Leu	Glu	Ala	Ala	Lys
1				5					10					15	
Glu Gly Arg															

(2) INFORMATION FOR SEQ ID NO:123:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

Tyr Tyr Trp Cys Pro Gly Gln Pro Phe Asp Pro Ala Trp Gly Pro
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

Asp Ile Gly Ser Glu Ser Thr Glu Asp Gln Gln Xaa Ala Val
 1 5 10

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

Ala Glu Glu Ser Ile Ser Thr Xaa Glu Xaa Ile Val Pro
 1 5 10

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

Asp Pro Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro
 1 5 10 15

Ser

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

Ala Pro Lys Thr Tyr Xaa Glu Glu Leu Lys Gly Thr Asp Thr Gly
 1 5 10 15

(2) INFORMATION FOR SEQ ID NO:128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

Asp Pro Ala Ser Ala Pro Asp Val Pro Thr Ala Ala Gln Leu Thr Ser
 1 5 10 15
 Leu Leu Asn Ser Leu Ala Asp Pro Asn Val Ser Phe Ala Asn
 20 25 30

(2) INFORMATION FOR SEQ ID NO:129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

Asp Pro Pro Asp Pro His Gln Xaa Asp Met Thr Lys Gly Tyr Tyr Pro
 1 5 10 15
 Gly Gly Arg Arg Xaa Phe
 20

(2) INFORMATION FOR SEQ ID NO:130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

Asp Pro Gly Tyr Thr Pro Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids

(D) OTHER INFORMATION: /note= "The Second Residue Can Be Either a Pro or Thr"

Xaa Xaa Gly Phe Thr Gly Pro Gln Phe Tyr
1 5 10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(D) OTHER INFORMATION: /note= "The Third Residue Can Be Either a Gln or Leu"

Xaa Pro Xaa Val Thr Ala Tyr Ala Gly
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Xaa Xaa Xaa Glu Lys Pro Phe Leu Arg
1 5

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

Xaa Asp Ser Glu Lys Ser Ala Thr Ile Lys Val Thr Asp Ala Ser
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

Ala Gly Asp Thr Xaa Ile Tyr Ile Val Gly Asn Leu Thr Ala Asp
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 15 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

Ala Pro Glu Ser Gly Ala Gly Leu Gly Gly Thr Val Gln Ala Gly
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 21 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

Xaa Tyr Ile Ala Tyr Xaa Thr Thr Ala Gly Ile Val Pro Gly Lys Ile
1 5 10 15

Asn Val His Leu Val
20

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 882 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

GCAACGCTGT CGTGGCCTTT GCGGTGATCG GTTTCGCCTC GCTGGCGGTG GCGGTGGCGG	60
TCACCATCCG ACCGACCGCG GCCTCAAAAC CGGTAGAGGG ACACCAAAAC GCCCAGCCAG	120
GGAAGTTCAT GCCGTTGTTG CCGACGCAAC AGCAGGCGCC GGTCCCGCCG CCTCCGCCCCG	180
ATGATCCCAC CGCTGGATTC CAGGGCGGCA CCATTCCGGC TGTACAGAAC GTGGTGCCGC	240
GGCCGGGTAC CTCACCCGGG GTGGGTGGGA CGCCGGCTTC GCCTGCGCCG GAAGCGCCGG	300
CCGTGCCCCG TGTGTGCCT GCCCCGGTGC CAATCCCGGT CCCGATCATC ATTCCCCCGT	360
TCCCGGGTTG GCAGCCTGGA ATGCCGACCA TCCCCACCGC ACCGCCGACG ACGCCGGTGA	420
CCACGTCGGC GACGACGCCG CCGACCACGC CGCCGACCAC GCCGGTGACC ACGCCGCCAA	480
CGACGCCGCC GACCACGCCG GTGACCACGC CGCCAACGAC GCCGCCGACC ACGCCGGTGA	540
CCACGCCACC AACGACCGTC GCCCCGACGA CCGTCGCCCC GACGACGGTC GCTCCGACCA	600
CCGTGCCCCC GACCACGGTC GCTCCAGCCA CCGCCACGCC GACGACCGTC GCTCCGACG	660
CGACGCAGCA GCCCAGCAA CAACCAACCC AACAGATGCC AACCAGCAG CAGACCGTGG	720
CCCCGAGAC GGTGGCGCCG GCTCCGACG CGCCGTCCGG TGGCCGCAAC GGCAGCGGCG	780
GGGGCGACTT ATTCGGCGGG TTCTGATCAC GGTCGCGGCT TCACTACGGT CGGAGGACAT	840
GGCCGGTGAT GCGGTGACGG TGGTGCTGCC CTGTCTCAAC GA	882

(2) INFORMATION FOR SEQ ID NO:139:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

CCATCAACCA ACCGCTCGCG CCGCCCGCGC CGCCGGATCC GCCGTCGCCG CCACGCCCCG	60
CGGTGCCTCC GGTGCCCCCG TTGCCGCGT CGCCGCCGTC GCCGCCGACC GGCTGGGTGC	120
CTAGGGCGCT GTTACCGCCC TGGTTGGCGG GGACGCCGCC GGCACCACCG GTACCGCCGA	180
TGGCGCCGTT GCCGCCGGCG GCACCGTTGC CACCGTTGCC ACCGTTGCCA CCGTTGCCGA	240
CCAGCCACCC GCCGCGACCA CCGGCACCGC CGGCGCCGCC CGCACCGCCG GCGTGCCCGT	300
TCGTGCCCCG ACCGCCGGCA CCGCCGTTGC CGCCGTCACC GCCGACGGAA CTACCGGCGG	360
ACGCGGCCTG CCCGCCGGCG CCGCCCGCAC CGCCATTGGC ACCGCCGTCA CCGCCGGCTG	420

GGAGTGCCGC GATTAGGGCA CTGACCGGCG CAACCAGCGC AAGTACTCTC GGTACCCGAG	480
CACTTCCAGA CGACACCACA GCACGGGGTT GTCGGCGGAC TGGGTGAAAT GGCAGCCGAT	540
AGCGGCTAGC TGTCGGCTGC GGTCAACCTC GATCATGATG TCGAGGTGAC CGTGACCGCG	600
CCCCCGAAG GAGGCGCTGA ACTCGGCGTT GAGCCGATCG GCGATCGGTT GGGGCAGTGC	660
CCAGGCCAAT ACGGGGATAC CGGGTGTGNA AGCCGCCGCG AGCGCAGCTT CGGTTGCGCG	720
ACNGTGGTCG GGGTGGCCTG TTACGCCGTT GTCNTCGAAC ACGAGTAGCA GGTCTGCTCC	780
GGCGAGGGCA TCCACCACGC GTTGCCTCAG CTCGT	815

(2) INFORMATION FOR SEQ ID NO:140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1152 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAGCCGCC GGCTGAGGTC TCAGATCAGA GAGTCTCCGG ACTCACCAGG GCGGTTTCAGC	60
CTTCTCCCAG AACAACTGCT GAAGATCCTC GCCCGCGAAA CAGGCGCTGA TTTGACGCTC	120
TATGACCGGT TGAACGACGA GATCATCCGG CAGATTGATA TGGCACCCTT GGGCTAACAG	180
GTGCGCAAGA TGGTGCAGCT GTATGTCTCG GACTCCGTGT CGCGGATCAG CTTTGCCGAC	240
GGCCGGGTGA TCGTGTGGAG CGAGGAGCTC GGCGAGAGCC AGTATCCGAT CGAGACGCTG	300
GACGGCATCA CGCTGTTTGG GCGGCCGACG ATGACAACGC CCTTCATCGT TGAGATGCTC	360
AAGCGTGAGC GCGACATCCA GCTCTTCACG ACCGACGGCC ACTACCAGGG CCGGATCTCA	420
ACACCCGACG TGTCATACGC GCCCGGGCTC CGTCAGCAAG TTCACCGCAC CGACGATCCT	480
GCGTTCTGCC TGTCGTTAAG CAAGCGGATC GTGTCGAGGA AGATCCTGAA TCAGCAGGCC	540
TTGATTCTGGG CACACACGTC GGGGCAAGAC GTTGCTGAGA GCATCCGCAC GATGAAGCAC	600
TCGCTGGCCT GGGTCGATCG ATCGGGCTCC CTGGCGGAGT TGAACGGGTT CGAGGGAAAT	660
GCCGCAAAGG CATACTTCAC CGCGCTGGGG CATCTCGTCC CGCAGGAGTT CGCATTCAG	720
GGCCGCTCGA CTCGGCCGCC GTTGGACGCC TTCAACTCGA TGGTCAGCCT CGGCTATTCTG	780
CTGCTGTACA AGAACATCAT AGGGGCGATC GAGCGTCACA GCCTGAACGC GTATATCGGT	840

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TTCTACACC AGGATTCACG AGGGCACGCA ACGTCTCGTG CCGAATTCGG CACGAGCTCC	900
GCTGAAACCG CTGGCCGGCT GCTCAGTGCC CGTACGTAAT CCGCTGCGCC CAGGCCGGCC	960
CGCCGGCCGA ATACCAGCAG ATCGGACAGC GAATTGCCGC CCAGCCGGTT GGAGCCGTGC	1020
ATACCGCCGG CACACTCACC GGCAGCGAAC AGGCCTGGCA CCGTGGCGGC GCCGGTGTCC	1080
GCGTCTACTT CGACACCGCC CATCACGTAG TGACACGTCG GCCCGACTTC CATTGCCTGC	1140
GTTCGGCACG AG	1152

(2) INFORMATION FOR SEQ ID NO:141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 655 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

CTCGTGCCGA TTCGGCAGGG TGTACTTGCC GGTGGTGTAN GCCGCATGAG TGCCGACGAC	60
CAGCAATGCG GCAACAGCAC GGATCCCGGT CAACGACGCC ACCCGGTCCA CGTGGGCGAT	120
CCGCTCGAGT CCGCCCTGGG CGGCTCTTTC CTTGGGCAGG GTCATCCGAC GTGTTTCCGC	180
CGTGGTTTGC CGCCATTATG CCGGCGCGCC GCGTCGGGCG GCCGGTATGG CCGAANGTCG	240
ATCAGCACAC CCGAGATACG GGTCTGTGCA AGCTTTTTGA GCGTCGCGCG GGGCAGCTTC	300
GCCGGCAATT CTACTAGCGA GAAGTCTGGC CCGATACGGA TCTGACCGAA GTCGCTGCGG	360
TGCAGCCCAC CCTCATTGGC GATGGCGCCG ACGATGGCGC CTGGACCGAT CTTGTGCCGC	420
TTGCCGACGG CGACGCGGTA GGTGGTCAAG TCCGGTCTAC GCTTGGGCCT TTGCGGACGG	480
TCCCAGCGCT GGTGCGGGTT GCGCCGCGAA AGCGGCGGGT CGGGTGCCAT CAGGAATGCC	540
TCACCGCCGC GGCACTGCAC GGCCAGTGCC GCGGCGATGT CAGCCATCGG GACATCATGC	600
TCGCGTTCAT ACTCCTCGAC CAGTCGGCGG AACAGCTCGA TTCCCGGACC GCCCA	655

(2) INFORMATION FOR SEQ ID NO:142:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

Asn	Ala	Val	Val	Ala	Phe	Ala	Val	Ile	Gly	Phe	Ala	Ser	Leu	Ala	Val	1	5	10	15
Ala	Val	Ala	Val	Thr	Ile	Arg	Pro	Thr	Ala	Ala	Ser	Lys	Pro	Val	Glu	20	25	30	
Gly	His	Gln	Asn	Ala	Gln	Pro	Gly	Lys	Phe	Met	Pro	Leu	Leu	Pro	Thr	35	40	45	
Gln	Gln	Gln	Ala	Pro	Val	Pro	Pro	Pro	Pro	Asp	Asp	Pro	Thr	Ala	50	55	60		
Gly	Phe	Gln	Gly	Gly	Thr	Ile	Pro	Ala	Val	Gln	Asn	Val	Val	Pro	Arg	65	70	75	80
Pro	Gly	Thr	Ser	Pro	Gly	Val	Gly	Gly	Thr	Pro	Ala	Ser	Pro	Ala	Pro	85	90	95	
Glu	Ala	Pro	Ala	Val	Pro	Gly	Val	Val	Pro	Ala	Pro	Val	Pro	Ile	Pro	100	105	110	
Val	Pro	Ile	Ile	Ile	Pro	Pro	Phe	Pro	Gly	Trp	Gln	Pro	Gly	Met	Pro	115	120	125	
Thr	Ile	Pro	Thr	Ala	Pro	Pro	Thr	Thr	Pro	Val	Thr	Thr	Ser	Ala	Thr	130	135	140	
Thr	Pro	Pro	Thr	Thr	Pro	Pro	Thr	Thr	Pro	Val	Thr	Thr	Pro	Pro	Thr	145	150	155	160
Thr	Pro	Pro	Thr	Thr	Pro	Val	Thr	Thr	Pro	Pro	Thr	Thr	Pro	Pro	Thr	165	170	175	
Thr	Pro	Val	Thr	Thr	Pro	Pro	Thr	Thr	Val	Ala	Pro	Thr	Thr	Val	Ala	180	185	190	
Pro	Thr	Thr	Val	Ala	Pro	Thr	Thr	Val	Ala	Pro	Thr	Thr	Val	Ala	Pro	195	200	205	
Ala	Thr	Ala	Thr	Pro	Thr	Thr	Val	Ala	Pro	Gln	Pro	Thr	Gln	Gln	Pro	210	215	220	
Thr	Gln	Gln	Pro	Thr	Gln	Gln	Met	Pro	Thr	Gln	Gln	Gln	Thr	Val	Ala	225	230	235	240
Pro	Gln	Thr	Val	Ala	Pro	Ala	Pro	Gln	Pro	Pro	Ser	Gly	Gly	Arg	Asn	245	250	255	
Gly	Ser	Gly	Gly	Gly	Asp	Leu	Phe	Gly	Gly	Phe	260	265							

(2) INFORMATION FOR SEQ ID NO:143:

145

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 174 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

```

Ile Asn Gln Pro Leu Ala Pro Pro Ala Pro Pro Asp Pro Pro Ser Pro
1           5           10           15

Pro Arg Pro Pro Val Pro Pro Val Pro Pro Leu Pro Pro Ser Pro Pro
          20           25           30

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

Ala Gly Thr Pro Pro Ala Pro Pro Val Pro Pro Met Ala Pro Leu Pro
          50           55           60

Pro Ala Ala Pro Leu Pro Pro Leu Pro Pro Leu Pro Pro Leu Pro Thr
65           70           75           80

Ser His Pro Pro Arg Pro Pro Ala Pro Pro Ala Pro Pro Ala Pro Pro
          85           90           95

Ala Cys Pro Phe Val Pro Val Pro Pro Ala Pro Pro Leu Pro Pro Ser
          100          105          110

Pro Pro Thr Glu Leu Pro Ala Asp Ala Ala Cys Pro Pro Ala Pro Pro
          115          120          125

Ala Pro Pro Leu Ala Pro Pro Ser Pro Pro Ala Gly Ser Ala Ala Ile
          130          135          140

Arg Ala Leu Thr Gly Ala Thr Ser Ala Ser Thr Leu Gly His Arg Ala
145          150          155          160

Leu Pro Asp Asp Thr Thr Ala Arg Gly Cys Arg Arg Thr Gly
          165          170

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(2) INFORMATION FOR SEQ ID NO:144:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

146

Gln Pro Pro Ala Glu Val Ser Asp Gln Arg Val Ser Gly Leu Thr Gly
 1 5 10 15
 Ala Val Gln Pro Ser Pro Arg Thr Thr Ala Glu Asp Pro Arg Pro Arg
 20 25 30
 Asn Arg Arg
 35

(2) INFORMATION FOR SEQ ID NO:145:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 104 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

Arg Ala Asp Ser Ala Gly Cys Thr Cys Arg Trp Cys Xaa Pro His Glu
 1 5 10 15
 Cys Arg Arg Pro Ala Met Arg Gln Gln His Gly Ser Arg Ser Thr Thr
 20 25 30
 Pro Pro Gly Pro Arg Gly Arg Ser Ala Arg Val Arg Pro Gly Arg Leu
 35 40 45
 Phe Pro Trp Ala Gly Ser Ser Asp Val Phe Pro Pro Trp Phe Ala Ala
 50 55 60
 Ile Met Pro Ala Arg Arg Val Gly Arg Pro Val Trp Pro Xaa Val Asp
 65 70 75 80
 Gln His Thr Arg Asp Thr Gly Leu Cys Lys Leu Phe Glu Arg Arg Ala
 85 90 95
 Gly Gln Leu Arg Arg Gln Phe Tyr
 100

(2) INFORMATION FOR SEQ ID NO:146:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 53 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid
 (A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

53

(2) INFORMATION FOR SEQ ID NO:147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 42 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

42

(2) INFORMATION FOR SEQ ID NO:148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR Primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(A) DESCRIPTION: /desc = "PCR primer"

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

GAGAGAATTC TCAGAAGCCC ATTTGCGAGG ACA

33

(2) INFORMATION FOR SEQ ID NO:152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 152..1273

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTC TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG C GTG AAA ATT CGT TTG CAT ACG	172
Val Lys Ile Arg Leu His Thr	
1 5	
CTG TTG GCC GTG TTG ACC GCT GCG CCG CTG CTG CTA GCA GCG GCG GGC	220
Leu Leu Ala Val Leu Thr Ala Ala Pro Leu Leu Leu Ala Ala Ala Gly	
10 15 20	
TGT GGC TCG AAA CCA CCG AGC GGT TCG CCT GAA ACG GGC GCC GGC GCC	268
Cys Gly Ser Lys Pro Pro Ser Gly Ser Pro Glu Thr Gly Ala Gly Ala	
25 30 35	
GGT ACT GTC GCG ACT ACC CCC GCG TCG TCG CCG GTG ACG TTG GCG GAG	316
Gly Thr Val Ala Thr Thr Pro Ala Ser Ser Pro Val Thr Leu Ala Glu	
40 45 50 55	
ACC GGT AGC ACG CTG CTC TAC CCG CTG TTC AAC CTG TGG GGT CCG GCC	364
Thr Gly Ser Thr Leu Leu Tyr Pro Leu Phe Asn Leu Trp Gly Pro Ala	
60 65 70	
TTT CAC GAG AGG TAT CCG AAC GTC ACG ATC ACC GCT CAG GGC ACC GGT	412
Phe His Glu Arg Tyr Pro Asn Val Thr Ile Thr Ala Gln Gly Thr Gly	
75 80 85	
TCT GGT GCC GGG ATC GCG CAG GCC GCC GCC GGG ACG GTC AAC ATT GGG	460
Ser Gly Ala Gly Ile Ala Gln Ala Ala Ala Gly Thr Val Asn Ile Gly	
90 95 100	
GCC TCC GAC GCC TAT CTG TCG GAA GGT GAT ATG GCC GCG CAC AAG GGC	508
Ala Ser Asp Ala Tyr Leu Ser Glu Gly Asp Met Ala Ala His Lys Gly	
105 110 115	
CTG ATG AAC ATC GCG CTA GCC ATC TCC GCT CAG CAG GTC AAC TAC AAC	556
Leu Met Asn Ile Ala Leu Ala Ile Ser Ala Gln Gln Val Asn Tyr Asn	
120 125 130 135	
CTG CCC GGA GTG AGC GAG CAC CTC AAG CTG AAC GGA AAA GTC CTG GCG	604
Leu Pro Gly Val Ser Glu His Leu Lys Leu Asn Gly Lys Val Leu Ala	
140 145 150	
GCC ATG TAC CAG GGC ACC ATC AAA ACC TGG GAC GAC CCG CAG ATC GCT	652
Ala Met Tyr Gln Gly Thr Ile Lys Thr Trp Asp Asp Pro Gln Ile Ala	
155 160 165	
GCG CTC AAC CCC GGC GTG AAC CTG CCC GGC ACC GCG GTA GTT CCG CTG	700
Ala Leu Asn Pro Gly Val Asn Leu Pro Gly Thr Ala Val Val Pro Leu	

150

170	175	180	
CAC CGC TCC GAC GGG TCC GGT GAC ACC TTC TTG TTC ACC CAG TAC CTG			748
His Arg Ser Asp Gly Ser Gly Asp Thr Phe Leu Phe Thr Gln Tyr Leu			
185	190	195	
TCC AAG CAA GAT CCC GAG GGC TGG GGC AAG TCG CCC GGC TTC GGC ACC			796
Ser Lys Gln Asp Pro Glu Gly Trp Gly Lys Ser Pro Gly Phe Gly Thr			
200	205	210	215
ACC GTC GAC TTC CCG GCG GTG CCG GGT GCG CTG GGT GAG AAC GGC AAC			844
Thr Val Asp Phe Pro Ala Val Pro Gly Ala Leu Gly Glu Asn Gly Asn			
220	225	230	
GGC GGC ATG GTG ACC GGT TGC GCC GAG ACA CCG GGC TGC GTG GCC TAT			892
Gly Gly Met Val Thr Gly Cys Ala Glu Thr Pro Gly Cys Val Ala Tyr			
235	240	245	
ATC GGC ATC AGC TTC CTC GAC CAG GCC AGT CAA CGG GGA CTC GGC GAG			940
Ile Gly Ile Ser Phe Leu Asp Gln Ala Ser Gln Arg Gly Leu Gly Glu			
250	255	260	
GCC CAA CTA GGC AAT AGC TCT GGC AAT TTC TTG TTG CCC GAC GCG CAA			988
Ala Gln Leu Gly Asn Ser Ser Gly Asn Phe Leu Leu Pro Asp Ala Gln			
265	270	275	
AGC ATT CAG GCC GCG GCG GCT GGC TTC GCA TCG AAA ACC CCG GCG AAC			1036
Ser Ile Gln Ala Ala Ala Ala Gly Phe Ala Ser Lys Thr Pro Ala Asn			
280	285	290	295
CAG GCG ATT TCG ATG ATC GAC GGG CCC GCC CCG GAC GGC TAC CCG ATC			1084
Gln Ala Ile Ser Met Ile Asp Gly Pro Ala Pro Asp Gly Tyr Pro Ile			
300	305	310	
ATC AAC TAC GAG TAC GCC ATC GTC AAC AAC CGG CAA AAG GAC GCC GCC			1132
Ile Asn Tyr Glu Tyr Ala Ile Val Asn Asn Arg Gln Lys Asp Ala Ala			
315	320	325	
ACC GCG CAG ACC TTG CAG GCA TTT CTG CAC TGG GCG ATC ACC GAC GGC			1180
Thr Ala Gln Thr Leu Gln Ala Phe Leu His Trp Ala Ile Thr Asp Gly			
330	335	340	
AAC AAG GCC TCG TTC CTC GAC CAG GTT CAT TTC CAG CCG CTG CCG CCC			1228
Asn Lys Ala Ser Phe Leu Asp Gln Val His Phe Gln Pro Leu Pro Pro			
345	350	355	
GCG GTG GTG AAG TTG TCT GAC GCG TTG ATC GCG ACG ATT TCC AGC			1273
Ala Val Val Lys Leu Ser Asp Ala Leu Ile Ala Thr Ile Ser Ser			
360	365	370	
TAGCCTCGTT GACCACCACG CGACAGCAAC CTCCGTCGGG CCATCGGGCT GCTTTGCGGA			1333
GCATGCTGGC CCGTGCCGGT GAAGTCGGCC GCGCTGGCCC GGCCATCCGG TGGTTGGGTG			1393
GGATAGGTGC GGTGATCCCG CTGCTTGCGC TGGTCTTGGT GCTGGTGGTG CTGGTCATCG			1453

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AGGCGATGGG TGCGATCAGG CTCAACGGGT TGCATTTCTT CACCGCCACC GAATGGAATC      1513
CAGGCAACAC CTACGGCGAA ACCGTTGTCA CCGACGCGTC GCCCATCCGG TCGGCGCCTA      1573
CTACGGGGCG TTGCCGCTGA TCGTCGGGAC GCTGGCGACC TCGGCAATCG CCCTGATCAT      1633
CGCGGTGCCG GTCTCTGTAG GAGCGGCGCT GGTGATCGTG GAACGGCTGC CGAAACGGTT      1693
GGCCGAGGCT GTGGGAATAG TCCTGGAATT GCTCGCCGGA ATCCCCAGCG TGGTCGTCGG      1753
TTTGTGGGGG GCAATGACGT TCGGGCCGTT CATCGCTCAT CACATCGCTC CGGTGATCGC      1813
TCACAACGCT CCCGATGTGC CGGTGCTGAA CTACTTGCGC GGCGACCCGG GCAACGGGGA      1873
GGGCATGTTG GTGTCCGGTC TGGTGTTGGC GGTGATGGTC GTTCCCATTA TCGCCACCAC      1933
CACTCATGAC CTGTTCCGGC AGGTGCCGGT GTTGCCCCGG GAGGGCGCGA TCGGGAATTC      1993

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(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

```

Val Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
 1             5             10             15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
          20             25             30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
          35             40             45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
          50             55             60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
          65             70             75             80
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
          85             90             95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
          100            105            110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
          115            120            125
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys

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152

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

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCACCGA ACAGCTGTTC TCCTCGCCGA	60
AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCGGG GGACGTCAAG GACGCCAAGC	120
GCGGAAATTG AAGAGCACAG AAAGGTATGG CGTGAAAATT CGTTTGATA CGCTGTTGGC	180
CGTGTGACC GCTGCGCCGC TGCTGCTAGC AGCGGCGGGC TGTGGCTCGA AACCACCGAG	240
CGGTTGCGCT GAAACGGGCG CCGGCGCCGG TACTGTCGCG ACTACCCCG CGTCGTCGCC	300
GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTCAACC TGTGGGGTCC	360
GGCCTTTCAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGGTGC	420
CGGGATCGCG CAGGCCGCCG CCGGGACGGT CAACATTGGG GCCTCCGACG CCTATCTGTC	480
GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGCTAGCCA TCTCCGCTCA	540
GCAGGTCAAC TACAACCTGC CCGGAGTGAG CGAGCACCTC AAGCTGAACG GAAAAGTCCT	600
GGCGGCCATG TACCAGGGCA CCATCAAAAC CTGGGACGAC CCGCAGATCG CTGCGCTCAA	660
CCCCGGCGTG AACCTGCCCC GCACCGCGGT AGTTCCGCTG CACCGCTCCG ACGGGTCCGG	720
TGACACCTTC TTGTTACCCC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC	780
GCCCCGCTTC GGCACCACCG TCGACTTCCC GGCGGTGCCG GGTGCGCTGG GTGAGAACGG	840
CAACGGCGGC ATGGTGACCG GTTGCGCCGA GACACCGGGC TGCGTGCCCT ATATCGGCAT	900
CAGCTTCCTC GACCAGGCCA GTCAACGGGG ACTCGGCGAG GCCCAACTAG GCAATAGCTC	960
TGGCAATTC TTGTTGCCCG ACGCGCAAAG CATTGAGGCC GCGGCGGCTG GCTTCGCATC	1020
GAAAACCCCG GCGAACCAGG CGATTTGAT GATCGACGGG CCCGCCCCGG ACGGCTACCC	1080
GATCATCAAC TACGAGTACG CCATCGTCAA CAACCGGCAA AAGGACGCCG CCACCGCGCA	1140
GACCTTGACG GCATTTCTGC ACTGGGCGAT CACCGACGGC AACAAGGCCT CGTTCCTCGA	1200
CCAGGTTTAT TTCCAGCCGC TGCCGCCCCG GGTGGTGAAG TTGTCTGACG CGTTGATCGC	1260
GACGATTTCC AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCGTC GGGCCATCGG	1320
GCTGCTTTGC GGAGCATGCT GGCCCGTGCC GGTGAAGTCG GCCGCGCTGG CCCGGCCATC	1380
CGGTGGTTGG GTGGGATAGG TGCGGTGATC CCGCTGCTTG CGCTGGTCTT GGTGCTGGTG	1440
GTGCTGGTCA TCGAGGCGAT GGGTGCGATC AGGCTCAACG GGTGTCATTT CTTACCCGCC	1500
ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTCGCCCATC	1560
CGGTGCGCGC CTACTACGGG GCGTTGCCGC TGATCGTCGG GACGCTGGCG ACCTCGGCAA	1620

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TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC      1680
TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCCTGGA ATTGCTCGCC GGAATCCCCA      1740
GCGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG      1800
CTCCGGTGAT CGCTCACAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC      1860
CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTT GGCGGTGATG GTCGTTCCCA      1920
TTATCGCCAC CACCACTCAT GACCTGTTCC GGCAGGTGCC GGTGTTGCCC CGGGAGGGCG      1980
CGATCGGGAA TTC                                                                1993

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(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 374 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

```

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

Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20              25              30

Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35              40              45

Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50              55              60

Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65              70              75              80

Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
85              90              95

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

Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115             120             125

Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130             135             140

Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
145             150             155             160

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155

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

(2) INFORMATION FOR SEQ ID NO:156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1777 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

GGTCTTGACC ACCACCTGGG TGTCGAAGTC GGTGCCCCGGA TTGAAGTCCA GGTACTCGTG 60
 GGTGGGGCGG GCGAAACAAT AGCGACAAGC ATGCGAGCAG CCGCGGTAGC CGTTGACGGT 120

GTAGCGAAAC GGCAACGCGG CCGCGTTGGG CACCTTGTTT AGCGCTGATT TGCACAACAC	180
CTCGTGGAAG GTGATGCCGT CGAATTGTGG CGCGCGAACG CTGCGGACCA GGCCGATCCG	240
CTGCAACCCG GCAGCGCCCG TCGTCAACGG GCATCCCGTT CACCGCGACG GCTTGCCGGG	300
CCCAACGCAT ACCATTATTC GAACAACCGT TCTATACTTT GTCAACGCTG GCCGCTACCG	360
AGCGCCGCAC AGGATGTGAT ATGCCATCTC TGCCCGCACA GACAGGAGCC AGGCCTTATG	420
ACAGCATTCT GCGTCGAGCC CTACGGGCAG CCGAAGTACC TAGAAATCGC CGGGAAGCGC	480
ATGGCGTATA TCGACGAAGG CAAGGGTGAC GCCATCGTCT TTCAGCACGG CAACCCACG	540
TCGTCTTACT TGTGGCGCAA CATCATGCCG CACTTGGAAG GGCTGGGCCG GCTGGTGGCC	600
TGCGATCTGA TCGGGATGGG CGCGTCGGAC AAGCTCAGCC CATCGGGACC CGACCGCTAT	660
AGCTATGGCG AGCAACGAGA CTTTTTGTTC GCGCTCTGGG ATGCGCTCGA CCTCGGCGAC	720
CACGTGGTAC TGGTGCTGCA CGACTGGGGC TCGGCGCTCG GCTTCGACTG GGCTAACCAG	780
CATCGCGACC GAGTGCAGGG GATCGCGTTC ATGGAAGCGA TCGTCACCCC GATGACGTGG	840
GCGGACTGGC CGCCGGCCGT GCGGGGTGTG TTCCAGGGTT TCCGATCGCC TCAAGGCGAG	900
CCAATGGCGT TGGAGCACAA CATCTTTGTC GAACGGGTGC TGCCCGGGGC GATCCTGCGA	960
CAGCTCAGCG ACGAGGAAAT GAACCACTAT CGGCGGCCAT TCGTGAACGG CGGCGAGGAC	1020
CGTCGCCCCA CGTTGTCTGT GCCACGAAAC CTTCCAATCG ACGGTGAGCC CGCCGAGGTC	1080
GTCGCGTTGG TCAACGAGTA CCGGAGCTGG CTCGAGGAAA CCGACATGCC GAAACTGTTC	1140
ATCAACGCCG AGCCCGGCGC GATCATCACC GGCCGCATCC GTGACTATGT CAGGAGCTGG	1200
CCCAACCAGA CCGAAATCAC AGTGCCCGGC GTGCATTTCT TTCAGGAGGA CAGCGATGGC	1260
GTCGTATCGT GGGCGGGCGC TCGGCAGCAT CGGCGACCTG GGAGCGCTCT CATTTACGA	1320
GACCAAGAAT GTGATTTCCG GCGAAGGCGG CGCCCTGCTT GTCAACTCAT AAGACTTCCT	1380
GCTCCGGGCA GAGATTCTCA GGGAAAAGGG CACCAATCGC AGCCGCTTCC TTCGCAACGA	1440
GGTCGACAAA TATACGTGGC AGGACAAAGG TCTTCCTATT TGCCCGAGCGA ATTAGTCGCT	1500
GCCTTTCTAT GGGCTCAGTT CGAGGAAGCC GAGCGGATCA CGCGTATCCG ATTGGACCTA	1560
TGGAACCGGT ATCATGAAAG CTTGGAATCA TTGGAACAGC GGGGGCTCCT GCGCCGTCCG	1620
ATCATCCAC AGGGCTGCTC TCACAACGCC CACATGTACT ACGTGTTACT AGCGCCAGC	1680
GCCGATCGGG AGGAGGTGCT GGCGCGTCTG ACGAGCGAAG GTATAGGCGC GGTCTTTCAT	1740

TACGTGCCGC TTCACGATTC GCCGGCCGGG CGTCGCT

1777

(2) INFORMATION FOR SEQ ID NO:157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

GAGATTGAAT CGTACCGGTC TCCTTAGCGG CTCCGTCCCG TGAATGCCCA TATCACGCAC	60
GGCCATGTTC TGGCTGTCTGA CCTTCGCCCC ATGCCCCGAC GTTGGTAAAC CCAGGGTTTG	120
ATCAGTAATT CCGGGGGACG GTTGCGGGAA GGCGGCCAGG ATGTGCGTGA GCCGCGGCGC	180
CGCCGTCGCC CAGGCGACCG CTGGATGCTC AGCCCCGGTG CGGCGACGTA GCCAGCGTTT	240
GGCGCGTGTC GTCCACAGTG GTACTCCGGT GACGACGCGG CGCGGTGCCT GGGTGAAGAC	300
CGTGACCGAC GCCGCCGATT CAGA	324

(2) INFORMATION FOR SEQ ID NO:158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1338 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

GCGGTACCGC CGCGTTGCGC TGGCACGGGA CCTGTACGAC CTGAACCACT TCGCCTCGCG	60
AACGATTGAC GAACCGCTCG TGCGGCGGCT GTGGGTGCTC AAGGTGTGGG GTGATGTCGT	120
CGATGACCGG CGCGGCACCC GGCCACTACG CGTCGAAGAC GTCCTCGCCG CCCGAGCGA	180
GCACGACTTC CAGCCCGACT CGATCGGCGT GCTGACCCGT CCTGTGCTA TGGCTGCCTG	240
GGAAGCTCGC GTTCGGAAGC GATTTGCGTT CCTCACTGAC CTCGACGCCG ACGAGCAGCG	300
GTGGGCCGCC TGCGACGAAC GGCACCGCCG CGAAGTGGAG AACGCGCTGG CGGTGCTGCG	360
GTCCTGATCA ACCTGCCGGC GATCGTGCCG TTCCGCTGGC ACGGTTGCGG CTGGACGCGG	420
CTGAATCGAC TAGATGAGAG CAGTTGGGCA CGAATCCGGC TGTGGTGGTG AGCAAGACAC	480
GAGTACTGTC ATCACTATTG GATGCACTGG ATGACCGGCC TGATTCAGCA GGACCAATGG	540
AACTGCCCCG GGCAAAACGT CTCGGAGATG ATCGGCGTCC CCTCGGAACC CTGCGGTGCT	600
GGCGTCATTC GGACATCGGT CCGGCTCGCG GGATCGTGGT GACGCCAGCG CTGAAGGAGT	660

GGAGCGCGGC GGTGCACGCG CTGCTGGACG GCCGGCAGAC GGTGCTGCTG CGTAAGGGCG	720
GGATCGGCGA GAAGCGCTTC GAGGTGGCGG CCCACGAGTT CTTGTTGTTC CCGACGGTCG	780
CGCACAGCCA CGCCGAGCGG GTTCGCCCCG AGCACCGCGA CCTGCTGGGC CCGGCGGCCG	840
CCGACAGCAC CGACGAGTGT GTGCTACTGC GGGCCGCAGC GAAAGTTGTT GCCGCACTGC	900
CGGTTAACCG GCCAGAGGGT CTGGACGCCA TCGAGGATCT GCACATCTGG ACCGCCGAGT	960
CGGTGCGCGC CGACCGGCTC GACTTTCGGC CCAAGCACAA ACTGGCCGTC TTGGTGGTCT	1020
CGGCGATCCC GCTGGCCGAG CCGGTCCGGC TGGCGCGTAG GCCCGAGTAC GGCGGTTGCA	1080
CCAGCTGGGT GCAGCTGCCG GTGACGCCGA CGTTGGCGGC GCCGGTGCAC GACGAGGCCG	1140
CGCTGGCCGA GGTCGCCGCC CGGGTCCGCG AGGCCGTGGG TTGACTGGGC GGCATCGCTT	1200
GGGTCTGAGC TGTACGCCCA GTCGGCGCTG CGAGTGATCT GCTGTCGGTT CGGTCCCTGC	1260
TGGCGTCAAT TGACGGCGCG GGCAACAGCA GCATTGGCGG CGCCATCCTC CGCGCGGCCG	1320
GCGCCCACCG CTACAACC	1338

(2) INFORMATION FOR SEQ ID NO:159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

CCGGCGGCAC CGGCGGCACC GCGGTACCG GCGGCAACGG CGCTGACGCC GCTGCTGTGG	60
TGGGCTTCGG CGCGAACGGC GACCCTGGCT TCGCTGGCGG CAAAGGCGGT AACGGCGGAA	120
TAGGTGGGGC CGCGGTGACA GCGGGGTGCG CCGGCGACGG CGGCACCGGC GGCAAAGGTG	180
GCACCGGCGG TGCCGGCGGC GCCGGCAACG ACGCCGGCAG CACCGGCAAT CCCGGCGGTA	240
AGGGCGGCGA CGGCGGGATC GCGGTGCCG GCGGGGCCGG CGGCGCGGCC GGCACCGGCA	300
ACGGCGGCCA TGCCGGCAAC C	321

(2) INFORMATION FOR SEQ ID NO:160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

```

GAAGACCCGG CCCC GCCATA TCGATCGGCT CGCCGACTAC TTTCGCCGAA CGTGCACGCG      60
GCGGCGTCGG GCTGATCATC ACCGGTGGCT ACGCGCCCAA CCGCACCGGA TGGCTGCTGC      120
CGTTGCCTC  CGAACTCGTC ACTTCGGCGC AAGCCC GACG GCACCGCCGA ATCACCAGGG      180
CGGTCCACGA TTCGGGTGCA AAGATCCTGC TGCAAATCCT GCACGCCGGA CGCTACGCCT      240
ACCACCCACT TGCGGTCAGC GCCTCGCCGA TCAAGGCGCC GATCACCCCG TTTCGTCCGC      300
GAGCACTATC GGCTCGCGGG GTCGAAGCGA CCATCGCGGA TTTCGCCCCG TGCGCGCAGT      360
TGGCCCCGCGA TGCCGGCTAC GACGGCGTCG AAATCATGGG CAGCGAAGGG TATCTGCTCA      420
ATCAGTTCCT GGCGCCGCGC ACCAACAAGC GCACCGACTC GTGGGGCGGC ACACCGGCCA      480
ACCGTCGCCG GT                                         492

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(2) INFORMATION FOR SEQ ID NO:161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

```

Phe Ala Gln His Leu Val Glu Gly Asp Ala Val Glu Leu Trp Arg Ala
1           5           10           15
Asn Ala Ala Asp Gln Ala Asp Pro Leu Gln Pro Gly Ser Ala Arg Arg
20          25          30
Gln Arg Ala Ser Arg Ser Pro Arg Arg Leu Ala Gly Pro Asn Ala Tyr
35          40          45
His Tyr Ser Asn Asn Arg Ser Ile Leu Cys Gln Arg Trp Pro Leu Pro
50          55          60
Ser Ala Ala Gln Asp Val Ile Cys His Leu Cys Pro His Arg Gln Glu
65          70          75          80
Pro Gly Leu Met Thr Ala Phe Gly Val Glu Pro Tyr Gly Gln Pro Lys
85          90          95
Tyr Leu Glu Ile Ala Gly Lys Arg Met Ala Tyr Ile Asp Glu Gly Lys
100         105         110
Gly Asp Ala Ile Val Phe Gln His Gly Asn Pro Thr Ser Ser Tyr Leu
115         120         125
Trp Arg Asn Ile Met Pro His Leu Glu Gly Leu Gly Arg Leu Val Ala

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160

130	135	140
Cys Asp Leu Ile Gly Met Gly Ala Ser Asp Lys Leu Ser Pro Ser Gly		
145	150	155 160
Pro Asp Arg Tyr Ser Tyr Gly Glu Gln Arg Asp Phe Leu Phe Ala Leu		
	165	170 175
Trp Asp Ala Leu Asp Leu Gly Asp His Val Val Leu Val Leu His Asp		
	180	185 190
Trp Gly Ser Ala Leu Gly Phe Asp Trp Ala Asn Gln His Arg Asp Arg		
	195	200 205
Val Gln Gly Ile Ala Phe Met Glu Ala Ile Val Thr Pro Met Thr Trp		
	210	215 220
Ala Asp Trp Pro Pro Ala Val Arg Gly Val Phe Gln Gly Phe Arg Ser		
	225	230 235 240
Pro Gln Gly Glu Pro Met Ala Leu Glu His Asn Ile Phe Val Glu Arg		
	245	250 255
Val Leu Pro Gly Ala Ile Leu Arg Gln Leu Ser Asp Glu Glu Met Asn		
	260	265 270
His Tyr Arg Arg Pro Phe Val Asn Gly Gly Glu Asp Arg Arg Pro Thr		
	275	280 285
Leu Ser Trp Pro Arg Asn Leu Pro Ile Asp Gly Glu Pro Ala Glu Val		
	290	295 300
Val Ala Leu Val Asn Glu Tyr Arg Ser Trp Leu Glu Glu Thr Asp Met		
	305	310 315 320
Pro Lys Leu Phe Ile Asn Ala Glu Pro Gly Ala Ile Ile Thr Gly Arg		
	325	330 335
Ile Arg Asp Tyr Val Arg Ser Trp Pro Asn Gln Thr Glu Ile Thr Val		
	340	345 350
Pro Gly Val His Phe Val Gln Glu Asp Ser Asp Gly Val Val Ser Trp		
	355	360 365
Ala Gly Ala Arg Gln His Arg Arg Pro Gly Ser Ala Leu Ile Ser Arg		
	370	375 380
Asp Gln Glu Cys Asp Phe Arg Arg Arg Arg Arg Pro Ala Cys Gln Leu		
	385	390 395 400
Ile Arg Leu Pro Ala Pro Gly Arg Asp Ser Gln Gly Lys Gly His Gln		
	405	410 415
Ser Gln Pro Leu Pro Ser Gln Arg Gly Arg Gln Ile Tyr Val Ala Gly		
	420	425 430

161

Gln Arg Ser Ser Tyr Leu Pro Ser Glu Leu Val Ala Ala Phe Leu Trp
 435 440 445

Ala Gln Phe Glu Glu Ala Glu Arg Ile Thr Arg Ile Arg Leu Asp Leu
 450 455 460

Trp Asn Arg Tyr His Glu Ser Phe Glu Ser Leu Glu Gln Arg Gly Leu
 465 470 475 480

Leu Arg Arg Pro Ile Ile Pro Gln Gly Cys Ser His Asn Ala His Met
 485 490 495

Tyr Tyr Val Leu Leu Ala Pro Ser Ala Asp Arg Glu Glu Val Leu Ala
 500 505 510

Arg Leu Thr Ser Glu Gly Ile Gly Ala Val Phe His Tyr Val Pro Leu
 515 520 525

His Asp Ser Pro Ala Gly Arg Arg
 530 535

(2) INFORMATION FOR SEQ ID NO:162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 284 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

Asn Glu Ser Ala Pro Arg Ser Pro Met Leu Pro Ser Ala Arg Pro Arg
 1 5 10 15

Tyr Asp Ala Ile Ala Val Leu Leu Asn Glu Met His Ala Gly His Cys
 20 25 30

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

Gly Asp Asp Arg Ala Gly Leu Gly Val Asp Glu Gln Phe Arg His Val
 50 55 60

Gly Phe Leu Glu Pro Ala Pro Val Leu Val Asp Gln Arg Asp Asp Leu
 65 70 75 80

Gly Gly Leu Thr Val Asp Trp Lys Val Ser Trp Pro Arg Gln Arg Gly
 85 90 95

Ala Thr Val Leu Ala Ala Val His Glu Trp Pro Pro Ile Val Val His
 100 105 110

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

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Asp Lys Asp Val Val Leu Gln Arg His Trp Leu Ala Leu Arg Arg Ser
 130 135 140
 Glu Thr Leu Glu His Thr Pro His Gly Arg Arg Pro Val Arg Pro Arg
 145 150 155 160
 His Arg Gly Asp Asp Arg Phe His Glu Arg Asp Pro Leu His Ser Val
 165 170 175
 Ala Met Leu Val Ser Pro Val Glu Ala Glu Arg Arg Ala Pro Val Val
 180 185 190
 Gln His Gln Tyr His Val Val Ala Glu Val Glu Arg Ile Pro Glu Arg
 195 200 205
 Glu Gln Lys Val Ser Leu Leu Ala Ile Ala Ile Ala Val Gly Ser Arg
 210 215 220
 Trp Ala Glu Leu Val Arg Arg Ala His Pro Asp Gln Ile Ala Gly His
 225 230 235 240
 Gln Pro Ala Gln Pro Phe Gln Val Arg His Asp Val Ala Pro Gln Val
 245 250 255
 Arg Arg Arg Gly Val Ala Val Leu Lys Asp Asp Gly Val Thr Leu Ala
 260 265 270
 Phe Val Asp Ile Arg His Ala Leu Pro Gly Asp Phe
 275 280

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

ATGAACATGT CGTCGGTGGT GGGTCGCAAG GCCTTTGCGC GATTCGCCGG CTACTCCTCC 60
 GCCATGCACG CGATCGCCGG TTTCTCCGAT GCGTTGCGCC AAGAGCTGCG GGGTAGCGGA 120
 ATCGCCGTCT CGGTGATCCA CCCGGCGCTG ACCCAGACAC CGCTGTTGGC CAACGTCGAC 180
 CCCGCCGACA TGCCGCCGCC GTTTCGCAGC CTCACGCCCA TTCCCGTTCA CTGGGTCGCG 240
 GCAGCGGTGC TTACGGTGT GGCG 264

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1171 base pairs

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- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

TAGTCGGCGA CGATGACGTC GCGGTCCAGG CCGACCGCTT CAAGCACCAG CGCGACCACG	60
AAGCCGGTGC GATCCTTACC CGCGAAGCAG TGGGTGAGCA CCGGGCGTCC GGCGGCAAGC	120
AGTGTGACGA CACGATGTAG CGCGCGCTGT GCTCCATTGC GCGTTGGGAA TTGGCGATAC	180
TCGTCCGGTCA TGTAGCGGGT GGCCGCGTCA TTTATCGACT GGCTGGATTG GCCGGACTCG	240
CCGTTGGACC CGTCATTGGT TAGCAGCCTC TTGAATGCGG TTTCGTGCGG CGCTGAGTCG	300
TCGGCGTCAT CATCGGCGAG GTCGGGGAAC GGCAGCAGGT GGACGTCGAT GCCGTCCGGA	360
ACCCGTCCTG GACCGCGGCG GGCAACCTCC CGGGACGACC GCAGGTCGGC AACGTCGGTG	420
ATCCCCAGCC GGCGCAGCGT TGCCCCCTCGT GCCGAATTCG GCACGAGGCT GGCGAGCCAC	480
CGGGCATCAC CAAGCAACGC TTGCCCAGTA CGGATCGTCA CTTCCGCATC CGGCAGACCA	540
ATCTCCTCGC CGCCCATCGT CAGATCCCCG TCGTGCGTTG ACAAGAACGG CCGCAGATGT	600
GCCAGCGGGT ATCGGAGATT GAACCGCGCA CGCAGTTCTT CAATCGCTGC GCGCTGCCGC	660
ACTATTGGCA CTTTCCGGCG GTCGCGGTAT TCAGCAAGCA TGCAGTCTC GACGAACTCG	720
CCCCACGTAA CCCACGGCGT AGCTCCCGGC GTGACGCGGA GGATCGGCGG GTGATCTTTG	780
CCGCCACGCT CGTAGCCGTT GATCCACCGC TTCGCGGTGC CGGCGGGGAG GCCGATCAGC	840
TTATCGACCT CGGCGTATGC CGACGGCAAG CTGGGCGCGT TCGTCGAGGT CAAGAACTCC	900
ACCATCGGCA CCGGCACCAA GGTGCCGCGC CTGACCTACG TCGGCGACGC CGACATCGGC	960
GAGTACAGCA ACATCGGCGC CTCCAGCGTG TTCGTCAACT ACGACGGTAC GTCCAAACGG	1020
CGCACCACCG TCGGTTTCGA CGTACGGACC GGGTCCGACA CCATGTTCTG GGCCCCAGTA	1080
ACCATCGGCG ACGGCGCGTA TACCGGGGCC GGCACAGTGG TGCGGGAGGA TGTCCCGCCG	1140
GGGGCGCTGG CAGTGTCGGC GGGTCCGCAA C	1171

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 227 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG 60
 ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT 120
 TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG 180
 GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCC 227

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 304 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

CCTCGCCACC ATGGGCGGGC AGGGCGGTAG CGGTGGCGCC GGCTCTACCC CAGGCGCCAA 60
 GGGCGCCAC GGCTTCACTC CAACCAGCGG CGGCGACGGC GGCGACGGCG GCAACGGCGG 120
 CAACTCCCAA GTGGTCGGCG GCAACGGCGG CGACGGCGGC AATGGCGGCA ACGGCGGCAG 180
 CGCCGGCACG GGCGGCAACG GCGGCCGCGG CGGCGACGGC GCGTTTGGTG GCATGAGTGC 240
 CAACGCCACC AACCCTGGTG AAAACGGGCC AAACGGTAAC CCCGGCGGCA ACGGTGGCGC 300
 CGGC 304

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1439 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

GTGGGACGCT GCCGAGGCTG TATAACAAGG ACAACATCGA CCAGCGCCGG CTCGGTGAGC 60
 TGATCGACCT ATTTAACAGT GCGCGCTTCA GCCGGCAGGG CGAGCACCGC GCCCGGGATC 120
 TGATGGGTGA GGTCTACGAA TACTTCCTCG GCAATTTTCG TCGCGCGGAA GGAAGCGGG 180
 GTGGCGAGTT CTTTACCCCG CCCAGCGTGG TCAAGGTGAT CGTGGAGGTG CTGGAGCCGT 240
 CGAGTGGGCG GGTGTATGAC CCGTGCTGCG GTTCCGGAGG CATGTTTGTG CAGACCGAGA 300
 AGTTCATCTA CGAACACGAC GGCATCCGA AGGATGTCTC GATCTATGGC CAGGAAAGCA 360
 TTGAGGAGAC CTGGCGGATG GCGAAGATGA ACCTCGCCAT CCACGGCATC GACAACAAGG 420

GGCTCGGCGC CCGATGGAGT GATACCTTCG CCCGCGACCA GCACCCGGAC GTGCAGATGG 480
 ACTACGTGAT GGCCAATCCG CCGTTCAACA TCAAAGACTG GGCCCGCAAC GAGGAAGACC 540
 CACGCTGGCG CTTGGGTGTT CCGCCCGCCA ATAACGCCAA CTACGCATGG ATTCAGCACA 600
 TCCTGTACAA CTTGGCGCCG GGAGGTCGGG CGGGCGTGGT GATGGCCAAC GGGTCGATGT 660
 CGTCGAACTC CAACGGCAAG GGGGATATTC GCGCGCAAAT CGTGGAGGCG GATTTGGTTT 720
 CCTGCATGGT CGCGTTACCC ACCCAGCTGT TCCGCAGCAC CGGAATCCCG GTGTGCCTGT 780
 GGTTTTTTCG CAAAAACAAG GCGGCAGGTA AGCAAGGGTC TATCAACCGG TCGGGGCAGG 840
 TGCTGTTTCAT CGACGCTCGT GAACTGGGCG ACCTAGTGGG CCGGGCCGAG CGGGCGCTGA 900
 CCAACGAGGA GATCGTCCGC ATCGGGGATA CCTTCCACGC GAGCACGACC ACCGGCAACG 960
 CCGGCTCCGG TGGTGCCGGC GGTAATGGGG GCACTGGCCT CAACGGCGCG GCGGGTGCTG 1020
 GCGGGGCCGG CGGCAACGCG GGTGTCGCCG GCGTGTCTTT CGGCAACGCT GTGGGCGGCG 1080
 ACGGCGGCAA CGGCGGCAAC GCGGGCCACG GCGGCGACGG CACGACGGGC GCGGCCGGCG 1140
 GCAAGGGCGG CAACGGCAGC AGCGGTGCCG CCAGCGGCTC AGGCGTCGTC AACGTCACCG 1200
 CCGGCCACGG CGGCAACGGC GGCAATGGCG GCAACGGCGG CAACGGCTCC GCGGGCGCCG 1260
 GCGGCCAGGG CCGTGCCGGC GGCAGCGCCG GCAACGGCGG CCACGGCGGC GGTGCCACCG 1320
 GCGGCGCCAG CGGCAAGGGC GGCAACGGCA CCAGCGGTGC CGCCAGCGGC TCAGGCGTCA 1380
 TCAACGTCAC CGCCGGCCAC GCGGCAACG GCGGCAATGG CCGCAACGGC GGCAACGGC 1439

(2) INFORMATION FOR SEQ ID NO:168:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 329 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

GGGCCGGCGG GGCCGATTT TCTCGTGCCT TGATTGTCGC TGGGGATAAC GGCGGTGATG 60
 GTGGTAACGG CGGGATGGGC GGGGCTGGCG GGGCTGGCGG CCCC GGCGGG GCCGGCGGCC 120
 TGATCAGCCT GCTGGGCGGC CAAGGCGCCG-GCGGGGCCGG CGGGACCGGC GGGGCCGGCG 180
 GTGTTGGCGG TGACGGCGGG GCCGGCGGCC CCGGCAACCA GGCTTCAAC GCAGGTGCCG 240
 GCGGGGCCGG CGGCCTGATC AGCCTGCTGG GCGGCCAAGG CGCCGGCGGG GCCGGCGGGA 300
 CCGGCGGGGC CGGCGGTGTT GGCGGTGAC 329

(2) INFORMATION FOR SEQ ID NO:169:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 80 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

GCAACGGTGG CAACGGCGGC ACCAGCACGA CCGTGGGGAT GGCCGGAGGT AACTGTGGTG 60
 CCGCCGGGCT GATCGGCAAC 80

(2) INFORMATION FOR SEQ ID NO:170:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 392 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

GGGCTGTGTC GCACTCACAC CGCCGCATTC GGCGACGTTG GCCGCCCAAT ATCCAGCTCA 60
 AGGCCTACTA CTTACCGTCG GAGGACCGCC GCATCAAGGT GCGGGTCAGC GCCCAAGGAA 120
 TCAAGGTCAT CGACCGCGAC GGGCATCGAG GCCGTCGTCG CGCGGCTCGG GCAGGATCCG 180
 CCCC GGCGCA CTTGCGCGCG CAAGCGGGCT CATCGCTCCG AACGGCGGCG ATCCTGTGAG 240
 CACA ACTGAT GCGCGCAAC GAGATTCGTC CAATTGTCAA GCCGTGTTG ACCGCAGGGA 300
 CCGGTTATAC GTATGTCAAC CTATGTCACT CGCAAGAACC GGCATAACGA TCCCGTGATC 360
 CGCCGACAGC CCACGAGTGC AAGACCGTTA CA 392

(2) INFORMATION FOR SEQ ID NO:171:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 535 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

ACCGGCGCCA CCGGCGGCAC CGGGTTCGCC GGTGGCGCCG GCGGGGCCGG CGGGCAGGGC 60
 GGTATCAGCG GTGCCGGCGG CACCAACGGC TCTGGTGGCG CTGGCGGCAC CGGCGGACAA 120
 GGCGGCGCCG GGGGCGCTGG CGGGGCCGGC GCCGATAACC CCACCGGCAT CGGCGGCGCC 180

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GGCGGCACCG GCGGCACCGG CGGAGCGGCC GGAGCCGGCG GGGCCGGTGG CGCCATCGGT	240
ACCGGCGGCA CCGGCGGCGC GGTGGGCAGC GTCGGTAACG CCGGGATCGG CCGTACCGGC	300
GGTACGGGTG GTGTCGGTGG TGCTGGTGGT GCAGGTGCGG CTGCGGCCGC TGGCAGCAGC	360
GCTACCGGTG GCGCCGGGTT CGCCGGCGGC GCCGGCGGAG AAGGCGGACC GGGCGGCAAC	420
AGCGGTGTGG GCGGCACCAA CGGCTCCGGC GGCGCCGGCG GTGCAGGCGG CAAGGGCGGC	480
ACCGGAGGTG CCGGCGGGTC CGGCGCGGAC AACCCACCG GTGCTGGTTT CGCCG	535

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 690 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

CCGACGTCGC CGGGGCGATA CGGGGGTCAC CGACTACTAC ATCATCCGCA CCGAGAATCG	60
GCCCGTGCTG CAACCGCTGC GGGCGGTGCC GGTCAATCGGA GATCCGCTGG CCGACCTGAT	120
CCAGCCGAAC CTGAAGGTGA TCGTCAACCT GGGCTACGGC GACCCGAACT ACGGCTACTC	180
GACGAGCTAC GCCGATGTGC GAACGCCGTT CGGGCTGTGG CCGAACGTGC CGCCTCAGGT	240
CATCGCCGAT GCCCTGGCCG CCGGAACACA AGAAGGCATC CTTGACTTCA CGGCCGACCT	300
GCAGGCGCTG TCCGCGCAAC CGCTCACGCT CCCGCAGATC CAGCTGCCGC AACCCGCCGA	360
TCTGGTGGCC GCGGTGGCCG CCGCACCGAC GCCGGCCGAG GTGGTGAACA CGCTCGCCAG	420
GATCATCTCA ACCAACTACG CCGTCCTGCT GCCCACCCTG GACATCGCCC TCGCCTGGTC	480
ACCACCCTGC CGCTGTACAC CACCCAACTG TTCGTCAGGC AACTCGCTGC GGGCAATCTG	540
ATCAACCGCA TCGGCTATCC CCTGGCGGCC ACCGTAGGTT TAGGCACGAT CGATAGCGGG	600
CGGCGTGGA TTGCTACCC TCCTCGCGGC GGCCTCGGAC ACCGTTGAA ACATCGAGGG	660
CCTCGTCACC TAACGGATT CCGACGGCAT	690

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

ACGGTGACGG CGGTACTGGC GGCGGCCACG GCGGCAACGG CGGGAATCCC GGGTGGCTCT	60
TGGGCACAGC CGGGGGTGGC GGCAACGGTG GCGCCGGCAG CACCGGTACT GCAGGTGGCG	120
GCTCTGGGGG CACCGGCGGC GACGGCGGGA CCGGCGGGCG TGGCGGCCTG TTAATGGGCG	180
CCGGCGCCGG CGGGCACGGT GGCCTGGCG GCGCGGGCGG TGCCGGTGTC GACGGTGGCG	240
GCGCCGGCGG GGCCGGCGGG GCCGGCGGCA ACGGCGGCGC CGGGGGTCAA GCCGCCCTGC	300
TGTTCTGGGCG CGGCGGCACC GGCGGAGCCG GCGGCTACGG CGGCGATGGC GGTGGCGGCG	360
GTGACGGCTT CGACGGCACG ATGGCCGGCC TGGGTGGTAC CGGTGGC	407

(2) INFORMATION FOR SEQ ID NO:174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 468 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GATCGGTCAG CGCATCGCCC TCGGCGGCAA GCGATTCCGC GGTCTCACCG AAGAACATCG	60
TGCACGCGGC GGC GCGGACC AGCCCGCTGC GCTGCGGCGC GTCGAACGCC TCCAGCAGGC	120
ACAGCCAGTC CTTGGCGGCC TCGGAGGCGA ACACGTCGGT GTCACCGGTG TAGATCGCCG	180
GGATGCCCCG CTCCGCCAAC GCATTCCGGC ACGCCCGCGC GTCTTTGTGA TGCTCGACGA	240
TCACCGCGAT GTCTGCGGCC ACCACGGGCC GCCCGGCGAA GGTGGCCCCG CTGGCCAGTA	300
GCGCCGCGAC GTCGGCGGCC AGGTCGTCGG GGATGTGCCG GCGCAGCGCT CCGGCGCGAC	360
GCCCCAAAAA CGACCCCTCA CCCAGCTGGG TCCGCTGGC ATATCCCTTG CCGTCCTGGG	420
CGATATTGGA CGCGCATGCC CCGACCGCGT ACAGGCCGGC CACCACCG	468

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GGTGGTAACG GCGGCCAGGG TGGCATCGGC GGCGCCGGCG AGAGAGGCGC CGACGGCGCC	60
GGCCCCAATG CTAACGGCGC AAACGGCGAG AACGGCGGTA GCGGTGGTAA CCGTGGCGAC	120

GGCGGCGCCG GCGGCAATGG CGGCGCGGGC GGCAACGCGC AGGCGGCGCG GTACACCGAC 180

GGCGCCACGG GCACCGGCGG CGACGGCGGC AACGGCGGC 219

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

TAGCTCCGGC GAGGGCGGCA AGGGCGGCGA CGGTGGCCAC GGCGGTGACG GCGTCGGCGG 60

CAACAGTTCC GTCACCCAAG GCGGCAGCGG CGGTGGCGGC GGCGCCGGCG GCGCCGGCGG 120

CAGCGGCTTT TTCGGCGGCA AGGGCGGCTT CGGCGGCGAC GGCGGTCAGG GCGGCCCCAA 180

CGGCGGCGGT ACCGTCGGCA CCGTGCCGG TGGCGCGGC AACGGCGGTG TCGGCGGCCG 240

GGGCGGCGAC GGCGTCTTTG CCGTGCCGG CGGCCAGGGC GGCTTCGGTG GGCAGGGCGG 300

CAATGGCGGC GGCTCCACCG GCGGCAACGG CGGCCTTGGC GGCGCGGGCG GTGGCGGAGG 360

CAACGCCCCG GCTCGTGCCG AATCCGGGCT GACCATGGAC AGCGCGGCCA AGTTTCGTGC 420

CATCGCATCA GGCGGTACT GCCCGAACA CCTGGAACAT CACCCGAGTT AGCGGGGCGC 480

ATTCCTGAT CACC 494

(2) INFORMATION FOR SEQ ID NO:177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 220 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGGCCGGTGG TGCCGCGGGC CAGCTCTTCA GCGCCGAGG CGCGGCGGGT GCCGTTGGGG 60

TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCGG AGCGGCCGGC GCCGACGCCC 120

CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCGTCGGCG 180

GCCAGAGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC 220

(2) INFORMATION FOR SEQ ID NO:178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

ATGGCGGCAA CGGGGGCCCC GCGGGTGCTG GCGGGGCCGG CGACTACAAT TTCCAACGGC	60
GGGCAGGGTG GTGCCGGCGG CCAAGGCGGC CAAGGCGGCC TGGGCGGGGC AAGCACCACC	120
TGATCGGCCT AGCCGCACCC GGGAAAGCCG ATCCAACAGG CGACGATGCC GCCTTCCTTG	180
CCGCGTTGGA CCAGGCCGGC ATCACCTACG CTGACCCAGG CCACGCCATA ACGGCCGCCA	240
AGGCGATGTG TGGGCTGTGT GCTAACGGCG TAACAGGTCT ACAGCTGGTC GCGGACCTGC	300
GGGACTACAA TCCCGGGCTG ACCATGGACA GCGCGGCCAA GTTCGCTGCC ATCGCATCAG	360
GCGCGTACTG CCCCGAACAC CTGGAACA	388

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

GCAAAGGCGG CACCGGCGGG GCCGGCATGA ACAGCCTCGA CCCGCTGCTA GCCGCCCAAG	60
ACGGCGGCCA AGGCGGCACC GGCGGCACCG GCGGCAACGC CGGCGCCGGC GGCACCAGCT	120
TCACCCAAGG CGCCGACGGC AACGCCGGCA ACGGCGGTGA CGGCGGGGTC GGCGGCAACG	180
GCGGAAACGG CGGAAACGGC GCAGACAACA CCACCACCGC CGCCGCCGGC ACCACAGGCG	240
GCGACGGCGG GGCCGGCGGG GCCGGCGGAA CCGGCGGAAC CGGCGGAGCC GCCGGCACCG	300
GCACCGGCGG CCAACAAGGC AACGGCGGCA ACGGCGGCAC CGGCGGCAAA GGCGGCACCG	360
GCGGCGACGG TGCACTCTCA GGCAGCACCG GTGGTGCCGG	400

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 538 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

GGCAACGGCG GCAACGGCGG CATCGCCGGC ATTGGGCGGC AACGGCGTTC CGGGACGGGC	60
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AGCGGCAACG GCGGCCAACG GCGGCAGCGG CGGCAACGGC GGCAACGCCG GCATGGGCGG 120
 CAACAGCGGC ACCGGCAGCG GCGACGGCGG TGCCGGCGGG AACGGCGGCG CGGCGGGCAC 180
 GGGCGGCACC GGGGGCGACG GCGGCCTCAC CGGTACTGGC GGCACCGGCG GCAGCGGTGG 240
 CACCGGCGGT GACGGCGGTA ACGGCGGCAA CGGAGCAGAT AACACCGCAA ACATGACTGC 300
 GCAGGCGGGC GGTGACGGTG GCAACGGCGG CGACGGTGGC TTCGGCGGCG GGGCCGGGGC 360
 CGGCGGCGGT GGCTTGACCG CTGGCGCCAA CGGCACCGGC GGGCAAGGCG GCGCCGGCGG 420
 CGATGGCGGC AACGGGGCCA TCGGCGGCCA CGGCCCACTC ACTGACGACC CCGGCGGCAA 480
 CGGGGGCACC GGGCGCAACG GCGGCACCGG CGGCACCGGC GGC CGCGGGCA TCGGCAGC 538

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 239 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

GGGCGGTGG TGCCGGGGC CAGCTCTTCA GCGCCGAGG CGCGGCGGGT GCCGTTGGGG 60
 TTGGCGGCAC CGGCGGCCAG GGTGGGGCTG GCGGTGCCG AGCGGCCGGC GCCGACGCC 120
 CCGCCAGCAC AGGTCTAACC GGTGGTACCG GGTTCGCTGG CGGGGCCGGC GGCGTCGGCG 180
 GCCACGGCGG CAACGCCATT GCCGGCGGCA TCAACGGCTC CGGTGGTGCC GGC GGCACC 239

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 985 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

AGCAGCGCTA CCGGTGGCGC CGGGTTCGCC GCGGCGCCG GCGGAGAAGG CGGAGCGGGC 60
 GGCAACAGCG GTGTGGGCGG CACCAACGGC TCCGGCGGCG CCGGCGGTGC AGGCGGCAAG 120
 GCGGCGACCG GAGGTGCCCG CGGGTCCGGC TCGGACAACC CCACCGGTGC TGGTTTCGCC 180
 GGTGGCGCCG GCGGCACAGG TGGCGCGGCC GCGCGCGGCG GGGCCGGCGG GGCGACCGGT 240
 ACCGGCGGCA CCGGCGGCGT TGTCGGCGCC ACCGGTAGTG CAGGCATCGG CCGGGCCGGC 300
 GGCGCGGCG GTGACGGCGG CGATGGGGCC AGCGGTCTCG GCCTGGGCCT CTCCGGCTTT 360

GACGGCGGCC AAGGCGGCCA AGGCGGGGCC GGCGGCAGCG CCGGCGCCGG CGGCATCAAC 420
 GGGGCCGGCG GGGCCGGCGG CAACGGCGGC GACGGCGGGG ACGGCGCAAC CGGTGCCGCA 480
 GGTCTCGGCG ACAACGGCGG GTTCGGCGGT GACGGTGGGG CCGGTGGCGC CGCCGGCAAC 540
 GGCGGCAACG CGGGCGTCGG CCTGACAGCC AAGGCCGGCG ACGGCGGCGC CGCGGGCAAT 600
 GGCGGCAACG GGGGCGCCGG CGGTGCTGGC GGGGCCGGCG ACAACAATTT CAACGGCGGC 660
 CAGGGTGGTG CCGGCGGCCA AGGCGGCCAA GGCGGCTTGG GCGGGGCAAG CACCACCTGA 720
 TCGGCCTAGC CGCACC CGG AAAGCCGATC CAACAGGCGA CGATGCCGCC TTCCTTGCCG 780
 CGTTGGACCA GGCCGGCATC ACCTACGCTG ACCCAGGCCA CGCCATAACG GCCGCCAAGG 840
 CGATGTGTGG GCTGTGTGCT AACGGCGTAA CAGGTCTACA GCTGGTCGCG GACCTGCGGG 900
 AATACAATCC CGGGCTGACC ATGGACAGCG CGGCCAAGTT CGCTGCCATC GCATCAGGCG 960
 CGTACTGCCC CGAACACCTG GAACA 985

(2) INFORMATION FOR SEQ ID NO:183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2138 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC 60
 CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTG CGATGCCGGC 120
 ATGAACGGGC GGCATCAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT 180
 AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG 240
 AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCATGGC GGACCCACCG ACTGATGTCC 300
 CCATCACACC GTGCGAACTC ACGGCGGCTA AAAACGCCGC CCAACAGCTG GTATTGTCCG 360
 CCGACAACAT GCGGGAATAC CTGGCGGCCG GTGCCAAAGA GCGGCAGCGT CTGGCGACCT 420
 CGCTGCGCAA CGCGGCCAAG GCGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG 480
 ACAACGACGG CGAAGGAACT GTGCAGGCAG AATCGGCCGG GGCCGTCGGA GGGGACAGTT 540
 CGGCCGAACT AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC 600
 TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTTTG 660

CGGATGGGTG GAACACTTTC AACCTGACGC TGCAAGGCGA CGTCAAGCGG TTCCGGGGGT	720
TTGACAACTG GGAAGGCGAT GCGGCTACCG CTTGCGAGGC TTCGCTCGAT CAACAACGGC	780
AATGGATACT CCACATGGCC AAATTGAGCG CTGCGATGGC CAAGCAGGCT CAATATGTCG	840
CGCAGCTGCA CGTGTGGGCT AGGCGGGAAC ATCCGACTTA TGAAGACATA GTCGGGCTCG	900
AACGGCTTTA CGCGGAAAAC CCTTCGGCCC GCGACCAAAT TCTCCCGGTG TACGCGGAGT	960
ATCAGCAGAG GTCGGAGAAG GTGCTGACCG AATACAACAA CAAGGCAGCC CTGGAACCGG	1020
TAAACCCGCC GAAGCCTCCC CCCGCCATCA AGATCGACCC GCCCCCGCCT CCGCAAGAGC	1080
AGGGATTGAT CCCTGGCTTC CTGATGCCGC CGTCTGACGG CTCCGGTGTG ACTCCCGGTA	1140
CCGGGATGCC AGCCGCACCG ATGGTTCCGC CTACCGGATC GCCGGGTGGT GGCCTCCCGG	1200
CTGACACGGC GCGCGAGCTG ACGTCGGCTG GCGGGAAGC CGCAGCGCTG TCGGGCGACG	1260
TGGCGGTCAA AGCGGCATCG CTCGGTGGCG GTGGAGGCGG CGGGGTGCCG TCGGCGCCGT	1320
TGGGATCCGC GATCGGGGGC GCCGAATCGG TGCGGCCCCG TGGCGTGGT GACATTGCCG	1380
GCTTAGGCCA GGGAAGGGCC GCGGCGGGC CCGCGCTGGG CGGCGGTGGC ATGGGAATGC	1440
CGATGGGTGC CGCGCATCAG GGACAAGGGG GCGCCAAGTC CAAGGGTTCT CAGCAGGAAG	1500
ACGAGGCGCT CTACACCGAG GATCGGGCAT GGACCGAGGC CGTCATTGGT AACCGTCGGC	1560
GCCAGGACAG TAAGGAGTCG AAGTGAGCAT GGACGAATTG GACCCGCATG TCGCCCGGGC	1620
GTTGACGCTG GCGGCGCGGT TTCAGTCGGC CCTAGACGGG ACGCTCAATC AGATGAACAA	1680
CGGATCCTTC CGCGCCACCG ACGAAGCCGA GACCGTCGAA GTGACGATCA ATGGGCACCA	1740
GTGGCTCACC GGCCTGCGCA TCGAAGATGG TTTGCTGAAG AAGCTGGGTG CCGAGGCGGT	1800
GGCTCAGCGG GTCAACGAGG CGCTGCACAA TGCGCAGGCC GCGGCGTCCG CGTATAACGA	1860
CGCGGCGGGC GAGCAGCTGA CCGCTGCGTT ATCGGCCATG TCCCGCGCGA TGAACGAAGG	1920
AATGGCCTAA GCCCATTGTT GCGGTGGTAG CGACTACGCA CCGAATGAGC GCCGCAATGC	1980
GGTCATTGAG CGCGCCCGAC ACGGCGTGAG TACGCATTGT CAATGTTTTG ACATGGATCG	2040
GCCGGGTTCG GAGGGCGCCA TAGTCCTGGT CGCCAATATT GCCGCAGCTA GCTGGTCTTA	2100
GGTTCGGTTA CGCTGGTTAA TTATGACGTC CGTTACCA	2138

(2) INFORMATION FOR SEQ ID NO:184:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 460 amino acids

(B) TYPE: amino acid

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(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

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Met Thr Gln Ser Gln Thr Val Thr Val Asp Gln Gln Glu Ile Leu Asn
 1             5             10             15
Arg Ala Asn Glu Val Glu Ala Pro Met Ala Asp Pro Pro Thr Asp Val
          20             25             30
Pro Ile Thr Pro Cys Glu Leu Thr Ala Ala Lys Asn Ala Ala Gln Gln
          35             40             45
Leu Val Leu Ser Ala Asp Asn Met Arg Glu Tyr Leu Ala Ala Gly Ala
          50             55             60
Lys Glu Arg Gln Arg Leu Ala Thr Ser Leu Arg Asn Ala Ala Lys Ala
        65             70             75             80
Tyr Gly Glu Val Asp Glu Glu Ala Ala Thr Ala Leu Asp Asn Asp Gly
          85             90             95
Glu Gly Thr Val Gln Ala Glu Ser Ala Gly Ala Val Gly Gly Asp Ser
          100            105            110
Ser Ala Glu Leu Thr Asp Thr Pro Arg Val Ala Thr Ala Gly Glu Pro
          115            120            125
Asn Phe Met Asp Leu Lys Glu Ala Ala Arg Lys Leu Glu Thr Gly Asp
          130            135            140
Gln Gly Ala Ser Leu Ala His Phe Ala Asp Gly Trp Asn Thr Phe Asn
          145            150            155            160
Leu Thr Leu Gln Gly Asp Val Lys Arg Phe Arg Gly Phe Asp Asn Trp
          165            170            175
Glu Gly Asp Ala Ala Thr Ala Cys Glu Ala Ser Leu Asp Gln Gln Arg
          180            185            190
Gln Trp Ile Leu His Met Ala Lys Leu Ser Ala Ala Met Ala Lys Gln
          195            200            205
Ala Gln Tyr Val Ala Gln Leu His Val Trp Ala Arg Arg Glu His Pro
          210            215            220
Thr Tyr Glu Asp Ile Val Gly Leu Glu Arg Leu Tyr Ala Glu Asn Pro
          225            230            235            240
Ser Ala Arg Asp Gln Ile Leu Pro Val Tyr Ala Glu Tyr Gln Gln Arg
          245            250            255
Ser Glu Lys Val Leu Thr Glu Tyr Asn Asn Lys Ala Ala Leu Glu Pro
          260            265            270

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Val Asn Pro Pro Lys Pro Pro Pro Ala Ile Lys Ile Asp Pro Pro Pro
 275 280 285
 Pro Pro Gln Glu Gln Gly Leu Ile Pro Gly Phe Leu Met Pro Pro Ser
 290 295 300
 Asp Gly Ser Gly Val Thr Pro Gly Thr Gly Met Pro Ala Ala Pro Met
 305 310 315 320
 Val Pro Pro Thr Gly Ser Pro Gly Gly Gly Leu Pro Ala Asp Thr Ala
 325 330 335
 Ala Gln Leu Thr Ser Ala Gly Arg Glu Ala Ala Ala Leu Ser Gly Asp
 340 345 350
 Val Ala Val Lys Ala Ala Ser Leu Gly Gly Gly Gly Gly Gly Val
 355 360 365
 Pro Ser Ala Pro Leu Gly Ser Ala Ile Gly Gly Ala Glu Ser Val Arg
 370 375 380
 Pro Ala Gly Ala Gly Asp Ile Ala Gly Leu Gly Gln Gly Arg Ala Gly
 385 390 395 400
 Gly Gly Ala Ala Leu Gly Gly Gly Gly Met Gly Met Pro Met Gly Ala
 405 410 415
 Ala His Gln Gly Gln Gly Gly Ala Lys Ser Lys Gly Ser Gln Gln Glu
 420 425 430
 Asp Glu Ala Leu Tyr Thr Glu Asp Arg Ala Trp Thr Glu Ala Val Ile
 435 440 445
 Gly Asn Arg Arg Arg Gln Asp Ser Lys Glu Ser Lys
 450 455 460

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 277 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

Ala Gly Asn Val Thr Ser Ala Ser Gly Pro His Arg Phe Gly Ala Pro
 1 5 10 15
 Asp Arg Gly Ser Gln Arg Arg Arg Arg His Pro Ala Ala Ser Thr Ala
 20 25 30
 Thr Glu Arg Cys Arg Phe Asp Arg His Val Ala Arg Gln Arg Cys Gly
 35 40 45

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

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

177

Arg Val Ala Ala Ser Phe Ile Asp Trp Leu Asp Ser Pro Asp Ser Pro
 1 5 10 15
 Leu Asp Pro Ser Leu Val Ser Ser Leu Leu Asn Ala Val Ser Cys Gly
 20 25 30
 Ala Glu Ser Ser Ala Ser Ser Ser Ala Arg Ser Gly Asn Gly Ser Arg
 35 40 45
 Trp Thr Ser Met Pro Ser Gly Thr Arg Pro Gly Pro Arg Arg Ala Thr
 50 55 60
 Ser Arg Asp Asp Arg Arg Ser Ala Thr Ser Val Ile Pro Ser Arg Arg
 65 70 75 80
 Ser Val Ala Pro Arg Ala Glu Phe Gly Thr Arg Leu Ala Ser His Arg
 85 90 95
 Ala Ser Pro Ser Asn Ala Cys Pro Val Arg Ile Val Thr Ser Ala Ser
 100 105 110
 Gly Arg Pro Ile Ser Ser Pro Pro Ile Val Arg Ser Arg Ser Cys Val
 115 120 125
 Asp Lys Asn Gly Arg Arg Cys Ala Ser Gly Tyr Arg Arg Leu Asn Arg
 130 135 140
 Ala Arg Ser Ser Ser Ile Ala Ala Arg Cys Arg Thr Ile Gly Thr Phe
 145 150 155 160
 Arg Arg Ser Arg Tyr Ser Ala Ser Met Arg Val Ser Thr Asn Ser Pro
 165 170 175
 His Val Thr His Gly Val Ala Pro Gly Val Thr Arg Arg Ile Gly Gly
 180 185 190

(2) INFORMATION FOR SEQ ID NO:187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

Gln Glu Arg Pro Gln Met Cys⁻ Gln Arg Val Ser Glu Ile Glu Pro Arg
 1 5 10 15
 Thr Gln Phe Phe Asn Arg Cys Ala Leu Pro His Tyr Trp His Phe Pro
 20 25 30
 Ala Val Ala Val Phe Ser Lys His Ala Ser Leu Asp Glu Leu Ala Pro

178

35 40 45

Arg Asn Pro Arg Arg Ser Ser Arg Arg Asp Ala Glu Asp Arg Arg Val
50 55 60

Ile Phe Ala Ala Thr Leu Val Ala Val Asp Pro Pro Leu Arg Gly Ala
65 70 75 80

Gly Gly Glu Ala Asp Gln Leu Ile Asp Leu Gly Val Cys Arg Arg Gln
85 90 95

Ala Gly Arg Val Arg Arg Gly Gln Glu Leu His His Arg His Arg His
100 105 110

Gln Gly Ala Ala Pro Asp Leu Arg Arg Arg Arg His Arg Arg Val
115 120 125

Gln Gln His Arg Arg Leu Gln Arg Val Arg Gln Leu Arg Arg Tyr Val
130 135 140

Gln Thr Ala His His Arg Arg Phe Ala Arg Thr Asp Arg Val Arg His
145 150 155 160

His Val Arg Gly Pro Ser Asn His Arg Arg Arg Arg Val Tyr Arg Gly
165 170 175

Arg His Ser Gly Ala Gly Gly Cys Pro Ala Gly Gly Ala Gly Ser Val
180 185 190

Gly Gly Ser Ala
195

(2) INFORMATION FOR SEQ ID NO:188:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 311 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS:
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

Val	Arg	Cys	Gly	Thr	Leu	Val	Pro	Val	Pro	Met	Val	Glu	Phe	Leu	Thr	
1				5					10					15		
Ser	Thr	Asn	Ala	Pro	Ser	Leu	Pro	Ser	Ala	Tyr	Ala	Glu	Val	Asp	Lys	
			20					25					30			
Leu	Ile	Gly	Leu	Pro	Ala	Gly	Thr	Ala	Lys	Arg	Trp	Ile	Asn	Gly	Tyr	
		35					40					45				
Glu	Arg	Gly	Gly	Lys	Asp	His	Pro	Pro	Ile	Leu	Arg	Val	Thr	Pro	Gly	
	50					55					60					
Ala	Thr	Pro	Trp	Val	Thr	Trp	Gly	Glu	Phe	Val	Glu	Thr	Arg	Met	Leu	

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

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2072 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

CTCGTGCCGA TTCGGCACGA GCTGAGCAGC CCAAGGGGCC GTTCGGCGAA GTCATCGAGG	60
CATTCGCCGA CGGGCTGGCC GGCAAGGGTA AGCAAATCAA CACCACGCTG AACAGCCTGT	120
CGCAGGCGTT GAACGCCTTG AATGAGGGCC GCGGCGACTT CTTCGCGGTG GTACGCAGCC	180
TGGCGCTATT CGTCAACGCG CTACATCAGG ACGACCAACA GTTCGTCGCG TTGAACAAGA	240
ACCTTGCGGA GTTCACCGAC AGGTTGACCC ACTCCGATGC GGACCTGTGC AACGCCATCC	300
AGCAATTCGA CAGCTTGCTC GCCGTCGCGC GCCCGTTCTT CGCCAAGAAC CGCGAGGTGC	360
TGACGCATGA CGTCAATAAT CTCGCGACCG TGACCACCAC GTTGCTGCAG CCCGATCCGT	420
TGGATGGGTT GGAGACCGTC CTGCACATCT TCCCAGCGCT GGCGGCGAAC ATTAACCAGC	480
TTTACCATCC GACACACGGT GCGTGGTGT CGCTTTCCGC GTTCACGAAT TTCGCCAACC	540
CGATGGAGTT CATCTGCAGC TCGATTGAGG CGGGTAGCCG GCTCGGTTAT CAAGAGTCGG	600
CCGAACTCTG TCGCAGTAT CTGGCGCCAG TCCTCGATGC GATCAAGTTC AACTACTTTC	660
CGTTCCGGCCT GAACGTGGCC AGCACCGCCT CGACACTGCC TAAAGAGATC GCGTACTCCG	720
AGCCCCGCTT GCAGCCGCCC AACGGGTACA AGGACACCAC GGTGCCCCGC ATCTGGGTGC	780
CGGATACGCC GTTGTACAC CGCAACACGC AGCCCGGTTG GGTGGTGGCA CCCGGGATGC	840
AAGGGGTTC GGTGGGACCG ATCAGCAGG GTTTGCTGAC GCCGGAGTCC CTGGCCGAAC	900
TCATGGGTGG TCCCGATATC GCCCCCTCCGT CGTCAGGGCT GCAAACCCCG CCCGGACCCC	960
CGAATGCSTA CGACGAGTAC CCCGTGCTGC CGCCGATCGG TTTACAGGCC CCACAGGTGC	1020
CGATACCACC GCCGCCTCCT GGGCCCCGAC TAATCCCGGG TCCGGTGCCA CCGGTCTTGG	1080
CGGCGATCGT GTTCCCAAGA GATCGCCCGG CAGCGTCGGA AACTTCGAC TACATGGGCC	1140
TCTTGTTGCT GTCGCCGGGC CTGGCGACCT TCCTGTTGCG GGTGTCATCT AGCCCCGCCC	1200
GTGGAACGAT GGCCGATCGG CACGTGTTGA TACCGGCGAT CACCGGCCTG GCGTTGATCG	1260
CGGCATTCTG CGCACATTCT TGGTACCGCA CAGAACATCC GCTCATAGAC ATGCGCTTGT	1320
TCCAGAACCG AGCGGTGCGC CAGGCCAACA TGACGATGAC GGTGCTCTCC CTCGGGCTGT	1380
TTGGCTCCTT CTTGCTGCTC CCGAGCTACC TCCAGCAAGT GTTGACCAA TCACCGATGC	1440
AATCGGGGGT GCATATCATC CCACAGGGCC TCGGTGCCAT GCTGGCGATG CCGATCGCCG	1500
GAGCGATGAT GGACCGACGG GGACCGGCCA AGATCGTGCT GGTGGGATC ATGCTGATCG	1560
CTGCGGGGTT GGGCACCTTC GCCTTTGGTG TCGCGCGGCA AGCGGACTAC TTACCCATTC	1620

TGCCGACCGG GCTGGCAATC ATGGGCATGG GCATGGGCTG CTCCATGATG CCACTGTCCG 1680
 GGGCGGCAGT GCAGACCCTG GCGCCACATC AGATCGCTCG CGGTTTCGACG CTGATCAGCG 1740
 TCAACCAGCA GGTGGGCGGT TCGATAGGGA CCGCACTGAT GTCGGTGCTG CTCACCTACC 1800
 AGTTCAATCA CAGCGAAATC ATCGCTACTG CAAAGAAAGT CGCACTGACC CCAGAGAGTG 1860
 GCGCCGGGCG GGGGGCGGCG GTTGACCCTT CCTCGCTACC GCGCCAAACC AACTTCGCGG 1920
 CCCAACTGCT GCATGACCTT TCGCACGCCT ACGCGGTGGT ATTCTGTGATA GCGACCGCGC 1980
 TAGTGGTCTC GACGCTGATC CCCGCGGCAT TCCTGCCGAA ACAGCAGGCT AGTCATCGAA 2040
 GAGCACCGTT GCTATCCGCA TGACGTCTGC TT 2072

(2) INFORMATION FOR SEQ ID NO:190:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1923 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TCACCCCGGA GAAGTCGTTT GTCGACGACC TGGACATCGA CTCGCTGTCT ATGGTCGAGA 60
 TCGCCGTGCA GACCGAGGAC AAGTACGGCG TCAAGATCCC CGACGAGGAC CTCGCCGGTC 120
 TCGGTACCGT CGGTGACGTT GTCGCCTACA TCCAGAAGCT CGAGGAAGAA AACCCGGAGG 180
 CGGCTCAGGC GTTGCGCGCG AAGATTGAGT CGGAGAACCC CGATGCGGCA CGAGCAGATC 240
 GGTGCGTTTC ACCCACATCG CAAGCTCGAG ACGCCCGTCT TCCTCTTGCA CGCTCAGCCA 300
 GGTGCGGCTG TCGCCGCCTT CCAGCAAGTG TTCCACCAC ACGAAGGGAC CCTCGCGAAA 360
 GGTGACTGAT CCGCGGACCA CATAGTCGAT GCCACCGTGG CTGACAATTG CGCCGGGTCC 420
 GAGTTGGCGG GGGCCGAATT GCGGCATTGC GTCGAAGGCC AGCGGATCCC GGCGCCCGCC 480
 CGGCGTGGCT GGTGTTTTGG GCCGCCGAT GGCCACGACG AGAACGACGA TGGCGGCGAT 540
 GAACAGCGCC ACGGCAATCA CGACCAGCAG ATTTCCACG CATACCCTCT CGTACCGCTG 600
 CGCCGCGGTT GGTGATCGG TCGCATATCG ATGGCGCCGT TTAACGTAAC AGCTTTCGCG 660
 GGACCGGGGG TCACAACGGG CGAGTTGTCC GGCCGGGAAC CCGGCAGGTC TCGCCGCGG 720
 TCACCCAGC TCACTGGTGC ACCATCCGGG TGTCGGTGAG CGTGCAACTC AAACACACTC 780
 AACGGCAACG GTTTCTCAGG TCACCAGCTC AACCTCGACC CGCAATCGCT CGTACGTTTC 840

GACCGCGCGC AGGTCGCGAG TCAGCAGCTT TGCGCCGGCA GCTTTCGCCG TGAAGCCGAC 900
 CAGGGCATCG TAGGTTGCGC CACCGGTGAC ATCGTGCTCG GCGAGGTGGT CCGTCAAGCC 960
 GCGATATGAG CAGGCATCCA GTGCCAGGTA GTTGCTGGAG GTGATGTCCG CCAAGTAGGC 1020
 GTGGACGGCA ACAGGGGCAA TACGATGCGG CGGTGGTAGC CGGGTCAAGA CCGAATAGGT 1080
 TTCCACAGCC GCGTGCGCGA TCAGATGGAC GCCACGGTTG AGCGCGCGCA CGGCGGCCCTC 1140
 GTGCCCTTCG TGCCAGGTCTG CGAATCCGGC AACCAGCAGC CTGGTGTCTG GTGCGATCAC 1200
 CGCCGTGTGC GATCGAGCGT TTCCCGAACG ATTTCTGTCG TCAACGGGGG CAGGGGACGT 1260
 TCTGGCCGTG CGACGAGAAC CGAGCCTTCC CGAACGAGTT CGACACCGGT CGGGGCCGGC 1320
 TCAATCTCGA TGCGCCCATC GCGCTCGGTG ATCTCCACCT GGTCGTTCCC GCGCAAGCCA 1380
 AGGCGCTCGC GAATCCGCTT GGGAAATCACC AGACGTCTCTG CGACATCGAT GGTGTGTTGCG 1440
 ATGGTAGGAA ATTTACCATC GCACGTTCCTA TAGGCGTGTC CTGCGCGGGA TGTGCGGACG 1500
 ATCCGCTAGC GTATCGAACG ATTGTTTCGG AAATGGCTGA GGGAGCGTGC GGTGCGGGTG 1560
 ATGGGTGTCTG ATCCCGGGTT GACCCGATGC GGGCTGTCTG TCATCGAGAG TGGGCGTGGT 1620
 CGGCAGCTCA CCGCGCTGGA TGTCGACGTG GTGCGCACAC CGTCGGATGC GGCCTTGGCG 1680
 CAGCGCCTGT TGGCCATCAG CGATGCCGTC GAGCACTGGC TGGACACCCA TCATCCGGAG 1740
 GTGGTGGCTA TCGAACGGGT GTTCTCTCAG CTCAACGTGA CCACGGTGAT GGGCACCGCG 1800
 CAGGCCGGCG GCGTGATCGC CCTGGCGGCG GCCAAACGTG GTGTCGACGT GCATTTCCAT 1860
 ACCCCAGCG AGGTCAAGGC GGCGGTCACT GGCAACGGTT CCGCAGACAA GGCTCAGGTC 1920
 ACC 1923

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1055 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

CTGGCGTGCC AGTGTACCG GCGATATGAE GTCGGCATT C AATTTGCGG CCCC GCCGGA 60
 CCCGTCGCCA CCAATCTGG ACCACCCGGT CCGTCAATTG CCGAAGGTG CCAAGTGGT 120
 GCCAATGTG GTGCTGGGTT TCTTGAACGA AGGCCTGCCG TATCGGGTGC CCTACCCCCA 180
 AACAAAGCCA GTCCAGGAAT CCGGTCCCGC GCGGCCGATT CCCAGCGGCA TCTGCTAGCC 240

GGGGATGGTT CAGACGTAAC GGTTGGCTAG GTCGAAACCC GCGCCAGGGC CGCTGGACGG	300
GCTCATGGCA GCGAAATTAG AAAACCCGGG ATATTGTCCG CGGATTGTCA TACGATGCTG	360
AGTGCTTGGT GGTTCTGTGT TAGCCATTGA GTGTGGATGT GTTGAGACCC TGGCCTGGAA	420
GGGGACAACG TGCTTTTGCC TCTTGGTCCG CCTTTGCCGC CCGACGCGGT GGTGGCGAAA	480
CGGGCTGAGT CGGGAATGCT CGGCGGGTTG TCGGTTCGCG TCAGCTGGGG AGTGGCTGTG	540
CCACCCGATG ATTATGACCA CTGGGCGCCT GCGCCGGAGG ACGGCGCCGA TGTCGATGTC	600
CAGGCGGCCG AAGGGGCGGA CGCAGAGGCC GCGGCCATGG ACGAGTGGGA TGAGTGGCAG	660
GCGTGGAACG AGTGGGTGGC GGAGAACGCT GAACCCCGCT TTGAGGTGCC ACGGAGTAGC	720
AGCAGCGTGA TTCCGCATTC TCCGGCGGCC GGCTAGGAGA GGGGGCGCAG ACTGTCGTTA	780
TTTGACCACT GATCGGCGGT CTCGGTGTTC CCGCGGCCGG CTATGACAAC AGTCAATGTG	840
CATGACAAGT TACAGGTATT AGGTCCAGGT TCAACAAGGA GACAGGCAAC ATGGCAACAC	900
GTTTTATGAC GGATCCGCAC GCGATGCGGG ACATGGCGGG CCGTTTTGAG GTGCACGCCC	960
AGACGGTGGA GGACGAGGCT CGCCGGATGT GGGCGTCCGC GCAAAACATC TCGGGNGCGG	1020
GCTGGAGTGG CATGGCCGAG GCGACCTCGC TAGAC	1055

(2) INFORMATION FOR SEQ ID NO:192:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

CCGCCTCGTT GTTGGCATA TCCGCCGCGG CCGCCTCGAC CGCACTGGCC GTGGCGTGTG	60
TCCGGGCTGA CCACCGGGAT CGCCGAACCA TCCGAGATCA CCTCGCAATG ATCCACCTCG	120
CGCAGCTGGT CACCCAGCCA CCGGGCGGTG TGCGACAGCG CCTGCATCAC CTTGGTATAG	180
CCGTCGCGCC CCAGCCGCAG GAAGTTGTAG TACTGGCCCA CCACCTGGTT ACCGGGACGG	240
GAGAAGTTCA GGGTGAAGGT CGGCATGTCG CCGCCGAGGT AGTTGACCCG GAAAACCAGA	300
TCCTCCGGCA GTGCTCGGG CCCGCGCCAC ACGACAAACC CGACGCCGGG ATAGGTCAG	359

(2) INFORMATION FOR SEQ ID NO:193:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

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AACGGGCCCCG TGGGCACCGC TCCTCTAAGG GCTCTCGTTG GTCGCATGAA GTGCTGGAAG      60
GATGCATCTT  GGCAGATTCC CGCCAGAGCA AAACAGCCGC TAGTCCTAGT CCGAGTCGCC      120
CGCAAAGTTC  CTCGAATAAC TCCGTACCCG GAGCGCCAAA CCGGGTCTCC TTCGCTAAGC      180
TGCGCGAACC  ACTTGAGGTT CCGGGACTCC TTGACGTCCA GACCGATTCTG TTCGAGTGGC      240
TGATCGGTTT  GCCGCGCTGG CGCGAATCCG CCGCCGAGCG GGGTGATGTC AACCCAGTGG      300
GTGGCCTGGA  AGAGGTGCTC TACGAGCTGT CTCCGATCGA GGACTTCTCC      350

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(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 679 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

```

Glu Gln Pro Lys Gly Pro Phe Gly Glu Val Ile Glu Ala Phe Ala Asp
1           5           10           15
Gly Leu Ala Gly Lys Gly Lys Gln Ile Asn Thr Thr Leu Asn Ser Leu
20          25          30
Ser Gln Ala Leu Asn Ala Leu Asn Glu Gly Arg Gly Asp Phe Phe Ala
35          40          45
Val Val Arg Ser Leu Ala Leu Phe Val Asn Ala Leu His Gln Asp Asp
50          55          60
Gln Gln Phe Val Ala Leu Asn Lys Asn Leu Ala Glu Phe Thr Asp Arg
65          70          75          80
Leu Thr His Ser Asp Ala Asp Leu Ser Asn Ala Ile Gln Gln Phe Asp
85          90          95
Ser Leu Leu Ala Val Ala Arg Pro Phe Phe Ala Lys Asn Arg Glu Val
100         105         110
Leu Thr His Asp Val Asn Asn Leu Ala Thr Val Thr Thr Leu Leu
115         120         125
Gln Pro Asp Pro Leu Asp Gly Leu Glu Thr Val Leu His Ile Phe Pro
130         135         140

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185

Thr Leu Ala Ala Asn Ile Asn Gln Leu Tyr His Pro Thr His Gly Gly
 145 150 155 160
 Val Val Ser Leu Ser Ala Phe Thr Asn Phe Ala Asn Pro Met Glu Phe
 165 170 175
 Ile Cys Ser Ser Ile Gln Ala Gly Ser Arg Leu Gly Tyr Gln Glu Ser
 180 185 190
 Ala Glu Leu Cys Ala Gln Tyr Leu Ala Pro Val Leu Asp Ala Ile Lys
 195 200 205
 Phe Asn Tyr Phe Pro Phe Gly Leu Asn Val Ala Ser Thr Ala Ser Thr
 210 215 220
 Leu Pro Lys Glu Ile Ala Tyr Ser Glu Pro Arg Leu Gln Pro Pro Asn
 225 230 235 240
 Gly Tyr Lys Asp Thr Thr Val Pro Gly Ile Trp Val Pro Asp Thr Pro
 245 250 255
 Leu Ser His Arg Asn Thr Gln Pro Gly Trp Val Val Ala Pro Gly Met
 260 265 270
 Gln Gly Val Gln Val Gly Pro Ile Thr Gln Gly Leu Leu Thr Pro Glu
 275 280 285
 Ser Leu Ala Glu Leu Met Gly Gly Pro Asp Ile Ala Pro Pro Ser Ser
 290 295 300
 Gly Leu Gln Thr Pro Pro Gly Pro Pro Asn Ala Tyr Asp Glu Tyr Pro
 305 310 315 320
 Val Leu Pro Pro Ile Gly Leu Gln Ala Pro Gln Val Pro Ile Pro Pro
 325 330 335
 Pro Pro Pro Gly Pro Asp Val Ile Pro Gly Pro Val Pro Pro Val Leu
 340 345 350
 Ala Ala Ile Val Phe Pro Arg Asp Arg Pro Ala Ala Ser Glu Asn Phe
 355 360 365
 Asp Tyr Met Gly Leu Leu Leu Leu Ser Pro Gly Leu Ala Thr Phe Leu
 370 375 380
 Phe Gly Val Ser Ser Ser Pro Ala Arg Gly Thr Met Ala Asp Arg His
 385 390 395 400
 Val Leu Ile Pro Ala Ile Thr Gly Leu Ala Leu Ile Ala Ala Phe Val
 405 410 415
 Ala His Ser Trp Tyr Arg Thr Glu His Pro Leu Ile Asp Met Arg Leu
 420 425 430
 Phe Gln Asn Arg Ala Val Ala Gln Ala Asn Met Thr Met Thr Val Leu

186

435	440	445
Ser Leu Gly Leu Phe Gly Ser Phe Leu Leu Leu Pro Ser Tyr Leu Gln		
450	455	460
Gln Val Leu His Gln Ser Pro Met Gln Ser Gly Val His Ile Ile Pro		
465	470	475
Gln Gly Leu Gly Ala Met Leu Ala Met Pro Ile Ala Gly Ala Met Met		
485	490	495
Asp Arg Arg Gly Pro Ala Lys Ile Val Leu Val Gly Ile Met Leu Ile		
500	505	510
Ala Ala Gly Leu Gly Thr Phe Ala Phe Gly Val Ala Arg Gln Ala Asp		
515	520	525
Tyr Leu Pro Ile Leu Pro Thr Gly Leu Ala Ile Met Gly Met Gly Met		
530	535	540
Gly Cys Ser Met Met Pro Leu Ser Gly Ala Ala Val Gln Thr Leu Ala		
545	550	555
Pro His Gln Ile Ala Arg Gly Ser Thr Leu Ile Ser Val Asn Gln Gln		
565	570	575
Val Gly Gly Ser Ile Gly Thr Ala Leu Met Ser Val Leu Leu Thr Tyr		
580	585	590
Gln Phe Asn His Ser Glu Ile Ile Ala Thr Ala Lys Lys Val Ala Leu		
595	600	605
Thr Pro Glu Ser Gly Ala Gly Arg Gly Ala Ala Val Asp Pro Ser Ser		
610	615	620
Leu Pro Arg Gln Thr Asn Phe Ala Ala Gln Leu Leu His Asp Leu Ser		
625	630	635
His Ala Tyr Ala Val Val Phe Val Ile Ala Thr Ala Leu Val Val Ser		
645	650	655
Thr Leu Ile Pro Ala Ala Phe Leu Pro Lys Gln Gln Ala Ser His Arg		
660	665	670
Arg Ala Pro Leu Leu Ser Ala		
675		

(2) INFORMATION FOR SEQ ID NO:195:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 120 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

Thr Pro Glu Lys Ser Phe Val Asp Asp Leu Asp Ile Asp Ser Leu Ser
 1 5 10 15
 Met Val Glu Ile Ala Val Gln Thr Glu Asp Lys Tyr Gly Val Lys Ile
 20 25 30
 Pro Asp Glu Asp Leu Ala Gly Leu Arg Thr Val Gly Asp Val Val Ala
 35 40 45
 Tyr Ile Gln Lys Leu Glu Glu Glu Asn Pro Glu Ala Ala Gln Ala Leu
 50 55 60
 Arg Ala Lys Ile Glu Ser Glu Asn Pro Asp Ala Ala Arg Ala Asp Arg
 65 70 75 80
 Cys Val Ser Pro Thr Ser Gln Ala Arg Asp Ala Arg Arg Pro Leu Ala
 85 90 95
 Arg Ser Ala Arg Leu Ala Cys Arg Arg Leu Pro Ala Ser Val Pro Thr
 100 105 110
 Thr Arg Arg Asp Pro Arg Glu Arg
 115 120

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

Leu Ala Cys Gln Cys His Arg Arg Tyr Asp Val Gly Ile Gln Phe Arg
 1 5 10 15
 Gly Pro Ala Gly Pro Val Ala Thr Gln Ser Gly Pro Pro Gly Pro Ser
 20 25 30
 Ile Ala Glu Gly Arg Gln Val Arg Ala Gln Cys Gly Ala Gly Phe Leu
 35 40 45
 Glu Arg Arg Pro Ala Val Ser Gly Ala Leu Pro Pro Asn Asn Ala Ser
 50 55 60
 Pro Gly Ile Arg Ser Arg Ala Ala Asp Ser Gln Arg His Leu Leu Ala
 65 70 75 80
 Gly Asp Gly Ser Asp Val Thr Val Gly
 85

(2) INFORMATION FOR SEQ ID NO:197:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 119 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

Ala Ser Leu Leu Ala Tyr Ser Ala Ala Ala Ser Thr Ala Leu Ala
 1 5 10 15
 Val Ala Cys Val Arg Ala Asp His Arg Asp Arg Arg Thr Ile Arg Asp
 20 25 30
 His Leu Ala Met Ile His Leu Ala Gln Leu Val Thr Gln Pro Pro Gly
 35 40 45
 Gly Val Arg Gln Arg Leu His His Leu Gly Ile Ala Val Ala Pro Gln
 50 55 60
 Pro Gln Glu Val Val Val Leu Ala His His Leu Val Thr Gly Thr Gly
 65 70 75 80
 Glu Val Gln Gly Glu Gly Arg His Val Ala Ala Glu Val Val Asp Pro
 85 90 95
 Glu Asn Gln Ile Leu Arg Gln Val Leu Gly Pro Ala Pro His Asp Lys
 100 105 110
 Pro Asp Ala Gly Ile Gly Gln
 115

(2) INFORMATION FOR SEQ ID NO:198:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

Arg Ala Arg Gly His Arg Ser Ser Lys Gly Ser Arg Trp Ser His Glu
 1 5 10 15
 Val Leu Glu Gly Cys Ile Leu Ala Asp Ser Arg Gln Ser Lys Thr Ala
 20 25 30
 Ala Ser Pro Ser Pro Ser Arg Pro Gln Ser Ser Ser Asn Asn Ser Val
 35 40 45
 Pro Gly Ala Pro Asn Arg Val Ser Phe Ala Lys Leu Arg Glu Pro Leu
 50 55 60

189

Glu Val Pro Gly Leu Leu Asp Val Gln Thr Asp Ser Phe Glu Trp Leu
 65 70 75 80
 Ile Gly Ser Pro Arg Trp Arg Glu Ser Ala Ala Glu Arg Gly Asp Val
 85 90 95
 Asn Pro Val Gly Gly Leu Glu Glu Val Leu Tyr Glu Leu Ser Pro Ile
 100 105 110
 Glu Asp Phe Ser
 115

(2) INFORMATION FOR SEQ ID NO:199:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 811 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

TGCTACGCAG CAATCGCTTT GGTGACAGAT GTGGATGCCG GCGTCGCTGC TGGCGATGGC 60
 GTGAAAGCCG CCGACGTGTT CGCCGCATTC GGGGAGAACA TCGAACTGCT CAAAAGGCTG 120
 GTGCGGGCCG CCATCGATCG GGTCGCCCAC GAGCGCACGT GCACGCACTG TCAACACCAC 180
 GCCGGTGTTT CGTTGCCGTT CGAGCTGCCA TGAGGGTGCT GCTGACCGGC GCGGCCGGCT 240
 TCATCGGGTC GCGCGTGGAT GCGGCGTTAC GGGCTGCGGG TCACGACGTG GTGGGCGTCG 300
 ACGCGCTGCT GCCCGCCGCG CACGGGCCAA ACCCGGTGCT GCCACCGGGC TGCCAGCGGG 360
 TCGACGTGCG CGACGCCAGC GCGCTGGCCC CGTTGTTGGC CCGTGTCGAT CTGGTGTGTC 420
 ACCAGGCCGC CATGGTGGGT GCCGGCGTCA ACGCCGCCGA CGCACCCGCC TATGGCGGCC 480
 ACAACGATTT CGCCACCACG GTGCTGCTGG CGCAGATGTT CGCCGCCGGG GTCCGCCGTT 540
 TGGTGCTGGC GTCGTCGATG GTGGTTTACG GGCAGGGGCG CTATGACTGT CCCCAGCATG 600
 GACCGGTCGA CCCGCTGCCG CGGCGGCGAG CCGACCTGGA CAATGGGGTC TTCGAGCACC 660
 GTTGCCCCGG GTGCGGCGAG CCAGTCATCT GGCAATTGGT CGACGAAGAT GCCCCGTTGC 720
 GCGCGCGCAG CCTGTACGCG GCAGCAAGAC CGCGCAGGAG CACTACGCGC TGGCGTGGTC 780
 GGAAACGAAT GGCGGTTCCG TGGTGGCGTT G 811

(2) INFORMATION FOR SEQ ID NO:200:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 966 base pairs
 - (B) TYPE: nucleic acid

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- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

GTCCCGCGAT GTGGCCGAGC ATGACTTTTCG GCAACACCGG CGTAGTAGTC GAAGATATCG	60
GACTTTGTGG TCCCGGTGGC GGGATAGAGC ACCTGTCGGC GTTGGTCAGC GTCACCCGTT	120
GCTCGGACGC CGAACCCATG CTTTCAACGT AGCCTGTCGG TCACACAAGT CGCGAGCGTA	180
ACGTCACGGT CAAATATCGC GTGGAATTTT GCCGTGACGT TCCGCTCGCG GACAATCAAG	240
GCATACTCAC TTACATGCGA GCCATTTGGA CGGGTTTCGAT CGCCTTCGGG CTGGTGAACG	300
TGCCCGTCAA GGTGTACAGC GCTACCGCAG ACCACGACAT CAGGTTCCAC CAGGTGCACG	360
CCAAGGACAA CGGACGCATC CGGTACAAGC GCGTCTGCGA GCGGTGTGGC GAGGTGGTGC	420
ACTACCGCGA TCTTGCCCGG GCCTACGAGT CCGGCGACGG CCAAATGGTG GCGATCACCG	480
ACGACGACAT CGCCAGCTTG CCTGAAGAAC GCAGCCGGGA GATCGAGGTG TTGGAGTTTCG	540
TCCCCGCCGC CGACGTGGAC CCGATGATGT TCGACCGCAG CTACTTTTTTG GAGCCTGATT	600
CGAAGTCGTC GAAATCGTAT GTGCTGCTGG CTAAGACACT CGCCGAGACC GACCGGATGG	660
CGATCGTGGA TCGCCCCACC GGCCGTGAAT GCAGGAAAAA TAAGAGCCGC TATCCACAAT	720
TCGGCGTCGA GCTCGGCTAC CACAAACGGT AGAACGATCG AGACATTCCC GAGCTGAAGT	780
GCGGCGCTAT AGAAGCCGCT CTGCGCGATT ATCAAACGCA AAATACGCTT ACTCATGCCA	840
TCGGCGCTGC TCACCCGATG CGACGTTTTT GCCACGCTCC ACCGCTGCC GCGCGACCTC	900
AAGTGGGCAT GCATCCCACC CGTTCCCGGA AACCGGTTCC GGCGGGTCGG CTCATCGCTT	960
CATCCT	966

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2367 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

CCGCACCGCC GGCAATACCG CCAGCGCCAC CGTTACCGCC GTTTGCGCCG TTGCCCCCGT	60
TGCCGCCCCGT CCCGCCGGCC CCGCCGATGG AGTTCTCATC GCCAAAAGTA CTGGCGTTGC	120
CACCGGAGCC GCGGTTGCCG CCGTCACCGC CAGCCCCGCC GACTCCACCG GCCCCACCGA	180

CTCCGCCGCT GCCACCGTTG CCGCCGTTGC CGATCAACAT GCCGCTGGCG CCACCCTTGC	240
CACCCACGCC ACCGGCTCCG CCCACCCCGC CGACACCAAG CGAGCTGCCG CCGGAGCCAC	300
CATCACCACC TACGCCACCG ACCGCCCAGA CACCAGCGAC CGGGTCTTCG TGAAACGTCG	360
CGGTGCCACC ACCGCCGCCG TTACCGCCAA CCCCACCGGC AACGCCGGCG CCGCCATCCC	420
CGCCGGCCCC GGCCTTGCCG CCGTTGCCGC CGTTGCCGAA CAACAACCCG CCGGCGCCGC	480
CGTTGCCGCC CGCGCCGCCG GTCCCGCCGG CGCCGCCGAC GCCAAGGCCG CTGCCGCCCT	540
TGCCGCCATC ACCACCCTTG CCGCCGACCA CATCGGGTTC TGCTCGGGG TCTGGGCTGT	600
CAAACCTCGC GATGCCAGCG TTGCCGCCGC TTCCCCCGGG CCCCCCGTG GCGCCGTCAC	660
CACCGATACC ACCCGCGCCA CCGGCGCCAC CGTTGCCGCC ATCACCGAAT AGCAACCCGC	720
CGGCGCCACC ATTGCCGCCA GCTCCCCCTG CGCCACCGTC GCGCCCGGAG GCGGCACTGG	780
CAGCCCCGTT ACCACCGAAA CCGCCGCTAC CACCGGTAGA GGTGGCAGTG GCGATGTGTA	840
CGAAAGCGCC GCCTCCGGCG CCGCCGCTAC CACCCCCACT GCCGGCGGCT ACACCGTCGG	900
ACCCGTTGCC ACCATCACC GCAAAGGCGC TCGCAATGTC GCCCTGCGCG ACTCCGCCGT	960
CGCCGCCGTT GCCGCCGCCG CCACCGGCAG CGGCGGTACC GCCGTCACCA CCGGCACCGC	1020
CGGTGGCCTT GCCCGAGCCT GCCGTGCGCG TGGCACCGTC GCCGCCGGTG CCACCGGTCG	1080
GCGTGCCGCG AGTGCCATGG CCGCCCGTGC CGCCGTGCGC GCCGGTTTGA TCACCGATGC	1140
CGGACACATC TGCCGGGCTG TCCCCGGTGC TGGCCGCGGG GCCGGGCGTG GGATTGACCC	1200
CGTTTGCCCC GCGGAGGCCG GCGCCGCCGG TACCACCGGC GCCGCCATGG CCGAACAGCC	1260
CGGCGTTGCC GCCGTTACCG CCCGCACCCC CGATGCCTGC GGCCACGCTG GTGCCGCCGA	1320
CACCGCCGTT GCCGCCGTTG CCCCACAACC ACCCCCCGTT CCCACCGGCA CCGCCGGCCG	1380
CGCCGGTACC ACCGGCCCCG CCGTTGCCGC CGTTGCCGAT CAACCCGGCC GCGCCTCCGC	1440
TGCCGCCGGT TTGACCGAAC CCGCCAGCCG CGCCGTTGCC ACCGTTGCCA AACAGCAACC	1500
CGCCGGCCCG GCCAGGCTGC CCGGGTGCCG TCCCGTCGGC GCCGTTTCCG ATCAACGGGC	1560
GCCCCAAAAG CGCCTCGGTG GCGGCATTCA CCGCACCCAG CAGACTCCGC TCAACAGCGG	1620
CTTCAGTGCT GGCATACCGA CCCGCGGCCG CAGTCAACGC CTGCACAAAC TGCTCGTGAA	1680
ACGCTGCCAC CTGTACGCTG AGCGCCTGAT ACTGCCGAGC ATGGGCCCCG AACAACCCCG	1740
CAATCGCCGC CGACACTTCA TCGGCAGCCG CAGCCACCAC TTCCGTCGTC GGGATCGCCG	1800
CGGCCGCATT AGCCGCGCTC ACCTGCGAAC CAATAGTCGA TAAATCCAAA GCCGCAGTTG	1860

CCAGCAGCTG CGGCGTCGCG ATCACCAAGG ACACCTCGCA CCTCCGGATA CCCCATATCG 1920
 CCGCACCGTG TCCCCAGCGG CCACGTGACC TTTGGTCGCT GGCTGGCGGC CCTGACTATG 1980
 GCCGCGACGG CCCTCGTTCT GATTGCCCCC GGCGCGCAGC TTGTTGCGCG AGTTGAAGAC 2040
 GGGAGGACAG GCCGAGCTTG GTGTAGACGT GGGTCAAGTG GGAATGCACG GTCCGCGGCG 2100
 AGATGAATAG GCGGACGCCG ATCTCCTTGT TGCTGAGTCC CTCACCGACC AGTAGAGCCA 2160
 CCTCAAGCTC TGTCGGTGTC AACGCGCCCC AGCCACTTGT CGGGCGTTTC CGTGCACCGC 2220
 GGCCTCGTTG CGCGTACGCG ATCGCCTCAT CGATCGATAA CGCAGTTCCT TCGGCCCAGG 2280
 CATCGTCGAA CTCGCTGTCA CCCATGGATT TTCGAAGGGT GGCTAGCGAC GAGTTACAGC 2340
 CCGCCTGGTA GATCCCGAAG CGGACCG 2367

(2) INFORMATION FOR SEQ ID NO:202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 376 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

Gln Pro Ala Gly Ala Thr Ile Ala Ala Ser Ser Pro Cys Ala Thr Val
 1 5 10 15
 Gly Ala Gly Gly Gly Thr Gly Ser Pro Val Thr Thr Glu Thr Ala Ala
 20 25 30
 Thr Thr Gly Arg Gly Gly Ser Gly Asp Val Tyr Glu Ser Ala Ala Ser
 35 40 45
 Gly Ala Ala Ala Thr Thr Pro Thr Ala Gly Gly Tyr Thr Val Gly Pro
 50 55 60
 Val Ala Thr Ile Thr Ala Lys Gly Ala Arg Asn Val Ala Leu Arg Asp
 65 70 75 80
 Ser Ala Val Ala Ala Val Ala Ala Ala Thr Gly Ser Gly Gly Thr
 85 90 95
 Ala Val Thr Thr Gly Thr Ala Gly Gly Leu Ala Arg Ala Cys Arg Arg
 100 105 110
 Gly Gly Thr Val Ala Ala Gly Ala Thr Gly Arg Arg Ala Gly Ser Ala
 115 120 125
 Met Ala Ala Arg Ala Ala Val Ala Ala Gly Leu Ile Thr Asp Ala Gly
 130 135 140

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

(2) INFORMATION FOR SEQ ID NO:203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2852 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

GGCCAAAACG CCCC GGCGAT CGCGGCCACC GAGGCCGCCT ACGACCAGAT GTGGGCCCCAG	60
GACGTGGCGG CGATGTTTGG CTACCATGCC GGGGCTTCGG CGGCCGTCTC GGCGTTGACA	120
CCGTTCGGCC AGGCGCTGCC GACCGTGGCG GGGCGCGGTG CGCTGGTCAG CGCGGCCGCG	180
GCTCAGGTGA CCACGCGGGT CTTCCGCAAC CTGGGCTTGG CGAACGTCCG CGAGGGCAAC	240
GTCCGCAACG GTAATGTCCG GAACTTCAAT CTCGGCTCGG CCAACATCGG CAACGGCAAC	300
ATCGGCAGCG GCAACATCGG CAGCTCCAAC ATCGGGTTTG GCAACGTGGG TCCTGGGTTG	360
ACCGCAGCGC TGAACAACAT CGGTTTCGGC AACACCGGCA GCAACAACAT CGGGTTTGGC	420
AACACCGGCA GCAACAACAT CGGGTTCGGC AATACCGGAG ACGGCAACCG AGGTATCGGG	480
CTCACGGGTA GCGGTTTGTT GGGGTTTCGGC GGCCTGAACT CGGGCACC GG CAACATCGGT	540
CTGTTCAACT CGGGCACC GG AAACGTCGGC ATCGGCAACT CGGGTACC GG GAACTGGGGC	600
ATTGGCAACT CGGGCAACAG CTACAACACC GGTTTTGGCA ACTCCGGCGA CGCCAACACG	660
GGCTTCTTCA ACTCCGGAAT AGCCAACACC GGCGTCGGCA ACGCCGGCAA CTACAACACC	720
GGTAGCTACA ACCCGGGCAA CAGCAATACC GGCGGCTTCA ACATGGGCCA GTACAACACG	780
GGCTACCTGA ACAGCGGCAA CTACAACACC GGCTTGGCAA ACTCCGGCAA TGTCAACACC	840
GGCGCCTTCA TTA CTGGCAA CTTCAACAAC GGCTTCTTGT GGCGCGGCGA CCACCAAGGC	900
CTGATTTTCG GGAGCCCCGG CTTCTTCAAC TCGACCAGTG CGCCGTCGTC GGGATTCTTC	960
AACAGCGGTG CCGGTAGCGC GTCCGGCTTC CTGAACTCCG GTGCCAACAA TTCTGGCTTC	1020
TTCAACTCTT CGTCGGGGGC CATCGGTAAC TCCGGCCTGG CAAACGCGGG CGTGCTGGTA	1080
TCGGGCGTGA TCAACTCGGG CAACACCGTA TCGGGTTTGT TCAACATGAG CCTGGTGGCC	1140
ATCACAACGC CGGCCTTGAT CTCGGGCTTC TTCAACACCG GAAGCAACAT GTCGGGATTT	1200
TTCGGTGGCC CACCGGTCTT CAATCTCGGC CTGGCAAACC GGGGCGTCGT GAACATTCTC	1260
GGCAACGCCA ACATCGGCAA TTACAACATT CTCGGCAGCG GAAACGTCGG TGA CTTC AAC	1320
ATCCTTGGCA GCGGCAACCT CGGCAGCCAA AACATCTTGG GCAGCGGCAA CGTCGGCAGC	1380
TTCAATATCG GCAGTGAAA CATCGGAGTA TTCAATGTCT GTTCCGGAAG CCTGGGAAAC	1440
TACAACATCG GATCCGAAA CCTCGGGATC TACAACATCG GTTTTGGAAA CGTCGGCGAC	1500
TACAACGTCG GCTTCGGGAA CGCGGGCGAC TTCAACCAAG GCTTTGCCAA CACCGGCAAC	1560
AACAACATCG GGTTCGCCAA CACCGGCAAC AACAACATCG GCATCGGGCT GTCCGGCGAC	1620

AACCAGCAGG GCTTCAATAT TGCTAGCGGC TGGAACTCGG GCACCGGCAA CAGCGGCCTG	1680
TTCAATTTCGG GCACCAATAA CGTTGGCATC TTCAACGCGG GCACCGGAAA CGTCGGCATC	1740
GCAAACTCGG GCACCGGGAA CTGGGGTATC GGGAAACCCG GTACCGACAA TACCGGCATC	1800
CTCAATGCTG GCAGCTACAA CACGGGCATC CTCAACGCCG GCGACTTCAA CACGGGCTTC	1860
TACAACACGG GCAGCTACAA CACCGGCGGC TTCAACGTG GTAACACCAA CACCGGCAAC	1920
TTCAACGTGG GTGACACCAA TACCGGCAGC TATAACCCGG GTGACACCAA CACCGGCTTC	1980
TTCAATCCCG GCAACGTCAA TACCGGCGCT TTCGACACGG GCGACTTCAA CAATGGCTTC	2040
TTGGTGGCGG GCGATAACCA GGGCCAGATT GCCATCGATC TCTCGGTCAC CACTCCATTC	2100
ATCCCCATAA ACGAGCAGAT GGTCAATTGAC GTACACAACG TAATGACCTT CGGCGGCAAC	2160
ATGATCACGG TCACCGAGGC CTCGACCGTT TTCCCCAAA CCTTCTATCT GAGCGGTTTG	2220
TTCTTCTTCG GCCCGGTCAA TCTCAGCGCA TCCACGCTGA CCGTTCCGAC GATCACCTC	2280
ACCATCGGCG GACCGACGGT GACCGTCCCC ATCAGCATTG TCGGTGCTCT GGAGAGCCGC	2340
ACGATTACCT TCCTCAAGAT CGATCCGGCG CCGGGCATCG GAAATTCGAC CACCAACCCC	2400
TCGTCCGGCT TCTTCAACTC GGGCACCGGT GGCACATCTG GCTTCCAAA CGTCGGCGGC	2460
GGCAGTTCAG GCGTCTGGAA CAGTGGTTTG AGCAGCGCGA TAGGGAATTC GGGTTTCCAG	2520
AACCTCGGCT CGCTGCAGTC AGGCTGGGCG AACCTGGGCA ACTCCGTATC GGGCTTTTTC	2580
AACACCAGTA CGGTGAACCT CTCCACGCCG GCCAATGTCT CGGGCCTGAA CAACATCGGC	2640
ACCAACCTGT CCGGCGTGTT CCGCGGTCCG ACCGGGACGA TTTTCAACGC GGGCCTTGCC	2700
AACCTGGGCC AGTTGAACAT CGGCAGCGCC TCGTGCCGAA TTCGGCACGA GTTAGATACG	2760
GTTTCAACAA TCATATCCGC GTTTTGCGGC AGTGCATCAG ACGAATCGAA CCCGGGAAGC	2820
GTAAGCGAAT AAACCGAATG GCGGCCTGTC AT	2852

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 943 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

Gly	Gln	Asn	Ala	Pro	Ala	Ile	Ala	Ala	Thr	Glu	Ala	Ala	Tyr	Asp	Gln
1				5					10					15	

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Met Trp Ala Gln Asp Val Ala Ala Met Phe Gly Tyr His Ala Gly Ala
 20 25 30
 Ser Ala Ala Val Ser Ala Leu Thr Pro Phe Gly Gln Ala Leu Pro Thr
 35 40 45
 Val Ala Gly Gly Gly Ala Leu Val Ser Ala Ala Ala Ala Gln Val Thr
 50 55 60
 Thr Arg Val Phe Arg Asn Leu Gly Leu Ala Asn Val Arg Glu Gly Asn
 65 70 75 80
 Val Arg Asn Gly Asn Val Arg Asn Phe Asn Leu Gly Ser Ala Asn Ile
 85 90 95
 Gly Asn Gly Asn Ile Gly Ser Gly Asn Ile Gly Ser Ser Asn Ile Gly
 100 105 110
 Phe Gly Asn Val Gly Pro Gly Leu Thr Ala Ala Leu Asn Asn Ile Gly
 115 120 125
 Phe Gly Asn Thr Gly Ser Asn Asn Ile Gly Phe Gly Asn Thr Gly Ser
 130 135 140
 Asn Asn Ile Gly Phe Gly Asn Thr Gly Asp Gly Asn Arg Gly Ile Gly
 145 150 155 160
 Leu Thr Gly Ser Gly Leu Leu Gly Phe Gly Gly Leu Asn Ser Gly Thr
 165 170 175
 Gly Asn Ile Gly Leu Phe Asn Ser Gly Thr Gly Asn Val Gly Ile Gly
 180 185 190
 Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn Ser Gly Asn Ser Tyr
 195 200 205
 Asn Thr Gly Phe Gly Asn Ser Gly Asp Ala Asn Thr Gly Phe Phe Asn
 210 215 220
 Ser Gly Ile Ala Asn Thr Gly Val Gly Asn Ala Gly Asn Tyr Asn Thr
 225 230 235 240
 Gly Ser Tyr Asn Pro Gly Asn Ser Asn Thr Gly Gly Phe Asn Met Gly
 245 250 255
 Gln Tyr Asn Thr Gly Tyr Leu Asn Ser Gly Asn Tyr Asn Thr Gly Leu
 260 265 270
 Ala Asn Ser Gly Asn Val Asn Thr Gly Ala Phe Ile Thr Gly Asn Phe
 275 280 285
 Asn Asn Gly Phe Leu Trp Arg Gly Asp His Gln Gly Leu Ile Phe Gly
 290 295 300
 Ser Pro Gly Phe Phe Asn Ser Thr Ser Ala Pro Ser Ser Gly Phe Phe

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305		310		315		320
Asn Ser Gly Ala Gly Ser Ala Ser Gly Phe Leu Asn Ser Gly Ala Asn						
	325			330		335
Asn Ser Gly Phe Phe Asn Ser Ser Ser Gly Ala Ile Gly Asn Ser Gly						
	340		345			350
Leu Ala Asn Ala Gly Val Leu Val Ser Gly Val Ile Asn Ser Gly Asn						
	355		360			365
Thr Val Ser Gly Leu Phe Asn Met Ser Leu Val Ala Ile Thr Thr Pro						
	370		375			380
Ala Leu Ile Ser Gly Phe Phe Asn Thr Gly Ser Asn Met Ser Gly Phe						
	385		390		395	400
Phe Gly Gly Pro Pro Val Phe Asn Leu Gly Leu Ala Asn Arg Gly Val						
	405		410			415
Val Asn Ile Leu Gly Asn Ala Asn Ile Gly Asn Tyr Asn Ile Leu Gly						
	420		425			430
Ser Gly Asn Val Gly Asp Phe Asn Ile Leu Gly Ser Gly Asn Leu Gly						
	435		440			445
Ser Gln Asn Ile Leu Gly Ser Gly Asn Val Gly Ser Phe Asn Ile Gly						
	450		455			460
Ser Gly Asn Ile Gly Val Phe Asn Val Gly Ser Gly Ser Leu Gly Asn						
	465		470		475	480
Tyr Asn Ile Gly Ser Gly Asn Leu Gly Ile Tyr Asn Ile Gly Phe Gly						
	485		490			495
Asn Val Gly Asp Tyr Asn Val Gly Phe Gly Asn Ala Gly Asp Phe Asn						
	500		505			510
Gln Gly Phe Ala Asn Thr Gly Asn Asn Asn Ile Gly Phe Ala Asn Thr						
	515		520			525
Gly Asn Asn Asn Ile Gly Ile Gly Leu Ser Gly Asp Asn Gln Gln Gly						
	530		535			540
Phe Asn Ile Ala Ser Gly Trp Asn Ser Gly Thr Gly Asn Ser Gly Leu						
	545		550		555	560
Phe Asn Ser Gly Thr Asn Asn Val Gly Ile Phe Asn Ala Gly Thr Gly						
	565		570			575
Asn Val Gly Ile Ala Asn Ser Gly Thr Gly Asn Trp Gly Ile Gly Asn						
	580		585			590
Pro Gly Thr Asp Asn Thr Gly Ile Leu Asn Ala Gly Ser Tyr Asn Thr						
	595		600			605

Gly Ile Leu Asn Ala Gly Asp Phe Asn Thr Gly Phe Tyr Asn Thr Gly
 610 615 620
 Ser Tyr Asn Thr Gly Gly Phe Asn Val Gly Asn Thr Asn Thr Gly Asn
 625 630 635 640
 Phe Asn Val Gly Asp Thr Asn Thr Gly Ser Tyr Asn Pro Gly Asp Thr
 645 650 655
 Asn Thr Gly Phe Phe Asn Pro Gly Asn Val Asn Thr Gly Ala Phe Asp
 660 665 670
 Thr Gly Asp Phe Asn Asn Gly Phe Leu Val Ala Gly Asp Asn Gln Gly
 675 680 685
 Gln Ile Ala Ile Asp Leu Ser Val Thr Thr Pro Phe Ile Pro Ile Asn
 690 695 700
 Glu Gln Met Val Ile Asp Val His Asn Val Met Thr Phe Gly Gly Asn
 705 710 715 720
 Met Ile Thr Val Thr Glu Ala Ser Thr Val Phe Pro Gln Thr Phe Tyr
 725 730 735
 Leu Ser Gly Leu Phe Phe Phe Gly Pro Val Asn Leu Ser Ala Ser Thr
 740 745 750
 Leu Thr Val Pro Thr Ile Thr Leu Thr Ile Gly Gly Pro Thr Val Thr
 755 760 765
 Val Pro Ile Ser Ile Val Gly Ala Leu Glu Ser Arg Thr Ile Thr Phe
 770 775 780
 Leu Lys Ile Asp Pro Ala Pro Gly Ile Gly Asn Ser Thr Thr Asn Pro
 785 790 795 800
 Ser Ser Gly Phe Phe Asn Ser Gly Thr Gly Gly Thr Ser Gly Phe Gln
 805 810 815
 Asn Val Gly Gly Gly Ser Ser Gly Val Trp Asn Ser Gly Leu Ser Ser
 820 825 830
 Ala Ile Gly Asn Ser Gly Phe Gln Asn Leu Gly Ser Leu Gln Ser Gly
 835 840 845
 Trp Ala Asn Leu Gly Asn Ser Val Ser Gly Phe Phe Asn Thr Ser Thr
 850 855 860
 Val Asn Leu Ser Thr Pro Ala Asn Val Ser Gly Leu Asn Asn Ile Gly
 865 870 875 880
 Thr Asn Leu Ser Gly Val Phe Arg Gly Pro Thr Gly Thr Ile Phe Asn
 885 890 895

Ala Gly Leu Ala Asn Leu Gly Gln Leu Asn Ile Gly Ser Ala Ser Cys
 900 905 910

Arg Ile Arg His Glu Leu Asp Thr Val Ser Thr Ile Ile Ser Ala Phe
 915 920 925

Cys Gly Ser Ala Ser Asp Glu Ser Asn Pro Gly Ser Val Ser Glu
 930 935 940

(2) INFORMATION FOR SEQ ID NO:205:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 53 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

GGATCCATAT GGGCCATCAT CATCATCATC ACGTGATCGA CATCATCGGG ACC

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(2) INFORMATION FOR SEQ ID NO:206:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 42 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

CCTGAATTCA GGCCTCGGTT GCGCCGGCCT CATCTTGAAC GA

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(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

GGATCCTGCA GGCTCGAAAC CACCGAGCGG T

31

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 31 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

CTCTGAATTC AGCGCTGGAA ATCGTCGCGA T

31

(2) INFORMATION FOR SEQ ID NO:209:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGATCCAGCG CTGAGATGAA GACCGATGCC GCT

33

(2) INFORMATION FOR SEQ ID NO:210:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 38 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

GGATATCTGC AGAATTCAGG TTAAAGCCC ATTTGCGA

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(2) INFORMATION FOR SEQ ID NO:211:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

CCGCATGCGA GCCACGTGCC CACAACGGCC

30

(2) INFORMATION FOR SEQ ID NO:212:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

CTTCATGGAA TTCTCAGGCC GGTAAGGTCC_GCTGCGG

37

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7676 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

TGGCGAATGG GACGCGCCCT GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG	60
CAGCGTGACC GCTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTTCGCTT TCTTCCCTTC	120
CTTCTCGCC ACGTTCGCGG GCTTTCCTCCG TCAAGCTCTA AATCGGGGGC TCCCTTTAGG	180
GTTCGATTT AGTGCTTTAC GGCACCTCGA CCCCCAAAAA CTTGATTAGG GTGATGGTTC	240
ACGTAGTGGG CCATCGCCCT GATAGACGGT TTTTCGCCCCT TTGACGTTGG AGTCCACGTT	300
CTTTAATAGT GGACTCTTGT TCCAAACTGG AACAACACTC AACCTATCT CGGTCTATTC	360
TTTTGATTTA TAAGGGATTT TGCCGATTTT GGCCTATTGG TTAAAAAATG AGCTGATTTA	420
ACAAAAATTT AACGCGAATT TTAACAAAAT ATTAACGTTT ACAATTTTCAG GTGGCACTTT	480
TCGGGGAAT GTGCGCGGAA CCCCTATTTG TTTATTTTTC TAAATACATT CAAATATGTA	540
TCCGCTCATG AATTAATTCT TAGAAAACT CATCGAGCAT CAAATGAAAC TGCAATTTAT	600
TCATATCAGG ATTATCAATA CCATATTTTT GAAAAAGCCG TTTCTGTAAT GAAGGAGAAA	660
ACTCACCGAG GCAGTTCCAT AGGATGGCAA GATCCTGGTA TCGGTCTGCG ATTCCGACTC	720
GTCCAACATC AATACAACCT ATTAATTTCC CCTCGTCAAA AATAAGGTTA TCAAGTGAGA	780
AATCACCATG AGTGACGACT GAATCCGGTG AGAATGGCAA AAGTTTATGC ATTTCTTTCC	840
AGACTTGTTT AACAGGCCAG CCATTACGCT CGTCATCAAA ATCACTCGCA TCAACCAAAC	900
CGTTATTCAT TCGTGATTGC GCCTGAGCGA GACGAAATAC GCGATCGCTG TTAAAAGGAC	960
AATTACAAAC AGGAATCGAA TGCAACCGGC GCAGGAACAC TGCCAGCGCA TCAACAATAT	1020
TTTCACCTGA ATCAGGATAT TCTTCTAATA CCTGGAATGC TGTTTTCCCG GGGATCGCAG	1080
TGGTGAGTAA CCATGCATCA TCAGGAGTAC GGATAAAATG CTTGATGGTC GGAAGAGGCA	1140
TAAATTCCGT CAGCCAGTTT AGTCTGACCA TCTCATCTGT AACATCATTG GCAACGCTAC	1200
CTTTGCCATG TTTCAGAAAC AACTCTGGCG CATCGGGCTT CCCATACAAT CGATAGATTG	1260
TCGCACCTGA TTGCCCCGACA TTATCGCGAG CCCATTTATA CCCATATAAA TCAGCATCCA	1320
TGTTGGAATT TAATCGCGGC CTAGAGCAAG ACGTTTCCCG TTGAATATGG CTCATAACAC	1380
CCCTTGATT ACTGTTTATG TAAGCAGACA GTTTTATTGT TCATGACCAA AATCCCTTAA	1440
CGTGAGTTTT CGTTCCACTG AGCGTCAGAC CCCGTAGAAA AGATCAAAGG ATCTTCTTGA	1500

GATCCTTTTT TTCTGCGCGT AATCTGCTGC TTGCAAACAA AAAAACCACC GCTACCAGCG	1560
GTGGTTTGTG TGCCGGATCA AGAGCTACCA ACTCTTTTTC CGAAGGTAAC TGGCTTCAGC	1620
AGAGCGCAGA TACCAAATAC TGTCTTCTA GTGTAGCCGT AGTTAGGCCA CCACTTCAAG	1680
AACTCTGTAG CACCGCCTAC ATACCTCGCT CTGCTAATCC TGTACCAGT GGCTGCTGCC	1740
AGTGGCGATA AGTCGTGTCT TACCGGGTTG GACTCAAGAC GATAGTTACC GGATAAGGCG	1800
CAGCGGTCCG GCTGAACGGG GGGTTCGTGC ACACAGCCCA GCTTGAGCG AACGACCTAC	1860
ACCGAACTGA GATACCTACA GCGTGAGCTA TGAGAAAGCG CCACGCTTCC CGAAGGGAGA	1920
AAGGCGGACA GGTATCCGGT AAGCGGCAGG GTCGGAACAG GAGAGCGCAC GAGGGAGCTT	1980
CCAGGGGGAA ACGCCTGGTA TCTTTATAGT CCTGTCCGGT TTCGCCACCT CTGACTTGAG	2040
CGTCGATTTT TGTGATGCTC GTCAGGGGGG CGGAGCCTAT GGAAAAACGC CAGCAACGCG	2100
GCCTTTTTAC GGTTCCTGGC CTTTGTCTGG CTTTTGCTC ACATGTTCTT TCCTGCGTTA	2160
TCCCCTGATT CTGTGGATAA CCGTATTACC GCCTTTGAGT GAGCTGATAC CGCTCGCCGC	2220
AGCCGAACGA CCGAGCGCAG CGAGTCAGTG AGCGAGGAAG CGGAAGAGCG CCTGATGCGG	2280
TATTTTCTCC TTACGCATCT GTGCGGTATT TCACACCGCA TATATGGTGC ACTCTCAGTA	2340
CAATCTGCTC TGATGCCGCA TAGTTAAGCC AGTATACT CCGCTATCGC TACGTGACTG	2400
GGTCATGGCT GCGCCCCGAC ACCCGCCAAC ACCCGCTGAC GCGCCCTGAC GGGCTTGTCT	2460
GCTCCCGGCA TCCGCTTACA GACAAGCTGT GACCGTCTCC GGGAGCTGCA TGTGTCAGAG	2520
GTTTTACCG TCATCACC GAACGCGGAG GCAGCTGCGG TAAAGCTCAT CAGCGTGGTC	2580
GTGAAGCGAT TCACAGATGT CTGCCTGTTT ATCCGCGTCC AGCTCGTTGA GTTTCTCCAG	2640
AAGCGTTAAT GTCTGGCTTC TGATAAAGCG GGCCATGTTA AGGGCGGTTT TTTCTGTTT	2700
GGTCACTGAT GCCTCCGTGT AAGGGGGATT TCTGTTTATG GGGGTAATGA TACCGATGAA	2760
ACGAGAGAGG ATGCTCACGA TACGGGTTAC TGATGATGAA CATGCCCGGT TACTGGAACG	2820
TTGTGAGGGT AAACAACCTG CCGTATGGAT GCGGCGGGAC CAGAGAAAAA TCACTCAGGG	2880
TCAATGCCAG CGCTTCGTTA ATACAGATGT AGGTGTTCCA CAGGGTAGCC AGCAGCATCC	2940
TGCGATGCAG ATCCGGAACA TAATGGTGCA GGGCGCTGAC TTCCGCGTTT CCAGACTTTA	3000
CGAAACACGG AAACCGAAGA CCATTCATGT TGTTGCTCAG GTCGCAGACG TTTTGCAGCA	3060
GCAGTCGCTT CACGTTCTGT CCGGTATCGG TGATTCATTC TGCTAACCAG TAAGGCAACC	3120
CCGCCAGCCT AGCCGGGTCC TCAACGACAG GAGCACGATC ATGCGCACCC GTGGGGCCGC	3180

CATGCCGGCG ATAATGGCCT GCTTCTCGCC GAAACGTTTG GTGGCGGGAC CAGTGACGAA 3240
GGCTTGAGCG AGGGCGTGCA AGATTCCGAA TACCGCAAGC GACAGGCCGA TCATCGTCGC 3300
GCTCCAGCGA AAGCGGTCCT CGCCGAAAAT GACCCAGAGC GCTGCCGGCA CCTGTCTTAC 3360
GAGTTGCATG ATAAAGAAGA CAGTCATAAG TCGGGCGACG ATAGTCATGC CCCGCGCCCA 3420
CCGGAAGGAG CTGACTGGGT TGAAGGCTCT CAAGGGCATC GGTCGAGATC CCGGTGCCTA 3480
ATGAGTGAGC TAACTTACAT TAATTGCGTT GCGCTCACTG CCCGCTTTCC AGTCGGGAAA 3540
CCTGTCTGTC CAGCTGCATT AATGAATCGG CCAACGCGCG GGGAGAGGCG GTTTGCGTAT 3600
TGGGCGCCAG GGTGGTTTTT CTTTTCACCA GTGAGACGGG CAACAGCTGA TTGCCCTTCA 3660
CCGCCTGGCC CTGAGAGAGT TGCAGCAAGC GGTCCACGCT GGTTCGCCCC AGCAGGCGAA 3720
AATCCTGTTT GATGGTGGTT AACGGCGGGA TATAACATGA GCTGTCTTCG GTATCGTCGT 3780
ATCCCACTAC CGAGATATCC GCACCAACGC GCAGCCCGGA CTCGGTAATG GCGCGCATTG 3840
CGCCAGCGC CATCTGATCG TTGGCAACCA GCATCGCAGT GGGAACGATG CCCTCATTCA 3900
GCATTTGCAT GGTTCGTTGA AAACCGGACA TGGCACTCCA GTCGCTTCC CGTTCGGCTA 3960
TCGGCTGAAT TTGATTGCGA GTGAGATATT TATGCCAGCC AGCCAGACGC AGACCGCCCG 4020
AGACAGAACT TAATGGGCCC GCTAACAGCG CGATTTGCTG GTGACCCAAT GCGACCAGAT 4080
GCTCCACGCC CAGTCGCGTA CCGTCTTCAT GGGAGAAAAT AATACTGTTG ATGGGTGTCT 4140
GGTCAGAGAC ATCAAGAAAT AACGCCGGAA CATTAGTGCA GGCAGCTTCC ACAGCAATGG 4200
CATCCTGGTC ATCCAGCGGA TAGTTAATGA TCAGCCCACT GACGCGTTGC GCGAGAAGAT 4260
TGTGCACCGC CGCTTTACAG GCTTCGACGC CGCTTCGTTT TACCATCGAC ACCACCAGC 4320
TGGCACCCAG TTGATCGGCG CGAGATTAA TCGCCGCGAC AATTTGCGAC GCGCGGTGCA 4380
GGGCCAGACT GGAGGTGGCA ACGCCAATCA GCAACGACTG TTTGCCCCGC AGTTGTTGTG 4440
CCACGCGGTT GGAATGTAA TTCAGCTCCG CCATCGCCGC TTCCACTTTT TCCCGCGTTT 4500
TCGAGAAAC GTGGCTGGCC TGGTTCACCA CGCGGGAAAC GGTCTGATAA GAGACACCGG 4560
CATACTCTGC GACATCGTAT AACGTTACTG GTTTCACATT CACCACCCTG AATTGACTCT 4620
CTTCCGGGCG CTATCATGCC ATACCGCGAA AGGTTTTGCG CCATTCGATG GTGTCCGGGA 4680
TCTCGACGCT CTCCCTTATG CGACTCCTGC ATTAGGAAGC AGCCAGTAG TAGGTTGAGG 4740
CCGTTGAGCA CCGCCGCGC AAGGAATGGT GCATGCAAGG AGATGGCGCC CAACAGTCCC 4800

CCGGCCACGG GGCCTGCCAC CATACCCACG CCGAAACAAG CGCTCATGAG CCCGAAGTGG 4860
CGAGCCCCGAT CTTCCCCATC GGTGATGTCG GCGATATAGG CGCCAGCAAC CGCACCTGTG 4920
GCGCCGGTGA TGCCGGCCAC GATGCGTCCG GCGTAGAGGA TCGAGATCTC GATCCCGCGA 4980
AATTAATACG ACTCACTATA GGGGAATTGT GAGCGGATAA CAATTCCCCT CTAGAAATAA 5040
TTTTGTTTAA CTTTAAGAAG GAGATATACA TATGGGCCAT CATCATCATC ATCACGTGAT 5100
CGACATCATC GGGACCAGCC CCACATCCTG GGAACAGGCG GCGGCGGAGG CGGTCCAGCG 5160
GGCGCGGGAT AGCGTCGATG ACATCCGCGT CGCTCGGGTC ATTGAGCAGG ACATGGCCGT 5220
GGACAGCGCC GGCAAGATCA CCTACCGCAT CAAGCTCGAA GTGTCGTTCA AGATGAGGCC 5280
GGCGCAACCG AGGGGCTCGA AACCACCGAG CGGTTGCGCT GAAACGGGCG CCGGCGCCGG 5340
TACTGTGCGG ACTACCCCCG CGTCGTGCGC GGTGACGTTG GCGGAGACCG GTAGCACGCT 5400
GCTCTACCCG CTGTTCAACC TGTGGGGTCC GGCCTTTTAC GAGAGGTATC CGAACGTCAC 5460
GATCACCGCT CAGGGCACCG GTTCTGGTGC CGGGATCGCG CAGGCCGCCG CCGGGACGGT 5520
CAACATTGGG GCCTCCGACG CCTATCTGTC GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT 5580
GATGAACATC GCGCTAGCCA TCTCCGCTCA GCAGGTCAAC TACAACCTGC CCGGAGTGAG 5640
CGAGCACCTC AAGCTGAACG GAAAAGTCCT GGCGGCCATG TACCAGGGCA CCATCAAAAC 5700
CTGGGACGAC CCGCAGATCG CTGCGCTCAA CCCC GGCGTG AACCTGCCCC GCACCGCGGT 5760
AGTTCCGCTG CACCGCTCCG ACGGGTCCGG TGACACCTTC TTGTTACCCC AGTACCTGTC 5820
CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC GCCCGGCTTC GGCACCACCG TCGACTTCCC 5880
GGCGGTGCCG GGTGCGCTGG GTGAGAACGG CAACGGCGGC ATGGTGACCG GTTGCGCCGA 5940
GACACCGGGC TGCGTGGCCT ATATCGGCAT CAGCTTCCTC GACCAGGCCA GTCAACGGGG 6000
ACTCGGCGAG GCCCAACTAG GCAATAGCTC TGGCAATTC TTGTTGCCCC ACGCGCAAAG 6060
CATTCAGGCC GCGGCGGCTG GCTTCGCATC GAAAACCCCG GCGAACCAGG CGATTTCGAT 6120
GATCGACGGG CCCGCCCCCG ACGGCTACCC GATCATCAAC TACGAGTACG CCATCGTCAA 6180
CAACCGGCAA AAGGACGCCG CCACCGCGCA GACCTTGAG GCATTTCTGC ACTGGGCGAT 6240
CACCGACGGC AACAAGGCCT CGTTCCTCGA CCAGGTTTCT TTCCAGCCGC TGCCGCCCGC 6300
GGTGGTGAAG TTGTCTGACG CGTTGATCGC GACGATTTCC AGCGCTGAGA TGAAGACCGA 6360
TGCCGCTACC CTCGCGCAGG AGGCAGGTAA TTTCGAGCGG ATCTCCGGCG ACCTGAAAAC 6420
CCAGATCGAC CAGGTGGAGT CGACGGCAGG TTCGTTGCAG GGCCAGTGGC GCGGCGCGGC 6480

GGGGACGGCC GCCCAGGCCG CGGTGGTGCG CTTCCAAGAA GCAGCCAATA AGCAGAAGCA 6540
 GGAACCTCGAC GAGATCTCGA CGAATATTCG TCAGGCCCGC GTCCAATACT CGAGGGCCGA 6600
 CGAGGAGCAG CAGCAGGCGC TGTCTCTCGA AATGGGCTTT GTGCCCACAA CGGCCGCCTC 6660
 GCCGCCGTCG ACCGCTGCAG CGCCACCCGC ACCGGCGACA CCTGTTGCCC CCCCACCACC 6720
 GGCCGCGGCC AACACGCCGA ATGCCCAGCC GGGCGATCCC AACGCAGCAC CTCCGCCGGC 6780
 CGACCCGAAC GCACCGCCGC CACCTGTCAT TGCCCCAAAC GCACCCCAAC CTGTCCGGAT 6840
 CGACAACCCG GTTGGAGGAT TCAGCTTCGC GCTGCCTGCT GGCTGGGTGG AGTCTGACGC 6900
 CGCCCACTTC GACTACGGTT CAGCACTCCT CAGCAAAACC ACCGGGGACC CGCCATTTC 6960
 CGGACAGCCG CCGCCGGTGG CCAATGACAC CCGTATCGTG CTCGGCCGGC TAGACCAAAA 7020
 GCTTTACGCC AGCGCCGAAG CCACCGACTC CAAGGCCGCG GCCCGGTTGG GCTCGGACAT 7080
 GGGTGAGTTC TATATGCCCT ACCCGGGCAC CCGGATCAAC CAGGAAACCG TCTCGCTTGA 7140
 CGCCAACGGG GTGTCTGGAA GCGCGTCGTA TTACGAAGTC AAGTTCAGCG ATCCGAGTAA 7200
 GCCGAACGGC CAGATCTGGA CGGGCGTAAT CGGCTCGCCC GCGGCGAACG CACCGGACGC 7260
 CGGGCCCCCT CAGCGCTGGT TTGTGGTATG GCTCGGGACC GCCAACAACC CGGTGGACAA 7320
 GGGCGCGGCC AAGGCGCTGG CCGAATCGAT CCGGCCTTTG GTCGCCCCGC CGCCGGCGCC 7380
 GGCACCGGCT CCTGCAGAGC CCGCTCCGGC GCCGGCGCCG GCCGGGGAAG TCGCTCCTAC 7440
 CCCGACGACA CCGACACCGC AGCGGACCTT ACCGGCCTGA GAATTCTGCA GATATCCATC 7500
 AACTGGCGG CCGCTCGAGC ACCACCACCA CCACCACTGA GATCCGGCTG CTAACAAAGC 7560
 CCGAAAGGAA GCTGAGTTGG CTGCTGCCAC CGCTGAGCAA TAACTAGCAT AACCCTTGG 7620
 GGCCTCTAAA CGGGTCTTGA GGGGTTTTTT GCTGAAAGGA GGAACATAT CCGGAT 7676

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

Met Gly His His His His His Val Ile Asp Ile Ile Gly Thr Ser
 1 5 10 15
 Pro Thr Ser Trp Glu Gln Ala Ala Ala Glu Ala Val Gln Arg Ala Arg

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20 25 30
 Asp Ser Val Asp Asp Ile Arg Val Ala Arg Val Ile Glu Gln Asp Met
 35 40 45
 Ala Val Asp Ser Ala Gly Lys Ile Thr Tyr Arg Ile Lys Leu Glu Val
 50 55 60
 Ser Phe Lys Met Arg Pro Ala Gln Pro Arg Gly Ser Lys Pro Pro Ser
 65 70 75 80
 Gly Ser Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro
 85 90 95
 Ala Ser Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr
 100 105 110
 Pro Leu Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn
 115 120 125
 Val Thr Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln
 130 135 140
 Ala Ala Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser
 145 150 155 160
 Glu Gly Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala
 165 170 175
 Ile Ser Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His
 180 185 190
 Leu Lys Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile
 195 200 205
 Lys Thr Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn
 210 215 220
 Leu Pro Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly
 225 230 235 240
 Asp Thr Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly
 245 250 255
 Trp Gly Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val
 260 265 270
 Pro Gly Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys
 275 280 285
 Ala Glu Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp
 290 295 300
 Gln Ala Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser
 305 310 315 320

Gly Asn Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Ala
 325 330 335
 Gly Phe Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp
 340 345 350
 Gly Pro Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile
 355 360 365
 Val Asn Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala
 370 375 380
 Phe Leu His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp
 385 390 395 400
 Gln Val His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp
 405 410 415
 Ala Leu Ile Ala Thr Ile Ser Ser Ala Glu Met Lys Thr Asp Ala Ala
 420 425 430
 Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile Ser Gly Asp Leu
 435 440 445
 Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly Ser Leu Gln Gly
 450 455 460
 Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala Ala Val Val Arg
 465 470 475 480
 Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu Asp Glu Ile Ser
 485 490 495
 Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg Ala Asp Glu Glu
 500 505 510
 Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe Val Pro Thr Thr Ala
 515 520 525
 Ala Ser Pro Pro Ser Thr Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro
 530 535 540
 Val Ala Pro Pro Pro Pro Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro
 545 550 555 560
 Gly Asp Pro Asn Ala Ala Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro
 565 570 575
 Pro Pro Val Ile Ala Pro Asn Ala Pro Gln Pro Val Arg Ile Asp Asn
 580 585 590
 Pro Val Gly Gly Phe Ser Phe Ala Leu Pro Ala Gly Trp Val Glu Ser
 595 600 605

Asp Ala Ala His Phe Asp Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr
 610 615 620
 Gly Asp Pro Pro Phe Pro Gly Gln Pro Pro Pro Val Ala Asn Asp Thr
 625 630 635 640
 Arg Ile Val Leu Gly Arg Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu
 645 650 655
 Ala Thr Asp Ser Lys Ala Ala Ala Arg Leu Gly Ser Asp Met Gly Glu
 660 665 670
 Phe Tyr Met Pro Tyr Pro Gly Thr Arg Ile Asn Gln Glu Thr Val Ser
 675 680 685
 Leu Asp Ala Asn Gly Val Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys
 690 695 700
 Phe Ser Asp Pro Ser Lys Pro Asn Gly Gln Ile Trp Thr Gly Val Ile
 705 710 715 720
 Gly Ser Pro Ala Ala Asn Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp
 725 730 735
 Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 454 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

GTGGCGGCGC	TGCGGCCGGC	CAGCAGAGCG	ATGTGCATCC	GTTTCGCGAAC	CTGATCGCGG	60
TCGACGATGA	GCGCGCCGAA	CGCCGCGACG	ACGAAGAACG	TCAGGAAGCC	GTCCAGCAGC	120
GCGGTCCGCG	CGGTGACGAA	GCTGACCCCG	TCGCAGATCA	GCAGCACCCC	GGCGATGGCG	180
CCGACCAATG	TCGACCGGCT	GATCCGCCGC	ACGATCCGCA	CCACCAGCGC	CACCAGGACC	240
ACACCCAGCA	GGGCGCCGGT	GAACCGCCAG	CCGAATCCGT	TGTGACCGAA	GATGGCCTCC	300

CCGATCGCGA TCAGCTGCTT ACCGACCGGC GGGTGAACCA CCAGGCCGTA CCCGGGGTTG 360
 TCTTCCACCC CATGGTTGTT CAGCACCTGC CAGGCCTGGC GGTGCGTAAT GCTTCTCGTC 420
 GAAGATGGGG GTGCCGGCAT CCGTCACCGA GCCC 454

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 470 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

TGCAGAAGTA CGGCGGATCC TCGGTGGCCG ACGCCGAACG GATTCGCCGC GTCGCCGAAC 60
 GCATCGTCGC CACCAAGAAG CAAGGCAATG ACGTCGTCGT CGTCGTCTCT GCCATGGGGG 120
 ATACCACCGA CGACCTGCTG GATCTGGCTC AGCAGGTGTG CCCGGCGCCG CCGCCTCGGG 180
 AGCTGGACAT GCTGCTTACC GCCGGTGAAC GCATCTCGAA TCGGTTGGTG GCCATGGCCA 240
 TCGAGTCGCT CGGCGCGCAT GCCCGGTCGT TCACCGGTTT GCAGGCCGGG GTGATCACCA 300
 CCGGCACCCA CGGCAACGCC AAGATCATCG ACGTCACGCC GGGGCGGCTG CAAACCGCCC 360
 TTGAGGAAGG GCGGGTCTGTC TTGGTGGCCG GATTCCAAGG GGTGAGCCAG GACACCAAGG 420
 ATGTCACGAC GTTGGGCGCG GCGGGCTCGG ACACCACCGC CGTCGCCATG 470

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 279 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

GGCCGGCGTA CCCGGCCGGG ACAAACAACG ATCGATTGAT ATCGATGAGA GACGGAGGAA 60
 TCGTGGCCCT TCCCCAGTTG ACCGACGAGC AGCGCGCGGC CGCGTTGGAG AAGGCTGCTG 120
 CCGCACGTCG AGCGCGAGCA GAGCTCAAGG ATCGGCTCAA GCGTGGCGGC ACCAACCTCA 180
 CCCAGGTCCT CAAGGACGCG GAGAGCGATG AAGTCTTGGG CAAAATGAAG GTGTCTGCGC 240
 TGCTTGAGGC CTTGCCAAAG GTGGGCAAGG TCCAGGCGC 279

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACACGGTCTGA	ACTCGACGAG	CCCCTCGTGG	AGGTGTCTGAC	CGACAAGGTC	GACACCGAAA	60
TCCCTCGCCG	GCCGCGGGTG	TGCTGACCAA	GATCATCGCC	CAAGAAGATG	ACACGGTCTGA	120
GGTCGGCGGC	GAGCTCTCTG	TCATTGGCGA	CGCCCATGAT	GCCGGCGAGG	CCGCGGTCCC	180
GGCACCCAG	AAAGTCTCTG	CCGGCCCAAC	CCGAATCCA			219

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TCGCTGCCGA	CATCGGCGCC	GCGCCCGCCC	CCAAGCCCGC	ACCCAAGCCC	GTCCCCGAGC	60
CAGCGCCGAC	GCCGAAGGCC	GAACCCGCAC	CATCGCCGCC	GGCGGCCCCAG	CCAGCCGGTG	120
CGGCCGAGGG	CGCACCGTAC	GTGACGCCGC	TGGTGCGAAA	GCTGGCGTCG	GAAAACAACA	180
TCGACCTCGC	CGGGGTGACC	GGCACCGGAG	TGGGTGGTCG	CATCCGCAAA	CAGGATGTGC	240
TGGCCGCGGC	TGAACAAAAG	AAGCGGGCGA	AAGCACCGGC	GCCGGCCGCC	CAGGCCGCCG	300
CCGCGCCGGC	CCGAAAGCG	CCGCCTGAAG	ATCCGATGCC	GC		342

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 515 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

GGGTCTTGGT	CAGTATCAGC	GCCGACGAGG	ACGCCACGGT	GCCCCGTCGGC	GGCGAGTTGG	60
CCCGGATCGG	TGTCGCTGCC	GACATCGGCG	CCGCGCCCGC	CCCCAAGCCC	GCACCCAAGC	120
CCGTCCCCGA	GCCAGCGCCG	ACGCCGAAGG	CCGAACCCGC	ACCATCGCCG	CCGGCGGCCC	180
AGCCAGCCGG	TGCGCCGAG	GGCGCACCGT	ACGTGACGCC	GCTGGTGCGA	AAGCTGGCGT	240
CGGAAAACAA	CATCGACCTC	GCCGGGGTGA	CCGGCACCCG	AGTGGGTGGT	CGCATCCGCA	300
AACAGGATGT	GCTGGCCGCG	GCTGAACAAA	AGAAGCGGGC	GAAAGCACCG	GCGCCCTGAG	360
CGCTTCATCA	CCCGGTTAAC	CAGCTTGCCC	CAGAAGCCGG	CTTCGACCTC	TTCGCGGGTC	420
TTGGTCCGCT	GCAGGCGGTC	GGCGAGCCAG	TTCAGGTTAG	GCGGCCGAAA	TCTTCCAGTT	480
CGCCAGGAAG	GGCACCCGGA	ACAGGGTCCG	CACCC			515

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 557 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

CCGACCCCAA	GGTGCAGATT	CAACAGGCCA	TTGAGGAAGC	ACAGCGCACC	CACCAAGCGC	60
TGACTCAACA	GGCGGCGCAA	GTGATCGGTA	ACCAGCGTCA	ATTGGAGATG	CGACTCAACC	120
GACAGCTGGC	GGACATCGAA	AAGCTTCAGG	TCAATGTGCG	CCAAGCCCTG	ACGCTGGCCG	180
ACCAGGCCAC	CGCCGCCGGA	GACGCTGCCA	AGGCCACC GA	ATACAACAAC	GCCGCCGAGG	240
CGTTCGCAGC	CCAGCTGGTG	ACCGCCGAGC	AGAGCGTCGA	AGACCTCAAG	ACGCTGCATG	300
ACCAGGCGCT	TAGCGCCGCA	GCTCAGGCCA	AGAAGGCCGT	CGAACGAAAT	GCGATGGTGC	360
TGCAGCAGAA	GATCGCCGAG	CGAACCAAGC	TGCTCAGCCA	GCTCGAGCAG	GCGAAGATGC	420
AGGAGCAGGT	CAGCGCATCG	TTGCGGTCTGA	TGAGTGAGCT	CGCCGCGCCA	GGCAACACGC	480
CGAGCCTCGA	CGAGGTGCGC	GACAAGATCG	AGCGTCGCTA	CGCCAACGCG	ATCGGTTCGG	540
CTGAACTTGC	CGAGAGT					557

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

CAGGATAGGT	TTGACATCC	ACCTGGGTTC	CGCACCCGGT	GCGCGACCGT	GTGATAGGCC	60
AGAGGTGGAC	CTGCGCCGAC	CGACGATCGA	TCGAGGAGTC	AACAGAAATG	GCCTTCTCCG	120
TCCAGATGCC	GGCACTCGGT	GAGAGCGTCA	CCGAGGGGAC	GGTTACCCGC	TGGCTCAAAC	180
AGGAAGGCGA	CACGGTCGAA	CTCGACGAGC	CCCTCGTGGA	GGT		223

(2) INFORMATION FOR SEQ ID NO:223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAGAAGTACA	TCTGCCGGTC	GATGTCGGCG	AACCACGGCA	GCCAACCGGC	GCAGTAGCCG	60
ACCAGGACCA	CCGCATAACG	CCAGTCCC GG	CGCACAAACA	TACGCCACCC	CGCGTATGCC	120
AGGACTGGCA	CCGCCAGCCA	CCACATCGCG	GGCGTGCCGA	CCAGCATCTC	GGCCTTGACG	180
CACGACTGTG	CGCCGCAGCC	TGCAACGTCT	TGCTGGTCTGA	TGGCGTACAG	CACCGGCCGC	240
AACGACATGG	GCCAGGTCCA	CGGTTTGGAT	TCCCAAGGGT	GGTAGTTGCC	TGCGGAATTC	300
GTCAGGCCCCG	CGTGGAAGTG	GAACGCTTTG	GCGGTGTATT	GCCAGAGCGA	GCGCACGGCG	360
TCGGGCAGCG	GAACAACCGA	GTTGCGACCG	ACCGCTTGAC	CGACCGCATG	CCGATCGATC	420
GCGGTCTCGG	ACGCGAACCA	CGGAGCGTAG	GTGGCCAGAT	AGACCGCGAA	CGGGATCAAC	480
CCCAGCGCAT	ACCCGCTGGG	AAGCACGTCA	CGCCGCACTG	TTCCCAGCCA	CGGTCTTTGC	540
ACTTGGTATG	AACGTCGCGC	CGCCACGTCA	ACGCCAGC			578

(2) INFORMATION FOR SEQ ID NO:224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224:

```

ACAACGATCG ATTGATATCG ATGAGAGACG GAGGAATCGT GGCCCTTCCC CAGTTGACCG      60
ACGAGCAGCG CGCGGCCGCG TTGGAGAAGG CTGCTGCCGC ACGTCGAGCG CGAGCAGAGC      120
TCAAGGATCG GCTCAAGCGT GCGGGCACCA ACCTCACCCA GGTCTCAAG GACGCGGAGA      180
GCGATGAAGT CTTGGGCAA ATGAAGGTGT CTGCGCTGCT TGAGGCCTTG CCAAAGGTGG      240
GCAAGGTCAA GGCGCAGGAG ATCATGACCG AGCTGGAAAT TGCGCCCCAC CCCGCCGCT      300
TCGTGGCCTC GGTGACCGTC AGCGCAAGGC CCTGCTGGAA AAGTTCGGCT CCGCCTAACC      360
CCGCCGCGCG ACGATGCGGG CCGGAAGGCC TGTGGTGGGC GTACCCCCGC ATACGGGGGA      420
GAAGCGGCCT GACAGGGCCA GCTCACAATT CAGGCCGAAC GCCCCGGTGG GGGGGAACCC      480
GCCC

```

(2) INFORMATION FOR SEQ ID NO:225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 537 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:225:

```

AGGACTGGCA CCGCCAGCCA CCACATCGCG GCGGTGCCGA CCAGCATCTC GGCCTTGACG      60
CACGACTGTG CGCCGCAGCC TGCAACGTCT TGCTGGTCTGA TGGCGTACAG CACCGGCCGC      120
AACGACATGG GCCAGGTCCA CGGTTTGGAT TCCCAAGGGT GGTAGTTGCC TGCGGAATTC      180
GTCAGGCCCC CGTGGAAGTG GAACGCTTTG GCGGTGTAGT GCCAGAGCGA GCGCACGGCG      240
TCGGGCAGCG GAACAACCGA GTTGCGACCG ACCGCTTGAC CGACCGCATG CCCGATCGATC      300
GCGGTCTCGG ACGCGAACCA CGGAGCGTAG GTGGCCAGAT AGACCGCGAA CCGGATCAAC      360
CCCAGCGCAT ACCCGCTGGG AAGCACGTCA CGCCGCACTG TCCCCAGCCA CCGTCTTTGC      420
ACTTGGTACT GACGTGCGCG CGCCACGTCG AACGCCAGCG CCATCGCGCC GAAGAACAGC      480
ACGAAGTACA CGCCGGACCA CTTGGTGGCG CAAGCCAATC CCAAGCAGCA CCCCGGC      537

```

(2) INFORMATION FOR SEQ ID NO:226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:226:

213

Gly Gly Ala Ala Ala Gly Gln Gln Ser Asp Val His Pro Phe Ala Asn
 1 5 10 15
 Leu Ile Ala Val Asp Asp Glu Arg Ala Glu Arg Arg Asp Asp Glu Glu
 20 25 30
 Arg Gln Glu Ala Val Gln Gln Arg Gly Pro Arg Gly Asp Glu Ala Asp
 35 40 45
 Pro Val Ala Asp Gln Gln His Pro Gly Asp Gly Ala Asp Gln Cys Arg
 50 55 60
 Pro Ala Asp Pro Pro His Asp Pro His His Gln Arg His Gln Asp His
 65 70 75 80
 Thr Gln Gln Gly Ala Gly Glu Pro Pro Ala Glu Ser Val Val Thr Glu
 85 90 95
 Asp Gly Leu Pro Asp Arg Asp Gln Leu Leu Thr Asp Arg Arg Val Asn
 100 105 110
 His Gln Ala Val Pro Gly Val Val Phe His Pro Met Val Val Gln His
 115 120 125
 Leu Pro Gly Leu Ala Val Arg
 130 135

(2) INFORMATION FOR SEQ ID NO:227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 156 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:227:

Gln Lys Tyr Gly Gly Ser Ser Val Ala Asp Ala Glu Arg Ile Arg Arg
 1 5 10 15
 Val Ala Glu Arg Ile Val Ala Thr Lys Lys Gln Gly Asn Asp Val Val
 20 25 30
 Val Val Val Ser Ala Met Gly Asp Thr Thr Asp Asp Leu Leu Asp Leu
 35 40 45
 Ala Gln Gln Val Cys Pro Ala Pro Pro Pro Arg Glu Leu Asp Met Leu
 50 55 60
 Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
 65 70 75 80
 Glu Ser Leu Gly Ala His Ala Arg Ser Phe Thr Gly Ser Gln Ala Gly
 85 90 95
 Val Ile Thr Thr Gly Thr His Gly Asn Ala Lys Ile Ile Asp Val Thr
 100 105 110
 Pro Gly Arg Leu Gln Thr Ala Leu Glu Glu Gly Arg Val Val Leu Val
 115 120 125
 Ala Gly Phe Gln Gly Val Ser Gln Asp Thr Lys Asp Val Thr Thr Leu
 130 135 140
 Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Met
 145 150 155

(2) INFORMATION FOR SEQ ID NO:228:

(i) SEQUENCE CHARACTERISTICS:

214

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:228:

```

Pro Ala Tyr Pro Ala Gly Thr Asn Asn Asp Arg Leu Ile Ser Met Arg
 1           5           10           15
Asp Gly Gly Ile Val Ala Leu Pro Gln Leu Thr Asp Glu Gln Arg Ala
      20           25           30
Ala Ala Leu Glu Lys Ala Ala Ala Arg Arg Ala Arg Ala Glu Leu
      35           40           45
Lys Asp Arg Leu Lys Arg Gly Gly Thr Asn Leu Thr Gln Val Leu Lys
      50           55           60
Asp Ala Glu Ser Asp Glu Val Leu Gly Lys Met Lys Val Ser Ala Leu
      65           70           75           80
Leu Glu Ala Leu Pro Lys Val Gly Lys Val Gln Ala
      85           90

```

(2) INFORMATION FOR SEQ ID NO:229:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:229:

```

Thr Val Glu Leu Asp Glu Pro Leu Val Glu Val Ser Thr Asp Lys Val
 1           5           10           15
Asp Thr Glu Ile Pro Ser Pro Ala Ala Gly Val Leu Thr Lys Ile Ile
      20           25           30
Ala Gln Glu Asp Asp Thr Val Glu Val Gly Gly Glu Leu Ser Val Ile
      35           40           45
Gly Asp Ala His Asp Ala Gly Glu Ala Ala Val Pro Ala Pro Gln Lys
      50           55           60
Val Ser Ala Gly Pro Thr Arg Ile
      65           70

```

(2) INFORMATION FOR SEQ ID NO:230:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:230:

Ala Ala Asp Ile Gly Ala Ala Pro Ala Pro Lys Pro Ala Pro Lys Pro
 1 5 10 15
 Val Pro Glu Pro Ala Pro Thr Pro Lys Ala Glu Pro Ala Pro Ser Pro
 20 25 30
 Pro Ala Ala Gln Pro Ala Gly Ala Ala Glu Gly Ala Pro Tyr Val Thr
 35 40 45
 Pro Leu Val Arg Lys Leu Ala Ser Glu Asn Asn Ile Asp Leu Ala Gly
 50 55 60
 Val Thr Gly Thr Gly Val Gly Gly Arg Ile Arg Lys Gln Asp Val Leu
 65 70 75 80
 Ala Ala Ala Glu Gln Lys Lys Arg Ala Lys Ala Pro Ala Pro Ala Ala
 85 90 95
 Gln Ala Ala Ala Pro Ala Pro Lys Ala Pro Pro Glu Asp Pro Met
 100 105 110
 Pro

(2) INFORMATION FOR SEQ ID NO:231:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:231:

Val Leu Val Ser Ile Ser Ala Asp Glu Asp Ala Thr Val Pro Val Gly
 1 5 10 15
 Gly Glu Leu Ala Arg Ile Gly Val Ala Ala Asp Ile Gly Ala Ala Pro
 20 25 30
 Ala Pro Lys Pro Ala Pro Lys Pro Val Pro Glu Pro Ala Pro Thr Pro
 35 40 45
 Lys Ala Glu Pro Ala Pro Ser Pro Pro Ala Ala Gln Pro Ala Gly Ala
 50 55 60
 Ala Glu Gly Ala Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Ser
 65 70 75 80
 Glu Asn Asn Ile Asp Leu Ala Gly Val Thr Gly Thr Gly Val Gly Gly
 85 90 95
 Arg Ile Arg Lys Gln Asp Val Leu Ala Ala Glu Gln Lys Lys Arg
 100 105 110
 Ala Lys Ala Pro Ala Pro
 115

(2) INFORMATION FOR SEQ ID NO:232:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:232:

```

Asp Pro Lys Val Gln Ile Gln Gln Ala Ile Glu Glu Ala Gln Arg Thr
 1           5           10           15
His Gln Ala Leu Thr Gln Gln Ala Ala Gln Val Ile Gly Asn Gln Arg
      20           25           30
Gln Leu Glu Met Arg Leu Asn Arg Gln Leu Ala Asp Ile Glu Lys Leu
      35           40           45
Gln Val Asn Val Arg Gln Ala Leu Thr Leu Ala Asp Gln Ala Thr Ala
      50           55           60
Ala Gly Asp Ala Ala Lys Ala Thr Glu Tyr Asn Asn Ala Ala Glu Ala
      65           70           75           80
Phe Ala Ala Gln Leu Val Thr Ala Glu Gln Ser Val Glu Asp Leu Lys
      85           90           95
Thr Leu His Asp Gln Ala Leu Ser Ala Ala Ala Gln Ala Lys Lys Ala
      100          105          110
Val Glu Arg Asn Ala Met Val Leu Gln Gln Lys Ile Ala Glu Arg Thr
      115          120          125
Lys Leu Leu Ser Gln Leu Glu Gln Ala Lys Met Gln Glu Gln Val Ser
      130          135          140
Ala Ser Leu Arg Ser Met Ser Glu Leu Ala Ala Pro Gly Asn Thr Pro
      145          150          155          160
Ser Leu Asp Glu Val Arg Asp Lys Ile Glu Arg Arg Tyr Ala Asn Ala
      165          170          175
Ile Gly Ser Ala Glu Leu Ala Glu Ser
      180          185

```

(2) INFORMATION FOR SEQ ID NO:233:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:233:

```

Val Ser Thr Ser Thr Trp Val Pro His Pro Val Arg Asp Arg Val Ile
 1           5           10           15
Gly Gln Arg Trp Thr Cys Ala Asp Arg Arg Ser Ile Glu Glu Ser Thr
      20           25           30
Glu Met Ala Phe Ser Val Gln Met Pro Ala Leu Gly Glu Ser Val Thr
      35           40           45
Glu Gly Thr Val Thr Arg Trp Leu Lys Gln Glu Gly Asp Thr Val Glu
      50           55           60
Leu Asp Glu Pro Leu Val Glu
      65           70

```

(2) INFORMATION FOR SEQ ID NO:234:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:234:

```

Glu Val His Leu Pro Val Asp Val Gly Glu Pro Arg Gln Pro Thr Gly
 1           5           10           15
Ala Val Ala Asp Gln Asp His Arg Ile Thr Pro Val Pro Ala His Lys
          20           25           30
His Thr Pro Pro Arg Val Cys Gln Asp Trp His Arg Gln Pro Pro His
          35           40           45
Arg Gly Arg Ala Asp Gln His Leu Gly Leu Asp Ala Arg Leu Cys Ala
          50           55           60
Ala Ala Cys Asn Val Leu Leu Val Asp Gly Val Gln His Arg Pro Gln
65           70           75           80
Arg His Gly Pro Gly Pro Arg Phe Gly Phe Pro Arg Val Val Val Ala
          85           90           95
Cys Gly Ile Arg Gln Ala Arg Val Glu Val Glu Arg Phe Gly Gly Val
          100          105          110
Leu Pro Glu Arg Ala His Gly Val Gly Gln Arg Asn Asn Arg Val Ala
          115          120          125
Thr Asp Arg Leu Thr Asp Arg Met Pro Ile Asp Arg Gly Leu Gly Arg
          130          135          140
Glu Pro Arg Ser Val Gly Gly Gln Ile Asp Arg Glu Arg Asp Gln Pro
145          150          155          160
Gln Arg Ile Pro Ala Gly Lys His Val Thr Pro His Cys Ser Gln Pro
          165          170          175
Arg Ser Leu His Leu Val
          180

```

(2) INFORMATION FOR SEQ ID NO:235:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 160 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:235:

```

Asn Asp Arg Leu Ile Ser Met Arg Asp Gly Gly Ile Val Ala Leu Pro
 1           5           10           15
Gln Leu Thr Asp Glu Gln Arg Ala Ala Ala Leu Glu Lys Ala Ala Ala
          20           25           30
Ala Arg Arg Ala Arg Ala Glu Leu Lys Asp Arg Leu Lys Arg Gly Gly
          35           40           45
Thr Asn Leu Thr Gln Val Leu Lys Asp Ala Glu Ser Asp Glu Val Leu
          50           55           60

```

218

Gly Lys Met Lys Val Ser Ala Leu Leu Glu Ala Leu Pro Lys Val Gly
 65 70 75 80
 Lys Val Lys Ala Gln Glu Ile Met Thr Glu Leu Glu Ile Ala Pro His
 85 90 95
 Pro Ala Ala Phe Val Ala Ser Val Thr Val Ser Ala Arg Pro Cys Trp
 100 105 110
 Lys Ser Ser Ala Pro Pro Asn Pro Ala Gly Arg Arg Cys Gly Pro Glu
 115 120 125
 Gly Leu Trp Trp Ala Tyr Pro Arg Ile Arg Gly Arg Ser Gly Leu Thr
 130 135 140
 Gly Pro Ala His Asn Ser Gly Arg Thr Pro Arg Trp Gly Gly Thr Arg
 145 150 155 160

(2) INFORMATION FOR SEQ ID NO:236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:236:

Asp Trp His Arg Gln Pro Pro His Arg Gly Arg Ala Asp Gln His Leu
 1 5 10 15
 Gly Leu Asp Ala Arg Leu Cys Ala Ala Cys Asn Val Leu Leu Val
 20 25 30
 Asp Gly Val Gln His Arg Pro Gln Arg His Gly Pro Gly Pro Arg Phe
 35 40 45
 Gly Phe Pro Arg Val Val Val Ala Cys Gly Ile Arg Gln Ala Arg Val
 50 55 60
 Glu Val Glu Arg Phe Gly Gly Val Val Pro Glu Arg Ala His Gly Val
 65 70 75 80
 Gly Gln Arg Asn Asn Arg Val Ala Thr Asp Arg Leu Thr Asp Arg Met
 85 90 95
 Pro Ile Asp Arg Gly Leu Gly Arg Glu Pro Arg Ser Val Gly Gly Gln
 100 105 110
 Ile Asp Arg Glu Arg Asp Gln Pro Gln Arg Ile Pro Ala Gly Lys His
 115 120 125
 Val Thr Pro His Cys Pro Gln Pro Arg Ser Leu His Leu Val Leu Thr
 130 135 140
 Ser Arg Arg His Val Glu Arg Gln Arg His Arg Ala Glu Glu Gln His
 145 150 155 160
 Glu Val His Ala Gly Pro Leu Gly Gly Ala Ser Gln Ser Gln Ala Ala
 165 170 175
 Pro Arg

(2) INFORMATION FOR SEQ ID NO:237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:237:

ATGCCAAGCC	GGTGCTGATG	CCCGAGCTCG	GCGAATCGGT	GACCGAGGGG	ACCGTCATTC	60
GTTGGCTGAA	GAAGATCGGG	GATTCGGTTC	AGGTTGACGA	GCCACTCGTG	GAGGTGTCCA	120
CCGACAAGGT	GGACACCGAG	ATCCCGTCCC	CGGTGGCTGG	GGTCTTGGTC	AGTATCAGCG	180
CCGACGAGGA	CGCCACGGTG	CCCGTCGGCG	GCGAGTTGGC	CCGGATCGGT	GTGCTGCCG	240
AGATCGGCGC	CGCGCCCGCC	CCCAAGCCCC	C			271

(2) INFORMATION FOR SEQ ID NO:238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:238:

Ala	Lys	Pro	Val	Leu	Met	Pro	Glu	Leu	Gly	Glu	Ser	Val	Thr	Glu	Gly	
1				5					10					15		
Thr	Val	Ile	Arg	Trp	Leu	Lys	Lys	Ile	Gly	Asp	Ser	Val	Gln	Val	Asp	
			20					25					30			
Glu	Pro	Leu	Val	Glu	Val	Ser	Thr	Asp	Lys	Val	Asp	Thr	Glu	Ile	Pro	
			35				40					45				
Ser	Pro	Val	Ala	Gly	Val	Leu	Val	Ser	Ile	Ser	Ala	Asp	Glu	Asp	Ala	
			50			55				60						
Thr	Val	Pro	Val	Gly	Gly	Glu	Leu	Ala	Arg	Ile	Gly	Val	Ala	Ala	Glu	
65					70					75					80	
Ile	Gly	Ala	Ala	Pro	Ala	Pro	Lys	Pro								
					85											

(2) INFORMATION FOR SEQ ID NO:239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:239:

GAGGTAGCGG	ATGGCCGGAG	GAGCACCCCA	GGACCGCGCC	CGAACCGCGG	GTGCCGGTCA	60
TCGATATGTG	GGCACC GTTC	GTTCCGTCCG	CCGAGGTCAT	TGACGAT		107

(2) INFORMATION FOR SEQ ID NO:240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 339 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:240:

```

ATGAAGTTGA AGTTTGCTCG CCTGAGTACT GCGATACTGG GTTGTGCAGC GGCGCTTGTG      60
TTTCCTGCCT CGGTTGCCAG CGCAGATCCA CCTGACCCGC ATCAGCCGGA CATGACGAAA      120
GGCTATTGCC CGGGTGGCCG ATGGGGTTTT GGC GACTTGG CCGTGTGCGA CGGCGAGAAG      180
TACCCCGACG GCTCGTTTTG GCACCACTGG ATGCAAACGT GGTTTACCGG CCCACAGTTT      240
TACTTCGATT GTGTCAGCGG CGGTGAGCCC CTCCCCGGCC CGCCGCCACC GGTGTTGC      300
GGTGGGGCAA TTCCGTCCGA GCAGCCCAAC GCTCCCTGA                               339

```

(2) INFORMATION FOR SEQ ID NO:241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 112 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:241:

```

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
 1           5           10           15
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
      20           25           30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
      35           40           45
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
      50           55           60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
      65           70           75           80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
      85           90           95
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
      100          105          110

```

(2) INFORMATION FOR SEQ ID NO:242:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 371 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:242:

```

GTGACCACGG TGGGCCTGCC ACCAACCCGG GCAGCGGCAG CCGCGGCGGC GCCGGCGGCT    60
CCGGCGGCAA CGGTGGCGCC GGGGGTAACG CCACCGGCTC AGGCGGCAAG GGCGGCGCCG    120
GTGGCAATGG CGGTGATGGG AGCTTCGGCG CTACCAGCGG CCCC GCCTCC ATCGGGGTCA    180
CGGGCGCCCC CGGCGGCAAC GGCGGCAAGG GCGGCGCCGG TGGCAGCAAC CCAACGGCT    240
CAGGTGGCGA CGGCGGCAAA GGCGGCAACG GCGGTGCCGG CGGCAACGGG GGCTCGATCG    300
GCGCCAACAG CGGCATCGTC GGCGGTCCG GTGGGGCCCG TGGCGCTGGC GGCGCCGCGC    360
GAAACGGCAG C

```

(2) INFORMATION FOR SEQ ID NO:243:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 424 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:243:

```

GTCCGGGTCC CACCACCGCG CCGGCGCGCC CCTAGCGGCC GGGCGCACCA GCCCCTTTTC    60
TTGACTCGTT CAAGAAAAGG GCCTTCTGTT TGGTCGGCCA TGTTGGCATG ATCGTGACCC    120
ATGGGCAACA TCGACGTCGA CATCTCGGCC AAGGTCTAGC TCCATGCGAA TCGCCGCCGC    180
GGTGGTGAGC ATCGGTCTAG CCGTCATAGC AGGGTTCGCG GTACCTGTTG CCGACGCACA    240
CCCGTCGGAG CCCGGGGTTG TGTCCTACGC GGTGCTCGGA AAGGGGTCGG TCGGCAACAT    300
CGTCGGCGCC CCAATGGGGT GGGAGGCGGT GTTCACCAAG CCGTCCAGG CGTTTGGGT    360
CGAATAACCG GCGTGCAACA ACTGGGTGGA CATCGGGCTG CCCGAGGTGT ACGACGATCC    420
CGAC

```

(2) INFORMATION FOR SEQ ID NO:244:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:244:

```

GCGATGGCGG CCGCGGGTAC CACCGCCAAT GTGGAACGGT TTCCCAACCC CAACGATCCT    60
TTGCATCTGG CGTCAATTGA CTTAGCCCCG GCCGATTTTC TCACCGAGGG CCACCGTCTA    120
AGGGCGGATG CGATCCTACT GCGCCGTACC GACCGGCTGC CTTTCGCCGA GCCGCCGGAT    180
TGGGACTTGG TGGAGTCGCA GTTGGCGACG ACCGTCACCG CCGACACGGT GCGCATCGAC    240
GTCATCGCCG ACGATATGCG TCCCGAACTG GCGGCGGCGT CCAAATCAC CGAATCGCTG    300
CGGCTCTACG ATTCGTC

```

(2) INFORMATION FOR SEQ ID NO:245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:245:

TGGCGTATGC	GCTTCGCAGC	CGGTGCCGCG	TCAACGCGCC	GGAGGCAATC	GCTTCGCTGC	60
CGAGGAATGG	TTCGATCACG	ATCGCAGTGT	GCCGTCGTGC	ACCGACACCG	CCGTCCAACG	120
TGAACTGAGG	GCGGAAAATC	GGCCGAAATC	TCGCCCTCAG	TTCACGCTCG	GCGCCTAACG	180
GTTCTGGAAG	TTGGGTGCGC	GCTTCTCGGC	GAACGCGCGC	GGGCCTTCCT	TGGCGTCGTC	240
GGACAGGAAG	ACCTTGATGC	CGATCTGGGT	GTCGATCTTG	AACGCCTCGT	TTTCGGGGCAT	300
GCACTCGGTC	TCGCGGATGG	ACCGCAAGAT	GGCCTGCACG	GCCAGGGGTC	CGTTAGCCGA	360
GATGGCGTCG	GCAAGTTCTA	GAACCTTGGT	CAACGCCTGG	CCGTCGGGCA	CACGTGGCCG	420
AT						422

(2) INFORMATION FOR SEQ ID NO:246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:246:

GCGTGCCGCT	GAACACCAGC	CCGCGGCTGC	CAGATCTCCC	GGAATCGGTA	GTGCCGCCGG	60
TGGCGTCGTT	GCTCTCCTGA	CGGGGCGCGG	CGACCATAAG	GTCGCTAATG	CCCAGGTAGC	120
GGCCCAGGTG	CATGGAGTCG	ATGATGATGC	GACTCTCCAG	CTCGCCGACC	GGGAGCTTGG	180
CATCGGGCCT	GATCAGCCAG	GACGCGTAGG	ACAAGTCGAT	CGAATGCATA	GTGGCCTCCA	240
GAGTGGCCGT	GCCACTTCCG	GCGTGCTCCA	CGGCAAATGC	CTTGATTTCT	AGCTCCGCGT	300
AGTGTTCCCG	CATCGCCTGC	GGGATGAATG	GGAACCGCAG	GATGGCGACA	AACGGGTCTG	360
ACCTCAGGTT	TGCCGCTTTG	CGCACAGTGG	TCGACAGCCG	GTACTCGGCA	TAAATGCTGG	420
CCCCGA						426

(2) INFORMATION FOR SEQ ID NO:247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 327 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:247:

AGACCGGCGA	GGGTGTGGTC	GCTGCCCGCG	GCATTGTCTGA	TAATCTGCGC	TGGGTGCGACG	60
CGCCGATCAA	CTAGTGAGGC	GCAACGCTAG	GCTTTGGGAT	ACCCACAGCT	AAAAAGTTTA	120
TCAAAGAAAC	GAAGAAGGTT	GCCATGAGCA	CTGTTGCCGC	CTACGCCGCC	ATGTCGGCGA	180
CCGAACCCCT	GACCAAGACC	ACGATCACCC	GTCGCGACCC	GGGCCCCGAC	GACATGGCGA	240
TCGACATCAA	ATTCGCCGGA	ATCTGTCTGCT	CGGACATCCA	TACCGTCCAA	ACCGAATGGG	300
GGCAACCGAA	TTTACCTGTG	GTCCCTG				327

(2) INFORMATION FOR SEQ ID NO:248:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:248:

```

Asp His Gly Gly Pro Ala Thr Asn Pro Gly Ser Gly Ser Arg Gly Gly
 1          5          10          15
Ala Gly Gly Ser Gly Gly Asn Gly Gly Ala Gly Gly Asn Ala Thr Gly
 20          25          30
Ser Gly Gly Lys Gly Gly Ala Gly Gly Asn Gly Gly Asp Gly Ser Phe
 35          40          45
Gly Ala Thr Ser Gly Pro Ala Ser Ile Gly Val Thr Gly Ala Pro Gly
 50          55          60
Gly Asn Gly Gly Lys Gly Gly Ala Gly Gly Ser Asn Pro Asn Gly Ser
 65          70          75          80
Gly Gly Asp Gly Gly Lys Gly Gly Asn Gly Gly Ala Gly Gly Asn Gly
 85          90          95
Gly Ser Ile Gly Ala Asn Ser Gly Ile Val Gly Gly Ser Gly Gly Ala
100          105          110
Gly Gly Ala Gly Gly Ala Gly Gly Asn Gly Ser
115          120

```

(2) INFORMATION FOR SEQ ID NO:249:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 104 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:249:

```

Met Ala Ala Ala Gly Thr Thr Ala Asn Val Glu Arg Phe Pro Asn Pro
 1          5          10          15
Asn Asp Pro Leu His Leu Ala Ser Ile Asp Phe Ser Pro Ala Asp Phe
 20          25          30
Val Thr Glu Gly His Arg Leu Arg Ala Asp Ala Ile Leu Leu Arg Arg
 35          40          45
Thr Asp Arg Leu Pro Phe Ala Glu Pro Pro Asp Trp Asp Leu Val Glu
 50          55          60
Ser Gln Leu Arg Thr Thr Val Thr Ala Asp Thr Val Arg Ile Asp Val
 65          70          75          80
Ile Ala Asp Asp Met Arg Pro Glu Leu Ala Ala Ser Lys Leu Thr
 85          90          95
Glu Ser Leu Arg Leu Tyr Asp Ser
100

```

(2) INFORMATION FOR SEQ ID NO:250:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 41 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:250:

```

Ala Tyr Ala Leu Arg Ser Arg Cys Arg Val Asn Ala Pro Glu Ala Ile
 1             5             10             15
Ala Ser Leu Pro Arg Asn Gly Ser Ile Thr Ile Ala Val Cys Arg Arg
          20             25             30
Ala Pro Thr Pro Pro Ser Asn Val Asn
 35             40

```

(2) INFORMATION FOR SEQ ID NO:251:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:251:

```

Val Pro Leu Asn Thr Ser Pro Arg Leu Pro Asp Leu Pro Asp Ser Val
 1             5             10             15
Val Pro Pro Val Ala Ser Leu Leu Ser
          20             25

```

(2) INFORMATION FOR SEQ ID NO:252:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:252:

```

Met Ser Thr Val Ala Ala Tyr Ala Ala Met Ser Ala Thr Glu Pro Leu
 1             5             10             15
Thr Lys Thr Thr Ile Thr Arg Arg Asp Pro Gly Pro His Asp Met Ala
          20             25             30
Ile Asp Ile Lys Phe Ala Gly Ile Cys Arg Ser Asp Ile His Thr Val
 35             40             45

```

Gln Thr Glu Trp Gly Gln Pro Asn Leu Pro Val Val Pro
 50 55 60

(2) INFORMATION FOR SEQ ID NO:253:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:253:

GCTTGGAGCC	CTGGAGCGAC	GGTGTGGGTC	TGGGGGTCGA	TTCGTTCTCG	GCGAAAGTCA	60
ACTAAAGACC	ACGTTGACAC	CCAACCGGCG	GCCCCGCGATG	GGCCGTCGCG	GCGTAGAAGC	120
TTTGACCGCG	GCGCGAAACG	TTCGCTGCTG	CGGCCCATGC	AGATCGCACA	CGCTTGCTTG	180
AACATCGGGT	GGAGCCGGTG	GTAACGCCAG	GCT			213

(2) INFORMATION FOR SEQ ID NO:254:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 367 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:254:

CCGAGCTGCT	GTTCGGCGCC	GGCGGTGCGG	GCGGCGCGGG	TGGGGCGGGC	ACCGACGGCG	60
GGCCCGGTGC	TACCGGCGGG	ACCGGCGGAC	ACGGCGGAGT	CGGCGGCGAC	GGCGGATGGC	120
TGGCACCCCG	CGGGGCCCGC	GGGGCCGGCG	GGCAAGGCGG	GGCAGGTGGT	GCCCGCAGCG	180
ATGGTGGCGC	GTTGGGTGGT	ACCGGCGGGA	CGGGCGGTAC	CGGCGGCGCC	GGTGGCGCCG	240
GCGGTCGCGG	CACACTGCTG	CTGGGCGCTG	GCGGACAGGG	CGGCCTCGGC	GGCGCCGGCG	300
GACAAGGCGG	CACCGGCGGG	GGCCGGCGGA	GATGGCGTTC	TGGGGGGTGT	CAGTGGCACT	360
GGTGGTA						367

(2) INFORMATION FOR SEQ ID NO:255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:255:

AAGGCGTGAT	TGGCAAGGCG	ACCGCGCAGC	GGCCCCGTAGC	CGCGGGACGG	CCCAGGCCCC	60
GACCGCAGCG	GCCGGTGTCT	GACCGGGTCA	GCGACCAGCG	GCGCTGACCG	TGCCGCTCGT	120
CTACTTCGAC	GCCAGCGCCT	TCGTCAAACCT	TCTCACCACC	GAGACAGGGA	GCTCGCTGGC	180

GTCCGCTCTA	TGGGACGGCT	GCGACGCCGC	ATTGTCCAAC	CGCCTGGCCT	ACCCCGAAGT	240
CCGCGCCGCA	CTCGCTGCAA	CGGGCCGCAA	TCACGACCTA	ACCGAATCCG	AGCTCGCCGA	300
CGCCGAGCGT	GACTGGGAGG	ACTTCTGGGC	CGCACCCGCC	CAGTCGAACT	CACCGCGACG	360
GTTGAACAGC	ACGCCGGGCA	CCTCGCCCCA	ACACATGCCT	TACGCGGAGC	CGACACCGTT	420

(2) INFORMATION FOR SEQ ID NO:256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:256:

CTCTTGTCGG	TGGCATCGGC	GGTACCGGCG	GAACCGGCGG	CAACGCCGGT	ATGCTCGCCG	60
GCGCCGCCGG	GGCCGGCGGT	GCCGGCGGGT	TCAGCTTCAG	CACTGCCGGT	GGGGCTGGCG	120
GCGCCGGCGG	GGCCGGTGGG	CTGTTACCA	CCGGCGGTGT	CGGCGGCGCC	GGTGGGCAGG	180
GTCACACGGG	CGGGGCGGGC	GGCGCCGGCG	GGGCCGCGCG	GTTGTTTGGT	GCCGGCGGCA	240
TGGGCGGGGC	GGGCGGATTC	GGGGATCACG	GAACGCTCGG	CACCGGCGGG	GCCGGCGGG	299

(2) INFORMATION FOR SEQ ID NO:257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:257:

Leu	Glu	Pro	Trp	Ser	Asp	Gly	Val	Gly	Leu	Gly	Val	Asp	Ser	Phe	Ser
1				5					10					15	
Ala	Lys	Val	Asn												
			20												

(2) INFORMATION FOR SEQ ID NO:258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:258:

Glu	Leu	Leu	Phe	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly	Gly	Ala	Gly
1				5				10						15	
Thr	Asp	Gly	Gly	Pro	Gly	Ala	Thr	Gly	Gly	Thr	Gly	Gly	His	Gly	Gly

```

      20      25      30
Val Gly Gly Asp Gly Gly Trp Leu Ala Pro Gly Gly Ala Gly Gly Ala
      35      40      45
Gly Gly Gln Gly Gly Ala Gly Gly Ala Arg Ser Asp Gly Gly Ala Leu
      50      55      60
Gly Gly Thr Gly Gly Thr Gly Gly Thr Gly Gly Ala Gly Gly Ala Gly
      65      70      75      80
Gly Arg Gly Thr Leu Leu Leu Gly Ala Gly Gly Gln Gly Gly Leu Gly
      85      90      95
Gly Ala Gly Gly Gln Gly Gly Thr Gly Gly Arg Arg Arg Trp Arg
      100      105      110
Ser Gly Gly Cys Gln Trp His Trp Trp
      115      120

```

(2) INFORMATION FOR SEQ ID NO:259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:259:

```

Gly Val Ile Gly Lys Ala Thr Ala Gln Arg Pro Val Ala Ala Gly Arg
 1           5           10           15
Pro Arg Pro Arg Pro Gln Arg Pro Val Ser Asp Arg Val Ser Asp Gln
      20      25      30
Arg Arg

```

(2) INFORMATION FOR SEQ ID NO:260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:260:

```

Leu Val Gly Gly Ile Gly Gly Thr Gly Gly Thr Gly Gly Asn Ala Gly
 1           5           10           15
Met Leu Ala Gly Ala Ala Gly Ala Gly Gly Ala Gly Gly Phe Ser Phe
      20      25      30
Ser Thr Ala Gly Gly Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe
      35      40      45
Thr Thr Gly Gly Val Gly Gly Ala Gly Gly Gln Gly His Thr Gly Gly
      50      55      60
Ala Gly Gly Ala Gly Gly Ala Gly Gly Leu Phe Gly Ala Gly Gly Met
      65      70      75      80

```

Gly Gly Ala Gly Gly Phe Gly Asp His Gly Thr Leu Gly Thr Gly Gly
 85 90 95
 Ala Gly Gly

(2) INFORMATION FOR SEQ ID NO:261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:261:

TCCTGTTTCGG	CGCCGGCGGG	GTGGGCGGTG	TTGGCGGTGA	CGGTGTGGCA	TTCCTGGGCA	60
CCGCCCCCGG	CGGGCCCCGT	GGTGCCGGCG	GGGCCGGTGG	GCTGTTTCAGC	GTCGGTGGGG	120
CCGGCGGGCG	CGGCGGAATC	GGATTGGTCG	GGAACAGCGG	TGCCGGGGGG	TCCGGCGGGT	180
CCGCCCTGCT	CTGGGGCGAC	GGCGGTGCCG	GCGGCGCGGG	TGGGGTCGGG	TCCACTACCG	240
GCGGTGCCGG	CGGGGCGGGC	GGCAACGCCA	GCCTGCTGGT	AA		282

(2) INFORMATION FOR SEQ ID NO:262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 415 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:262:

CGGCACGAGC	CGTGCTACTG	GTCAACTGAT	GCCCTGATTG	TGACCTTCCC	GGCGCCGGAT	60
CAGTGCTTCT	CAGGACCGAC	GTAATATTCT	AAAACCAATC	CGGCCGCCGA	GGCGAGGATG	120
AATGCCACAC	CGGCGGCGAT	CAGCCACGGG	AGCCACAACG	CGATGCCGAC	CGCTGCCACC	180
GAGCCGGACA	ACGCGACCAT	GATCGGCCAC	CAGCTATGCG	GACTGAAGAA	TCCAAGTTCT	240
CCTGCGCCGT	CGCTGATTTT	AGCGCCTTCG	TAGTCCTCGG	GCCGGGAATC	TAACCGGCGG	300
GCCACAAACC	GGAAGAAGGT	GGCGACGATC	AACGCCATGC	CGCCGGTGAG	CGCCAACGCA	360
ATGGTGCCAG	CCCCTCGAC	ACCACCGGTG	GCGAACATCG	AGGTCAACAC	GCCGT	415

(2) INFORMATION FOR SEQ ID NO:263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 373 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:263:

TCACCGCGTG AACGGTTCGT AACACTGATA CGTATGCTTG TCAGCGAGCA GATCAAGTCC	60
AGTCCGACCA ATGCCAGGAG ATCATCGGCT AGGCTCACGG TTTCGCCTGG GACGAGACGG	120
TATTGAGTTC TGGCGTTGGA CGGTCCGTGG CGTGGTGGGA AGTCTGACGC GGCATCAGAA	180
CGGTTGTCAA TACCAGTCTT TGGGGGATAT GGCCTATTG GTGTCGTCGG GCCGCTCCAC	240
CGGATCCCTT TTCGAACGTT GCGCAAGCGC GGTCCAGTTA CGGCCTGTTC ACTGCGCGCT	300
GGCGTAGCTG CGCGGCCTCG ATCGGTTTGA ACGTCATCGC AATTCCTCGCA ATGGGTGAGT	360
ACCTGACGCT CCT	373

(2) INFORMATION FOR SEQ ID NO:264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 423 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:264:

CCAAACCGGA CAGGCCGCA GCGACGGTCG GAAGTTGCAC CACGGTGCGC GCTCCATGTA	60
GCCAACCGGT GACCACGGCG TAGACAGCAG ATCCGTGGAT CGCGCGTTCG GTGTCGTCCG	120
GGCCGAGTAC CCGCGGGCCG AACCGCAGCG ACCAAAGCAA CGCGATCGAT ACGGGGATCG	180
CCACTCGTGC CGAATTCGAG CTCCGTCGAC AAGCTTGCGG CCGCACTCGA ACCCGGGTGA	240
ATGATTGAGT TTAAACCGCT TAGCAATAAC TAGCATAACC CCTTGGGGCC TCTAAACGGG	300
TCTTGAGGGG TTTTGTGCTG AAAGGAGGAA CTATATCCGG ATAACCTGGC GTAGTAGCGA	360
AGAGGCCCCG ACCGATCGCC CTTCCCAACA GTTGCGCAGC CTGAATGGCG AATGGACGCG	420
CCC	423

(2) INFORMATION FOR SEQ ID NO:265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:265:

AGTGGCCAGC CGGTGCGCCA ATGCATCCAG CTCCCGGTAC GTCAGCTGAC CATCCGCCCCA	60
ACTGACCGCC ACCGAGTCAG GCTGTGCCGC AGCGATTTTC GCGAACCAGG TATGCACCGC	120
GGGTGCCGAC GTCGTCACAT CCGGCAGGCC GGGTGCGGTC GGATCGTGCT CGCCGTCCAG	180
CAGAATGTCG ACGTCGCGCA GCGGCCGATC CCACCGGCTG ACCAAGCGCT GTAACACAGC	240
CAGCACCCGC CTGCCGAGGC TTTCGGGCGC CATCGTGCCC AGCGCACCGT CGAGCACCTC	300
CACTAGCAGC GTGAGCTCAC CGGTGCTGCG GTGCGCGGCG ACGGTCACCG GAAAGTGCGA	360
CAAACCTCTT AGCGCCACCG GACGGAACGT CACCCCGTTT GCGA	404

(2) INFORMATION FOR SEQ ID NO:266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 421 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:266:

GTCCTGGTCG	CAGGCTGTTT	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCCC	60
ACCATCGAAC	CCGCCCAACC	GGCGGTGTCA	CCGCCTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTCT	ACAACGGCAC	CCGCCAATTG	180
GTGGCTCTGC	GCCCCGGGCG	CGATTCTGGC	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
ATGCACGTTG	CACCGCGCGT	CATTTTCTTG	CCGGGCCCCG	CAGCCGCGTT	GACCAGCGAC	300
GACCACGGCA	CGGCCTTCCT	TGCCGCCCCG	GGCGGCTACT	TCGTGGCCGA	CCTGTCCTCC	360
GGTCACACCG	CACGAGTGAA	TGTCGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420
C						421

(2) INFORMATION FOR SEQ ID NO:267:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:267:

ATGCATATCA	CGCTCAACGC	CATCCTGCGT	GCGATCTTCG	GGGCCGGCGG	CAGTGAACCTA	60
GACGAGCTGC	GCCGCCTCAT	TCCGCCGTGG	GTCACGCTGG	GCTCGCGCCT	GGCGGCGCTA	120
CCGAAACCCA	AACGCGACTA	TGGCCGCCTT	AGCCCGTGGG	GCCGGCTGGC	CGAGTGGCGG	180
CGCCAGTACG	ACACTGTGAT	CGACGAGCTC	ATCGAAGCCG	AGCGGGCCGA	CCCGAACTTC	240
GCCGATCGGA	CCGACGTTTT	GGCGTTGATG	CTGCGCAGCA	CTTACGACGA	CGGTTCCATC	300
ATGTCGCGCA	AGGACATTGG	CGACGAACTG	CTCACGCTGC	TTGCCGCGCG	GCACGAAACC	360
ACGGCGGCGA	CATGGGCTGG	GCGTTCGAAC	GGCTCAACCG	GCACCCCGAC	GTGCTCGCGG	420
CTCTGG						426

(2) INFORMATION FOR SEQ ID NO:268:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 522 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:268:

GTCCTGGTCG	CAGGCTGTTT	TTCGAACCCG	CTGGCTAACT	TCGCACCCGG	GTATCCGCCC	60
ACCATCGAAC	CCGCCCAACC	GGCGGTGTCA	CCGCCTACTT	CGCAAGACCC	GGCCGGTGCA	120
GTGCGACCAC	TGAGCGGCCA	CCCCCGGGCG	GCACTATTCT	ACAACGGCAC	CCGCCAATTG	180
GTGGCTCTGC	GCCCCGGGCG	CGATTCTGGC	GCACCCGCCA	GCATCATGGT	CTTCGATGAC	240
GTGCACGTTG	CACCGCGCGT	CATTTTCTTG	CCGGGCCCCG	CAGCCGCGTT	GACCAGCGAC	300
GACCACGGCA	CGGCCTTCCT	TGCCGCCCCG	GGCGGCTACT	TCGTGGCCGA	CCTGTCCTCC	360
GGTCACACCG	CACGAGTGAA	TGTCGCTGAC	GCAGCGCACA	CCGATTTCAC	CGCGATCGCC	420

CGCCGCTCCG ACGCAAGCT GGTGCTGGGC AGCGCAGATG GCGCCGTCTA CACGCTTGCC 480
 AAGAACCCGC AGTTGACCGG CGTCGGCGCC GCCACCGTAG CC 522

(2) INFORMATION FOR SEQ ID NO:269:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 739 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:269:

GCTGGGGCGC	ACCGCCGTCC	GGCGGCCCCA	GCCCCTGGGC	CCAGACCCCG	CGCAAAACCA	60
ACCCGTGGCC	CTTAGTGGCC	GGCGCCGCCG	CCGTCTGTGCT	CGTCCTCGTG	TTGGGCGCCA	120
TCGGCATCTG	GATCGCCATC	CGGCCCAAGC	CGGTACAGCC	GCCTCAGCCG	GTTGCGGAGG	180
AGCGCCTTAG	CGCCCTACTG	CTGAACCTCT	CAGAAGTCAA	CGCCGTGATG	GGCTCGTCGT	240
CCATGCAGCC	GGGCAAACCG	ATCACATCGA	TGGACTCTTC	GCCGGTGACG	GTGTCCCTGC	300
CGGACTGCCA	GGGCGCGCTG	TATACCAGCC	AGGATCCGGT	GTATGCCGGC	ACCGGCTACA	360
CCGCCATCAA	CGGCTTGATT	TCATCCGAGC	CGGGCGACAA	CTACGAACAT	TGGGTGAACC	420
AAGCCGTCTG	CGCCTTTCCG	ACCGCCGACA	AAGCCCCGCG	GTTCGTGCAG	ACTTCGGCCG	480
ACAAATGGAA	GAAGTGCACA	GGCAAGACGG	TCACCGTCAC	GAATAAGGCC	AAGACCTACC	540
GGTGGACGTT	TGCCGACGTC	AAAGGCAGCC	CGCCGACGAT	CACGGTGATA	GACACCCAAG	600
AAGGCGCTGA	GGGCTGGGAA	TGCCAACGCG	CGATGAGCGT	GGCCAACAAT	GTGGTTGTCTG	660
ACGTCAACGC	ATGCGGGTAC	CAGATCACCA	ATCAAGCAGG	CCAGATCGCC	GCCAAGATCT	720
GTTGACAAAG	TCAACAAGG					739

(2) INFORMATION FOR SEQ ID NO:270:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:270:

AGACGTCGTC	GAGGCCGCCA	TCGCCCCGCG	CGAAGCCGTT	AACCCGGCAC	TGAACGCGTT	60
GGCGTATGC						69

(2) INFORMATION FOR SEQ ID NO:271:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 523 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:271:

ACTGCACCCG	GCAGGCGCGA	CCAACGGATC	GGGTCAACTA	GCACTGCCGG	TGGAGGCGCC	60
CCCGCGGTCT	GTGCCTTCCC	ACGGGGAACC	CTTGGGCAGC	GCGGCTCCAG	AAGGGTTGGA	120
GGGAGAGTTC	GACGACCGTA	TCGACGAGCG	GTTCCCGGTC	TTCAGCTCGG	CCAGTCTCGC	180
CGAAGCGCTG	CCGGGTCCGC	TGACCCCGAT	GACGCTGGAT	GTCCAGTTGA	GTGGACTGCG	240
CGCGGCCGGT	CGGGCGATGG	GTCGGGTACT	GGCGCTTGGC	GGTGTCTGTT	CCGATGAGTG	300
GGAGAGAAGA	GCCATCGCGG	TGTTTCGGTCA	CCGCCCGTAT	ATCGGAGTGT	CGGCCAATAT	360
TGTGGCCGCC	GCCCAACTGC	CGGGGTGGGA	CGCGCAGGCC	GTAACCCGGC	GGGCACTGGG	420
CGAGCAACCG	CAGGTCACTG	AGCTGCTTCC	GTTTGGTTCGA	CCGCAACTTG	CGGGCGGACC	480
GCTCGGCTCG	GTCGCGAAGG	TGGTCGTGAC	GGCACGGTCG	CTG		523

(2) INFORMATION FOR SEQ ID NO:272:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:272:

GTGTGGGTGT	CGTCGGGGTA	GGAGCGACTT	CCCCGGCCGG	CGCCGGCGCC	GGAGCGGGCT	60
CTGCAGGAAC	CGGTGCCGGC	GCCGGCGGCG	GGGCGACCAA	AGGCCGGATC	GATTCGGCCA	120
GCGCCTTGGC	CGCGCCCTTG	TCCACCGGGT	TGTTGGCGGT	CCCGAGCCAT	ACCACAAACC	180
AACGCTGAAG	GGGCCCGGCG	TCCGGTGCCT	TCGCCCGGGG	CGAC		224

(2) INFORMATION FOR SEQ ID NO:273:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:273:

TGAACTGACT	GGCCCGCTCG	ATCGGCGGCG	GCGGCGTGTC	ATAGCTGCGC	CGCCAGGCCA	60
TGAACTGCTC	TTCGCCATAG	CGGGCCTTGG	TCTCGGCCTT	GTCCAAACCC	TGCAGCGCGC	120
CGTAGTGGCG	TTCGTTGAGC	CGCCAGCTAC	GCCGCACGGG	AATCCAGAGC	CGATCGGCGC	180
TGTCCAACGC	CAGATGCGCG	GTGGTGATCG	CGCGCCGCAG	CAACGAGGTG	TAGAGCACGT	240
CGGGCAATAG	GTCGTGTTCC	GCGATCAGCT	CGCCGCTTCG	AACCGCCTCT	GCCTGGCCCT	300
TGTCCGTCAG	GCCGACATCG	ACCCAGCCGG	TGAACAGGTT	GAGGGCATTG	CAGTCGCTCT	360
CGCCGTGGCG	CAGCAACACC	AGGCTGCCAG	TGTTTGCCAT	ACCGGCAAGT	CTCTACGCA	420
CTCCCGCACT	CCTCATCGTG	GACCAAAATG	CCCGAATTCT	CCTCGGTCCG	CTGCGCAGCG	480
CGTTCATACC	GCCGAGGTGG	TCGGCACCGT	AACGGCCGGT	T		521

(2) INFORMATION FOR SEQ ID NO:274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 426 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:274:

CTCCAGGCTC	ATTCGCTCGA	ACAAAGCCAC	CCGGCCGTAC	AGCGGACGCC	CCCATTCTGTT	60
GTCGTGATAG	TCGCGGTACA	GCTGGGCATC	GGGCCCTGGA	CGAACCTCCG	CCCAGGGGCA	120
GCGAACCAGC	CCGTCGCCGC	TCACGCGGGG	TCAGAACGGT	AGTGCACGAC	AGTCTCGCCG	180
CGCGAAGGGT	TTGACGCGTC	AGACTCGGCC	TCGGCGTCTT	CCGACGAGGC	GTGGATCGCC	240
CCGAGCTGAG	AGCGTAGCGC	CTCGAGCTCA	CGGCCGAGCC	GTTCCAGCAC	CCAGTCCACC	300
TCGCTGGTCT	TGTTCCCGCG	CAGCACCTGC	GTGAACCTGA	CCGCGTCGAC	ATCGGCGCGG	360
GTGACCCCGA	ACGCCGGCAG	CGTCGTCGCC	GTCTGTCGCC	GCGGCAGGGG	CGGCAACTGC	420
TCGCCA						426

(2) INFORMATION FOR SEQ ID NO:275:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 219 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:275:

GCGGACACGG	CGGACAAAGC	GCAATCGGCC	TCGGCGGCGG	CGCCGGCGGC	GACGGGGGCC	60
AGGGCGGCGC	CGGCCGCGGA	CTGTGGGGTA	CTGGCGGCGC	CGGCGGACAC	GGCGGGGCAA	120
GGCGGTGGTA	CCGGGGGGCC	ACCGCTGCCC	GGTCAGGCAG	GCATGGGCGC	CGCGGGTGGC	180
GCCGGTGGGC	TGATCGGCAA	CGGCGGGGCC	GGCGGCGAC			219

(2) INFORMATION FOR SEQ ID NO:276:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 571 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:276:

AAGATCATCG	GCGCCGCTCC	TTAGCATCGC	TGCGCTCTGC	ATCGTCGCCG	GCGCGGATCA	60
CGGAGGTCCG	GCCTTGTACC	CCACTCCTCG	AACGGTCAGC	ACCACAGTCG	GGTTCTCGGG	120
ATCCTTTTCG	ACCTTGCCCC	GCAGACGCTG	GACATGCACG	TTCACCAGCC	TGGTATCGGC	180
TGGGTGCCGG	TAACCCCATATA	CCTGTTTCGAG	CAGCACATCA	CGAGTAAACA	CCTGGCGCGG	240
CTTGCGCGCC	AATGCGACCA	ACAGGTCGAA	TTCCAGCGGT	GTCAACGAGA	TCTGCTCACC	300
GTTGCGAGTG	ACCTTGTGCG	CCGGTACGTC	GATTTCTACG	TCGGCGATGG	ACAGCATCTC	360
GGCGGGTTCG	TCGTCGTTGC	GGCGCAGCCG	CGCCCGCACC	CGCGCAACCA	GCTCCTTGGG	420
CTTGAACGGC	TTCATGATGT	AGTCGTCGGC	GCCCCACTCC	AGACCCAGCA	CCACATCCAC	480
GGTGTGCGTC	TTTGCGGTGA	GCATCACGAT	CGGAACACCG	GAATCGGCGC	GCAACACCCG	540
GCACACGTCG	ATGCCGTTCA	TACCGGGGCA	A			571

(2) INFORMATION FOR SEQ ID NO:277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:277:

```

Leu Phe Gly Ala Gly Gly Val Gly Gly Val Gly Gly Asp Gly Val Ala
 1             5             10             15
Phe Leu Gly Thr Ala Pro Gly Gly Pro Gly Gly Ala Gly Gly Ala Gly
 20             25             30
Gly Leu Phe Ser Val Gly Gly Ala Gly Gly Ala Gly Gly Ile Gly Leu
 35             40             45
Val Gly Asn Ser Gly Ala Gly Gly Ser Gly Gly Ser Ala Leu Leu Trp
 50             55             60
Gly Asp Gly Gly Ala Gly Gly Ala Gly Gly Val Gly Ser Thr Thr Gly
 65             70             75             80
Gly Ala Gly Gly Ala Gly Gly Asn Ala Ser Leu Leu Val
             85             90

```

(2) INFORMATION FOR SEQ ID NO:278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:278:

```

Met Pro Pro Val Ser Ala Asn Ala Met Val Pro Ala His Ser Thr Pro
 1             5             10             15
Pro Val Ala Asn Ile Glu Val Asn Thr Pro
             20             25

```

(2) INFORMATION FOR SEQ ID NO:279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:279:

Lys Pro Asp Arg Pro Ala Ala Thr Val Gly Ser Cys Thr Thr Val Arg
 1 5 10 15
 Ala Pro Cys Ser Gln Pro Val Thr Thr Ala
 20 25

(2) INFORMATION FOR SEQ ID NO:280:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:280:

Trp Pro Ala Gly Arg Pro Met His Pro Ala Pro Gly Thr Ser Ala Asp
 1 5 10 15
 His Pro Pro Asn
 20

(2) INFORMATION FOR SEQ ID NO:281:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 140 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:281:

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1 5 10 15
 Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
 20 25 30
 Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
 35 40 45
 Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
 50 55 60
 Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
 65 70 75 80
 Met His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
 85 90 95
 Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
 100 105 110
 Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala
 130 135 140

(2) INFORMATION FOR SEQ ID NO:282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:282:

```

Met His Ile Thr Leu Asn Ala Ile Leu Arg Ala Ile Phe Gly Ala Gly
 1           5           10           15
Gly Ser Glu Leu Asp Glu Leu Arg Arg Leu Ile Pro Pro Trp Val Thr
          20           25           30
Leu Gly Ser Arg Leu Ala Ala Leu Pro Lys Pro Lys Arg Asp Tyr Gly
          35           40           45
Arg Leu Ser Pro Trp Gly Arg Leu Ala Glu Trp Arg Arg Gln Tyr Asp
          50           55           60
Thr Val Ile Asp Glu Leu Ile Glu Ala Glu Arg Ala Asp Pro Asn Phe
65           70           75           80
Ala Asp Arg Thr Asp Val Leu Ala Leu Met Leu Arg Ser Thr Tyr Asp
          85           90           95
Asp Gly Ser Ile Met Ser Arg Lys Asp Ile Gly Asp Glu Leu Leu Thr
          100          105          110
Leu Leu Ala Ala Gly His Glu Thr Thr Ala Ala Thr Trp Ala Gly Arg
          115          120          125
Ser Asn Gly Ser Thr Gly Thr Pro Thr Cys Ser Arg Leu Trp
          130          135          140

```

(2) INFORMATION FOR SEQ ID NO:283:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 163 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:283:

```

Val Leu Val Ala Gly Cys Ser Ser Asn Pro Leu Ala Asn Phe Ala Pro
 1           5           10           15
Gly Tyr Pro Pro Thr Ile Glu Pro Ala Gln Pro Ala Val Ser Pro Pro
          20           25           30
Thr Ser Gln Asp Pro Ala Gly Ala Val Arg Pro Leu Ser Gly His Pro
          35           40           45
Arg Ala Ala Leu Phe Asp Asn Gly Thr Arg Gln Leu Val Ala Leu Arg
          50           55           60
Pro Gly Ala Asp Ser Ala Ala Pro Ala Ser Ile Met Val Phe Asp Asp
65           70           75           80
Val His Val Ala Pro Arg Val Ile Phe Leu Pro Gly Pro Ala Ala Ala
          85           90           95
Leu Thr Ser Asp Asp His Gly Thr Ala Phe Leu Ala Ala Arg Gly Gly
          100          105          110

```

237

Tyr Phe Val Ala Asp Leu Ser Ser Gly His Thr Ala Arg Val Asn Val
 115 120 125
 Ala Asp Ala Ala His Thr Asp Phe Thr Ala Ile Ala Arg Arg Ser Asp
 130 135 140
 Gly Lys Leu Val Leu Gly Ser Ala Asp Gly Ala Val Tyr Thr Leu Ala
 145 150 155 160
 Lys Asn Pro

(2) INFORMATION FOR SEQ ID NO:284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

Trp Gly Ala Pro Pro Ser Gly Gly Pro Ser Pro Trp Ala Gln Thr Pro
 1 5 10 15
 Arg Lys Thr Asn Pro Trp Pro Leu Val Ala Gly Ala Ala Val Val
 20 25 30
 Leu Val Leu Val Leu Gly Ala Ile Gly Ile Trp Ile Ala Ile Arg Pro
 35 40 45
 Lys Pro Val Gln Pro Pro Gln Pro Val Ala Glu Glu Arg Leu Ser Ala
 50 55 60
 Leu Leu Leu Asn Ser Ser Glu Val Asn Ala Val Met Gly Ser Ser Ser
 65 70 75 80
 Met Gln Pro Gly Lys Pro Ile Thr Ser Met Asp Ser Ser Pro Val Thr
 85 90 95
 Val Ser Leu Pro Asp Cys Gln Gly Ala Leu Tyr Thr Ser Gln Asp Pro
 100 105 110
 Val Tyr Ala Gly Thr Gly Tyr Thr Ala Ile Asn Gly Leu Ile Ser Ser
 115 120 125
 Glu Pro Gly Asp Asn Tyr Glu His Trp Val Asn Gln Ala Val Val Ala
 130 135 140
 Phe Pro Thr Ala Asp Lys Ala Arg Ala Phe Val Gln Thr Ser Ala Asp
 145 150 155 160
 Lys Trp Lys Asn Cys Ala Gly Lys Thr Val Thr Val Thr Asn Lys Ala
 165 170 175
 Lys Thr Tyr Arg Trp Thr Phe Ala Asp Val Lys Gly Ser Pro Pro Thr
 180 185 190
 Ile Thr Val Ile Asp Thr Gln Glu Gly Ala Glu Gly Trp Glu Cys Gln
 195 200 205
 Arg Ala Met Ser Val Ala Asn Asn Val Val Val Asp Val Asn Ala Cys
 210 215 220
 Gly Tyr Gln Ile Thr Asn Gln Ala Gly Gln Ile Ala Ala Lys Ile Cys
 225 230 235 240

(2) INFORMATION FOR SEQ ID NO:285:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:285:

```

Asp Val Val Glu Ala Ala Ile Ala Arg Ala Glu Ala Val Asn Pro Ala
 1             5             10             15
Leu Asn Ala Leu Ala Tyr
                20

```

(2) INFORMATION FOR SEQ ID NO:286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:286:

```

Leu His Pro Ala Gly Ala Thr Asn Gly Ser Gly Gln Leu Ala Leu Pro
 1             5             10             15
Val Glu Ala Pro Pro Arg Ser Val Pro Ser His Gly Glu Pro Leu Gly
                20             25             30
Ser Ala Ala Pro Glu Gly Leu Glu Gly Glu Phe Asp Asp Arg Ile Asp
                35             40             45
Glu Arg Phe Pro Val Phe Ser Ser Ala Ser Leu Ala Glu Ala Leu Pro
                50             55             60
Gly Pro Leu Thr Pro Met Thr Leu Asp Val Gln Leu Ser Gly Leu Arg
 65             70             75             80
Ala Ala Gly Arg Ala Met Gly Arg Val Leu Ala Leu Gly Gly Val Val
                85             90             95
Ala Asp Glu Trp Glu Arg Arg Ala Ile Ala Val Phe Gly His Arg Pro
                100            105            110
Tyr Ile Gly Val Ser Ala Asn Ile Val Ala Ala Ala Gln Leu Pro Gly
                115            120            125
Trp Asp Ala Gln Ala Val Thr Arg Arg Ala Leu Gly Glu Gln Pro Gln
                130            135            140
Val Thr Glu Leu Leu Pro Phe Gly Arg Pro Gln Leu Ala Gly Gly Pro
 145            150            155            160
Leu Gly Ser Val Ala Lys Val Val Val Thr Ala Arg Ser Leu
                165            170

```

(2) INFORMATION FOR SEQ ID NO:287:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:287:

```

Val Gly Val Val Gly Val Gly Ala Thr Ser Pro Ala Gly Ala Gly Ala
 1           5           10           15
Gly Ala Gly Ser Ala Gly Thr Gly Ala Gly Ala Gly Gly Gly Ala Thr
      20           25           30
Lys Gly Arg Ile Asp Ser Ala Ser Ala Leu Ala Ala Pro Leu Ser Thr
      35           40           45
Gly Leu Leu Ala Val Pro Ser His Thr Thr Asn Gln Arg
 50           55           60

```

(2) INFORMATION FOR SEQ ID NO:288:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:288:

```

Met Ala Asn Thr Gly Ser Leu Val Leu Leu Arg His Gly Glu Ser Asp
 1           5           10           15
Trp Asn Ala Leu Asn Leu Phe Thr Gly Trp Val Asp Val Gly Leu Thr
      20           25           30
Asp Lys Gly Gln Ala Glu Ala Val Arg Ser Gly Glu Leu Ile Ala Glu
      35           40           45
His Asp Leu Leu Pro Asp Val Leu Tyr Thr Ser Leu Leu Arg Arg Ala
      50           55           60
Ile Thr Thr Ala His Leu Ala Leu Asp Ser Ala Asp Arg Leu Trp Ile
      65           70           75           80
Pro Val Arg Arg Ser Trp Arg Leu Asn Glu Arg His Tyr Gly Ala Leu
      85           90           95
Gln Gly Leu Asp Lys Ala Glu Thr Lys Ala Arg Tyr Gly Glu Glu Gln
      100          105          110
Phe Met Ala Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Ile Glu
      115          120          125
Arg Gly Ser Gln Phe
      130

```

(2) INFORMATION FOR SEQ ID NO:289:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:289:

```

Pro Gly Ser Phe Ala Arg Thr Lys Pro Pro Gly Arg Thr Ala Asp Ala
 1             5             10             15
Pro Ile Arg Cys Arg Asp Ser Arg Gly Thr Ala Gly His Arg Ala Leu
          20             25             30
Asp Glu Pro Pro Pro Arg Gly Ser Glu Pro Ala Arg Arg Ser Arg
      35             40             45
Gly Val Arg Thr Val Val His Asp Ser Leu Ala Ala Arg Arg Val
 50             55             60

```

(2) INFORMATION FOR SEQ ID NO:290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:290:

```

Gly His Gly Gly Gln Ser Ala Ile Gly Leu Gly Gly Gly Ala Gly Gly
 1             5             10             15
Asp Gly Gly Gln Gly Gly Ala Gly Arg Gly Leu Trp Gly Thr Gly Gly
          20             25             30
Ala Gly Gly His Gly Gly Ala Arg Arg Trp Tyr Arg Gly Pro Thr Ala
      35             40             45
Ala Arg Ser Gly Arg His Gly Arg Arg Gly Trp Arg Arg Trp Ala Asp
 50             55             60
Arg Gln Arg Arg Gly Arg Arg Arg
55             70

```

(2) INFORMATION FOR SEQ ID NO:291:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:291:

```

Asp His Arg Arg Arg Ser Leu Ala Ser Leu Arg Ser Ala Ser Ser Pro
 1             5             10             15
Ala Arg Ile Thr Glu Val Arg Pro Cys Thr Pro Leu Leu Glu Arg Ser
          20             25             30
Ala Pro Gln Ser Gly Ser Arg Asp Pro Phe Arg Pro Trp Pro Ala Asp
      35             40             45
Ala Gly His Ala Arg Ser Pro Ala Trp Tyr Arg Leu Gly Ala Gly Asn
 50             55             60

```

Pro Ile Pro Val Arg Ala Ala His His Glu
65 70

(2) INFORMATION FOR SEQ ID NO:292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 174 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:292:

CCGCACGTAA CACCGTGAAT TGAAGGGAGC CGCTGGTCAT GGGCCGATTC TATCCGTGGG	60
CGAACGGTTA TTGACGGCCC GGAGGCCACT CCGTGCCAC CAAGTGGTGA CTCAGCGCGT	120
TTTCACGGCA ACGAACGGCG GACACACCAC TTGACATTCT ACAGCACGGC CGCG	174

(2) INFORMATION FOR SEQ ID NO:293:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 404 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:293:

TCGCAAACGG GGTGACGTC CGTCCGGTGG CGCTAGAGAG TTTGTCGCAC TTTCCGGTGA	60
CCGTCGCGCG GCACCGCAGC ACCGGTGAGC TCACGCTGCT AGTGGAGGTG CTCGACGGTG	120
CGCTGGGCAC GATGGCGCCC GAAAGCCTCG GCAGGCGGGT GCTGGCTGTG TTACAGCGCT	180
TGGTCAGCCG GTGGGATCGG CCGCTGCGCG ACGTCGACAT TCTGCTGGAC GGCGAGCACG	240
ATCCGACCGC ACCCGGCCTG CCGGATGTGA CGACGTCGGC ACCCGCGGTG CATACCCGGT	300
TCGCCGAAAT CGCTGCGGCA CAGCCTGACT CCGTGGCGGT CAGTTGGGCG GATGGTCAGC	360
TGACGTACCG GGAGCTGGAT GCATTGGCCG ACCGGCTGGC CACT	404

(2) INFORMATION FOR SEQ ID NO:294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:294:

Ala Asn Gly Val Thr Phe Arg Pro Val Ala Leu Glu Ser Leu Ser His	
1 5 10 15	
Phe Pro Val Thr Val Ala Ala His Arg Ser Thr Gly Glu Leu Thr Leu	
20 25 30	

Leu Val Glu Val Leu Asp Gly Ala Leu Gly Thr Met Ala Pro Glu Ser
 35 40 45
 Leu Gly Arg Arg Val Leu Ala Val Leu Gln Arg Leu Val Ser Arg Trp
 50 55 60
 Asp Arg Pro Leu Arg Asp Val Asp Ile Leu Leu Asp Gly Glu His Asp
 65 70 75 80
 Pro Thr Ala Pro Gly Leu Pro Asp Val Thr Thr Ser Ala Pro Ala Val
 85 90 95
 His Thr Arg Phe Ala Glu Ile Ala Ala Gln Pro Asp Ser Val Ala
 100 105 110
 Val Ser Trp Ala Asp Gly Gln Leu Thr Tyr Arg Glu Leu Asp Ala Leu
 115 120 125
 Ala Asp Arg Leu Ala Thr
 130

(2) INFORMATION FOR SEQ ID NO:295:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 526 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:295:

GCTTCGACGG	CTACGAGTAC	CTGTTCTGGG	TGGGTTGTGC	GGGCGCCTAC	GACGACAAGG	60
CCAAGAAGAC	CACCAAGGCC	GTCCGCCGAGC	TGTTCCGCCGT	CGCCGGGGTG	AAATACTTGG	120
TGCTGGGCGC	TGGGGAAACC	TGCAACGGCG	ACTCGGCGCG	CCGCTCCGGC	AACGAGTTCC	180
TCTTCCAGCA	GCTGGCACAA	CAGGCCGTCG	AGACCCTGGA	CGGTTTGTTT	GAGGGTGTGG	240
AGACCGTCGA	CCGCAAGATC	GTTGTACCTT	GCCCCCACTG	CTTCAACACC	ATCGGCAAGG	300
AATATCGGCA	GCTGGGCGCC	AACTACACCG	TGCTGCACCA	CACCCAGCTG	CTCAATCGGT	360
TGGTGCGCGA	CAAGAGGCTG	GTCCCTGTCA	CTCCGGTTTC	TCAGGACATC	ACCTACCACG	420
ACCCGTGCTA	CCTGGGTCGG	CACAACAAGG	TCTACGAGGC	ACCACGGGAG	CTGATCGGTG	480
CCGCGGGGGC	CACCTGAGCC	GAGATGCCGC	GCCATGCCGA	CCGCAG		526

(2) INFORMATION FOR SEQ ID NO:296:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:296:

CTCGCCGCCG	TGATCTGGCC	GGCGAACTTC	GTCAGTGCAT	CCAGACCCCA	ACGATCATCG	60
ATCAGGCCGA	TGCCCATGAT	CACCGCACCG	GCCACCAGCA	CCGCGGGCAT	GCCGGTGGAA	120
TAGACGAACC	CCCGGGTGAG	TGCCGAAGC	TGGGAGGCAA	GAAAGACGGC	GCCGACAATG	180
CCCAGGAACA	TCGCCAACCC	ACCCATCCGA	GGGGTAGGCG	TGACGTGCAC	ATCTCGCTCC	240
CGCGGGTAGG	CGACGGCTCC	CAGGCGACTG	GCCAGCATCC	GCACCGGACC	GGTCGCAAAA	300
TAGGTGATGA	TCGCCGCGGT	CAGCCCCACC	AGCGCAAGCT	CACGCAGCGG	GACACCGGCG	360

CCGCGATAGG ACAGGGCGAG CAAGCCACCG GCAACGCCCG CCACATCGCT GGACACCTCG 420
 AGACCGTACT GCACCAACCT GAAGAGCTGA AACTCGCCG AACGTGCAAC AGCTGCGAAC 480
 AATTGGG 487

(2) INFORMATION FOR SEQ ID NO:297:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 528 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:297:

ACGAAGCGCG AGAATATGAG CCGGGGCAAC CCGGCATGTA CGAGCTTGAG TTCCCGGCGC 60
 CTCAGCTGTC GTCGTCCGAC GGCCGTGGTC CCGTGTTGGT GCACGCTTTG GAAGGTTTCT 120
 CCGACGCCGG CCATGCGATC CGGCTGGCCG CCGCCACCT CAAGGCGGCC CTGGACACAG 180
 AGCTGGTCGC GTCCTTCGCG ATCGATGAAC TACTGGACTA CCGCTCGCGG CGGCCATTAA 240
 TGACTTTCAA GACCGATCAT TTCACCACT CCGATGATCC TGAGCTAAGC CTGTATGCGC 300
 TGCGCGACAG CATCGGCACC CCATTCTGTC TGCTGGCGGG TTTGGAGCCG GACCTGAAGT 360
 GGGAGCGGTT CATCACCGCC GTCCGATTGC TGGCCGAGCG CCTGGGTGTA CGGCAGAACC 420
 ATCGGCCTGG GCACCGTCCC GATGGCCGTT CCGCACACAC GACCGATCAC GATGACCGCT 480
 CATTCCAACA ACCGGGAGCT ATCTCCGATT TTCAACCGTT CGATCTCC 528

(2) INFORMATION FOR SEQ ID NO:298:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:298:

CCAAGCCCGT CAAGGAGCCG GTGCCGGCCT TGCCTCCGGT GCCGCCGACG CCGGCGTTGC 60
 CGCCGTTGCC GCCGTTGCCG CCGGTACCGG GGTTCCTTAC GGTGCCGCCG CCCGGCAGCA 120
 TGGCCCCGCT GTTTAGGCCG TTTTCGCCGG CCCC GCCGTC ACCGGCTTTG CCGCCATCGC 180
 CGCCGTTGCC GCCGCTGGTG GGGGTGGCGG CCTGGTTGAC GTATTGTTCC ACCGGCCCGG 240
 CCCTTGACCC TTTGGCGGTG TCGATCGCGG CGTCGATGGA TCCGCCGACC ACGACGTGCG 300
 AAGCCTCGCC TGCCGCCGCA GCCGCCAAC TGTGTCGCGG CTCCTGCGAT TTGGCCCCGG 360
 CCGACGAGAT GATGGGCACC ACCGGAGCCT GCGGCCGTCT GGGGGAGGCC AGCGCGGGTT 420
 CGCGGTCACG CCATACGCGA CCGTGCGCCG CCGCTTCGGA GATTTCAGG CTGCGTTGCA 480
 CCAGATCGAG CAGCGGTGTG CCCAGGACT GGGTTAGCCC GTTGGCGCCG CCGTTGTAGC 540
 GGCGAGCGCA ATATCGGTGC CCACTCGACC CAACCGCGAC TCCATAAGCG ACACCATTCG 600
 CGGTTGATGC 610

(2) INFORMATION FOR SEQ ID NO:299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid

244

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:299:

```

Phe Asp Gly Tyr Glu Tyr Leu Phe Trp Val Gly Cys Ala Gly Ala Tyr
 1           5           10           15
Asp Asp Lys Ala Lys Lys Thr Thr Lys Ala Val Ala Glu Leu Phe Ala
 20           25           30
Val Ala Gly Val Lys Tyr Leu Val Leu Gly Ala Gly Glu Thr Cys Asn
 35           40           45
Gly Asp Ser Ala Arg Arg Ser Gly Asn Glu Phe Leu Phe Gln Gln Leu
 50           55           60
Ala Gln Gln Ala Val Glu Thr Leu Asp Gly Leu Phe Glu Gly Val Glu
 65           70           75           80
Thr Val Asp Arg Lys Ile Val Val Thr Cys Pro His Cys Phe Asn Thr
 85           90           95
Ile Gly Lys Glu Tyr Arg Gln Leu Gly Ala Asn Tyr Thr Val Leu His
 100          105          110
His Thr Gln Leu Leu Asn Arg Leu Val Arg Asp Lys Arg Leu Val Pro
 115          120          125
Val Thr Pro Val Ser Gln Asp Ile Thr Tyr His Asp Pro Cys Tyr Leu
 130          135          140
Gly Arg His Asn Lys Val Tyr Glu Ala Pro Arg Glu Leu Ile Gly Ala
 145          150          155          160
Ala Gly Ala Thr

```

(2) INFORMATION FOR SEQ ID NO:300:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 161 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:300:

```

Arg Arg Arg Asp Leu Ala Gly Glu Leu Arg Gln Cys Ile Gln Thr Pro
 1           5           10           15
Thr Ile Ile Asp Gln Ala Asp Ala His Asp His Arg Thr Gly His Gln
 20           25           30
His Arg Gly His Ala Gly Gly Ile Asp Glu Pro Pro Gly Glu Cys Arg
 35           40           45
Lys Leu Gly Gly Lys Lys Asp Gly Ala Asp Asn Ala Gln Glu His Arg
 50           55           60
Gln Pro Thr His Pro Arg Gly Arg Arg Asp Val His Ile Ser Leu Pro
 65           70           75           80
Arg Val Gly Asp Gly Ser Gln Ala Thr Gly Gln His Pro His Arg Thr
 85           90           95
Gly Arg Lys Ile Gly Asp Asp Arg Arg Gly Gln Pro Asp Gln Arg Lys

```

245

```

          100              105              110
Leu Thr Gln Arg Asp Thr Gly Ala Ile Gly Gln Gly Glu Gln Ala
      115              120              125
Thr Gly Asn Ala Gly His Ile Ala Gly His Leu Glu Thr Val Leu His
      130              135              140
Gln Pro Glu Glu Leu Asn Thr Arg Arg Thr Cys Asn Ser Cys Glu Gln
145              150              155              160
Leu

```

(2) INFORMATION FOR SEQ ID NO:301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:301:

```

Glu Ala Arg Glu Tyr Glu Pro Gly Gln Pro Gly Met Tyr Glu Leu Glu
 1              5              10              15
Phe Pro Ala Pro Gln Leu Ser Ser Ser Asp Gly Arg Gly Pro Val Leu
      20              25              30
Val His Ala Leu Glu Gly Phe Ser Asp Ala Gly His Ala Ile Arg Leu
      35              40              45
Ala Ala Ala His Leu Lys Ala Ala Leu Asp Thr Glu Leu Val Ala Ser
      50              55              60
Phe Ala Ile Asp Glu Leu Leu Asp Tyr Arg Ser Arg Arg Pro Leu Met
55              70              75              80
Thr Phe Lys Thr Asp His Phe Thr His Ser Asp Asp Pro Glu Leu Ser
      85              90              95
Leu Tyr Ala Leu Arg Asp Ser Ile Gly Thr Pro Phe Leu Leu Ala
      100              105              110
Gly Leu Glu Pro Asp Leu Lys Trp Glu Arg Phe Ile Thr Ala Val Arg
      115              120              125
Leu Leu Ala Glu Arg Leu Gly Val Arg Gln Asn His Arg Pro Gly His
      130              135              140
Arg Pro Asp Gly Arg Ser Ala His Thr Thr Asp His Asp Asp Arg Ser
145              150              155              160
Phe Gln Gln Pro Gly Ala Ile Ser Asp Phe Gln Pro Phe Asp Leu
      165              170              175

```

(2) INFORMATION FOR SEQ ID NO:302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:302:

```

Lys Pro Val Lys Glu Pro Val Pro Ala Leu Pro Pro Val Pro Pro Thr
 1           5           10           15
Pro Ala Leu Pro Pro Leu Pro Pro Leu Pro Pro Val Pro Gly Phe Pro
          20           25           30
Thr Val Pro Pro Pro Gly Ser Met Ala Pro Leu Phe Arg Pro Phe Ser
          35           40           45
Pro Ala Pro Pro Ser Pro Ala Leu Pro Pro Ser Pro Pro Leu Pro Pro
          50           55           60
Leu Val Gly Val Ala Ala Trp Leu Thr Tyr Cys Ser Thr Gly Pro Ala
65           70           75           80
Leu Asp Pro Leu Ala Val Ser Ile Ala Ala Ser Met Asp Pro Pro Thr
          85           90           95
Thr Thr Cys Glu Ala Ser Pro Ala Ala Ala Ala Ala Gln Leu Cys Arg
          100          105          110
Gly Ser Cys Asp Leu Ala Pro Ala Asp Glu Met Met Gly Thr Thr Gly
          115          120          125
Ala Cys Gly Arg Leu Gly Glu Ala Ser Ala Gly Ser Arg Ser Arg His
          130          135          140
Thr Arg Arg Cys Ala Ala Ala Ser Glu Ile Cys Arg Leu Arg Cys Thr
          145          150          155          160
Arg Ser Ser Ser Gly Val Pro Arg Asp Trp Val Ser Pro Leu Ala Pro
          165          170          175
Pro Leu

```

(2) INFORMATION FOR SEQ ID NO:303:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 921 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:303:

```

AATTCGGCAC GARCAGCACC AACACCGGCT TCTTCAACTC CGGCGACGTC AATACCGGTA      60
TCGGCAACAC CGGCAGCTTC AACACCGGCA GCTTCAATCC GGGCGATTCC AACACCGGGG      120
ATTTCAACCC ANGCACTAC CACACGGGGA CTCGGAAACA CCGGCGATTT TACACCGGCS      180
CCTTCATCTC CGGCAGCTAC AGCAACGGGT CTTGTGGAGT GGAAATTATC AGGGCTCATT      240
GGNTGCACCC GGSCTTRCGA ATCCCTCGKG CCAATTCAAC TCCTCNACAA GCTTGCGGCC      300
GCACTCSAGC CCGGTGAAT GATTGAGTTT AACCGCTNAN CAATAACTAG CATAACCCCT      360
TKGGGCTCT AAACGGGTCT TGAAGGGTTT TTTGCTGAAA GGANGAACTA TATCCGGATA      420
ACTGGCGTAN TACGAAAAGC CGCACCGATC GCCTTCCCAA CAGTTGCGCA CCKGAATGGC      480
AATGGACCNC CTKTTACCG GSCATTAAACN CGGGGGTGTN GGKGTACCC CCACGTNACC      540
GCTACCTTGC CANNSSCTN RSGCCGTCTT TCSTTTCTTC CTTCTCTCTC CCMCTTCGCC      600
GGTTCCCNCT AGCTCTAAAT CGGGGNCC CTTMGGGTTC CAATTATTGC TTACNGSCCC      660
CCACCCAAA AAYTNATNG GGTAAATGTC CCTTMTTGGG CNTCCCCCTA WTNANNGTTT      720
TCCCCCTTNA CTTTGRSTCC CTTCTTATW NTGAMNCTNT TTCCACYGGA AAAMNCTCCA      780
CCNTTYSSES TTTCTTTGA WTTATMRGGR AATTSCAATY CCGCYTTKGG TTMAANTTAA      840
CYTATTTTNA ATTTTCCCGM TTTTMMNATR TTNSNCKCGM KNCTCCNRKA SSGNTTTCCT      900
CCCCCYTTSS GKTYCCCRN G

```

(2) INFORMATION FOR SEQ ID NO:304:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1082 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:304:

```

AATTCGGCAC GAGATANGGG CGCACCAGGG TCCGCAGCCG GCGGGACCGT CGCCAGCACC      60
ACCGGGGTCA ACAGCACCAC GGTGGCGTCC ANG CAGAGCG CCGCGGTGAT GCGGCGCGAG      120
ACGGCRAACA CCTGCCGTAG CAGTCGGTGC GACTCCGCGC TCGCTCGANC CATGGCCGCG      180
CCGGCTGCCT CGAACANGCC TTCGTCTGTC ACAGCTTAGC CAGCANCCAA ACCGCACCCA      240
GAAACCCACA CGCCCGCCGC CCCGGANACC TGCGCCATCG KCTGCTGGGG CGANATCCCC      300
CGATCGCTNA CANGATGACC GCTGCCGGAA CGCCGCCGCT GCCTCCGGGC AGCCGCGTGG      360
GCSGGGCAAC CGCGAACCCA NGAACACGGC AAGCAGTATC ANCGCAACAG CAATTGTCAA      420
GGGCTAAACG CTTCACATCC AGGGATCTCG CGGCGCCACA CCGTCGGMTC TGCAGSGCGA      480
CCCCNTCCTN GGGCGGNAC TCNTCAAAGA TGCNGATCNA CAGKCTAGGT CTTGCGCCGA      540
TATGSAAGGN CCCAACGGNT TTAAAGCGGC SAAAAAATC TCCCANTGGA TAAAATCAGC      600
CGGGGANCCC CCCGTGSCMM NGTCYCGGKC ATTNTTCAAC MGGTTTNACG GCGGKTGCNG      660
GCCAACTKGC CAAAMTTAAG KTNNGGGNTY CGGGGCGGTA ACCGGCNNTK NGCCCCCTTAA      720
AAAACCGGNC YTTTCTKGAT TAMMACCGGN CCCCCAWTGG CGGKTGKTCC CANGNTYAAC      780
AMCCYCCCCS MNGGGKTGGS SAACCCTTCC CGNNGGGTTC NTKGTTSCYT AWMCCCCCGG      840
AAACCSGKYG GGKTGGCRTN WASSAMNCCC CMNGYYTCTT TAAAGGCCAN KNRAAWGKYT      900
CCTTGGAAGW CCTNCAATYC GAAAAYYCTC CTYMMGSSCN CTTKCWRTYN NRNGGGAACS      960
AMWTNYCCNC GWTTCAWTCG GGTCCGASMN AAACKCTTTY TTTTYCGSSC STCCMGGSNC      1020
SGGTKNANAN AAASATTTMC YYCNNNANKK YYCSSGCTT CYKMGRNRNR GMGAACCCGR      1080
GS                                                                1082

```

(2) INFORMATION FOR SEQ ID NO:305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 990 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:305:

```

AATTGGCACG AGTGATCGCG CTGAAGCCGG TAGCGCGGGT GGCTCGGGTG GTTTGCGAAC      60
RAAATCCGCT CGANGTGGTC TCGGTAGGCG GTGTCCANAA CCGTGGCGCG GTGCCGCGG      120
ATCTGATCGG CGCGGCCGTA GTGCACGTCG GCGGGCGTGT GCAGTCCGAT GCCGGAATGC      180
TTGTGTTCTG GGTGTGTACCA GCCGAAGAAC CGGTGCGAGT GCACCCGGGC CGCCTCGATC      240
GACTCGAACC GTTTGCGGAA ATCGGGCCGG TACTTGAAGG TCTYGAAGT GGCCTCAGAC      300
AACGGGTTGT CTTGCTGGTG TCGGGGCGTG AGTGCGACTT GGTGACACCG AAGTCGGCCA      360
NCANCAATGC CACCGGTTTG GAACTCATCC ACAACCCCG TCCGCGTCMA GGTCACCTGT      420
NCGGCGCTAA TTTNYTGGGC GGCAAGGGTT TGCCGAYCAN KCCGCTCGGC CAAAACCTCG      480
ANTCNCSCCA AGGCCNCCAT CCNCCCAAAC AMGTTACGGG ANAAAANATY CAAAGAYCAC      540
CYTCCGGKTN TTATANCTYC CCYTTTGSTY GGGCCCCCN CYYTGKKNAT ACCCCTNCCA      600

```

AWTCCCCAACN	CCCKCCAANA	RCYKGGGGGCC	CCCNCCAACC	CGGGKGAACA	WTAATTTTAAA	660
CCCYAACMAW	ACTWMMNACC	CNNGGGSCCY	AAMCGTYYNR	AGGTTTTTCT	NAAAGAAASA	720
ANTCGGAAMC	CGGNTSTACC	AAAAASCCCK	CCNWTCCCTC	CRASATTGSC	NCCSAAWKSA	780
AKGCCCCCN	Y	TCSGCNWN	NC	CSGCGGKKKT	KKGTTNCCCT	WMRCWMWYTS
CKYYSMYCC	CCCCCTCCCM	CTCCGNKTCC	CCAMCCYANC	MGGCCCCCYTM	GKCCCCWKNT	840
YKGGCCCCC	AMMNNNGGGG	WGACCCTNGG	CCCCMKRRGM	TCCCNANTGA	MCCTCWGNRA	900
MKYCCNRAR	ANMCCSCNCC	NGCNCRCCKNN				960
						990

(2) INFORMATION FOR SEQ ID NO:306:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 223 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:306:

AATTCGGGTG	GCAACGCGGG	CCTGTTCCGC	AACGGCGGCG	CCGGTGGTGC	CGGTGGGGCT	60
GGTGGTGGCG	CCGGCGGCGC	GGGCGGTAA	GCGGGGTGGT	TTGGTCATGG	GGGCGCTGGC	120
GGCGTGGGTG	GTGTANGTGC	GGCCGGGGCC	AACGGTGCTA	CGCCCGGTCA	GGATGGGGCG	180
GCTGGTGTG	CCGGGTCGGA	CRACRCTCGT	GCCGCTCGTG	CCG		223

(2) INFORMATION FOR SEQ ID NO:307:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:307:

AATTCGGCAC	GANGCGGCAA	CGGTGGCAGC	GGCGGCACGT	CNGTTGCCAC	CGGGGGGGGCC	60
GGGAACGGCG	GTGCCGGCGG	CGCCGGCGGC	GGGGCCGGGC	TGATCGGCAA	CGGCSGCAAC	120
GGCGGCAGTG	GCGGAATGGG	CGATGCCCCG	GGCGGCACCG	GCGTCNGCGG	CATCRGTGGG	180
CTGTTGTTGG	GTTTGGACRG	CGCCAACGCC	CCGGCCAGCA	CCAACCCGCT	GCACACCGCG	240
CAGCACAGGC	GTTGGCCGCA	GTCAACGCGC	CCATCCAGGC	CGTGACCGGG	CGCCCCCTGAT	300
CGGCAACGCG	CCAACGGCGC	CCCGGGCAAC	GGGGCCCCCG	GCRGGCACGG	CGGGTGTTTG	360
TTCGGCGGCG	GAAGGAACGG	CGGGTCCGGC	GTCANCRGCG	GGGCGGGCGG	AAATGCCG	418

(2) INFORMATION FOR SEQ ID NO:308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1049 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:308:

AATTCGGCAC	GAGGGGCACG	ATCGCATACA	GCGCTCGCGG	CAGACCCGCC	CGATACAGCA	60
GCTCGGCACA	CGCGAGCGCA	CAATACGGCG	TCTGGCTGTC	CGGCTTGARC	ACCACCGCGT	120
TACCGGCCAC	CAGCGCGGGC	ACCGAGTCCG	ACACCGTAAG	CGTCATGGGG	TAGTTCCACG	180
GCGAGATCAC	CCCCACCACG	CCCTTCGGTT	GATAGCACAC	CGTGGTCTTG	CCTATCCCGG	240
GCAGCAGCGG	CTGTGCCTTA	CGGGGCTTCA	GCAGGTCCAC	ACAGACTCGT	GCSTTATAAT	300
TNCGCSTTCC	GCGATCAGAT	CGACAATTTT	CTCTTGCGCC	GCCCATCGGG	CCTTGCCCCG	360
CTCGGCTTGC	AGGAAGTCCA	TGAAGAACTC	GCGGTTCTCG	ATNAACAGGT	CGCGATAGCG	420
GCSGATGACT	GCAGCTCGCT	CGATNACGGG	ACCTTCGCCA	GTCGGTCTGC	GCCGCGCGAN	480
CTTCCGCGAA	TGCCGCTTCG	ACTTCCGCGG	NCGTGCCAAC	GGAATCNTAT	CACGGGTTGC	540
CGGTAAAAAC	TCCTCAATST	NCYGGTCGAA	ATTCCGCAAC	TTCTTATCCC	GGCAGGTRCC	600
AACSANNCAA	ACCTCGGCAA	GGTTAGGTTT	TCCCCNCTT	YCAAAAATNC	GGKTTTTGGN	660
CMAATTTTCG	CKCNATGKTG	MCAAGGMTCT	CKAANAAKCS	GGGTCYTCTN	NTCNGKGGAK	720
CCAAAMGGKT	TTGGGGMAGC	GKNMNCCAA	CCTWACCCTG	KTKAANGGNW	TTCCCCCGG	780
GGGAKKNGA	ATYCYCCSNA	NCCCRGGGGG	GNMCARATTC	TYCCGGMCTC	CTCKGGAWTC	840
WGMGSTTTCC	CAAAAAACSC	CCCAAATTMM	TTTTTCCRCN	TRTTGANACW	CTTTTKARCA	900
MMCSSAARNS	ANMCNCTCYC	CKCTKTGKTK	AAAAAGNAYW	CCCCMAAATT	TYTAWTTSSC	960
CCSCGCGGGN	CCCNCTNTTT	TSCNMTWCTM	WNYTNCRMCC	MMMSNCKSNG	KKGGNRCCNN	1020
CRCCSNCCCM	AAWYNTKGYN	KNTATMAGC				1049

(2) INFORMATION FOR SEQ ID NO:309:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:309:

AATTCGGCAC	GAGGGAATCG	AGAATCCCGG	AATGGTGAAG	CCTCGGTGCC	TGCCGTTACG	60
CCAAGAKTCA	GGGTGAGCGG	CCCCCGGTG	GGAATGCTGA	SGCCAACCGG	GAAAAGGGTG	120
AGGGCTGGGG	TGGAATAACT	GAANGTTACT	GGGATGAAAA	ACCCGGTATT	GATATGTATT	180
GGGCCGATCA	ANGTTGTGGG	AATGGGGGAA	GGCTGAGGGC	GACCTGTTGG	ATTTGGGGAA	240
TTGTYRTGGA	CRAKACWGGC	CAGCCMGCGT	GATGGTTTGG	TTSAANTTTT	GTGCCGSCCA	300
CANGGTGATG	GGATTGATTT	TGATGGGGCC	SATCGAAATA	TTGGGTATGC	CNACGCCSAA	360
CGAGATYGCC	GGGACGTTCA	TGGGCGGGAC	AACCMASGGT	CCSANGTAAK	GGTTTCCTTN	420
ATNTTGATCG	GGATTCCGGA	ACTMTSTCGA	TGSGCTCSAY	MTSATSGCCC	NACNCCWCCG	480
YTTATTTTMS	GCTNAYGGGA	ATBAMRGGA	CAAYNTCCCT	CCCMGGAAAA	ACCAACMSGC	540
CCTGGTNSYC	CNCCCRCCNC	AKAACCCRTT	KCTGTRSTMC	CCSMAAATNA	CSCCSCSTTS	600
NACTCCNCSG	AANTNSCCCC	CCSCXNNTT	ATSTYCCCGK	GTTCCCCCMC	CCCTTNAAMC	660
TCCCCGGTTA	ACCCCCWTNT	SNCNCCCCCS	YTAAKMNCRG	GCTTSTTNCT	CCCCCYTRMK	720
CNCCCCCTCK	SAMCWNCNC	CTCKAACNAC	CCCKCYKGS	TNCCCAATNT	WCMWCKCCNS	780
KTTNTMCTKC	CCAAAYTNCRC	CCNCRCTCCC	CKKSTSTCAM	WTATAAAACC	WCWYAWYNNK	840
KCNCWMAWTA	MGACWCTCNY	NCCCCNCNCK	NTTKTAMWCC	CKMCCCKCSW	TWCYCKCSCC	900
CCMTCTMNAC	YCCCCCKKTY	NKWMCCCTTC	CCCCCCTCCC	MCNMBMKTCT	YCSGKTWCWC	960
NCYNTTMTCN	CYNANMCKCK	KTCTCTTCN	CRNTCTCCCC	CCWCCCCCCV	KKCTCTSKCC	1020
CNCNCTCCSC	MMKGSC					1036

(2) INFORMATION FOR SEQ ID NO:310:

(i) SEQUENCE CHARACTERISTICS:

250

- (A) LENGTH: 1036 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:310:

AATTCGGCAC	GAGATCATGA	ATAGCGGGCT	GGTCAGCACC	GAAGTGGTCG	GCGATCTCGC	60
GAGCAAGTCT	CGTCTGCTCG	CCCAGCAGGA	GGTCGGCATC	GATGCGGACA	CCTGCGATGT	120
CTTGATGGT	GTTCAATTGC	AGGTAAGGCC	GACGCCGCAG	CTTTGCTAGC	AGGGTGTCTT	180
GGCTCTTCGC	ACGTGAGGTA	ACCAATAACT	CCGACGCAGA	CCAACTCCGG	CCCTCGATCC	240
GGGTACCAGG	CTCCGCCGGA	GCCAGCCGTT	GTGCCCCCTG	GGCCGAAGGT	CAGCTGCTGT	300
GCGATCGAAG	TAAGAAACCG	CGCCATGCCC	GTGCGCAAGT	ACGACTGACC	GAGCAAACGA	360
ACGATCGTCG	TCCTTTCCGT	GGGGGTAATC	GANCCCAGCA	ACCGCACGAG	CCACCAATCA	420
TTGGGATTTC	GCCACTGACC	GACCAACCGC	CTGTGCGACA	CCCCAGCGGA	ATTGGTGGTC	480
TTCCCGGGGG	CCGCNAACGG	AATCANCGSG	ACGCGCTCGC	CGAASCANCC	GCATANCCNT	540
ACATANCAAC	GGNNTCTGCG	CCCACATTTT	GGGSTTMTGC	CCCTCNGCAA	CSSNAAYNCC	600
CCCAATTTCY	AACNAAAAAA	TTGGYCCATY	ARNGTYCTCM	CCAAAAACCN	AWTCCCKTA	660
TCCCCCGGGG	GGGRCCCCYY	NMNAAAACGG	CCCWWAANCC	CCSGGGCSCC	CGGGTTRWTN	720
CCCCCTGTGC	GCCCNCCSGG	TTTGGTCMCM	GGSCMTNWN	GGGNTGCSCC	CCCNCAAAAA	780
AAAAAYCKNG	NCAAATYAAA	CCCKYCMAAA	ASKTGGGSSC	CCCMARCCGG	GGKAACKWWA	840
ANTTAANCCN	KAAAAAAWW	NCANNMCCCC	NGGGNCCTAA	GGKYTTAGGG	GTTSTTNANG	900
AAAAAATMTC	CANATMNSSK	TTNNAAAAAA	ASCCSWAKCC	CCCNNNKKN	CCAAWKAARR	960
SRCCTTCGGG	TNWNNSGGGG	KKKKKTNCMS	KMNMMTTWGR	CCCNCCGCCN	NNTWKCCCTN	1020
TCCNYGGNGC	RNCAGN					1036

(2) INFORMATION FOR SEQ ID NO:311:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1060 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:311:

AATTCGGCAC	GAGTCGATTC	GATCGAACAC	GCCCCGACCT	GGCCAGGCCA	CATGGGCGCG	60
GCCATGGCCA	ACGCCTACTC	GGCCAACCCG	AATCCATTTC	GCGTCTCACC	GCAACCCCCG	120
AAACCGGCGA	CCGCGGCATG	GATCAACCCG	CCCACCCAG	ATCCGAAATA	GCGTCCACAT	180
AATGAGACAC	TGGCGCAAAG	AGCTTGACAG	GCGCCGCACC	ACGCAAGCTG	TTAGACGTGT	240
CGGTCTTGCA	AGAAGCGGGT	TGGCCACCCA	AGATCACGCC	GCCCAAGGGC	ATCGAGTCAA	300
CGTTGCGGTG	GTATCGCGCT	AACGTGCGCG	CCGCCAAGAA	ATGACGGTGC	GCATTACCAT	360
GGCCCTGCTG	ATCACCTTTG	GCCACCTGCG	CACCANAACT	ATGANCAGCC	TTATGCCGAG	420
TCTCGTGGAC	ATCGGCAGCC	GCTTCAAAAA	CTCCTTGTCG	ACAATSGTAT	TGCTGANCCG	480
CCGAATTCTT	NTRCTTGCAA	SAACACTNCA	TGTTNCSGGT	NAACAACCYT	GGTTNGAAAA	540
ACANCCAATA	TTGAANTCCC	ANTCGGGCAM	GAACCN GTTM	CGGAAGKTGK	TGGGAACGAA	600
TGKTGCCCAA	AAATCCCGGG	NGGTRAAAW	CCCN SNATGG	MSAATTTTSC	CTNGAACAA	660
AAAAGGTCCA	AGKYCAAAGG	NGCCCCCCCC	SGNAAATTGG	TGAACSCAKA	WYANRTTCCC	720
WWWTNCAAAT	MTTNGGGTCC	KNNTCCCCWT	AAANGGGSCN	CCCCNCCRG	GMGTYTCCCC	780
NWNMGGMG	CYYCSCCCCA	AAAAAAAMMM	MTTTCSGKGG	SMGGKKCCCC	CCSGGTYWGG	840
GKKYTTAAAC	CCGGKGGGTN	CAAAAAANAN	ACCCCCCAMS	NGGGGGGAAA	ATTTGNAAWT	900

AAGGKKKTKC	SCMACCCCAA	AAANMMNNCN	AWNCCCGMGK	SARGGGGRNY	TTMKAGGGMG	960
GNYYYYCCCW	YCGGGGGGNA	NAAYAAAAGK	NGSNGRGAAT	NTTNTTTTGT	RSSSRNKTTT	1020
TYNTCCTYCN	CCNMGNRWWG	SRAMNTGKTS	NSSGGGSGGC			1060

(2) INFORMATION FOR SEQ ID NO:312:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1040 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:312:

AATTCGGCAC	GAGCTTCACC	AAAGAGCTGA	CATGCCGGGT	GATGCGACAT	CGCATCGAGG	60
GCAATACGGG	CATGGATGAN	CCGAANGGAN	TCTGGCGTTC	GCTCAACTGG	ATTACGGTTC	120
CCAAGGTGAA	ACGCTTTGCG	GCGAAAGATG	CGACGCTTAA	CTTGCGCTTC	CACCGTGCAA	180
TGTTNGTATG	GATGCTGGAA	CCGCGCTGAC	NGATAANGAA	TTGCTGGTTC	GCCGGGCGACN	240
ATGGATGGTC	CKSTTTTCNC	TCCGCSGTTA	AATTGCSTGT	GCATCATCTG	GCAGGCTATG	300
TTCCCGCTAC	RCTGCAGCCC	ATCATGGATG	TGCGGCTAAC	GAANAAGTTA	TGACATGGCG	360
CAAGCGAMTC	GGGCATSCNC	GCGGCAMTTT	CGCAACCTGC	TGTGTNTGAA	GCGTMTCAAC	420
CGAATGCGGC	GCTYAAAAGC	NGGCTTGCCT	TGATTMMAAC	CNAACCCNTN	CNATYCTTTG	480
CCGNGNMNTG	CGTTCTCTCC	AACTCCGKKG	SYTGCCNCCG	TGAAACCCMA	CTNCCCCCCC	540
GTTGGACTTA	MRTNTTCAAA	AAMCGGMTNA	ACCSGAATNN	SAACCTNCCR	TCAAANTAMM	600
SAANTCGGGC	TTYGGGNRCC	CCCCNGAAYW	TTCKNCNGGG	GMNNTYCTCN	GGTTYNGGCG	660
SAAACNTTTG	CCRTNCYMN	TTTACAMGGC	NCMTNMTTGM	GGGSCSNNA	GWCCCGGGKK	720
TNTTTNCAAW	TCNCNSKTTT	TTKGGGGGGG	GGCYGRTRMC	NCGGGCCCCC	GGCCCKKMAA	780
AAAAAMCMSA	RRCNCYGGG	KKCCCCCCCM	NNATNGGGCG	YKCRAAACAA	ACCCCAANRA	840
TNGNGMGGGC	SMACCSGNGN	GYNAAAKGGT	TSNSCTMANM	MKGMANNNCT	SGMSCCMNSN	900
NCTGMGGGKT	TTKGNNGARN	AANAMKMGM	RCGGNCGCN	GAAAGGGSMS	GSCKSCNNGN	960
NGASNGWMGN	CRNNGANRCC	NCNGYGNMRN	NNGNNNGNN	GGGRKNACN	NMKMCAWSMC	1020
NSNMMGNNS	CGYMTNKCGC					1040

(2) INFORMATION FOR SEQ ID NO:313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:313:

AATTCGGCAC	GAGACAANGG	CGTGAAATGG	GATCCGGCCG	AGCTGGGGCC	CGTCGTCAGC	60
GACCTGTTGG	CCAAGTCGCG	GCCGCCGGTT	CCGGTCTATG	GGGCCTAGTT	ATCTGCGCCG	120
AGCGTGAAC	CAGGGCGAGA	TTTCGGCCGT	TTTCTCGCCC	TGGCTTCACG	TTTCGGCGAAG	180
TKGGGAACGG	TCAGGGTTTC	CAAACCACGA	TCGGGATCGT	GCGGTTCGGT	CAGGACTGGT	240
ANTCCTGATA	CTTKGGTACA	TCGTGACCAA	CTGTGGNCAA	TATTCGGCGC	GCTCCTCGTC	300
NGTCGCGTCC	CGCGCGGTAA	GGTCCANCAC	TTCTTTTTTC	TCGTGCCG		348

(2) INFORMATION FOR SEQ ID NO:314:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:314:

AATTCGGCAC	GAGAGACCGG	GTCGTTGACC	AACGGACGCT	TGGGCGCGGG	CCCCTTGCGT	60
GGCATCAGCC	CTTCTCCTTC	TTAGCGCCGT	AACGGCTGCG	TGCCTGTTTG	CGGTTCTTGA	120
CACCCTGCGT	ATCCAGCGAA	CCGCGGATGA	TCTTGTAAGC	CACACCAGGC	AGGTCCTTCA	180
CCCGGCCGCC	GCGCACCAGC	ACCATCGAGT	GCTCCTGCAG	GTTGTGGCCC	TCGCCGGGAA	240
TGTACGCCGT	GACCTCGAAC	TGACTCGTCA	CTTCACGCGG	GCAACCTTCC	GAAGCGCCGA	300
GTTCGGCTTC	TTCGGAGTGG	TGGCTCGTGC	CG			332

(2) INFORMATION FOR SEQ ID NO:315:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:315:

AATTCGGCAC	RAGTCGGTCT	AGACGGATTTC	AATGCTCCCG	CGAGCACCTC	GCCACTGCAC	60
ACCCTGCAGC	AAAATGTGCT	CAATGTGGTG	AACGAGCCCT	TCCAGACGCT	CACCGGCCGC	120
CCGCTGATCG	GCAACGGCGC	CAACGGGACT	CCTGGAACCG	GGGCTGACGC	GGGGCCGGCG	180
GGTGGCTGTT	CGGCAACGGC	GGCAACGGCG	GGTCCGGGGC	GAACGGAACC	AACGGCGGGG	240
ACGTGGGGAC	GCGCCCGGCG	GGATTTCTTC	GCACCGGSGC	ACCGGCGGGG	CCGGCGGCGT	300
CGCACAAACG	CACCGGCGGG	GACGCNGCGC	CCGTNGGGCG	GCTTCTKGAT	GGGCTCCGGC	360
GGTNACGCGG	CACGGCGGCG	CCCGGCTCAC	CGCCNGTTGG	GACGCGGGGA	CGCGTNACCC	420
CGATCTTCTT	CCGCNCCCCG	GAAACCGCGG	GGCCGGCCCC	ACATTAKACC	CGGCGGNACC	480
GCGGMCCCCG	CGGAACGGNG	GGYNTTTTCC	AACGGCGGGG	CCGCGGAACC	GNMGGSTGTT	540
CCTTNGGSGA	AGGNCCAAKT	CCCGKCTANC	YYAATCCCCG	ANGGKTGAMC	CTSATGSNCA	600
MYTTMAGGAA	CYTNNCCANT	KTTSGRACCW	CRCNNGGAAA	ASRAWNKNGT	KGGCAAACNA	660
NNTNCTYTKN	NATTKGGNNA	AAAANCCCTY	CCWCSGRAC	NCCCCCNGM	GRGMCNNTNN	720
NTTTYGNCNN	CCCGGSNAAM	RNTTKATTTT	NGGGGGNTCN	GGGTKMNNNA	AACCCCAAAM	780
MNRNNKCSA	ANGGGKSNGC	NKNNMMNSGT	TTTYCKNMRA	MRNWTYKNKN	NTCNGARSRN	840
NAAMCNSNK	NGKKKNKAA	ARNNTTWKTN	KNSCNNNCNN	GRRNGVRGGC	CKMKGSNMNG	900
MCWHNAWRNG	NNGSNCNCKC	NNKMNAAAAA	AASGGVNCKS	NSMKNNKKKG	NRGGGGGGGG	960
GG						962

(2) INFORMATION FOR SEQ ID NO:316:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:316:

AATTCGGCAC	RAGAAGACGC	CCGAANGTTT	GCGCTGGCTC	TACAACTTCA	TCAARGCGCA	60
GGGGGAACGC	AACTTCGGCA	AGATCTACGT	TCGCTTCCCC	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGGC	GCACCGCACG	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GGCTTGCGTT	180
GCAGAAGATG	TCGTTGAGG	TGGCCTGGAG	GATTTTGCAN	GCGACGCCNG	TGACCGCGAC	240
GGGTTTGTG	TCCGCACTGC	TGCTCACCAC	CCGCGGCACC	GCGTTGACCT	CGACCAGCTG	300
CACCACTCGT	GCCGCTCGTG	CCG				323

(2) INFORMATION FOR SEQ ID NO:317:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1034 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:317:

AATTCGCAGT	GTGTGTGGCG	GCGTCCAGAA	GAAGATGATC	GCGAACATCG	CCAGCGCCGG	60
CCAGGCTATG	GTGCCGTGA	TGGCCGACCA	GCCGATCATC	ACCGGCATAC	AGCCGGCCGC	120
CCCACCCAC	ACCACGTTCT	GTGACGTGCG	TCGCTTGAGC	CAAAGCGTGT	AGACRAACAC	180
ATAAACGCG	ACGGTGACCA	GGGCCAGCAC	CCCCGCCAGC	AGGTTCGTGG	CGCACCATAG	240
CCAGAAGAAC	GAGATCACCG	TCNACGTCAC	CCGAGTGCCA	ACGCGTTTCG	GGTCGGCACC	300
GCTTCCCGCG	CCAAGGGCCG	GCGCGCGGTT	CGCTTCATCA	CCTTGTCGAT	ATCGGCGTCG	360
GCNACCAGTT	GAGCGTGTTG	GCGCCGGCGG	CSGCCATCAT	CCGCGCGACN	ANCGTGTTGA	420
GCATGANCA	GCGATGAATG	GCGCCGCGGC	TCGTGCCGCT	CGTGCCGAAT	TCAACTCCGT	480
CNACAACCTG	CGGNCGCACT	CGAACCCGGG	TGAATGAWTG	AATTTAAACC	GSTSAACANT	540
AACTACATAA	CCCTTGGGGG	CTCTTAACCG	GTYYTGAANG	GGTTTTTTGC	TTAAAGGAAG	600
AACYATTTCC	GGATANCTGG	CSTTNWTARC	GAAAAGGCCC	CRCCCATNGC	CCTCCACAGT	660
TTSCCCCTGA	ATGGSAAATG	MNCNCCYKNR	CNGGGNCTTT	AACRCSGGCG	GGNTTTTGKT	720
MCCCNCTKA	CNTTMMMTGC	ARNNCNGGCC	SKCCCTTCKK	TNTYCCCTCC	NTCCCCCNST	780
TNCNGKTCCC	CNNAMNYTNW	ACGGGGGGCC	YTNNGGKCRM	TWTKKTTTGG	GCCCCMCCCC	840
MAAANASAA	GGGKRNNGTY	CSTTTGGCNC	CCCAMAARGG	NYCCCCCAM	YTNRRKMCSY	900
CNNTNKGGMN	CTGTNCKNCG	GAARAMAMCC	KCCCCGNSTS	STTNGTYWAG	GNRWKGNRSG	960
CCSCCCCGGY	MNMNAAYAWN	WMNATNCNNS	STNANMAKKN	NNNNNNNSCN	WNGNGNNTCN	1020
SCNSNGGKBC	CSCC					1034

(2) INFORMATION FOR SEQ ID NO:318:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:318:

AATTCGGCAC	GAGCCACAT	CCGGGGCCGC	TCGTTGCATG	ACTCGTTCGT	CATCGTCGAC	60
RAGGCACAGT	CGCTGGAGCG	CAATGTGTTG	CTGACCGTGC	TGTCCCGGTT	GGGGACCGGT	120
TCCCCGGTGG	TGTTGACCCA	CGACATCGCC	CAGCGCGACA	ACCTGCGGGT	CGGCCGCCAC	180
GACGGGTCGC	CGCGGTGATC	GAGAAGCTCA	AAGGTCATCC	GTTGTTCCGC	CACATCACCT	240
TGCTGCGCAG	TGAGCGCTCG	CCGATCGCCG	CGCTGGTCAC	GAGATGCTCG	ANGAGATCAC	300
CGGGCCGCGC	TGAGTGCGCC	TCCCGCGAGC	A			331

(2) INFORMATION FOR SEQ ID NO:319:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1026 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:319:

AATTCGGCAC	GAGATCGTCA	CCCTGGCGAC	CAGTGCACCC	AGGCCACGCC	ACCAGTTACG	60
GCTGATGGGC	CAGAAGATGG	ACCAGGTGCT	GCCCATCCCC	CCCACCGCAC	TGCAGTGAG	120
CACCGGGATC	GCGGTCCTCA	GCTACGGCGA	TRAGCTGGTG	TTCGGCATCA	CCGCTGACTA	180
TGACGCCCGC	TCCGAAATGC	AGCAGCTGGT	CAACGGTATC	GAAGTGGGTG	TGGCGCGTCT	240
GGTGGCGCTC	ANCGACAATT	CCGTGCTGCT	GTTTACAAGG	ATCGGCSTAA	GCGTTCATCC	300
CGCGCACTCC	CCANCGCCGC	GCGGCSGGGG	CGGCCCTCTG	TGCCGACCGC	CCGAGCGCGT	360
CACTGACGCC	ATCTCCGTCG	GCGTTAACCC	CGTGAGAAGG	TGGGTCGTGC	GCAAGTTGGG	420
CCCGGTCACC	ATCNATCCGC	GCCGCCATGA	CGCNGTGCTG	TTCCACACCA	CNTSNGACNC	480
CCCCCAGGAA	CTGGTCCGGC	AMTNCAGGAA	NTYCGTGTGG	GCACCNGCTT	CTTCCGKTRT	540
GGCYTAAACT	TCCNATSTTN	CSGCSGGCCT	CTGGCGTTNC	GNCCGGGGCCG	NTCTTNCCAA	600
ATCGGSMMAA	ATCCCCANMC	AAACCCCCCG	GGTCTTGSGG	GCSGGGNGGC	GGCCNAWNCC	660
AAACCCCCCC	NTTAAANTCT	TTGKTNCCNN	CNCSGGCNC	NCNAANSCAN	CCCTTTKGGC	720
NCTTCCCCCC	CCCAWTTTAA	CCGAKCGSCN	AAAYCCAAGY	TMMGKCCYCY	KNAAAAAAAAA	780
AATTTGSCSG	CCCCAANTAA	ATTCCCNGGC	CCYTTGGGGG	CGRANCNYNT	TTTMCCSNSS	840
TKGNNAAMC	NGGANCCSGG	KAAYTMMTKG	NAAYCGCCSN	AAMBNTTTTC	TAANNCCCCN	900
YNCCCSGAAA	ATTNNAMAAM	CMNNKTGSNG	GGGGKTT SNC	SGKKGRAGGM	AAAAAANRSN	960
SKTTNMCNNN	SANMNCNSNN	SGGNSNNNNN	NNNCNCGYKC	CSNAANMCCC	CGCGGGGGGG	1020
CCMMCC						1026

(2) INFORMATION FOR SEQ ID NO:320:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 324 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:320:

AATTCGGCAC	GAGAAGACGC	CCGARNGTST	GCGCTGGCTC	TACAACTTCA	TCAARGCGCA	60
NGGGGAACGC	AACTTCGGCA	AGATCTACGT	TCGCTTCCCC	GAAGCGGTCT	CGATGCGCCA	120
GTACCTCGGC	GCACCGCACG	GCGAGCTGAC	CCAGGATCCG	GCCGCGAAAC	GGCTTGCGTT	180
GCAGAAGATG	TCGTTGAGG	TGGCCTGGAN	GATTTTGCAN	GCGACGCCNG	TNACCGCGAC	240
GGGTTTKGTG	TCCGCACTGC	TGCTCACCAC	CCGCSGCACC	GCGTTGACGC	TCGACCAGCT	300

GCACCACTCG TGCCGCTCGT GCCG

324

(2) INFORMATION FOR SEQ ID NO:321:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:321:

AATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCCGCGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGCCGC	CGGTGGCGTC	GTTGCTCTCC	TGACGGGGCG	CGGCGACCAT	AAGGTCGCTM	120
ATGCCCAGGT	AGCGGCCCAG	GTGCATGGAG	TCGATGATGA	TGCGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCGT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGCCT	CCAGAGTGGC	CGTGCAMTTC	CNGCGTGCTC	CACGGCAAAT	GCCTTGATTT	300
CTACTCCGCG	TANTGTTCCC	GCATCGCCTG	CGGGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANCTCAGGT	TTGCCGCTTT	GCGCACAGTG	GTCNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GCGCCGACGG	CGCCACNAT	AANAACGGGC	ACNACAATCG	480
CCGCCCCGGT	CACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCCCCANCG	CTCAANCCGT	540
CCCGAACGCC	TCNTCCGGCG	NACTTTTCTT	NNAWTAAGTG	CCGCTTCCGK	CCCTGGNGCA	600
WTAAATGGGA	AACCCTTNCC	CCACCTTGAA	GGGGTTGTTG	NATTTTTACT	GSTAACCCCG	660
AATTNTTCCG	GANTCGGTCTN	KCCGGGSTTT	YSTNTTCCCC	ACCTTNGNAN	GGGCCGGCCA	720
AGSTTTTCTT	SYTGAAGGGG	GAAACCCAAC	TTTNTYTYYN	AACCSNMNAA	MYMTTTYCSG	780
MNAASCCNKT	CCCCTTTAAC	CAMGSGGTN	AACCGKTMNG	NGGKTAAAAA	GGGSKNNKTG	840
NCCCCYMANG	GGGGGAAAAA	TSTKTCNNCG	GGGCCKAAAW	ACCMMMMYGN	GTGKKKNKSS	900
GCSAAATTTT	NMMRAACTKN	GGGGCCSSGA	NNTTTNAAAG	MSCCCCCSNN	GSTGKCCCN	960
NTTTCNNAA	WMKKGKNWNM	SNMNSCSNGG	GKYNSSGGSNN	NNAAGMGGGG		1010

(2) INFORMATION FOR SEQ ID NO:322:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1010 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:322:

AATTCGGCAC	GANGCGTGCC	GCTNAACACC	AGCCCCGCGC	TGCCAGATAT	CCCGGACTCG	60
GTAGTGCCGC	CGGTGGCGTC	GTTGCTCTCC	TGACGGGGCG	CGGCGACCAT	AAGGTCGCTM	120
ATGCCCAGGT	AGCGGCCCAG	GTGCATGGAG	TCGATGATGA	TGCGACTCTC	CAGCTCGCCG	180
ACCGGGAGCT	TGGCATCGGG	CCTGATCAGC	CAGGACGCGT	AGGACAAGTC	GATCGAATGC	240
ATAGTGGCCT	CCAGAGTGGC	CGTGCAMTTC	CNGCGTGCTC	CACGGCAAAT	GCCTTGATTT	300
CTACTCCGCG	TANTGTTCCC	GCATCGCCTG	CGGGATGAAT	GGGAACCGCA	SGATGGCGAC	360
GAACGGGTCT	GANCTCAGGT	TTGCCGCTTT	GCGCACAGTG	GTCNACANCC	GGTACTCGGC	420
ATANATCTGG	CCCNAAATCG	GCGCCGACGG	CGCCACNAT	AANAACGGGC	ACNACAATCG	480
CCGCCCCGGT	CACCCNAACA	ACANCTTGSC	ATCGGATTTT	GTCCCCANCG	CTCAANCCGT	540
CCCGAACGCC	TCNTCCGGCG	NACTTTTCTT	NNAWTAAGTG	CCGCTTCCGK	CCCTGGNGCA	600
WTAAATGGGA	AACCCTTNCC	CCACCTTGAA	GGGGTTGTTG	NATTTTTACT	GSTAACCCCG	660

AATTNTTCCG	GANTCGGTCN	KCCGGGSTTT	YSTNTTCCCC	ACCTTNGNAN	GGGCCGGCCA	720
AGSTTTTCTT	SYTGAAGGGG	GAAACCCAAC	TTTNTYTYYN	AACCSCMNAA	MYMTTTYCSG	780
MNAASCCNKT	CCCCTTTAAC	CAMGSGGTN	AACCGKTMNG	NGGKTAAAAA	GGGSKNNKTG	840
NCCCCYMANG	GGGGGAAAA	TSTKTCNNCG	GGGCCKAAAW	ACCMMMYGN	GTGKKKNKSS	900
GCSAAATTTT	NMMRAACTKN	GGGGCCSSGA	NNTTTNAAAG	MSCCCCCSNN	GSTGKCCCN	960
NTTTCNNAA	WMKKGKNWNM	SNMNSCSNGG	GKYNSSGGSNN	NNAAGMGGGG		1010

(2) INFORMATION FOR SEQ ID NO:323:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1092 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:323:

NGNGGGGWNS	NTCAYCAYCA	YCACSGGGYW	CWATTGCGGC	CGCAWCTTGT	MAASAGATCT	60
CGAAYTCGGC	AMGAGGGAMT	CKCTMGCNCC	GCTGTGCAAN	CCAATRAGGC	CTRATAATTY	120
CCACTCCACA	AAAAACCGTT	GTGTGTAYYT	SCCGRAATR	AAGGCGCCGG	TNTCAACWYC	180
GCCGGTKTTY	CCRATYCCCG	TKTTGTAMCT	GCCKGGGTSR	AAAYCCCCGG	TGTTGGAYCC	240
CCGGATTGAA	ACTGCCGGKT	TGAAACTGCC	GKTTTSGCSA	TCCGGKWATT	GAMSTCRCGG	300
ATTAAAAAAC	CGGKKTGGN	GCTGSNCGTG	CCAAATNCGR	AYCCRATAYC	CCATGGCCTG	360
KYCTYCTCK	YCGGTACCCA	AAYCTGGGTA	TCCTATACTG	GYCCCTAAAK	GCAAWYCKGG	420
GCTGYCMMTK	TTGCKGSGT	CCNAATTTAS	CACCASCGET	TCCTTCCATA	CCNAAACNCG	480
CKTGGGCWCC	AGMCCGRAAA	AAAKAATAAT	RAKAAKGGTG	CATNYCCAAA	ACCNCCGCCN	540
CCCNANTNCN	ATCCGNTNCC	MSCNCCCCCA	GCGGTNAAGK	TKSGGAAYTT	CTMMAACCCC	600
CAAANCCCCA	TAACNTNCGR	GAASAAACCC	CTYCNCGGGG	GYCNWNCAAA	ACASCNTTAT	660
FTGCTKSTTT	CGGGMWCCGT	GCCGCCNAAA	YCCCAAATA	CTTTYTGCGT	CCNAGAKAAA	720
ACCNCGGGCN	CCMCCCSNAA	NWTATYTCTT	KGGCAANCCC	CSAAACCTTR	TCMNACCNC	780
ATRMTCCTTT	CCCCVSCAAT	TGGYCGGRAT	NCGSNCCYTY	TCAAARKKSC	CAKWWNNGNG	840
GRRNNACCM	ACCCCAAGTY	CCMNAAAAATN	GKCCCCGCTC	CNAACACGNK	TYTCCSAAA	900
ASCCCWCCCC	CCCCCCCRAA	AACCCCCNA	RKANTNCCCA	AAAACNYNGK	GGCCCCCCCC	960
CAAACMAAAA	AMCCCCSGM	RMACSGGGGN	NMCCCCGKKK	KKTTTTCTTT	TKCCMRSCCC	1020
AAMGCAMWSY	KSKTNMAAAA	GGAAGRANCN	TYCCSANANM	TCCCNWRSW	CCGSWGMGNA	1080
GAASMCCCCC	CS					1092

(2) INFORMATION FOR SEQ ID NO:324:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:324:

GGGGGGGNNN	NATACATCWT	CYGTGYACCG	GGGMTCTAKT	GGCGGGCCGC	AATCTNGTCA	60
ASAGATCTCT	NAMTTGGGGC	ACAAAAACTW	GACAAASYMT	CGNGCNMTCC	GTGTCTNKA	120
TCGCAAAACG	NGTRACASAC	ASACACRTAT	GTGTGCCAC	CASCAAYTCK	TTGGGACCTC	180
GCTRACCGGY	TGCCCRNACG	CCACGYTGCS	CWTCTATCCC	RACGCCGGCC	ACGGGYGGGG	240

ATATTCCAGG	CACCACGCCC	AGTTTGGTGG	ACAATGCCCT	GGCAKTTTCC	TCRAANTTCG	300
TGAAACCGAA	TTCNSMTTGA	ACCNCCAARG	CCCCSNCCNR	AACARTTGGG	WTCCGCGGTT	360
CTCCCCACCG	KTTTCCGGGG	GTNTCGGCAN	AANCGCACCC	WTGGWTTCTM	TCNCCGCACC	420
GGGCGGACAA	NTCGGGTTGC	AATTTTGCR	AYCGGGGCCG	GGATTCCSCA	AACGGGTGCC	480
GAAACTGTTY	YCRAAMACCG	GGAKCCGCAA	TTTCCGGGCR	ANAAATTTCN	YCNCACTACT	540
GCTTRTACTT	CCCCGACCGT	AACMANTTTC	ATCGTCNTNN	CCTCTGCCCT	TGGGGCAGGG	600
CKAAAYACCG	CMTTKGGTTT	CGCAACCTGC	GGCCCAANTC	CCNAMCCRCA	CTTTCNATTT	660
GGNTCGAATT	SCCCCCCGGT	RANAACCCSC	NTGGCCNNYT	CGGASSAAAA	NGGGCCCTNT	720
KGGCNSCCCC	AGTAANACCC	TACCNAYTS	CAWTCTTTGC	CAAASSTKGG	ACGAANSKTG	780
GGNTTCCGGK	ATTTYTYTGS	GGNCNCCCTN	TATNGGSNTN	GGGCCCKCYN	NCSTKTGKCA	840
NASSKAYCCS	NGNKGGGGGT	ACCCCCCTMG	GGGGGTTTTT	NSSGCCCCCC	AWAYGNKSTG	900
GCCCCCNNGG	GGAACAATWT	MWWTMCNSGG	GGGAAWTTTT	NTSTGGAMCS	SGGACYCCCR	960
GGGGGKTTTT	TCCCCNCNSA	NNAWANGGGG	GGGGGANAYT	NTGNSGNGGG	KWNTTTTATTT	1020
YTYCYCCTM	TKACMSGGGG	GTTTKKAKNG	GGGGGAGAAA	ANAAAAAATA	RAKGGYKNTT	1080
TSKNCACTCT	GKWNWNWANR	NAGAGKTCCT	CKCKCCNCSG	SNTTTCTTTT	MGNSGSYGGG	1140
GNNGNNAAAA	ACNKSRRMAC	KCSYTYCCCG	CGYCTCCTCC	NCNGGGGYGS	NGSCGNSTYN	1200
GNNKGRKWT	TNTMGNCGTN	SCCTCCNCCC	GCKNKNTGTC	TMTCNMYGSG	C	1251

(2) INFORMATION FOR SEQ ID NO:325:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1099 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:325:

AAYTCGGCAC	MGAGTATCAC	CAAKCTGYGT	GGCCCAGCAA	AGTGGAGCTA	TTACTACCTG	60
TATGTGATCC	TCRACATCTY	CTCCCGCTAC	KTGGTCGGGT	GGATGGTGGC	CTCGKTKGAK	120
TCRAAGGTCT	TGGCCRAACG	GCTGATCGCG	CAAACCCTTG	CGCCCAGCAC	ATCAKCGCCG	180
AACAGCTGAC	CTGCMCGCCG	ACCGGGGGYC	GNCAATAACT	CCAAACCGGT	GGCMCTGCTG	240
CTGGCCNACY	CCGTGTCCCA	ANTCGAACTC	ASCCSGCNMA	CCAKMAACKA	NAACCGTTGT	300
CTGAAGCCCA	GTTCAAAAAC	CTCAAGTWCC	GGCCCRACCT	CCCGAAACGG	TNCGAGTCKA	360
TCRSAGGSGG	CCGGGTGCMC	TGCAACCGGT	TCTTCGGNTG	GTRCAMCCCN	AAAMCAAGCA	420
TTCCGGGMTC	CGMMTGCCCA	CGCCGCCAAS	TTTMTACGG	GCSGSCCNAT	CAAATTCGCC	480
GGGAACSGSN	CCMCKTCKNK	GGAMACGCCC	TWCCAAAACC	CYCGAACGGK	ATCCTTCKGY	540
NAACNCCCGA	RCNCCCKSKT	TCCGGGCTTC	NMSGCGAATA	CCCKNSCMNT	CCGAATCCAA	600
TTCCCMKYGG	CTTTTYYYCC	CCCCGGCCCC	AAAYNGGGYC	CCTASSNMKC	KNCCAMNANT	660
CCNWATCTGG	NGGTCCCNAN	KYYGGCGTTC	NMAATSAMNA	NMNRGGGTYT	TSCYACCMN	720
AACCGKNKNG	KCCCCMKCTK	MANAAKATT	RATCAMKWNG	GGNKCKCNCN	NAAMACCSCN	780
CNCYNWYTC	TMYCSSKWGC	GCSMYNANCA	SNGGGGAGGW	GGSGRMKMCT	CTMTCTCNCT	840
MGCGCCKNTN	TYCKSGAKAT	ACASMNKTCC	GCGCNGCCGN	MAAMANRAKA	CTAKCCGYGN	900
CCSNSTMNTN	CTSNNMKMNN	TCCWMWNATC	NTYYGKKCNN	KCTMKATNWC	CSCTSKCNCK	960
MRAMTCKTYG	SNMTCTCTCA	TCNCTCKKSC	SNMSKNTCKC	KSCNCCNCWN	CNKCNMKCWN	1020
GGNSTCRCCY	TCTMNNNTCS	AGCKCGSKNC	WACNCACACK	NGWCTYTTCC	WKNNMKCNKM	1080
TCKCKCACRG	MTMTCWCCS					1099

(2) INFORMATION FOR SEQ ID NO:326:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 296 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:326:

GNGNTATACA	TCWCTGTGYA	CCSAGGATCW	ANTGCGGCCG	MAAKCTWSTM	CASAGATCTC	60
AAAYTCTGCA	MGAGCGGCAC	AKAKYSTCGT	CCMRACCCGG	CAYACWCCWG	CNCGCCCCWT	120
CTTRGACCGG	GGCKATASMC	ACCGTTGGCC	CCGGCNCGCA	CCTACACCAC	CCACGCCGCC	180
AGCGCCCCCW	TRAMCAAACC	ACCCCGCKTT	TACCGCCCCG	GCCGCCGGGG	CCACCACCAG	240
CCCCACCGGC	ACCACCGGCG	CCGCCGTTGC	CAAAACAGGC	CCGCKTTTGC	CACCRA	296

(2) INFORMATION FOR SEQ ID NO:327:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:327:

NGNGSGNKMY	ATCATCWTTT	TGCACCSNGG	MTCWATTGCG	GCCGCAATCT	TSTMNASAGA	60
TCTCGAAYTC	GGCANGARCA	TCTGCGCGGN	GAATGTCCAA	AWGTCWKTA	CGGCMATCGG	120
TTTGCCGYCA	ACCACKCTRT	SCAKATGCGG	GCCAMWTYCA	AACCRATTAT	TTGGGYCGAG	180
AAAATTTMCG	CKTGTRASCA	ACCTGCAGCG	GGTCAASCAA	CAGCCTCTRA	ACCGTAAATY	240
CKTAGGTNKT	YCCGGCAACA	ASCYCRATAA	TSCGGCCCCG	AMCCACAAAA	CCTGANINGT	300
TNTTCNCRAA	NCCGGTYCCC	GRAGGGGTSA	ACTGCSGTAR	GCTTNTCWYC	NCCTTRACAT	360
TAAACCCCCC	CGGNTCWTCG	CCGCGCCCAA	ATYCYTGCCC	WTKGCNACCA	YCCCANCTTG	420
CSGTATGGTS	RAANCASTSG	GCRAACGGTM	MCCSTACCKC	TGGCTGATYC	KTCGGNTCCS	480
SNAATTCGGG	GATTTACGGS	CAMGGTTAAY	CCAGGYCCCC	TNTGCTCKY	CNACAACCSG	540
ATCMWCNCCG	TACCTKTAA	AATTCTTTGT	GGTGGAACCC	AWYCKAAAAA	NMTNTYCCCN	600
TCCAMGGGGG	CYCGGAAKKT	CNACNTGGKT	NACCCCTNCC	YTTGAASTTT	TCYTGNNCCC	660
GGCCCKAAAS	ANACCSGAKC	CCCGGAAYCS	WTAGGCTCN	TGCCCCSTTA	AATTKGNCYC	720
AATCCCKCAA	CGCTCCCCGG	GGTCSSCCMT	TAAAMTTCCC	CCCKSCASNG	GAATYCYKSG	780
GCWGTMAATW	CCNCCNTTTT	CYYGKNAAAC	SCCCCCWKGN	GSCTYCCCCN	SNTTSSGCCS	840
GGTTSGAMYC	AAAATWNGGG	MMCNRAGNCG	SGNAMCCSCN	GKKGGGSATW	TKAAYCYGG	900
GGGGGTCNYC	CCCCRCSNAA	AAGYGTKGGC	KCCSSSCTYC	CCMARTTTYT	CNGGMRCMAM	960
ACCANGGGNG	CTCCCGTNCW	WGGCTCCCSN	SNSMAMAAAN	NKCKCKKGGG	CKGARRNMNA	1020
MCTCSNGNGG	WTCCCKNKTC	NSCNSGNCGS	YGGNSASWCC	YNYCNCCACA	ANC	1073

(2) INFORMATION FOR SEQ ID NO:328:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1166 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:328:

CGCCCCGTTT	TTMMMTTCAY	TCATTACCCG	GGMTCTAGTG	CGGCCGCAAK	CTTGTCACACA	60
GATCTCGAAY	TCGGCAGMAS	ACAATSTCGG	GTKGGGCAAT	GTCNGGTGGG	GCAACTTTTGG	120
GCTCGGRAAT	YCGGGGTAA	CGCCGGGTCT	RATGGGTSTG	GGTAATATCG	GGTTTGGTAA	180
TGCCGGCAGC	TACAATTTTCG	GTTTGGCAAA	ATATGGGTGT	GGGCAATATN	GGGTYCGCTA	240
ACACCGSCAS	TGGRAATTTC	GGTATTSSGT	NACCGGTTRAY	AACTGACCG	GGTNCGGTGG	300
TTYCAATACC	GGTAACGGGA	ATGTSSGTTS	YYYACYCCGS	GSAACGGNWW	YTTNGKTCCT	360
TMMCNTSSM	CCKSAAMTSM	KMGSTSTYCT	MTYCNNGGAS	TAMTYNMCCC	CCGWAYCKSC	420
WAYCCCTCGT	CATYCCMCMC	SGSGYCCTCA	MNCCACCCTG	NGYYCCCTCC	MKMTTCYCAT	480
CMNTCCGGTW	CCTNTMMNCC	CSCNCRYCTC	AMCNCTKSGK	CACCNATMYC	CSACKCHTCT	540
MCYMCSCAKN	MTTCCCTCN	CCTYTNNCCA	MCMCSCTCTM	TCMAACTCKC	CCGGYCKCNC	600
MYCTCTCKCC	AYNMAACCKK	TYCYWCNWYC	YMYCKCKCAG	WYKNMCTCCW	ACTCTMYNTT	660
TCTCTCNKCC	CMKACCKNTT	CTCWCSCCCC	CCACAKAYMC	YAWCMTMTCC	MCTCKACSCC	720
CYYCNYYCCM	NMCWCMTWC	TWNAKCANCN	TTCTTCTCTC	MMYMTMAACKC	WCNNTCNCKK	780
SGACCTCTCT	ACTKMKCKKM	TCTCCTTMCK	CCYMWCNCTC	MKYNCCCTCC	NMTCTMCKYT	840
CCTCNMCMRY	CYYAKCAKC	NMCTCCCCAN	KMCAKCTKCT	CCCCCAKMKC	ACNCKCCCWC	900
CCTCCTATCC	WCTCTCWCTY	ATCTCKCTCW	CNYCMYMKMC	ACNCKCYAYT	CNACTMNMWN	960
CCANCNCTCT	CTNYCTCWCK	ACGTCKCKCK	CTMCKCNMYC	NRWCTYRCCT	CKKCCNCCRN	1020
CKNMCMKCTM	CTCTCCWMKM	TCCCWCCCAT	CTMMKSTCTC	WCNMTCCCT	CNKCCYNYNT	1080
KCYTYCCMYG	CTTCKNTCMT	MCCWCCYATC	TCTMKCCTCT	CWCACYMCAC	WMTTACWNCC	1140
ACTCTCTRCW	CKCKCMCCR	MTCTCB				1166

(2) INFORMATION FOR SEQ ID NO:329:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1230 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:329:

NGNGGNNNT	CWTACATCWN	TCTNCACCSG	NGMTCWATTG	CGCGCCGCAW	NCTTGTMNAS	60
AGAATCTCN	AACTCGGCAC	ANATGTCTTT	TSTMTAKTGT	GGCGGGGNGC	CACGCCKTAT	120
GTGYGCCTGG	GYTRACCCAA	CCCCGCGGCS	CGGGCCRACC	AGGCGGGGRA	TSCAGGCCGC	180
GGCGGCCGCG	GCGGYTATAT	RAAGCGCCGY	TTTTKTRATA	ACGGTSCCGC	CGCCGGGTRA	240
TTACGGGCAA	AACTCGGKTT	TTGGGTRTAT	AACGCTAATT	GCAACCAWTT	TTTYCGGGTC	300
AAAAACYCGG	CGWGCANATC	NCGGGYCNCT	RAGGCGCATT	YMCGCCAAAA	WTNTGGGCGC	360
AAAACCCCKT	TSYTATTTTN	TGGGCTATSC	GGYTGTCTCG	GCAAACGCTY	CCCGGGTTAA	420
TCCCKTCCGC	GGCGCCGCCN	AAAAACCACC	AATYCCGYTG	GGGGTGKYCC	CMCAGGCSGT	480
TGCTYCGNGY	CACCTGGCCA	AAAYCCCAWT	AKATTGGGTG	SCYKTSCTCG	TTSYTGCGCY	540
CAATTACCCC	CNCGGNAAAA	GRRAAANA	ATCNTCCNTT	TGCTCGGYCA	YCTTTMTTGG	600
SAAAAGGGGC	ATGGCSCGGT	TYTTTACCT	CAAYCCCCNA	NCANTWACCT	YTCCSCCCGG	660
GGGGNCANAA	CGSTTNGCTC	CGSGGNAKCC	TKGTMCCCGN	ATCNAAAGGC	CNGAATTTGG	720
TYYSSTYCNA	ATTWTWKKKY	CCCCWCNTTG	YAAAAAKCCA	AAASAKCCCK	YCNCAMMYKT	780
NGGGGTYSYG	GCCKNYCTTK	SNMTTAAACC	CYCCCCAAAA	YYNSGGGKKT	TCCGCYNSAT	840
KCCACCNCKK	GNGGGGGGNA	SAAAAAAAAY	TTTYCCSAAA	ATCCCACCYY	TCYKTKSTRY	900
AMACCCCTT	TYMKKAYTC	CKYSCNATTC	SGMTTCWAAA	TYCCGYGGCT	TNTTCCCCCK	960
CSGGNGCCCC	AAWTTTGKTT	YNCNANTTYC	CCCNAAAMNCM	AWTMGGGGKS	KCCATTCTGG	1020
SCYTMAANTA	AAANAANGGG	NKTTTYCTY	MANAAACACN	GTGKCNCCN	CNAAMAAASN	1080
AKMAAAKAGN	KKKMTKNNSA	AANCCNCCCC	CTSTYTNYTT	NKTNMNCCKC	CYGGKKNKGM	1140
SWSWYNTTCT	NCCCRCCCCC	YNYNKTGANA	AAMMNCYCCS	GGSTMCRNAN	ASNMTTCTCK	1200
STSTNGMGCC	KMBASNANAN	MCAMWKWYCC				1230

(2) INFORMATION FOR SEQ ID NO:330:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1022 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:330:

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NGNGGGGKNNNA  TMAYCWTCTC  ACSSGGTCTA  TGCGGCGCAW  CTMGTMAASA  GATCTCNAAY      60
TCGGGCAMNAN   GCATMTCMMC  CATATATAAC  CATTGCGTCS  GYWTGCAWCT  CRAAWCTGTC     120
CTTCSKGCCG    TTKTACRAAG  GTGGMWTGYT  CWTYCCTRAA  SCCCTCRATC  TCKTKTATYC     180
CTKGGGGCTYC   ACTTTAACSG  RATKSCTGCC  TTKTAYCATT  RATGCAAWTA  WTGGYCRAWT     240
KTTGCAGGCC    RACGGCWYCT  TTTYCCGCRA  GRACAAATNGA  TTGGAWYCGC  TYCGCRAGGC     300
CCGGCACCAR    ACCGGGCNCC  AAAGGYCCGC  GCAAWTSCCT  GGKTCAAAAA  TGGTGCAAAC     360
AAAMCNATCC    CCGGYTTRAC  CGCAGYTAMC  ACAAKAAAAT  TCCCWTGGCC  GCACCAWNNT     420
TTYCRATCWY    CWYCCCCACC  TTRAACCTGK  YTGCSGTATT  GCCTKCCTGC  CTCRACAGCM     480
YCNCCCKTCA    AACCTGCGGT  GACTCCAAC  GGTCTGGYCG  AASGGGGGYT  CAMCGGACAA     540
AACCCCRANNN   TCGCCAAATT  TTCNCCCCC  CYCGGGAAAN  GKTGATMTTC  TCSNAACCSA     600
CMGGGNNTW     NAACCTGAA   CSSSGSNKGA  MYNSCCSGGA  ANTTTTCCCT  TYNGGGCGRN     660
AAANCCTTTT    AAGGTACCCC  KGGNGGGGKG  CCCYYTTGGG  AAAACAACCC  CKATTGGKTT     720
TGGAAATNTT    TKCNCCCCCA  TTCNSGGGGG  GGGCCCCAMC  CMMCTTTTN  TCMSCNMTYY     780
YCYYGGAAT     TNYTCGCCSG  GAAYYCGGSM  CCKGYCTTAA  NCCCCMNWGG  GKYSTGSNAR     840
GGRATMAWWT    TYSTTTYMC   CCGGCNNCCC  CCCAKMCNT   KGNTGAACMA  AAKCSGGGG      900
GSCNMWYMY     YCNNGNRTT   TNRGSSNMT   TYMAAAMMAN  GGGGKYWTYY  CKCCNGSCNN     960
GKTYSGGGST    TTTCCNTTTS  GGGSSATYKG  MACCCCKTMT  AYCCGGGGGT  NTKTKYCCCC    1020
SC                                                     1022

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(2) INFORMATION FOR SEQ ID NO:331:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1083 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:331:

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NNCGNNKNTA    TAMAYCWYCT  NCACCSGGGA  TCWATTGCGG  CCGCAATCTT  STMAASAGAT      60
CTCKAAYTCG    GCAMGANCCG  CAWCTATTTG  KGTGRASCGC  ACCAGCGRGA  CCTCGCSGKT     120
CKTTYCTTGC    AGRGAGGCC  TGGGTGGCRC  CGGTGGCAAT  GCCAACCGCC  CCCCAAAACN     180
CCGCAAATMY    CRAAAAACAA  CCCSGGGGTA  GKTCCSGGCC  GCCAAATMAA  TAACCGTKTT     240
AACKCAGGCN    ACGGCCAAC  GGYCCCGCCC  AACCAAGCNA  CCTCCCCSCC  NATAGGYCCG     300
GTGGGGGGCTG   CCKTATYKCC  AASTCGTCAY  CTCNACGGGM  CGGYCCMCWT  TCCGCCTCAT     360
CCGTCTCTCC    TTMMATTTTC  CRTCCACYKG  GCGGGGAACY  TTTTNTYCN  CCTTGSCMAN     420
CACCNAAGGY    CNAAAATTNC  CCMTGCCKYG  SNNCAAAYGR  GATTGGGGTY  CGKKTNTNT      480
TCNMCCMAAC    CCCCNTTINA  CGCCCCMATC  CCYTWATACC  CCCWWMCMNS  ANGKTTGNSA     540
AAKTNNCCCC    AAATRCCAAA  MTTCTTCGCC  NTTMTWMCY   YYCCTTTCCC  CMCCCWNAAA     600
GGSCCRCCVY    TCGGGAANTY  TCCCNCAAA  AWTCAWCCM   TTTCCCNCCA  AGAAWTTCSG     660

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SACTCCTTTN	TTCNGGGNAM	ATANATYYTT	YCKTNGGGSK	TTCCGMTNCN	AMMAATNTCC	720.
RGGGKAAMCC	AGKNTNNTCC	YYYYCCCCAA	NNTYCCYKGG	RMCMYNNYCY	TTAAANRASR	780
SAACCCKSGG	GKCYNCNCSS	TARCCCCCAM	KAAAATTTCC	CCCSSKTTTC	TYYNKKMRW	840
CCCCCSAAM	ACTMTWAYTT	TCCCKCGNNN	TTTSYCKCS	KCAMWMMTG	KKNCTTTTTT	900
YCSCMATAMA	CTTNGGKCCT	NTCNYGSGCG	CMAAANAAGG	CGCGSTTCTN	TTCWMAMACA	960
YNTSGNMMMA	SAAKAKWATA	AWNNTTRKKYK	TKNNCCCNCC	CKCKCTTSNN	TNKCCMCSKS	1020
GGGKNWNKKR	GWCTCCWCNC	CKCCCNCKNK	CCKWATMCCC	CCCCSKCCGM	NCCMMNTTTKT	1080
CCC						1083

(2) INFORMATION FOR SEQ ID NO:332:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1069 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:332:

GGGGNNKYAT	MCAYCWTCTS	YACSGGGMNC	TATTGCGGCC	GCAWYTNCTM	GASAGATCTC	60
GAAYTCGGCA	MGAAAAAAGW	GATGTGCTGG	ACCTTMCCGC	GCGGGACGCR	ACCRACAAAG	120
RAASCGCGCC	ANAATATTGG	CCACAKTTGG	TCACATATTT	ACCCAATTMT	AYCAGGGAYT	180
MCCATTCCCKG	GGACCRACCG	CACAATCCCR	ATSKTGGTTT	GCRAACCCTR	ACCGTCCCCA	240
MYTYCGCCRA	STTGAACCAG	GGCRAAAAAA	CGGCCRAAWY	CTCGCCCTGA	NTCCCGCTCS	300
GCGCNAATAA	CTAGGCCCCAT	TKAACGGAAC	CGGNGGCCSC	NANTTGGCCA	ACAGGTCCCTR	360
ACAAAGGGGC	CCCASYCGG	CCGWTCCCW	TTYCACNCCC	TNKTCTCKTG	CCGAATYCGG	420
WTCCRATNYC	CCWTGGGCCT	TKTKYCKYC	KYCGGTNCCA	AWTCTNGGTA	TNCTATRGKG	480
TCCCCTAAAT	SCANATCTGG	GCKYCCATTT	NCTGGSNTTC	NATTTAMMAN	SRRCGGTTCT	540
TTCTTTCCRA	AACCGSNTGG	GCCCNMCCA	AAAAATGATN	ATAATAATGK	YGSCTTTCAA	600
ACCCCGCCCC	CCCATTCTRW	CSGTTCCANC	CCCCNGNGGT	TAAGKTGGGA	ATTTYTNAMC	660
YCNARGCCCT	NATTTSGGNA	AAAACCYCYC	GGGYCTCAAA	CMNYTTTTTT	GSKSSNTCGG	720
GCTCRTTCSC	CAAAACCCAA	ATTNTYNYGG	GGYCKTNAA	ACMCGGYCRC	RCCGGAAATT	780
TTTTTGTTTC	AACCCCAACC	TTTTCAASCC	NTTTYTYT	TRCCSSCSMN	TNGSSGGGNT	840
KSSCCNTTCY	RARKKCCNMN	GGGGGWYCYN	CCCCRMNTTT	CTTTTTTTTT	CCGTNNMAAM	900
NGKTCTTCA	AASMCCCCC	SCCCCNNSAA	ACCCCTNAR	GTTTTYCMMA	AANNWYNGN	960
KNCCCCCCCC	MMNAAAAAY	YCSCCGNRN	ACSMNGGGA	MCCCCCGGSN	NTTRKTTTTT	1020
TNCMSGYCCC	CSRMASYTTT	TKAMAMANRR	GAMNSMTTTY	TNNRGWNK		1069

(2) INFORMATION FOR SEQ ID NO:333:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:333:

NGNGGGGKWK	MATACATCWT	TCTTCACGSG	GGATCWATTG	CGGGCCGCAW	TCTNGTMCAA	60
SAGATCTCGA	TYTCGGGCAM	NACCCACCWC	TCCRAAAAAA	ACCCRAAWCT	CGGGSKCTYC	120
GARAAGTGTT	GCCCGCKTTR	AATTTAACAA	ATTCACTGTC	ANAGTGTCAC	GGCKTTACWT	180

YCCCGGCAAA	GGGGCCACAA	CCTGCAGRGA	SCACYCRATG	GKTGYTGKTS	CNCGGGCGGG	240.
CCGGKTNAAG	GGACCTGCCT	GGGKTGCS	TMCAANATC	WYCCGCGGGT	YCGCTGGRAT	300
MCNCAGGGGT	GTCAAAAAAC	CGCAAACAGG	CACSCCANCC	NTTTACGGGS	CTTAAAAANGA	360
AAAAGGGCTG	ATGCCCCCAA	GGGGGCCCCG	NCCCAACCTT	CCGTTGGTCA	ACAACCCCGT	420
CTCTCKTGCC	RAATCCGRWT	CCRATNYCNC	CWTGGCCTTK	TCKYCTYCTY	CGGTACCCAA	480
ATCTGGGTAT	CCTATASTGT	CCCCTAAWTT	CCAAATCTGG	GCTGTCCATT	TSCTTGGCNT	540
TCCAAATTTA	CCANCAACGG	TTTCTTNCAT	NCCAAAAACC	GNTKGGCKCC	NRACCCRAAA	600
AAATGAATAA	TAATAANNGG	KCNNTTYCNA	ACCNCCCCCC	CCCNATTCCA	TYSNGTTCCA	660
NMNCCCCCAG	NGGKTAGGTK	GGGAAANYYC	TCMACCYCA	ANCCCTWARS	TTTTNGRAAT	720
KAAACCCTYC	YCNGGGTCWW	TYMAAAAAMA	NTTATTTGGN	NGNTTTCGGG	MWNCKRKNST	780
SCCAAAATCC	MAAATANTTT	YTTGGTYCNA	TWAAAAAMCG	YGNCNMNCCC	GGAAAAWTTT	840
TTNTGKTTSA	ACCCCAAAAC	YTTTTCMNAA	NCSSKTTTTY	CYTTCCCCCC	AMNWTGGGYS	900
GGGNATKGYG	SCYTNTCTTA	TKTKYTYMTW	CMGGGGGGNN	MKMTCMCCCC	CCMTTTYCY	960
NYWRTTTTTN	KCCCCKTNMR	NNRAANNGGN	YTCSYNANAA	AAGCNCCCCC	SCCKNCCCNA	1020
AAAAWCCCCN	NNNARAKTNT	TTMKANNRMN	SCKCNKNGKY	YCCCCCCCWC	YNMNNAAAAA	1080
AATMYCCNCC	RASANMCASM	NMGGRGNRSC	CCCCCCCSTT	NNNNTMTTNT	TTTTTTCRA	1140
GAGCKCCSCG	MNNANMKNC	CTTTTTKNC	NNGNNGNGNN	GGNGMNCKCC	CCNAGAAMWK	1200
CTKSTCCCKS						1210

(2) INFORMATION FOR SEQ ID NO:334:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1105 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:334:

NGSSSNGNNA	TMCATCWYCT	GYACSGGGMT	CWATTGCGGC	CGCAACTNGT	MAASAGATCT	60
CGAAYTCGGC	AAKANACACC	ACCGCCGTGT	MTATACACCG	CAAATGTTCT	GKTGCGCAAA	120
ACCGAGACGC	GCCGGCCGCG	GGGYTCCAAC	GCKTTACYTR	ACCCGCCAGY	TCAGTGTTTRA	180
AACCGGTGYT	RAGGGCCGCA	CCCAACWTAA	ACGCTTTAKC	CAAGRAWYTG	GKTGGCCCCG	240
AGCCACCTGY	TGTGGYTGCC	CTCWYCGGTG	GTAGCGCCGG	TTANCGCCGG	TTGCGCGYTC	300
AMCASCSCGC	CGGTRATCCC	AKCNWTCCCC	CGGCCMRACC	CACCGGGCAC	TTTGRACGGT	360
GCCGCCAATT	CAAAKYCYCT	GRWTCCTTCM	AAACACCACR	AAGGCCACCM	CCMSCACCNA	420
ATMGGGRACT	TTAAGGCCCA	GGCAAAACCT	NTRAKCNCCT	CCCGGGCRAA	GGTCCSGCAA	480
SCRATCCMAA	AAAAKCKNAT	TTCCCCCAGC	AKCAACCCAA	MMCGSTTTGC	TGCTTCCGGA	540
TTCGAAMCCA	ATTMCWGGKT	NCNWGGGAAA	AACASCNNCC	NWTAKCCMGG	CCCMCGGGCA	600
ATTTCSGRAA	SAACCCCTNY	CCCGGGTTTT	YCCTGCTCMG	GCCCAANACC	CCCGGGAATC	660
AAAAASGGTC	GGNCAAANGG	GCMAAACCCS	SACCCMACTT	WTTCCRCTTN	GGGGGGSCWN	720
CKNGTTTTAA	AWKSCCTCY	CTSCCCAAAY	TCGGKCMAAA	NNGRKTGGGK	TTNGGCNACC	780
NTTTCGCGKC	CCGGGKGK	WGKYCTMNMA	CSTTTNTTTT	SCCCCYKAAA	NYSCCCCCCC	840
CGSSSCCCCG	CCCGGGGGGA	NNTTTTTAMA	GKTTYCCCCCT	CCCCAMAAAA	ANACCCCN	900
CCSGGSCCCT	TTKRWAAAMN	KCTSCCCNG	GNGGGGKCM	GGKTTATTMT	NNNCCSCCCC	960
TCCGCGSAAA	AAATAKMTT	SYCCCCCNC	CTCKNCNKR	GKAMSMSCGC	TCCCYCTCNC	1020
GCNKNTWAAN	ARSNCCKNN	CCNCYKCCGS	NSNGKCNWCD	NCCSTSSNCT	NKGCNCKNCN	1080
KAAANAAYNC	NGSMSTSSMN	CNKCC				1105

(2) INFORMATION FOR SEQ ID NO:335:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 936 base pairs

- (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:335:

NGSNSNKNMNM	TAMAYCWYYC	TSCACSNNGA	ACWANTGCGG	CCRMAWCTNS	TMKASAGATC	60
TMGAAYTCGG	CAAGAGCGGC	AAGAGTGTGT	GCATCTGGTC	ANAGTSTMTA	CRCGGTGCCG	120
CSGGTGKGT	GASCACMCAT	NTGCGRACAC	CAAACCCCKTC	GCGGGYCACC	GGCKTCGCCT	180
GCAAAYCCT	CCAGGCCACC	TCRAACAAYW	YCTYCTGCAA	CGCARGCCGT	TYCGCGGCCG	240
RATCCTGGKT	CASYCGCK	TGCGGTGCCC	AAGKTACTGG	CSCAYCAAAA	CCGCTCCGGG	300
RAACRAACKT	AAWTYTGCCG	AATTTCTNTC	CCCTGCGCCT	TGATAAATTT	NTNAAGCCAC	360
CGCAAMCCTY	CGGGCKTCTC	CTCKTGCCRA	ATYCGRWTCC	RATAYCGCCA	TGGCCTNKTC	420
KYCTYCKYCS	GTACCCAAAT	CTTGGGTATC	CTATANTKYC	CCWAAANRCA	AWTCTGGGCK	480
KTCCATKTSC	TGGSKTCCRA	ATTTAMMACA	NCGGTTTCTT	TCWTACCAAA	AACCSNTGGG	540
CCCCRACCRA	AAAAGATAA	TAATAAKGTG	CWWWCAAAAC	CCCGCCCCCC	RRTTCAAYCG	600
GTCCARCACC	CCANGNGGTN	AGGTNGGAAT	TYTMAACCCC	CAGCCCATAA	SNTTNSGNAA	660
AAACCCCCCN	GGGYMYCAA	AMMCTTTTGT	GGGMTTCSGS	CCATKGYKCC	AAAACCAAAA	720
TMTTTCYGGT	CRWAAAAACC	GGCCCNCCCG	NAAATTTTTT	GKCAACCCCA	AACCTTTMAM	780
CCNNNTTCYY	YCCNSACAA	TNGGSGGNKN	NGSSCNTTYT	TWTTTTYYNNA	GGGGGGRRWC	840
SNCCCCNAAN	YYCNAANKG	NKCCCGSNMA	AAAGAGANTT	YCMKAAAAAC	CCCCNCNCCC	900
NAAAYACCCC	MAAAKWTTTCM	AAASMSCNNG	YCCCCC			936

(2) INFORMATION FOR SEQ ID NO:336:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1042 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:336:

NNNGNKNNNY	ATMMAYTCWY	YCTSCACCSG	GGNNWCWATT	GCGGCCRMAW	KCTTGTMAAS	60
AGATCTMNAA	YTCGGCACAG	ASSSGCACAG	ASCCGCGGCG	CTATYCMYCC	GYTGCTCATG	120
CTCAACACGC	TCKTCGGCGW	GRATAATGGC	NCGCCGCGCG	CGCCAACACG	YTCAAYTGCT	180
TCGCCAACGC	CATATNTCAA	CAAGGTRATA	AAASCAAAAC	CGCSCGCCGY	GCCCTTGGGC	240
SCGGRAASCG	GTGCCAACCC	RAAACNCKTT	GGGCACYCGG	KTSRACTTTA	AASGGTAATC	300
TCKTCCTCCT	GGGCTATGGT	GCGCCACAAA	CCTSYTGGCG	WGGGTCTGGC	CCTGGGYCAC	360
CGYCRCNTTT	TATNTNTCK	YCTACACNCT	TKGGTYCAAC	CAACCCACTT	CACMAAATTG	420
TTTTGGGKTG	GGGSSGCCGG	YTGTNNCCGK	TAATAATCSG	NTGKTCSGCC	MYCACC GGWA	480
CCATANCCTG	GCCGGCSCTG	GCAAATTTCC	SAAATCATYT	CCTTCTGRAC	CCCCACAMRC	540
CTNSAAATCC	GRATCAATNC	CCCNKGGCTT	NTCYCTCTCN	GTRCCCAATY	TGGTTTCTAT	600
RKTNCCCYAA	TSCAATTGGS	TTYCCRTTSC	YGSTTCCAAN	TTNACAAMAS	GGTTTTYTCMT	660
ACCAAAACCC	NTGGSCCNNA	CMNAAAANKA	RAAAANAKGG	KCTTTYAAAC	CCCCCCCTAT	720
TCAWYCGGTN	CMRNWCCCCG	NGKAAGGKGN	GAAAYTTHRA	CCCAANCCMT	ARSTTSGNAK	780
AAACCCYYCG	GGGTSMCAAA	MKNTWTTSSC	CTTCGGMCTT	YCCAAATMSA	AAATYYTCKK	840
KRMNAAAAMC	YGNCCCCSAA	ANATTTTTGT	NAAMCCCKMA	YYTRTTWMCC	WTTTTCCYCC	900
CCMCNNSNSG	GNTNCCCTTY	TYATTTCYMM	MCRNNSGACN	CCCCMNTYTT	TWTTCKWCN	960
MMARGSNNTY	RGRMMNMNCC	CCNCCCNNAK	MTCCNCAAAK	NTTTNAACNN	NNKYCKCCCC	1020
CCCMWMNKNC	CCCCMNCMTT	TM				1042

(2) INFORMATION FOR SEQ ID NO:337:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1073 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:337:

```

NNSGSGMKKK ATAMATCWCT CTSYACCSNG GMTCWATTGC GGCCGMAWTC TNGTMAASAG      60
ATCTCGAAYT CGGCAAANAK ACGCMAYGTC AAGTGTRAYY CGGTACACATA TCMTCGCGNG      120
TCAACMCCAA AGCCGNGTCA CCGYCTCCCT GGGGCGCCAC CCCCATCGGT RATGCAACYT      180
CGCGCGCCAC CGYCAAAAGG KTCWTTTRAGG CGCTAAAGGT CAMCAATTCC TRAGGTMCN      240
CACCGTTNTT TGGCCCGCCC RAWTYCTRAC CCGCAATWTC GGTAATCGGR AATTGGGCGW      300
YCGGCTTGGG CAATAAGKTN TTGGGCAACG GCGGRWTCYC NCTGGCCGRA ATTCNCNCAT      360
TCCKTTAACG GKTGRACCGT TTYCCCGGYT GCCGTAAYTG YTYCNTGGGC GCCYTCGGCC      420
CRNAGCASY CRCTAACGGY CMCCAGGCAA TACCKTTGGC TTTRAACCAC CGGRATNAAY      480
TGKTACCCAC YTCAASSGTS CTGRANTTRK TNTCNTGRAA AANMCCACCN AACCCGGNTT      540
RATCTGCTTC MTCANCWTTT SCCGGGTCTT GCCGTTTTGR AAYCTTNATC CMTYCAAAAG      600
GTTTAMTTTC CCAANRAATT CGGYTTGCCA CCTTGGCCGS GGCTGGTTM CGMWCCPTRR      660
AMATCCNCCS GCGGGSAAAN AMTTSGGNTT SGSCCGGTCC CCCGNAATAT YCNTGGNCCT      720
GNAAATTGSS GGGATCCCN GSGNAYCCGG CCWTKGGGGK TNCCCAGTTG GWACAATTYC      780
WKCCGTTCCA AACCCGGGNC CGGGGGGTGG GSCCCTTTT CCTMYNNAAA AAGKGTGTGN      840
NYYTTTTCCG CNRAANTTCA CCSKCNKTNT GGNCCNAACY YYCAANTTC CANACCTTTA      900
AASAAANCYK YGKTYCCCC TTTTMCSSGS SANCCCCCM NMSSKNCGGG AAAAAAGNK      960
TYNGCCTTAN CNSNKTKTNT TNKTYCCCC NMWNNNSNMCY NCBKKCNKRY NGNSNMNCCT      1020
MKYSKCNWNN SNNNNNKCNG GSNCSGMKYM CMNNCNGMYK NGNKSNNCCC MSC      1073

```

(2) INFORMATION FOR SEQ ID NO:338:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:338:

```

GNSNGNKNTN TMCAVCWYCT SCACSGGGTC TATTGCGGCC GCAATYTNGT CKASAGATCT      60
CGATYTCGGC AMNANAARTG TCGTCGTCAA TTTCAGKKTG GTCKTCAAAY GGGCCAGGCC      120
GNGACCRACA CCCTGNGTCA CCCAAAANAC CAACAGCWTC AAATWTCAAG GCCRAGGCSC      180
TRTCAATYCC CRASAKTTA ACCGTKTCCW TCRAAGGTGC CRAACCAGGC ACCCAGYTCA      240
CCGCCSGGCA AWTGCGGCTG CCGGCCGNTN TCAGCCTGAT TYCTGACCCT RWTCTGTSGG      300
TGGYCAMCNT GGTGAAGGCC CWWCCGCCNA AGAACTGGAG GGCRAATTCC CAGGANCCNA      360
GRAACCCNAG GAACCCGCGG TAKAANCCGG CRAAACCRAG GCCGYTGGCN ATTCNATTA      420
NAMSGGTTTG CRACNTGGCC RAACCGTTTT CTTGGTCGGC CTCGGCAACC CTGGACCANT      480
TACCCCKTNC CCGGNMCMAC CYCGGGTNTT TGKYCCCAAT NTGCYCCCGC GNRANTNGGC      540
CNAATTCCAG GGCNCCANCT TTCCGGCCCN AATTCCCYTG GTTAATCACC GGCNCNCCT      600
GGTTTTGGGC AACCCCNYS CTTMTTTAAA CATTCGSCC CAAATGGGNC STTGGSAAT      660

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TCTNTYCGGT	GGGGCSGGCR	ANMYTTCTCT	YCCNAASAN	CTTAMYCCAN	TTCGSSNTCC	720
CGGKCAAAWS	NGGGGGGNA	AAGGGCCCC	CGGNTSCKCC	GGGGKKGCCC	CYGGKTTCAA	780
AANTTTCSGG	GKTSTMSCGG	NVTCSCCCCC	CSGCCAAGRA	CCGNGGTTTT	TTTTTGAACC	840
KCMANTCSSA	AMCCGCCSSC	CCCMAGGS	GCTNAAWGR	RAYTTNKSCC	CNNAAACSGG	900
CCCCCAKYTY	SGGKTTCNMC	CNCCSGKKGT	CCMTSTTTMM	MRCCCTTTGN	GNKTTTTTTAN	960
MGSCCTTNMC	CACCCCYCK	GGGKCSMNNA	GAAKTMYWKC	CNGGGGNAN	RSCCCCCNN	1020
GSKGGGGKG	MGAGYSCCKT	CTKGCNCNN	YKNTTCCCC	C		1061

(2) INFORMATION FOR SEQ ID NO:339:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 986 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:339:

GNNGNNNKWN	ATMCAYCWYY	CTSCACCSGG	GMTCWATTGC	GGCCGCAWKY	TNGTMAASAG	60
ATCTMGAAYT	CGGCACANAG	CGGCACAGAG	TGTGTGCATC	TGTGTCANAG	CTGTCAACGC	120
GGTGCCGCSG	GTGGTRASCA	CMCATTGCGR	AACACCAAAC	CCGTCCGCGG	GYCACCGGCK	180
TCGCCTGCAA	AAVCCTCCAG	GCCACCYCRA	AACAAYWYCT	CCTGCAACSC	ARSCCGTTYC	240
GCGGCCGRAT	CCTGGKYCAS	YTCGCCKTGC	GGTGCGCCAA	GGTACTGGCS	CWYCRANACC	300
GCTYCGGGRA	ACCNAACGTA	AATCTTGCCN	AATTTGCNTT	CCCCCTSCCC	TTRATNAATT	360
TGTTAAACCA	CGAAACCTY	CGGGCKTCTC	CTCKTGCCRA	WTCCGRWTCC	RATNYCGCCA	420
TGGCCTNKTC	KYCTYCKYCS	GTMCCCAAAT	CTTGGTATCC	TATATTGTCC	CTAAATGCAA	480
ATCTKGGCTG	TCCATNTGCT	GGCGTTCAAA	TTWAMANCAG	NGGTTTCTTY	CTTCCNAAAC	540
CCSTTGCCCC	CAAACCNAAA	AATGATNATA	ATAATGGTGC	TNTCAAACCC	CGCNCCTATY	600
CNATCSGKCC	AMMCCCCRGN	GGKTANKKGG	GNAATTCTMM	AACCCCAAGC	CATAASNTTG	660
SGANAAACCY	NCNCMGGYCA	CCAAAACANY	NTTNTTGGNY	SSNTTCGGMN	YCATGGCTNN	720
CMAAAACCCA	AATACTNYYG	GGYCCAATAA	AAMMMSGGYC	SAMCCGGAAG	WTTTTYTTGN	780
KYNAAACCN	AAKCTTTTTT	CNAACCCDAN	WNTYCCTNCC	RCRCMANTGG	CNSGGARTKT	840
SSSCTTNCCA	ATGKYCCMAA	AGNGGGRANA	CCARCCCCAA	TTCTTNNNTN	KNKNCCCNST	900
TRNAAAAGGG	GKNTYNCMAA	AASCNCNCNC	NCNCTCCCAA	AAKAMCCCCN	AAAGAKNTCN	960
NAANASKYSN	NNNSCCCCCC	CCMMMN				986

(2) INFORMATION FOR SEQ ID NO:340:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1074 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:340:

NGNGGGNKRN	ATMMAYCWCT	SATYYACCSN	GGMMNWATTG	CGGCCRMATW	CTNGTMKASA	60
GATCTMGAAA	YTCGGCAAAG	AGYATKCTCG	GGGGCCAGAT	TTNTGGCCCG	CAACCGCCGC	120
ACTTTGCAYW	TCAACAKTCC	SGGTGCCCCA	AAAAAWTCWT	ACCCCATMC	TYCKTGCSAM	180
ASYTGCGCCC	RATTRAACAC	CCGGCCGGCW	TGCTGCGCCA	GGTATTYCAS	CAGYTCAAAY	240
YCTTTKTAGK	TAAAATCCAG	CSGGCGGCCA	CNCAGCCGGG	CGGKTAGGT	GCCTYCRTCA	300

ATMACCAGCY	CGCCAGGGY	CACCTTGCCC	AAAAYCTCCT	GGGTCAGCCA	AATTYCCGCS	360
CCGGCCAACM	ACCANCCGCA	TYCTGGCNTC	AATCYCACCG	GGCCCGGTGY	TAAAMMANMA	420
GRATCTCKTC	MANCCCCCAN	TCAGCSYTNA	CNGCMACAGC	CCGCCTTCTT	CAMACCGCCA	480
RTACCGGGWT	CAACCGGCCS	GTCAAACCTCA	ACAGGCGGNC	AGGCCTCCCC	CGGANSAAAG	540
GTCTTACSCC	NNYAANAAAA	MAAGNTCTGT	TTTCCCCCTC	CASAASNAAA	AANCCCCSGC	600
CGGGCCTTCN	NMMGGGTTTG	GGGMANANAA	AARCNCCGNN	GGAACGNATC	CGAAAMCTCC	660
CAAGTCNCMT	TWAWAACYCN	NNAACCCCCC	ANTTTTGGGA	AAGGNTCCCC	NTTMYCCCCC	720
TTTTASGKTS	GGGMMYYCTY	TAAAAAATT	CCCCAAAAAG	CCCCGGGAAG	GGTCMAMCTG	780
GGNAAATTTT	CAAMCCNWGK	TTNTTYNGGT	TMCGGGGGRA	AATTYCNCTC	CCYNNNGGG	840
CSSGSNNNAT	TAYGGMSNMT	TTTNNAAWTM	NSGKKTSAAM	YNNKCCMNNN	SNNMSMANNK	900
TNAMCKCCCN	CCTCNGNGKY	CSCYNCCCSG	GNAGNGGRAS	MKCCNANMAA	AYASGNTTNK	960
CGGAAMMCNN	AATKGNNNSC	CCGGASMCMN	NNNMAAATMT	CNCNKCSNN	AANRGMACRN	1020
CCCNSSNGMN	RRGAARMTNY	YCCCCGSKM	GKGNKAAAAG	GKYCCCCCM	AAAG	1074

(2) INFORMATION FOR SEQ ID NO:341:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:341:

NGNGNCNKNT	MTACATCWTT	CTGCACCSGG	GNTCWANTGC	GGCCGCAWKY	TTGTGASAG	60
ATCTCGAAYT	CGGCAMGAGG	ACWCTCGCRA	CGCCCCACA	NACTCTGGCG	TGTGTACCCC	120
ATTGNGCGCK	TCACGCGCCC	AYTGANCCAK	TNCACTGGGG	TGCCGTYCGC	CKTGC CGGC	180
GGCCTCACGG	CKCTSCWTCT	RAAGGCWTGG	CGCACCGCAT	TCGGTTTTCT	RAACGCTGGG	240
AAAWTGGCCA	GCCGTCTGGC	TCATGGGNTC	TACGCAACGC	CNGCCCCCAA	CRCTTTCTTA	300
AATCCGGYCC	NTCCTGANCS	CTTTGAAYCC	CGGGGSAAGA	ACTGGTTGCS	CNCGAYCTGC	360
TCGAACCTTRK	TCNAAATCCC	GCANAKTGTT	TCNTAMGYCC	CNCCGGAAGG	NGAACCTACT	420
TTCNGGWANG	TCGGCNKCCG	GCGCTTATCA	STCCTGATCA	ACGGGGAACT	GGYKNNSTTG	480
KGGGAAAAAG	RRCCTCAATG	MTYGGTCKC	GCTGCGKANC	CGCSCCTGK	GYCGCNAATG	540
GAAGGCSMAG	GGTTAANGCC	MTYCNYYCCR	RSCCGTSTGA	SGKWTTYCGG	MGGANKAMNN	600
NNKMAMWTTK	TCRNGGGCCW	ATSTSCCGGG	CKSTTAKAGA	ANACTYCKW	WCCGTNTYSC	660
SAAAGNTKCS	GCGMGTTTTS	SCCKMGANGN	YCTGATTTSA	GGGGGKYKCC	CCCGGGGTYC	720
CGAAWKWRKY	CCYAGGGGGM	GNYSAGCSC	CGMNNATNAG	AGNAAGGKTT	RYGSTSKNCC	780
TYTNKGGACC	WSCNNCWSAK	ANAACNNKKT	TGCSCCNTMS	AGNKTNKGRT	YCCNKTSTTC	840
TAAGAGGAGC	TATKMKCGCC	CKTGGANGMM	GAGWGMGCGC	KYCCCSNKRT	TCNTNGWAAA	900
TATKSAGMGG	TKCCGMAGMK	CCSCGTTTKT	TKTGANAAMN	MSMRKNKKTG	CGMGYTCTSC	960
GGGNTTTGTA	GAGTAKTCGS	CSCSSMWGAC	WCSGMCMGNG	AGKNKTNNTS	YANTGARGCY	1020
MNNSKTMKMT	MSCSCGCGNA	GGAGNGCCCC	CSANGMSTGY	NKGGNMSSNG	ARAKGATGGS	1080
GGCCNCGMNN	MGMGGANMGA	SANNGMGMR	GGGGGKTGKC	TCKCSCCGNS	CSANGRAGAA	1140
GKTCNGSCGC	CGMGGKYGKT	KTKTKNKTGG	YSTCMSSMM	NAGAAAAGAG	AGGGC	1195

(2) INFORMATION FOR SEQ ID NO:342:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3572 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:342:

CCATCTGATC	GTTGGCAACC	AGCATCGCAG	TGGGAACGAT	GCCCTCATTC	AGCATTTGCA	60
TGGTTTGTG	AAAACCGGAC	ATGGCACTCC	AGTCGCCTTC	CCGTTCCGCT	ATCGGCTGAA	120
TTTGATTGCG	AGTGAGATAT	TTATGCCAGC	CAGCCAGACG	CAGACGCGCC	GAGACAGAAC	180
TTAATGGGCC	CGCTAACAGC	GCGATTTGCT	GGTGACCCAA	TGCGACCAGA	TGCTCCACGC	240
CCAGTCGCGT	ACCGTCTTCA	TGGGAGAAAA	TAATACTGTT	GATGGGTGTC	TGGTCAGAGA	300
CATCAAGAAA	TAACGCCGGA	ACATTAGTGC	AGGCAGCTTC	CACAGCAATG	GCATCCTGGT	360
CATCCAGCGG	ATAGTTAATG	ATCAGCCCAC	TGACGCGTTG	CGCGAGAAGA	TTGTGCACCG	420
CCGCTTTTACA	GGCTTCGACG	CCGCTTCGTT	CTACCATCGA	CACCACCACG	CTGGCACCCA	480
GTTGATCGGC	GCGAGATTTA	ATCGCCGCGA	CAATTTCGCG	CGGCGCGTGC	AGGGCCAGAC	540
TGGAGGTGGC	AACGCCAATC	AGCAACGACT	GTTTGCCCGC	CAGTTGTTGT	GCCACGCGGT	600
TGGGAATGTA	ATTCAGCTCC	GCCATCGCCG	CTTCCACTTT	TTCCCGCGTT	TTCGCAGAAA	660
CGTGGCTGGC	CTGGTTCACC	ACGCGGGAAA	CGTCTGTATA	AGAGACACCG	GCATACTCTG	720
CGACATCGTA	TAACGTTACT	GGTTTCACAT	TCACCACCCT	GAATTGACTC	TCTTCCGGGC	780
GCTATCATGC	CATACGCGA	AAGGTTTTGC	GCCATTCGAT	GGTGTCGGG	ATCTCGACGC	840
TCTCCCTTAT	GCGACTCCTG	CATTAGGAAG	CAGCCCAGTA	GTAGGTTGAG	GCCGTTGAGC	900
ACCGCCGCGC	CAAGGAATGG	TGCATGCAAG	GAGATGGCGC	CCAACAGTCC	CCCGGCCACG	960
GGGCTTGCCA	CCATACCCAC	GCCGAAACAA	GCGCTCATGA	GCCGAAGTG	GCGAGCCCGA	1020
TCTTCCCCAT	CGGTGATGTC	GGCGATATAG	GCGCCAGCAA	CCGCACCTGT	GGCGCCGGTG	1080
ATGCCGGCCA	CGATGCGTCC	GGCGTAGAGG	ATCGAGATCT	CGATCCCGCG	AAATTAATAC	1140
GACTCACTAT	AGGGGAATTG	TGAGCGGATA	ACAATTCCCC	TCTAGAAATA	ATTTTGTTTA	1200
ACTTTAAGAA	GGAGATATAC	ATATGGGCCA	TCATCATCAT	CATCACGTGA	TCGTGATCAT	1260
CGGGACCAGC	CCCACATCCT	GGGAACAGGC	GGCGGCGGAG	GCGGTCCAGC	GGGCGCGGGA	1320
TAGCGTCGAT	GACATCCGCG	TCGCTCGGGT	CATTGAGCAG	GACATGGCCG	TGGACAGCGC	1380
CGGCAAGATC	ACCTACCGCA	TCAAGCTCGA	AGTGTGCTTC	AAGATGAGGC	CGGCGCAACC	1440
GAGGGGCTCG	AAACCACCGA	GCGGTTGCGC	TGAAACGGGC	GCCGGCGCCG	GTACTGTTCG	1500
GACTACCCCC	GCGTCGTCGC	CGGTGACGTT	GGCGGAGACC	GGTAGCACGC	TGCTCTACCC	1560
GCTGTTCAAC	CTGTGGGGTC	CGGCCCTTCA	CGAGAGGTAT	CCGAACGTCA	CGATCACCGC	1620
TCAGGGCACC	GGTTCTGGTG	CCGGGATCGC	GCAGGCCGCC	GCCGGGACGG	TCAACATTGG	1680
GGCCTCCGAC	GCCTATCTGT	CGGAAGGTGA	TATGGCCGCG	CACAAGGGGC	TGATGAACAT	1740
CGCGCTAGCC	ATCTCCGCTC	AGCAGGTCAA	CTACAACCTG	CCCGGAGTGA	GCGAGCACTT	1800
CAAGCTGAAC	GGAAAAGTCC	TGGCGGCCAT	GTACCAGGGC	ACCATCAAAA	CCTGGGACGA	1860
CCCGCAGATC	GCTGCGCTCA	ACCCCGCGGT	GAACCTGCCC	GGCACC GCGG	TAGTTCCGCT	1920
GCACCGCTCC	GACGGGTCCG	GTGACACCTT	CTTGTTTACC	CAGTACCTGT	CCAAGCAAGA	1980
TCCCGAGGGC	TGGGGCAAGT	CGCCCGGCTT	CGGCACCACC	GTGACTTCC	CGGCGGTGCC	2040
GGGTGCGCTG	GGTGAGAACG	GCAACGGCGG	CATGGTGACC	GGTTGCGCCG	AGACACCGGG	2100
CTGCGTGGCC	TATATCGGCA	TCAGCTTCCT	CGACCAGGCC	AGTCAACGGG	GACTCGGCGA	2160
GGCCCAACTA	GGCAATAGCT	CTGGCAATTT	CTTGTTGCCC	GACGCGCAAA	GCATTCAGGC	2220
CGCGGCGGCT	GGCTTCGCAT	CGAAAACCCC	GGCGAACCAG	GCGATTTCTGA	TGATCGACGG	2280
GCCCGCCCCG	GACGGGTACC	CGATCATCAA	CTACGAGTAC	GCCATCGTCA	ACAACCGGCA	2340
AAAGGACGCC	GCCACCGCGC	AGACCTTGCA	GGCATTTCTG	CACTGGGCGA	TCACCGACGG	2400
CAACAAGGCC	TCGTTCCCTG	ACCAGGTTCA	TTTCCAGCCG	CTGCCGCCCG	CGGTGGTGAA	2460
GTTGTCTGAC	GCGTTGATCG	CGACGATTTT	CAGCGCTGAG	ATGAAGACCG	ATGCCGCTAC	2520
CCTCGCGCAG	GAGGCAGGTA	ATTTTCGAGC	GATCTCCGGC	GACCTGAAAA	CCCAGATCGA	2580
CCAGGTGGAG	TCGACGGCAG	GTTCTGTTCA	GGGCCAGTGG	CGCGGCGCGG	CGGGGACGGC	2640
CGCCCAGGCC	GCGGTGGTGC	GCTTCCAAGA	AGCAGCCAAT	AAGCAGAAGC	AGGAACTCGA	2700
CGAGATCTCG	ACGAATATTC	GTCAGGCCGG	CGTCCAATAC	TCGAGGGCCG	ACGAGGAGCA	2760
GCAGCAGGCG	CTGTCTTCGC	AAATGGGCTT	TGGATTTCAGC	TTGCGGCTGC	CTGCTGGCTG	2820
GGTGGAGTCT	GACGCCGCCC	ACTTCGACTA	CGGTTTCAGCA	CTCCTCAGCA	AAACCACCGG	2880
GGACCCGCCA	TTTCCCGGAC	AGCCCGCCGC	GGTGGCCAAT	GACACCCGTA	TCGTGCTCGG	2940
CCGGCTAGAC	CAAAAGCTTT	ACGCCAGCGC	CGAAGCCACC	GACTCCAAGG	CCGCGGCCCG	3000
GTTGGGCTCG	GACATGGGTG	AGTTCTATAT	GCCCTACCCG	GGCACCCGGA	TCAACCAGGA	3060

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AACCGTCTCG CTYGACGCCA ACGGGGTGTC TGGAAGCGCG TCGTATTACG AAGTCAAGTT 3120
CAGCGATCCG AGTAAGCCGA ACGGCCAGAT CTGGACGGGC GTAATCGGCT CGCCCGCGGC 3180
GAACGCACCG GACGCCGGGC CCCCTCAGCG CTGGTTTGTG GTATGGGCTCG GGACCGCCAA 3240
CAACCCGGTG GACAAGGGCG CGGCCAAGGC GCTGGCCGAA TCGATCCGGC CTTTGGTTCG 3300
CCCGCCGCGG GCGCCGGCCG GGAAGTCGC TCCTACCCCG ACGACACCGA CACCGCAGCG 3360
GACCTTACCG GCCTGAGAAT TCTGCAGATA TCCATCACAC TGGCGGCCGC TCGAGCACCA 3420
CCACCACCAC CACTGAGATC CGGCTGCTAA CAAAGCCCGA AAGGAAGCTG AGTTGGCTGC 3480
TGCCACCGCT GAGCAATAAC TAGCATAACC CCTTGGGGCC TCTAACGGG TCTTGAGGGG 3540
TTTTTTGCTG AAAGGAGGAA CTATATCCGG AT 3572

```

(2) INFORMATION FOR SEQ ID NO:343:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:343:

```

Val Gln Phe Gln Ser Gly Gly Asp Asn Ser Pro Ala Val Tyr Xaa Xaa
 1             5             10             15
Asp Gly Xaa Arg
      20

```

(2) INFORMATION FOR SEQ ID NO:344:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:344:

```

Thr Thr Val Pro Xaa Val Thr Glu Ala Arg
 1             5             10

```

(2) INFORMATION FOR SEQ ID NO:345:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:345:

```

Thr Thr Pro Ser Xaa Val Ala Phe Ala Arg

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269

1 5 10

(2) INFORMATION FOR SEQ ID NO:346:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:346:

Asp Ala Gly Lys Xaa Ala Gly Xaa Asp Val Xaa Arg
1 5 10

(2) INFORMATION FOR SEQ ID NO:347:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:347:

Thr Xaa Glu Glu Xaa Gln Glu Ser Phe Asn Ser Ala Ala Pro Gly Asn
1 5 10 15
Xaa Lys

(2) INFORMATION FOR SEQ ID NO:348:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:348:

CTAGTTAGTA CTCAGTCGCA GACCGTG

27

(2) INFORMATION FOR SEQ ID NO:349:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:349:

GCAGTGACGA ATTCACTTCG ACTCC

25

(2) INFORMATION FOR SEQ ID NO:350:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2412 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:350:

CATATGGGCC	ATCATCATCA	TCATCACGTG	ATCGACATCA	TCGGGACCAG	CCCCACATCC	60
TGGGAACAGG	CGGCGGCGGA	GGCGGTCCAG	CGGGCGCGGG	ATAGCGTCGA	TGACATCCGC	120
GTCGCTCGGG	TCATTGAGCA	GGACATGGCC	GTGGACAGCG	CCGGCAAGAT	CACCTACCGC	180
ATCAAGCTCG	AAGTGTCTG	CAAGATGAGG	CCGGCGCAAC	CGAGGGGCTC	GAAACCACCG	240
AGCGGTTTCG	CTGAAACGGG	CGCCGGCGCC	GGTACTGTCTG	CGACTACCCC	CGCGTCGTCG	300
CCGGTGACGT	TGGCGGAGAC	CGGTAGCACG	CTGCTCTACC	CGCTGTTCAA	CCTGTGGGGT	360
CCGGCCTTTC	ACGAGAGGTA	TCCGAACGTC	ACGATCACCG	CTCAGGGCAC	CGGTTCTGGT	420
GCCGGGATCG	CGCAGGCCGC	CGCCGGGACG	GTCAACATTG	GGGCCTCCGA	CGCCTATCTG	480
TCGGAAGGTG	ATATGGCCGC	GCACAAGGGG	CTGATGAACA	TCGCGCTAGC	CATCTCCGCT	540
CAGCAGGTCA	ACTACAACCT	GCCCGGAGTG	AGCGAGCACC	TCAAGCTGAA	CGGAAAAGTC	600
CTGGCGGCCA	TGTACCAGGG	CACCATCAAA	ACCTGGGACG	ACCCGCAGAT	CGCTGCGCTC	660
AACCCCGGCG	TGAACCTGCC	CGGCACCGCG	GTAGTTCCGC	TGCACCGCTC	CGACGGGTCC	720
GGTGACACCT	TCTTGTTCAC	CCAGTACCTG	TCCAAGCAAG	ATCCCGAGGG	CTGGGGCAAG	780
TCGCCCGGCT	TCGGCACCCAC	CGTCGACTTC	CCGGCGGTGC	CGGGTGCCTG	GGGTGAGAAC	840
GGCAACGGCG	GCATGGTGAC	CGGTTGCGCC	GAGACACCGG	GCTGCGTGGC	CTATATCGGC	900
ATCAGCTTCC	TCGACCAGGC	CAGTCAACGG	GGACTCGGCG	AGGCCCAACT	AGGCAATAGC	960
TCTGGCAATT	TCTTGTTGCC	CGACGCGCAA	AGCATTCAGG	CCGCGGCGGC	TGGCTTCGCA	1020
TCGAAAACCC	CGGCGAACCA	GGCGATTTTC	ATGATCGACG	GGCCCGCCCC	GGACGGCTAC	1080
CCGATCATCA	ACTACGAGTA	CGCCATCGTC	AACAACCGGC	AAAAGGACGC	CGCCACCGCG	1140
CAGACCTTGC	AGGCATTTCT	GCACTGGGCG	ATCACCGACG	GCAACAAGGC	CTCGTTCCCTC	1200
GACCAGGTTT	ATTTCCAGCC	GCTGCCGCCG	GCGGTGGTGA	AGTTGTCTGA	CGCGTTGATC	1260
GCGACGATTT	CCAGCGCTGA	GATGAAGACC	GATGCCGCTA	CCCTCGCGCA	GGAGGCAGGT	1320
AATTTTCGAG	GGATCTCCGG	CGACCTGAAA	ACCCAGATCG	ACCAGGTGGA	GTGACGGCA	1380
GGTTCGTTGC	AGGGCCAGTG	GCGCGGCGCG	GCGGGGACGG	CCGCCCAGGC	CGCGGTGGTG	1440
CGCTTCCAAG	AAGCAGCCAA	TAAGCAGAAG	CAGGAACCTG	ACGAGATCTC	GACGAATATT	1500
CGTCAGGCCG	GCGTCCAATA	CTCGAGGGCC	GACGAGGAGC	AGCAGCAGGC	GCTGTCTCTG	1560
CAAATGGGCT	TTGTGCCAC	AACGGCCGCC	TCGCCGCCGT	CGACCGCTGC	AGCGCCACCC	1620
GCACCGGCGA	CACCTGTTGC	CCCCCACCA	CCGGCCGCCG	CCAACACGCC	GAATGCCCAG	1680
CCGGGCGATC	CCAACGCAGC	ACCTCCGCCG	GCCGACCCGA	ACGCACCGCC	GCCACCTGTC	1740
ATTGCCCCAA	ACGCACCCCA	ACCTGTCCGG	ATCGACAACC	CGGTTGGAGG	ATTCAGCTTC	1800
GCGCTGCCTG	CTGGCTGGGT	GGAGTCTGAC	GCCGCCCACT	TCGACTACGG	TTCAGCACTC	1860
CTCAGCAAAA	CCACCGGGGA	CCCGCCATTT	CCCGGACAGC	CGCCGCCGGT	GGCCAATGAC	1920
ACCCGTATCG	TGCTCGGCCG	GCTAGACCAA	AAGCTTTACG	CCAGCGCCGA	AGCCACCGAC	1980
TCCAAGGCCG	CGGCCCGGTT	GGGCTCGGAC	ATGGGTGAGT	TCTATATGCC	CTACCCGGGC	2040
ACCCGGATCA	ACCAGGAAAC	CGTCTCGCTC	GACGCCAACG	GGGTGTCTGG	AAGCGCGTCG	2100
TATTACGAAG	TCAAGTTCAG	CGATCCGAGT	AAGCCGAACG	GCCAGATCTG	GACGGGCGTA	2160

ATCGGCTCGC	CCGCGGCGAA	CGCACC GGAC	GCCGGGCCCC	CTCAGCGCTG	GTTTGTGGTA	2220
TGGCTCGGGA	CCGCCAACAA	CCCGGTGGAC	AAGGGCGCGG	CCAAGGCGCT	GGCCGAATCG	2280
ATCCGGCCTT	TGGTCGCCCC	GCCGCCGGCG	CCGGCACC GG	CTCCTGCAGA	GCCCGCTCCG	2340
GCGCCGGCGC	CGGCCGGGGA	AGTCGCTCCT	ACCCCGACGA	CACCGACACC	GCAGCGGACC	2400
TTACCGGCCT	GA					2412

(2) INFORMATION FOR SEQ ID NO:351:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 802 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:351:

Met	Gly	His	His	His	His	His	His	Val	Ile	Asp	Ile	Ile	Gly	Thr	Ser	1	5	10	15
Pro	Thr	Ser	Trp	Glu	Gln	Ala	Ala	Ala	Glu	Ala	Val	Gln	Arg	Ala	Arg	20	25	30	
Asp	Ser	Val	Asp	Asp	Ile	Arg	Val	Ala	Arg	Val	Ile	Glu	Gln	Asp	Met	35	40	45	
Ala	Val	Asp	Ser	Ala	Gly	Lys	Ile	Thr	Tyr	Arg	Ile	Lys	Leu	Glu	Val	50	55	60	
Ser	Phe	Lys	Met	Arg	Pro	Ala	Gln	Pro	Arg	Gly	Ser	Lys	Pro	Pro	Ser	65	70	75	80
Gly	Ser	Pro	Glu	Thr	Gly	Ala	Gly	Ala	Gly	Thr	Val	Ala	Thr	Thr	Pro	85	90	95	
Ala	Ser	Ser	Pro	Val	Thr	Leu	Ala	Glu	Thr	Gly	Ser	Thr	Leu	Leu	Tyr	100	105	110	
Pro	Leu	Phe	Asn	Leu	Trp	Gly	Pro	Ala	Phe	His	Glu	Arg	Tyr	Pro	Asn	115	120	125	
Val	Thr	Ile	Thr	Ala	Gln	Gly	Thr	Gly	Ser	Gly	Ala	Gly	Ile	Ala	Gln	130	135	140	
Ala	Ala	Ala	Gly	Thr	Val	Asn	Ile	Gly	Ala	Ser	Asp	Ala	Tyr	Leu	Ser	145	150	155	160
Glu	Gly	Asp	Met	Ala	Ala	His	Lys	Gly	Leu	Met	Asn	Ile	Ala	Leu	Ala	165	170	175	
Ile	Ser	Ala	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His		180	185	190	
Leu	Lys	Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile	195	200	205	
Lys	Thr	Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn	210	215	220	
Leu	Pro	Gly	Thr	Ala	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly		225	230	235	240
Asp	Thr	Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly	245	250	255	
Trp	Gly	Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val	260	265	270	
Pro	Gly	Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys	275	280	285	
Ala	Glu	Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp				

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290		295		300
Gln Ala Ser Gln Arg Gly	Leu Gly Glu Ala	Gln Leu Gly Asn Ser Ser		
305	310	315		320
Gly Asn Phe Leu Leu Pro Asp Ala	Gln Ser Ile Gln Ala Ala Ala			
	325	330		335
Gly Phe Ala Ser Lys Thr Pro Ala	Asn Gln Ala Ile Ser Met Ile Asp			
	340	345		350
Gly Pro Ala Pro Asp Gly Tyr Pro	Ile Ile Asn Tyr Glu Tyr Ala Ile			
	355	360		365
Val Asn Asn Arg Gln Lys Asp Ala	Ala Thr Ala Gln Thr Leu Gln Ala			
	370	375		380
Phe Leu His Trp Ala Ile Thr Asp	Gly Asn Lys Ala Ser Phe Leu Asp			
385	390	395		400
Gln Val His Phe Gln Pro Leu Pro	Pro Ala Val Val Lys Leu Ser Asp			
	405	410		415
Ala Leu Ile Ala Thr Ile Ser Ser	Ala Glu Met Lys Thr Asp Ala Ala			
	420	425		430
Thr Leu Ala Gln Glu Ala Gly Asn	Phe Glu Arg Ile Ser Gly Asp Leu			
	435	440		445
Lys Thr Gln Ile Asp Gln Val Glu	Ser Thr Ala Gly Ser Leu Gln Gly			
	450	455		460
Gln Trp Arg Gly Ala Ala Gly Thr	Ala Ala Gln Ala Ala Val Val Arg			
465	470	475		480
Phe Gln Glu Ala Ala Asn Lys Gln	Lys Gln Glu Leu Asp Glu Ile Ser			
	485	490		495
Thr Asn Ile Arg Gln Ala Gly Val	Gln Tyr Ser Arg Ala Asp Glu Glu			
	500	505		510
Gln Gln Gln Ala Leu Ser Ser Gln	Met Gly Phe Val Pro Thr Thr Ala			
	515	520		525
Ala Ser Pro Pro Ser Thr Ala Ala	Ala Pro Pro Ala Pro Ala Thr Pro			
	530	535		540
Val Ala Pro Pro Pro Pro Ala Ala	Ala Asn Thr Pro Asn Ala Gln Pro			
545	550	555		560
Gly Asp Pro Asn Ala Ala Pro Pro	Pro Ala Asp Pro Asn Ala Pro Pro			
	565	570		575
Pro Pro Val Ile Ala Pro Asn Ala	Pro Gln Pro Val Arg Ile Asp Asn			
	580	585		590
Pro Val Gly Gly Phe Ser Phe Ala	Leu Pro Ala Gly Trp Val Glu Ser			
	595	600		605
Asp Ala Ala His Phe Asp Tyr Gly	Ser Ala Leu Leu Ser Lys Thr Thr			
	610	615		620
Gly Asp Pro Pro Phe Pro Gly Gln	Pro Pro Pro Val Ala Asn Asp Thr			
625	630	635		640
Arg Ile Val Leu Gly Arg Leu Asp	Gln Lys Leu Tyr Ala Ser Ala Glu			
	645	650		655
Ala Thr Asp Ser Lys Ala Ala Ala	Arg Leu Gly Ser Asp Met Gly Glu			
	660	665		670
Phe Tyr Met Pro Tyr Pro Gly Thr	Arg Ile Asn Gln Glu Thr Val Ser			
	675	680		685
Leu Asp Ala Asn Gly Val Ser Gly	Ser Ala Ser Tyr Tyr Glu Val Lys			
	690	695		700
Phe Ser Asp Pro Ser Lys Pro Asn	Gly Gln Ile Trp Thr Gly Val Ile			
705	710	715		720
Gly Ser Pro Ala Ala Asn Ala Pro	Asp Ala Gly Pro Pro Gln Arg Trp			
	725	730		735

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Phe Val Val Trp Leu Gly Thr Ala Asn Asn Pro Val Asp Lys Gly Ala
 740 745 750
 Ala Lys Ala Leu Ala Glu Ser Ile Arg Pro Leu Val Ala Pro Pro Pro
 755 760 765
 Ala Pro Ala Pro Ala Pro Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala
 770 775 780
 Gly Glu Val Ala Pro Thr Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu
 785 790 795 800
 Pro Ala

(2) INFORMATION FOR SEQ ID NO:352:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:352:

GGATCCAAAC CACCGAGCGG TTCGCCTGAA ACGG

34

(2) INFORMATION FOR SEQ ID NO:353:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 37 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:353:

CGCTGCGAAT TCACCTCCGG AGGAAATCGT CGCGATC

37

(2) INFORMATION FOR SEQ ID NO:354:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1962 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:354:

CATATGGGCC ATCATCATCA TCATCACGGA TCCAAACCAC CGAGCGGTTC GCCTGAAACG	60
GGCGCCGGCG CCGGTACTGT CGCGACTACC CCCGCGTCGT CGCCGGTGAC GTTGGCGGAG	120
ACCGGTAGCA CGCTGCTCTA CCCGCTGTTC AACCTGTGGG GTCCGGCCTT TCACGAGAGG	180
TATCCGAACG TCACGATCAC CGCTCAGGGC ACCGGTTCTG GTGCCGGGAT CGCGCAGGCC	240

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GCCGCCGGGA CGGTCAACAT TGGGGCCTCC GACGCCTATC TGTCGGAAGG TGATATGGCC 300
GCGCACAAAGG GGCTGATGAA CATCGCGCTA GCCATCTCCG CTCAGCAGGT CAACTACAAC 360
CTGCCCCGAG TGAGCGAGCA CCTCAAGCTG AACGGAAAAG TCCTGGCGGC CATGTACCAG 420
GGCACCATCA AAACCTGGGA CGACCCGCAG ATCGCTGCGC TCAACCCCGG CGTGAACCTG 480
CCCGGCACCG CGGTAGTTCC GCTGCACCGC TCCGACGGGT CCGGTGACAC CTTCTTGTTT 540
ACCCAGTACC TGTCCAAGCA AGATCCCGAG GGCTGGGGCA AGTCGCCCCG CTTGCGGCACC 600
ACCGTCGACT TCCCGGCGGT GCCGGGTGCG CTGGGTGAGA ACGGCAACGG CGGCATGGTG 660
ACCGGTTGCG CCGAGACACC GGGCTGCGTG GCCTATATCG GCATCAGCTT CCTCGACCAG 720
GCCAGTCAAC GGGGACTCGG CGAGGCCCAA CTAGGCAATA GCTCTGGCAA TTTCTTGTTG 780
CCCGACGCGC AAAGCATTCA GGCCGCGGCG GCTGGCTTCG CATCGAAAAC CCCGCGGAAC 840
CAGGCGATTT CGATGATCGA CGGGCCCGCC CCGGACGGCT ACCCGATCAT CCACTACGAG 900
TACGCCATCG TCAACAACCG GCAAAAGGAC GCCGCCACCG CGCAGACCTT GCAGGCATTT 960
CTGCACTGGG CGATCACCGA CGGCAACAAG GCCTCGTTCC TCGACCAGGT TCATTTCCAG 1020
CCGCTGCCGC CCGCGGTGGT GAAGTTGTCT GACGCGTTGA TCGCGACGAT TTCCTCCGGA 1080
GGTGGCAGTG GGGGAGGCTC AGGTGGAGGT TCTGGCGGGA GCGTGCCAC AACGGCCGCC 1140
TCGCCCCCGT CGACCGCTGC AGCGCCACCC GCACCGGCGA CACCTGTTGC CCCCCACCA 1200
CCGGCCGCCG CCAACACGCC GAATGCCCG CCGGGCGATC CCAACGCAGC ACCTCCGCCG 1260
GCCGACCCGA ACGCACCGCC GCCACCTGTC ATTGCCCAA ACGCACCCCA ACCTGTCCGG 1320
ATCGACAACC CGGTTGGAGG ATTCAGCTTC GCGCTGCCTG CTGGCTGGGT GGAGTCTGAC 1380
GCCGCCCACT TCGACTACGG TTCAGCACTC CTCAGCAAAA CCACCGGGGA CCCGCCATTT 1440
CCCGGACAGC CGCCGCCGGT GGCCAATGAC ACCCGTATCG TGCTCGGCCG GCTAGACCAA 1500
AAGCTTTACG CCAGCGCCGA AGCCACCGAC TCCAAGGCCG CGGCCCGGTT GGGCTCGGAC 1560
ATGGGTGAGT TCTATATGCC CTACCCGGGC ACCCGGATCA ACCAGGAAAC CGTCTCGCTC 1620
GACGCCAACG GGGTGTCTGG AAGCGCGTCG TATTACGAAG TCAAGTTCAG CGATCCGAGT 1680
AAGCCGAACG GCCAGATCTG GACGGGCGTA ATCGGCTCGC CCGCGGCGAA CGCACCGGAC 1740
GCCGGGCCCC CTCAGCGCTG GTTGTGGTA TGGCTCGGGA CCGCCAACAA CCCGGTGGAC 1800
AAGGGCGCGG CCAAGGCGCT GGCCGAATCG ATCCGGCCTT TGGTCGCCCC GCCCGCGGCG 1860
CCGGCACCGG CTCCTGCAGA GCGCGCTCCG GCGCCGGCGC CGGCCGGGGA AGTCGCTCCT 1920
ACCCCGACGA CACCGACACC GCAGCGGACC TTACCGGCCT GA 1962

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(2) INFORMATION FOR SEQ ID NO:355:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:355:

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Met Gly His His His His His Gly Ser Lys Pro Pro Ser Gly Ser
 1           5           10           15
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
 20           25           30
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
 35           40           45
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
 50           55           60
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
 65           70           75           80
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
 85           90           95
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser

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	100		105		110										
Ala	Gln	Gln	Val	Asn	Tyr	Asn	Leu	Pro	Gly	Val	Ser	Glu	His	Leu	Lys
	115							120				125			
Leu	Asn	Gly	Lys	Val	Leu	Ala	Ala	Met	Tyr	Gln	Gly	Thr	Ile	Lys	Thr
	130					135						140			
Trp	Asp	Asp	Pro	Gln	Ile	Ala	Ala	Leu	Asn	Pro	Gly	Val	Asn	Leu	Pro
145					150					155					160
Gly	Thr	Ala	Val	Val	Pro	Leu	His	Arg	Ser	Asp	Gly	Ser	Gly	Asp	Thr
				165					170					175	
Phe	Leu	Phe	Thr	Gln	Tyr	Leu	Ser	Lys	Gln	Asp	Pro	Glu	Gly	Trp	Gly
			180					185					190		
Lys	Ser	Pro	Gly	Phe	Gly	Thr	Thr	Val	Asp	Phe	Pro	Ala	Val	Pro	Gly
	195						200					205			
Ala	Leu	Gly	Glu	Asn	Gly	Asn	Gly	Gly	Met	Val	Thr	Gly	Cys	Ala	Glu
	210					215					220				
Thr	Pro	Gly	Cys	Val	Ala	Tyr	Ile	Gly	Ile	Ser	Phe	Leu	Asp	Gln	Ala
225					230					235					240
Ser	Gln	Arg	Gly	Leu	Gly	Glu	Ala	Gln	Leu	Gly	Asn	Ser	Ser	Gly	Asn
				245					250					255	
Phe	Leu	Leu	Pro	Asp	Ala	Gln	Ser	Ile	Gln	Ala	Ala	Ala	Ala	Gly	Phe
			260					265					270		
Ala	Ser	Lys	Thr	Pro	Ala	Asn	Gln	Ala	Ile	Ser	Met	Ile	Asp	Gly	Pro
	275					280						285			
Ala	Pro	Asp	Gly	Tyr	Pro	Ile	Ile	Asn	Tyr	Glu	Tyr	Ala	Ile	Val	Asn
	290					295				300					
Asn	Arg	Gln	Lys	Asp	Ala	Ala	Thr	Ala	Gln	Thr	Leu	Gln	Ala	Phe	Leu
305					310					315					320
His	Trp	Ala	Ile	Thr	Asp	Gly	Asn	Lys	Ala	Ser	Phe	Leu	Asp	Gln	Val
			325						330					335	
His	Phe	Gln	Pro	Leu	Pro	Pro	Ala	Val	Val	Lys	Leu	Ser	Asp	Ala	Leu
			340					345					350		
Ile	Ala	Thr	Ile	Ser	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly
	355					360						365			
Gly	Ser	Gly	Gly	Ser	Val	Pro	Thr	Thr	Ala	Ala	Ser	Pro	Pro	Ser	Thr
	370					375					380				
Ala	Ala	Ala	Pro	Pro	Ala	Pro	Ala	Thr	Pro	Val	Ala	Pro	Pro	Pro	Pro
385					390					395					400
Ala	Ala	Ala	Asn	Thr	Pro	Asn	Ala	Gln	Pro	Gly	Asp	Pro	Asn	Ala	Ala
			405						410					415	
Pro	Pro	Pro	Ala	Asp	Pro	Asn	Ala	Pro	Pro	Pro	Pro	Val	Ile	Ala	Pro
			420					425					430		
Asn	Ala	Pro	Gln	Pro	Val	Arg	Ile	Asp	Asn	Pro	Val	Gly	Gly	Phe	Ser
	435					440					445				
Phe	Ala	Leu	Pro	Ala	Gly	Trp	Val	Glu	Ser	Asp	Ala	Ala	His	Phe	Asp
	450				455					460					
Tyr	Gly	Ser	Ala	Leu	Leu	Ser	Lys	Thr	Thr	Gly	Asp	Pro	Pro	Phe	Pro
465					470					475					480
Gly	Gln	Pro	Pro	Pro	Val	Ala	Asn	Asp	Thr	Arg	Ile	Val	Leu	Gly	Arg
			485						490					495	
Leu	Asp	Gln	Lys	Leu	Tyr	Ala	Ser	Ala	Glu	Ala	Thr	Asp	Ser	Lys	Ala
			500					505					510		
Ala	Ala	Arg	Leu	Gly	Ser	Asp	Met	Gly	Glu	Phe	Tyr	Met	Pro	Tyr	Pro
	515						520					525			
Gly	Thr	Arg	Ile	Asn	Gln	Glu	Thr	Val	Ser	Leu	Asp	Ala	Asn	Gly	Val
	530					535					540				

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Ser	Gly	Ser	Ala	Ser	Tyr	Tyr	Glu	Val	Lys	Phe	Ser	Asp	Pro	Ser	Lys
545					550					555					560
Pro	Asn	Gly	Gln	Ile	Trp	Thr	Gly	Val	Ile	Gly	Ser	Pro	Ala	Ala	Asn
				565						570					575
Ala	Pro	Asp	Ala	Gly	Pro	Pro	Gln	Arg	Trp	Phe	Val	Val	Trp	Leu	Gly
			580					585						590	
Thr	Ala	Asn	Asn	Pro	Val	Asp	Lys	Gly	Ala	Ala	Lys	Ala	Leu	Ala	Glu
		595					600					605			
Ser	Ile	Arg	Pro	Leu	Val	Ala	Pro	Pro	Pro	Ala	Pro	Ala	Pro	Ala	Pro
610						615					620				
Ala	Glu	Pro	Ala	Pro	Ala	Pro	Ala	Pro	Ala	Gly	Glu	Val	Ala	Pro	Thr
625					630					635					640
Pro	Thr	Thr	Pro	Thr	Pro	Gln	Arg	Thr	Leu	Pro	Ala				
				645					650						

CLAIMS

1. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Val-Asp-Ala-Val-Ile-Asn-Thr-Thr-Cys-Asn-Tyr-Gly-Gln-Val-Val-Ala-Ala-Leu; (SEQ ID No. 120)
- (b) Ala-Val-Glu-Ser-Gly-Met-Leu-Ala-Leu-Gly-Thr-Pro-Ala-Pro-Ser; (SEQ ID No. 121)
- (c) Ala-Ala-Met-Lys-Pro-Arg-Thr-Gly-Asp-Gly-Pro-Leu-Glu-Ala-Ala-Lys-Glu-Gly-Arg; (SEQ ID No. 122)
- (d) Tyr-Tyr-Trp-Cys-Pro-Gly-Gln-Pro-Phe-Asp-Pro-Ala-Trp-Gly-Pro; (SEQ ID No. 123)
- (e) Asp-Ile-Gly-Ser-Glu-Ser-Thr-Glu-Asp-Gln-Gln-Xaa-Ala-Val; (SEQ ID No. 124)
- (f) Ala-Glu-Glu-Ser-Ile-Ser-Thr-Xaa-Glu-Xaa-Ile-Val-Pro; (SEQ ID No. 125)
- (g) Asp-Pro-Glu-Pro-Ala-Pro-Pro-Val-Pro-Thr-Thr-Ala-Ala-Ser-Pro-Pro-Ser; (SEQ ID No. 126)
- (h) Ala-Pro-Lys-Thr-Tyr-Xaa-Glu-Glu-Leu-Lys-Gly-Thr-Asp-Thr-Gly; (SEQ ID No. 127)
- (i) Asp-Pro-Ala-Ser-Ala-Pro-Asp-Val-Pro-Thr-Ala-Ala-Gln-Leu-Thr-Ser-Leu-Leu-Asn-Ser-Leu-Ala-Asp-Pro-Asn-Val-Ser-Phe-Ala-Asn; (SEQ ID No. 128) and
- (j) Ala-Pro-Glu-Ser-Gly-Ala-Gly-Leu-Gly-Gly-Thr-Val-Gln-Ala-Gly; (SEQ ID No. 136)

wherein Xaa may be any amino acid.

2. A polypeptide comprising an immunogenic portion of an *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative

substitutions and/or modifications, wherein said antigen has an N-terminal sequence selected from the group consisting of:

- (a) Asp-Pro-Pro-Asp-Pro-His-Gln-Xaa-Asp-Met-Thr-Lys-Gly-Tyr-Tyr-Pro-Gly-Gly-Arg-Arg-Xaa-Phe; (SEQ ID No. 129) and
- (b) Xaa-Tyr-Ile-Ala-Tyr-Xaa-Thr-Thr-Ala-Gly-Ile-Val-Pro-Gly-Lys-Ile-Asn-Val-His-Leu-Val; (SEQ ID No. 137), wherein Xaa may be any amino acid.

3. A polypeptide comprising an immunogenic portion of a soluble *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 1, 2, 4-10, 13-25, 52, 99 and 101 or a complement thereof under moderately stringent conditions.

4. A polypeptide comprising an immunogenic portion of a *M. tuberculosis* antigen, or a variant of said antigen that differs only in conservative substitutions and/or modifications, wherein said antigen comprises an amino acid sequence encoded by a DNA sequence selected from the group consisting of the sequences recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 26-51, 138, 139, 163-183, 201, 240, 242-247, 253-256, 295-298, 309, 316, 318-320, 322, 324, 328, 329, 333, 335, 337, 339 and 341 or a complement thereof under moderately stringent conditions.

5. A DNA molecule comprising a nucleotide sequence encoding a polypeptide according to any one of claims 1-4.

6. An expression vector comprising a DNA molecule according to claim 5.

7. A host cell transformed with an expression vector according to claim 6.
8. The host cell of claim 7 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cells.
9. A pharmaceutical composition comprising one or more polypeptides according to any one of claims 1-4 and a physiologically acceptable carrier.
10. A pharmaceutical composition comprising one or more DNA molecules according to claim 5 and a physiologically acceptable carrier.
11. A pharmaceutical composition comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and a physiologically acceptable carrier.
12. A vaccine comprising one or more polypeptides according to any one of claims 1-4 and a non-specific immune response enhancer.
13. A vaccine comprising:
a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
a non-specific immune response enhancer.
14. A vaccine comprising:
one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and

a non-specific immune response enhancer.

15. The vaccine of claims 12-14 wherein the non-specific immune response enhancer is an adjuvant.

16. A vaccine comprising one or more DNA molecules according to claim 5 and a non-specific immune response enhancer.

17. A vaccine comprising one or more DNA sequences recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and a non-specific immune response enhancer.

18. The vaccine of claims 16 or 17 wherein the non-specific immune response enhancer is an adjuvant.

19. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to any one of claims 9-11.

20. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to any one of claims 12-18.

21. A fusion protein comprising two or more polypeptides according to any one of claims 1-4.

22. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and ESAT-6.

23. A fusion protein comprising one or more polypeptides according to any one of claims 1-4 and the *M. tuberculosis* antigen 38 kD (SEQ ID NO:155).

24. A pharmaceutical composition comprising a fusion protein according to any one of claims 21-23 and a physiologically acceptable carrier.

25. A vaccine comprising a fusion protein according to any one of claims 21-23 and a non-specific immune response enhancer.

26. The vaccine of claim 25 wherein the non-specific immune response enhancer is an adjuvant.

27. A method for inducing protective immunity in a patient, comprising administering to a patient a pharmaceutical composition according to claim 24.

28. A method for inducing protective immunity in a patient, comprising administering to a patient a vaccine according to claims 25 or 26.

29. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with one or more polypeptides according to any one of claims 1-4; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

30. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

31. A method for detecting tuberculosis in a patient, comprising:

(a) contacting dermal cells of a patient with one or more polypeptides encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308,

310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and

(b) detecting an immune response on the patient's skin and therefrom detecting tuberculosis in the patient.

32. The method of any one of claims 29-31 wherein the immune response is induration.

33. A diagnostic kit comprising:

- (a) a polypeptide according to any one of claims 1-4; and
- (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

34. A diagnostic kit comprising:

- (a) a polypeptide having an N-terminal sequence selected from the group consisting of sequences recited in SEQ ID NO: 134 and 135; and
- (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

35. A diagnostic kit comprising:

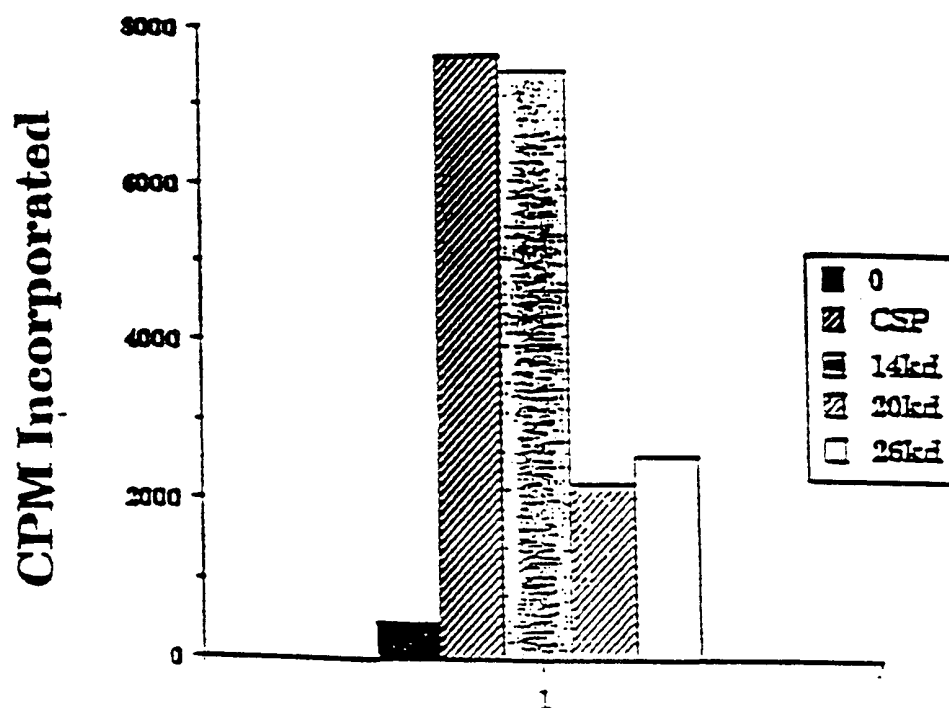
- (a) a polypeptide encoded by a DNA sequence selected from the group consisting of SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347, the complements of said sequences, and DNA sequences that hybridize to a sequence recited in SEQ ID Nos.: 3, 11, 12, 140, 141, 156-160, 189-193, 199, 200, 203, 215-225, 237, 239, 261-276, 292, 293, 303-308, 310-315, 317, 321, 323, 325-327, 330-332, 334, 336, 338, 340 and 342-347; and
- (b) apparatus sufficient to contact said polypeptide with the dermal cells of a patient.

36. A diagnostic kit comprising:

- (a) a fusion protein according to any one of claims 21-23; and
- (b) apparatus sufficient to contact said fusion protein with the dermal cells of a patient.

37. A fusion protein according to claim 23 comprising an amino acid sequence selected from the group consisting of sequences recited in SEQ ID NO: 153, 209, 351 and 355.

D7 T Cell Proliferation



D7 IFN γ

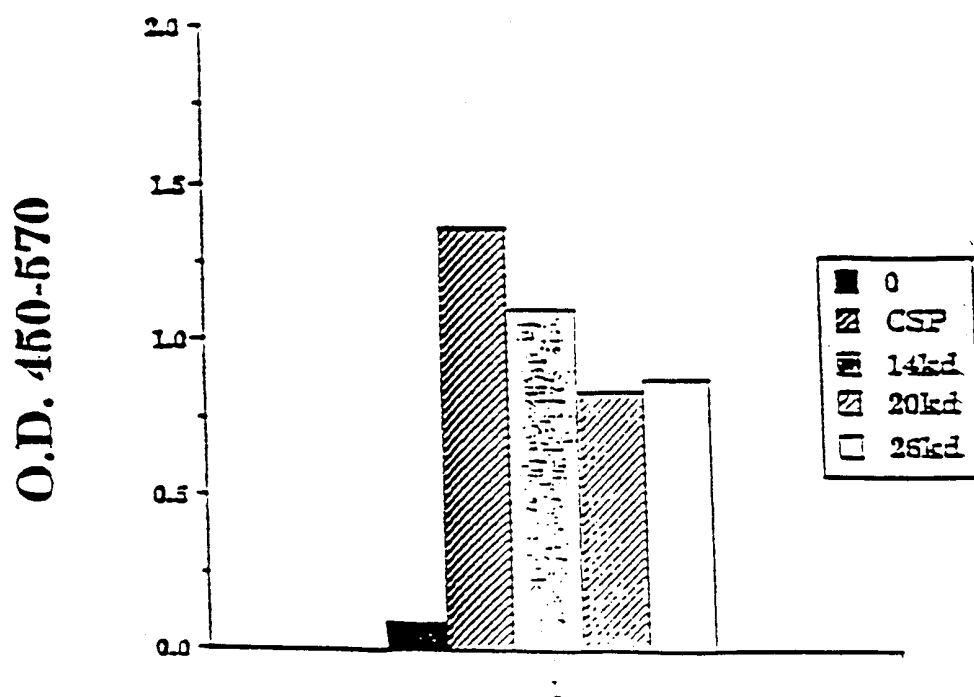


FIG. 1

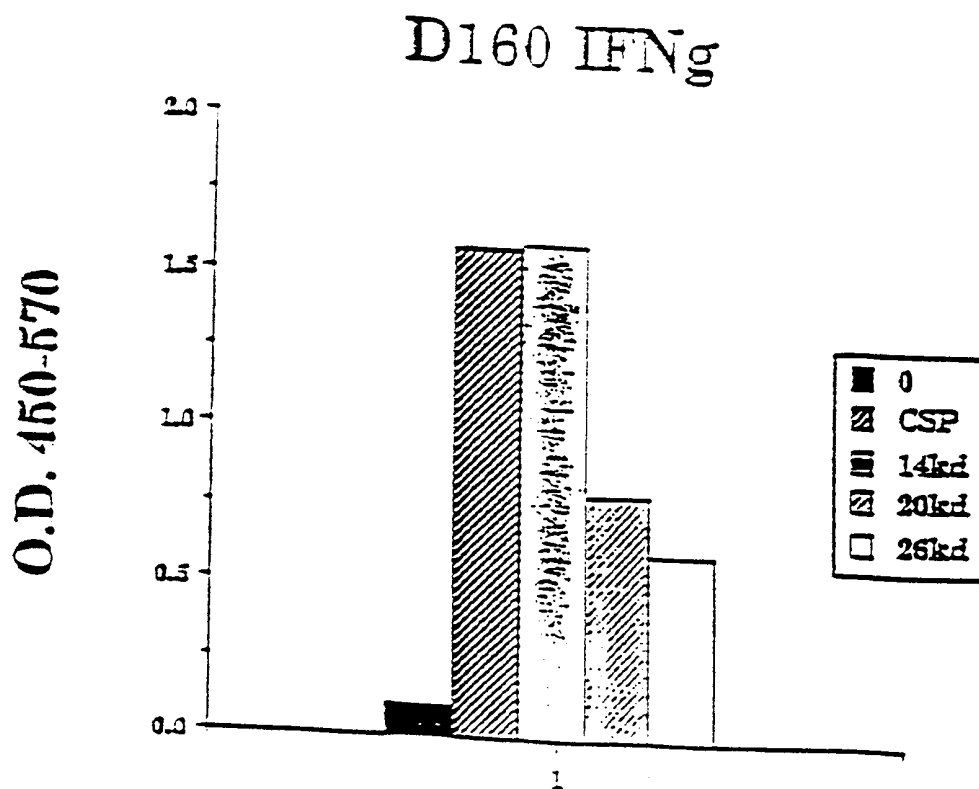
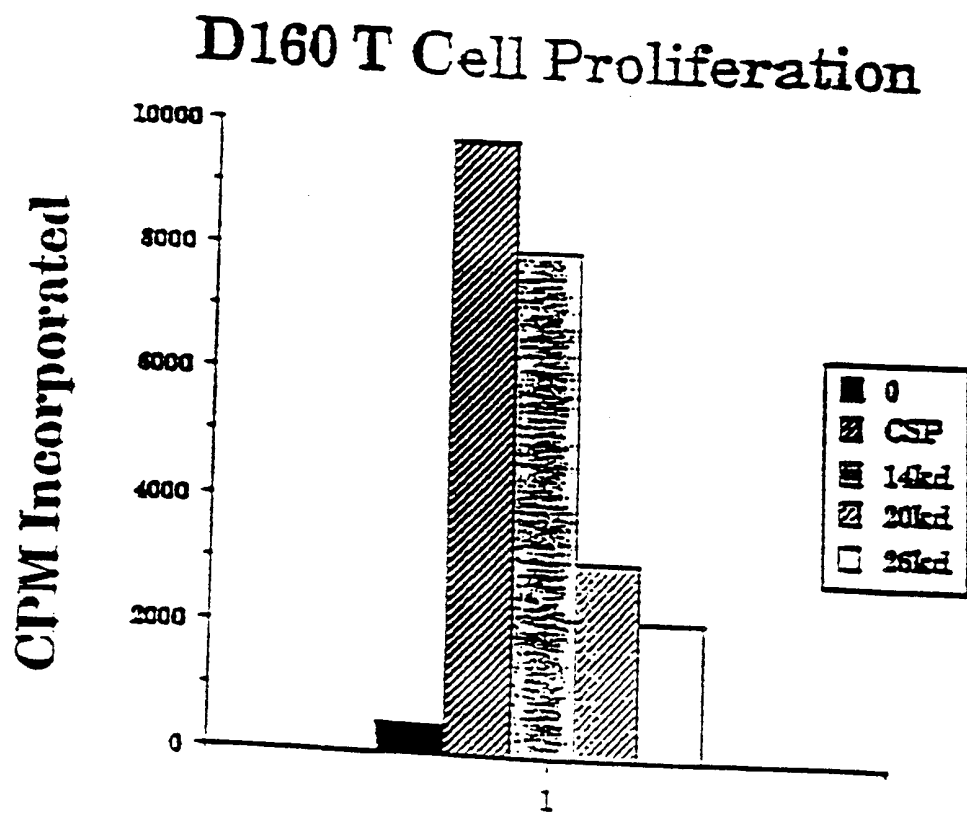


FIG. 1B

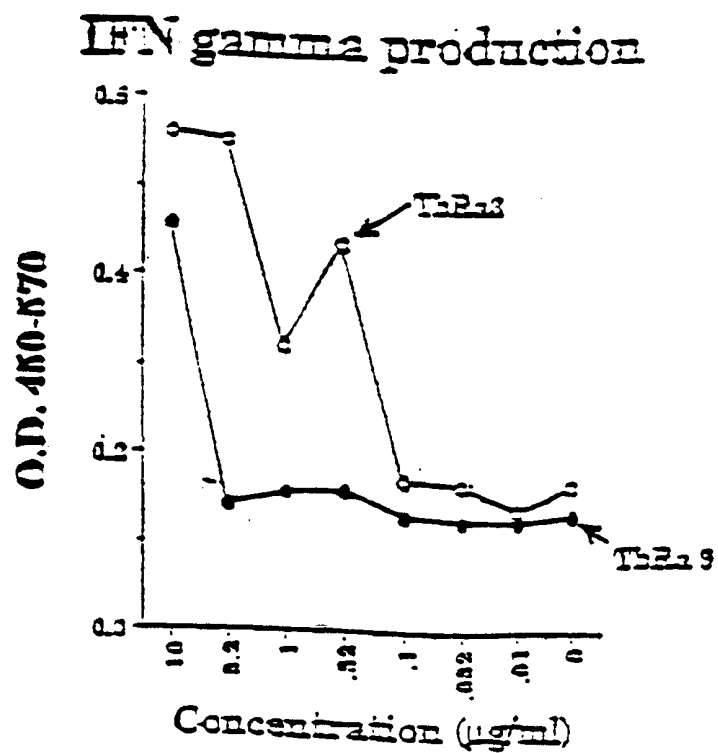
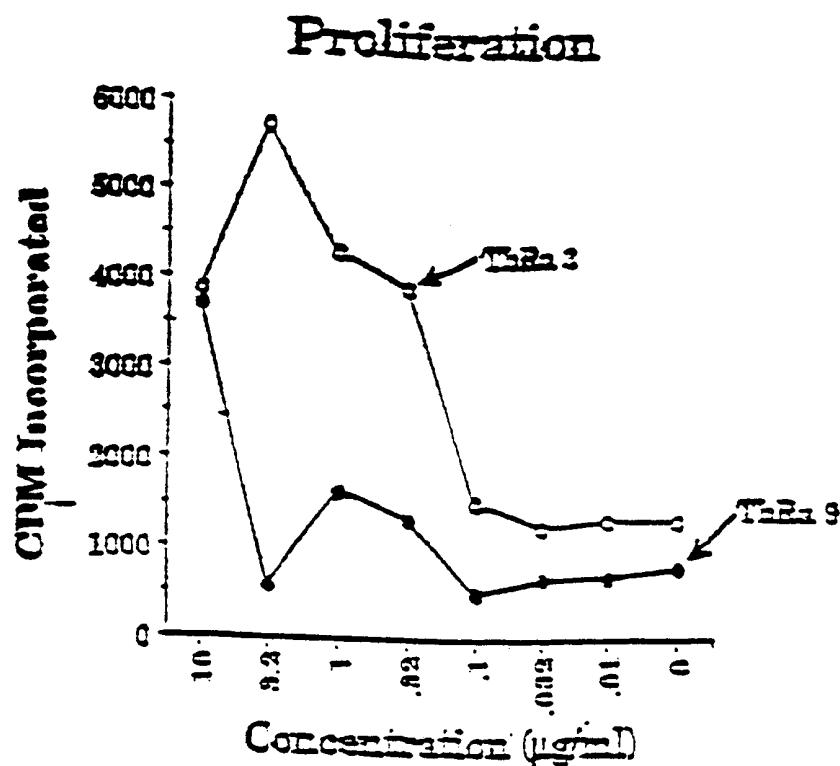
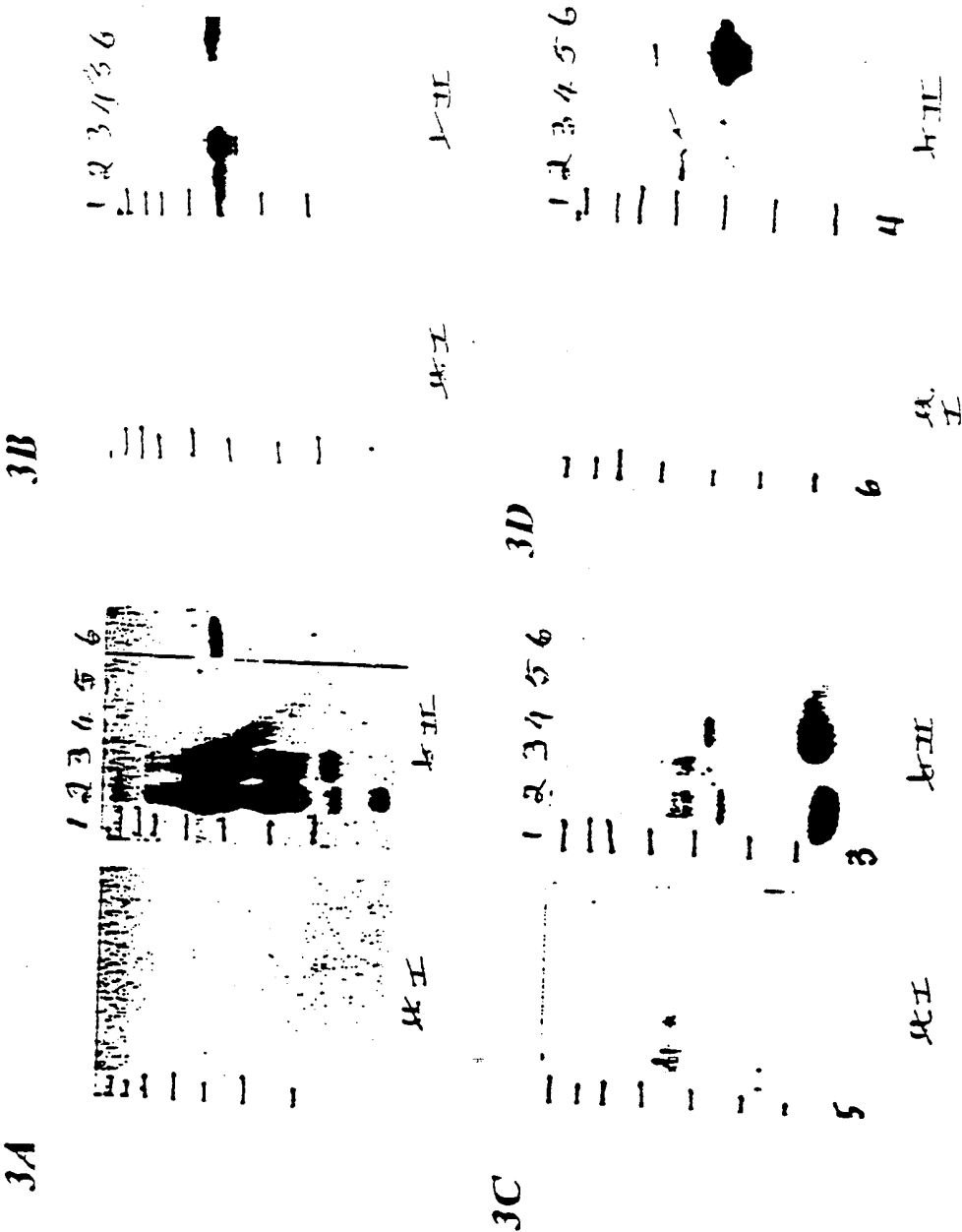


FIG. 2



FIGS. 3 A-D

**T cell clone 131TbH9
responds poorly to CSP**

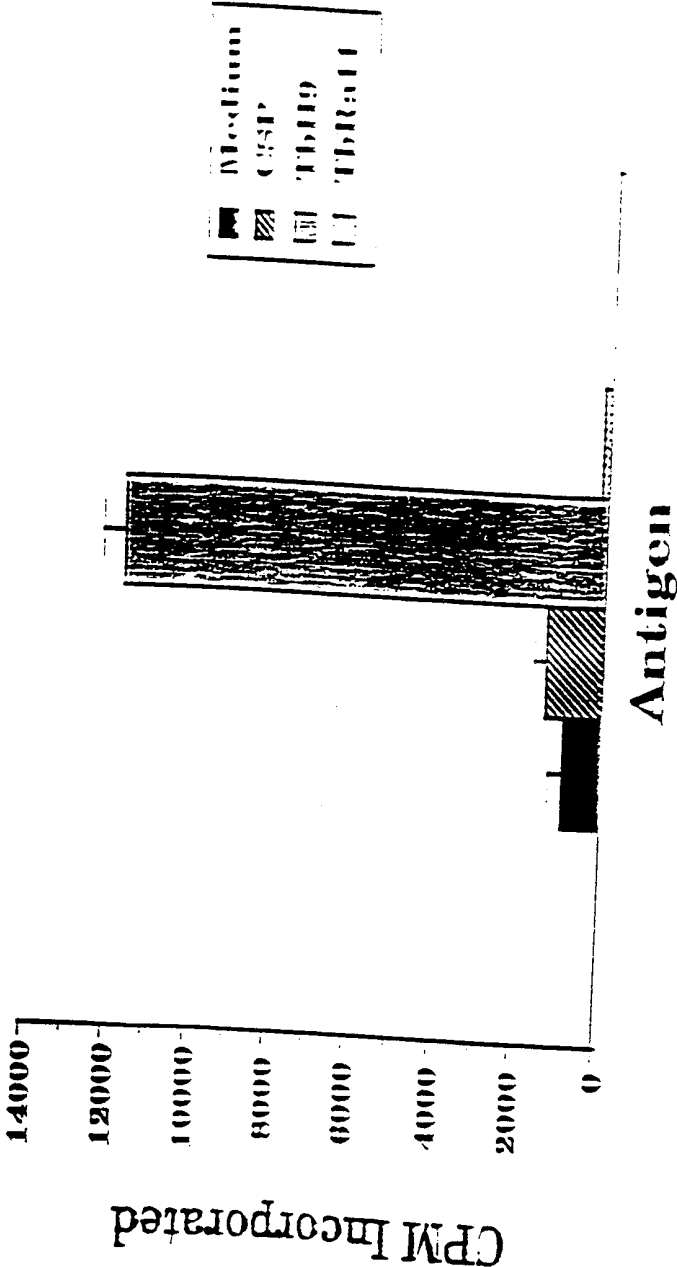


FIG. 4A

T Cell Clone PPD 800-10 IFN γ Production

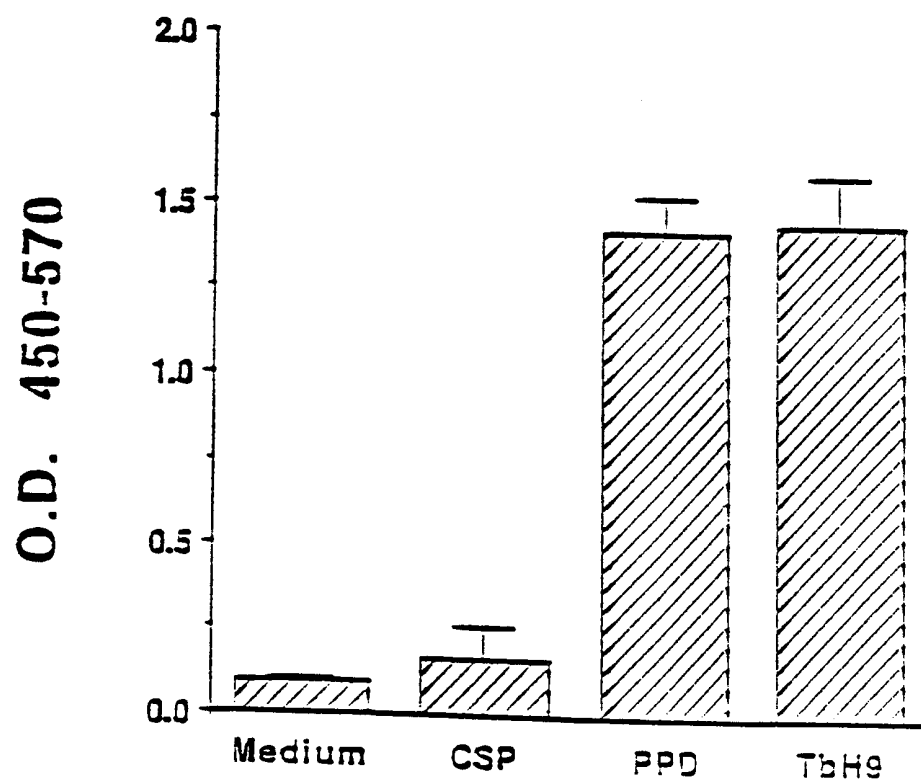
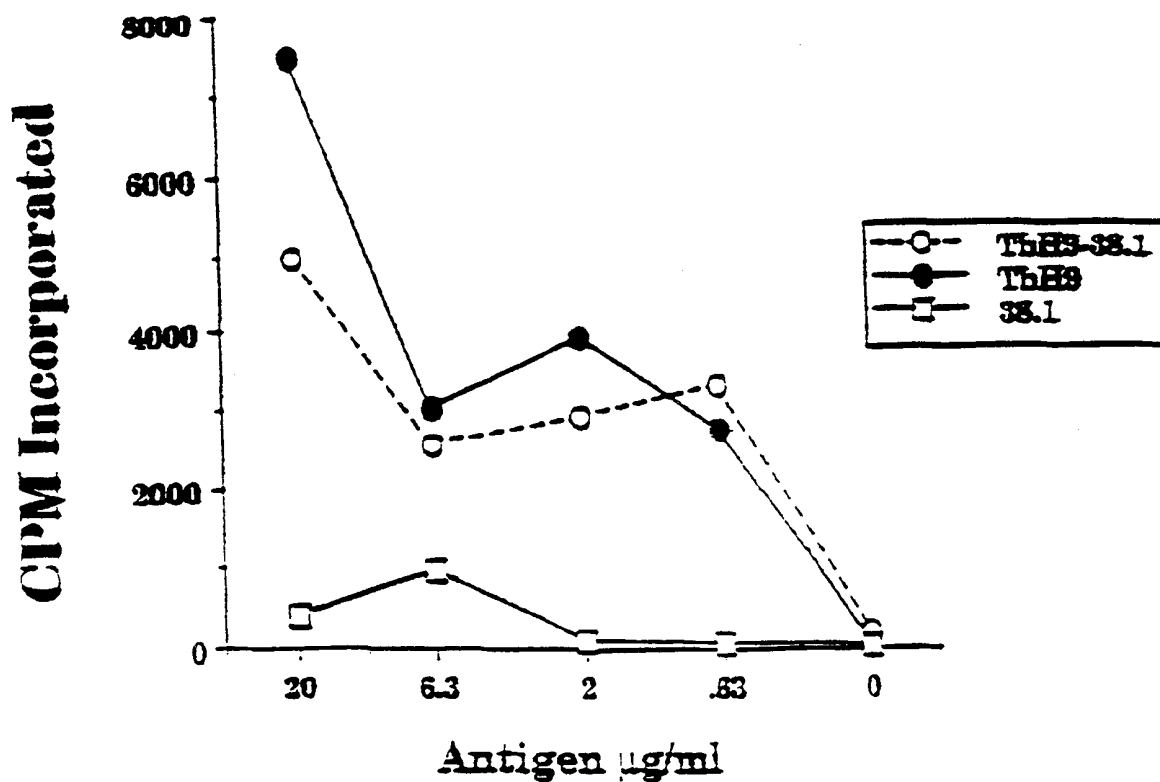
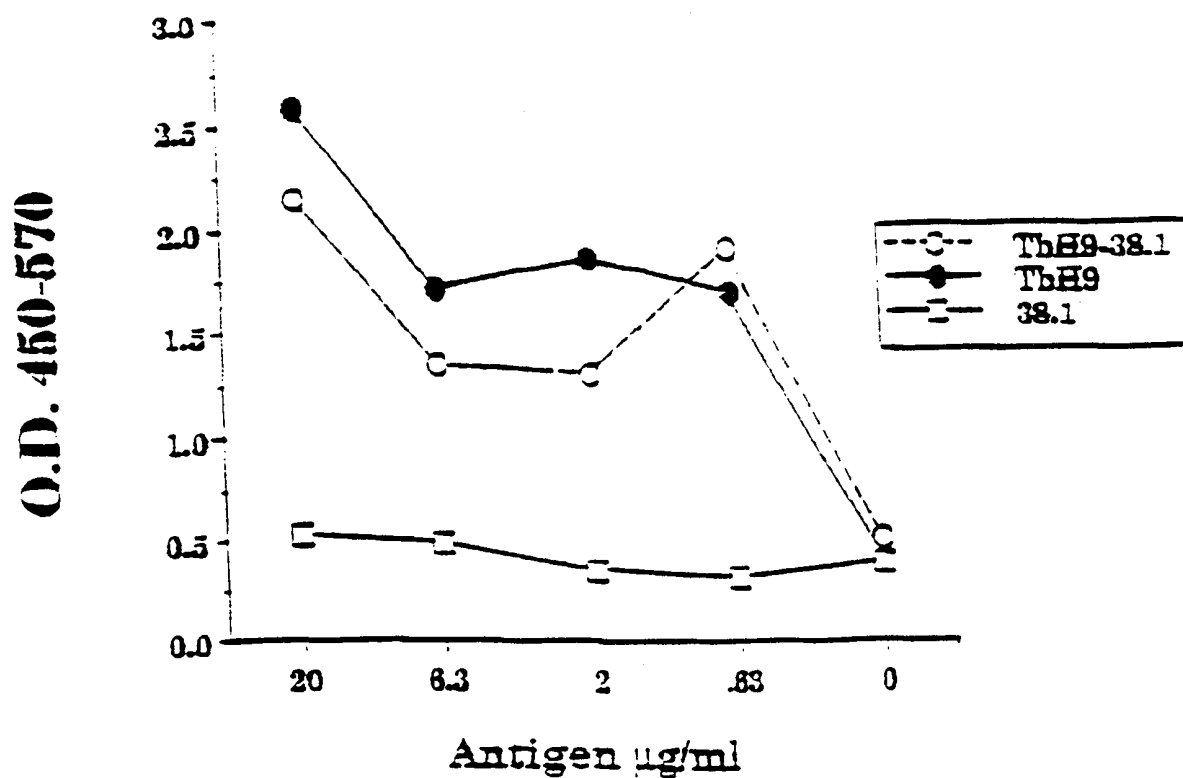


FIG. 4B

D131 T Cell Proliferation

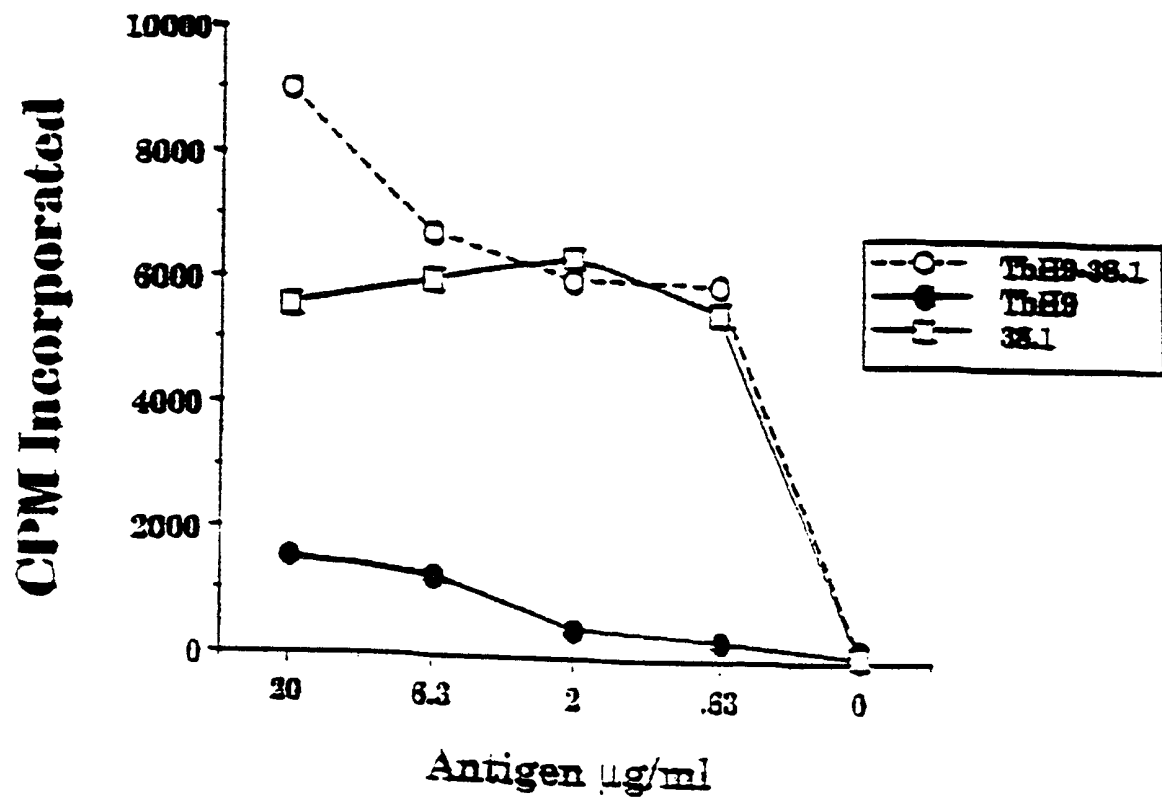


D131 IFN γ

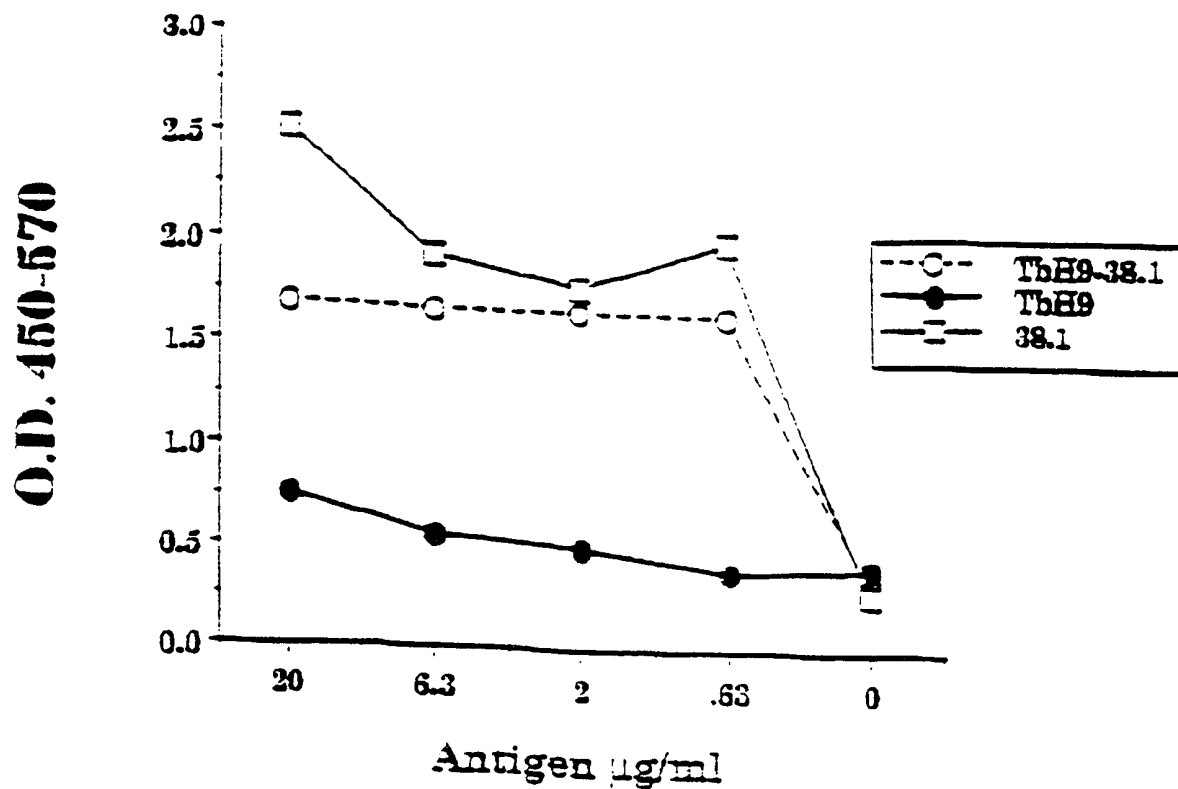


FIGS. 5 A-B

D184 T Cell Proliferation

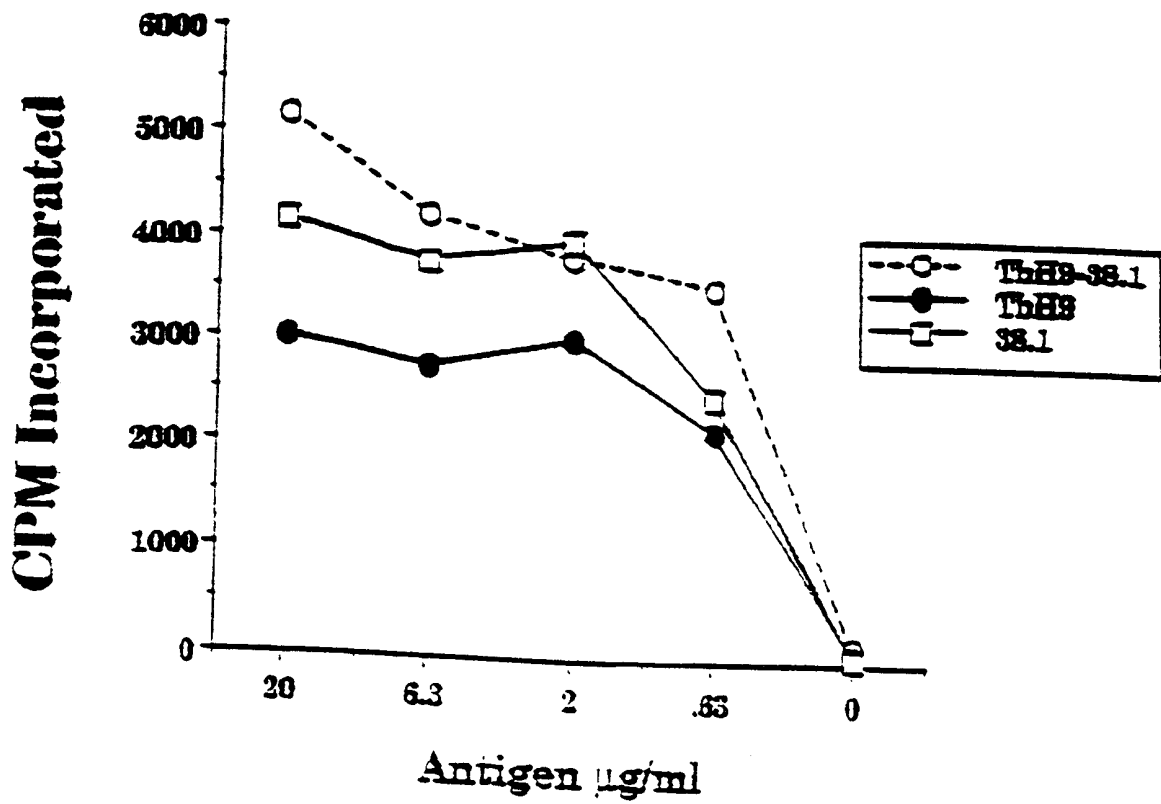


D184 IFN γ

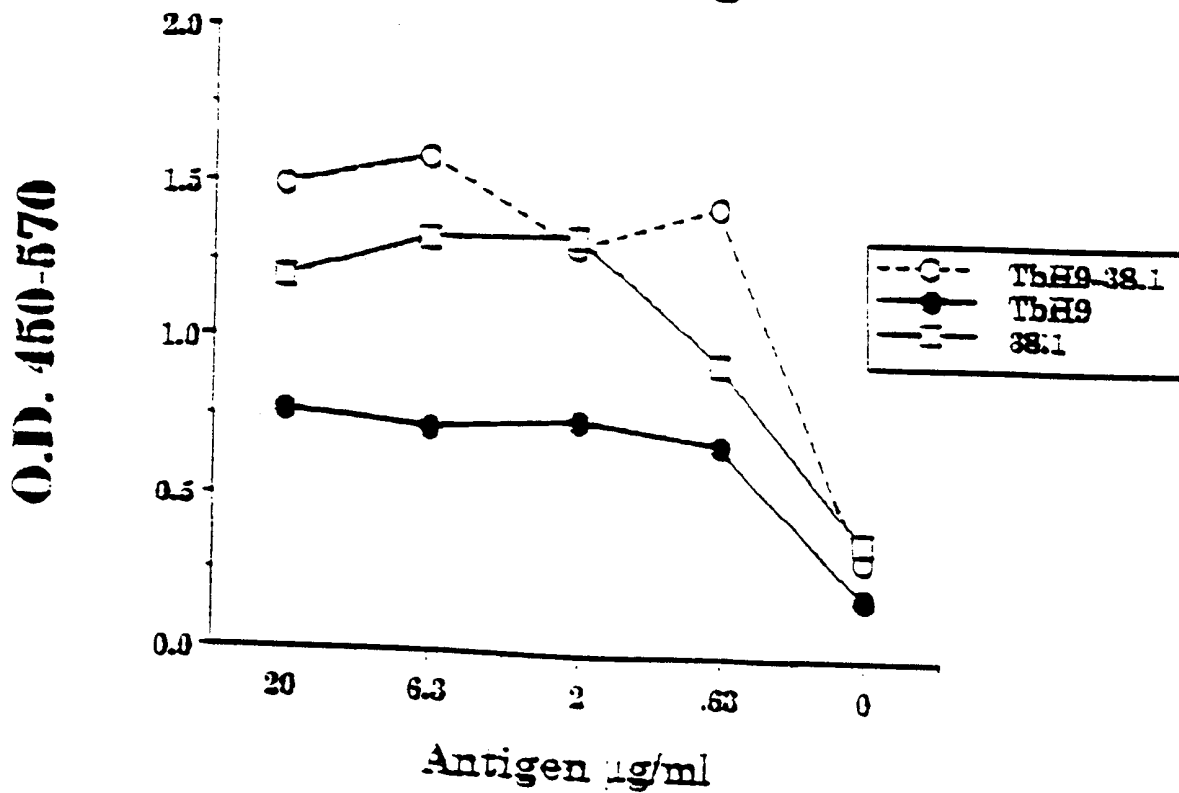


FIGS. 6 A-B

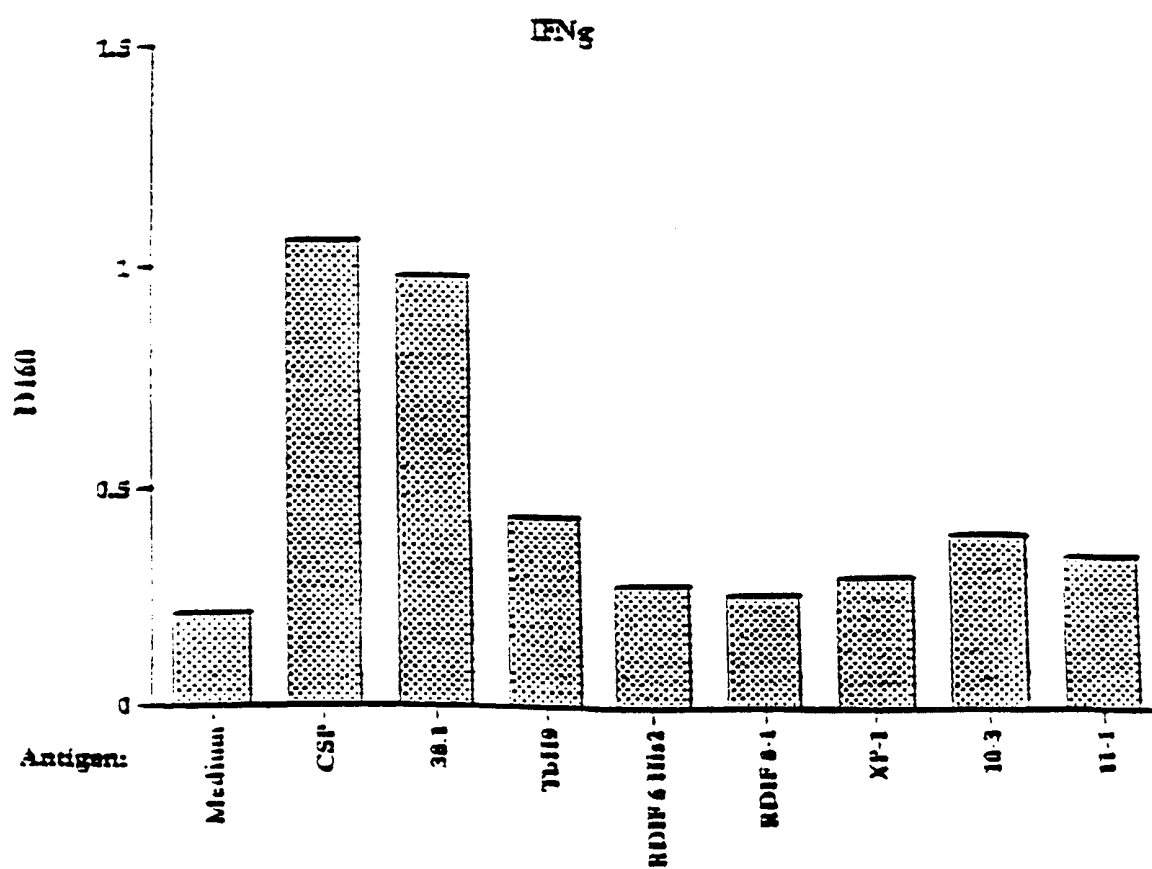
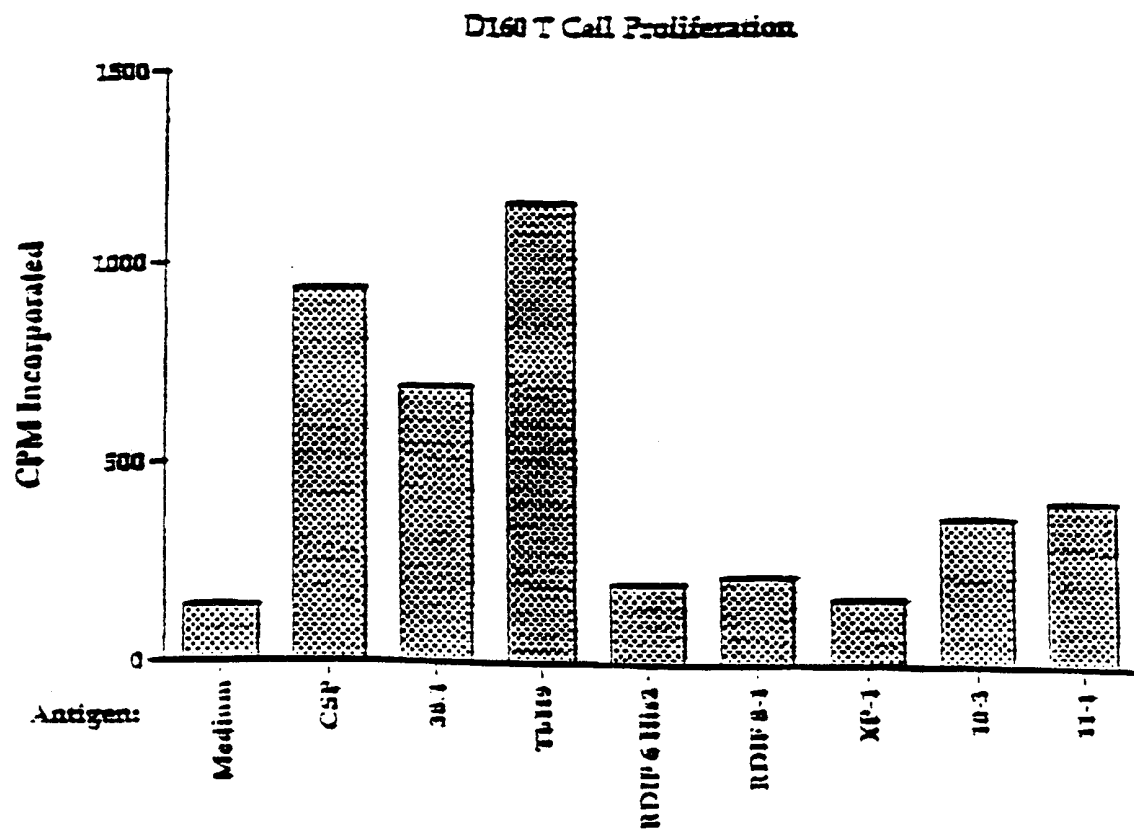
D201 T Cell Proliferation

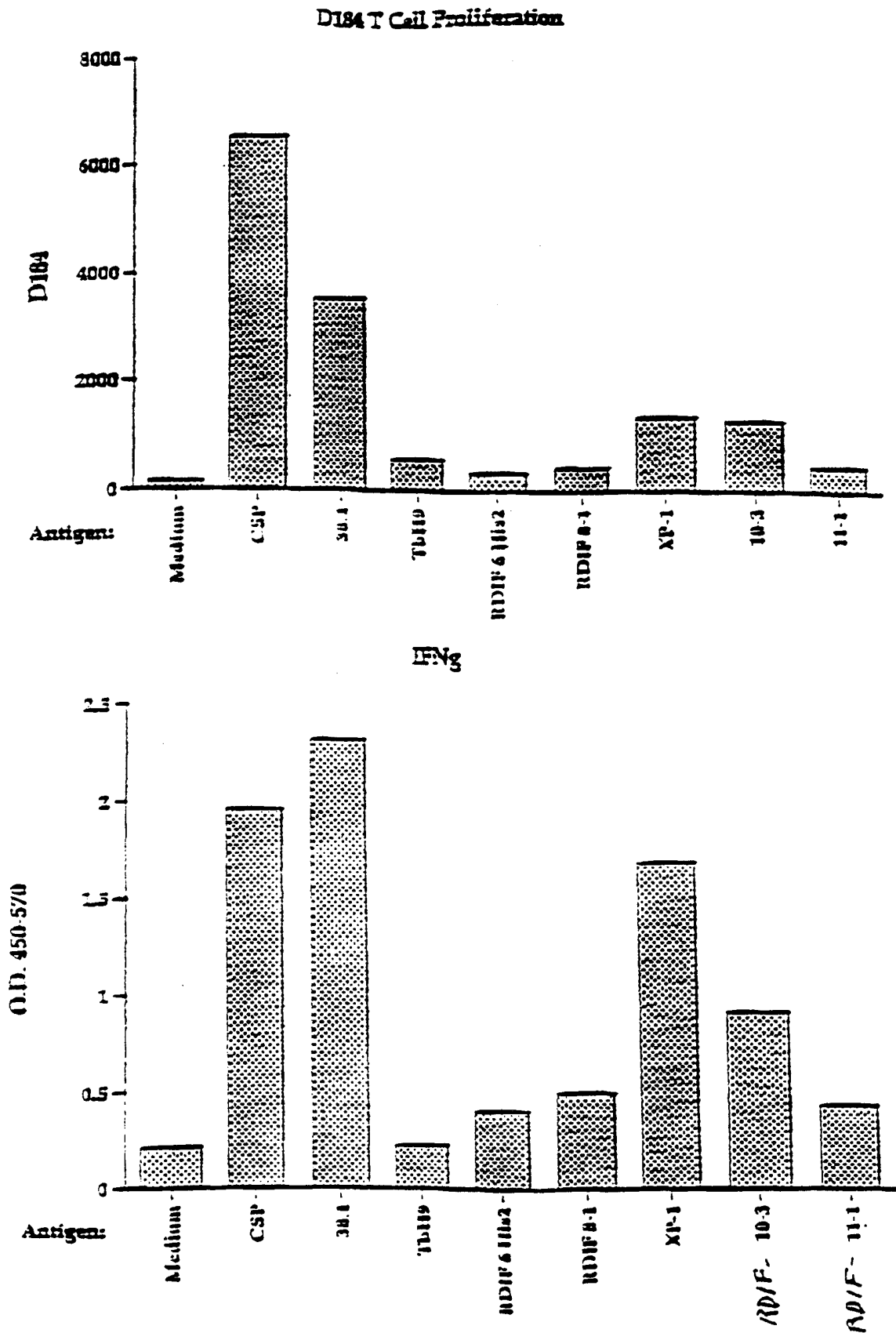


D201 IFNg



FIGS. 7A-B

**FIGS. 8A-B**

**FIGS. 9A-B**

**Tuberculosis: Protection of Cynomolgus Monkeys
with Recombinant Antigens of Mtb**

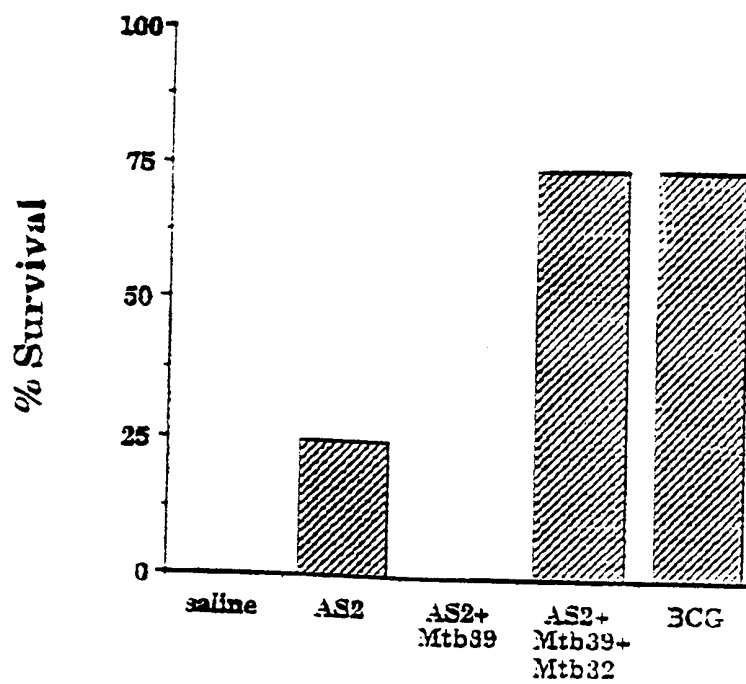
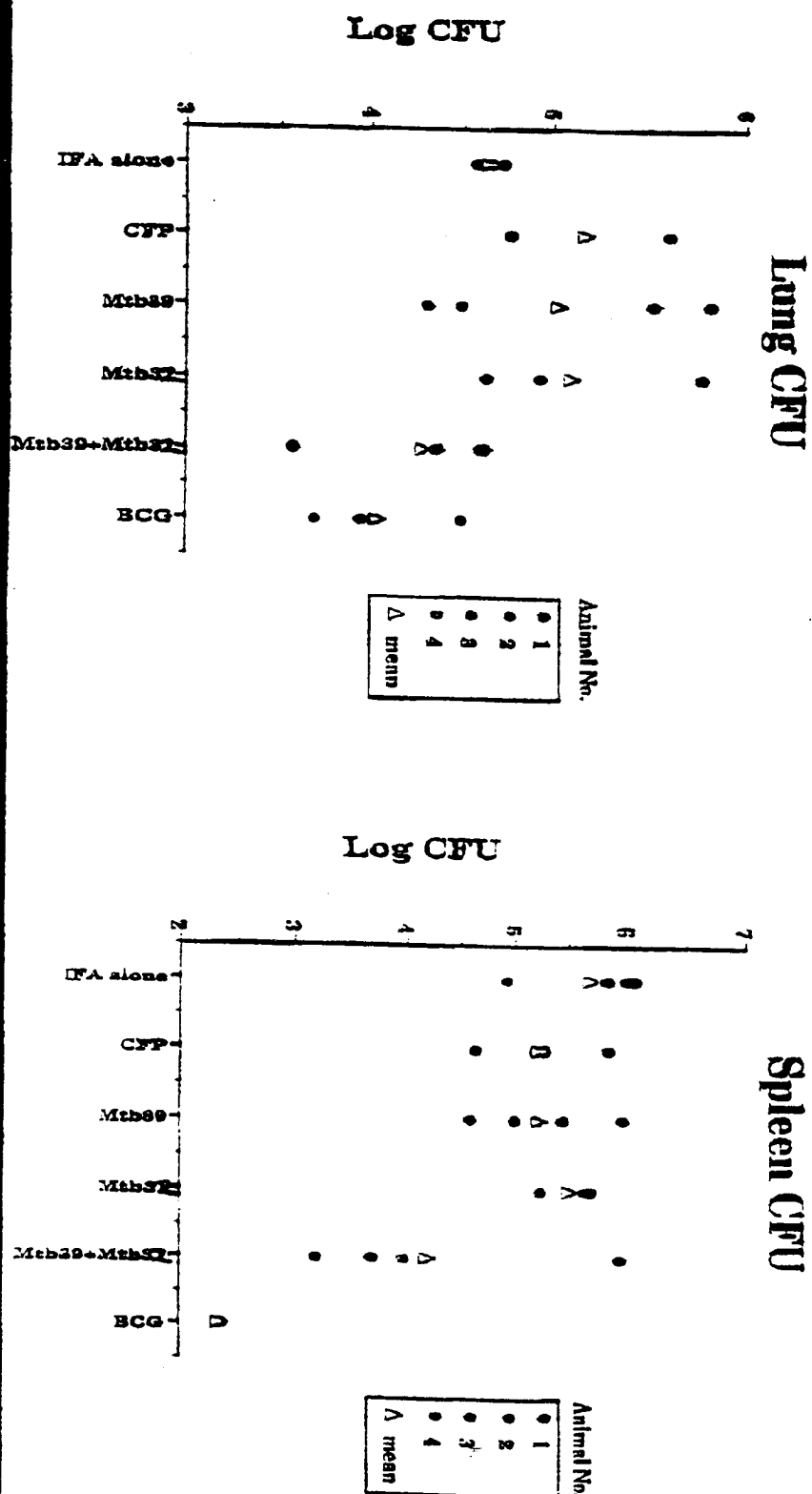


FIG. 10

Aerosol TB challenge of Vaccinated Guinea Pigs



FIGS. 11 A-B

DNA Immunized mice challenged with aerosol TB (lung CFU)

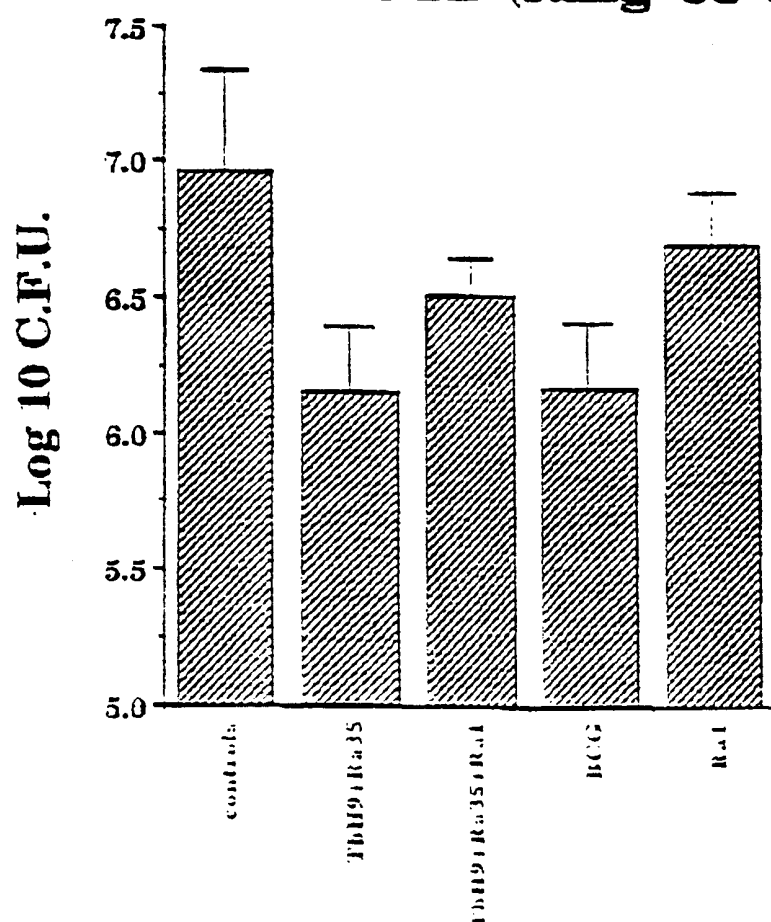


FIG. 12