



US 20060160159A1

(19) **United States**

(12) **Patent Application Publication**  
**Handfield et al.**

(10) **Pub. No.: US 2006/0160159 A1**  
(43) **Pub. Date: Jul. 20, 2006**

(54) **IDENTIFICATION OF ACTINOBACILLUS  
ACTINOMYCETEMCOMITANS ANTIGENS  
FOR USE IN THE DIAGNOSIS, TREATMENT,  
AND MONITORING OF PERIODONTAL  
DISEASES**

(75) Inventors: **Martin Handfield**, Gainesville, FL  
(US); **Jeffrey Daniel Hillman**,  
Gainesville, FL (US); **Ann  
Progulske-Fox**, Keystone Heights, FL  
(US)

Correspondence Address:  
**MCDONNELL BOEHNEN HULBERT &  
BERGHOFF LLP**  
**300 S. WACKER DRIVE**  
**32ND FLOOR**  
**CHICAGO, IL 60606 (US)**

(73) Assignee: **University of Florida Research Founda-  
tion**

(21) Appl. No.: **11/333,747**

(22) Filed: **Jan. 17, 2006**

**Related U.S. Application Data**

(60) Division of application No. 09/995,493, filed on Nov.  
28, 2001, now Pat. No. 7,052,860.  
Continuation-in-part of application No. PCT/US02/  
37235, filed on Nov. 20, 2002.  
Continuation-in-part of application No. PCT/US03/  
32645, filed on Oct. 15, 2003.

**Publication Classification**

(51) **Int. Cl.**  
**G01N 33/554** (2006.01)  
**G01N 33/569** (2006.01)  
(52) **U.S. Cl.** ..... **435/7.32**

(57) **ABSTRACT**

Antibodies, polypeptides, and polynucleotides are provided  
for the detection, prevention, amelioration and treatment of  
diseases caused by *Actinobacillus actinomycetemcomitans*.

**IDENTIFICATION OF ACTINOBACILLUS  
ACTINOMYCETEMCOMITANS ANTIGENS FOR  
USE IN THE DIAGNOSIS, TREATMENT, AND  
MONITORING OF PERIODONTAL DISEASES**

GOVERNMENT INTERESTS

[0001] This invention was made with Government support under Grant Number RO1 DE 13523 awarded by the National Institutes of Health (National Institute for Dental and Craniofacial Research, NIDCR). The Government has certain rights in the invention.

TECHNICAL AREA OF THE INVENTION

[0002] This invention provides methods and compositions for the diagnosis, treatment, preventions, and amelioration of diseases caused by *Actinobacillus actinomycetemcomitans*.

BACKGROUND OF THE INVENTION

[0003] *Actinobacillus actinomycetemcomitans* (Aa) is the principal etiologic agent of early-onset periodontitis including localized and generalized prepubertal periodontitis, localized and generalized juvenile periodontitis, and rapidly progressive or refractory adult periodontitis. Currently, diagnosis of these diseases is made by X-ray analysis usually long after the onset of the disease and after considerable damage to the supporting bone and tissue has occurred. Tooth loss is the ultimate detrimental effect of destructive periodontal disease. A national survey of the United States revealed a prevalence of localized juvenile periodontitis of 0.53% and of generalized juvenile periodontitis of 0.13%. Loe & Brown, *J. Periodontol.* 62:608-616 (1991). Findings from a number of studies corroborate the conclusion that early-onset disease is similar in other industrialized countries and is more frequent in developing countries. Loe & Brown, *J. Periodontol.* 62:608-616 (1991). Therefore, methods of early diagnosis of early-onset periodontitis, localized and generalized juvenile periodontitis, and rapidly progressive or refractory adult periodontitis are needed in the art. In addition, certain types of adult periodontitis, which in general is a very common condition affecting over half the adult population, are likely to be caused by Aa. Furthermore, Aa can cause extra-oral diseases such as endocarditis, thyroid gland abscesses, urinary tract infections, brain abscesses, and vertebral osteomyelitis.

[0004] There are antibiotic, surgical, and mechanical therapies for the treatment of Aa induced periodontitis, but no means for prevention. Tetracycline has been widely used in the treatment of early-onset periodontitis. There remains a concern, however, of strains developing resistance to tetracycline as well as the possibility of overgrowth of other pathogenic microorganisms. Given the incidence of these diseases, a safe vaccine for Aa is needed. A vaccine can be, for example, a multivalent vaccine. Control of periodontal disease is also very important in light of recent attention to the possible role of periodontal infections as risk factors for systemic disease (e.g., coronary heart disease).

[0005] While most people have Aa as a normal member of their dental plaque, it usually does not cause disease. However, when Aa does cause disease, the host mounts an enormous immune response that is inevitably futile, presumably because the immune response is directed against

the wrong Aa antigens. Providing the most appropriate periodontal treatment requires making an accurate diagnosis, performing optimum treatment, and monitoring the patient's response to therapy.

[0006] Currently, standard microbiological tests for Aa detect only the presence of Aa in dental plaque, and do not specifically identify disease activity. For this reason these tests have a low positive predictive value. Because Aa is normally found in the plaque of even healthy individuals, the application of these tests is limited in their usefulness to those who present with certain clinical manifestations of disease, including for example, patients with advanced attachment loss and bone loss before the age of 25, patients aged about 25-35 with rapid destruction of attachment and bone in a relatively short period of time (rapidly progressive periodontitis), and patients who continue to lose attachment despite stringent treatment (refractory periodontitis).

[0007] DNA probe technology has been developed to identify the presence of Aa in dental plaque, but this technology is unable to distinguish between Aa that is normally part of the dental plaque community and Aa that is involved in an actual disease process. Therefore, these DNA probes do not identify Aa involved in a disease process.

[0008] Therefore, methods of diagnosing, monitoring, treating, preventing, or ameliorating a disease caused by Aa are needed in the art.

SUMMARY OF THE INVENTION

[0009] It is an object of the invention to provide methods and compositions for the treatment, amelioration, and prevention of diseases caused by Aa. This and other objects of the invention are provided by one or more of the embodiments described below.

[0010] One embodiment of the invention provides a purified immunogenic polypeptide comprising at least 5 contiguous amino acids of an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID

NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, and SEQ ID NO:234 (“the polypeptide SEQ IDs”). While each of these polypeptide sequences are collectively referred to as “the polypeptide SEQ IDs” and are presented together in a group, each of these sequences can be separately considered and claimed.

[0011] Another embodiment of the invention provides a purified polypeptide comprising an amino acid sequence selected from the group consisting of “the polypeptide SEQ IDs.”

[0012] Yet another embodiment of the invention provides a purified polynucleotide comprising a sequence that encodes a “polypeptide SEQ ID.”

[0013] Still another embodiment of the invention provides a purified polynucleotide comprising at least about 15 contiguous nucleic acids of a sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231 and SEQ ID NO:233 (“the polynucleotide SEQ IDs”). While each of these polynucleotide sequences are

collectively referred to as “the polynucleotide SEQ IDs” and are presented together in a group, each of these sequences can be separately considered and claimed.

[0014] Even another embodiment of the invention provides a purified polynucleotide comprising the nucleotide sequence of “the polynucleotide SEQ IDs” or degenerate variants thereof.

[0015] Another embodiment of the invention provides an expression vector comprising a “polynucleotide SEQ ID” operably linked to an expression control sequence. The vector can be in a cultured cell.

[0016] Still another embodiment of the invention provides an antibody or a fragment thereof that specifically binds to a polypeptide of “the polypeptide SEQ IDs.” An antibody fragment can be, for example, a Fab or F(ab)<sub>2</sub> fragment. The antibody can be a monoclonal antibody or a polyclonal antibody. The antibody can be present in a pharmaceutical composition along with a pharmaceutically acceptable carrier.

[0017] Yet another embodiment of the invention provides a method for treating, ameliorating, or preventing a disease caused by *A. actinomycetemcomitans*. The method comprises administering to an animal an antibody of the invention or fragment thereof. A disease caused by *A. actinomycetemcomitans* is thereby treated, ameliorated, or prevented. A disease caused by *A. actinomycetemcomitans* can be selected from the group consisting of localized prepubertal periodontitis, generalized prepubertal periodontitis, localized juvenile periodontitis, generalized juvenile periodontitis, rapidly progressive adult periodontitis, refractory adult periodontitis, endocarditis, thyroid gland abscess, urinary tract infection, brain abscess and vertebral osteomyelitis.

[0018] Even another embodiment of the invention provides a method of detecting the presence of *A. actinomycetemcomitans* or an *A. actinomycetemcomitans* antigen in a test sample. The method comprises contacting a test sample with an antibody of the invention that specifically binds *A. actinomycetemcomitans* or an *A. actinomycetemcomitans* antigen under conditions that allow formation of an immunocomplex between the antibody and the *A. actinomycetemcomitans* or the *A. actinomycetemcomitans* antigen and detecting an immunocomplex. Detection of the immunocomplex indicates the presence of *A. actinomycetemcomitans* or an *A. actinomycetemcomitans* antigen in the test sample. The detected *A. actinomycetemcomitans* antigen can be an antigen that is expressed in vivo during infection of an animal.

[0019] Another embodiment of the invention provides a pharmaceutical composition that comprises a polypeptide of the invention and a pharmaceutically acceptable carrier.

[0020] Still another embodiment of the invention provides a method of eliciting an immune response. The method comprises administering a polypeptide of the invention to an animal, wherein an immune response is elicited.

[0021] Yet another embodiment of the invention provides a method of treating, preventing, or ameliorating a disease or infection caused by *A. actinomycetemcomitans*. The method comprises administering a polypeptide of the invention to an animal, wherein the disease or infection is treated, prevented, or ameliorated.

[0022] Even another embodiment of the invention provides a composition comprising a polynucleotide of the invention and a pharmaceutically acceptable carrier. The polynucleotide can be DNA. The polynucleotide can be in a plasmid.

[0023] Another method of the invention provides a method of eliciting an immune response comprising administering a purified polynucleotide of the invention to an animal, wherein an immune response is elicited. Still another embodiment of the invention provides a method of treating, preventing, or ameliorating a disease or infection caused by *A. actinomycetemcomitans*. The method comprises administering a purified polynucleotide of the invention to an animal, wherein the disease or infection is treated, prevented, or ameliorated.

[0024] Yet another embodiment of the invention provides a method for identifying the presence of a first *A. actinomycetemcomitans* polynucleotide. The method comprises contacting a test sample suspected of containing a first *A. actinomycetemcomitans* polynucleotide with a second polynucleotide, wherein the second polynucleotide is a polynucleotide of the invention, under hybridization conditions. A hybridized first and second polynucleotide complex is detected. The presence of a hybridized first and second polynucleotide indicates the presence of a first polynucleotide in the test sample.

#### DETAILED DESCRIPTION OF THE INVENTION

##### Method of Identification of Polynucleotides and Polypeptides

[0025] A method for identifying nucleotide sequences that are important to a microorganism's ability to cause disease has been applied to Aa, the principal etiologic agent of early-onset periodontitis including localized prepubertal periodontitis, generalized prepubertal periodontitis, localized juvenile periodontitis, generalized juvenile periodontitis, rapidly progressive adult periodontitis, and refractory adult periodontitis. Aa can also cause endocarditis, thyroid gland abscess, urinary tract infection, brain abscess and vertebral osteomyelitis. The method used to identify polynucleotide and polypeptide sequences of the invention is termed *in vivo* induced antigen technology (IVIAT). See Handfield et al., Trends Microbiol. 336:336-339 (2000); WO 01/11081.

[0026] Briefly, IVIAT comprises obtaining a sample of antibodies against Aa antigens that are expressed by Aa *in vivo* and *in vitro* and adsorbing the antibodies with cells or cellular extracts of Aa that have been grown *in vitro*. An example of a sample of antibodies that can be used is sera from patients who have been or are infected with Aa. The unadsorbed antibodies are isolated and are used to probe an expression library of Aa DNA. Reactive clones are isolated and the cloned fragments sequenced.

[0027] IVIAT was used to identify polynucleotides of Aa that are expressed only when Aa is engaged in actually causing disease in animals, and in particular humans. Important environmental signals that normally cause Aa to turn on virulence genes during an infection are missing when the bacteria are grown in the laboratory. Therefore, many of the best targets for diagnostic and vaccine strategies were unknown. IVIAT methodology was used to identify poly-

nucleotides that are specifically turned on during growth of Aa in a human host and not during routine laboratory growth. These polynucleotides and corresponding polypeptides and antibodies are useful in developing diagnostic tests for Aa to identify, for example, subjects who are in early stages of infection and for monitoring response to therapy, and for developing vaccines or treatments to prevent or treat diseases caused by Aa in susceptible animals.

[0028] Aa antigens identified by IVIAT have a high predictive value with regard to diseases caused by Aa, for example, periodontal diseases. Diagnostic tests for Aa can be useful in applications such as screening children whose mothers have a history of periodontitis to determine if the children have acquired a predisposition for the disease. Diseases known to be associated with periodontitis before puberty include Papillon-Lefevre syndrome (PLS), hypophosphatasia, neutropenias, leukocyte adhesion deficiency (LAD), Chediak-Higashi syndrome, Down's syndrome, leukemia, histiocytosis X, early-onset Type I diabetes, and acro-dynia. Children with these diseases are candidates for Aa testing. Additionally, other preadolescent children who are less prone to periodontitis would benefit from an Aa diagnostic test since there are no other predictors or known risk factors.

##### Polypeptides

[0029] Purified polypeptides of the invention can either be full-length polypeptides or fragments of polypeptides. For example, fragments of polypeptides of the invention can comprise about 5, 10, 25, 50, 100, or 200 amino acids of polypeptides of the invention. Examples of polypeptides of the invention include those shown in SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, SEQ ID NO:38, SEQ ID NO:40, SEQ ID NO:42, SEQ ID NO:44, SEQ ID NO:46, SEQ ID NO:48, SEQ ID NO:50, SEQ ID NO:52, SEQ ID NO:54, SEQ ID NO:56, SEQ ID NO:58, SEQ ID NO:60, SEQ ID NO:62, SEQ ID NO:64, SEQ ID NO:66, SEQ ID NO:68, SEQ ID NO:70, SEQ ID NO:72, SEQ ID NO:74, SEQ ID NO:76, SEQ ID NO:78, SEQ ID NO:80, SEQ ID NO:82, SEQ ID NO:84, SEQ ID NO:86, SEQ ID NO:88, SEQ ID NO:90, SEQ ID NO:92, SEQ ID NO:94, SEQ ID NO:96, SEQ ID NO:98, SEQ ID NO:100, SEQ ID NO:102, SEQ ID NO:104, SEQ ID NO:106, SEQ ID NO:108, SEQ ID NO:110, SEQ ID NO:112, SEQ ID NO:114, SEQ ID NO:116, SEQ ID NO:118, SEQ ID NO:120, SEQ ID NO:122, SEQ ID NO:124, SEQ ID NO:126, SEQ ID NO:128, SEQ ID NO:130, SEQ ID NO:132, SEQ ID NO:134, SEQ ID NO:136, SEQ ID NO:138, SEQ ID NO:140, SEQ ID NO:142, SEQ ID NO:144, SEQ ID NO:146, SEQ ID NO:148, SEQ ID NO:150, SEQ ID NO:152, SEQ ID NO:154, SEQ ID NO:156, SEQ ID NO:158, SEQ ID NO:160, SEQ ID NO:162, SEQ ID NO:164, SEQ ID NO:166, SEQ ID NO:168, SEQ ID NO:170, SEQ ID NO:172, SEQ ID NO:174, SEQ ID NO:176, SEQ ID NO:178, SEQ ID NO:180, SEQ ID NO:182, SEQ ID NO:184, SEQ ID NO:186, SEQ ID NO:188, SEQ ID NO:190, SEQ ID NO:192, SEQ ID NO:194, SEQ ID NO:196, SEQ ID NO:198, SEQ ID NO:200, SEQ ID NO:202, SEQ ID NO:204, SEQ ID NO:206, SEQ ID NO:208, SEQ ID NO:210, SEQ ID

NO:212, SEQ ID NO:214, SEQ ID NO:216, SEQ ID NO:218, SEQ ID NO:220, SEQ ID NO:222, SEQ ID NO:224, SEQ ID NO:226, SEQ ID NO:228, SEQ ID NO:230, SEQ ID NO:232, and SEQ ID NO:234. These polypeptides will be referred to as "the polypeptide SEQ IDs." Homologous amino acid sequences that are at least about 75, or about 90, 96, 98, or 99% identical to the polypeptide sequences shown in the polypeptide SEQ IDs are also Aa polypeptides. Homologous amino acid sequences retain biological activity, i.e., are biologically functional equivalents.

[0030] Percent sequence identity has an art recognized meaning and there are a number of methods to measure identity between two polypeptide or polynucleotide sequences. See, e.g., Lesk, Ed., *Computational Molecular Biology*, Oxford University Press, New York, (1988); Smith, Ed., *Biocomputing: Informatics And Genome Projects*, Academic Press, New York, (1993); Griffin & Griffin, Eds., *Computer Analysis Of Sequence Data, Part I*, Humana Press, New Jersey, (1994); von Heinje, *Sequence Analysis In Molecular Biology*, Academic Press, (1987); and Gribskov & Devereux, Eds., *Sequence Analysis Primer*, M Stockton Press, New York, (1991). Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux et al., *Nuc. Acids Res.* 12:387 (1984)), BLASTP, BLASTN, FASTA (Atschul et al., *J. Molec. Biol.* 215:403 (1990)), and Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research Park, 575 Science Drive, Madison, Wis. 53711) which uses the local homology algorithm of Smith and Waterman (*Adv. App. Math.*, 2:482-489 (1981)). For example, the computer program ALIGN which employs the FASTA algorithm can be used, with an affine gap search with a gap open penalty of -12 and a gap extension penalty of -2.

[0031] When using any of the sequence alignment programs to determine whether a particular sequence is, for instance, about 95% identical to a reference sequence, the parameters are set such that the percentage of identity is calculated over the full length of the reference polynucleotide and that gaps in identity of up to 5% of the total number of nucleotides in the reference polynucleotide are allowed.

[0032] Variants of polypeptides shown in the polypeptide SEQ IDs and fragments thereof are also included in the invention. A variant is a polypeptide that differs from a polypeptide SEQ ID or fragment thereof, only in conservative substitutions and/or modifications, such that the antigenic properties of the polypeptide are substantially the same as the original polypeptide. Variants can generally be identified by modifying one of the polypeptide sequences of the invention, and evaluating the antigenic properties of the modified polypeptide using, for example, an immunohistochemical assay, an enzyme-linked immunosorbant assay (ELISA), a radioimmunoassay (RIA), or a western blot assay. Polypeptides of the invention can comprise at least 1, 5, 10, 25, 50, or 100 conservative amino acid substitutions.

[0033] 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 hydrophobic 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.

[0034] Variants can also (or alternatively) be modified by, for example, the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydrophobic nature of the polypeptide. For example, a polypeptide can 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 can also be conjugated to a linker or other 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 can be conjugated to an immunoglobulin Fc region.

[0035] Polypeptides of the invention further comprise biologically functional equivalents of at least about 5, 10, 25, 50, 100, or 200 amino acids of the polypeptides shown in the polypeptide SEQ IDs. A polypeptide is a biological equivalent if it reacts substantially the same as a polypeptide of the invention in an assay such as an immunohistochemical assay, an ELISA, an RIA, or a western blot assay, e.g. has 90-110% of the activity of the original polypeptide. In one embodiment, the assay is a competition assay wherein the biologically equivalent polypeptide is capable of reducing binding of the polypeptide of the invention to a corresponding reactive antigen or antibody by about 80, 95, 99, or 100%.

[0036] Polypeptides of the invention can comprise an antigen that is recognized by an antibody reactive against Aa. The antigen can comprise one or more epitopes (or antigenic determinants). An epitope can be a linear epitope, sequential epitope or a conformational epitope. Epitopes within a polypeptide of the invention can be identified by several methods. See, e.g., U.S. Pat. No. 4,554,101; Jameson & Wolf, *CABIOS*: 181-186(1988). For example, a polypeptide of the invention can be isolated and screened. A series of short peptides, which together span an entire polypeptide sequence, can be prepared by proteolytic cleavage. By starting with, for example, 100-mer polypeptide fragments, each fragment can be tested for the presence of epitopes recognized in an ELISA. For example, in an ELISA assay an Aa polypeptide, such as a 100-mer polypeptide fragment, is attached to a solid support, such as the wells of a plastic multi-well plate. A population of antibodies are labeled, added to the solid support and allowed to bind to the unlabeled antigen, under conditions where non-specific adsorption is blocked, and any unbound antibody and other proteins are washed away. Antibody binding is detected by, for example, a reaction that converts a colorless substrate into a colored reaction product. Progressively smaller and overlapping fragments can then be tested from an identified 100-mer to map the epitope of interest.

[0037] A polypeptide of the invention can be produced recombinantly. A polynucleotide encoding a polypeptide of the invention can be introduced into a recombinant expression vector, which can be expressed in a suitable expression host cell system using techniques well known in the art. A variety of bacterial, yeast, plant, mammalian, and insect expression systems are available in the art and any such

expression system can be used. Optionally, a polynucleotide encoding a polypeptide can be translated in a cell-free translation system. A polypeptide can also be chemically synthesized.

[0038] If desired, a polypeptide can be produced as a fusion protein, which can also contain other amino acid sequences, such as amino acid linkers or signal sequences, as well as ligands useful in protein purification, such as glutathione-S-transferase, histidine tag, and staphylococcal protein A. More than one polypeptide of the invention can be present in a fusion protein.

#### Polynucleotides

[0039] Polynucleotides of the invention contain less than an entire microbial genome and can be single- or double-stranded DNA or RNA. The polynucleotides can be purified free of other components, such as proteins and lipids. The polynucleotides of the invention encode the polypeptides described above. Polynucleotides of the invention can also comprise other nucleotide sequences, such as sequences coding for linkers, signal sequences, heterologous signal sequences, TMR stop transfer sequences, transmembrane domains, or ligands useful in protein purification such as glutathione-S-transferase, histidine tag, and staphylococcal protein A.

[0040] Polynucleotides of the invention are shown in SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, SEQ ID NO:35, SEQ ID NO:37, SEQ ID NO:39, SEQ ID NO:41, SEQ ID NO:43, SEQ ID NO:45, SEQ ID NO:47, SEQ ID NO:49, SEQ ID NO:51, SEQ ID NO:53, SEQ ID NO:55, SEQ ID NO:57, SEQ ID NO:59, SEQ ID NO:61, SEQ ID NO:63, SEQ ID NO:65, SEQ ID NO:67, SEQ ID NO:69, SEQ ID NO:71, SEQ ID NO:73, SEQ ID NO:75, SEQ ID NO:77, SEQ ID NO:79, SEQ ID NO:81, SEQ ID NO:83, SEQ ID NO:85, SEQ ID NO:87, SEQ ID NO:89, SEQ ID NO:91, SEQ ID NO:93, SEQ ID NO:95, SEQ ID NO:97, SEQ ID NO:99, SEQ ID NO:101, SEQ ID NO:103, SEQ ID NO:105, SEQ ID NO:107, SEQ ID NO:109, SEQ ID NO:111, SEQ ID NO:113, SEQ ID NO:115, SEQ ID NO:117, SEQ ID NO:119, SEQ ID NO:121, SEQ ID NO:123, SEQ ID NO:125, SEQ ID NO:127, SEQ ID NO:129, SEQ ID NO:131, SEQ ID NO:133, SEQ ID NO:135, SEQ ID NO:137, SEQ ID NO:139, SEQ ID NO:141, SEQ ID NO:143, SEQ ID NO:145, SEQ ID NO:147, SEQ ID NO:149, SEQ ID NO:151, SEQ ID NO:153, SEQ ID NO:155, SEQ ID NO:157, SEQ ID NO:159, SEQ ID NO:161, SEQ ID NO:163, SEQ ID NO:165, SEQ ID NO:167, SEQ ID NO:169, SEQ ID NO:171, SEQ ID NO:173, SEQ ID NO:175, SEQ ID NO:177, SEQ ID NO:179, SEQ ID NO:181, SEQ ID NO:183, SEQ ID NO:185, SEQ ID NO:187, SEQ ID NO:189, SEQ ID NO:191, SEQ ID NO:193, SEQ ID NO:195, SEQ ID NO:197, SEQ ID NO:199, SEQ ID NO:201, SEQ ID NO:203, SEQ ID NO:205, SEQ ID NO:207, SEQ ID NO:209, SEQ ID NO:211, SEQ ID NO:213, SEQ ID NO:215, SEQ ID NO:217, SEQ ID NO:219, SEQ ID NO:221, SEQ ID NO:223, SEQ ID NO:225, SEQ ID NO:227, SEQ ID NO:229, SEQ ID NO:231, and SEQ ID NO:233. These polynucleotides will be referred to as the "polynucleotide SEQ IDs."

[0041] Degenerate nucleotide sequences encoding polypeptides of the invention, as well as homologous nucleotide sequences that are at least about 75, or about 90, 96, 98, or 99% identical to the nucleotide sequences shown in the polynucleotide SEQ IDs and the complements thereof are also polynucleotides of the invention. Percent sequence identity can be calculated as described in the "Polypeptides" section. Degenerate nucleotide sequences are polynucleotides that encode a polypeptide shown in the polypeptide SEQ IDs or fragments thereof, but differ in nucleic acid sequence from the sequence given in the polynucleotide SEQ IDs, due to the degeneracy of the genetic code. Complementary DNA (cDNA) molecules, species homologs, and variants of Aa polynucleotides that encode biologically functional Aa polypeptides also are Aa polynucleotides. A polynucleotide of the invention can comprise about 5, 10, 15, 50, 100, or 200 nucleotides of a nucleic acid sequence shown in the polynucleotide SEQ IDs.

[0042] Polynucleotides of the invention can be isolated from nucleic acid sequences present in, for example, a biological sample, such as plaque, saliva, crevicular fluid, sputum, blood, serum, plasma, urine, feces, cerebrospinal fluid, amniotic fluid, wound exudate, or tissue, from an infected individual. Polynucleotides can also be synthesized in the laboratory, for example, using an automatic synthesizer. An amplification method such as PCR can be used to amplify polynucleotides from either genomic DNA or cDNA encoding the polypeptides.

[0043] Polynucleotides of the invention can comprise coding sequences for naturally occurring polypeptides or can encode altered sequences which do not occur in nature. If desired, polynucleotides can be cloned into an expression vector comprising expression control elements, including for example, origins of replication, promoters, enhancers, or other regulatory elements that drive expression of the polynucleotides of the invention in host cells. An expression vector can be, for example, a plasmid, such as pBR322, pUC, or ColE1, or an adenovirus vector, such as an adenovirus Type 2 vector or Type 5 vector. Optionally, other vectors can be used, including but not limited to Sindbis virus, simian virus 40, alphavirus vectors, poxvirus vectors, and cytomegalovirus and retroviral vectors, such as murine sarcoma virus, mouse mammary tumor virus, Moloney murine leukemia virus, and Rous sarcoma virus. Minichromosomes such as MC and MC 1, bacteriophages, phagemids, yeast artificial chromosomes, bacterial artificial chromosomes, virus particles, virus-like particles, cosmids (plasmids into which phage lambda cos sites have been inserted) and replicons (genetic elements that are capable of replication under their own control in a cell) can also be used.

[0044] Methods for preparing polynucleotides operably linked to an expression control sequence and expressing them in a host cell are well-known in the art. See, e.g., U.S. Pat. No. 4,366,246. A polynucleotide of the invention is operably linked when it is positioned adjacent to one or more expression control elements, which direct transcription and/or translation of the polynucleotide.

[0045] A vector comprising a polynucleotide of the invention can be transformed into, for example, bacterial, yeast, insect, or mammalian cells so that the polypeptides of the invention can be expressed in and isolated from cell culture.

Any of those techniques that are available in the art can be used to introduce polynucleotides into the host cells. These include, but are not limited to, transfection with naked or encapsulated nucleic acids, cellular fusion, protoplast fusion, viral infection, and electroporation.

[0046] Polynucleotides of the invention can be used, for example, as probes or primers, for example PCR primers, to detect the presence of Aa polynucleotides in a sample, such as a biological sample. The ability of such probes and primers to specifically hybridize to Aa polynucleotide sequences will enable them to be of use in detecting the presence of complementary sequences in a given sample. Polynucleotide probes and primers of the invention can hybridize to complementary sequences in a sample such as a biological sample, including plaque, saliva, crevicular fluid, sputum, blood, urine, feces, cerebrospinal fluid, amniotic fluid, wound exudate, or tissue. Polynucleotides from the sample can be, for example, subjected to gel electrophoresis or other size separation techniques or can be immobilized without size separation. The polynucleotide probes or primers can be labeled. Suitable labels, and methods for labeling probes and primers are known in the art, and include, for example, radioactive labels incorporated by nick translation or by kinase, biotin labels, fluorescent labels, chemiluminescent labels, bioluminescent labels, metal chelator labels and enzyme labels. The polynucleotides from the sample are contacted with the probes or primers under hybridization conditions of suitable stringencies.

[0047] Depending on the application, varying conditions of hybridization can be used to achieve varying degrees of selectivity of the probe or primer towards the target sequence. For applications requiring high selectivity, relatively stringent conditions can be used, such as low salt and/or high temperature conditions, such as provided by a salt concentration of from about 0.02 M to about 0.15 M salt at temperatures of from about 50° C. to about 70° C. For applications requiring less selectivity, less stringent hybridization conditions can be used. For example, salt conditions from about 0.14 M to about 0.9M salt, at temperatures ranging from about 20° C. to about 55° C. The presence of a hybridized complex comprising the probe or primer and a complementary polynucleotide from the test sample indicates the presence of Aa or an Aa polynucleotide sequence in the sample.

#### Antibodies

[0048] Antibodies of the invention are antibody molecules that specifically and stably bind to an Aa polypeptide of the invention or fragment thereof. An antibody of the invention can be a polyclonal antibody, a monoclonal antibody, a single chain antibody (scFv), or a fragment of an antibody. Fragments of antibodies are a portion of an intact antibody comprising the antigen binding site or variable region of an intact antibody, wherein the portion is free of the constant heavy chain domains of the Fc region of the intact antibody. Examples of antibody fragments include Fab, Fab', Fab'-SH, F(ab')<sub>2</sub> and F<sub>v</sub> fragments.

[0049] An antibody of the invention can be any antibody class, including for example, IgG, IgM, IgA, IgD and IgE. An antibody or fragment thereof binds to an epitope of a polypeptide of the invention. An antibody can be made in vivo in suitable laboratory animals or in vitro using recom-

binant DNA techniques. Means for preparing and characterizing antibodies are well known in the art. See, e.g., Dean, *Methods Mol. Biol.* 80:23-37 (1998); Dean, *Methods Mol. Biol.* 32:361-79 (1994); Baileg, *Methods Mol. Biol.* 32:381-88 (1994); Gullick, *Methods Mol. Biol.* 32:389-99 (1994); Drenckhahn et al. *Methods Cell. Biol.* 37:7-56 (1993); Morrison, *Ann. Rev. Immunol.* 10:239-65 (1992); Wright et al. *Crit. Rev. Immunol.* 12:125-68(1992). For example, polyclonal antibodies can be produced by administering a polypeptide of the invention to an animal, such as a human or other primate, mouse, rat, rabbit, guinea pig, goat, pig, cow, sheep, donkey, or horse. Serum from the immunized animal is collected and the antibodies are purified from the plasma by, for example, precipitation with ammonium sulfate, followed by chromatography, such as affinity chromatography. Techniques for producing and processing polyclonal antibodies are known in the art.

[0050] Additionally, monoclonal antibodies directed against epitopes present on a polypeptide of the invention can also be readily produced. For example, normal B cells from a mammal, such as a mouse, which was immunized with a polypeptide of the invention can be fused with, for example, HAT-sensitive mouse myeloma cells to produce hybridomas. Hybridomas producing Aa-specific antibodies can be identified using RIA or ELISA and isolated by cloning in semi-solid agar or by limiting dilution. Clones producing Aa-specific antibodies are isolated by another round of screening. Monoclonal antibodies can be screened for specificity using standard techniques, for example, by binding a polypeptide of the invention to a microtiter plate and measuring binding of the monoclonal antibody by an ELISA assay. Techniques for producing and processing monoclonal antibodies are known in the art. See e.g., Kohler & Milstein, *Nature*, 256:495 (1975). Particular isotypes of a monoclonal antibody can be prepared directly, by selecting from the initial fusion, or prepared secondarily, from a parental hybridoma secreting a monoclonal antibody of a different isotype by using a sib selection technique to isolate class-switch variants. See Steplewski et al., *P.N.A.S. U.S.A.* 82:8653 1985; Spria et al., *J. Immunolog. Meth.* 74:307, 1984. Monoclonal antibodies of the invention can also be recombinant monoclonal antibodies. See, e.g., U.S. Pat. No. 4,474,893; U.S. Pat. No. 4,816,567. Antibodies of the invention can also be chemically constructed. See, e.g., U.S. Pat. No. 4,676,980.

[0051] Antibodies of the invention can be chimeric (see, e.g., U.S. Pat. No. 5,482,856), humanized (see, e.g., Jones et al., *Nature* 321:522 (1986); Reichmann et al., *Nature* 332:323 (1988); Presta, *Curr. Op. Struct. Biol.* 2:593 (1992)), or human antibodies. Human antibodies can be made by, for example, direct immortalization, phage display, transgenic mice, or a Trimeria methodology, see e.g., Reissner et al., *Trends Biotechnol.* 16:242-246 (1998).

[0052] Antibodies, either monoclonal and polyclonal, which are directed against Aa antigens, are particularly useful for detecting the presence of Aa or Aa antigens in a sample, such as a serum sample from an Aa-infected human. An immunoassay for Aa or an Aa antigen can utilize one, antibody or several antibodies. An immunoassay for Aa or an Aa antigen can use, for example, a monoclonal antibody directed towards an Aa epitope, a combination of monoclonal antibodies directed towards epitopes of one Aa polypeptide, monoclonal antibodies directed towards

epitopes of different Aa polypeptides, polyclonal antibodies directed towards the same Aa antigen, polyclonal antibodies directed towards different Aa antigens, or a combination of monoclonal and polyclonal antibodies. Immunoassay protocols can be based upon, for example, competition, direct reaction, or sandwich type assays using, for example, labeled antibody. Antibodies of the invention can be labeled with any type of label known in the art, including, for example, fluorescent, chemiluminescent, radioactive, enzyme, colloidal metal, radioisotope and bioluminescent labels.

[0053] Antibodies of the invention or fragments thereof can be bound to a support and used to detect the presence of Aa or an Aa antigen. Supports include, for example, glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses, polyacrylamides, agaroses and magnetite.

[0054] Polyclonal or monoclonal antibodies of the invention can further be used to isolate Aa organisms or Aa antigens by immunoaffinity columns. The antibodies can be affixed to a solid support by, for example, adsorption or by covalent linkage so that the antibodies retain their immunoselective activity. Optionally, spacer groups can be included so that the antigen binding site of the antibody remains accessible. The immobilized antibodies can then be used to bind Aa organisms or Aa antigens from a sample, such as a biological sample including saliva, plaque, crevicular fluid, sputum, blood, urine, feces, cerebrospinal fluid, amniotic fluid, wound exudate, or tissue. The bound Aa organisms or Aa antigens are recovered from the column matrix by, for example, a change in pH.

[0055] Antibodies of the invention can also be used in immunolocalization studies to analyze the presence and distribution of a polypeptide of the invention during various cellular events or physiological conditions. Antibodies can also be used to identify molecules involved in passive immunization and to identify molecules involved in the biosynthesis of non-protein antigens. Identification of such molecules can be useful in vaccine development. Antibodies of the invention, including, for example, monoclonal antibodies and single chain antibodies, can be used to monitor the course of amelioration of a disease caused by Aa. By measuring the increase or decrease of Aa antibodies to Aa proteins in a test sample from an animal, it can be determined whether a particular therapeutic regimen aimed at ameliorating the disorder is effective. Antibodies can be detected and/or quantified using for example, direct binding assays such as RIA, ELISA, or western blot assays.

[0056] An antibody of the invention can be used in a method of the diagnosis of Aa infection by obtaining a test sample from an animal suspected of having an Aa infection. The test sample is contacted with an antibody of the invention under conditions enabling the formation of an antibody-antigen complex (i.e., an immunocomplex). The amount of antibody-antigen complexes can be determined by methodology known in the art. A level that is higher than that formed in a control sample indicates an Aa infection. Alternatively, a polypeptide of the invention can be contacted with a test sample. Aa antibodies in a positive body sample will form an antigen-antibody complex under suitable conditions. The amount of antibody-antigen complexes can be determined by methods known in the art.

Methods of Treatment, Amelioration, or Prevention of a Disease Caused by Aa

[0057] Polypeptides, polynucleotides, and antibodies of the invention can be used to treat, ameliorate, or prevent a disease caused by Aa, such as early-onset periodontitis including localized and generalized prepubertal periodontitis, localized and generalized juvenile periodontitis, and rapidly progressive or refractory adult periodontitis, endocarditis, thyroid gland abscesses, urinary tract infections, brain abscesses, and vertebral osteomyelitis.

[0058] For example, an antibody, such as a monoclonal antibody of the invention or fragments thereof, can be administered to an animal, such as a human. In one embodiment of the invention an antibody or fragment thereof is administered to an animal in a pharmaceutical composition comprising a pharmaceutically acceptable carrier. A pharmaceutical composition comprises a therapeutically effective amount of an antibody or fragments thereof. A therapeutically effective amount is an amount effective in alleviating the symptoms of Aa infection or in reducing the amount of Aa organisms in a subject.

[0059] Polypeptides or polynucleotides of the invention can be used to elicit an immune response in a host. An immunogenic polypeptide or polynucleotide is a polypeptide or polynucleotide of the invention that is capable of inducing an immune response in an animal. An immunogenic polypeptide or polynucleotide of the invention is particularly useful in sensitizing an immune system of an animal such that, as one result, an immune response is produced that ameliorates or prevents the effect of Aa infection. The elicitation of an immune response in animal model can be useful to determine, for example, optimal doses or administration routes. Elicitation of an immune response can also be used to treat, prevent, or ameliorate a disease or infection caused by Aa. An immune response includes humoral immune responses or cell mediated immune responses, or a combination thereof. An immune response can also comprise the promotion of a generalized host response, e.g., by promoting the production of defensins.

[0060] The generation of an antibody titer by an animal against Aa can be important in protection from infection and clearance of infection. Detection and/or quantification of antibody titers after delivery of a polypeptide or polynucleotide can be used to identify epitopes that are particularly effective at eliciting antibody titers. Epitopes responsible for a strong antibody response to Aa can be identified by eliciting antibodies directed against Aa polypeptides of different lengths. Antibodies elicited by a particular polypeptide epitope can then be tested using, for example, an ELISA assay to determine which polypeptides contain epitopes that are most effective at generating a strong response. Polypeptides or fusion proteins that contain these epitopes or polynucleotides encoding the epitopes can then be constructed and used to elicit a strong antibody response.

[0061] A polypeptide, polynucleotide, or antibody of the invention can be administered to a mammal, such as a mouse, rabbit, guinea pig, macaque, baboon, chimpanzee, human, cow, sheep, pig, horse, dog, cat, or to animals such as chickens or ducks, to elicit antibodies in vivo. Injection of a polynucleotide has the practical advantages of simplicity of construction and modification. Further, injection of a

polynucleotide results in the synthesis of a polypeptide in the host. Thus, the polypeptide is presented to the host immune system with native post-translational modifications, structure, and conformation. A polynucleotide can be delivered to a subject as "naked DNA."

[0062] Administration of a polynucleotide, polypeptide, or antibody can be by any means known in the art, including intramuscular, intravenous, intrapulmonary, intramuscular, intradermal, intraperitoneal, or subcutaneous injection, aerosol, intranasal, infusion pump, suppository, mucosal, topical, and oral, including injection using a biological ballistic gun ("gene gun"). A polynucleotide, polypeptide, or antibody can be accompanied by a protein carrier for oral administration. A combination of administration methods can also be used to elicit an immune response. Antibodies can be administered at a daily dose of about 0.5 mg to about 200 mg. In one embodiment of the invention antibodies are administered at a daily dose of about 20 to about 100 mg.

[0063] Pharmaceutically acceptable carriers and diluents for therapeutic use are well known in the art and are described in, for example, Remington's Pharmaceutical Sciences, Mack Publishing Co. (A. R. Gennaro ed. (1985)). The carrier should not itself induce the production of antibodies harmful to the host. Such carriers include, but are not limited to, large, slowly metabolized, macromolecules, such as proteins, polysaccharides such as latex functionalized sepharose, agarose, cellulose, cellulose beads and the like, polylactic acids, polyglycolic acids, polymeric amino acids such as polyglutamic acid, polylysine, and the like, amino acid copolymers, peptoids, lipitoids, and inactive, avirulent virus particles or bacterial cells. Liposomes, hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesives can also be used as a carrier for a composition of the invention.

[0064] Pharmaceutically acceptable salts can also be used in compositions of the invention, for example, mineral salts such as hydrochlorides, hydrobromides, phosphates, or sulfates, as well as salts of organic acids such as acetates, propionates, malonates, or benzoates. Especially useful protein substrates are serum albumins, keyhole limpet hemocyanin, immunoglobulin molecules, thyroglobulin, ovalbumin, tetanus toxoid, and other proteins well known to those of skill in the art. Compositions of the invention can also contain liquids or excipients, such as water, saline, phosphate buffered saline, Ringer's solution, Hank's solution, glucose, glycerol, dextrose, malodextrin, ethanol, or the like, singly or in combination, as well as substances such as wetting agents, emulsifying agents, tonicity adjusting agents, detergent, or pH buffering agents. Additional active agents, such as bacteriocidal agents can also be used.

[0065] If desired, co-stimulatory molecules, which improve immunogen presentation to lymphocytes, such as B7-1 or B7-2, or cytokines such as MIP1 $\alpha$ , GM-CSF, IL-2, and IL-12, can be included in a composition of the invention. Optionally, adjuvants can also be included in a composition. Adjuvants are substances that can be used to nonspecifically augment a specific immune response. Generally, an adjuvant and a polypeptide of the invention are mixed prior to presentation to the immune system, or presented separately, but are presented into the same site of the animal. Adjuvants can include, for example, oil adjuvants (e.g. Freund's complete and incomplete adjuvants) mineral salts (e.g.

Alk(SO<sub>4</sub>)<sub>2</sub>; AlNa(SO<sub>4</sub>)<sub>2</sub>, AlNH<sub>4</sub>(SO<sub>4</sub>), Silica, Alum, Al(OH)<sub>3</sub>, and Ca<sub>3</sub>(PO<sub>4</sub>)<sub>2</sub>), polynucleotides (i.e. Polyic and Poly AU acids), and certain natural substances (e.g. wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, *Bordetella pertussis* and members of the genus *Brucella*). Adjuvants which can be used include, but are not limited to MF59-0, aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637), referred to as nor-MDP), N-acetyl-muramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-di-pamitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE), and RIBI, which contains three components extracted from bacteria, monophosphoryl lipid A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/Tween 80 emulsion.

[0066] The compositions of the invention can be formulated into ingestible tablets, buccal tablets, troches, capsules, elixirs, suspensions, syrups, wafers, injectable formulations, mouthwashes, dentrifices, and the like. The percentage of one or more polypeptides, polynucleotides, or antibodies of the invention in such compositions and preparations can vary from 0.1% to 60% of the weight of the unit.

[0067] Administration of polypeptides or polynucleotides can elicit an immune response in the animal that lasts for at least 1 week, 1 month, 3 months, 6 months, 1 year, or longer. Optionally, an immune response can be maintained in an animal by providing one or more booster injections of the polypeptide or polynucleotide at 1 month, 3 months, 6 months, 1 year, or more after the primary injection. If desired, co-stimulatory molecules or adjuvants can also be provided before, after, or together with the compositions.

[0068] A composition of the invention comprising a polypeptide, polynucleotide, or a combination thereof is administered in a manner compatible with the particular composition used and in an amount that is effective to elicit an immune response as detected by, for example, an ELISA. A polynucleotide can be injected intramuscularly to a large mammal, such as a baboon, chimpanzee, or human, at a dose of 1 ng/kg, 10 ng/kg, 100 ng/kg, 1000 ng/kg, 0.001 mg/kg, 0.1 mg/kg, or 0.5 mg/kg. A polypeptide can be injected intramuscularly to a large mammal, such as a human, at a dose of 0.01, 0.05, 0.5, 0.75, 1.0, 1.5, 2.0, 2.5, 5 or 10 mg/kg.

[0069] Polypeptides, polynucleotides, or antibodies, or a combination thereof can be administered either to an animal that is not infected with Aa or can be administered to an Aa-infected animal. The particular dosages of polynucleotide, polypeptides, or antibodies in a composition will depend on many factors including, but not limited to the species, age, gender, concurrent medication, general condition of the mammal to which the composition is administered, and the mode of administration of the composition. An effective amount of the composition of the invention can be readily determined using only routine experimentation.

[0070] The materials for use in a method of the invention can be present in a kit. A kit can comprise one or more elements used in the method. For example, a kit can contain an antibody of the invention in a container and Aa polypeptides in another container. The kit and containers are labeled with their contents and the kit includes instructions for use of the elements in the containers. The constituents of the kit can be present in, for example, liquid or lyophilized form.

[0071] All references cited in this disclosure are incorporated herein by reference.

---

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 234

<210> SEQ ID NO 1  
 <211> LENGTH: 560  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(555)

<400> SEQUENCE: 1

```

agc gat tgg ctg gca ttt atg tta agc ggc gaa ctg gcg gtg gaa cct      48
Ser Asp Trp Leu Ala Phe Met Leu Ser Gly Glu Leu Ala Val Glu Pro
1           5           10           15

tcc aat gcg ggc acg acc ggc atg ttg aac ctg aca aca cgt caa tgg      96
Ser Asn Ala Gly Thr Thr Gly Met Leu Asn Leu Thr Thr Arg Gln Trp
          20           25           30

tcg ccg gaa tta ctg gat atg gcg ggg tta aat tca aat att ctg acg     144
Ser Pro Glu Leu Leu Asp Met Ala Gly Leu Asn Ser Asn Ile Leu Thr
          35           40           45

ccg ata aaa gaa acc ggt acg cgt tta ggt gaa gtg act tca gaa gtt     192
Pro Ile Lys Glu Thr Gly Thr Arg Leu Gly Glu Val Thr Ser Glu Val
          50           55           60

gca caa caa acc ggt tta ata cag ggc aca ccg gtt gtg gtc ggc ggc     240
Ala Gln Gln Thr Gly Leu Ile Gln Gly Thr Pro Val Val Val Gly Gly
          65           70           75           80

ggg gac gtg cag tta ggt tgt att ggt tta ggc gtc acc gag ccc gct     288
Gly Asp Val Gln Leu Gly Cys Ile Gly Leu Gly Val Thr Glu Pro Ala
          85           90           95

caa gcg gca gtt atc ggc ggt acg ttc tgg caa caa gtg gtg aat tta     336
Gln Ala Ala Val Ile Gly Gly Thr Phe Trp Gln Gln Val Val Asn Leu
          100          105          110

ccg cag gcg gtg acc gac ccg gaa atg aat gta cgt att aac ccg cac     384
Pro Gln Ala Val Thr Asp Pro Glu Met Asn Val Arg Ile Asn Pro His
          115          120          125

gtt atc ccg ccg tta gta cag gcg gaa tcc att agc ttt ttc acc aga     432
Val Ile Pro Pro Leu Val Gln Ala Glu Ser Ile Ser Phe Phe Thr Arg
          130          135          140

tta acc atg gcg tgg ttc cgt gat gca ttt tgc gaa gaa gaa aag aga     480
Leu Thr Met Arg Trp Phe Arg Asp Ala Phe Cys Glu Glu Glu Lys Arg
          145          150          155          160

ctg gcg gaa aaa ctg ggt acc gat gct tat gcg ttg ctg gaa caa atg     528
Leu Ala Glu Lys Leu Gly Thr Asp Ala Tyr Ala Leu Leu Glu Gln Met
          165          170          175

gcg gaa cgc gtg ccc gtc ggc gcc aat gacgt
Ala Glu Arg Val Pro Val Gly Ala Asn
          180          185

```

<210> SEQ ID NO 2  
 <211> LENGTH: 185  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 2

Ser Asp Trp Leu Ala Phe Met Leu Ser Gly Glu Leu Ala Val Glu Pro

-continued

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

<210> SEQ ID NO 3  
 <211> LENGTH: 573  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(573)

<400> SEQUENCE: 3

tgt gat acc gac att gaa cgt tat ctg gat gaa ggg cta atc tcc ctc	48
Cys Asp Thr Asp Ile Glu Arg Tyr Leu Asp Glu Gly Leu Ile Ser Leu	
1 5 10 15	
aat ccg cgc ccg tcg aac gat aaa att aat ggc gcc aca att gat gtg	96
Asn Pro Arg Pro Ser Asn Asp Lys Ile Asn Gly Ala Thr Ile Asp Val	
20 25 30	
cgt ttg ggc aat tcc ttc cgc gta ttt cgt gaa cat tcc gcc cct tac	144
Arg Leu Gly Asn Ser Phe Arg Val Phe Arg Glu His Ser Ala Pro Tyr	
35 40 45	
att gat ttg agc ggt ccg aaa gaa gaa gtg tcg gcg cag ttg gaa tcg	192
Ile Asp Leu Ser Gly Pro Lys Glu Glu Val Ser Ala Gln Leu Glu Ser	
50 55 60	
gtc atg agc gat gaa atg att atc ggt gat gac gaa gcc ttc ttt tta	240
Val Met Ser Asp Glu Met Ile Ile Gly Asp Asp Glu Ala Phe Phe Leu	
65 70 75 80	
cat ccc ggc gtg ctg gcg ctt gcc acg act ttg gaa tca gta aaa ctg	288
His Pro Gly Val Leu Ala Leu Ala Thr Thr Leu Glu Ser Val Lys Leu	
85 90 95	
ccg gcg aat att atc ggt tgg ctg gac ggg cgt tct tct ttg gcg cgt	336
Pro Ala Asn Ile Ile Gly Trp Leu Asp Gly Arg Ser Ser Leu Ala Arg	
100 105 110	
ttg ggg ttg atg gta cac gtc acc gcc cat cgt atc gac cca ggc tgg	384
Leu Gly Leu Met Val His Val Thr Ala His Arg Ile Asp Pro Gly Trp	

-continued

115	120	125	
gaa ggc aaa atc gtg ttg gaa ttt tac aat tcc ggc aaa tta ccg tta			432
Glu Gly Lys Ile Val Leu Glu Phe Tyr Asn Ser Gly Lys Leu Pro Leu			
130	135	140	
gcg tta cgc ccg aat atg att atc ggc gcc ttg agt ttc gaa gtg tta			480
Ala Leu Arg Pro Asn Met Ile Ile Gly Ala Leu Ser Phe Glu Val Leu			
145	150	155	160
agc gga ccg gcg gcg cgt ccg tac agc agc cgc aaa gac gca aaa tac			528
Ser Gly Pro Ala Ala Arg Pro Tyr Ser Ser Arg Lys Asp Ala Lys Tyr			
165	170	175	
aag aac caa caa aat gcc gtt gcc agc cgc att gat gag gac aaa			573
Lys Asn Gln Gln Asn Ala Val Ala Ser Arg Ile Asp Glu Asp Lys			
180	185	190	

<210> SEQ ID NO 4  
 <211> LENGTH: 191  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 4

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

<210> SEQ ID NO 5  
 <211> LENGTH: 798  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(798)

<400> SEQUENCE: 5

atg aac get att cag cct gaa gat aag agc ttt tgg ctt ttc act cag				48
Met Asn Ala Ile Gln Pro Glu Asp Lys Ser Phe Trp Leu Phe Thr Gln				
1	5	10	15	

-continued

```

aga tca aaa ata cat tta att gac ggc aag ctt cct ttc ggc aat gcc      96
Arg Ser Lys Ile His Leu Ile Asp Gly Lys Leu Pro Phe Gly Asn Ala
      20                      25                      30

acc gaa ctg ggt ttc gtc ggg ctt cat gct atg cgc atc ggc gaa tgg      144
Thr Glu Leu Gly Phe Val Gly Leu His Ala Met Arg Ile Gly Glu Trp
      35                      40                      45

ctg gag caa ccg tta tat ttg gtg gaa acc caa ccg aac gac aac cgc      192
Leu Glu Gln Pro Leu Tyr Leu Val Glu Thr Gln Pro Asn Asp Asn Arg
      50                      55                      60

acc tat ttt tct tta cgc gat caa ctg ccg ctg ccg caa gcg caa ttt      240
Thr Tyr Phe Ser Leu Arg Asp Gln Leu Pro Leu Pro Gln Ala Gln Phe
      65                      70                      75                      80

aat ctg ttg agc tgc ggc gtg gag tta aat cat ttc tat cag acc cat      288
Asn Leu Leu Ser Cys Gly Val Glu Leu Asn His Phe Tyr Gln Thr His
      85                      90                      95

caa ttc tgc gga aag tgc ggt gga aaa acc gag caa atg cag gag gaa      336
Gln Phe Cys Gly Lys Cys Gly Gly Lys Thr Glu Gln Met Gln Glu Glu
      100                      105                      110

tgg gcg gta aaa tgc cgt gcc tgc ggt ttt cat acc tat ccc gtc att      384
Trp Ala Val Lys Cys Arg Ala Cys Gly Phe His Thr Tyr Pro Val Ile
      115                      120                      125

tgc cct tcc att atc gtt gca gta cga cac gat tca caa atc ctg ctg      432
Cys Pro Ser Ile Ile Val Ala Val Arg His Asp Ser Gln Ile Leu Leu
      130                      135                      140

gca aat cat atg cgc cac aaa ggc ggc att tac acc acg ttg gcg ggt      480
Ala Asn His Met Arg His Lys Gly Gly Ile Tyr Thr Thr Leu Ala Gly
      145                      150                      155                      160

ttt gtg gaa gta ggc gaa acc ttt gag gat gcg gta cat cgc gaa att      528
Phe Val Glu Val Gly Glu Thr Phe Glu Asp Ala Val His Arg Glu Ile
      165                      170                      175

tgg gag gaa acc caa atc aaa gta aaa aat ttg cgt tat ttc gac agc      576
Trp Glu Glu Thr Gln Ile Lys Val Lys Asn Leu Arg Tyr Phe Asp Ser
      180                      185                      190

cag cct tgg gcg ttt cct aat tcg caa atg gtg ggt ttt tta gcc gat      624
Gln Pro Trp Ala Phe Pro Asn Ser Gln Met Val Gly Phe Leu Ala Asp
      195                      200                      205

tat gaa gga ggc gag att act att cag cgt gaa gaa ctt tat gac gca      672
Tyr Glu Gly Gly Glu Ile Thr Ile Gln Arg Glu Glu Leu Tyr Asp Ala
      210                      215                      220

caa tgg ttt gat tgc gac caa ccg ttg ccc gaa ctg cca ccg cac ggc      720
Gln Trp Phe Asp Cys Asp Gln Pro Leu Pro Glu Leu Pro Pro His Gly
      225                      230                      235                      240

acc atc gca cgc aaa tta att gaa acc aca ctt gaa ttg tgt aaa cag      768
Thr Ile Ala Arg Lys Leu Ile Glu Thr Thr Leu Glu Leu Cys Lys Gln
      245                      250                      255

cat aaa ata aac cat aat aag gaa cgg gca      798
His Lys Ile Asn His Asn Lys Glu Arg Ala
      260                      265

```

&lt;210&gt; SEQ ID NO 6

&lt;211&gt; LENGTH: 266

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 6

```

Met Asn Ala Ile Gln Pro Glu Asp Lys Ser Phe Trp Leu Phe Thr Gln
1          5          10          15

```

-continued

---

Arg Ser Lys Ile His Leu Ile Asp Gly Lys Leu Pro Phe Gly Asn Ala  
 20 25 30

Thr Glu Leu Gly Phe Val Gly Leu His Ala Met Arg Ile Gly Glu Trp  
 35 40 45

Leu Glu Gln Pro Leu Tyr Leu Val Glu Thr Gln Pro Asn Asp Asn Arg  
 50 55 60

Thr Tyr Phe Ser Leu Arg Asp Gln Leu Pro Leu Pro Gln Ala Gln Phe  
 65 70 75 80

Asn Leu Leu Ser Cys Gly Val Glu Leu Asn His Phe Tyr Gln Thr His  
 85 90 95

Gln Phe Cys Gly Lys Cys Gly Gly Lys Thr Glu Gln Met Gln Glu Glu  
 100 105 110

Trp Ala Val Lys Cys Arg Ala Cys Gly Phe His Thr Tyr Pro Val Ile  
 115 120 125

Cys Pro Ser Ile Ile Val Ala Val Arg His Asp Ser Gln Ile Leu Leu  
 130 135 140

Ala Asn His Met Arg His Lys Gly Gly Ile Tyr Thr Thr Leu Ala Gly  
 145 150 155 160

Phe Val Glu Val Gly Glu Thr Phe Glu Asp Ala Val His Arg Glu Ile  
 165 170 175

Trp Glu Glu Thr Gln Ile Lys Val Lys Asn Leu Arg Tyr Phe Asp Ser  
 180 185 190

Gln Pro Trp Ala Phe Pro Asn Ser Gln Met Val Gly Phe Leu Ala Asp  
 195 200 205

Tyr Glu Gly Gly Glu Ile Thr Ile Gln Arg Glu Glu Leu Tyr Asp Ala  
 210 215 220

Gln Trp Phe Asp Cys Asp Gln Pro Leu Pro Glu Leu Pro Pro His Gly  
 225 230 235 240

Thr Ile Ala Arg Lys Leu Ile Glu Thr Thr Leu Glu Leu Cys Lys Gln  
 245 250 255

His Lys Ile Asn His Asn Lys Glu Arg Ala  
 260 265

<210> SEQ ID NO 7  
 <211> LENGTH: 770  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(768)

<400> SEQUENCE: 7

aaa atc caa agt ttg ctg cat cct gat gtt aaa ccg atg gtt tta ccg 48  
 Lys Ile Gln Ser Leu Leu His Pro Asp Val Lys Pro Met Val Leu Pro  
 1 5 10 15

aac ccg att tcc gtt gaa atg tcc gcc atg cgt gtt tca tta ttg acc 96  
 Asn Pro Ile Ser Val Glu Met Ser Ala Met Arg Val Ser Leu Leu Thr  
 20 25 30

ggg tta ttg ggc gca gtg att tat aat caa aac cgc caa caa agt cgc 144  
 Gly Leu Leu Gly Ala Val Ile Tyr Asn Gln Asn Arg Gln Gln Ser Arg  
 35 40 45

gtg cgt ttg ttt gag cac ggt tta cgt ttt att ccg gac gaa aag gcc 192  
 Val Arg Leu Phe Glu His Gly Leu Arg Phe Ile Pro Asp Glu Lys Ala  
 50 55 60

gaa ttc ggc gtg cac caa gag ccg gtt ttt gcc gcg gtg atg aca ggg 240

-continued

Glu Phe Gly Val His Gln Glu Pro Val Phe Ala Ala Val Met Thr Gly	
65 70 75 80	
tta aaa tca aac gaa cag tgg agc gaa aaa gcc gta ccg gca gat ttt	288
Leu Lys Ser Asn Glu Gln Trp Ser Glu Lys Ala Val Pro Ala Asp Phe	
85 90 95	
tac gac tta aaa ggc tac att gaa aac tta ctt tcg tta agt tct gct	336
Tyr Asp Leu Lys Gly Tyr Ile Glu Asn Leu Leu Ser Leu Ser Ser Ala	
100 105 110	
gga aat cgg gca aaa ttt gta gca aaa tca tac aca gca ttg cat ccg	384
Gly Asn Arg Ala Lys Phe Val Ala Lys Ser Tyr Thr Ala Leu His Pro	
115 120 125	
ggt caa tct gcg gcc att atg ctg gat ggt gaa gaa atc gga ttt att	432
Gly Gln Ser Ala Ala Ile Met Leu Asp Gly Glu Glu Ile Gly Phe Ile	
130 135 140	
ggt caa ctt cac ccg act atc gcg caa aaa att ggt ctt acc gga aaa	480
Gly Gln Leu His Pro Thr Ile Ala Gln Lys Ile Gly Leu Thr Gly Lys	
145 150 155 160	
gca ttt gtt tgt gaa att tcg gtc gca cac att tct cga cga gaa gtc	528
Ala Phe Val Cys Glu Ile Ser Val Ala His Ile Ser Arg Arg Glu Val	
165 170 175	
gcc cgt gcc aaa gaa att tcc cgt ttc cct gct aat cgt cgt gat ttg	576
Ala Arg Ala Lys Glu Ile Ser Arg Phe Pro Ala Asn Arg Arg Asp Leu	
180 185 190	
gcg gtt gtg gtt gcg gat aat atc cct gca aat gac gtg ctg gaa gtg	624
Ala Val Val Val Ala Asp Asn Ile Pro Ala Asn Asp Val Leu Glu Val	
195 200 205	
tgt cgt aca gca ggc gga gat aaa tta acc caa atc aat tta ttt gat	672
Cys Arg Thr Ala Gly Gly Asp Lys Leu Thr Gln Ile Asn Leu Phe Asp	
210 215 220	
gtt tac cac gga acc ggt gtt gct gca ggg cat aag agc tta gct atc	720
Val Tyr His Gly Thr Gly Val Ala Ala Gly His Lys Ser Leu Ala Ile	
225 230 235 240	
agc tta gta att caa gat aat gaa aaa acc ctt gaa gaa gat gaa att	768
Ser Leu Val Ile Gln Asp Asn Glu Lys Thr Leu Glu Glu Asp Glu Ile	
245 250 255	
aa	770

<210> SEQ ID NO 8  
 <211> LENGTH: 256  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 8

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

-continued

	100		105		110										
Gly	Asn	Arg	Ala	Lys	Phe	Val	Ala	Lys	Ser	Tyr	Thr	Ala	Leu	His	Pro
	115						120					125			
Gly	Gln	Ser	Ala	Ala	Ile	Met	Leu	Asp	Gly	Glu	Glu	Ile	Gly	Phe	Ile
	130					135					140				
Gly	Gln	Leu	His	Pro	Thr	Ile	Ala	Gln	Lys	Ile	Gly	Leu	Thr	Gly	Lys
	145				150					155					160
Ala	Phe	Val	Cys	Glu	Ile	Ser	Val	Ala	His	Ile	Ser	Arg	Arg	Glu	Val
				165						170				175	
Ala	Arg	Ala	Lys	Glu	Ile	Ser	Arg	Phe	Pro	Ala	Asn	Arg	Arg	Asp	Leu
			180							185				190	
Ala	Val	Val	Val	Ala	Asp	Asn	Ile	Pro	Ala	Asn	Asp	Val	Leu	Glu	Val
			195				200					205			
Cys	Arg	Thr	Ala	Gly	Gly	Asp	Lys	Leu	Thr	Gln	Ile	Asn	Leu	Phe	Asp
	210					215					220				
Val	Tyr	His	Gly	Thr	Gly	Val	Ala	Ala	Gly	His	Lys	Ser	Leu	Ala	Ile
	225				230					235					240
Ser	Leu	Val	Ile	Gln	Asp	Asn	Glu	Lys	Thr	Leu	Glu	Glu	Asp	Glu	Ile
				245					250					255	

<210> SEQ ID NO 9  
 <211> LENGTH: 141  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(141)

<400> SEQUENCE: 9

gat	cag	cct	gat	tat	gtc	aac	gcc	gtc	gct	tgc	ctg	gaa	acg	gcg	ctt	48
Asp	Gln	Pro	Asp	Tyr	Val	Asn	Ala	Val	Ala	Cys	Leu	Glu	Thr	Ala	Leu	
1			5					10						15		
tct	ccc	ttc	gca	ttg	ctt	gat	gaa	tta	caa	cg	att	gaa	cag	gaa	caa	96
Ser	Pro	Phe	Ala	Leu	Leu	Asp	Glu	Leu	Gln	Arg	Ile	Glu	Gln	Glu	Gln	
			20				25					30				
ggg	cg	gtc	cg	ctt	cg	ctg	tgg	ggt	gag	cg	aca	tta	gat	ctg		141
Gly	Arg	Val	Arg	Leu	Arg	Arg	Trp	Gly	Glu	Arg	Thr	Leu	Asp	Leu		
	35					40					45					

<210> SEQ ID NO 10  
 <211> LENGTH: 47  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 10

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

<210> SEQ ID NO 11  
 <211> LENGTH: 597  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS

-continued

&lt;222&gt; LOCATION: (1)..(597)

&lt;400&gt; SEQUENCE: 11

```

ggt ctg agt ttt act ttc ctt tca tca ttg gct ttt gca gaa tct tgg      48
Gly Leu Ser Phe Thr Phe Leu Ser Ser Leu Ala Phe Ala Glu Ser Trp
1           5           10           15

act atg cat att tcc gaa gat ggc gtg ata acc gat aaa acc gct caa      96
Thr Met His Ile Ser Glu Asp Gly Val Ile Thr Asp Lys Thr Ala Gln
                20           25           30

cag ctt aat ccg gct agg tat gcc gga gct gtg tac aaa caa caa ttt      144
Gln Leu Asn Pro Ala Arg Tyr Ala Gly Ala Val Tyr Lys Gln Gln Phe
                35           40           45

tct ttt tct gac agc ggc ggg caa ggt aaa acc act tac att aat caa      192
Ser Phe Ser Ser Asp Ser Gly Gly Gln Gly Lys Thr Thr Tyr Ile Asn Gln
                50           55           60

aat aac ggc aag aaa ttc gat cct aaa aat gct gct gat gtg agt gaa      240
Asn Asn Gly Lys Lys Phe Asp Pro Lys Asn Ala Ala Asp Val Ser Glu
                65           70           75           80

ttg ggt aaa agc atc gcc ttt gaa gtg ttt gag att aaa gaa aat aaa      288
Leu Gly Lys Ser Ile Ala Phe Glu Val Phe Glu Ile Lys Glu Asn Lys
                85           90           95

gac tct cac tca gta ttt gaa tcc gcc gcc gcc att tgt tac gcc ttc      336
Asp Ser His Ser Val Phe Glu Ser Gly Ala Gly Ile Cys Tyr Gly Phe
                100           105           110

aaa tat acc gat ggc gtc gcg ttc acc gat tct aca acc tat tat gta      384
Lys Tyr Thr Asp Gly Val Ala Phe Thr Asp Ser Thr Thr Tyr Tyr Val
                115           120           125

gat aaa tcc aag cag caa tat tac gcc agt atc atc gcc gcc acc gta      432
Asp Lys Ser Lys Gln Gln Tyr Tyr Ala Ser Ile Ile Gly Ala Thr Val
                130           135           140

tct tct gac gtg gaa ccg aaa aac gtg caa tat gcg ccg gtg ttt aat      480
Ser Ser Asp Val Glu Pro Lys Asn Val Gln Tyr Ala Pro Val Phe Asn
                145           150           155           160

att cag gat ccc gag tta gat aaa gaa gta aag tcg gaa gaa caa cga      528
Ile Gln Asp Pro Glu Leu Asp Lys Glu Val Lys Ser Glu Glu Gln Arg
                165           170           175

aac ggt aaa acc ttg att aat aaa aat ttg caa aag agc aga gaa att      576
Asn Gly Lys Thr Leu Ile Asn Lys Asn Leu Gln Lys Ser Arg Glu Ile
                180           185           190

ctt tct aac gta gtt tgt aag      597
Leu Ser Asn Val Val Cys Lys
                195

```

&lt;210&gt; SEQ ID NO 12

&lt;211&gt; LENGTH: 199

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 12

```

Gly Leu Ser Phe Thr Phe Leu Ser Ser Leu Ala Phe Ala Glu Ser Trp
1           5           10           15

Thr Met His Ile Ser Glu Asp Gly Val Ile Thr Asp Lys Thr Ala Gln
                20           25           30

Gln Leu Asn Pro Ala Arg Tyr Ala Gly Ala Val Tyr Lys Gln Gln Phe
                35           40           45

Ser Phe Ser Asp Ser Gly Gly Gln Gly Lys Thr Thr Tyr Ile Asn Gln
                50           55           60

```

-continued

---

Asn Asn Gly Lys Lys Phe Asp Pro Lys Asn Ala Ala Asp Val Ser Glu  
 65 70 75 80

Leu Gly Lys Ser Ile Ala Phe Glu Val Phe Glu Ile Lys Glu Asn Lys  
 85 90 95

Asp Ser His Ser Val Phe Glu Ser Gly Ala Gly Ile Cys Tyr Gly Phe  
 100 105 110

Lys Tyr Thr Asp Gly Val Ala Phe Thr Asp Ser Thr Thr Tyr Tyr Val  
 115 120 125

Asp Lys Ser Lys Gln Gln Tyr Tyr Ala Ser Ile Ile Gly Ala Thr Val  
 130 135 140

Ser Ser Asp Val Glu Pro Lys Asn Val Gln Tyr Ala Pro Val Phe Asn  
 145 150 155 160

Ile Gln Asp Pro Glu Leu Asp Lys Glu Val Lys Ser Glu Glu Gln Arg  
 165 170 175

Asn Gly Lys Thr Leu Ile Asn Lys Asn Leu Gln Lys Ser Arg Glu Ile  
 180 185 190

Leu Ser Asn Val Val Cys Lys  
 195

<210> SEQ ID NO 13  
 <211> LENGTH: 288  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(288)

<400> SEQUENCE: 13

atg caa aaa ttg tta ctc gtc aca gtg att agt ggt gtt tta gtt gct 48  
 Met Gln Lys Leu Leu Leu Val Thr Val Ile Ser Gly Val Leu Val Ala  
 1 5 10 15

tgt tct tct aag gct cca caa atc aat caa gct cct tta gat aag cag 96  
 Cys Ser Ser Lys Ala Pro Gln Ile Asn Gln Ala Pro Leu Asp Lys Gln  
 20 25 30

aca gtt gaa gct tat caa gcg aaa gtg tat agc ggt aat acg gtg tcg 144  
 Thr Val Glu Ala Tyr Gln Ala Lys Val Tyr Ser Gly Asn Thr Val Ser  
 35 40 45

aag aaa tat caa gta aga gac gtt aaa ccg gaa gac aat gtg tta aat 192  
 Lys Lys Tyr Gln Val Arg Asp Val Lys Pro Glu Asp Asn Val Leu Asn  
 50 55 60

gct agt gat tcg gaa ccg aaa acc gtg att tat cgc gag cgt cag cca 240  
 Ala Ser Asp Ser Glu Pro Lys Thr Val Ile Tyr Arg Glu Arg Gln Pro  
 65 70 75 80

aga ctg gtt gtg aca ccg agc att ggc tat tat cgc ggt tgg cac tgg 288  
 Arg Leu Val Val Thr Pro Ser Ile Gly Tyr Tyr Arg Gly Trp His Trp  
 85 90 95

<210> SEQ ID NO 14  
 <211> LENGTH: 96  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 14

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

Cys Ser Ser Lys Ala Pro Gln Ile Asn Gln Ala Pro Leu Asp Lys Gln  
 20 25 30



-continued

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

<210> SEQ ID NO 17  
 <211> LENGTH: 374  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(372)

<400> SEQUENCE: 17

cac cgt tta ccg gaa atg att aac caa att cgc ggt ggc aaa agt gct 48  
 His Arg Leu Pro Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ala  
 1 5 10 15  
 gtg gtg gat att agt ttc ccg gaa atc gaa aaa ttc gac ccg ttg ccg 96  
 Val Val Asp Ile Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro  
 20 25 30  
 gaa ccg cgc gca gaa ggc ccg act gcc ttt gtt tct atc atg gaa ggc 144  
 Glu Pro Arg Ala Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly  
 35 40 45  
 tgt aat aaa tac tgt act tac tgc gtg gtg cct tat acc cgt ggc gag 192  
 Cys Asn Lys Tyr Cys Thr Tyr Cys Val Val Pro Tyr Thr Arg Gly Glu  
 50 55 60  
 gaa gtt agc cgt ccg gtg gat gat att tta ttt gaa att gcc cag ttg 240  
 Glu Val Ser Arg Pro Val Asp Asp Ile Leu Phe Glu Ile Ala Gln Leu  
 65 70 75 80  
 gcg gag caa ggc gtg cgc gaa gtg aat ttg ctc gcc cag aac gtg aac 288  
 Ala Glu Gln Gly Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn  
 85 90 95  
 gcc tat cgt ggt ccg aca ttt gat gcc gat att tgc acc ttc gcc gaa 336  
 Ala Tyr Arg Gly Pro Thr Phe Asp Gly Asp Ile Cys Thr Phe Ala Glu  
 100 105 110  
 ttg ttg cgt ttg gta gcg gcc att gac ggt atc gat cg 374  
 Leu Leu Arg Leu Val Ala Ala Ile Asp Gly Ile Asp  
 115 120

<210> SEQ ID NO 18  
 <211> LENGTH: 124  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 18

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

-continued

35	40	45	
Cys Asn Lys Tyr Cys Thr Tyr Cys Val Val Pro Tyr Thr Arg Gly Glu			
50	55	60	
Glu Val Ser Arg Pro Val Asp Asp Ile Leu Phe Glu Ile Ala Gln Leu			
65	70	75	80
Ala Glu Gln Gly Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn			
85	90		95
Ala Tyr Arg Gly Pro Thr Phe Asp Gly Asp Ile Cys Thr Phe Ala Glu			
100	105		110
Leu Leu Arg Leu Val Ala Ala Ile Asp Gly Ile Asp			
115	120		
<210> SEQ ID NO 19			
<211> LENGTH: 158			
<212> TYPE: DNA			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(156)			
<400> SEQUENCE: 19			
cta agc gta ttc aac tac gcc cat ttg ccg agc cgt ttt gcc gga cag			48
Leu Ser Val Phe Asn Tyr Ala His Leu Pro Ser Arg Phe Ala Gly Gln			
1	5	10	15
gcg aaa atc aag gat tgg cag ttg ccg aaa ccg gaa gcg aaa ctg gaa			96
Ala Lys Ile Lys Asp Trp Gln Leu Pro Lys Pro Glu Ala Lys Leu Glu			
20	25		30
att ctg caa aaa acc atc gaa acg ctg ggc aac gcc ggt tac aaa ttt			144
Ile Leu Gln Lys Thr Ile Glu Thr Leu Gly Asn Ala Gly Tyr Lys Phe			
35	40		45
atc ggc atg gat ca			158
Ile Gly Met Asp			
50			
<210> SEQ ID NO 20			
<211> LENGTH: 52			
<212> TYPE: PRT			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<400> SEQUENCE: 20			
Leu Ser Val Phe Asn Tyr Ala His Leu Pro Ser Arg Phe Ala Gly Gln			
1	5	10	15
Ala Lys Ile Lys Asp Trp Gln Leu Pro Lys Pro Glu Ala Lys Leu Glu			
20	25		30
Ile Leu Gln Lys Thr Ile Glu Thr Leu Gly Asn Ala Gly Tyr Lys Phe			
35	40		45
Ile Gly Met Asp			
50			
<210> SEQ ID NO 21			
<211> LENGTH: 1098			
<212> TYPE: DNA			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(1095)			
<400> SEQUENCE: 21			
aat cag atg aat aaa acc tta aaa att tca ttg ttt gcc atg att tcc			48

-continued

Asn	Gln	Met	Asn	Lys	Thr	Leu	Lys	Ile	Ser	Leu	Phe	Ala	Met	Ile	Ser	
1				5					10					15		
gcg	tta	gct	ttt	aat	acc	atg	gca	aat	aca	caa	ccg	tta	gcc	gtg	ttg	96
Ala	Leu	Ala	Phe	Asn	Thr	Met	Ala	Asn	Thr	Gln	Pro	Leu	Ala	Val	Leu	
			20					25					30			
gaa	ccg	cag	gta	aac	tat	caa	cag	tta	ctc	acc	caa	cgg	cag	gtg	gtg	144
Glu	Pro	Gln	Val	Asn	Tyr	Gln	Gln	Leu	Leu	Thr	Gln	Arg	Gln	Val	Val	
		35				40					45					
gat	gat	tta	atc	gcg	cag	gcg	gtg	aaa	atc	caa	aat	tca	ccg	gcg	cgg	192
Asp	Asp	Leu	Ile	Ala	Gln	Ala	Val	Lys	Ile	Gln	Asn	Ser	Pro	Ala	Arg	
	50				55					60						
gtg	tcc	aat	gcg	ggc	ttt	acc	gca	aaa	ttg	cca	agc	aac	atg	gaa	cgc	240
Val	Ser	Asn	Ala	Gly	Phe	Thr	Ala	Lys	Leu	Pro	Ser	Asn	Met	Glu	Arg	
65				70					75					80		
att	gcc	gcg	att	ttg	ttg	gaa	gcc	tat	gaa	ttg	gaa	cct	tac	cgc	gtt	288
Ile	Ala	Ala	Ile	Leu	Leu	Glu	Ala	Tyr	Glu	Leu	Glu	Pro	Tyr	Arg	Val	
			85					90						95		
gat	ttt	ctg	ttc	ggc	gca	gca	aat	gcc	aac	att	tac	aac	ggc	aat	acg	336
Asp	Phe	Leu	Phe	Gly	Ala	Ala	Asn	Ala	Asn	Ile	Tyr	Asn	Gly	Asn	Thr	
			100					105					110			
gac	aaa	gcc	atc	gag	ctt	tac	caa	aaa	gtg	ctc	acg	gtg	gcg	cct	gat	384
Asp	Lys	Ala	Ile	Glu	Leu	Tyr	Gln	Lys	Val	Leu	Thr	Val	Ala	Pro	Asp	
		115					120					125				
gat	gtg	aaa	gca	cat	att	tat	tta	acc	gcg	tgg	aat	cgt	ttt	aaa	caa	432
Asp	Val	Lys	Ala	His	Ile	Tyr	Leu	Thr	Ala	Trp	Asn	Arg	Phe	Lys	Gln	
	130				135					140						
aac	caa	ggg	gaa	acc	gac	aaa	tac	ttc	acc	cgc	tta	aaa	gcg	ctg	gca	480
Asn	Gln	Gly	Glu	Thr	Asp	Lys	Tyr	Phe	Thr	Arg	Leu	Lys	Ala	Leu	Ala	
145				150						155				160		
ccg	caa	aaa	gca	gcg	gaa	ctg	gag	cag	gtc	ttc	aag	att	att	gat	aac	528
Pro	Gln	Lys	Ala	Ala	Glu	Leu	Glu	Gln	Val	Phe	Lys	Ile	Ile	Asp	Asn	
			165					170						175		
gcc	gca	agc	caa	ccg	att	agc	gat	aaa	ttg	gcg	aat	aaa	ttg	ccg	gcg	576
Ala	Ala	Ser	Gln	Pro	Ile	Ser	Asp	Lys	Leu	Ala	Asn	Lys	Leu	Pro	Ala	
			180					185					190			
gat	tcc	gcc	att	att	acc	ttg	ggt	tat	gcg	tta	aat	ccg	gac	ggc	agt	624
Asp	Ser	Ala	Ile	Ile	Thr	Leu	Gly	Tyr	Ala	Leu	Asn	Pro	Asp	Gly	Ser	
		195				200						205				
atg	cac	gac	att	ttg	att	cag	cgt	ttg	gaa	aaa	acc	ttg	gaa	atc	gcc	672
Met	His	Asp	Ile	Leu	Ile	Gln	Arg	Leu	Glu	Lys	Thr	Leu	Glu	Ile	Ala	
		210				215						220				
aaa	caa	aat	cct	gat	gca	ttg	att	att	gtc	acc	ggc	ggc	atg	ccg	caa	720
Lys	Gln	Asn	Pro	Asp	Ala	Leu	Ile	Ile	Val	Thr	Gly	Gly	Met	Pro	Gln	
225				230						235				240		
aat	aat	cgt	acg	gaa	ggg	gca	tta	atg	aaa	caa	tgg	ctg	att	aac	aaa	768
Asn	Asn	Arg	Thr	Glu	Gly	Ala	Leu	Met	Lys	Gln	Trp	Leu	Ile	Asn	Lys	
			245					250						255		
ggc	atc	gat	gcc	aaa	cgc	att	tat	gcc	gac	aat	tac	gcc	cgt	tca	acg	816
Gly	Ile	Asp	Ala	Lys	Arg	Ile	Tyr	Ala	Asp	Asn	Tyr	Ala	Arg	Ser	Thr	
			260				265						270			
gtg	gaa	aat	gcg	tta	ttt	tcc	cgt	tac	gcc	ttg	gcg	aaa	cac	cat	atc	864
Val	Glu	Asn	Ala	Leu	Phe	Ser	Arg	Tyr	Ala	Leu	Ala	Lys	His	His	Ile	
		275				280						285				
aaa	cac	gcc	tcc	ctc	atc	agc	tcc	ggt	agc	cat	gtg	cgg	cgc	ggt	cag	912
Lys	His	Ala	Ser	Leu	Ile	Ser	Ser	Gly	Ser	His	Val	Arg	Arg	Gly	Gln	
		290				295					300					
gcg	ttg	ttt	gaa	atc	gcc	gcc	ttg	gaa	tcc	ggt	ccg	caa	aac	atc	aaa	960

-continued

---

```

Ala Leu Phe Glu Ile Ala Ala Leu Glu Ser Gly Pro Gln Asn Ile Lys
305                310                315                320

atc gaa acg gtg gcg gcg cta gac aaa ccg tta gac gaa tta caa aaa    1008
Ile Glu Thr Val Ala Ala Leu Asp Lys Pro Leu Asp Glu Leu Gln Lys
                325                330                335

gtg agt gaa aaa gat tta ttg gga atc tat cgc gac agc ctg aaa acc    1056
Val Ser Glu Lys Asp Leu Leu Gly Ile Tyr Arg Asp Ser Leu Lys Thr
                340                345                350

atg ggc ttg cca atg ttt aat agc gga gca cta caa gat taa    1098
Met Gly Leu Pro Met Phe Asn Ser Gly Ala Leu Gln Asp
                355                360                365

```

```

<210> SEQ ID NO 22
<211> LENGTH: 365
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 22

```

```

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

Ala Leu Ala Phe Asn Thr Met Ala Asn Thr Gln Pro Leu Ala Val Leu
                20                25                30

Glu Pro Gln Val Asn Tyr Gln Gln Leu Leu Thr Gln Arg Gln Val Val
                35                40                45

Asp Asp Leu Ile Ala Gln Ala Val Lys Ile Gln Asn Ser Pro Ala Arg
50                55                60

Val Ser Asn Ala Gly Phe Thr Ala Lys Leu Pro Ser Asn Met Glu Arg
65                70                75                80

Ile Ala Ala Ile Leu Leu Glu Ala Tyr Glu Leu Glu Pro Tyr Arg Val
                85                90                95

Asp Phe Leu Phe Gly Ala Ala Asn Ala Asn Ile Tyr Asn Gly Asn Thr
100                105                110

Asp Lys Ala Ile Glu Leu Tyr Gln Lys Val Leu Thr Val Ala Pro Asp
115                120                125

Asp Val Lys Ala His Ile Tyr Leu Thr Ala Trp Asn Arg Phe Lys Gln
130                135                140

Asn Gln Gly Glu Thr Asp Lys Tyr Phe Thr Arg Leu Lys Ala Leu Ala
145                150                155                160

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

Ala Ala Ser Gln Pro Ile Ser Asp Lys Leu Ala Asn Lys Leu Pro Ala
180                185                190

Asp Ser Ala Ile Ile Thr Leu Gly Tyr Ala Leu Asn Pro Asp Gly Ser
195                200                205

Met His Asp Ile Leu Ile Gln Arg Leu Glu Lys Thr Leu Glu Ile Ala
210                215                220

Lys Gln Asn Pro Asp Ala Leu Ile Ile Val Thr Gly Gly Met Pro Gln
225                230                235                240

Asn Asn Arg Thr Glu Gly Ala Leu Met Lys Gln Trp Leu Ile Asn Lys
245                250                255

Gly Ile Asp Ala Lys Arg Ile Tyr Ala Asp Asn Tyr Ala Arg Ser Thr
260                265                270

Val Glu Asn Ala Leu Phe Ser Arg Tyr Ala Leu Ala Lys His His Ile
275                280                285

```

-continued

Lys His Ala Ser Leu Ile Ser Ser Gly Ser His Val Arg Arg Gly Gln  
 290 295 300  
 Ala Leu Phe Glu Ile Ala Ala Leu Glu Ser Gly Pro Gln Asn Ile Lys  
 305 310 315 320  
 Ile Glu Thr Val Ala Ala Leu Asp Lys Pro Leu Asp Glu Leu Gln Lys  
 325 330 335  
 Val Ser Glu Lys Asp Leu Leu Gly Ile Tyr Arg Asp Ser Leu Lys Thr  
 340 345 350  
 Met Gly Leu Pro Met Phe Asn Ser Gly Ala Leu Gln Asp  
 355 360 365

<210> SEQ ID NO 23  
 <211> LENGTH: 134  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(132)

<400> SEQUENCE: 23

ttg gat caa ttc ccg tcc gac gtt tat caa ggc ggc gcg ggc act tcc 48  
 Leu Asp Gln Phe Pro Ser Asp Val Tyr Gln Gly Gly Ala Gly Thr Ser  
 1 5 10 15  
 gtc aac atg aat acg aac gaa gtg gtt gcg aat ctg gca ttg gaa att 96  
 Val Asn Met Asn Thr Asn Glu Val Val Ala Asn Leu Ala Leu Glu Ile  
 20 25 30  
 tta gga cac aaa aaa ggc gaa tat aat tat ttg gat cc 134  
 Leu Gly His Lys Lys Gly Glu Tyr Asn Tyr Leu Asp  
 35 40

<210> SEQ ID NO 24  
 <211> LENGTH: 44  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 24

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

<210> SEQ ID NO 25  
 <211> LENGTH: 380  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(378)

<400> SEQUENCE: 25

gat ccg aac agc ttc aaa ctg cgc ggc gaa ttg agc cac ggc aaa gac 48  
 Asp Pro Asn Ser Phe Lys Leu Arg Gly Glu Leu Ser His Gly Lys Asp  
 1 5 10 15  
 gtg gaa atc gac atg aac gtg att tta aac ggc aaa gtg cg g tta gga 96  
 Val Glu Ile Asp Met Asn Val Ile Leu Asn Gly Lys Val Arg Leu Gly  
 20 25 30  
 aat ccg gtg aaa atc ggt gca ggt tgt gtg ttg act aac tgc gac atc 144

-continued

---

```

Asn Arg Val Lys Ile Gly Ala Gly Cys Val Leu Thr Asn Cys Asp Ile
   35                               40                               45
ggc gat gac gtg gaa atc aaa ccg tat tcc gtg ctg gaa gat gcc tcc   192
Gly Asp Asp Val Glu Ile Lys Pro Tyr Ser Val Leu Glu Asp Ala Ser
   50                               55                               60
gta ggc gcc aat gcc gcc atc gga ccg ttc tcc cgc tta cgt ccg ggc   240
Val Gly Ala Asn Ala Ala Ile Gly Pro Phe Ser Arg Leu Arg Pro Gly
   65                               70                               75
ggc gac ttg gcg gaa aac acc cac gtg ggc aat ttc gtg gaa atc aaa   288
Ala Asp Leu Ala Glu Asn Thr His Val Gly Asn Phe Val Glu Ile Lys
   85                               90                               95
aaa gcg tac atc ggc aaa ggc tcc aaa gtg aac cac tta acc tat gtg   336
Lys Ala Tyr Ile Gly Lys Gly Ser Lys Val Asn His Leu Thr Tyr Val
   100                              105                              110
ggc gac gcg gaa atc ggc aaa gat tgt aac ata ggc gca ggc gt       380
Gly Asp Ala Glu Ile Gly Lys Asp Cys Asn Ile Gly Ala Gly
   115                              120                              125

```

```

<210> SEQ ID NO 26
<211> LENGTH: 126
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```
<400> SEQUENCE: 26
```

```

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

```

```

<210> SEQ ID NO 27
<211> LENGTH: 468
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(468)

```

```
<400> SEQUENCE: 27
```

```

att ggt cgc caa ctt gct cag ttg ctc aac atg gat ttt gta gat acc   48
Ile Gly Arg Gln Leu Ala Gln Leu Leu Asn Met Asp Phe Val Asp Thr
 1                               5                               10                               15
gac gca gaa att gaa gaa cgc gcc ggc gca gat att ggc tgg att ttt   96
Asp Ala Glu Ile Glu Glu Arg Ala Gly Ala Asp Ile Gly Trp Ile Phe
 20                              25                              30
gat gtt gag ggc gaa gcc ggt ttc cgt aaa aga gaa gaa cgt att att   144
Asp Val Glu Gly Glu Ala Gly Phe Arg Lys Arg Glu Glu Arg Ile Ile

```

-continued

35	40	45	
aac gaa tta acg caa cgc caa ggc atc gtg tta tct acc ggc ggc ggt Asn Glu Leu Thr Gln Arg Gln Gly Ile Val Leu Ser Thr Gly Gly Gly			192
50	55	60	
gca gtg tta tct aag gac aat cga aac cag ctt gcc gcg cgc ggt att Ala Val Leu Ser Lys Asp Asn Arg Asn Gln Leu Ala Ala Arg Gly Ile			240
65	70	75	80
gtg att tat ctg gaa acc act gtt gaa aag caa tat caa cgc acc cag Val Ile Tyr Leu Glu Thr Thr Val Glu Lys Gln Tyr Gln Arg Thr Gln			288
85	90		
cgg gat aaa aag cgc ccg ctt ttg caa gat gtt gcc gat ccg cgt cag Arg Asp Lys Lys Arg Pro Leu Leu Gln Asp Val Ala Asp Pro Arg Gln			336
100	105	110	
gtg ttg gaa gat ttg gcg aaa atc cgc aat ccg ctg tat gaa gac gta Val Leu Glu Asp Leu Ala Lys Ile Arg Asn Pro Leu Tyr Glu Asp Val			384
115	120	125	
gca gac att acc ctc cct act gat gac caa agt gcc aag gta atg gca Ala Asp Ile Thr Leu Pro Thr Asp Asp Gln Ser Ala Lys Val Met Ala			432
130	135	140	
acg cag att atc gac ttg att gat aac tat aac ggt Thr Gln Ile Ile Asp Leu Ile Asp Asn Tyr Asn Gly			468
145	150	155	

<210> SEQ ID NO 28  
 <211> LENGTH: 156  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 28

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

<210> SEQ ID NO 29  
 <211> LENGTH: 307  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(306)

-continued

&lt;400&gt; SEQUENCE: 29

```

gcc tcc cgc agt ggc gat gcc gat gag cgt gtc atg gat tcc aac gat      48
Ala Ser Arg Ser Gly Asp Ala Asp Glu Arg Val Met Asp Ser Asn Asp
1           5           10           15

tta gaa aaa gag cgc ggc atc act att tta gcg aaa aat act gcc att      96
Leu Glu Lys Glu Arg Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile
           20           25           30

aac tgg aat agc tac cgt att aac att gta gac acc ccg ggg cac gcg      144
Asn Trp Asn Ser Tyr Arg Ile Asn Ile Val Asp Thr Pro Gly His Ala
           35           40           45

gac ttc ggt ggc gaa gtg gaa cgc gta ctt tcc atg gtg gat tcc gta      192
Asp Phe Gly Gly Glu Val Glu Arg Val Leu Ser Met Val Asp Ser Val
           50           55           60

tta ttg atg gtg gat gcc ttc gac ggc ccg atg ccg caa acc cgt ttt      240
Leu Leu Met Val Asp Ala Phe Asp Gly Pro Met Pro Gln Thr Arg Phe
           65           70           75           80

gtt acg caa aaa gcc ttc tcc cac ggt tta aaa cct atc gta gtc atc      288
Val Thr Gln Lys Ala Phe Ser His Gly Leu Lys Pro Ile Val Val Ile
           85           90           95

aat aaa gtt gac cgc ccg g
Asn Lys Val Asp Arg Pro
           100

```

&lt;210&gt; SEQ ID NO 30

&lt;211&gt; LENGTH: 102

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 30

```

Ala Ser Arg Ser Gly Asp Ala Asp Glu Arg Val Met Asp Ser Asn Asp
1           5           10           15

Leu Glu Lys Glu Arg Gly Ile Thr Ile Leu Ala Lys Asn Thr Ala Ile
           20           25           30

Asn Trp Asn Ser Tyr Arg Ile Asn Ile Val Asp Thr Pro Gly His Ala
           35           40           45

Asp Phe Gly Gly Glu Val Glu Arg Val Leu Ser Met Val Asp Ser Val
           50           55           60

Leu Leu Met Val Asp Ala Phe Asp Gly Pro Met Pro Gln Thr Arg Phe
           65           70           75           80

Val Thr Gln Lys Ala Phe Ser His Gly Leu Lys Pro Ile Val Val Ile
           85           90           95

Asn Lys Val Asp Arg Pro
           100

```

&lt;210&gt; SEQ ID NO 31

&lt;211&gt; LENGTH: 891

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(891)

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: misc\_feature

&lt;222&gt; LOCATION: (882)..(882)

&lt;223&gt; OTHER INFORMATION: n is any nucleotide a, g, c, or t.

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: misc\_feature

&lt;222&gt; LOCATION: (888)..(888)

&lt;223&gt; OTHER INFORMATION: n is any nucleotide a, g, c, or t.

-continued

&lt;400&gt; SEQUENCE: 31

atg gct atc gta caa tcc aaa tct gcc cgc tac cgt tta tgg gtg acc	48
Met Ala Ile Val Gln Ser Lys Ser Ala Arg Tyr Arg Leu Trp Val Thr	
1 5 10 15	
cat ttg ctg ctg att gca ttt att tgt ctg att att ttc ccg tta ctg	96
His Leu Leu Leu Ile Ala Phe Ile Cys Leu Ile Ile Phe Pro Leu Leu	
20 25 30	
atg gtg atc ggc att tcc ctg cgc ccg ggc aac ctc gct ttg ggc gat	144
Met Val Ile Gly Ile Ser Leu Arg Pro Gly Asn Leu Ala Leu Gly Asp	
35 40 45	
ttg att ccg aaa caa att tcc tgg gaa cac tgg cag gcg gcg ctt ggc	192
Leu Ile Pro Lys Gln Ile Ser Trp Glu His Trp Gln Ala Ala Leu Gly	
50 55 60	
ttt tat gtg gta cac gcc gac ggt tct gtc aca cca ccg ccg ttc ccg	240
Phe Tyr Val Val His Ala Asp Gly Ser Val Thr Pro Pro Phe Pro	
65 70 75 80	
gtg ttg ttg tgg ttg tgg aac tcc att aaa gtg gcg acc atc acc tcc	288
Val Leu Leu Trp Leu Trp Asn Ser Ile Lys Val Ala Thr Ile Thr Ser	
85 90 95	
gtg ggt atc gtt gtt atg tcc acc act tgc gcc tac gct ttc gcg ccg	336
Val Gly Ile Val Val Met Ser Thr Thr Cys Ala Tyr Ala Phe Ala Arg	
100 105 110	
atg aaa ttc aaa ggc aaa aaa acc atc ttg caa ggc atg tta att ttc	384
Met Lys Phe Lys Gly Lys Lys Thr Ile Leu Gln Gly Met Leu Ile Phe	
115 120 125	
caa atg ttc cct gcg gtg ttg tct ttg gtc gcc tta tac gcc tta ttc	432
Gln Met Phe Pro Ala Val Leu Ser Leu Val Ala Leu Tyr Ala Leu Phe	
130 135 140	
gat cgc ctc ggt caa tat atc ccg ttc ctc ggc tta aac acc cac ggc	480
Asp Arg Leu Gly Gln Tyr Ile Pro Phe Leu Gly Leu Asn Thr His Gly	
145 150 155 160	
ggc gtg att ttc gct tac ttg ggc ggt atc gcc ttg cac gtt tgg acc	528
Gly Val Ile Phe Ala Tyr Leu Gly Gly Ile Ala Leu His Val Trp Thr	
165 170 175	
atc aaa ggc tat ttt gaa acc atc gac gga tcc ctg gaa gaa gct gcc	576
Ile Lys Gly Tyr Phe Glu Thr Ile Asp Gly Ser Leu Glu Glu Ala Ala	
180 185 190	
gcc tta gac ggc gct acc cca tgg cag gca ttc cgc tta att tta cta	624
Ala Leu Asp Gly Ala Thr Pro Trp Gln Ala Phe Arg Leu Ile Leu Leu	
195 200 205	
cct ctc tcc gta ccg att ctg gcg gtg gtc ttc att ctt tcc ttc atc	672
Pro Leu Ser Val Pro Ile Leu Ala Val Val Phe Ile Leu Ser Phe Ile	
210 215 220	
gcc gcc att acc gaa gtg ccg gtc gcc tcg cta tta tta cgc gat gtc	720
Ala Ala Ile Thr Glu Val Pro Val Ala Ser Leu Leu Leu Arg Asp Val	
225 230 235 240	
aac agc tac acc ctg gcg gtg gga atg caa caa tat ctc tac ccg caa	768
Asn Ser Tyr Thr Leu Ala Val Gly Met Gln Gln Tyr Leu Tyr Pro Gln	
245 250 255	
aac tac ctt tgg ggc gac ttc gcc gct gca gcg gtg ctt tcc gct att	816
Asn Tyr Leu Trp Gly Asp Phe Ala Ala Ala Val Leu Ser Ala Ile	
260 265 270	
cct att acc ctc gtg ttc tta ctg gca caa cgc tgg tta atc ggc gga	864
Pro Ile Thr Leu Val Phe Leu Leu Ala Gln Arg Trp Leu Ile Gly Gly	
275 280 285	
tta acg gca ggt ggg gtn aar ggn tga	891

-continued

Leu Thr Ala Gly Gly Val Lys Gly  
290 295

<210> SEQ ID NO 32  
<211> LENGTH: 296  
<212> TYPE: PRT  
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 32

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

<210> SEQ ID NO 33  
<211> LENGTH: 323  
<212> TYPE: DNA  
<213> ORGANISM: Actinobacillus actinomycetemcomitans  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(321)

-continued

&lt;400&gt; SEQUENCE: 33

```

aat gtt tat ggc ggt acc aaa gcc ttt gta aaa caa ttt agc tta aac      48
Asn Val Tyr Gly Gly Thr Lys Ala Phe Val Lys Gln Phe Ser Leu Asn
1          5          10          15

cta cgt gcc gat ctt gcc gga acc aat att cgc gtt tcc aat gta gaa      96
Leu Arg Ala Asp Leu Ala Gly Thr Asn Ile Arg Val Ser Asn Val Glu
          20          25          30

ccg gga ctg tgc ggc ggc acg gaa ttt tct aac gta cgt ttt aaa ggc      144
Pro Gly Leu Cys Gly Gly Thr Glu Phe Ser Asn Val Arg Phe Lys Gly
          35          40          45

gat aac gcc cgc gcg gaa aaa ctc tac gaa aac gta caa tat gtt acg      192
Asp Asn Ala Arg Ala Glu Lys Leu Tyr Glu Asn Val Gln Tyr Val Thr
          50          55          60

cca caa gat att gcc aat atc gtg ttg tgg ctc aat caa caa ccg gaa      240
Pro Gln Asp Ile Ala Asn Ile Val Leu Trp Leu Asn Gln Gln Pro Glu
          65          70          75          80

cac gtc aac att aac cgc att gaa gtg atg ccg acg gcg caa acc ttc      288
His Val Asn Ile Asn Arg Ile Glu Val Met Pro Thr Ala Gln Thr Phe
          85          90          95

gcc ccg ctt aat gta gca agg aat tta aat tta ga                        323
Ala Pro Leu Asn Val Ala Arg Asn Leu Asn Leu
          100          105

```

&lt;210&gt; SEQ ID NO 34

&lt;211&gt; LENGTH: 107

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 34

```

Asn Val Tyr Gly Gly Thr Lys Ala Phe Val Lys Gln Phe Ser Leu Asn
1          5          10          15

Leu Arg Ala Asp Leu Ala Gly Thr Asn Ile Arg Val Ser Asn Val Glu
          20          25          30

Pro Gly Leu Cys Gly Gly Thr Glu Phe Ser Asn Val Arg Phe Lys Gly
          35          40          45

Asp Asn Ala Arg Ala Glu Lys Leu Tyr Glu Asn Val Gln Tyr Val Thr
          50          55          60

Pro Gln Asp Ile Ala Asn Ile Val Leu Trp Leu Asn Gln Gln Pro Glu
          65          70          75          80

His Val Asn Ile Asn Arg Ile Glu Val Met Pro Thr Ala Gln Thr Phe
          85          90          95

Ala Pro Leu Asn Val Ala Arg Asn Leu Asn Leu
          100          105

```

&lt;210&gt; SEQ ID NO 35

&lt;211&gt; LENGTH: 585

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(585)

&lt;400&gt; SEQUENCE: 35

```

atg gcg gaa acg att tta aac ccg tat ttc ggg gaa ttc gcc gga atg      48
Met Ala Glu Thr Ile Leu Asn Pro Tyr Phe Gly Glu Phe Gly Gly Met
1          5          10          15

tat gtg ccg gaa att cta gtg ccg gtg ttg caa cag ttg gaa aaa gcg      96

```

-continued

Tyr	Val	Pro	Glu	Ile	Leu	Val	Pro	Val	Leu	Gln	Gln	Leu	Glu	Lys	Ala	
			20					25					30			
ttt	gta	gaa	gcc	aag	gcg	gat	cct	gca	ttt	cag	cgc	gaa	ttt	cag	gat	144
Phe	Val	Glu	Ala	Lys	Ala	Asp	Pro	Ala	Phe	Gln	Arg	Glu	Phe	Gln	Asp	
		35					40					45				
tta	ttg	aaa	aat	tat	gcc	ggc	aga	ccc	acc	gca	ctt	acc	ctt	tgt	cgc	192
Leu	Leu	Lys	Asn	Tyr	Ala	Gly	Arg	Pro	Thr	Ala	Leu	Thr	Leu	Cys	Arg	
		50				55					60					
aat	ctc	acc	aaa	ggc	acc	aac	gcc	aaa	atc	tat	tta	aaa	cgg	gaa	gat	240
Asn	Leu	Thr	Lys	Gly	Thr	Asn	Ala	Lys	Ile	Tyr	Leu	Lys	Arg	Glu	Asp	
		65			70					75					80	
tta	tta	cac	ggc	ggc	gca	cat	aaa	acc	aac	cag	gta	tta	ggt	cag	att	288
Leu	Leu	His	Gly	Gly	Ala	His	Lys	Thr	Asn	Gln	Val	Leu	Gly	Gln	Ile	
			85						90					95		
ttg	ctt	gcc	aaa	cgc	atg	ggc	aaa	acc	cgc	att	att	gcc	gaa	acc	ggc	336
Leu	Leu	Ala	Lys	Arg	Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	
			100					105					110			
gcg	gga	cag	cac	ggt	gtc	gcc	act	gct	ctc	gcc	tgc	gcc	atg	ttg	gat	384
Ala	Gly	Gln	His	Gly	Val	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Met	Leu	Asp	
		115					120					125				
atg	ccg	tgc	cgt	ggt	tat	atg	ggc	gcg	aaa	gat	gtg	gaa	cgc	caa	tcg	432
Met	Pro	Cys	Arg	Val	Tyr	Met	Gly	Ala	Lys	Asp	Val	Glu	Arg	Gln	Ser	
		130				135					140					
ccg	aat	gtg	ttt	cgt	atg	cgt	tta	atg	ggc	acg	gaa	gtg	gta	ccg	gtg	480
Pro	Asn	Val	Phe	Arg	Met	Arg	Leu	Met	Gly	Thr	Glu	Val	Val	Pro	Val	
		145			150					155					160	
caa	aaa	ggt	tcc	tgt	tct	ttg	aaa	gac	gct	tgc	tgc	gaa	gcc	atg	cgt	528
Gln	Lys	Gly	Ser	Cys	Ser	Leu	Lys	Asp	Ala	Cys	Cys	Glu	Ala	Met	Arg	
			165					170						175		
gac	tggt	tcg	gca	aat	tat	gaa	aat	acg	cac	tat	ttg	ctc	ggc	aca	gcg	576
Asp	Trp	Ser	Ala	Asn	Tyr	Glu	Asn	Thr	His	Tyr	Leu	Leu	Gly	Thr	Ala	
			180					185					190			
gca	ggt	ccg														585
Ala	Gly	Pro														
		195														

<210> SEQ ID NO 36  
 <211> LENGTH: 195  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 36

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

-continued

Ala Gly Gln His Gly Val Ala Thr Ala Leu Ala Cys Ala Met Leu Asp  
 115 120 125  
 Met Pro Cys Arg Val Tyr Met Gly Ala Lys Asp Val Glu Arg Gln Ser  
 130 135 140  
 Pro Asn Val Phe Arg Met Arg Leu Met Gly Thr Glu Val Val Pro Val  
 145 150 155 160  
 Gln Lys Gly Ser Cys Ser Leu Lys Asp Ala Cys Cys Glu Ala Met Arg  
 165 170 175  
 Asp Trp Ser Ala Asn Tyr Glu Asn Thr His Tyr Leu Leu Gly Thr Ala  
 180 185 190  
 Ala Gly Pro  
 195

<210> SEQ ID NO 37  
 <211> LENGTH: 543  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(543)

<400> SEQUENCE: 37

atg tcg cac gta ttt caa atc tca aga gaa att atg aca gct tta aat	48
Met Ser His Val Phe Gln Ile Ser Arg Glu Ile Met Thr Ala Leu Asn	
1 5 10 15	
gta ctt att tac ccg gaa gag cac ctt aaa gtg gtt tgc gat ccg gtc	96
Val Leu Ile Tyr Pro Glu Glu His Leu Lys Val Val Cys Asp Pro Val	
20 25 30	
gtg gaa gtc aat gac aac acg cgt aag att att gat aat atg ttt gat	144
Val Glu Val Asn Asp Asn Thr Arg Lys Ile Ile Asp Asn Met Phe Asp	
35 40 45	
acc atg tat cag gaa ggc ggt atc ggc cta gcg gca ccg cag gtg gat	192
Thr Met Tyr Gln Glu Gly Ile Gly Leu Ala Ala Pro Gln Val Asp	
50 55 60	
att tta cag cgt att atc act att gat att gag ggt gac aaa caa aac	240
Ile Leu Gln Arg Ile Ile Thr Ile Asp Ile Glu Gly Asp Lys Gln Asn	
65 70 75 80	
cag tta gtg ttg att aac cct gaa att ttg gaa tcg gaa ggt gaa acc	288
Gln Leu Val Leu Ile Asn Pro Glu Ile Leu Glu Ser Glu Gly Glu Thr	
85 90 95	
gga att gaa gag ggt tgt ttg tcg att ccc gga ttt cgt gcg tta gtg	336
Gly Ile Glu Glu Gly Cys Leu Ser Ile Pro Gly Phe Arg Ala Leu Val	
100 105 110	
cca cgt aaa gag aaa gtg act gta aaa gcg ctg gat cgt cat ggt aaa	384
Pro Arg Lys Glu Lys Val Thr Val Lys Ala Leu Asp Arg His Gly Lys	
115 120 125	
gaa ttc acc tta aaa gcc gat ggt ctg ttg gca att tgt att cag cat	432
Glu Phe Thr Leu Lys Ala Asp Gly Leu Leu Ala Ile Cys Ile Gln His	
130 135 140	
gaa att gat cat tta aac ggt att ctt ttt gtg gat tat ctc tct cca	480
Glu Ile Asp His Leu Asn Gly Ile Leu Phe Val Asp Tyr Leu Ser Pro	
145 150 155 160	
ttg aaa cgt cag cgg att aaa gaa aag ctg att aaa atg aaa aag cag	528
Leu Lys Arg Gln Arg Ile Lys Glu Lys Leu Ile Lys Met Lys Lys Gln	
165 170 175	
atg gaa aag caa aaa	543
Met Glu Lys Gln Lys	
180	

-continued

<210> SEQ ID NO 38  
 <211> LENGTH: 181  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 38

```

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

```

<210> SEQ ID NO 39  
 <211> LENGTH: 353  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(351)

<400> SEQUENCE: 39

```

cgc ggc gtg aca ccg gaa cta ttc gcc gac tgg tta aaa cag tta cat      48
Arg Gly Val Thr Pro Glu Leu Phe Ala Asp Trp Leu Lys Gln Leu His
1          5          10          15
cag gcg ggc gta aaa gtg gtg ttg gac agc agt aac gcc gca ttg acc      96
Gln Ala Gly Val Lys Val Val Leu Asp Ser Ser Asn Ala Ala Leu Thr
20          25          30
gcc ggc tta acg gcg caa cct tgg ttg gtt aaa ccg aat cat cgt gag      144
Ala Gly Leu Thr Ala Gln Pro Trp Leu Val Lys Pro Asn His Arg Glu
35          40          45
ttg gaa gcc tgg att ggt cat gcg ctg ccg acc ttg gac gac att atc      192
Leu Glu Ala Trp Ile Gly His Ala Leu Pro Thr Leu Asp Asp Ile Ile
50          55          60
gcg gcg gcg aaa aaa ctg aaa gca caa gcc att gct aac gtg att att      240
Ala Ala Ala Lys Lys Leu Lys Ala Gln Gly Ile Ala Asn Val Ile Ile
65          70          75          80

```

-continued

---

```

tcc atg ggc gcc aac ggt tcg ttg tgg ttg agc gat aca gcc gtc gta      288
Ser Met Gly Ala Asn Gly Ser Leu Trp Leu Ser Asp Thr Ala Val Val
      85                               90                               95

cag gcg caa ccg ccg aaa tgc gaa aac gtg gtc agc acc gtg ggc gcg      336
Gln Ala Gln Pro Pro Lys Cys Glu Asn Val Val Ser Thr Val Gly Ala
      100                               105                               110

ggc gat tct atg gtg gc      353
Gly Asp Ser Met Val
      115

```

```

<210> SEQ ID NO 40
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 40

```

```

Arg Gly Val Thr Pro Glu Leu Phe Ala Asp Trp Leu Lys Gln Leu His
 1                               5                               10                               15

Gln Ala Gly Val Lys Val Val Leu Asp Ser Ser Asn Ala Ala Leu Thr
 20                               25                               30

Ala Gly Leu Thr Ala Gln Pro Trp Leu Val Lys Pro Asn His Arg Glu
 35                               40                               45

Leu Glu Ala Trp Ile Gly His Ala Leu Pro Thr Leu Asp Asp Ile Ile
 50                               55                               60

Ala Ala Ala Lys Lys Leu Lys Ala Gln Gly Ile Ala Asn Val Ile Ile
 65                               70                               75                               80

Ser Met Gly Ala Asn Gly Ser Leu Trp Leu Ser Asp Thr Ala Val Val
 85                               90                               95

Gln Ala Gln Pro Pro Lys Cys Glu Asn Val Val Ser Thr Val Gly Ala
 100                               105                               110

Gly Asp Ser Met Val
 115

```

```

<210> SEQ ID NO 41
<211> LENGTH: 367
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(366)

```

```

<400> SEQUENCE: 41

```

```

atg aaa aaa tgg ttt atg ctg tta ctt ccg ctg aca ttt atc ggc agc      48
Met Lys Lys Trp Phe Met Leu Leu Leu Pro Leu Thr Phe Ile Gly Ser
 1                               5                               10                               15

ctt tgg gcg cag gaa gcg cct tcc ccc ttt ctt gcc ggg gaa tta ccg      96
Leu Trp Ala Gln Glu Ala Pro Ser Pro Phe Leu Ala Gly Glu Leu Pro
 20                               25                               30

gca gcg caa aaa atc gaa aaa gtc tta agc gcc ggt aat ccg agt gat      144
Ala Ala Gln Lys Ile Glu Lys Val Leu Ser Ala Gly Asn Pro Ser Asp
 35                               40                               45

gcg tta ttg ctg gcc gcc gcg ccg caa aaa atg gtc gga ctg gcg ggc      192
Ala Leu Leu Leu Ala Ala Ala Pro Gln Lys Met Val Gly Leu Ala Gly
 50                               55                               60

ttt aag atg gca tcc aaa ggc ggc aaa tta ttt cct gtg caa caa caa      240
Phe Lys Met Ala Ser Lys Gly Gly Lys Leu Phe Pro Val Gln Gln Gln
 65                               70                               75                               80

gcg ttg ccg acc atc ggc aaa att gcc gga aag ggc agt acg ttt tcc      288

```

-continued

---

```

Ala Leu Pro Thr Ile Gly Lys Ile Ala Gly Lys Gly Ser Thr Phe Ser
      85                               90                               95

gcc gaa aaa atc gtg gcg ctt caa ccg aat ttg att att gat gtg ggc    336
Ala Glu Lys Ile Val Ala Leu Gln Pro Asn Leu Ile Ile Asp Val Gly
      100                               105                               110

aat gtg gcg ccg aat tac atc gat cag gca a    367
Asn Val Ala Pro Asn Tyr Ile Asp Gln Ala
      115                               120
    
```

```

<210> SEQ ID NO 42
<211> LENGTH: 122
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans
    
```

<400> SEQUENCE: 42

```

Met Lys Lys Trp Phe Met Leu Leu Leu Pro Leu Thr Phe Ile Gly Ser
 1      5      10      15

Leu Trp Ala Gln Glu Ala Pro Ser Pro Phe Leu Ala Gly Glu Leu Pro
 20      25      30

Ala Ala Gln Lys Ile Glu Lys Val Leu Ser Ala Gly Asn Pro Ser Asp
 35      40      45

Ala Leu Leu Leu Ala Ala Ala Pro Gln Lys Met Val Gly Leu Ala Gly
 50      55      60

Phe Lys Met Ala Ser Lys Gly Gly Lys Leu Phe Pro Val Gln Gln Gln
 65      70      75      80

Ala Leu Pro Thr Ile Gly Lys Ile Ala Gly Lys Gly Ser Thr Phe Ser
      85      90      95

Ala Glu Lys Ile Val Ala Leu Gln Pro Asn Leu Ile Ile Asp Val Gly
 100      105      110

Asn Val Ala Pro Asn Tyr Ile Asp Gln Ala
 115      120
    
```

```

<210> SEQ ID NO 43
<211> LENGTH: 4593
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(4593)
    
```

<400> SEQUENCE: 43

```

gtc ttt aaa gta atc tgg tgt aaa aca tct cag aca tgg att gcc gta    48
Val Phe Lys Val Ile Trp Cys Lys Thr Ser Gln Thr Trp Ile Ala Val
 1      5      10      15

tct gaa cta tct aaa gct ttt tcc ctt tct acc act aca gat ata cct    96
Ser Glu Leu Ser Lys Ala Phe Ser Leu Ser Thr Thr Thr Asp Ile Pro
 20      25      30

aaa aaa act aaa ata ttc att gct gca gcc ccg tta tta ttt ctc tcc    144
Lys Lys Thr Lys Ile Phe Ile Ala Ala Ala Pro Leu Leu Phe Leu Ser
 35      40      45

ttt aat acc aac gct tac att gct ata ggt tct gtt gaa aac aat tct    192
Phe Asn Thr Asn Ala Tyr Ile Ala Ile Gly Ser Val Glu Asn Asn Ser
 50      55      60

gtg aaa tcc gag ggg gca gaa gcc tcc cca aac aag aga aag gga agc    240
Val Lys Ser Glu Gly Ala Glu Ala Ser Pro Asn Lys Arg Lys Gly Ser
 65      70      75      80

caa gca tta aat tat tac aac ccc ggt agt aaa tca tat gat gat aaa    288
Gln Ala Leu Asn Tyr Tyr Asn Pro Gly Ser Lys Ser Tyr Asp Asp Lys
    
```



-continued

385	390	395	400	
gta gct gtt gca aac gcc ggt aaa gag cgt cga att att aat gtt gcc Val Ala Val Ala Asn Ala Gly Lys Glu Arg Arg Ile Ile Asn Val Ala 405 410 415				1248
ggt ggt cgt aat gat act gat gca gtg aat att gcc cag tta aaa ttc Gly Gly Arg Asn Asp Thr Asp Ala Val Asn Ile Ala Gln Leu Lys Phe 420 425 430				1296
gtg aat gat aac tta gcc aag tcc atc gca ggc gcc ggt tat aac ggc Val Asn Asp Asn Leu Ala Lys Ser Ile Ala Gly Ala Gly Tyr Asn Gly 435 440 445				1344
tat gaa aca gac gga cat act tac aaa gca ccg gta ttt agt att aaa Tyr Glu Thr Asp Gly His Thr Tyr Lys Ala Pro Val Phe Ser Ile Lys 450 455 460				1392
aat acc aac tat cac gat gtc aaa aca gct gtt gaa gcg gca caa acc Asn Thr Asn Tyr His Asp Val Lys Thr Ala Val Glu Ala Ala Gln Thr 465 470 475 480				1440
aat tat gta agt gta aat agc act aat aca gca gcc gat agt aat tac Asn Tyr Val Ser Val Asn Ser Thr Asn Thr Ala Ala Asp Ser Asn Tyr 485 490 495				1488
gac aat aaa ggg gct aaa gca gta ggt tct att gcg tta ggc gaa aaa Asp Asn Lys Gly Ala Lys Ala Val Gly Ser Ile Ala Leu Gly Glu Lys 500 505 510				1536
gcc aca aca gga acg gcg gca atg aac tct att gcc att ggt tta aac Ala Thr Thr Gly Thr Ala Ala Met Asn Ser Ile Ala Ile Gly Leu Asn 515 520 525				1584
agc aat gtt agc ggc caa aat acc gtt gca ttg ggt gcc aat atc acc Ser Asn Val Ser Gly Gln Asn Thr Val Ala Leu Gly Ala Asn Ile Thr 530 535 540				1632
gcg aca acc aac ggt tcc gtc att tta gga aat tcc tcc acc acg gaa Ala Thr Thr Asn Gly Ser Val Ile Leu Gly Asn Ser Ser Thr Thr Glu 545 550 555 560				1680
ggt tca cat cct gtt tca aat gtt agc agt gcg act gtt aac gga tat Gly Ser His Pro Val Ser Asn Val Ser Ser Ala Thr Val Asn Gly Tyr 565 570 575				1728
acc tac tca ggt ttt acc ggc acg gta aaa gag tcg gga cat ttt gtg Thr Tyr Ser Gly Phe Thr Gly Thr Val Lys Glu Ser Gly His Phe Val 580 585 590				1776
agc att ggt tca aaa ggc aat gag cgt caa att aaa aat gtg gca gca Ser Ile Gly Ser Lys Gly Asn Glu Arg Gln Ile Lys Asn Val Ala Ala 595 600 605				1824
ggt aat gtt gcg gca aac tca acc gat gcc gtt aat ggc tct caa tta Gly Asn Val Ala Ala Asn Ser Thr Asp Ala Val Asn Gly Ser Gln Leu 610 615 620				1872
ttt gct gtc gcc agt cgt gta gaa caa ggt tgg caa atc act tcc ggc Phe Ala Val Ala Ser Arg Val Glu Gln Gly Trp Gln Ile Thr Ser Gly 625 630 635 640				1920
gta gaa aat ggt ggt act caa aat ggc gca gcc tca aca gca aca atc Val Glu Asn Gly Gly Thr Gln Asn Gly Ala Ala Ser Thr Ala Thr Ile 645 650 655				1968
aaa ccg agt aac caa gtg aag cta ctg gca gga aag aat tta gca gtc Lys Pro Ser Asn Gln Val Lys Leu Leu Ala Gly Lys Asn Leu Ala Val 660 665 670				2016
aaa caa aac ggc act aac ttc acc ttc tca acc caa gaa aat gtc acg Lys Gln Asn Gly Thr Asn Phe Ser Thr Phe Ser Thr Gln Glu Asn Val Thr 675 680 685				2064
ttc act aat gtt acg acc caa gat cta act gca aca ggc aac acc act Phe Thr Asn Val Thr Thr Gln Asp Leu Thr Ala Thr Gly Asn Thr Thr 690 695 700				2112

-continued

690	695	700	
ggt aag aac ttc agc gtt caa aat ggc gga acc atc aat atg gga aat Val Lys Asn Phe Ser Val Gln Asn Gly Gly Thr Ile Asn Met Gly Asn 705 710 715 720			2160
aat cgc att acc ggt gtc gct gaa ggc act caa gat gac gac gcg gtt Asn Arg Ile Thr Gly Val Ala Glu Gly Thr Gln Asp Asp Asp Ala Val 725 730 735			2208
aac ttt aaa caa tta aaa agc ctt ctt ggt ggc tcc gca tca acg gaa Asn Phe Lys Gln Leu Lys Ser Leu Leu Gly Gly Ser Ala Ser Thr Glu 740 745 750			2256
att gtt gag aaa aaa gca gct caa gcc gga gat gaa aac ctg gcg gat Ile Val Glu Lys Lys Ala Ala Gln Ala Gly Asp Glu Asn Leu Ala Asp 755 760 765			2304
att agc gta gca aat ggt aaa aac gcc ggc gat atg ggt gcg aaa tac Ile Ser Val Ala Asn Gly Lys Asn Ala Gly Asp Met Gly Ala Lys Tyr 770 775 780			2352
gaa gta tct gta tcc aaa aaa gcc gta caa agt gcc gca aaa gaa gcg Glu Val Ser Val Ser Lys Lys Ala Val Gln Ser Ala Ala Lys Glu Ala 785 790 795 800			2400
ggt aaa gtg aca ggt tcg gca ccg att aat gta aac aaa aca gat gta Val Lys Val Thr Gly Ser Ala Pro Ile Asn Val Asn Lys Thr Asp Val 805 810 815			2448
aat ggc gtt gat act tat gcc gta acc ttt aat ggc aca gaa gcg gcg Asn Gly Val Asp Thr Tyr Ala Val Thr Phe Asn Gly Thr Glu Ala Ala 820 825 830			2496
aaa tct atc cca tta act tat aaa gct aac ggt agc ggt gat aaa acc Lys Ser Ile Pro Leu Thr Tyr Lys Ala Asn Gly Ser Gly Asp Lys Thr 835 840 845			2544
gtc atg ttg gat aaa gga tta aac ttt acc aat ggt atg atg aca acc Val Met Leu Asp Lys Gly Leu Asn Phe Thr Asn Gly Met Met Thr Thr 850 855 860			2592
gct tcc gtg gca aat gac ggt gtg gtg aaa tat gac gtc aat tta tcc Ala Ser Val Ala Asn Asp Gly Val Val Lys Tyr Asp Val Asn Leu Ser 865 870 875 880			2640
acc att aaa gta gaa gat ggc aag gct gcc gta gcc ggt aca ccg ggc Thr Ile Lys Val Glu Asp Gly Lys Ala Ala Val Ala Gly Thr Pro Gly 885 890 895			2688
aca aat ggc gcc aac ggc act gat ggc aaa gat ggc gta gcg acg gtt Thr Asn Gly Ala Asn Gly Thr Asp Gly Lys Asp Gly Val Ala Thr Val 900 905 910			2736
aaa aat gtg gta gag gcg tta aat aat gcc gca tgg aca ata act gcc Lys Asn Val Val Glu Ala Leu Asn Asn Ala Ala Trp Thr Ile Thr Ala 915 920 925			2784
tct aaa tct gac ggc gaa gtc gtc agc aat gca tct aat tcc gtt aaa Ser Lys Ser Asp Gly Glu Val Val Ser Asn Ala Ser Asn Ser Val Lys 930 935 940			2832
aat ggg gat acg gtg act tat gat gcc ggc aaa aac atc aaa att act Asn Gly Asp Thr Val Thr Tyr Asp Ala Gly Lys Asn Ile Lys Ile Thr 945 950 955 960			2880
caa aga gat aaa aaa ttc tct ttt gcc acc aaa gat aat gtt gaa ttt Gln Arg Asp Lys Lys Phe Ser Phe Ala Thr Lys Asp Asn Val Glu Phe 965 970 975			2928
act tct gtg acc acg ggc aat acc aaa tta acc ggt aat ggt gta gaa Thr Ser Val Thr Thr Gly Asn Thr Lys Leu Thr Gly Asn Gly Val Glu 980 985 990			2976
atc acc aac ggc cct aaa ctt acc caa tca ggt gtg gat gca gcc ggt Ile Thr Asn Gly Pro Lys Leu Thr Gln Ser Gly Val Asp Ala Gly Gly 3024			

-continued

995		1000				1005									
aag Lys	aaa Ile	atc Thr	acc Asn	aat Val	gta Val	gca Ala	gat Asp	ggc Gly	gtt Val	att Ile	gca Ala	gct Ala	aac Asn	agc Ser	3069
1010					1015						1020				
aaa Lys	gat Asp	gcc Ala	gtg Val	aat Asn	ggc Gly	ggt Gly	caa Gln	tta Leu	ttc Phe	gct Ala	gaa Glu	act Thr	gca Ala	aaa Lys	3114
1025					1030						1035				
gcc Ala	aaa Lys	act Thr	acg Thr	gtt Val	gag Glu	aaa Lys	ggt Gly	gat Asp	gat Asp	aat Asn	att Ile	caa Gln	atc Ile	aca Thr	3159
1040					1045						1050				
tca Ser	gaa Glu	act Thr	gca Ala	acg Thr	gac Asp	gga Gly	cat His	att Ile	aac Asn	tat Tyr	aaa Lys	gtg Val	gca Ala	tta Leu	3204
1055					1060						1065				
aat Asn	cct Pro	agc Ser	ttg Leu	acc Thr	gtc Val	gga Gly	cca Pro	aga Arg	aca Thr	aat Asn	ggt Gly	cac His	ccg Pro	atc Ile	3249
1070					1075						1080				
acc Thr	att Ile	gat Asp	ggt Gly	aat Asn	aac Asn	ggc Gly	tat Tyr	att Ile	acc Thr	ggt Gly	tta Leu	acc Thr	aat Asn	aca Thr	3294
1085					1090						1095				
agc Ser	tggt Trp	acg Thr	ggc Gly	gcg Ala	cca Pro	aca Thr	acc Thr	ggt Gly	cgt Arg	gca Ala	gca Ala	acg Thr	gaa Glu	gat Asp	3339
1100					1105						1110				
caa Gln	tta Leu	tct Ser	ata Ile	gtc Val	gat Asp	aaa Lys	aaa Lys	ttc Phe	gat Asp	aat Asn	aag Lys	gtt Val	tct Ser	tta Leu	3384
1115					1120						1125				
ggc Gly	ggt Gly	gac Asp	aac Asn	ggt Gly	agt Ser	acc Thr	aca Thr	gag Glu	aaa Lys	tcc Ser	ttg Leu	tct Ser	cac His	aac Asn	3429
1130					1135						1140				
ggc Gly	gga Gly	atc Ile	aaa Lys	ttt Phe	aat Asn	atc Ile	aaa Lys	ggc Gly	gga Gly	gac Asp	agc Ser	caa Gln	aaa Lys	tat Tyr	3474
1145					1150						1155				
gtg Val	acg Thr	aca Thr	tca Ser	gga Gly	tcc Ser	ggc Gly	gat Asp	gat Asp	gtc Val	acg Thr	gtg Val	gat Asp	ctt Leu	gcc Ala	3519
1160					1165						1170				
caa Gln	acc Thr	aca Thr	aaa Lys	aat Asn	aag Lys	atc Ile	gac Asp	aat Asn	gcg Ala	gca Ala	gat Asp	aaa Lys	gat Asp	ctc Leu	3564
1175					1180						1185				
ggc Ala	aac Asn	att Ile	acc Thr	gat Asp	aat Asn	ggt Gly	aaa Lys	aaa Lys	ggt Val	att Ile	acc Thr	gct Ala	tta Leu	ggc Gly	3609
1190					1195						1200				
gct Ala	gta Val	gtg Val	aaa Lys	gcg Ala	gct Ala	gat Asp	tct Ser	acg Thr	att Ile	acg Thr	gta Val	act Thr	gac Asp	gaa Glu	3654
1205					1210						1215				
acc Thr	gat Asp	aat Asn	acg Thr	aca Thr	gga Gly	caa Gln	aaa Lys	acc Thr	tac Tyr	aaa Lys	atc Ile	aaa Lys	gcc Ala	aat Asn	3699
1220					1225						1230				
att Ile	cca Pro	aca Thr	ccg Pro	gaa Glu	aaa Lys	aca Thr	gca Ala	atg Met	gct Ala	ccc Pro	ggc Gly	aac Asn	aat Asn	aca Thr	3744
1235					1240						1245				
acc Thr	att Ile	gaa Glu	ggt Gly	gat Asp	ggc Gly	tca Ser	gcc Ala	gcc Ala	aat Asn	ccg Pro	ttt Phe	aaa Lys	gtg Val	aat Asn	3789
1250					1255						1260				
ctg Leu	aaa Lys	gat Asp	gat Asp	tta Leu	gcg Ala	cta Leu	ggt Gly	caa Gln	aaa Lys	gac Asp	gct Ala	aac Asn	ggc Gly	gta Val	3834
1265					1270						1275				
acc Thr	ggt Gly	aaa Lys	gat Asp	tct Ser	tcc Ser	att Ile	aaa Lys	gtg Val	aac Asn	ggc Gly	aaa Lys	gat Asp	ggc Gly	tcc Ser	3879
1280					1285						1290				

-continued

1280	1285	1290	
ggt gtg gcg att aac ggt Gly Val Ala Ile Asn Gly 1295	aaa gac ggt tcc att gca Lys Asp Gly Ser Ile Ala 1300	tta aat ggc Leu Asn Gly 1305	3924
aaa gac ggt gcg aat cct Lys Asp Gly Ala Asn Pro 1310	gtc acc atc aaa acg gcg Val Thr Ile Lys Thr Ala 1315	caa ggt cct Gln Gly Pro 1320	3969
gcc ggt gtg aat gaa acc Ala Gly Val Asn Glu Thr 1325	aat ccc aaa gac cgt tta Asn Pro Lys Asp Arg Leu 1330	atg gtg aat Met Val Asn 1335	4014
aac gac gct gtt gca acc Asn Asp Ala Val Ala Thr 1340	ctt aaa gac ggc tta aaa Leu Lys Asp Gly Leu Lys 1345	ttc gcc gga Phe Ala Gly 1350	4059
gat aac agc acc gaa gtc Asp Asn Ser Thr Glu Val 1355	atc act aaa acc tta aat Ile Thr Lys Thr Leu Asn 1360	caa aaa ctg Gln Lys Leu 1365	4104
gaa att gtg ggt ggt gca Glu Ile Val Gly Gly Ala 1370	gat aaa aac aaa tta tct Asp Lys Asn Lys Leu Ser 1375	gac aac aat Asp Asn Asn 1380	4149
atc ggc gta aat gcc aat Ile Gly Val Asn Ala Asn 1385	aac ggc aaa ctg gaa gtg Asn Gly Lys Leu Glu Val 1390	aaa tta gcc Lys Leu Ala 1395	4194
aaa gag ttg aat gag tta Lys Glu Leu Asn Glu Leu 1400	acc agt gcg caa ttc aag Thr Ser Ala Gln Phe Lys 1405	aat ggc gac Asn Gly Asp 1410	4239
aac aca acg gtt atc aat Asn Thr Thr Val Ile Asn 1415	ggc aat ggc ata aca att Gly Asn Gly Ile Thr Ile 1420	acc ccg aaa Thr Pro Lys 1425	4284
gat ccg aca aag gcg gtc Asp Pro Thr Lys Ala Val 1430	agc tta acg gat aaa gga Ser Leu Thr Asp Lys Gly 1435	cta aac aat Leu Asn Asn 1440	4329
ggt ggt aat caa att gtg Gly Gly Asn Gln Ile Val 1445	aac att gac agc gga tta Asn Ile Asp Ser Gly Leu 1450	aaa caa gcc Lys Gln Ala 1455	4374
gac ggt tca aca gtt gct Asp Gly Ser Thr Val Ala 1460	tta aaa gac gcc tca ggt Leu Lys Asp Ala Ser Gly 1465	gat acc tta Asp Thr Leu 1470	4419
aaa aat gcg gcg aat atc Lys Asn Ala Ala Asn Ile 1475	ggc gat tta caa aaa tcc Gly Asp Leu Gln Lys Ser 1480	att aac gac Ile Asn Asp 1485	4464
att acc gac gca agt aaa Ile Thr Asp Ala Ser Lys 1490	aac ggc ggc ttc ggt tta Asn Gly Gly Phe Gly Leu 1495	agc gat gac Ser Asp Asp 1500	4509
aat ggc gca acc gct aaa Asn Gly Ala Thr Ala Lys 1505	gcc aac tta ggt gaa acc Ala Asn Leu Gly Glu Thr 1510	cgt gaa agt Arg Glu Ser 1515	4554
gaa agg cga tgg cag tgt Glu Arg Arg Trp Gln Cys 1520	tat tac aaa agt agt tac Tyr Tyr Lys Ser Ser Tyr 1525	cga Arg 1530	4593

&lt;210&gt; SEQ ID NO 44

&lt;211&gt; LENGTH: 1531

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 44

Val Phe Lys Val Ile Trp Cys Lys Thr Ser Gln Thr Trp Ile Ala Val  
 1 5 10 15

-continued

---

Ser Glu Leu Ser Lys Ala Phe Ser Leu Ser Thr Thr Thr Asp Ile Pro  
                   20                                  25                                  30  
 Lys Lys Thr Lys Ile Phe Ile Ala Ala Ala Pro Leu Leu Phe Leu Ser  
                   35                                  40                                  45  
 Phe Asn Thr Asn Ala Tyr Ile Ala Ile Gly Ser Val Glu Asn Asn Ser  
                   50                                  55                                  60  
 Val Lys Ser Glu Gly Ala Glu Ala Ser Pro Asn Lys Arg Lys Gly Ser  
                   65                                  70                                  75                                  80  
 Gln Ala Leu Asn Tyr Tyr Asn Pro Gly Ser Lys Ser Tyr Asp Asp Lys  
                   85                                  90                                  95  
 Asp Lys Pro Ser Asn Pro Glu Arg Arg Tyr Ser Asn Gly Glu Ala Tyr  
                   100                                  105                                  110  
 Gly Ile Ala Ile Gly Lys Asn Thr Asp Val Arg Asp Ser Ser Lys Asp  
                   115                                  120                                  125  
 Ser Asn Gly Ile Ala Leu Gly Asp Tyr Ser Lys Ala Thr Gly Gly Leu  
                   130                                  135                                  140  
 Ala Met Ala Leu Gly Ser Phe Ser Arg Ala Glu Lys Asn Gly Gly Ile  
                   145                                  150                                  155                                  160  
 Ala Ile Gly Ile Ala Ser Arg Ser Ser Gly Ile Asn Ser Leu Ala Met  
                   165                                  170                                  175  
 Met Arg Gln Ser Ala Ala Thr Gly Asp Tyr Ser Thr Ala Ile Gly Ser  
                   180                                  185                                  190  
 Val Ala Trp Ala Ala Gly Gln Ser Ser Phe Ala Leu Gly Ala Ser Ala  
                   195                                  200                                  205  
 Thr Ala Lys Gly Asn Gln Ser Ile Ala Ile Gly Ser Leu Glu Gln Lys  
                   210                                  215                                  220  
 Ile Ser Pro Asn Gly Ser Gly Val Pro Ile Thr Lys Tyr Asn Gly Leu  
                   225                                  230                                  235                                  240  
 Asp Asn Thr Gln Thr Asn Gly Asn Arg Ser Met Ala Leu Gly Thr Ala  
                   245                                  250                                  255  
 Ala Lys Thr Asn Gly Asp Asp Ser Phe Ala Ile Gly Tyr Lys Ala His  
                   260                                  265                                  270  
 Thr Gly Glu Phe Lys Val Glu His Asp Asn Tyr Leu Lys Glu Asn Val  
                   275                                  280                                  285  
 Thr Ser Pro Asp Leu Ser Lys Lys Ala Asp Lys Ala Ile Ala Val Gly  
                   290                                  295                                  300  
 Thr Ser Ala Leu Ala Gln Lys Glu Ser Ala Ile Ala Phe Gly Tyr Gln  
                   305                                  310                                  315                                  320  
 Ala Asn Ala Ser Gly Ile Asn Ala Ile Ser Leu Gly Ala Asn Ala Lys  
                   325                                  330                                  335  
 Ala Ser Gln Asp Asn Val Val Ala Ile Gly Lys Tyr Ala Thr Ala Thr  
                   340                                  345                                  350  
 Glu Ser Gly Ser Met Ala Ile Gly Gln Gly Ala Lys Ser Thr Phe Lys  
                   355                                  360                                  365  
 Asn Ser Leu Ala Leu Gly Thr Gly Thr Ile Val Asn Ser Val Asp Gly  
                   370                                  375                                  380  
 Gly Gln Ser Lys Phe Thr Ala Gln Asn Tyr Asp Ala Asn Asn Gly Val  
                   385                                  390                                  395                                  400  
 Val Ala Val Ala Asn Ala Gly Lys Glu Arg Arg Ile Ile Asn Val Ala  
                   405                                  410                                  415

-continued

---

Gly Gly Arg Asn Asp Thr Asp Ala Val Asn Ile Ala Gln Leu Lys Phe  
 420 425 430

Val Asn Asp Asn Leu Ala Lys Ser Ile Ala Gly Ala Gly Tyr Asn Gly  
 435 440 445

Tyr Glu Thr Asp Gly His Thr Tyr Lys Ala Pro Val Phe Ser Ile Lys  
 450 455 460

Asn Thr Asn Tyr His Asp Val Lys Thr Ala Val Glu Ala Ala Gln Thr  
 465 470 475 480

Asn Tyr Val Ser Val Asn Ser Thr Asn Thr Ala Ala Asp Ser Asn Tyr  
 485 490 495

Asp Asn Lys Gly Ala Lys Ala Val Gly Ser Ile Ala Leu Gly Glu Lys  
 500 505 510

Ala Thr Thr Gly Thr Ala Ala Met Asn Ser Ile Ala Ile Gly Leu Asn  
 515 520 525

Ser Asn Val Ser Gly Gln Asn Thr Val Ala Leu Gly Ala Asn Ile Thr  
 530 535 540

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

Gly Ser His Pro Val Ser Asn Val Ser Ser Ala Thr Val Asn Gly Tyr  
 565 570 575

Thr Tyr Ser Gly Phe Thr Gly Thr Val Lys Glu Ser Gly His Phe Val  
 580 585 590

Ser Ile Gly Ser Lys Gly Asn Glu Arg Gln Ile Lys Asn Val Ala Ala  
 595 600 605

Gly Asn Val Ala Ala Asn Ser Thr Asp Ala Val Asn Gly Ser Gln Leu  
 610 615 620

Phe Ala Val Ala Ser Arg Val Glu Gln Gly Trp Gln Ile Thr Ser Gly  
 625 630 635 640

Val Glu Asn Gly Gly Thr Gln Asn Gly Ala Ala Ser Thr Ala Thr Ile  
 645 650 655

Lys Pro Ser Asn Gln Val Lys Leu Leu Ala Gly Lys Asn Leu Ala Val  
 660 665 670

Lys Gln Asn Gly Thr Asn Phe Thr Phe Ser Thr Gln Glu Asn Val Thr  
 675 680 685

Phe Thr Asn Val Thr Thr Gln Asp Leu Thr Ala Thr Gly Asn Thr Thr  
 690 695 700

Val Lys Asn Phe Ser Val Gln Asn Gly Gly Thr Ile Asn Met Gly Asn  
 705 710 715 720

Asn Arg Ile Thr Gly Val Ala Glu Gly Thr Gln Asp Asp Asp Ala Val  
 725 730 735

Asn Phe Lys Gln Leu Lys Ser Leu Leu Gly Gly Ser Ala Ser Thr Glu  
 740 745 750

Ile Val Glu Lys Lys Ala Ala Gln Ala Gly Asp Glu Asn Leu Ala Asp  
 755 760 765

Ile Ser Val Ala Asn Gly Lys Asn Ala Gly Asp Met Gly Ala Lys Tyr  
 770 775 780

Glu Val Ser Val Ser Lys Lys Ala Val Gln Ser Ala Ala Lys Glu Ala  
 785 790 795 800

Val Lys Val Thr Gly Ser Ala Pro Ile Asn Val Asn Lys Thr Asp Val  
 805 810 815

Asn Gly Val Asp Thr Tyr Ala Val Thr Phe Asn Gly Thr Glu Ala Ala

-continued

820				825				830							
Lys	Ser	Ile	Pro	Leu	Thr	Tyr	Lys	Ala	Asn	Gly	Ser	Gly	Asp	Lys	Thr
	835						840					845			
Val	Met	Leu	Asp	Lys	Gly	Leu	Asn	Phe	Thr	Asn	Gly	Met	Met	Thr	Thr
	850					855					860				
Ala	Ser	Val	Ala	Asn	Asp	Gly	Val	Val	Lys	Tyr	Asp	Val	Asn	Leu	Ser
865					870					875				880	
Thr	Ile	Lys	Val	Glu	Asp	Gly	Lys	Ala	Ala	Val	Ala	Gly	Thr	Pro	Gly
				885						890				895	
Thr	Asn	Gly	Ala	Asn	Gly	Thr	Asp	Gly	Lys	Asp	Gly	Val	Ala	Thr	Val
			900					905						910	
Lys	Asn	Val	Val	Glu	Ala	Leu	Asn	Asn	Ala	Ala	Trp	Thr	Ile	Thr	Ala
		915					920					925			
Ser	Lys	Ser	Asp	Gly	Glu	Val	Val	Ser	Asn	Ala	Ser	Asn	Ser	Val	Lys
	930					935					940				
Asn	Gly	Asp	Thr	Val	Thr	Tyr	Asp	Ala	Gly	Lys	Asn	Ile	Lys	Ile	Thr
945					950					955					960
Gln	Arg	Asp	Lys	Lys	Phe	Ser	Phe	Ala	Thr	Lys	Asp	Asn	Val	Glu	Phe
				965						970				975	
Thr	Ser	Val	Thr	Thr	Gly	Asn	Thr	Lys	Leu	Thr	Gly	Asn	Gly	Val	Glu
			980					985						990	
Ile	Thr	Asn	Gly	Pro	Lys	Leu	Thr	Gln	Ser	Gly	Val	Asp	Ala	Gly	Gly
		995					1000					1005			
Lys	Lys	Ile	Thr	Asn	Val	Ala	Asp	Gly	Val	Ile	Ala	Ala	Asn	Ser	
	1010					1015					1020				
Lys	Asp	Ala	Val	Asn	Gly	Gly	Gln	Leu	Phe	Ala	Glu	Thr	Ala	Lys	
	1025					1030					1035				
Ala	Lys	Thr	Thr	Val	Glu	Lys	Gly	Asp	Asp	Asn	Ile	Gln	Ile	Thr	
	1040					1045					1050				
Ser	Glu	Thr	Ala	Thr	Asp	Gly	His	Ile	Asn	Tyr	Lys	Val	Ala	Leu	
	1055					1060					1065				
Asn	Pro	Ser	Leu	Thr	Val	Gly	Pro	Arg	Thr	Asn	Gly	His	Pro	Ile	
	1070					1075					1080				
Thr	Ile	Asp	Gly	Asn	Asn	Gly	Tyr	Ile	Thr	Gly	Leu	Thr	Asn	Thr	
	1085					1090					1095				
Ser	Trp	Thr	Gly	Ala	Pro	Thr	Thr	Gly	Arg	Ala	Ala	Thr	Glu	Asp	
	1100					1105					1110				
Gln	Leu	Ser	Ile	Val	Asp	Lys	Lys	Phe	Asp	Asn	Lys	Val	Ser	Leu	
	1115					1120					1125				
Gly	Gly	Asp	Asn	Gly	Ser	Thr	Thr	Glu	Lys	Ser	Leu	Ser	His	Asn	
	1130					1135					1140				
Gly	Gly	Ile	Lys	Phe	Asn	Ile	Lys	Gly	Gly	Asp	Ser	Gln	Lys	Tyr	
	1145					1150					1155				
Val	Thr	Thr	Ser	Gly	Ser	Gly	Asp	Asp	Val	Thr	Val	Asp	Leu	Ala	
	1160					1165					1170				
Gln	Thr	Thr	Lys	Asn	Lys	Ile	Asp	Asn	Ala	Ala	Asp	Lys	Asp	Leu	
	1175					1180					1185				
Ala	Asn	Ile	Thr	Asp	Asn	Gly	Lys	Lys	Val	Ile	Thr	Ala	Leu	Gly	
	1190					1195					1200				
Ala	Val	Val	Lys	Ala	Ala	Asp	Ser	Thr	Ile	Thr	Val	Thr	Asp	Glu	
	1205					1210					1215				

-continued

Thr Asp Asn Thr Thr Gly Gln Lys Thr Tyr Lys Ile Lys Ala Asn  
 1220 1225 1230  
 Ile Pro Thr Pro Glu Lys Thr Ala Met Ala Pro Gly Asn Asn Thr  
 1235 1240 1245  
 Thr Ile Glu Gly Asp Gly Ser Ala Ala Asn Pro Phe Lys Val Asn  
 1250 1255 1260  
 Leu Lys Asp Asp Leu Ala Leu Gly Gln Lys Asp Ala Asn Gly Val  
 1265 1270 1275  
 Thr Gly Lys Asp Ser Ser Ile Lys Val Asn Gly Lys Asp Gly Ser  
 1280 1285 1290  
 Gly Val Ala Ile Asn Gly Lys Asp Gly Ser Ile Ala Leu Asn Gly  
 1295 1300 1305  
 Lys Asp Gly Ala Asn Pro Val Thr Ile Lys Thr Ala Gln Gly Pro  
 1310 1315 1320  
 Ala Gly Val Asn Glu Thr Asn Pro Lys Asp Arg Leu Met Val Asn  
 1325 1330 1335  
 Asn Asp Ala Val Ala Thr Leu Lys Asp Gly Leu Lys Phe Ala Gly  
 1340 1345 1350  
 Asp Asn Ser Thr Glu Val Ile Thr Lys Thr Leu Asn Gln Lys Leu  
 1355 1360 1365  
 Glu Ile Val Gly Gly Ala Asp Lys Asn Lys Leu Ser Asp Asn Asn  
 1370 1375 1380  
 Ile Gly Val Asn Ala Asn Asn Gly Lys Leu Glu Val Lys Leu Ala  
 1385 1390 1395  
 Lys Glu Leu Asn Glu Leu Thr Ser Ala Gln Phe Lys Asn Gly Asp  
 1400 1405 1410  
 Asn Thr Thr Val Ile Asn Gly Asn Gly Ile Thr Ile Thr Pro Lys  
 1415 1420 1425  
 Asp Pro Thr Lys Ala Val Ser Leu Thr Asp Lys Gly Leu Asn Asn  
 1430 1435 1440  
 Gly Gly Asn Gln Ile Val Asn Ile Asp Ser Gly Leu Lys Gln Ala  
 1445 1450 1455  
 Asp Gly Ser Thr Val Ala Leu Lys Asp Ala Ser Gly Asp Thr Leu  
 1460 1465 1470  
 Lys Asn Ala Ala Asn Ile Gly Asp Leu Gln Lys Ser Ile Asn Asp  
 1475 1480 1485  
 Ile Thr Asp Ala Ser Lys Asn Gly Gly Phe Gly Leu Ser Asp Asp  
 1490 1495 1500  
 Asn Gly Ala Thr Ala Lys Ala Asn Leu Gly Glu Thr Arg Glu Ser  
 1505 1510 1515  
 Glu Arg Arg Trp Gln Cys Tyr Tyr Lys Ser Ser Tyr Arg  
 1520 1525 1530

<210> SEQ ID NO 45  
 <211> LENGTH: 565  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(564)

<400> SEQUENCE: 45

caa gaa atc att aac cta gcg cct aaa ggc tta att acc gcc gcc agc

48

-continued

Gln	Glu	Ile	Ile	Asn	Leu	Ala	Pro	Lys	Gly	Leu	Ile	Thr	Ala	Ala	Ser	
1				5					10						15	
cct	tat	tta	tac	ggt	gta	acc	cgt	agt	gat	ttg	gaa	aaa	atc	gtc	atc	96
Pro	Tyr	Leu	Tyr	Gly	Val	Thr	Arg	Ser	Asp	Leu	Glu	Lys	Ile	Val	Ile	
			20					25					30			
atg	ggc	gtg	tgg	ttt	gaa	gac	atg	aaa	acc	ctc	gcg	ccc	tac	tgg	caa	144
Met	Gly	Val	Trp	Phe	Glu	Asp	Met	Lys	Thr	Leu	Ala	Pro	Tyr	Trp	Gln	
		35					40					45				
atc	acc	ggc	acg	ccc	acc	ggt	gtc	aac	ttt	gac	gaa	cgc	aac	gcc	atg	192
Ile	Thr	Gly	Thr	Pro	Thr	Gly	Val	Asn	Phe	Asp	Glu	Arg	Asn	Ala	Met	
		50				55					60					
atc	ggc	aaa	acc	ctc	gcc	gaa	cgc	tta	aac	ctg	aaa	gtg	ggc	agt	aag	240
Ile	Gly	Lys	Thr	Leu	Ala	Glu	Arg	Leu	Asn	Leu	Lys	Val	Gly	Ser	Lys	
65					70					75					80	
ctg	acc	tta	agc	ctg	aat	tcg	gta	gat	aaa	cac	cag	ttt	acg	att	aaa	288
Leu	Thr	Leu	Ser	Leu	Asn	Ser	Val	Asp	Lys	His	Gln	Phe	Thr	Ile	Lys	
				85					90					95		
gcc	atc	gtg	gaa	gcg	ggc	gac	gcc	acc	gac	aat	atg	ctc	atc	gtg	agc	336
Ala	Ile	Val	Glu	Ala	Gly	Asp	Ala	Thr	Asp	Asn	Met	Leu	Ile	Val	Ser	
			100						105					110		
ctg	gat	ttc	gcg	caa	aac	tgg	ctg	gaa	aaa	gaa	aac	ttt	gcc	acc	aat	384
Leu	Asp	Phe	Ala	Gln	Asn	Trp	Leu	Glu	Lys	Glu	Asn	Phe	Ala	Thr	Asn	
		115					120					125				
gcc	ctg	ctt	aac	gtg	aaa	aat	gat	cag	ggg	caa	gtg	gaa	caa	ttc	gca	432
Ala	Leu	Leu	Asn	Val	Lys	Asn	Asp	Gln	Gly	Gln	Val	Glu	Gln	Phe	Ala	
		130				135					140					
cag	caa	ctt	cag	caa	caa	tat	ccc	gat	ttg	gat	att	cat	ccg	atc	cgc	480
Gln	Gln	Leu	Gln	Gln	Gln	Tyr	Pro	Asp	Leu	Asp	Ile	His	Pro	Ile	Arg	
145					150					155					160	
aaa	gtc	tcc	gcc	tcc	gaa	ggg	caa	att	ctg	gat	aag	att	aaa	ggc	ttg	528
Lys	Val	Ser	Ala	Ser	Glu	Gly	Gln	Ile	Leu	Asp	Lys	Ile	Lys	Gly	Leu	
				165					170					175		
atg	ggc	ttg	att	tcc	gtg	gtg	att	ctg	att	tta	gcc	a				565
Met	Gly	Leu	Ile	Ser	Val	Val	Ile	Leu	Ile	Leu	Ala					
				180					185							

&lt;210&gt; SEQ ID NO 46

&lt;211&gt; LENGTH: 188

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 46

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

-continued

```

Leu Asp Phe Ala Gln Asn Trp Leu Glu Lys Glu Asn Phe Ala Thr Asn
   115                               120                               125

Ala Leu Leu Asn Val Lys Asn Asp Gln Gly Gln Val Glu Gln Phe Ala
   130                               135                               140

Gln Gln Leu Gln Gln Gln Tyr Pro Asp Leu Asp Ile His Pro Ile Arg
   145                               150                               155                               160

Lys Val Ser Ala Ser Glu Gly Gln Ile Leu Asp Lys Ile Lys Gly Leu
   165                               170                               175

Met Gly Leu Ile Ser Val Val Ile Leu Ile Leu Ala
   180                               185
    
```

```

<210> SEQ ID NO 47
<211> LENGTH: 668
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(666)
    
```

<400> SEQUENCE: 47

```

gcc aat cgg atc att gaa atc aaa gat ggt gaa att atc agt gat acg      48
Ala Asn Arg Ile Ile Glu Ile Lys Asp Gly Glu Ile Ile Ser Asp Thr
1                               5                               10                               15

caa aaa cgt cag gta aaa agt gcg gtt aaa aat cca agt gtt ttt aaa      96
Gln Lys Arg Gln Val Lys Ser Ala Val Lys Asn Pro Ser Val Phe Lys
20                               25                               30

ggt cgt ttc ggt ttc agc aaa gat caa ctt atg gaa gcc ttc cgt atg     144
Gly Arg Phe Gly Phe Ser Lys Asp Gln Leu Met Glu Ala Phe Arg Met
35                               40                               45

tcc gtc agt gcc att gta gcg cac aaa atg cgc tca ttg ctg acc atg     192
Ser Val Ser Ala Ile Val Ala His Lys Met Arg Ser Leu Leu Thr Met
50                               55                               60

ctg gga att atc atc ggg atc act tcc gtc gtt tcc gtg gtg gcg tta     240
Leu Gly Ile Ile Ile Gly Ile Thr Ser Val Val Ser Val Val Ala Leu
65                               70                               75                               80

gga aat ggt tca caa caa aag att ttg gaa aat att cgc ggt atc ggc     288
Gly Asn Gly Ser Gln Gln Lys Ile Leu Glu Asn Ile Arg Gly Ile Gly
85                               90                               95

aca aac aca atg acg att ttt aac ggt aat ggt ttc ggt gac cgt cgt     336
Thr Asn Thr Met Thr Ile Phe Asn Gly Asn Gly Phe Gly Asp Arg Arg
100                              105                              110

tca cgg cac att caa aac cta aaa atc agc gat gcc aat acg tta tcg     384
Ser Arg His Ile Gln Asn Leu Lys Ile Ser Asp Ala Asn Thr Leu Ser
115                              120                              125

aaa caa agt tat att caa agc gtt act cca aat acc tct tcc agc ggc     432
Lys Gln Ser Tyr Ile Gln Ser Val Thr Pro Asn Thr Ser Ser Ser Gly
130                              135                              140

att tta gtg gtc ggt aac aaa tcc ttc aca tcc gcc aat tta tat ggt     480
Ile Leu Val Val Gly Asn Lys Ser Phe Thr Ser Ala Asn Leu Tyr Gly
145                              150                              155                              160

atc ggt gaa caa tat ttt gat gta gaa ggc ttg aag tta aaa cag ggc     528
Ile Gly Glu Gln Tyr Phe Asp Val Glu Gly Leu Lys Leu Lys Gln Gly
165                              170                              175

cgt tta tta acc gag gac gat gtg gat caa agc aac cag gtg gtc gtg     576
Arg Leu Leu Thr Glu Asp Asp Val Thr Ser Asn Gln Ser Asn Gln Val Val
180                              185                              190

ctg gac gaa agt gca aaa aaa gcc att ttt gcc aac gaa aat ccc ctt     624
Leu Asp Glu Ser Ala Lys Lys Ala Ile Phe Ala Asn Glu Asn Pro Leu
    
```

-continued

---

```

195                200                205
ggc aaa acg gtg att ttt aat aag cga cca ttt cgt gtc att gg      668
Gly Lys Thr Val Ile Phe Asn Lys Arg Pro Phe Arg Val Ile
  210                215                220

```

```

<210> SEQ ID NO 48
<211> LENGTH: 222
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 48

```

```

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

```

```

<210> SEQ ID NO 49
<211> LENGTH: 276
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(276)

```

```

<400> SEQUENCE: 49

```

```

atg aga atg cac aat cct cca cac ccg gga gaa ctg tta aaa gaa tat      48
Met Arg Met His Asn Pro Pro His Pro Gly Glu Leu Lys Glu Tyr
 1                    5                10                15
att gat ggc gtg agt gtc acg aag gtt gcc caa aaa tta ggt gtt tcg      96
Ile Asp Gly Val Ser Val Thr Lys Val Ala Gln Lys Leu Gly Val Ser
 20                25                30
cgt gtt acg ctt tcc cgc att ctt aat ggg aaa gca agt ata acg cct      144

```



-continued

```

tac gat aaa gcc gcg agt aaa acg cat tta tct gcg tcc att cct gat      336
Tyr Asp Lys Ala Ala Ser Lys Thr His Leu Ser Ala Ser Ile Pro Asp
      100                      105                      110

acc gac cgt atg tgg tat agt ata gga gcc acc tat aaa ttc acc ccg      384
Thr Asp Arg Met Trp Tyr Ser Ile Gly Ala Thr Tyr Lys Phe Thr Pro
      115                      120                      125

aat tta tct gtt gat gtc gcc ttc gct cat tta cgt ggt aag aag aaa      432
Asn Leu Ser Val Asp Val Gly Phe Ala His Leu Arg Gly Lys Lys Lys
      130                      135                      140

cat ttt gtt gag acc caa aat atc aag ggg tta ttg ctt gtt gag gcg      480
His Phe Val Glu Thr Gln Asn Ile Lys Gly Leu Leu Leu Val Glu Ala
      145                      150                      155                      160

gat tac acc act aaa gcc acc gct aac ctc tac ggt ttg aat cta aat      528
Asp Tyr Thr Thr Lys Ala Thr Ala Asn Leu Tyr Gly Leu Asn Leu Asn
      165                      170                      175

tac cgt ttc                                                                537
Tyr Arg Phe

```

```

<210> SEQ ID NO 52
<211> LENGTH: 179
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 52

```

```

Gln His Asn Gly Val Leu Gly Pro Tyr Ile Gly Lys Gly Ser Leu Thr
1                      5                      10                      15

Leu Lys Leu Pro Ala Tyr Trp Glu Leu Ser Gly Phe His Gln Leu Thr
      20                      25                      30

Asp Gln Trp Ala Ile His Tyr Ser Tyr Lys Tyr Thr Glu Trp Ser Arg
      35                      40                      45

Phe Lys Glu Leu Arg Gly Lys Tyr Gln Asp Gly Ser Gly Tyr Glu Ala
      50                      55                      60

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

Thr Thr Tyr Ser Leu Asn Asp Ala Leu Thr Leu Arg Ala Gly Leu Ala
      85                      90                      95

Tyr Asp Lys Ala Ala Ser Lys Thr His Leu Ser Ala Ser Ile Pro Asp
      100                      105                      110

Thr Asp Arg Met Trp Tyr Ser Ile Gly Ala Thr Tyr Lys Phe Thr Pro
      115                      120                      125

Asn Leu Ser Val Asp Val Gly Phe Ala His Leu Arg Gly Lys Lys Lys
      130                      135                      140

His Phe Val Glu Thr Gln Asn Ile Lys Gly Leu Leu Leu Val Glu Ala
      145                      150                      155                      160

Asp Tyr Thr Thr Lys Ala Thr Ala Asn Leu Tyr Gly Leu Asn Leu Asn
      165                      170                      175

Tyr Arg Phe

```

```

<210> SEQ ID NO 53
<211> LENGTH: 548
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(546)

```

-continued

&lt;400&gt; SEQUENCE: 53

```

gga cca agt gtc acc aag gac ggc att cac gcc aat gat aag aaa atc      48
Gly Pro Ser Val Thr Lys Asp Gly Ile His Ala Asn Asp Lys Lys Ile
1          5          10          15

acc ggt gta aaa gac ggt gaa att tca gcc cat agt aaa gag gcg gtg      96
Thr Gly Val Lys Asp Gly Glu Ile Ser Ala His Ser Lys Glu Ala Val
          20          25          30

aac ggt agc caa tta cat caa acc aac caa aat gtg acg aat tta gcc      144
Asn Gly Ser Gln Leu His Gln Thr Asn Gln Asn Val Thr Asn Leu Ala
          35          40          45

aac aat gtg gac aaa ggg ctg aat ttc caa gga gac aat caa gaa gtc      192
Asn Asn Val Asp Lys Gly Leu Asn Phe Gln Gly Asp Asn Gln Glu Val
          50          55          60

aca gtt aat cgt aaa tta ggc gat caa ctt aac att cgc ggc ggt gcg      240
Thr Val Asn Arg Lys Leu Gly Asp Gln Leu Asn Ile Arg Gly Gly Ala
65          70          75          80

gat ccg aag aaa tta aca caa aat aat atc ggc gtg acc gca gat aaa      288
Asp Pro Lys Lys Leu Thr Gln Asn Asn Ile Gly Val Thr Ala Asp Lys
          85          90          95

aac ggc acc atg acc gtt cag ctg gcg aag gaa gtt aat ctc ggc gca      336
Asn Gly Thr Met Thr Val Gln Leu Ala Lys Glu Val Asn Leu Gly Ala
          100          105          110

gat ggc agc ctt act gta ggc aat acc acg gtc aat aac gac ggt gtt      384
Asp Gly Ser Leu Thr Val Gly Asn Thr Thr Val Asn Asn Asp Gly Val
          115          120          125

acg att aaa gac ggt cca agc atg aca agc cac ggc atc aac gcc ggc      432
Thr Ile Lys Asp Gly Pro Ser Met Thr Ser His Gly Ile Asn Ala Gly
          130          135          140

ggc aaa cga att gct aac gtt gcg aaa ggg aaa gca ccg acg gat gca      480
Gly Lys Arg Ile Ala Asn Val Ala Lys Gly Lys Ala Pro Thr Asp Ala
145          150          155          160

gta aat atg agt cag ctt caa gac gtc ggc agt gcc att aat aat cgc      528
Val Asn Met Ser Gln Leu Gln Asp Val Gly Ser Ala Ile Asn Asn Arg
          165          170          175

att gat aac att gat aag cg      548
Ile Asp Asn Ile Asp Lys
          180

```

&lt;210&gt; SEQ ID NO 54

&lt;211&gt; LENGTH: 182

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 54

```

Gly Pro Ser Val Thr Lys Asp Gly Ile His Ala Asn Asp Lys Lys Ile
1          5          10          15

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

Asn Gly Ser Gln Leu His Gln Thr Asn Gln Asn Val Thr Asn Leu Ala
          35          40          45

Asn Asn Val Asp Lys Gly Leu Asn Phe Gln Gly Asp Asn Gln Glu Val
          50          55          60

Thr Val Asn Arg Lys Leu Gly Asp Gln Leu Asn Ile Arg Gly Gly Ala
65          70          75          80

Asp Pro Lys Lys Leu Thr Gln Asn Asn Ile Gly Val Thr Ala Asp Lys
          85          90          95

```

-continued

---

Asn Gly Thr Met Thr Val Gln Leu Ala Lys Glu Val Asn Leu Gly Ala  
 100 105 110

Asp Gly Ser Leu Thr Val Gly Asn Thr Thr Val Asn Asn Asp Gly Val  
 115 120 125

Thr Ile Lys Asp Gly Pro Ser Met Thr Ser His Gly Ile Asn Ala Gly  
 130 135 140

Gly Lys Arg Ile Ala Asn Val Ala Lys Gly Lys Ala Pro Thr Asp Ala  
 145 150 155 160

Val Asn Met Ser Gln Leu Gln Asp Val Gly Ser Ala Ile Asn Asn Arg  
 165 170 175

Ile Asp Asn Ile Asp Lys  
 180

<210> SEQ ID NO 55  
 <211> LENGTH: 168  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(168)

<400> SEQUENCE: 55

atg gat cac ttt ccg ccg ctt tgg ctt ttt cgg tta aac agc tta atg 48  
 Met Asp His Phe Pro Pro Leu Trp Leu Phe Arg Leu Asn Ser Leu Met  
 1 5 10 15

ctt ctt ttg ctg ctt ctt ccg ttg cat aaa cct gtt caa aat cca ccg 96  
 Leu Leu Leu Leu Leu Leu Pro Leu His Lys Pro Val Gln Asn Pro Pro  
 20 25 30

tgc agt cag aac cgt caa tca ccg tac cca cct cga cac aac agc aaa 144  
 Cys Ser Gln Asn Arg Gln Ser Pro Tyr Pro Pro Arg His Asn Ser Lys  
 35 40 45

ctt ttg ctt ctt ccg cct gac att 168  
 Leu Leu Leu Leu Pro Pro Asp Ile  
 50 55

<210> SEQ ID NO 56  
 <211> LENGTH: 56  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 56

Met Asp His Phe Pro Pro Leu Trp Leu Phe Arg Leu Asn Ser Leu Met  
 1 5 10 15

Leu Leu Leu Leu Leu Leu Pro Leu His Lys Pro Val Gln Asn Pro Pro  
 20 25 30

Cys Ser Gln Asn Arg Gln Ser Pro Tyr Pro Pro Arg His Asn Ser Lys  
 35 40 45

Leu Leu Leu Leu Pro Pro Asp Ile  
 50 55

<210> SEQ ID NO 57  
 <211> LENGTH: 492  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(492)

<400> SEQUENCE: 57

-continued

```

atg acg aac aaa cca aaa tcc ggg ctc tca ttt ttg tgg tta agt acg      48
Met Thr Asn Lys Pro Lys Ser Gly Leu Ser Phe Leu Trp Leu Ser Thr
1          5          10          15

ctg gca ttt atc gcc gat att ttt acc aaa tac tta atc gta agc cat      96
Leu Ala Phe Ile Ala Asp Ile Phe Thr Lys Tyr Leu Ile Val Ser His
          20          25          30

ttt gaa tac ggc gaa agc gta aat atc ctg ccg att ttt aat ttg acc      144
Phe Glu Tyr Gly Glu Ser Val Asn Ile Leu Pro Ile Phe Asn Leu Thr
          35          40          45

tat gtg ggt aac ttt ggc gcc gct ttt agt ttc ctg gcg gat cat gac      192
Tyr Val Gly Asn Phe Gly Ala Ala Phe Ser Phe Leu Ala Asp His Asp
          50          55          60

ggg tgg caa aaa ttc ttt ttc ctt gcg ttg gca gtg ggg att tcc gcc      240
Gly Trp Gln Lys Phe Phe Phe Leu Ala Leu Ala Val Gly Ile Ser Ala
65          70          75          80

atg ttg gtt tat ttt tta atg aaa aat cgc cat gaa caa aaa ctg ctg      288
Met Leu Val Tyr Phe Leu Met Lys Asn Arg His Glu Gln Lys Leu Leu
          85          90          95

aat gcc gcc tac gct ttg att atc ggc gcc gct ttg ggc aat gcg gcg      336
Asn Ala Ala Tyr Ala Leu Ile Ile Gly Gly Ala Leu Gly Asn Ala Ala
          100          105          110

gat cgt ctg tat cac ggc tat gtg gtg gat ttt tta gat ttc tat tgg      384
Asp Arg Leu Tyr His Gly Tyr Val Val Asp Phe Leu Asp Phe Tyr Trp
          115          120          125

cgg gat tgg cat tat ccc gtg ttt aac ctg gcg gat att gcc att tgt      432
Arg Asp Trp His Tyr Pro Val Phe Asn Leu Ala Asp Ile Ala Ile Cys
          130          135          140

gtg ggt gcc ggt ttg att gcc ttg gat gcg ttc aaa aac ggc aat aaa      480
Val Gly Ala Gly Leu Ile Ala Leu Asp Ala Phe Lys Asn Gly Asn Lys
145          150          155          160

cag gaa tgt aaa      492
Gln Glu Cys Lys

```

```

<210> SEQ ID NO 58
<211> LENGTH: 164
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 58

```

```

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

Leu Ala Phe Ile Ala Asp Ile Phe Thr Lys Tyr Leu Ile Val Ser His
          20          25          30

Phe Glu Tyr Gly Glu Ser Val Asn Ile Leu Pro Ile Phe Asn Leu Thr
          35          40          45

Tyr Val Gly Asn Phe Gly Ala Ala Phe Ser Phe Leu Ala Asp His Asp
          50          55          60

Gly Trp Gln Lys Phe Phe Phe Leu Ala Leu Ala Val Gly Ile Ser Ala
65          70          75          80

Met Leu Val Tyr Phe Leu Met Lys Asn Arg His Glu Gln Lys Leu Leu
          85          90          95

Asn Ala Ala Tyr Ala Leu Ile Ile Gly Gly Ala Leu Gly Asn Ala Ala
          100          105          110

Asp Arg Leu Tyr His Gly Tyr Val Val Asp Phe Leu Asp Phe Tyr Trp
          115          120          125

Arg Asp Trp His Tyr Pro Val Phe Asn Leu Ala Asp Ile Ala Ile Cys

```

-continued

130	135	140	
Val Gly Ala Gly Leu Ile Ala Leu Asp Ala Phe Lys Asn Gly Asn Lys			
145	150	155	160
Gln Glu Cys Lys			
<210> SEQ ID NO 59			
<211> LENGTH: 453			
<212> TYPE: DNA			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(453)			
<400> SEQUENCE: 59			
atg gct aaa ttg tat ttt tac tat tcc acc atg aat gca gga aaa tcc			48
Met Ala Lys Leu Tyr Phe Tyr Tyr Ser Thr Met Asn Ala Gly Lys Ser			
1	5	10	15
acc acc ttg ttg caa tct tcc tat aat tac cgc gaa cgt aac atg aac			96
Thr Thr Leu Leu Gln Ser Ser Tyr Asn Tyr Arg Glu Arg Asn Met Asn			
	20	25	30
acg ctg gtt tat aca gcg gcg ata gac gat cgt ttc ggc gta ggg cag			144
Thr Leu Val Tyr Thr Ala Ala Ile Asp Asp Arg Phe Gly Val Gly Gln			
	35	40	45
gtg act tcc cgc atc ggg att agc gaa cgg gcg aat acc ttt acc cgc			192
Val Thr Ser Arg Ile Gly Ile Ser Glu Arg Ala Asn Thr Phe Thr Arg			
	50	55	60
aat acg aat ttg ttc gct gaa att gaa caa cat ctg gcg cag gag ccg			240
Asn Thr Asn Leu Phe Ala Glu Ile Glu Gln His Leu Ala Gln Glu Pro			
65	70	75	80
ctt cat tgt att ttg gtg gat gag gca cag ttt tta acc aaa gaa cag			288
Leu His Cys Ile Leu Val Asp Glu Ala Gln Phe Leu Thr Lys Glu Gln			
	85	90	95
gtt tat caa ctg agc gat gtg gtg gat aaa cta cat att ccc gtg ttg			336
Val Tyr Gln Leu Ser Asp Val Val Asp Lys Leu His Ile Pro Val Leu			
	100	105	110
tgc tac ggt ttg cgc acc gat ttc caa gcg gaa tta ttt gaa ggc agt			384
Cys Tyr Gly Leu Arg Thr Asp Phe Gln Ala Glu Leu Phe Glu Gly Ser			
	115	120	125
cgc tat tta ctg gcg tgg gcg gat cag ctg gaa gaa ctc aaa acc att			432
Arg Tyr Leu Leu Ala Trp Ala Asp Gln Leu Glu Glu Leu Lys Thr Ile			
	130	135	140
tgt tac tgc ggt cgc aaa gcc			453
Cys Tyr Cys Gly Arg Lys Ala			
145	150		

&lt;210&gt; SEQ ID NO 60

&lt;211&gt; LENGTH: 151

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 60

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

-continued

50	55	60	
Asn Thr Asn Leu Phe Ala Glu Ile Glu Gln His Leu Ala Gln Glu Pro 65 70 75 80			
Leu His Cys Ile Leu Val Asp Glu Ala Gln Phe Leu Thr Lys Glu Gln 85 90 95			
Val Tyr Gln Leu Ser Asp Val Val Asp Lys Leu His Ile Pro Val Leu 100 105 110			
Cys Tyr Gly Leu Arg Thr Asp Phe Gln Ala Glu Leu Phe Glu Gly Ser 115 120 125			
Arg Tyr Leu Leu Ala Trp Ala Asp Gln Leu Glu Glu Leu Lys Thr Ile 130 135 140			
Cys Tyr Cys Gly Arg Lys Ala 145 150			
<p>&lt;210&gt; SEQ ID NO 61                  &lt;211&gt; LENGTH: 643                  &lt;212&gt; TYPE: DNA                  &lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans                  &lt;220&gt; FEATURE:                  &lt;221&gt; NAME/KEY: CDS                  &lt;222&gt; LOCATION: (1)..(642)</p>			
<p>&lt;400&gt; SEQUENCE: 61</p>			
tat aac gaa aaa act tac gaa aat gac tta acc gca aaa gaa atc ttc Tyr Asn Glu Lys Thr Tyr Glu Asn Asp Leu Thr Ala Lys Glu Ile Phe 1 5 10 15			48
gta act tat gta ttg aaa aac aaa ttg tta tgg tac atc gcc att gct Val Thr Tyr Val Leu Lys Asn Lys Leu Leu Trp Tyr Ile Ala Ile Ala 20 25 30			96
aac gtg ttc gtt tac tta atc cgc tac ggc gta ttg aaa tgg tct ccg Asn Val Phe Val Tyr Leu Ile Arg Tyr Gly Val Leu Lys Trp Ser Pro 35 40 45			144
gtt tac ttg agt gaa gtg aaa cac ttc aac atc aaa ggt acc gca tgg Val Tyr Leu Ser Glu Val Lys His Phe Asn Ile Lys Gly Thr Ala Trp 50 55 60			192
gca tac acc att tat gaa ttg cgc gcc gtt ccg ggt aca tta ctt tgc Ala Tyr Thr Ile Tyr Glu Leu Ala Ala Val Pro Gly Thr Leu Leu Cys 65 70 75 80			240
ggt tgg gta tct gac cat gta ttc aaa ggt aaa cgt ggc tta acc ggt Gly Trp Val Ser Asp His Val Phe Lys Gly Lys Arg Gly Leu Thr Gly 85 90 95			288
ttc atc ttt atg att tta acc acc gca gcg gta gcc aca tac tgg atg Phe Ile Phe Met Ile Leu Thr Thr Ala Ala Val Ala Thr Tyr Trp Met 100 105 110			336
aac cct gca aca ccg gaa gct gag ctt gca aac tac agc gca tgg tat Asn Pro Ala Thr Pro Glu Ala Glu Leu Ala Asn Tyr Ser Ala Trp Tyr 115 120 125			384
gaa aac cca tac caa tta acc gac ttt att ttg atg acc tta atc ggt Glu Asn Pro Tyr Gln Leu Thr Asp Phe Ile Leu Met Thr Leu Ile Gly 130 135 140			432
ttc tta atc tac ggc cct gtg atg cta atc ggc ttg cac gcc ctt gaa Phe Leu Ile Tyr Gly Pro Val Met Leu Ile Gly Leu His Ala Leu Glu 145 150 155 160			480
ctt gca ccg aaa aaa gcg gca ggt acc gca gca ggt ttc acc ggt tta Leu Ala Pro Lys Lys Ala Ala Gly Thr Ala Ala Gly Phe Thr Gly Leu 165 170 175			528
ttc ggt tac tta ggc ggt acc gtg tct gca tca gca gtt atc ggt tgg			576

-continued

---

```

Phe Gly Tyr Leu Gly Gly Thr Val Ser Ala Ser Ala Val Ile Gly Trp
      180                               185                               190

gca gcc caa cac tac ggc tgg gac ggc ggt ttt tac gtg atg atc ggc      624
Ala Ala Gln His Tyr Gly Trp Asp Gly Gly Phe Tyr Val Met Ile Gly
      195                               200                               205

ggt ggt atc tta ccg gtc a
Gly Gly Ile Leu Pro Val
      210

```

```

<210> SEQ ID NO 62
<211> LENGTH: 214
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 62

```

```

Tyr Asn Glu Lys Thr Tyr Glu Asn Asp Leu Thr Ala Lys Glu Ile Phe
1      5      10      15

Val Thr Tyr Val Leu Lys Asn Lys Leu Leu Trp Tyr Ile Ala Ile Ala
20     25     30

Asn Val Phe Val Tyr Leu Ile Arg Tyr Gly Val Leu Lys Trp Ser Pro
35     40     45

Val Tyr Leu Ser Glu Val Lys His Phe Asn Ile Lys Gly Thr Ala Trp
50     55     60

Ala Tyr Thr Ile Tyr Glu Leu Ala Ala Val Pro Gly Thr Leu Leu Cys
65     70     75     80

Gly Trp Val Ser Asp His Val Phe Lys Gly Lys Arg Gly Leu Thr Gly
85     90     95

Phe Ile Phe Met Ile Leu Thr Thr Ala Ala Val Ala Thr Tyr Trp Met
100    105    110

Asn Pro Ala Thr Pro Glu Ala Glu Leu Ala Asn Tyr Ser Ala Trp Tyr
115    120    125

Glu Asn Pro Tyr Gln Leu Thr Asp Phe Ile Leu Met Thr Leu Ile Gly
130    135    140

Phe Leu Ile Tyr Gly Pro Val Met Leu Ile Gly Leu His Ala Leu Glu
145    150    155    160

Leu Ala Pro Lys Lys Ala Ala Gly Thr Ala Ala Gly Phe Thr Gly Leu
165    170    175

Phe Gly Tyr Leu Gly Gly Thr Val Ser Ala Ser Ala Val Ile Gly Trp
180    185    190

Ala Ala Gln His Tyr Gly Trp Asp Gly Gly Phe Tyr Val Met Ile Gly
195    200    205

Gly Gly Ile Leu Pro Val
210

```

```

<210> SEQ ID NO 63
<211> LENGTH: 333
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(333)

```

```

<400> SEQUENCE: 63

```

```

gaa tgg gcg gga acg cct tat cgt atc ggc gga caa agt cgc agt ggc      48
Glu Trp Ala Gly Thr Pro Tyr Arg Ile Gly Gly Gln Ser Arg Ser Gly
1      5      10      15

```

## -continued

---

```

gtg gat tgc tcc ggt ttc gtg caa acc acc ttt ttc gat cgc ttc ggc      96
Val Asp Cys Ser Gly Phe Val Gln Thr Thr Phe Phe Asp Arg Phe Gly
      20                      25                      30

ata aaa ttg ccg cga caa acc aaa gat cag gca aat tac ggt cag tat      144
Ile Lys Leu Pro Arg Gln Thr Lys Asp Gln Ala Asn Tyr Gly Gln Tyr
      35                      40                      45

att gaa aaa ggc gat att caa acc ggt gat ttg gtg ttc ttt aaa acc      192
Ile Glu Lys Gly Asp Ile Gln Thr Gly Asp Leu Val Phe Phe Lys Thr
      50                      55                      60

ggt cgc ggt cct cat ggc tat cat gtg ggc att tat gtg aag gaa gac      240
Gly Arg Gly Pro His Gly Tyr His Val Gly Ile Tyr Val Lys Glu Asp
      65                      70                      75                      80

aaa ttt ctg cac gcg tct act aag ggt ggc gtg att tat tcc tcg ttg      288
Lys Phe Leu His Ala Ser Thr Lys Gly Gly Val Ile Tyr Ser Ser Leu
      85                      90                      95

aac agc gat tat tgg cgt aag gca tat tgg cag gca aga cga att      333
Asn Ser Asp Tyr Trp Arg Lys Ala Tyr Trp Gln Ala Arg Arg Ile
      100                      105                      110

```

```

<210> SEQ ID NO 64
<211> LENGTH: 111
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```
<400> SEQUENCE: 64
```

```

Glu Trp Ala Gly Thr Pro Tyr Arg Ile Gly Gly Gln Ser Arg Ser Gly
1      5      10      15

Val Asp Cys Ser Gly Phe Val Gln Thr Thr Phe Phe Asp Arg Phe Gly
      20                      25                      30

Ile Lys Leu Pro Arg Gln Thr Lys Asp Gln Ala Asn Tyr Gly Gln Tyr
      35                      40                      45

Ile Glu Lys Gly Asp Ile Gln Thr Gly Asp Leu Val Phe Phe Lys Thr
      50                      55                      60

Gly Arg Gly Pro His Gly Tyr His Val Gly Ile Tyr Val Lys Glu Asp
      65                      70                      75                      80

Lys Phe Leu His Ala Ser Thr Lys Gly Gly Val Ile Tyr Ser Ser Leu
      85                      90                      95

Asn Ser Asp Tyr Trp Arg Lys Ala Tyr Trp Gln Ala Arg Arg Ile
      100                      105                      110

```

```

<210> SEQ ID NO 65
<211> LENGTH: 423
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(423)

```

```
<400> SEQUENCE: 65
```

```

atg aaa aaa cgt tgc aca tgg gcg gaa aac tca caa att tat cag gat      48
Met Lys Lys Arg Cys Thr Trp Ala Glu Asn Ser Gln Ile Tyr Gln Asp
1      5      10      15

tac cac gac aac gaa tgg ggt aaa cca caa ttt gat gat cgc aaa tta      96
Tyr His Asp Asn Glu Trp Gly Lys Pro Gln Phe Asp Asp Arg Lys Leu
      20                      25                      30

ttt gaa aaa ctg tgt ctg gaa ggg cag caa gcg ggc ctg tcg tgg att      144
Phe Glu Lys Leu Cys Leu Glu Gly Gln Gln Ala Gly Leu Ser Trp Ile
      35                      40                      45

```

-continued

---

```

acg gta tta aaa aaa cgg gaa gct tat cgg cag gcg ttt ttc cat ttt 192
Thr Val Leu Lys Lys Arg Glu Ala Tyr Arg Gln Ala Phe Phe His Phe
    50                55                60

gat ccg cac aaa gtc gca gca atg act gat gcc gat atc gat cac tgt 240
Asp Pro His Lys Val Ala Ala Met Thr Asp Ala Asp Ile Asp His Cys
    65                70                75                80

atg caa aat aca ggc tta att cgc cat cgc gct aaa tta cag gca atc 288
Met Gln Asn Thr Gly Leu Ile Arg His Arg Ala Lys Leu Gln Ala Ile
    85                90                95

gtc acc aat gcg cgg gcg ttt ctt gcc atg caa aag tgc ggt gaa aat 336
Val Thr Asn Ala Arg Ala Phe Leu Ala Met Gln Lys Cys Gly Glu Asn
    100                105                110

ttc agt cat ttt att tgg tct ttc gtg aat cat cag ccg caa att cat 384
Phe Ser His Phe Ile Trp Ser Phe Val Asn His Gln Pro Gln Ile His
    115                120                125

gac gtg ccc gag tta agc cat gtg ccg gcg caa acg gca 423
Asp Val Pro Glu Leu Ser His Val Pro Ala Gln Thr Ala
    130                135                140

```

```

<210> SEQ ID NO 66
<211> LENGTH: 141
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 66

```

```

Met Lys Lys Arg Cys Thr Trp Ala Glu Asn Ser Gln Ile Tyr Gln Asp
1                5                10                15

Tyr His Asp Asn Glu Trp Gly Lys Pro Gln Phe Asp Asp Arg Lys Leu
20                25                30

Phe Glu Lys Leu Cys Leu Glu Gly Gln Gln Ala Gly Leu Ser Trp Ile
35                40                45

Thr Val Leu Lys Lys Arg Glu Ala Tyr Arg Gln Ala Phe Phe His Phe
50                55                60

Asp Pro His Lys Val Ala Ala Met Thr Asp Ala Asp Ile Asp His Cys
65                70                75                80

Met Gln Asn Thr Gly Leu Ile Arg His Arg Ala Lys Leu Gln Ala Ile
85                90                95

Val Thr Asn Ala Arg Ala Phe Leu Ala Met Gln Lys Cys Gly Glu Asn
100                105                110

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

Asp Val Pro Glu Leu Ser His Val Pro Ala Gln Thr Ala
130                135                140

```

```

<210> SEQ ID NO 67
<211> LENGTH: 375
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(375)

```

```

<400> SEQUENCE: 67

```

```

gac atc gtt aca ttt acc caa aaa cgc tgc ccg ttt aat cac atg acg 48
Asp Ile Val Thr Phe Thr Gln Lys Arg Cys Pro Phe Asn His Met Thr
1                5                10                15

gtg gcg tat caa aaa agt gcg gtc ata aat tgc ggc gga tat gag gat 96
Val Ala Tyr Gln Lys Ser Ala Val Ile Asn Cys Gly Gly Tyr Glu Asp

```

-continued

20	25	30	
tta cag gaa gat tat tat ttg tgg atc aaa ctg gtg gcg caa ggg cag			144
Leu Gln Glu Asp Tyr Tyr Leu Trp Ile Lys Leu Val Ala Gln Gly Gln			
35	40	45	
cgc gta gca aat tta ccc gat att ttg gtc tat gcg cgc gtc ggc aac			192
Arg Val Ala Asn Leu Pro Asp Ile Leu Val Tyr Ala Arg Val Gly Asn			
50	55	60	
ggc atg gta ggg cga cgc cgt ggt tta aac caa gcc aaa gcg gaa tgg			240
Gly Met Val Gly Arg Arg Arg Gly Leu Asn Gln Ala Lys Ala Glu Trp			
65	70	75	
cgc tta ttt aag cta aaa cac cat ctt ggc att cag gga ttt tta tcc			288
Arg Leu Phe Lys Leu Lys His His Leu Gly Ile Gln Gly Phe Leu Ser			
85	90	95	
ggg cta ttc act ttt gtc ctg cgt tcc ggt gcc aga tta ttg ccg aca			336
Gly Leu Phe Thr Phe Val Leu Arg Ser Gly Ala Arg Leu Leu Pro Thr			
100	105	110	
tca tta ctg aaa aac atc tat caa acc ttt tta aga aaa			375
Ser Leu Leu Lys Asn Ile Tyr Gln Thr Phe Leu Arg Lys			
115	120	125	

<210> SEQ ID NO 68  
 <211> LENGTH: 125  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 68

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

<210> SEQ ID NO 69  
 <211> LENGTH: 1005  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1005)

<400> SEQUENCE: 69

tcc ggt aaa tcc gtc ggc gta aat acc atg att tta agc ctg ctt tac			48
Ser Gly Lys Ser Val Gly Val Asn Thr Met Ile Leu Ser Leu Leu Tyr			
1	5	10	15
cgc gtt aaa ccg gaa gaa gtg aaa ttc atc atg att gac ccg aaa gtg			96
Arg Val Lys Pro Glu Glu Val Lys Phe Ile Met Ile Asp Pro Lys Val			
20	25	30	

-continued

gtg gaa ttg tct att tat aat gat att ccg cat ctt tta acg gaa gtg Val Glu Leu Ser Ile Tyr Asn Asp Ile Pro His Leu Leu Thr Glu Val 35 40 45	144
gtc acg gac atg aaa aaa gcg gca aac gcg ttg cgc tgg tgt gta gac Val Thr Asp Met Lys Lys Ala Ala Asn Ala Leu Arg Trp Cys Val Asp 50 55 60	192
gaa atg gag cgc cgt tat caa tta ttg tct gct ttg cgg gtg cgt aat Glu Met Glu Arg Arg Tyr Gln Leu Leu Ser Ala Leu Arg Val Arg Asn 65 70 75 80	240
att gaa gga ttt aac gag aaa gtt gat gaa tat gag gcc tta aat atg Ile Glu Gly Phe Asn Glu Lys Val Asp Glu Tyr Glu Ala Leu Asn Met 85 90 95	288
ccg att ccg aac ccg tta tgg aag ccg ggc gat tcc atg gat act ttg Pro Ile Pro Asn Pro Leu Trp Lys Pro Gly Asp Ser Met Asp Thr Leu 100 105 110	336
ccg cca cca tta gaa aaa ctg agt tac att gtg gtg att gtg gat gaa Pro Pro Pro Leu Glu Lys Leu Ser Tyr Ile Val Val Ile Val Asp Glu 115 120 125	384
ttc gcc gat ttg atg atg gtg gca ggc aaa cag gtg gaa gag ctt atc Phe Ala Asp Leu Met Met Val Ala Gly Lys Gln Val Glu Glu Leu Ile 130 135 140	432
gca cgt ttg gcg caa aaa gcc cgt gcg gtg ggg att cac tta att ttg Ala Arg Leu Ala Gln Lys Ala Arg Ala Val Gly Ile His Leu Ile Leu 145 150 155 160	480
gca acc caa ccg cct tcc gta gat gtg att acc ggt ttg att aaa gcg Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Leu Ile Lys Ala 165 170 175	528
aac gta ccg agt cga att gcg ttt act gtg gcg act aaa att gac tcg Asn Val Pro Ser Arg Ile Ala Phe Thr Val Ala Thr Lys Ile Asp Ser 180 185 190	576
cgt act att ctt gat gca ggc ggt gcg gaa tcc tta ttg ggt aaa ggt Arg Thr Ile Leu Asp Ala Gly Glu Ala Glu Ser Leu Leu Gly Lys Gly 195 200 205	624
gat atg ctg tat tcc cca cag ggt tct acc gaa tta gtc cgt att cac Asp Met Leu Tyr Ser Pro Gln Gly Ser Thr Glu Leu Val Arg Ile His 210 215 220	672
ggt gcc ttt atg act gat gac gaa gtc gtg cgc gtg gta gat gat tgg Gly Ala Phe Met Thr Asp Asp Glu Val Val Arg Val Val Asp Asp Trp 225 230 235 240	720
aaa gca cgc ggt aaa ccg aat tac att gat ggt att tta gag ggt gat Lys Ala Arg Gly Lys Pro Asn Tyr Ile Asp Gly Ile Leu Glu Gly Asp 245 250 255	768
gaa gaa gat gcc ggt gcg gaa cgc tta agt gag cgt ggc ggc gaa acc Glu Glu Asp Ala Gly Ala Glu Arg Leu Ser Glu Arg Gly Gly Glu Thr 260 265 270	816
gac ggg ttg ttt gat gaa gtg gta gag ttt gtg gtc agc aca ggc acc Asp Gly Leu Phe Asp Glu Val Val Glu Phe Val Val Ser Thr Gly Thr 275 280 285	864
acg tct att tct gcg att caa cgc cgt ttc cga gta ggc ttt aac cgt Thr Ser Ile Ser Ala Ile Gln Arg Arg Phe Arg Val Gly Phe Asn Arg 290 295 300	912
gcc gcc aat att atg gat cag ctg gaa gag cag ggc att gtt tcg ccg Ala Ala Asn Ile Met Asp Gln Leu Glu Glu Gln Gly Ile Val Ser Pro 305 310 315 320	960
gtg caa aac ggt aaa cgt gaa gtg ttg gcg cgc agt gcg gat tat Val Gln Asn Gly Lys Arg Glu Val Leu Ala Arg Ser Ala Asp Tyr 325 330 335	1005

-continued

SEQ ID NO 70

&lt;211&gt; LENGTH: 335

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 70

```

Ser Gly Lys Ser Val Gly Val Asn Thr Met Ile Leu Ser Leu Leu Tyr
1          5          10          15
Arg Val Lys Pro Glu Glu Val Lys Phe Ile Met Ile Asp Pro Lys Val
20          25          30
Val Glu Leu Ser Ile Tyr Asn Asp Ile Pro His Leu Leu Thr Glu Val
35          40          45
Val Thr Asp Met Lys Lys Ala Ala Asn Ala Leu Arg Trp Cys Val Asp
50          55          60
Glu Met Glu Arg Arg Tyr Gln Leu Leu Ser Ala Leu Arg Val Arg Asn
65          70          75          80
Ile Glu Gly Phe Asn Glu Lys Val Asp Glu Tyr Glu Ala Leu Asn Met
85          90          95
Pro Ile Pro Asn Pro Leu Trp Lys Pro Gly Asp Ser Met Asp Thr Leu
100         105         110
Pro Pro Pro Leu Glu Lys Leu Ser Tyr Ile Val Val Ile Val Asp Glu
115         120         125
Phe Ala Asp Leu Met Met Val Ala Gly Lys Gln Val Glu Glu Leu Ile
130         135         140
Ala Arg Leu Ala Gln Lys Ala Arg Ala Val Gly Ile His Leu Ile Leu
145         150         155         160
Ala Thr Gln Arg Pro Ser Val Asp Val Ile Thr Gly Leu Ile Lys Ala
165         170         175
Asn Val Pro Ser Arg Ile Ala Phe Thr Val Ala Thr Lys Ile Asp Ser
180         185         190
Arg Thr Ile Leu Asp Ala Gly Gly Ala Glu Ser Leu Leu Gly Lys Gly
195         200         205
Asp Met Leu Tyr Ser Pro Gln Gly Ser Thr Glu Leu Val Arg Ile His
210         215         220
Gly Ala Phe Met Thr Asp Asp Glu Val Val Arg Val Val Asp Asp Trp
225         230         235         240
Lys Ala Arg Gly Lys Pro Asn Tyr Ile Asp Gly Ile Leu Glu Gly Asp
245         250         255
Glu Glu Asp Ala Gly Ala Glu Arg Leu Ser Glu Arg Gly Gly Glu Thr
260         265         270
Asp Gly Leu Phe Asp Glu Val Val Glu Phe Val Val Ser Thr Gly Thr
275         280         285
Thr Ser Ile Ser Ala Ile Gln Arg Arg Phe Arg Val Gly Phe Asn Arg
290         295         300
Ala Ala Asn Ile Met Asp Gln Leu Glu Glu Gln Gly Ile Val Ser Pro
305         310         315         320
Val Gln Asn Gly Lys Arg Glu Val Leu Ala Arg Ser Ala Asp Tyr
325         330         335

```

&lt;210&gt; SEQ ID NO 71

&lt;211&gt; LENGTH: 426

-continued

```

<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(426)

<400> SEQUENCE: 71
atg tcg cct aat tat cct tat att aaa aca ttg gtt ata ttt cct ctg      48
Met Ser Pro Asn Tyr Pro Tyr Ile Lys Thr Leu Val Ile Phe Pro Leu
1          5          10          15

ctt gct caa ctt atc ggc acc atc atc agc att tgt gtg gat gac aat      96
Leu Ala Gln Leu Ile Gly Thr Ile Ile Ser Ile Cys Val Asp Asp Asn
          20          25          30

act gac agt ttt ctc ggc act gcc gac gtg atc ctt ttt agt ctg tta      144
Thr Asp Ser Phe Leu Gly Thr Ala Asp Val Ile Leu Phe Ser Leu Leu
          35          40          45

tcg act ttt atc gtg gca acc gtg ccc gct ttt ttg att gca ctg tgg      192
Ser Thr Phe Ile Val Ala Thr Val Pro Ala Phe Leu Ile Ala Leu Trp
          50          55          60

aca aaa att tat cgc tat acg cgc tat aac atg atg gcg att gtg tta      240
Thr Lys Ile Tyr Arg Tyr Thr Arg Tyr Asn Met Met Ala Ile Val Leu
65          70          75          80

atc tcg ctg att atc gct ttt tgt tat ggc aac gta gct agc ttt atc      288
Ile Ser Leu Ile Ile Ala Phe Cys Tyr Gly Asn Val Ala Ser Phe Ile
          85          90          95

tac atg acg ttc tct cag cca aac atg acg ttt ggt att tgg ctg cgt      336
Tyr Met Thr Phe Ser Gln Pro Asn Met Thr Phe Gly Ile Trp Leu Arg
          100          105          110

agc ggc ggc att gat atg gcg ttt tta ctg agt ttc ggc atg gcg ttg      384
Ser Gly Ile Ile Asp Met Ala Phe Leu Leu Ser Phe Gly Met Ala Leu
          115          120          125

tat tca gtt ctt gtc ttg cct ttg ttg tta ccg caa acc aga      426
Tyr Ser Val Leu Val Leu Pro Leu Leu Leu Pro Gln Thr Arg
          130          135          140

```

```

<210> SEQ ID NO 72
<211> LENGTH: 142
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 72
Met Ser Pro Asn Tyr Pro Tyr Ile Lys Thr Leu Val Ile Phe Pro Leu
1          5          10          15

Leu Ala Gln Leu Ile Gly Thr Ile Ile Ser Ile Cys Val Asp Asp Asn
          20          25          30

Thr Asp Ser Phe Leu Gly Thr Ala Asp Val Ile Leu Phe Ser Leu Leu
          35          40          45

Ser Thr Phe Ile Val Ala Thr Val Pro Ala Phe Leu Ile Ala Leu Trp
          50          55          60

Thr Lys Ile Tyr Arg Tyr Thr Arg Tyr Asn Met Met Ala Ile Val Leu
          65          70          75          80

Ile Ser Leu Ile Ile Ala Phe Cys Tyr Gly Asn Val Ala Ser Phe Ile
          85          90          95

Tyr Met Thr Phe Ser Gln Pro Asn Met Thr Phe Gly Ile Trp Leu Arg
          100          105          110

Ser Gly Gly Ile Asp Met Ala Phe Leu Leu Ser Phe Gly Met Ala Leu
          115          120          125

```

-continued

---

Tyr Ser Val Leu Val Leu Pro Leu Leu Leu Pro Gln Thr Arg  
 130 135 140

<210> SEQ ID NO 73  
 <211> LENGTH: 600  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(600)

<400> SEQUENCE: 73

gta tct caa caa aac cgc tgc gga ttc cac cac gga ttc aat aat gaa 48  
 Val Ser Gln Gln Asn Arg Cys Gly Phe His His Gly Phe Asn Asn Glu  
 1 5 10 15

aga gga aaa ata atc atg ttg gca aga atg tta ttt caa tcc tgg cgt 96  
 Arg Gly Lys Ile Ile Met Leu Ala Arg Met Leu Phe Gln Ser Trp Arg  
 20 25 30

tat gat tta aag cgc aaa ctc ctc gcc att gtg acc att ttc ctc gct 144  
 Tyr Asp Leu Lys Arg Lys Leu Leu Ala Ile Val Thr Ile Phe Leu Ala  
 35 40 45

gcc gga tta att tcc gcc ttg ctt gcg gtg tcc atc gac atc ggc gac 192  
 Ala Gly Leu Ile Ser Ala Leu Leu Ala Val Ser Ile Asp Ile Gly Asp  
 50 55 60

aaa atg gcg aaa gag ctt aaa tcc tac ggc gcc aat att ctg gtg gag 240  
 Lys Met Ala Lys Glu Leu Lys Ser Tyr Gly Ala Asn Ile Leu Val Glu  
 65 70 75 80

ccc gcc agc agc gcc att ttg cct gat gaa gtg agc cgt aat aat tct 288  
 Pro Ala Ser Ser Ala Ile Leu Pro Asp Glu Val Ser Arg Asn Asn Ser  
 85 90 95

ctc gcc acg caa gat ttt ttg gac gaa aaa gaa ctg ccg aac att aaa 336  
 Leu Ala Thr Gln Asp Phe Leu Asp Glu Lys Glu Leu Pro Asn Ile Lys  
 100 105 110

gac att ttt tgg cgt aac aat att gta ggc ttc gcc ccg tta ctc agc 384  
 Asp Ile Phe Trp Arg Asn Asn Ile Val Gly Phe Ala Pro Leu Leu Ser  
 115 120 125

gca caa gtc aaa gcc gat gga cca aac ggc aag gcg caa gac atc gac 432  
 Ala Gln Val Lys Ala Asp Gly Pro Asn Gly Lys Ala Gln Asp Ile Asp  
 130 135 140

att ctc ggc acg ttt ttt gat cat caa atc gcc gtg ccg gat gaa gac 480  
 Ile Leu Gly Thr Phe Phe Asp His Gln Ile Ala Val Pro Asp Glu Asp  
 145 150 155 160

gat tac cac acc ggg caa aaa atc atc aac cct tat tgg cag gtg gaa 528  
 Asp Tyr His Thr Gly Gln Lys Ile Ile Asn Pro Tyr Trp Gln Val Glu  
 165 170 175

ggc gaa tgg gtg aac gat gcc acc gat gat ttc agc gaa cag gtt cct 576  
 Gly Glu Trp Val Asn Asp Ala Thr Asp Asp Phe Ser Glu Gln Val Pro  
 180 185 190

gcg tta ctc ggc gca caa ctt gcc 600  
 Ala Leu Leu Gly Ala Gln Leu Ala  
 195 200

<210> SEQ ID NO 74  
 <211> LENGTH: 200  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 74

Val Ser Gln Gln Asn Arg Cys Gly Phe His His Gly Phe Asn Asn Glu  
 1 5 10 15



-continued

```

atg gaa gaa atc ggt gga tgg agt act aac atg atc acc gaa gac att 384
Met Glu Glu Ile Gly Gly Trp Ser Thr Asn Met Ile Thr Glu Asp Ile
      115                      120                      125

gat att agc tgg aaa att caa att gcc ggt tac aac atc atg tac gaa 432
Asp Ile Ser Trp Lys Ile Gln Ile Ala Gly Tyr Asn Ile Met Tyr Glu
      130                      135                      140

cca cgc gca ctc tgc tgg gtg ctt atg ccg gaa agc ata aaa ggg ctt 480
Pro Arg Ala Leu Cys Trp Val Leu Met Pro Glu Ser Ile Lys Gly Leu
      145                      150                      155                      160

tat aaa cag cgt ttg cgt tgg gca caa ggc ggt gcg gaa act atc atg 528
Tyr Lys Gln Arg Leu Arg Trp Ala Gln Gly Gly Ala Glu Thr Ile Met
      165                      170                      175

aag tat ttt tcg aaa ata tgg cat tgg cgg aat cgt cgc ttg tgg cca 576
Lys Tyr Phe Ser Lys Ile Trp His Trp Arg Asn Arg Arg Leu Trp Pro
      180                      185                      190

atg tat att gag tat ttt gct acc gtt 603
Met Tyr Ile Glu Tyr Phe Ala Thr Val
      195                      200

```

```

<210> SEQ ID NO 76
<211> LENGTH: 201
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 76

```

```

Glu Pro Arg Ile Thr Ala Leu His Gln Glu Asn Gln Gly Lys Ala Ser
1          5          10          15

Ala Leu Asn His Gly Leu Thr Val Ala Lys Gly Lys Tyr Val Ala Cys
20         25         30

Ile Asp Gly Asp Ala Val Leu Asp Tyr Tyr Ala Leu Asp Tyr Met Val
35         40         45

Gln Ala Leu Glu Gln Asp Pro Lys Tyr Ala Ala Thr Thr Gly Asn Pro
50         55         60

Arg Val Arg Asn Arg Ser Thr Ile Leu Gly Arg Leu Gln Val Ser Glu
65         70         75         80

Phe Ser Ser Ile Ile Gly Leu Ile Lys Arg Ala Gln Gly Leu Met Gly
85         90         95

Thr Ile Phe Thr Val Ser Gly Val Cys Cys Leu Phe Arg Lys Asp Val
100        105        110

Met Glu Glu Ile Gly Gly Trp Ser Thr Asn Met Ile Thr Glu Asp Ile
115        120        125

Asp Ile Ser Trp Lys Ile Gln Ile Ala Gly Tyr Asn Ile Met Tyr Glu
130        135        140

Pro Arg Ala Leu Cys Trp Val Leu Met Pro Glu Ser Ile Lys Gly Leu
145        150        155        160

Tyr Lys Gln Arg Leu Arg Trp Ala Gln Gly Gly Ala Glu Thr Ile Met
165        170        175

Lys Tyr Phe Ser Lys Ile Trp His Trp Arg Asn Arg Arg Leu Trp Pro
180        185        190

Met Tyr Ile Glu Tyr Phe Ala Thr Val
195        200

```

```

<210> SEQ ID NO 77
<211> LENGTH: 759
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

-continued

---

```

<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(759)

<400> SEQUENCE: 77

atg cga tat ttg aaa caa aca aca att tca ctg tta att ttg acc gca      48
Met Arg Tyr Leu Lys Gln Thr Thr Ile Ser Leu Leu Ile Leu Thr Ala
1          5          10          15

ctt tcc tcc tcc ttt gcc aat cag cac aag gcg aca acg cat aaa gcg      96
Leu Ser Ser Ser Phe Ala Asn Gln His Lys Ala Thr Thr His Lys Ala
20          25          30

aat gtt gcc cat acg cac gcc aaa ccg gag caa cac cac gca gaa tta     144
Asn Val Ala His Thr His Ala Lys Pro Glu Gln His His Ala Glu Leu
35          40          45

gaa cgg cta aaa cag cgt gca act ttt ctg cag tta gaa agc ctg ctg     192
Glu Arg Leu Lys Gln Arg Ala Thr Phe Leu Gln Leu Glu Ser Leu Leu
50          55          60

aaa agt gcg gtc aaa aat aac ggc gtt ttt atc aac caa act gta ttc     240
Lys Ser Ala Val Lys Asn Asn Gly Val Phe Ile Asn Gln Thr Val Phe
65          70          75          80

ctg aaa ctg att gag gat ttg aaa ggc tat ccg ttg caa aca gat gcc     288
Leu Lys Leu Ile Glu Asp Leu Lys Gly Tyr Pro Leu Gln Thr Asp Ala
85          90          95

ata gcg gct tat ttc gac gcc tgc att aaa agc gta aat cac gac aca     336
Ile Ala Ala Tyr Phe Asp Ala Cys Ile Lys Ser Val Asn His Asp Thr
100         105         110

tcg aag gga gaa gtt aag gcg cta aaa cag gac att gag caa ttt atc     384
Ser Lys Gly Glu Val Lys Ala Leu Lys Gln Asp Ile Glu Gln Phe Ile
115        120        125

gaa aag cat ccg act cat ttt cta cgg gaa aaa ttg gaa caa aga ctt     432
Glu Lys His Pro Thr His Phe Leu Arg Glu Lys Leu Glu Gln Arg Leu
130        135        140

ttt acc tta ttt atc aac acg gaa gat ctt gaa ggc tta gtt ggt tac     480
Phe Thr Leu Phe Ile Asn Thr Glu Asp Leu Glu Gly Leu Val Gly Tyr
145        150        155        160

gcg caa cgg gtt aaa ccg aaa ggg ttg gaa gcc caa ctt gca gtg ttg     528
Ala Gln Arg Val Lys Pro Lys Gly Leu Glu Ala Gln Leu Ala Val Leu
165        170        175

aat gcc gaa tat caa ctg ggg cgc aaa cgt gcc gaa tct gat aaa aat     576
Asn Ala Glu Tyr Gln Leu Gly Arg Lys Arg Ala Glu Ser Asp Lys Asn
180        185        190

ccg aat gcg aat gtg tcg aaa atc atc gcc cgt tat gag caa ctt tgg     624
Pro Asn Ala Asn Val Ser Lys Ile Ile Ala Arg Tyr Glu Gln Leu Trp
195        200        205

tta aac aat agt gaa ctg cca aac gat gcg cag cta cgg gca aaa tgg     672
Leu Asn Asn Ser Glu Leu Pro Asn Asp Ala Gln Leu Arg Ala Lys Trp
210        215        220

tat tcc gac ggc ggc aga atg gca gaa aaa gtg tat caa aaa gct gag     720
Tyr Ser Asp Gly Gly Arg Met Ala Glu Lys Val Tyr Gln Lys Ala Glu
225        230        235        240

aat ctc ttt atc aaa aac aat gta aaa ggc ttg gaa ttg                 759
Asn Leu Phe Ile Lys Asn Asn Val Lys Gly Leu Glu Leu
245        250

<210> SEQ ID NO 78
<211> LENGTH: 253
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

-continued

<400> SEQUENCE: 78

```

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

<210> SEQ ID NO 79

<211> LENGTH: 624

<212> TYPE: DNA

<213> ORGANISM: Actinobacillus actinomycetemcomitans

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(624)

<400> SEQUENCE: 79

```

gtc ggt caa tgg acg gag aaa ggt aac caa acg gaa aat cgc gat aat      48
Val Gly Gln Trp Thr Glu Lys Gly Asn Gln Thr Glu Asn Arg Asp Asn
1      5      10      15
tcc gat ccg tcc ggt tta ggt tgt act ctt ggt tgg ggc ttt gca tgg      96
Ser Asp Pro Ser Gly Leu Gly Cys Thr Leu Gly Trp Gly Phe Ala Trp
20     25     30
cca gca aac cgc cgc gtg ctt tat agc cgc gcc tct ttg gat att aac      144
Pro Ala Asn Arg Arg Val Leu Tyr Ser Arg Ala Ser Leu Asp Ile Asn
35     40     45
ggg aat cct tgg gat aaa cac cgt caa ctg atc aaa tgg aac ggt aaa      192
Gly Asn Pro Trp Asp Lys His Arg Gln Leu Ile Lys Trp Asn Gly Lys
50     55     60
    
```

-continued

```

aac tgg aac tgg ttt gat att gcc gac tac ggc act caa cca cca ggt      240
Asn Trp Asn Trp Phe Asp Ile Ala Asp Tyr Gly Thr Gln Pro Pro Gly
65                               70                               75                               80

tcc gat acc aga cca ttt atg atg tca gcc gaa ggt gtt gga cgc tta      288
Ser Asp Thr Arg Pro Phe Met Met Ser Ala Glu Gly Val Gly Arg Leu
85                               90                               95

ttt gcc gtt gat aaa att aat agc gga ccg ttc ccg gaa cac tat gaa      336
Phe Ala Val Asp Lys Ile Asn Ser Gly Pro Phe Pro Glu His Tyr Glu
100                              105                              110

ccg att gaa agt ccg att gat acg aat ccg ctt cat ccg aat gtg gta      384
Pro Ile Glu Ser Pro Ile Asp Thr Asn Pro Leu His Pro Asn Val Val
115                              120                              125

tca gat ccg acg gtg cgt att tac aaa gaa gat cgc gag ttt atc ggc      432
Ser Asp Pro Thr Val Arg Ile Tyr Lys Glu Asp Arg Glu Phe Ile Gly
130                              135                              140

tca aat aaa gaa tat ccg ttt gtg gca aca act tat cgt cta acc gaa      480
Ser Asn Lys Glu Tyr Pro Phe Val Ala Thr Thr Tyr Arg Leu Thr Glu
145                              150                              155                              160

cat ttc cac agt tgg acc gcg caa tct gcc att aac atc atc gca caa      528
His Phe His Ser Trp Thr Ala Gln Ser Ala Ile Asn Ile Ile Ala Gln
165                              170                              175

ccg caa caa ttt gtg gaa atc ggt gaa aaa ttg gca gaa gaa aaa ggt      576
Pro Gln Gln Phe Val Glu Ile Gly Glu Lys Leu Ala Glu Glu Lys Gly
180                              185                              190

atc caa aaa ggc gat atg gta cgt att acc tcc aaa ccg ggc tat att      624
Ile Gln Lys Gly Asp Met Val Arg Ile Thr Ser Lys Arg Gly Tyr Ile
195                              200                              205

```

```

<210> SEQ ID NO 80
<211> LENGTH: 208
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 80

```

```

Val Gly Gln Trp Thr Glu Lys Gly Asn Gln Thr Glu Asn Arg Asp Asn
1                               5                               10                               15

Ser Asp Pro Ser Gly Leu Gly Cys Thr Leu Gly Trp Gly Phe Ala Trp
20                              25                              30

Pro Ala Asn Arg Arg Val Leu Tyr Ser Arg Ala Ser Leu Asp Ile Asn
35                              40                              45

Gly Asn Pro Trp Asp Lys His Arg Gln Leu Ile Lys Trp Asn Gly Lys
50                              55                              60

Asn Trp Asn Trp Phe Asp Ile Ala Asp Tyr Gly Thr Gln Pro Pro Gly
65                               70                               75                               80

Ser Asp Thr Arg Pro Phe Met Met Ser Ala Glu Gly Val Gly Arg Leu
85                               90                               95

Phe Ala Val Asp Lys Ile Asn Ser Gly Pro Phe Pro Glu His Tyr Glu
100                              105                              110

Pro Ile Glu Ser Pro Ile Asp Thr Asn Pro Leu His Pro Asn Val Val
115                              120                              125

Ser Asp Pro Thr Val Arg Ile Tyr Lys Glu Asp Arg Glu Phe Ile Gly
130                              135                              140

Ser Asn Lys Glu Tyr Pro Phe Val Ala Thr Thr Tyr Arg Leu Thr Glu
145                              150                              155                              160

His Phe His Ser Trp Thr Ala Gln Ser Ala Ile Asn Ile Ile Ala Gln

```

-continued

165	170	175	
Pro Gln Gln Phe Val Glu Ile Gly	Glu Lys Leu Ala Glu Glu Lys Gly		
180	185	190	
Ile Gln Lys Gly Asp Met Val Arg	Ile Thr Ser Lys Arg Gly Tyr Ile		
195	200	205	
<210> SEQ ID NO 81			
<211> LENGTH: 534			
<212> TYPE: DNA			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(534)			
<400> SEQUENCE: 81			
att cct ggc tta att gaa ggc gca tcg gaa gga gca ggc ttg ggt atc			48
Ile Pro Gly Leu Ile Glu Gly Ala Ser Glu Gly Ala Gly Leu Gly Ile			
1 5 10 15			
cgc ttc ctg aaa cac ttg gaa cgt tgc cgc gtg ttg att cat ttg gtg			96
Arg Phe Leu Lys His Leu Glu Arg Cys Arg Val Leu Ile His Leu Val			
20 25 30			
gat atc aac cca att gat gat tcc aac ccg gcg gat aac gtg gcg att			144
Asp Ile Asn Pro Ile Asp Asp Ser Asn Pro Ala Asp Asn Val Ala Ile			
35 40 45			
atc gaa tcg gaa ttg ttc caa tac agc gag tcc ttg gcg gaa aaa ccg			192
Ile Glu Ser Glu Leu Phe Gln Tyr Ser Glu Ser Leu Ala Glu Lys Pro			
50 55 60			
cgc tgg ctg gtg ttc aac aaa atc gat acg ctc agt gat gaa gaa gcc			240
Arg Trp Leu Val Phe Asn Lys Ile Asp Thr Leu Ser Asp Glu Glu Ala			
65 70 75 80			
cat gcg cga gcg aaa gag atc acc gaa cgt ctg ggc cgg gag gaa ggt			288
His Ala Arg Ala Lys Glu Ile Thr Glu Arg Leu Gly Arg Glu Glu Gly			
85 90 95			
tat tat tta att tcc gcc gcc acc ggt aaa aac gcc ccg caa ctg tgc			336
Tyr Tyr Leu Ile Ser Ala Ala Thr Gly Lys Asn Ala Pro Gln Leu Cys			
100 105 110			
cgc gat att atg gac ttc ctg gaa gcc cac ccg gcg aaa aca gaa aaa			384
Arg Asp Ile Met Asp Phe Leu Glu Ala His Pro Arg Lys Thr Glu Lys			
115 120 125			
acg ccg gta gaa aat gaa gaa gtc aaa ttc aaa tgg gaa gat tat cat			432
Thr Pro Val Glu Asn Glu Glu Val Lys Phe Lys Trp Glu Asp Tyr His			
130 135 140			
cag gag caa ttg gaa aat gcc gat gtt gat gat gaa gag gat aat gac			480
Gln Glu Gln Leu Glu Ala Asp Val Asp Asp Glu Glu Asp Asn Asp			
145 150 155 160			
tgg gat gac tgg tcg gaa gac gat gaa gaa ggc gtg gaa att atc tat			528
Trp Asp Asp Trp Ser Glu Asp Asp Glu Glu Gly Val Glu Ile Ile Tyr			
165 170 175			
aag cct			534
Lys Pro			

<210> SEQ ID NO 82  
 <211> LENGTH: 178  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 82

Ile Pro Gly Leu Ile Glu Gly Ala Ser Glu Gly Ala Gly Leu Gly Ile			
1 5 10 15			

-continued

```

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

Lys Pro
    
```

```

<210> SEQ ID NO 83
<211> LENGTH: 372
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(372)
    
```

<400> SEQUENCE: 83

```

atg tta acg gaa agt gcg gtc gtt att gag tac gaa tcc ggc aga gcc      48
Met Leu Thr Glu Ser Ala Val Val Ile Glu Tyr Glu Ser Gly Arg Ala
1                5                10                15

aaa gtg aaa tgc caa tca caa agc gca tgc ggc gct tgc gcg gca aaa      96
Lys Val Lys Cys Gln Ser Gln Ser Ala Cys Gly Ala Cys Ala Ala Lys
      20                25                30

ccg gcg tgc ggt aat tct gcc ttg tcg gaa tta gcc agc agc ggc gcg      144
Pro Ala Cys Gly Asn Ser Ala Leu Ser Glu Leu Ala Ser Ser Gly Ala
      35                40                45

cgc ggc gaa cat att ttc acc atc gag acc att acg oca ctg aaa atc      192
Arg Gly Glu His Ile Phe Thr Ile Glu Thr Ile Thr Pro Leu Lys Ile
      50                55                60

ggg caa cgg gtg gaa atc ggt ttg tcc gaa cgt tcc tta atc aaa tcc      240
Gly Gln Arg Val Glu Ile Gly Leu Ser Glu Arg Ser Leu Ile Lys Ser
      65                70                75                80

gcc ttg ctc atg tat tgc gtg ccg cta ttt act tta tta ttc agc acg      288
Ala Leu Leu Met Tyr Cys Val Pro Leu Phe Thr Leu Leu Phe Ser Thr
      85                90                95

tta tta ttt gat tcg ctg ttt gcc cat gag ctc gtc agc gtc ttt ttt      336
Leu Leu Phe Asp Ser Leu Phe Ala His Glu Leu Val Ser Val Phe Phe
      100               105               110

atc ttc att tcc act gca ctt tct ttc ctt ggt gtg      372
Ile Phe Ile Ser Thr Ala Leu Ser Phe Leu Gly Val
      115                120
    
```

-continued

<210> SEQ ID NO 84  
 <211> LENGTH: 124  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 84

```

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

```

<210> SEQ ID NO 85  
 <211> LENGTH: 629  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(627)

<400> SEQUENCE: 85

```

att tct tcc ggt tcc tta ttg ctt gcc gtg ctt tat aaa cgc aat cgc      48
Ile Ser Ser Gly Ser Leu Leu Leu Ala Val Leu Tyr Lys Arg Asn Arg
1           5           10           15
aaa ccg gaa aaa aca agc gaa aac tgg att att cgc agt gct gcg atc      96
Lys Pro Glu Lys Thr Ser Glu Asn Trp Ile Ile Arg Ser Ala Ala Ile
20           25           30
tta gcg cct ggc acg gtg att atc ggt tta ttg ctg ttg att ttc cac      144
Leu Ala Pro Gly Thr Val Ile Ile Gly Leu Leu Leu Leu Ile Phe His
35           40           45
ttg gcg cgc cct tgg acg ttc tgg tat ttg atg ttt aac tac cag ttc      192
Leu Ala Arg Pro Trp Thr Phe Trp Tyr Leu Met Phe Asn Tyr Gln Phe
50           55           60
aat tcc gtg atg tcc atg ggg gta ctg tta ttc caa atc tat atg gcg      240
Asn Ser Val Met Ser Met Gly Val Leu Leu Phe Gln Ile Tyr Met Ala
65           70           75           80
gcg gtt ctc ctc tgg att gcg att ctc ttt aaa aat gaa ctt gcc gcc      288
Ala Val Leu Leu Trp Ile Ala Ile Leu Phe Lys Asn Glu Leu Ala Ala
85           90           95
ttg ctc gat aga ttt tta ccg aaa tta aaa ttt atc gtg aaa tgg att      336
Leu Leu Asp Arg Phe Leu Pro Lys Leu Lys Phe Ile Val Lys Trp Ile
100          105          110
ttc gcc tgt gaa cgc att acc aac ccg ttg gaa ctg ttc ctg ttg ttc      384
Phe Ala Cys Glu Arg Ile Thr Asn Pro Leu Glu Leu Phe Leu Leu Phe
115          120          125
ctt gcg gtg ttg cta ggc gct tat acc ggt ttc tta ttg tcg gcg tta      432

```



-continued

---

```

<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(264)

<400> SEQUENCE: 87

tgg gat gcc att gag aaa tgt att cag gaa tgg caa ccg gcg cgt att      48
Trp Asp Ala Ile Glu Lys Cys Ile Gln Glu Trp Gln Pro Ala Arg Ile
1           5           10           15

gtg gtc ggt ttg cca ctg aat atg gat ggt acg gaa cag ccc tta acg      96
Val Val Gly Leu Pro Leu Asn Met Asp Gly Thr Glu Gln Pro Leu Thr
          20           25           30

ttg cgt gcc aaa aag ttt gct aag cgt ttg cac gga cgt ttt aac gtg     144
Leu Arg Ala Lys Lys Phe Ala Lys Arg Leu His Gly Arg Phe Asn Val
          35           40           45

ccg gtg gat tta cag gac gaa cgt ctt acc acc acc gaa gcg cgt agc     192
Pro Val Asp Leu Gln Asp Glu Arg Leu Thr Thr Thr Glu Ala Arg Ser
          50           55           60

gaa att ttc agt cgt ggt ggt tat cgc gcc tta aat aaa agc aaa gtg     240
Glu Ile Phe Ser Arg Gly Gly Tyr Arg Ala Leu Asn Lys Ser Lys Val
65           70           75           80

gac ggc att tcc gcc tgt ttg att tt                                  266
Asp Gly Ile Ser Ala Cys Leu Ile
          85

```

```

<210> SEQ ID NO 88
<211> LENGTH: 88
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 88

Trp Asp Ala Ile Glu Lys Cys Ile Gln Glu Trp Gln Pro Ala Arg Ile
1           5           10           15

Val Val Gly Leu Pro Leu Asn Met Asp Gly Thr Glu Gln Pro Leu Thr
          20           25           30

Leu Arg Ala Lys Lys Phe Ala Lys Arg Leu His Gly Arg Phe Asn Val
          35           40           45

Pro Val Asp Leu Gln Asp Glu Arg Leu Thr Thr Thr Glu Ala Arg Ser
          50           55           60

Glu Ile Phe Ser Arg Gly Gly Tyr Arg Ala Leu Asn Lys Ser Lys Val
65           70           75           80

Asp Gly Ile Ser Ala Cys Leu Ile
          85

```

```

<210> SEQ ID NO 89
<211> LENGTH: 567
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(567)

```

```

<400> SEQUENCE: 89

caa caa gta aaa gcg ccg gga gaa gcc aaa tcc gac gta tgg caa ttg      48
Gln Gln Val Lys Ala Pro Gly Glu Ala Lys Ser Asp Val Trp Gln Leu
1           5           10           15

gta gaa ttc tcc aaa tat ttc acc acc gat gaa atg tgg ccg gcg gaa      96
Val Glu Phe Ser Lys Tyr Phe Thr Thr Asp Glu Met Trp Pro Ala Glu
          20           25           30

att ctg gac aaa aat ccg gaa tac aaa ggc aaa acc tta tat gac gtg     144

```

-continued

Ile	Leu	Asp	Lys	Asn	Pro	Glu	Tyr	Lys	Gly	Lys	Thr	Leu	Tyr	Asp	Val	
		35					40					45				
tta	tac	cgc	aac	ggt	caa	gta	gat	aaa	ttc	ccg	tta	agc	gaa	ttg	gcg	192
Leu	Tyr	Arg	Asn	Gly	Gln	Val	Asp	Lys	Phe	Pro	Leu	Ser	Glu	Leu	Ala	
	50				55						60					
gaa	gga	caa	ttg	aat	gat	gag	tcc	tat	cac	ttc	ggt	ttc	tac	ttg	caa	240
Glu	Gly	Gln	Leu	Asn	Asp	Glu	Ser	Tyr	His	Phe	Gly	Phe	Tyr	Leu	Gln	
65				70						75				80		
aaa	ggc	tta	ttt	gag	gaa	tac	gcc	tcc	ttc	ggt	cgc	ggt	cac	gga	cat	288
Lys	Gly	Leu	Phe	Glu	Glu	Tyr	Ala	Ser	Phe	Gly	Arg	Gly	His	Gly	His	
			85						90					95		
gac	ttg	gca	tcg	ttc	gat	act	tac	cac	aaa	gca	cgc	ggt	tta	cgc	tgg	336
Asp	Leu	Ala	Ser	Phe	Asp	Thr	Tyr	His	Lys	Ala	Arg	Gly	Leu	Arg	Trp	
			100					105					110			
ccg	gtg	gtg	gac	ggc	aaa	gaa	acc	tta	tgg	cgt	tat	cgc	gaa	ggc	tac	384
Pro	Val	Val	Asp	Gly	Lys	Glu	Thr	Leu	Trp	Arg	Tyr	Arg	Glu	Gly	Tyr	
		115					120					125				
gac	ccg	tat	gtc	aaa	gaa	ggg	gaa	ggt	gtg	gcg	ttc	tac	ggc	tat	ccg	432
Asp	Pro	Tyr	Val	Lys	Glu	Gly	Glu	Gly	Val	Ala	Phe	Tyr	Gly	Tyr	Pro	
	130					135					140					
gat	aaa	aaa	gcg	att	att	ctt	gcc	gtg	cct	tat	gag	ccg	cct	gcg	gaa	480
Asp	Lys	Lys	Ala	Ile	Ile	Leu	Ala	Val	Pro	Tyr	Glu	Pro	Pro	Ala	Glu	
145				150						155				160		
tca	ccg	gac	gaa	gaa	tac	gat	ttg	tgg	tta	tgt	acc	ggt	cgc	gtg	ttg	528
Ser	Pro	Asp	Glu	Glu	Tyr	Asp	Leu	Trp	Leu	Cys	Thr	Gly	Arg	Val	Leu	
			165					170						175		
gaa	cac	tgg	cac	acc	ggc	acc	atg	acc	cgt	cgt	gta	cca				567
Glu	His	Trp	His	Thr	Gly	Thr	Met	Thr	Arg	Arg	Val	Pro				
			180					185								

<210> SEQ ID NO 90  
 <211> LENGTH: 189  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <400> SEQUENCE: 90

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

-continued

Ser Pro Asp Glu Glu Tyr Asp Leu Trp Leu Cys Thr Gly Arg Val Leu  
 165 170 175

Glu His Trp His Thr Gly Thr Met Thr Arg Arg Val Pro  
 180 185

<210> SEQ ID NO 91  
 <211> LENGTH: 563  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(561)

<400> SEQUENCE: 91

cgc aaa cct ttc tat ttt tcc gct gaa aaa gat ggc att ggt gta gaa 48  
 Pro Lys Pro Phe Tyr Phe Ser Ala Glu Lys Asp Gly Ile Gly Val Glu  
 1 5 10 15

att gcg ttg caa tgg aac gac ggt tac gcg gaa aac att tat tgt ttc 96  
 Ile Ala Leu Gln Trp Asn Asp Gly Tyr Ala Glu Asn Ile Tyr Cys Phe  
 20 25 30

acc aac aac att ccg caa cgg gac ggc ggt acg cac tta gcc ggt ttc 144  
 Thr Asn Asn Ile Pro Gln Arg Asp Gly Gly Thr His Leu Ala Gly Phe  
 35 40 45

cgt ggc gca atg acc cgc acc ttg aac aac tac atg gaa aac gaa ggc 192  
 Arg Gly Ala Met Thr Arg Thr Leu Asn Asn Tyr Met Glu Asn Glu Gly  
 50 55 60

tac acc aag aaa tcc aaa gtg gcg act tcc ggt gat gat gcc cgt gaa 240  
 Tyr Thr Lys Lys Ser Lys Val Ala Thr Ser Gly Asp Asp Ala Arg Glu  
 65 70 75 80

ggc ttg gtg gcg gtg att tcc gtg aaa gta ccg gat ccg aaa ttc tct 288  
 Gly Leu Val Ala Val Ile Ser Val Lys Val Pro Asp Pro Lys Phe Ser  
 85 90 95

tct caa aca aaa gac aaa ctg gtt tcc tcc gaa gtg aaa agt gcg gtg 336  
 Ser Gln Thr Lys Asp Lys Leu Val Ser Ser Glu Val Lys Ser Ala Val  
 100 105 110

gaa tcc ctg atg aac gaa tat tta caa acc tat ttg ttg gaa aac ccg 384  
 Glu Ser Leu Met Asn Glu Tyr Leu Gln Thr Tyr Leu Leu Glu Asn Pro  
 115 120 125

aac gat gta aaa atc atc gtg acc aaa att att gat gcc gcg cgt gcc 432  
 Asn Asp Val Lys Ile Ile Val Thr Lys Ile Ile Asp Ala Ala Arg Ala  
 130 135 140

cgt gaa gcc gcc cgc aaa gcc cgc gaa atg acc cgt cgt aaa ggc gcg 480  
 Arg Glu Ala Ala Arg Lys Ala Arg Glu Met Thr Arg Arg Lys Gly Ala  
 145 150 155 160

ttg gat tta ggc ggc ttg ccg ggc aaa ttg gcg gat tgt cag gaa cgc 528  
 Leu Asp Leu Gly Gly Leu Pro Gly Lys Leu Ala Asp Cys Gln Glu Arg  
 165 170 175

gat ccg gcg tta tcc gag ctt tac atc gtg gag gg 563  
 Asp Pro Ala Leu Ser Glu Leu Tyr Ile Val Glu  
 180 185

<210> SEQ ID NO 92  
 <211> LENGTH: 187  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 92

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



-continued

```

acc att ttc cag cga atc cgc gaa caa atg tac caa gat ttt cct aat      432
Thr Ile Phe Gln Arg Ile Arg Glu Gln Met Tyr Gln Asp Phe Pro Asn
   130                               135                               140

aaa aaa cag ttt act atc act gaa aat cga gta agt gtt att gcc cct      480
Lys Lys Gln Phe Thr Ile Thr Glu Asn Arg Val Ser Val Ile Ala Pro
   145                               150                               155                               160

tcc tcc gtt att aag cca cgc ctt gcc ttg gca gct gca att ttt gat      528
Ser Ser Val Ile Lys Pro Arg Leu Ala Leu Ala Ala Ala Ile Phe Asp
   165                               170                               175

cag cag ttt aaa ggg gtt gaa gtt gat gat ttt tct tac ttg gat caa      576
Gln Gln Phe Lys Gly Val Glu Val Asp Asp Phe Ser Tyr Leu Asp Gln
   180                               185                               190

ccg cgt gaa aat ttg caa cac aat aat gat aca acc cgt tat aaa acc      624
Pro Arg Glu Asn Leu Gln His Asn Asn Asp Thr Thr Arg Tyr Lys Thr
   195                               200                               205

ttt                                                                627
Phe

```

```

<210> SEQ ID NO 94
<211> LENGTH: 209
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 94

```

```

Lys Gln Gln Leu Ala Ala Ala Leu Ala Arg Gln Glu Gln Lys Gln Ile
 1                               5                               10                               15

Ile Val Leu Gln Lys Lys Leu Thr Ser Leu Ser Ser Leu Ser Pro Gln
 20                               25                               30

Arg Leu Ala Gln Gln Ile Arg Thr Thr Glu Lys Ile Leu Thr Arg Ile
 35                               40                               45

Phe Lys Thr Glu Lys Asn Leu Thr Pro Lys Phe Ile Asp Tyr Leu Tyr
 50                               55                               60

Phe Glu Pro Ile Glu Thr Ala Asp Asp Thr Leu Met Gln Glu Met Lys
 65                               70                               75                               80

Lys Asn Leu Leu Ile Ser Phe Leu Ala Asn Glu Arg Ala Gln Ile Tyr
 85                               90                               95

Ile Lys Asp Met Pro Asn Ala Asn Gln Phe Val Gln Leu Leu Thr Glu
100                               105                               110

Lys Gly Ala Lys Thr Thr Gln Ile Ser Val Leu Ala Glu Pro Ala Lys
115                               120                               125

Thr Ile Phe Gln Arg Ile Arg Glu Gln Met Tyr Gln Asp Phe Pro Asn
130                               135                               140

Lys Lys Gln Phe Thr Ile Thr Glu Asn Arg Val Ser Val Ile Ala Pro
145                               150                               155                               160

Ser Ser Val Ile Lys Pro Arg Leu Ala Leu Ala Ala Ala Ile Phe Asp
165                               170                               175

Gln Gln Phe Lys Gly Val Glu Val Asp Asp Phe Ser Tyr Leu Asp Gln
180                               185                               190

Pro Arg Glu Asn Leu Gln His Asn Asn Asp Thr Thr Arg Tyr Lys Thr
195                               200                               205

Phe

```

```

<210> SEQ ID NO 95
<211> LENGTH: 270

```

-continued

---

```

<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(270)

<400> SEQUENCE: 95

tct gac aat acg caa tat ttt tgc ccg gcg gga tta agc gag gag cgt      48
Ser Asp Asn Thr Gln Tyr Phe Cys Pro Ala Gly Leu Ser Glu Glu Arg
1           5           10           15

gaa cag gag ctc cgc cgt ttg gta aaa cag gcc tat gat gtg gtg ggc      96
Glu Gln Glu Leu Arg Arg Leu Val Lys Gln Ala Tyr Asp Val Val Gly
           20           25           30

tgt cgt ggt tgg agc cgt att gat gtg atg gcg gat gcg gaa gga aag     144
Cys Arg Gly Trp Ser Arg Ile Asp Val Met Ala Asp Ala Glu Gly Lys
           35           40           45

ttc cgt ttg gtg gaa gtt aat acc aac cct gcc atg acc agc cac agt     192
Phe Arg Leu Val Glu Val Asn Thr Asn Pro Gly Met Thr Ser His Ser
           50           55           60

tta ttc ccg aaa tcg gcg gca acg gtc ggc tat tct ttt gcg cag ttg     240
Leu Phe Pro Lys Ser Ala Ala Thr Val Gly Tyr Ser Phe Ala Gln Leu
65           70           75           80

gtt gag aaa att tta gag ttg agc gcg gaa                               270
Val Glu Lys Ile Leu Glu Leu Ser Ala Glu
           85           90

```

```

<210> SEQ ID NO 96
<211> LENGTH: 90
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 96

Ser Asp Asn Thr Gln Tyr Phe Cys Pro Ala Gly Leu Ser Glu Glu Arg
1           5           10           15

Glu Gln Glu Leu Arg Arg Leu Val Lys Gln Ala Tyr Asp Val Val Gly
           20           25           30

Cys Arg Gly Trp Ser Arg Ile Asp Val Met Ala Asp Ala Glu Gly Lys
           35           40           45

Phe Arg Leu Val Glu Val Asn Thr Asn Pro Gly Met Thr Ser His Ser
           50           55           60

Leu Phe Pro Lys Ser Ala Ala Thr Val Gly Tyr Ser Phe Ala Gln Leu
65           70           75           80

Val Glu Lys Ile Leu Glu Leu Ser Ala Glu
           85           90

```

```

<210> SEQ ID NO 97
<211> LENGTH: 379
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(378)

<400> SEQUENCE: 97

ggg gaa tat ttc ggt cct tat ccg aat gcc ggt gca gtg cgc gaa acc     48
Gly Glu Tyr Phe Gly Pro Tyr Pro Asn Ala Gly Ala Val Arg Glu Thr
1           5           10           15

ctg tct tta tta caa aaa ctg ttc ccc att cgg cag tgt gaa aac tcc     96
Leu Ser Leu Leu Gln Lys Leu Phe Pro Ile Arg Gln Cys Glu Asn Ser
           20           25           30

```

-continued

```

gtg tat aac aac cgt tcg cgc ccc tgt ttg cag tat caa atc ggg cgt      144
Val Tyr Asn Asn Arg Ser Arg Pro Cys Leu Gln Tyr Gln Ile Gly Arg
      35                40                45

tgt ctg gcg cct tgc gta aag ggc tat gtg acc gat gaa gcc tat gcg      192
Cys Leu Ala Pro Cys Val Lys Gly Tyr Val Thr Asp Glu Ala Tyr Ala
      50                55                60

cag cag gtc aat ttc gcc cgc ttg ttt tta caa gga aaa gat caa cag      240
Gln Gln Val Asn Phe Ala Arg Leu Phe Leu Gln Gly Lys Asp Gln Gln
      65                70                75                80

gtg ctg gat cat ttg gtg aag caa atg gaa cag gca agt cag caa ctg      288
Val Leu Asp His Leu Val Lys Gln Met Glu Gln Ala Ser Gln Gln Leu
      85                90                95

aat ttt gaa gaa gcg gca cgc gtt cgt gat caa att cag gca gtg cgg      336
Asn Phe Glu Glu Ala Ala Arg Val Arg Asp Gln Ile Gln Ala Val Arg
      100                105                110

gca gta att gaa aaa caa ttt gtc gcc aac gat cgc cat gac g          379
Ala Val Ile Glu Lys Gln Phe Val Ala Asn Asp Arg His Asp
      115                120                125

```

&lt;210&gt; SEQ ID NO 98

&lt;211&gt; LENGTH: 126

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 98

```

Gly Glu Tyr Phe Gly Pro Tyr Pro Asn Ala Gly Ala Val Arg Glu Thr
1      5      10      15

Leu Ser Leu Leu Gln Lys Leu Phe Pro Ile Arg Gln Cys Glu Asn Ser
20     25     30

Val Tyr Asn Asn Arg Ser Arg Pro Cys Leu Gln Tyr Gln Ile Gly Arg
35     40     45

Cys Leu Ala Pro Cys Val Lys Gly Tyr Val Thr Asp Glu Ala Tyr Ala
50     55     60

Gln Gln Val Asn Phe Ala Arg Leu Phe Leu Gln Gly Lys Asp Gln Gln
65     70     75     80

Val Leu Asp His Leu Val Lys Gln Met Glu Gln Ala Ser Gln Gln Leu
85     90     95

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

Ala Val Ile Glu Lys Gln Phe Val Ala Asn Asp Arg His Asp
115    120    125

```

&lt;210&gt; SEQ ID NO 99

&lt;211&gt; LENGTH: 625

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(624)

&lt;400&gt; SEQUENCE: 99

```

gca aaa acc tta gat ttt cag tcc gca ggg ccg gaa aaa ctc ccg aaa      48
Ala Lys Thr Leu Asp Phe Gln Ser Ala Gly Pro Glu Lys Leu Pro Lys
1      5      10      15

ttt caa ccg cac ttt ttg gcg caa agc caa caa tta atc gac att tgc      96
Phe Gln Pro His Phe Leu Ala Gln Ser Gln Gln Leu Ile Asp Ile Cys
20     25     30

```

-continued

```

cgc cgc ctg aca ccg gcg gat att gct tcg ctc atg tct atc agc gac 144
Arg Arg Leu Thr Pro Ala Asp Ile Ala Ser Leu Met Ser Ile Ser Asp
      35                40                45

aaa ctt gcc ggg ttg aat gcc gca cgt ttc gcc gaa tgg cag ttg gaa 192
Lys Leu Ala Gly Leu Asn Ala Ala Arg Phe Ala Glu Trp Gln Leu Glu
      50                55                60

cat aac gaa cac aat gcc aaa gcg gcg gtg tat gcc ttt aga ggc gat 240
His Asn Glu His Asn Ala Lys Ala Ala Val Tyr Ala Phe Arg Gly Asp
      65                70                75                80

gtt tac acc gcc ttg gac gtg gat tcc tta agc aat gac gat atg ttg 288
Val Tyr Thr Gly Leu Asp Val Asp Ser Leu Ser Asn Asp Asp Met Leu
      85                90                95

ttt gca caa cag cat ttg cgc att ttg tcc ggg tta tat ggg ctg tta 336
Phe Ala Gln Gln His Leu Arg Ile Leu Ser Gly Leu Tyr Gly Leu Leu
      100                105                110

acg ccg ctg gat ttg att cag cct tat cgt ttg gaa atg ggc acc aaa 384
Thr Pro Leu Asp Leu Ile Gln Pro Tyr Arg Leu Glu Met Gly Thr Lys
      115                120                125

tta gcc aac gcc aaa gcc gcc gat ttg tat gcc ttt tgg cat ggt ttg 432
Leu Ala Asn Gly Lys Gly Ala Asp Leu Tyr Ala Phe Trp His Gly Leu
      130                135                140

gtg atg cag gcg tta caa cag gcg att gat gaa caa cag gac gat gtt 480
Val Met Gln Ala Leu Gln Gln Ala Ile Asp Glu Gln Gln Asp Asp Val
      145                150                155                160

ttg gtg aat ctg gcg tcc gat gaa tat tat aaa tcg gta caa ccg tcg 528
Leu Val Asn Leu Ala Ser Asp Glu Tyr Tyr Lys Ser Val Gln Pro Ser
      165                170                175

aat tta acg gcg caa atc att aaa ccg gtg ttc ctg gat aat aaa aac 576
Asn Leu Thr Ala Gln Ile Ile Lys Pro Val Phe Leu Asp Asn Lys Asn
      180                185                190

ggc aaa tat aaa att atc agt ttc tac gcg aaa aaa gcc cgc ggt tta a 625
Gly Lys Tyr Lys Ile Ile Ser Phe Tyr Ala Lys Lys Ala Arg Gly Leu
      195                200                205

```

&lt;210&gt; SEQ ID NO 100

&lt;211&gt; LENGTH: 208

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 100

```

Ala Lys Thr Leu Asp Phe Gln Ser Ala Gly Pro Glu Lys Leu Pro Lys
1      5      10      15

Phe Gln Pro His Phe Leu Ala Gln Ser Gln Gln Leu Ile Asp Ile Cys
20     25     30

Arg Arg Leu Thr Pro Ala Asp Ile Ala Ser Leu Met Ser Ile Ser Asp
35     40     45

Lys Leu Ala Gly Leu Asn Ala Ala Arg Phe Ala Glu Trp Gln Leu Glu
50     55     60

His Asn Glu His Asn Ala Lys Ala Ala Val Tyr Ala Phe Arg Gly Asp
65     70     75     80

Val Tyr Thr Gly Leu Asp Val Asp Ser Leu Ser Asn Asp Asp Met Leu
85     90     95

Phe Ala Gln Gln His Leu Arg Ile Leu Ser Gly Leu Tyr Gly Leu Leu
100    105    110

Thr Pro Leu Asp Leu Ile Gln Pro Tyr Arg Leu Glu Met Gly Thr Lys
115    120    125

```

-continued

Leu Ala Asn Gly Lys Gly Ala Asp Leu Tyr Ala Phe Trp His Gly Leu  
 130 135 140  
 Val Met Gln Ala Leu Gln Gln Ala Ile Asp Glu Gln Gln Asp Asp Val  
 145 150 155 160  
 Leu Val Asn Leu Ala Ser Asp Glu Tyr Tyr Lys Ser Val Gln Pro Ser  
 165 170 175  
 Asn Leu Thr Ala Gln Ile Ile Lys Pro Val Phe Leu Asp Asn Lys Asn  
 180 185 190  
 Gly Lys Tyr Lys Ile Ile Ser Phe Tyr Ala Lys Lys Ala Arg Gly Leu  
 195 200 205

<210> SEQ ID NO 101  
 <211> LENGTH: 500  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(498)

<400> SEQUENCE: 101

cac tgc ttt ata ccg cca tcg cta tgg ctt gct tac cgg cgt atg ccg 48  
 His Cys Phe Ile Pro Pro Ser Leu Trp Leu Ala Tyr Arg Arg Met Pro  
 1 5 10 15  
 aag aag ttt tta ccc ttg ggc aaa ttg agg tga ttg ccg ata gat caa 96  
 Lys Lys Phe Leu Pro Leu Gly Lys Leu Arg Leu Pro Ile Asp Gln  
 20 25 30  
 cgg att taa gca cca cac gca ttg aac agg ctg act tac aga aaa aca 144  
 Arg Ile Ala Pro His Ala Leu Asn Arg Leu Thr Tyr Arg Lys Thr  
 35 40 45  
 atc aaa cca atg tcg ccg agg tgg cga aaa cca cac cgg gcg tat ttt 192  
 Ile Lys Pro Met Ser Pro Arg Trp Arg Lys Pro His Arg Ala Tyr Phe  
 50 55 60  
 tgg atc gta gcg gcg cac gca atg aac ata att tgt tgg tac gcg gat 240  
 Trp Ile Val Ala Ala His Ala Met Asn Ile Ile Cys Trp Tyr Ala Asp  
 65 70 75  
 tta aag cca atc gcg tgc cag tgt tta ttg acg gca ttc ccg tgt atg 288  
 Leu Lys Pro Ile Ala Cys Gln Cys Leu Leu Thr Ala Phe Arg Cys Met  
 80 85 90  
 tgc cct atg acg gca ata tgg aca ttg gtc gct tca cca cct tcg att 336  
 Cys Pro Met Thr Ala Ile Trp Thr Leu Val Ala Ser Pro Pro Ser Ile  
 95 100 105 110  
 tat ccc gca ttg ata ttt cca agg gcg caa gtt ccg tgc ttt atg gcg 384  
 Tyr Pro Ala Leu Ile Phe Pro Arg Ala Gln Val Pro Cys Phe Met Ala  
 115 120 125  
 cca aca cgc tgg gcg gtg cgg taa atc tca tta cgc aaa aac cga cca 432  
 Pro Thr Arg Trp Ala Val Arg Ile Ser Leu Arg Lys Asn Arg Pro  
 130 135 140  
 aac cgt ttg aag gca cta tcg gct acg gat ttg ctc acg gta gaa gcg 480  
 Asn Arg Leu Lys Ala Leu Ser Ala Thr Asp Leu Leu Thr Val Glu Ala  
 145 150 155  
 gca gca ccg gca cca atc aa 500  
 Ala Ala Arg Ala Pro Ile  
 160

<210> SEQ ID NO 102  
 <211> LENGTH: 26  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

-continued

&lt;400&gt; SEQUENCE: 102

His Cys Phe Ile Pro Pro Ser Leu Trp Leu Ala Tyr Arg Arg Met Pro  
 1 5 10 15  
 Lys Lys Phe Leu Pro Leu Gly Lys Leu Arg  
 20 25

&lt;210&gt; SEQ ID NO 103

&lt;211&gt; LENGTH: 7

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 103

Leu Pro Ile Asp Gln Arg Ile  
 1 5

&lt;210&gt; SEQ ID NO 104

&lt;211&gt; LENGTH: 100

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 104

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

&lt;210&gt; SEQ ID NO 105

&lt;211&gt; LENGTH: 30

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 105

Ile Ser Leu Arg Lys Asn Arg Pro Asn Arg Leu Lys Ala Leu Ser Ala  
 1 5 10 15  
 Thr Asp Leu Leu Thr Val Glu Ala Ala Ala Arg Ala Pro Ile  
 20 25 30

&lt;210&gt; SEQ ID NO 106

&lt;211&gt; LENGTH: 303

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(303)

&lt;400&gt; SEQUENCE: 106

gca ttc ttc tcc tta ttt tcc att atc atg agc ggc aga tta aaa gaa

48

-continued

---

```

Ala Phe Phe Ser Leu Phe Ser Ile Ile Met Ser Gly Arg Leu Lys Glu
1      5      10      15
ttg ggc gaa cac tta aac gaa acc ggc tct ttc aaa gtg ggc atg att      96
Leu Gly Glu His Leu Asn Glu Thr Gly Ser Phe Lys Val Gly Met Ile
      20      25      30
tgg aaa gct ttt atc gtc atc acc acc ggt gta ctg gct ttc atg cta      144
Trp Lys Ala Phe Ile Val Ile Thr Thr Gly Val Leu Ala Phe Met Leu
      35      40      45
tac aaa gaa gca ggc aaa gtg ctc acc aaa ggc tac gaa ggc tat ccg      192
Tyr Lys Glu Ala Gly Lys Val Leu Thr Lys Gly Tyr Glu Gly Tyr Pro
      50      55      60
gac cgg ttc gtc aac acc ttc ggc tgg ggc atg gca atc gct ttg gtg      240
Asp Arg Phe Val Asn Thr Phe Gly Trp Gly Met Ala Ile Ala Leu Val
65      70      75      80
atc atc gca ttc ctg ctt tcc cgc ctg ccg tgg aaa cac tta acg caa      288
Ile Ile Ala Phe Leu Leu Ser Arg Leu Pro Trp Lys His Leu Thr Gln
      85      90      95
aca caa gga gaa aaa      303
Thr Gln Gly Glu Lys
      100

```

```

<210> SEQ ID NO 107
<211> LENGTH: 101
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 107

```

```

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

```

```

<210> SEQ ID NO 108
<211> LENGTH: 465
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(465)

```

```

<400> SEQUENCE: 108

```

```

gtg ttt ata acc gct tgc aac aat ata aac ttc ccg aga tcg gtc tcg      48
Val Phe Ile Thr Ala Cys Asn Asn Ile Asn Phe Pro Arg Ser Val Ser
1      5      10      15
gga ggc ttc agg ttt acg aac ttt gac tac act aaa cag aga acg gat      96
Gly Gly Phe Arg Phe Thr Asn Phe Asp Tyr Thr Lys Gln Arg Thr Asp
      20      25      30
ctc ttt taa gta ttc atc aaa acc ttc ccc ctg aaa aac ttt tac tac      144

```

-continued

---

```

Leu Phe      Val Phe Ile Lys Thr Phe Pro Leu Lys Asn Phe Tyr Tyr
          35          40          45

aaa act tcc ttt att agc gag aat ctg ctt gca cat atc aag cgc aag    192
Lys Thr Ser Phe Ile Ser Glu Asn Leu Leu Ala His Ile Lys Arg Lys
          50          55          60

ttc tac caa ata cat cgc acg cgg aat atc cac tga tgg cat ccc act    240
Phe Tyr Gln Ile His Arg Thr Arg Asn Ile His      Trp His Pro Thr
          65          70          75

gaa att cgg tgc cat atc tga cat cac cac atc tac ttt gcc ttc acc    288
Glu Ile Arg Cys His Ile      His His His Ile Tyr Phe Ala Phe Thr
          80          85          90

gac ccg ctc caa taa aat gtt taa cac att ttc atc acg gaa atc gcc    336
Asp Pro Leu Gln      Asn Val      His Ile Phe Ile Thr Glu Ile Ala
          95          100          105

ttg tag aaa atc cac gcc tac aat agg atc cat ttc cag aag atc aca    384
Leu      Lys Ile His Ala Tyr Asn Arg Ile His Phe Gln Lys Ile Thr
          110          115          120

ggc aat aat ccg tcc att gcg ccc aat ttg gct tac cac ata ctg cga    432
Gly Asn Asn Pro Ser Ile Ala Pro Asn Leu Ala Tyr His Ile Leu Arg
          125          130          135

cca tcc gcc cgg cgc tgc acc taa atc aac cac    465
Pro Ser Ala Arg Arg Cys Thr      Ile Asn His
          140          145

```

```

<210> SEQ ID NO 109
<211> LENGTH: 34
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 109

```

```

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

Gly Gly Phe Arg Phe Thr Asn Phe Asp Tyr Thr Lys Gln Arg Thr Asp
          20          25          30

```

```

Leu Phe

```

```

<210> SEQ ID NO 110
<211> LENGTH: 40
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 110

```

```

Val Phe Ile Lys Thr Phe Pro Leu Lys Asn Phe Tyr Tyr Lys Thr Ser
1          5          10          15

Phe Ile Ser Glu Asn Leu Leu Ala His Ile Lys Arg Lys Phe Tyr Gln
          20          25          30

Ile His Arg Thr Arg Asn Ile His
          35          40

```

```

<210> SEQ ID NO 111
<211> LENGTH: 10
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 111

```

```

Trp His Pro Thr Glu Ile Arg Cys His Ile
1          5          10

```

-continued

---

```

<210> SEQ ID NO 112
<211> LENGTH: 13
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 112

His His His Ile Tyr Phe Ala Phe Thr Asp Pro Leu Gln
1           5           10

<210> SEQ ID NO 113
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 113

His Ile Phe Ile Thr Glu Ile Ala Leu
1           5

<210> SEQ ID NO 114
<211> LENGTH: 37
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 114

Lys Ile His Ala Tyr Asn Arg Ile His Phe Gln Lys Ile Thr Gly Asn
1           5           10           15

Asn Pro Ser Ile Ala Pro Asn Leu Ala Tyr His Ile Leu Arg Pro Ser
20           25           30

Ala Arg Arg Cys Thr
35

<210> SEQ ID NO 115
<211> LENGTH: 630
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(630)

<400> SEQUENCE: 115

gaa ctg ggc tgg gga ggt tgg tgg ttc tgg gat ccg gtg gaa aat gcg      48
Glu Leu Gly Trp Gly Gly Trp Trp Phe Trp Asp Pro Val Glu Asn Ala
1           5           10           15

tcg ctc atg ccg tgg ttg ctc ggc ttg gca ttg ttg cac agt tta atc      96
Ser Leu Met Pro Trp Leu Leu Gly Leu Ala Leu Leu His Ser Leu Ile
20           25           30

gtc agc gaa aaa cgc gga att ttt aat tac tgg acg acc tta ttt tcc      144
Val Ser Glu Lys Arg Gly Ile Phe Asn Tyr Trp Thr Thr Leu Phe Ser
35           40           45

ttg ttg gca ttt gcc ttc agc gta tta ggc acg ttt atc gtg cgc tcc      192
Leu Leu Ala Phe Ala Phe Ser Val Leu Gly Thr Phe Ile Val Arg Ser
50           55           60

ggc gcg ctt acc tcc gta cac gct ttc gct gtg gac agc caa cgc ggc      240
Gly Ala Leu Thr Ser Val His Ala Phe Ala Val Asp Ser Gln Arg Gly
65           70           75           80

tcg gca tta tta ctg att ttc ttc ctg ctc acc gtg ggt tct ctc ggt      288
Ser Ala Leu Leu Leu Ile Phe Phe Leu Leu Thr Val Gly Ser Leu Gly
85           90           95

tta ttc gcg ttc aaa gcc aat ttg cag caa cgc cgc gtc aaa tta acg      336
Leu Phe Ala Phe Lys Ala Asn Leu Gln Gln Arg Arg Val Lys Leu Thr
100          105          110

```

-continued

```

ctg ctt tcc aaa gaa agt gcg gtg ctt ttt ttg aat gtt tta ttg agt      384
Leu Leu Ser Lys Glu Ser Ala Val Leu Phe Leu Asn Val Leu Leu Ser
      115                      120                      125

atc gcc acc gtt agc acc ttt ctc ggc acc ttt tat ccc atg ctg ttc      432
Ile Ala Thr Val Ser Thr Phe Leu Gly Thr Phe Tyr Pro Met Leu Phe
      130                      135                      140

caa gcc atg aat tgg ggt tcc att tcc gtc ggt gcg cct tat ttc aac      480
Gln Ala Met Asn Trp Gly Ser Ile Ser Val Gly Ala Pro Tyr Phe Asn
      145                      150                      155                      160

agt att ttc ttg ccg ctg ctt acg ctg att tta atc gcc atg gtg ttt      528
Ser Ile Phe Leu Pro Leu Leu Thr Leu Ile Leu Ile Ala Met Val Phe
      165                      170                      175

tcc ctc ggc ttg cac tgg gcg aag gcg gac aaa ggc att ttg ttt aaa      576
Ser Leu Gly Leu His Trp Ala Lys Ala Asp Lys Gly Ile Leu Phe Lys
      180                      185                      190

cgc gcg gcg ttg tta ctg ccg tct ttg ttg atc gct tat ttt atg att      624
Arg Ala Ala Leu Leu Leu Pro Ser Leu Leu Ile Ala Tyr Phe Met Ile
      195                      200                      205

cgt cag      630
Arg Gln
      210

<210> SEQ ID NO 116
<211> LENGTH: 210
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 116

Glu Leu Gly Trp Gly Gly Trp Trp Phe Trp Asp Pro Val Glu Asn Ala
1                      5                      10                      15

Ser Leu Met Pro Trp Leu Leu Gly Leu Ala Leu Leu His Ser Leu Ile
20                      25                      30

Val Ser Glu Lys Arg Gly Ile Phe Asn Tyr Trp Thr Thr Leu Phe Ser
35                      40                      45

Leu Leu Ala Phe Ala Phe Ser Val Leu Gly Thr Phe Ile Val Arg Ser
50                      55                      60

Gly Ala Leu Thr Ser Val His Ala Phe Ala Val Asp Ser Gln Arg Gly
65                      70                      75                      80

Ser Ala Leu Leu Leu Ile Phe Phe Leu Leu Thr Val Gly Ser Leu Gly
85                      90                      95

Leu Phe Ala Phe Lys Ala Asn Leu Gln Gln Arg Arg Val Lys Leu Thr
100                      105                      110

Leu Leu Ser Lys Glu Ser Ala Val Leu Phe Leu Asn Val Leu Leu Ser
115                      120                      125

Ile Ala Thr Val Ser Thr Phe Leu Gly Thr Phe Tyr Pro Met Leu Phe
130                      135                      140

Gln Ala Met Asn Trp Gly Ser Ile Ser Val Gly Ala Pro Tyr Phe Asn
145                      150                      155                      160

Ser Ile Phe Leu Pro Leu Leu Thr Leu Ile Leu Ile Ala Met Val Phe
165                      170                      175

Ser Leu Gly Leu His Trp Ala Lys Ala Asp Lys Gly Ile Leu Phe Lys
180                      185                      190

Arg Ala Ala Leu Leu Leu Pro Ser Leu Leu Ile Ala Tyr Phe Met Ile
195                      200                      205

```

-continued

Arg Gln  
210

&lt;210&gt; SEQ ID NO 117

&lt;211&gt; LENGTH: 876

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(876)

&lt;400&gt; SEQUENCE: 117

```

act cac cct gtg cat att tcg atg caa tat atg gca gat gaa gtt aaa      48
Thr His Pro Val His Ile Ser Met Gln Tyr Met Ala Asp Glu Val Lys
1          5          10          15

aaa tta aca aat ggt gaa gtg gtg atc cga att tac cca aat agc cag      96
Lys Leu Thr Asn Gly Glu Val Val Ile Arg Ile Tyr Pro Asn Ser Gln
          20          25          30

ctt ggt agc cag cgt gaa tca atg gaa tta ttg caa tcc ggg tca cta      144
Leu Gly Ser Gln Arg Glu Ser Met Glu Leu Leu Gln Ser Gly Ser Leu
          35          40          45

gat atg gca aaa tca aac gca agt gaa tta gaa gca ttt gag cca tct      192
Asp Met Ala Lys Ser Asn Ala Ser Glu Leu Glu Ala Phe Glu Pro Ser
          50          55          60

tat ggt gca tac aat att ccg tat ctt ttc cat aat gtt gat cat tat      240
Tyr Gly Ala Tyr Asn Ile Pro Tyr Leu Phe His Asn Val Asp His Tyr
65          70          75          80

tat cgt gct cta ctt gat cct gaa gtt ggg caa aaa att ctt gat tca      288
Tyr Arg Ala Leu Leu Asp Pro Glu Val Gly Gln Lys Ile Leu Asp Ser
          85          90          95

tca aag ggc aaa ggt ttc att ggg ttg act tat tat gat ggt ggt gcg      336
Ser Lys Gly Lys Gly Phe Ile Gly Leu Thr Tyr Tyr Asp Gly Gly Ala
          100          105          110

cgt agt ttc tat gcg ggt aag gca att aaa tcg cct gcg gac ctc aaa      384
Arg Ser Phe Tyr Ala Gly Lys Ala Ile Lys Ser Pro Ala Asp Leu Lys
          115          120          125

ggg atg aaa att cgc gtt caa cca agc cca acc gca gta gaa atg atc      432
Gly Met Lys Ile Arg Val Gln Pro Ser Pro Thr Ala Val Glu Met Ile
          130          135          140

aaa tta atg ggt gct tct cca aca cct tta gct tat ggt gaa ctc tat      480
Lys Leu Met Gly Ala Ser Pro Thr Pro Leu Ala Tyr Gly Glu Leu Tyr
145          150          155          160

acc gca ctc caa caa aaa gtg gtt gat ggc gcg gaa aat aac caa aca      528
Thr Ala Leu Gln Gln Lys Val Val Asp Gly Ala Glu Asn Asn Gln Thr
          165          170          175

gca tta acc tta tct cgt cat ggt gaa gtg gct aaa ttc ttt agt gaa      576
Ala Leu Thr Leu Ser Arg His Gly Glu Val Ala Lys Phe Phe Ser Glu
          180          185          190

gat gaa cat act atg att cct gat gtg ctc gta att ggt caa aaa tct      624
Asp Glu His Thr Met Ile Pro Asp Val Leu Val Ile Gly Gln Lys Ser
          195          200          205

tgg gat aaa tta act cca gaa caa caa aat gca ctt aaa aaa gcc gct      672
Trp Asp Lys Leu Thr Pro Glu Gln Gln Asn Ala Leu Lys Lys Ala Ala
210          215          220

gat gat tca atg atg tat cac aaa gat tta tgg caa aaa atg att gct      720
Asp Asp Ser Met Met Tyr His Lys Asp Leu Trp Gln Lys Met Ile Ala
225          230          235          240

gaa acc act caa gaa gct aaa gat aaa ttg ggt gta gaa ttt gtg aaa      768
Glu Thr Thr Gln Glu Ala Lys Asp Lys Leu Gly Val Glu Phe Val Lys

```



-continued

Leu Ala Thr Lys  
290

<210> SEQ ID NO 119  
<211> LENGTH: 303  
<212> TYPE: DNA  
<213> ORGANISM: Actinobacillus actinomycetemcomitans  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(303)

<400> SEQUENCE: 119

```

atg agt gtt tta agt tat gcc caa aaa atc ggg caa gcc tta atg gta      48
Met Ser Val Leu Ser Tyr Ala Gln Lys Ile Gly Gln Ala Leu Met Val
1           5           10           15

ccc gtt gcc gtt ttg ccg gca gcc gcc gta tta atg ggg atc ggc tat      96
Pro Val Ala Val Leu Pro Ala Ala Ala Val Leu Met Gly Ile Gly Tyr
           20           25           30

tgg ctt gac ccg gac ggc tgg ggc gca aac agc caa ctt gcc gcc tta      144
Trp Leu Asp Pro Asp Gly Trp Gly Ala Asn Ser Gln Leu Ala Ala Leu
           35           40           45

tta atc aag tcc ggc gcg gca atc atc gat aac atg ggc tta tta ttc      192
Leu Ile Lys Ser Gly Ala Ala Ile Ile Asp Asn Met Gly Leu Leu Phe
           50           55           60

gcc gtg ggc gta gca ttc ggg ttg tcc aaa gac aag cac ggt tct gct      240
Ala Val Gly Val Ala Phe Gly Leu Ser Lys Asp Lys His Gly Ser Ala
           65           70           75           80

gcg ctt tcc ggt tta gtg ggc tat tat gtg gtc act acc cta ctc gcc      288
Ala Leu Ser Gly Leu Val Gly Tyr Tyr Val Val Thr Thr Leu Leu Ala
           85           90           95

cct ggc gcc gta gcg      303
Pro Gly Gly Val Ala
           100

```

<210> SEQ ID NO 120  
<211> LENGTH: 101  
<212> TYPE: PRT  
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 120

```

Met Ser Val Leu Ser Tyr Ala Gln Lys Ile Gly Gln Ala Leu Met Val
1           5           10           15

Pro Val Ala Val Leu Pro Ala Ala Ala Val Leu Met Gly Ile Gly Tyr
           20           25           30

Trp Leu Asp Pro Asp Gly Trp Gly Ala Asn Ser Gln Leu Ala Ala Leu
           35           40           45

Leu Ile Lys Ser Gly Ala Ala Ile Ile Asp Asn Met Gly Leu Leu Phe
           50           55           60

Ala Val Gly Val Ala Phe Gly Leu Ser Lys Asp Lys His Gly Ser Ala
           65           70           75           80

Ala Leu Ser Gly Leu Val Gly Tyr Tyr Val Val Thr Thr Leu Leu Ala
           85           90           95

Pro Gly Gly Val Ala
           100

```

<210> SEQ ID NO 121  
<211> LENGTH: 590  
<212> TYPE: DNA  
<213> ORGANISM: Actinobacillus actinomycetemcomitans

-continued

```

<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(588)

<400> SEQUENCE: 121

gaa tat aaa aat ctt gct gtt gct tat atc cgt atg tct acg gag cat      48
Glu Tyr Lys Asn Leu Ala Val Ala Tyr Ile Arg Met Ser Thr Glu His
1          5          10          15

cag gaa ttt tca ccg gat ata caa cgt cgc ttc att caa aaa tat gct      96
Gln Glu Phe Ser Pro Asp Ile Gln Arg Arg Phe Ile Gln Lys Tyr Ala
          20          25          30

aag gaa caa ggg ctt ata ctc act agg gaa tac cta gat gag gga agg     144
Lys Glu Gln Gly Leu Ile Leu Thr Arg Glu Tyr Leu Asp Glu Gly Arg
          35          40          45

agt gga tta agc gca gaa aaa cgt cct cag ttt tta tca ctc att aat     192
Ser Gly Leu Ser Ala Glu Lys Arg Pro Gln Phe Leu Ser Leu Ile Asn
          50          55          60

ttt gta caa tcc ggt aat gct gat ttt tca cat att ctt gtt tat gac     240
Phe Val Gln Ser Gly Asn Ala Asp Phe Ser His Ile Leu Val Tyr Asp
65          70          75          80

att agc cga tgg ggg cgc ttt cta aat att gat gaa tct gca cat tat     288
Ile Ser Arg Trp Gly Arg Phe Leu Asn Ile Asp Glu Ser Ala His Tyr
          85          90          95

gaa caa att tgt tca aaa atg ggg att aaa gtg cat tac tgt gca gaa     336
Glu Gln Ile Cys Ser Lys Met Gly Ile Lys Val His Tyr Cys Ala Glu
          100          105          110

cct ttt aag gga aac gac att ggt tct caa att ttt aaa gcg gta aaa     384
Pro Phe Lys Gly Asn Asp Ile Gly Ser Gln Ile Phe Lys Ala Val Lys
          115          120          125

cgt tgg tct gcc gga gaa tac tgt cgt gag cta ggt gaa aaa gtt ttt     432
Arg Trp Ser Ala Gly Glu Tyr Cys Arg Glu Leu Gly Glu Lys Val Phe
          130          135          140

aat ggg cag aag aat ttg att gag cgc gga ttt cgt caa ggt gga cca     480
Asn Gly Gln Lys Asn Leu Ile Glu Arg Gly Phe Arg Gln Gly Gly Pro
          145          150          155          160

gct gga ttt ggg tta aga cgc cta tta tta agt gct gat ggt tcg cca     528
Ala Gly Phe Gly Leu Arg Arg Leu Leu Leu Ser Ala Asp Gly Ser Pro
          165          170          175

aaa ttt gaa cta aaa acg ggt gac agg aag agt ttg cag tcg gat cgt     576
Lys Phe Glu Leu Lys Thr Gly Asp Arg Lys Ser Leu Gln Ser Asp Arg
          180          185          190

gtc att ctt att gc          590
Val Ile Leu Ile
          195

```

```

<210> SEQ ID NO 122
<211> LENGTH: 196
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 122

Glu Tyr Lys Asn Leu Ala Val Ala Tyr Ile Arg Met Ser Thr Glu His
1          5          10          15

Gln Glu Phe Ser Pro Asp Ile Gln Arg Arg Phe Ile Gln Lys Tyr Ala
          20          25          30

Lys Glu Gln Gly Leu Ile Leu Thr Arg Glu Tyr Leu Asp Glu Gly Arg
          35          40          45

Ser Gly Leu Ser Ala Glu Lys Arg Pro Gln Phe Leu Ser Leu Ile Asn

```

-continued

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

<210> SEQ ID NO 123  
 <211> LENGTH: 531  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(531)

<400> SEQUENCE: 123

ttt tta acc aaa gat aaa atc aag cag gca ata cag gca cag caa cag	48
Phe Leu Thr Lys Asp Lys Ile Lys Gln Ala Ile Gln Ala Gln Gln Gln	
1 5 10 15	
gaa ctg tta cta caa gtg atc ccg cag gat tac ttc aat aat gat ctg	96
Glu Leu Leu Leu Gln Val Ile Pro Gln Asp Tyr Phe Asn Asn Asp Leu	
20 25 30	
acg cag gct tgt tat gca ccg caa gcg ggg aca tta caa gtc gtg gag	144
Thr Gln Ala Cys Tyr Ala Pro Gln Ala Gly Thr Leu Gln Val Val Glu	
35 40 45	
ata agc aaa ata tgc acg gca aag aaa gac ggc gtg act act gcc tat	192
Ile Ser Lys Ile Cys Thr Ala Lys Lys Asp Gly Val Thr Thr Ala Tyr	
50 55 60	
gcc ttt gaa agc acg gcg cat gat ggc tat tcc ggc gat att cat att	240
Ala Phe Glu Ser Thr Ala His Asp Gly Tyr Ser Gly Asp Ile His Ile	
65 70 75 80	
ttg gtg ggc atg aaa cct gat ggc gaa gtg ctt ggc gtg cgc att acg	288
Leu Val Gly Met Lys Pro Asp Gly Glu Val Leu Gly Val Arg Ile Thr	
85 90 95	
gaa cac cac gaa acc ccg gga tta ggc gat aaa att gaa acc cgc att	336
Glu His His Glu Thr Pro Gly Leu Gly Asp Lys Ile Glu Thr Arg Ile	
100 105 110	
tcc aac tgg gtt tta agt ttt gat cat cag gtt atc agc aac gaa aat	384
Ser Asn Trp Val Leu Ser Phe Asp His Gln Val Ile Ser Asn Glu Asn	
115 120 125	
gcc gca gaa tgg gcg gtg aaa aaa gac ggc ggt aaa ttc gat caa ttc	432
Ala Ala Glu Trp Ala Val Lys Lys Asp Gly Gly Lys Phe Asp Gln Phe	
130 135 140	



-continued

tca aat gaa aaa agc att tgg aaa acg att ttc att cag ggc atc tgg 192  
 Ser Asn Glu Lys Ser Ile Trp Lys Thr Ile Phe Ile Gln Gly Ile Trp  
 50 55 60

acc aac aat tcc acc gtg gtg caa ctg ctt ggg ttg tgt ccg ctg ctg 240  
 Thr Asn Asn Ser Thr Val Val Gln Leu Leu Gly Leu Cys Pro Leu Leu  
 65 70 75 80

gcg gtg tcc aac tcc gtg acc aac gcc ctc ggg ctg ggt tta gcc acc 288  
 Ala Val Ser Asn Ser Val Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr  
 85 90 95

atg ctt gtg ctg acg tgt acg aac acg gta gtt tct ctt ttc cgt aag 336  
 Met Leu Val Leu Thr Cys Thr Asn Thr Val Val Ser Leu Phe Arg Lys  
 100 105 110

cac atc ccc aat gaa atc cgc att ccg att tat gtg atg atc atc gca 384  
 His Ile Pro Asn Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala  
 115 120 125

acc acg gta acc gct gtg caa tta ttg atg aat gcc tat acc tac gcg 432  
 Thr Thr Val Thr Ala Val Gln Leu Leu Met Asn Ala Tyr Thr Tyr Ala  
 130 135 140

ctt tat caa tct ctc ggg att ttt att ccg ctc atc gtc acc aac tgt 480  
 Leu Tyr Gln Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys  
 145 150 155 160

att gtg atc ggt cgc gcc gaa gcc ttt gct tcc aag aac agc att tcc 528  
 Ile Val Ile Gly Arg Ala Glu Ala Phe Ala Ser Lys Asn Ser Ile Ser  
 165 170 175

cat tcc gcc ttt gac ggt ttt tcc atg gga tta ggg atg tta ttc agt 576  
 His Ser Ala Phe Asp Gly Phe Ser Met Gly Leu Gly Met Leu Phe Ser  
 180 185 190

tta gta gcg ctc ggc gcc atc cgc gaa atc atc ggc aac ggt act tta 624  
 Leu Val Ala Leu Gly Gly Ile Arg Glu Ile Ile Gly Asn Gly Thr Leu  
 195 200 205

ttt gac ggc atc gaa aat ttg ctg ggc gat tgg gct aaa ttc atg cgg 672  
 Phe Asp Gly Ile Glu Asn Leu Leu Gly Asp Trp Ala Lys Phe Met Arg  
 210 215 220

att gaa ttt ttc cac aat gac agt aat ctg tta ctt gcg att ttg cct 720  
 Ile Glu Phe Phe His Asn Asp Ser Asn Leu Leu Leu Ala Ile Leu Pro  
 225 230 235 240

ccc ggc gca ttt att ggt tta gct ttg ttg tta gcc tta aaa aat gta 768  
 Pro Gly Ala Phe Ile Gly Leu Ala Leu Leu Leu Ala Leu Lys Asn Val  
 245 250 255

ata gat aca aaa aag 783  
 Ile Asp Thr Lys Lys  
 260

&lt;210&gt; SEQ ID NO 126

&lt;211&gt; LENGTH: 261

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 126

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

Ser Ala Val Asp Lys Lys Gln His Phe Leu Asn Val Gly Ser Ala Asn  
 20 25 30

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

Ser Asn Glu Lys Ser Ile Trp Lys Thr Ile Phe Ile Gln Gly Ile Trp  
 50 55 60

-continued

Thr Asn Asn Ser Thr Val Val Gln Leu Leu Gly Leu Cys Pro Leu Leu  
65 70 75 80

Ala Val Ser Asn Ser Val Thr Asn Ala Leu Gly Leu Gly Leu Ala Thr  
85 90 95

Met Leu Val Leu Thr Cys Thr Asn Thr Val Val Ser Leu Phe Arg Lys  
100 105 110

His Ile Pro Asn Glu Ile Arg Ile Pro Ile Tyr Val Met Ile Ile Ala  
115 120 125

Thr Thr Val Thr Ala Val Gln Leu Leu Met Asn Ala Tyr Thr Tyr Ala  
130 135 140

Leu Tyr Gln Ser Leu Gly Ile Phe Ile Pro Leu Ile Val Thr Asn Cys  
145 150 155 160

Ile Val Ile Gly Arg Ala Glu Ala Phe Ala Ser Lys Asn Ser Ile Ser  
165 170 175

His Ser Ala Phe Asp Gly Phe Ser Met Gly Leu Gly Met Leu Phe Ser  
180 185 190

Leu Val Ala Leu Gly Gly Ile Arg Glu Ile Ile Gly Asn Gly Thr Leu  
195 200 205

Phe Asp Gly Ile Glu Asn Leu Leu Gly Asp Trp Ala Lys Phe Met Arg  
210 215 220

Ile Glu Phe Phe His Asn Asp Ser Asn Leu Leu Leu Ala Ile Leu Pro  
225 230 235 240

Pro Gly Ala Phe Ile Gly Leu Ala Leu Leu Leu Ala Leu Lys Asn Val  
245 250 255

Ile Asp Thr Lys Lys  
260

<210> SEQ ID NO 127  
 <211> LENGTH: 627  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(627)

<400> SEQUENCE: 127

atg aat ttt act aaa acg cta tat att ttt aaa tat act ggc gaa ctt 48  
 Met Asn Phe Thr Lys Thr Leu Tyr Ile Phe Lys Tyr Thr Gly Glu Leu  
 1 5 10 15

ttc gcg att ttt att tat aat gaa gac gct atg ttt tta aat ata cat 96  
 Phe Ala Ile Phe Ile Tyr Asn Glu Asp Ala Met Phe Leu Asn Ile His  
 20 25 30

cgt tat att ttt ctc aca ttc tgt tgg ggt aac atc atg aaa ttt gaa 144  
 Arg Tyr Ile Phe Leu Thr Phe Cys Trp Gly Asn Ile Met Lys Phe Glu  
 35 40 45

gtc att tac aaa ttc ctg ttg ttg tgt gtg ctg att atc agt ttg ttg 192  
 Val Ile Tyr Lys Phe Leu Leu Leu Cys Val Leu Ile Ile Ser Leu Leu  
 50 55 60

tgt gtt gtg ata agc ggc gcc gga tta ttc tac ggt tgg caa ttg agc 240  
 Cys Val Val Ile Ser Gly Ala Gly Leu Phe Tyr Gly Trp Gln Leu Ser  
 65 70 75 80

atg ctg ttc aat att cat gtg agc ttt gcc gtt ttg ctg gtc gcc gcg 288  
 Met Leu Phe Asn Ile His Val Ser Phe Ala Val Leu Leu Val Ala Ala  
 85 90 95

ttg tta ctg cat att ctg aac cgc aaa aat aaa ttg gcg aaa atc aat 336

-continued

---

```

Leu Leu Leu His Ile Leu Asn Arg Lys Asn Lys Leu Ala Lys Ile Asn
    100                               105                               110

acc caa ttt gcc gat ttg gtc tta cac aat aaa tac ccg agt tat tgc      384
Thr Gln Phe Ala Asp Leu Val Leu His Asn Lys Tyr Pro Ser Tyr Cys
    115                               120                               125

aat tta gac cgc ttg atc atg acg ttc gag cat ttt tcc gtt gtg caa      432
Asn Leu Asp Arg Leu Ile Met Thr Phe Glu His Phe Ser Val Val Gln
    130                               135                               140

att gcc gaa cag tta aac ctg gat ttg gat gcg ctg cta aaa gaa ctc      480
Ile Ala Glu Gln Leu Asn Leu Asp Leu Asp Ala Leu Leu Lys Glu Leu
    145                               150                               155                               160

gcc gaa gga aaa ata aac gtc aaa aat tcc cac agc act tta cgg gag      528
Ala Glu Gly Lys Ile Asn Val Lys Asn Ser His Ser Thr Leu Arg Glu
    165                               170                               175

aat ttt ccc cat aat gat gaa aag att ttt gct gcg atc acc atc gtg      576
Asn Phe Pro His Asn Asp Glu Lys Ile Phe Ala Ala Ile Thr Ile Val
    180                               185                               190

ctg caa ctt cgt tta att aat cct atc cct gct ttt aac tta aaa gga      624
Leu Gln Leu Arg Leu Ile Asn Pro Ile Pro Ala Phe Asn Leu Lys Gly
    195                               200                               205

cat                                                                 627
His
    
```

```

<210> SEQ ID NO 128
<211> LENGTH: 209
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans
    
```

<400> SEQUENCE: 128

```

Met Asn Phe Thr Lys Thr Leu Tyr Ile Phe Lys Tyr Thr Gly Glu Leu
 1          5          10          15

Phe Ala Ile Phe Ile Tyr Asn Glu Asp Ala Met Phe Leu Asn Ile His
 20          25          30

Arg Tyr Ile Phe Leu Thr Phe Cys Trp Gly Asn Ile Met Lys Phe Glu
 35          40          45

Val Ile Tyr Lys Phe Leu Leu Leu Cys Val Leu Ile Ile Ser Leu Leu
 50          55          60

Cys Val Val Ile Ser Gly Ala Gly Leu Phe Tyr Gly Trp Gln Leu Ser
 65          70          75          80

Met Leu Phe Asn Ile His Val Ser Phe Ala Val Leu Leu Val Ala Ala
 85          90          95

Leu Leu Leu His Ile Leu Asn Arg Lys Asn Lys Leu Ala Lys Ile Asn
100          105          110

Thr Gln Phe Ala Asp Leu Val Leu His Asn Lys Tyr Pro Ser Tyr Cys
115          120          125

Asn Leu Asp Arg Leu Ile Met Thr Phe Glu His Phe Ser Val Val Gln
130          135          140

Ile Ala Glu Gln Leu Asn Leu Asp Leu Asp Ala Leu Leu Lys Glu Leu
145          150          155          160

Ala Glu Gly Lys Ile Asn Val Lys Asn Ser His Ser Thr Leu Arg Glu
165          170          175

Asn Phe Pro His Asn Asp Glu Lys Ile Phe Ala Ala Ile Thr Ile Val
180          185          190

Leu Gln Leu Arg Leu Ile Asn Pro Ile Pro Ala Phe Asn Leu Lys Gly
195          200          205
    
```

-continued

His

```

<210> SEQ ID NO 129
<211> LENGTH: 663
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(663)

<400> SEQUENCE: 129

gtg caa tct tac gag cag caa agt aat aac ggc gtg ccg att caa ttc      48
Val Gln Ser Tyr Glu Gln Gln Ser Asn Asn Gly Val Pro Ile Gln Phe
1                               5                               10                               15

cag cag tta gac caa tca caa acc gtt gaa ccg acc gtg ttg gat aat      96
Gln Gln Leu Asp Gln Ser Gln Thr Val Glu Pro Thr Val Leu Asp Asn
                20                               25                               30

ctg acc ccg caa acc gat aac act gtc gcg caa caa cct gct gcg gaa     144
Leu Thr Pro Gln Thr Asp Asn Thr Val Ala Gln Gln Pro Ala Ala Glu
                35                               40                               45

acc aat acg caa aat gtc aat gcc ggc gcc ata gaa ccg caa gcg gtg     192
Thr Asn Thr Gln Asn Val Asn Ala Gly Ala Ile Glu Pro Gln Ala Val
                50                               55                               60

gaa caa ggg gca acc acc tcc gtt gct gag caa acg aca act gcg gcg     240
Glu Gln Gly Ala Thr Thr Ser Val Ala Glu Gln Thr Thr Thr Ala Ala
65                               70                               75                               80

gta gaa aat aaa ccg gca gaa gtc aaa ccg gaa gag gtc gaa acc gtt     288
Val Glu Asn Lys Pro Ala Glu Val Lys Pro Glu Glu Val Glu Thr Val
                85                               90                               95

aaa ccg agt gag cct gca aaa gcg caa gaa gcc gtc aaa ccg cgt caa     336
Lys Pro Ser Glu Pro Ala Lys Ala Gln Glu Ala Val Lys Pro Arg Gln
                100                              105                              110

cat cag gaa agc gtg aaa aaa gag ccg gtg aaa acc gat aaa gtg aaa     384
His Gln Glu Ser Val Lys Lys Glu Pro Val Lys Thr Asp Lys Val Lys
                115                              120                              125

cag gct gaa aaa gcg act gct aaa aat caa ccg act aaa tcg gca aaa     432
Gln Ala Glu Lys Ala Thr Ala Lys Asn Gln Pro Thr Lys Ser Ala Lys
                130                              135                              140

acc gaa aaa gaa gta cgg gat att tta gaa ggc aaa aca acg act atc     480
Thr Glu Lys Glu Val Arg Asp Ile Leu Glu Gly Lys Thr Thr Thr Ile
145                              150                              155                              160

acc aaa gca gca gcc ggt agc aaa acc tta acc att ccg caa ggc gtg     528
Thr Lys Ala Ala Ala Gly Ser Lys Thr Leu Thr Ile Pro Gln Gly Val
                165                              170                              175

acc tta atg cag gtg ttc cgt gac aac cat cta cct gtc ggt gat gtg     576
Thr Leu Met Gln Val Phe Arg Asp Asn His Leu Pro Val Gly Asp Val
                180                              185                              190

aat gcc atg acc aaa gcc aaa ggc gta ggc aag gtg tta agc agc ttc     624
Asn Ala Met Thr Lys Ala Lys Gly Val Gly Lys Val Leu Ser Ser Phe
                195                              200                              205

aag ccg ggt gat aag gta cag gtt tcc ctg aat gca caa                 663
Lys Pro Gly Asp Lys Val Gln Val Ser Leu Asn Ala Gln
                210                              215                              220

```

```

<210> SEQ ID NO 130
<211> LENGTH: 221
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

-continued

<400> SEQUENCE: 130

```

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

<210> SEQ ID NO 131

<211> LENGTH: 478

<212> TYPE: DNA

<213> ORGANISM: Actinobacillus actinomycetemcomitans

<220> FEATURE:

<221> NAME/KEY: CDS

<222> LOCATION: (1)..(477)

<400> SEQUENCE: 131

```

atg tta aaa aaa atc tta cat tcc gca ctc atc ggt ttg gtt acg gca      48
Met Leu Lys Lys Ile Leu His Ser Ala Leu Ile Gly Leu Val Thr Ala
1      5      10      15
ggt gtg att ttg ttt gtg cta ccg aaa atc acc ggg aaa tcc gtg tta      96
Gly Val Ile Leu Phe Val Leu Pro Lys Ile Thr Gly Lys Ser Val Leu
20      25      30
ccg gag caa gaa atc gcc tct tat aaa gat gca gtg cgt att gct tcg      144
Pro Glu Gln Glu Ile Ala Ser Tyr Lys Asp Ala Val Arg Ile Ala Ser
35      40      45
ccg gcg gtt gtg aac gtt tat aat cag gcg ttt act tct tcg tcc gcg      192
Pro Ala Val Val Asn Val Tyr Asn Gln Ala Phe Thr Ser Ser Ser Ala
50      55      60
caa ttg cag gtg aat aac ctc ggt tcg gcc gtg atc atg tca aaa gac      240
Gln Leu Gln Val Asn Asn Leu Gly Ser Gly Val Ile Met Ser Lys Asp
65      70      75      80
ggt tat att ctg acg aac aaa cac gtt att caa aat gcc gat caa att      288
    
```

-continued

---

Gly	Tyr	Ile	Leu	Thr	Asn	Lys	His	Val	Ile	Gln	Asn	Ala	Asp	Gln	Ile		
				85					90					95			
gta	gta	gcg	ttg	caa	aac	ggg	cat	att	ttt	gat	gcg	gcg	ctc	att	ggt		336
Val	Val	Ala	Leu	Gln	Asn	Gly	His	Ile	Phe	Asp	Ala	Ala	Leu	Ile	Gly		
			100					105					110				
tcc	gat	tct	tta	acg	gat	ttg	gca	gta	tta	aaa	att	aaa	gcg	gat	aat		384
Ser	Asp	Ser	Leu	Thr	Asp	Leu	Ala	Val	Leu	Lys	Ile	Lys	Ala	Asp	Asn		
		115				120						125					
tta	tcc	acg	att	ccg	caa	aat	ctc	agc	cgt	ccg	gtg	cat	gtg	gga	gat		432
Leu	Ser	Thr	Ile	Pro	Gln	Asn	Leu	Ser	Arg	Pro	Val	His	Val	Gly	Asp		
		130				135					140						
gtg	gcg	ctg	gca	atc	ggc	aat	ccg	tat	aac	ctg	ggg	caa	agc	gtg	t		478
Val	Ala	Leu	Ala	Ile	Gly	Asn	Pro	Tyr	Asn	Leu	Gly	Gln	Ser	Val			
145					150					155							

&lt;210&gt; SEQ ID NO 132

&lt;211&gt; LENGTH: 159

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 132

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

&lt;210&gt; SEQ ID NO 133

&lt;211&gt; LENGTH: 537

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(537)

&lt;400&gt; SEQUENCE: 133

gcc	ggc	tgg	cag	ata	aaa	aat	aac	aaa	cct	ttt	gac	ggt	aaa	gac	tgg		48
Ala	Gly	Trp	Gln	Ile	Lys	Asn	Asn	Lys	Pro	Phe	Asp	Gly	Lys	Asp	Trp		
1			5					10						15			
acc	cgt	tgg	gtc	gat	gcg	aga	gaa	tcc	gga	gcc	att	gcc	ggt	gca	gta		96
Thr	Arg	Trp	Val	Asp	Ala	Arg	Glu	Ser	Gly	Ala	Ile	Ala	Gly	Ala	Val		
		20					25						30				

-continued

gaa ttt aac aat tat gtc aat tct cat aaa ggc aaa atg ttc tat gtg	144
Glu Phe Asn Asn Tyr Val Asn Ser His Lys Gly Lys Met Phe Tyr Val	
35 40 45	
tca aat cgc aaa gac agt aat gaa aaa gca ggt acc att gat gac atg	192
Ser Asn Arg Lys Asp Ser Asn Glu Lys Ala Gly Thr Ile Asp Asp Met	
50 55 60	
aaa cgt tta ggc ttt acc ggt gtt gat gaa tca tcc ctt tat ctg aaa	240
Lys Arg Leu Gly Phe Thr Gly Val Asp Glu Ser Ser Leu Tyr Leu Lys	
65 70 75 80	
aaa gat aaa tcc gcc aaa tct gcc cgt ttt gca gaa att gaa agt caa	288
Lys Asp Lys Ser Ala Lys Ser Ala Arg Phe Ala Glu Ile Glu Ser Gln	
85 90 95	
ggc tat gac atc gtg ctt tat gta ggc gac aac ctg gat gat ttc ggt	336
Gly Tyr Asp Ile Val Leu Tyr Val Gly Asp Asn Leu Asp Asp Phe Gly	
100 105 110	
gat gca aca cac ggt aaa tta aat gcg gat cgt cga gac ttt gtt gct	384
Asp Ala Thr His Gly Lys Leu Asn Ala Asp Arg Arg Asp Phe Val Ala	
115 120 125	
aaa aac cag gcg aaa ttc ggt aaa act tat atc gtt tta cct aat ccg	432
Lys Asn Gln Ala Lys Phe Gly Lys Thr Tyr Ile Val Leu Pro Asn Pro	
130 135 140	
aat tac ggt ggt tgg gaa ggc ggt tta gcc aaa gac tac ttt aaa ggt	480
Asn Tyr Gly Gly Trp Glu Gly Gly Leu Ala Lys Asp Tyr Phe Lys Gly	
145 150 155 160	
gat tcc caa agc aaa gtt gat gcc cgc tta aat gta att aag gca tgg	528
Asp Ser Gln Ser Lys Val Asp Ala Arg Leu Asn Val Ile Lys Ala Trp	
165 170 175	
agt gga aaa	537
Ser Gly Lys	

<210> SEQ ID NO 134  
 <211> LENGTH: 179  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <400> SEQUENCE: 134

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

-continued

---

Asp Ser Gln Ser Lys Val Asp Ala Arg Leu Asn Val Ile Lys Ala Trp  
 165 170 175

Ser Gly Lys

<210> SEQ ID NO 135  
 <211> LENGTH: 765  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(765)

<400> SEQUENCE: 135

atg tgg ata ttt tac aac acc cgg aca ttc gtg ccg aat tac cgg ctt 48  
 Met Trp Ile Phe Tyr Asn Thr Arg Thr Phe Val Pro Asn Tyr Arg Leu  
 1 5 10 15

atg cca act ggc cga cat tcc cgc aat tat ggg tgg aag gcg agc tca 96  
 Met Pro Thr Gly Arg His Ser Arg Asn Tyr Gly Trp Lys Ala Ser Ser  
 20 25 30

tcg gtg gtt gcg aca tcg tgt tgg aaa tgt acc aac aag gtg agc tta 144  
 Ser Val Val Ala Thr Ser Cys Trp Lys Cys Thr Asn Lys Val Ser Leu  
 35 40 45

aaa cct tgt tac aag agg ttg ccg caa gac atc cgc aag cgt aaa aac 192  
 Lys Pro Cys Tyr Lys Arg Leu Pro Gln Asp Ile Arg Lys Arg Lys Asn  
 50 55 60

gcg ttt caa aat gac cgt act ttg gtt tcc gga gtg ccg ttt ttt gct 240  
 Ala Phe Gln Asn Asp Arg Thr Leu Val Ser Gly Val Arg Phe Phe Ala  
 65 70 75 80

gct tgg cgc agg gaa aaa cag gcg gtt tgt gct ata att ctc cgc aaa 288  
 Ala Trp Arg Arg Glu Lys Gln Ala Val Cys Ala Ile Ile Leu Arg Lys  
 85 90 95

ttt tta ccg cac ttt agg atc aat atg tcg ttt caa ttc aac gcg atc 336  
 Phe Leu Pro His Phe Arg Ile Asn Met Ser Phe Gln Phe Asn Ala Ile  
 100 105 110

gcc tta ctt ttg gtg att tta att tta tta ggt gta ctc agc cac aac 384  
 Ala Leu Leu Leu Val Ile Leu Ile Leu Leu Gly Val Leu Ser His Asn  
 115 120 125

agt tcc atc acc att tcc gct gcc gta ttg ctc atc atg caa caa acc 432  
 Ser Ser Ile Thr Ile Ser Ala Ala Val Leu Leu Ile Met Gln Gln Thr  
 130 135 140

ttg ctc gca aaa tat att cct tac ttg gaa aaa tac ggc ttg agc atc 480  
 Leu Leu Ala Lys Tyr Ile Pro Tyr Leu Glu Lys Tyr Gly Leu Ser Ile  
 145 150 155 160

ggt atc gta att tta acc atc ggc gta cta agc ccg ttg gtt tcc ggc 528  
 Gly Ile Val Ile Leu Thr Ile Gly Val Leu Ser Pro Leu Val Ser Gly  
 165 170 175

aga att caa ctg cct ggc ttg tcg gca ttt ttt agc tgg cga atg ttt 576  
 Arg Ile Gln Leu Pro Gly Leu Ser Ala Phe Phe Ser Trp Arg Met Phe  
 180 185 190

gtt gcc att ggc gtc ggc gta tta gtg gcg tgg ctt gcc ggc aaa ggc 624  
 Val Ala Ile Gly Val Gly Val Leu Val Ala Trp Leu Ala Gly Lys Gly  
 195 200 205

gtt ccg ctc atg ggg gaa gag cct gtt ctg gta acc ggc ttg gtt atc 672  
 Val Pro Leu Met Gly Glu Glu Pro Val Leu Val Thr Gly Leu Val Ile  
 210 215 220

ggc acc att atc ggc gtt tct ttt ctc ggt ggt att ccc gtt ggt ccc 720  
 Gly Thr Ile Ile Gly Val Ser Phe Leu Gly Gly Ile Pro Val Gly Pro  
 225 230 235 240



-continued

gtg act atc ggt gcg ttt gcg gcg cac ggt tta agc caa gtg ttg gac	96
Val Thr Ile Gly Ala Phe Ala Ala His Gly Leu Ser Gln Val Leu Asp	
20 25 30	
gcg aaa gcc tta gcg tgg att gac acc ggc gtg aaa tat caa atg ttc	144
Ala Lys Ala Leu Ala Trp Ile Asp Thr Gly Val Lys Tyr Gln Met Phe	
35 40 45	
cac acc ctc gcc atc atg gga atc ggc atc gca caa tta tgt cgc gaa	192
His Thr Leu Ala Ile Met Gly Ile Gly Ile Ala Gln Leu Cys Arg Glu	
50 55 60	
cca ttt gcc gcc aac aaa agc gcc aat gtt gcc gcc ggc gcg tgg tca	240
Pro Phe Ala Ala Asn Lys Ser Ala Asn Val Ala Ala Gly Ala Trp Ser	
65 70 75 80	
ttc gga atc ctt ctc ttt agc ggc agt tta tac gcc ctc gca ctt ggc	288
Phe Gly Ile Leu Leu Phe Ser Gly Ser Leu Tyr Ala Leu Ala Leu Gly	
85 90 95	
tca ggt aaa ttt atg gtt tgg ctc acg ccc atc ggc ggc acg cta ttt	336
Ser Gly Lys Phe Met Val Trp Leu Thr Pro Ile Gly Gly Thr Leu Phe	
100 105 110	
tta atc ggc tgg ctt ggt tta gct tac ggc gct ttc aaa agt aaa tca	384
Leu Ile Gly Trp Leu Gly Leu Ala Tyr Gly Ala Phe Lys Ser Lys Ser	
115 120 125	
gaa	387
Glu	

<210> SEQ ID NO 138  
 <211> LENGTH: 129  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 138

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

<210> SEQ ID NO 139  
 <211> LENGTH: 684  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(684)  
 <400> SEQUENCE: 139

-continued

---

```

atc aat ttg gca cat aat tat cag caa aaa tgg cag gcg gac atc ggt      48
Ile Asn Leu Ala His Asn Tyr Gln Gln Lys Trp Gln Ala Asp Ile Gly
1          5          10          15

cgg cac gcc gtg cag tat ttt gct tac gat aac ccg cgg gcg gat ttt      96
Arg His Ala Val Gln Tyr Phe Ala Tyr Asp Asn Pro Arg Ala Asp Phe
          20          25          30

tac gcc gaa caa att cat ttc tcc gaa caa ggc gcc tat ttc tta ctc      144
Tyr Ala Glu Gln Ile His Phe Ser Glu Gln Gly Ala Tyr Phe Leu Leu
          35          40          45

cac acg ccg caa ggc cgc gtg caa atc aat tca ccg tat ttg ggt gag      192
His Thr Pro Gln Gly Arg Val Gln Ile Asn Ser Pro Tyr Leu Gly Glu
          50          55          60

cat aat atc tct aat gcg ttg gcg gca act gcc ttg gcg atg aac gtg      240
His Asn Ile Ser Asn Ala Leu Ala Ala Thr Ala Leu Ala Met Asn Val
65          70          75          80

ggg gcc acc acg gcg cag gtg aaa aaa ggg ttg gaa acg ccc tct ttg      288
Gly Ala Thr Thr Ala Gln Val Lys Lys Gly Leu Glu Thr Pro Ser Leu
          85          90          95

gtg aaa ggg cgt ttg ttc ccg att cag cct tgt gaa aat ctg tta ttg      336
Val Lys Gly Arg Leu Phe Pro Ile Gln Pro Cys Glu Asn Leu Leu Leu
          100          105          110

ctg gac gat act tac aac gcc aat gtg gga tct atg aaa tcg gcg att      384
Leu Asp Thr Tyr Asn Ala Asn Val Gly Ser Met Lys Ser Ala Ile
          115          120          125

tcc gtg tta caa aaa tat cct gct ttt cgc gtc ttt gtt gtt ggt gat      432
Ser Val Leu Gln Lys Tyr Pro Ala Phe Arg Val Phe Val Val Gly Asp
          130          135          140

atg ggc gaa tta ggc gat aat gcg caa ctt tgc cat caa gag gtg ggg      480
Met Gly Glu Leu Gly Asp Asn Ala Gln Leu Cys His Gln Glu Val Gly
145          150          155          160

gag ttc gct cat gcc gcc aag tta gac tta gtg ctt tct ttc ggg tgt      528
Glu Phe Ala His Ala Ala Lys Leu Asp Leu Val Leu Ser Phe Gly Cys
          165          170          175

tcc agt ggc gtt ata agt gcg gtt aat tcg gga cgc cat ttt acc gat      576
Ser Ser Gly Val Ile Ser Ala Val Asn Ser Gly Arg His Phe Thr Asp
          180          185          190

aaa acg gaa ctt gta act tat tta aca ccg att att caa caa caa tta      624
Lys Thr Glu Leu Val Thr Tyr Leu Thr Pro Ile Ile Gln Gln Gln Leu
          195          200          205

gca caa caa aaa gtc gtt gtt ttg gtg aaa gga tca cgc agc atg aaa      672
Ala Gln Gln Lys Val Val Val Leu Val Lys Gly Ser Arg Ser Met Lys
          210          215          220

atg gaa gaa gtg
Met Glu Glu Val
225

```

&lt;210&gt; SEQ ID NO 140

&lt;211&gt; LENGTH: 228

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 140

```

Ile Asn Leu Ala His Asn Tyr Gln Gln Lys Trp Gln Ala Asp Ile Gly
1          5          10          15

Arg His Ala Val Gln Tyr Phe Ala Tyr Asp Asn Pro Arg Ala Asp Phe
          20          25          30

Tyr Ala Glu Gln Ile His Phe Ser Glu Gln Gly Ala Tyr Phe Leu Leu
          35          40          45

```

-continued

His Thr Pro Gln Gly Arg Val Gln Ile Asn Ser Pro Tyr Leu Gly Glu  
 50 55 60

His Asn Ile Ser Asn Ala Leu Ala Ala Thr Ala Leu Ala Met Asn Val  
 65 70 75 80

Gly Ala Thr Thr Ala Gln Val Lys Lys Gly Leu Glu Thr Pro Ser Leu  
 85 90 95

Val Lys Gly Arg Leu Phe Pro Ile Gln Pro Cys Glu Asn Leu Leu Leu  
 100 105 110

Leu Asp Asp Thr Tyr Asn Ala Asn Val Gly Ser Met Lys Ser Ala Ile  
 115 120 125

Ser Val Leu Gln Lys Tyr Pro Ala Phe Arg Val Phe Val Val Gly Asp  
 130 135 140

Met Gly Glu Leu Gly Asp Asn Ala Gln Leu Cys His Gln Glu Val Gly  
 145 150 155 160

Glu Phe Ala His Ala Ala Lys Leu Asp Leu Val Leu Ser Phe Gly Cys  
 165 170 175

Ser Ser Gly Val Ile Ser Ala Val Asn Ser Gly Arg His Phe Thr Asp  
 180 185 190

Lys Thr Glu Leu Val Thr Tyr Leu Thr Pro Ile Ile Gln Gln Leu  
 195 200 205

Ala Gln Gln Lys Val Val Val Leu Val Lys Gly Ser Arg Ser Met Lys  
 210 215 220

Met Glu Glu Val  
 225

<210> SEQ ID NO 141  
 <211> LENGTH: 267  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(267)

<400> SEQUENCE: 141

gat ggc ggt aag gcg ggt tcg agg tat gca ggt att atc tat aaa tct 48  
 Asp Gly Gly Lys Ala Gly Ser Arg Tyr Ala Gly Ile Ile Tyr Lys Ser  
 1 5 10 15

gtg aag cca tat ttt cgt ggt gat agt cgt ttt ttt ggt aag gtc tgt 96  
 Val Lys Pro Tyr Phe Arg Gly Asp Ser Arg Phe Phe Gly Lys Val Cys  
 20 25 30

gat att aga att gag ctt tct agt gat ggc act att tta tct tac caa 144  
 Asp Ile Arg Ile Glu Leu Ser Ser Asp Gly Thr Ile Leu Ser Tyr Gln  
 35 40 45

aag gtc tcc ggg cca aat gat tta tgt ggg gcg gct tta aat gct att 192  
 Lys Val Ser Gly Pro Asn Asp Leu Cys Gly Ala Ala Leu Asn Ala Ile  
 50 55 60

ggt caa acc aga aaa atg aac gaa ccg cct acg ccg gaa gaa tat gaa 240  
 Gly Gln Thr Arg Lys Met Asn Glu Pro Pro Thr Pro Glu Glu Tyr Glu  
 65 70 75 80

ata ttt aaa agg tcc att gta acc ttt 267  
 Ile Phe Lys Arg Ser Ile Val Thr Phe  
 85

<210> SEQ ID NO 142  
 <211> LENGTH: 89  
 <212> TYPE: PRT

-continued

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 142

```

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

```

&lt;210&gt; SEQ ID NO 143

&lt;211&gt; LENGTH: 683

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(681)

&lt;400&gt; SEQUENCE: 143

```

ggt gcc tta tat ttt gta ttc agt ctg atg ggc gtg ttc gcc agt ttg      48
Gly Ala Leu Tyr Phe Val Phe Ser Leu Met Gly Val Phe Ala Ser Leu
1           5           10           15
tta tcc acc gcg cgc ggc ggc tgg att ggt atc cct ttt gtt ctc ctg      96
Leu Ser Thr Ala Arg Gly Gly Trp Ile Gly Ile Pro Phe Val Leu Leu
                20           25           30
tta atc ctc ttt gct tat cgt cgt tat tta tcg aaa aaa ttc gtc gcc     144
Leu Ile Leu Phe Ala Tyr Arg Arg Tyr Leu Ser Lys Lys Phe Val Ala
                35           40           45
ggc ttt ttt att gtg ctt gcc ctg att gta aca acc gtt gcg atg ttg     192
Gly Phe Phe Ile Val Leu Ala Leu Ile Val Thr Thr Val Ala Met Leu
                50           55           60
cca aat acc aaa att aaa gaa cgc att gcc gcc gca gaa tac gac atc     240
Pro Asn Thr Lys Ile Lys Glu Arg Ile Ala Ala Ala Glu Tyr Asp Ile
65           70           75           80
atc gcc tat ttt caa caa aat aac ggt tct acc tcc gtc ggc gcc cgt     288
Ile Ala Tyr Phe Gln Gln Asn Asn Gly Ser Thr Ser Val Gly Ala Arg
                85           90           95
ttt gat atg tgg aaa agc gtg atg tta atg acg cag gaa aaa ccg att     336
Phe Asp Met Trp Lys Ser Val Met Leu Met Thr Gln Glu Lys Pro Ile
                100          105          110
ttc ggt tgg ggc gta caa ggg gtc agc gaa aaa cgc aaa ctg caa tat     384
Phe Gly Trp Gly Val Gln Gly Val Ser Glu Lys Arg Lys Leu Gln Tyr
                115          120          125
gag caa ggt ttg ata agc caa tat gcc gcc gcc ttt aac cac gcg cac     432
Glu Gln Gly Leu Ile Ser Gln Tyr Ala Ala Ala Phe Asn His Ala His
                130          135          140
aac caa tat ttt gat gat tta tcc aaa cgc ggc gca tta ggt tta ctc     480
Asn Gln Tyr Phe Asp Asp Leu Ser Lys Arg Gly Ala Leu Gly Leu Leu
145          150          155
gcc tta ctc ggc gta ttt tta gtg ccg ttg cgt ttc ttt ata cgg cat     528
Ala Leu Leu Gly Val Phe Leu Val Pro Leu Arg Phe Phe Ile Arg His
                165          170          175

```

-continued

```

ctc aaa agc gtc gat tta gaa ctg aaa ctc gtt tcg ttg tta ggt gcg      576
Leu Lys Ser Val Asp Leu Glu Leu Lys Leu Val Ser Leu Leu Gly Ala
      180                      185                      190

gtt cat att gtc tcc gtg atg ttc tac tgt ttc agc caa ggc ttt ttc      624
Val His Ile Val Ser Val Met Phe Tyr Cys Phe Ser Gln Gly Phe Phe
      195                      200                      205

agc cat aac tcg ggc aat att ttc tat ttt ttc ccg gtg att gtg ttt      672
Ser His Asn Ser Gly Asn Ile Phe Tyr Phe Phe Pro Val Ile Val Phe
      210                      215                      220

tac gcc ttg gt      683
Tyr Ala Leu
225

```

```

<210> SEQ ID NO 144
<211> LENGTH: 227
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 144

```

```

Gly Ala Leu Tyr Phe Val Phe Ser Leu Met Gly Val Phe Ala Ser Leu
 1      5      10      15

Leu Ser Thr Ala Arg Gly Gly Trp Ile Gly Ile Pro Phe Val Leu Leu
 20     25     30

Leu Ile Leu Phe Ala Tyr Arg Arg Tyr Leu Ser Lys Lys Phe Val Ala
 35     40     45

Gly Phe Phe Ile Val Leu Ala Leu Ile Val Thr Thr Val Ala Met Leu
 50     55     60

Pro Asn Thr Lys Ile Lys Glu Arg Ile Ala Ala Ala Glu Tyr Asp Ile
 65     70     75     80

Ile Ala Tyr Phe Gln Gln Asn Asn Gly Ser Thr Ser Val Gly Ala Arg
 85     90     95

Phe Asp Met Trp Lys Ser Val Met Leu Met Thr Gln Glu Lys Pro Ile
100    105    110

Phe Gly Trp Gly Val Gln Gly Val Ser Glu Lys Arg Lys Leu Gln Tyr
115    120    125

Glu Gln Gly Leu Ile Ser Gln Tyr Ala Ala Ala Phe Asn His Ala His
130    135    140

Asn Gln Tyr Phe Asp Asp Leu Ser Lys Arg Gly Ala Leu Gly Leu Leu
145    150    155    160

Ala Leu Leu Gly Val Phe Leu Val Pro Leu Arg Phe Phe Ile Arg His
165    170    175

Leu Lys Ser Val Asp Leu Glu Leu Lys Leu Val Ser Leu Leu Gly Ala
180    185    190

Val His Ile Val Ser Val Met Phe Tyr Cys Phe Ser Gln Gly Phe Phe
195    200    205

Ser His Asn Ser Gly Asn Ile Phe Tyr Phe Phe Pro Val Ile Val Phe
210    215    220

Tyr Ala Leu
225

```

```

<210> SEQ ID NO 145
<211> LENGTH: 408
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:

```

-continued

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(408)

&lt;400&gt; SEQUENCE: 145

```

gcc gat tat ggc atc gac tat ggt aac gat ttc gta ggt atc att gaa      48
Ala Asp Tyr Gly Ile Asp Tyr Gly Asn Asp Phe Val Gly Ile Ile Glu
1           5           10           15

gga aaa ttg aag tta aac aaa tca acg tta cat gat aat aac gcc tcc      96
Gly Lys Leu Lys Leu Asn Lys Ser Thr Leu His Asp Asn Asn Ala Ser
           20           25           30

ggc tac cgt ggc aaa ctg aac gaa aag gca cgt ttg ggc gta agt tac      144
Gly Tyr Arg Gly Lys Leu Asn Glu Lys Ala Arg Leu Gly Val Ser Tyr
           35           40           45

tta caa ggc tat cgc gta aca cca agc att ctt cct tat gcc aaa gtt      192
Leu Gln Gly Tyr Arg Val Thr Pro Ser Ile Leu Pro Tyr Ala Lys Val
           50           55           60

ggg gtg caa act gct aaa ttt gaa agt gag gtt cgt aca cgc aac tac      240
Gly Val Gln Thr Ala Lys Phe Glu Ser Glu Val Arg Thr Arg Asn Tyr
           65           70           75           80

tca gct acg cat agt gat acc aaa aac ggt ata ggt ttt ggt gcg ggt      288
Ser Ala Thr His Ser Asp Thr Lys Asn Gly Ile Gly Phe Gly Ala Gly
           85           90           95

gtt aag gtc aat ctg gta ccg gac ttt gag cta agc ttg gaa tat tta      336
Val Lys Val Asn Leu Val Pro Asp Phe Glu Leu Ser Leu Glu Tyr Leu
           100          105          110

agg act cat aac aaa ttt gat ggt caa aag tta aga ggt aat gta tat      384
Arg Thr His Asn Lys Phe Asp Gly Gln Lys Leu Arg Gly Asn Val Tyr
           115          120          125

agc acc aac gct aca tat cgt ttc      408
Ser Thr Asn Ala Thr Tyr Arg Phe
           130          135

```

&lt;210&gt; SEQ ID NO 146

&lt;211&gt; LENGTH: 136

&lt;212&gt; TYPE: PRT

<213> ORGANISM: *Actinobacillus actinomycetemcomitans*

&lt;400&gt; SEQUENCE: 146

```

Ala Asp Tyr Gly Ile Asp Tyr Gly Asn Asp Phe Val Gly Ile Ile Glu
1           5           10           15

Gly Lys Leu Lys Leu Asn Lys Ser Thr Leu His Asp Asn Asn Ala Ser
           20           25           30

Gly Tyr Arg Gly Lys Leu Asn Glu Lys Ala Arg Leu Gly Val Ser Tyr
           35           40           45

Leu Gln Gly Tyr Arg Val Thr Pro Ser Ile Leu Pro Tyr Ala Lys Val
           50           55           60

Gly Val Gln Thr Ala Lys Phe Glu Ser Glu Val Arg Thr Arg Asn Tyr
           65           70           75           80

Ser Ala Thr His Ser Asp Thr Lys Asn Gly Ile Gly Phe Gly Ala Gly
           85           90           95

Val Lys Val Asn Leu Val Pro Asp Phe Glu Leu Ser Leu Glu Tyr Leu
           100          105          110

Arg Thr His Asn Lys Phe Asp Gly Gln Lys Leu Arg Gly Asn Val Tyr
           115          120          125

Ser Thr Asn Ala Thr Tyr Arg Phe
           130          135

```

-continued

```

<210> SEQ ID NO 147
<211> LENGTH: 426
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(426)

<400> SEQUENCE: 147

atg aaa aaa att ctt acc gca ctt ttt tgc agt tgt ctc att tcc cct      48
Met Lys Lys Ile Leu Thr Ala Leu Phe Cys Ser Cys Leu Ile Ser Pro
1          5          10          15

ctc aca aac gct gaa acc ttg tct gat ggt tta cca cca cag gca gct      96
Leu Thr Asn Ala Glu Thr Leu Ser Asp Gly Leu Pro Pro Gln Ala Ala
20          25          30

ggt gat tat gtg ttc ttg gac ccg cat caa aac aat acg gat ata caa     144
Gly Asp Tyr Val Phe Leu Asp Pro His Gln Asn Asn Thr Asp Ile Gln
35          40          45

ttt cgt tta aaa ctt aaa ggc aaa caa tgg ctg gca gac ggt tcc caa     192
Phe Arg Leu Lys Leu Lys Gly Lys Gln Trp Leu Ala Asp Gly Ser Gln
50          55          60

aat gcc ggc aaa agc tgg tcg cct gtg tgc gaa gtc agt ggc gaa tgc     240
Asn Ala Gly Lys Ser Trp Ser Pro Val Cys Glu Val Ser Gly Glu Cys
65          70          75          80

aaa ctg gag aca tcc tcc aaa gcg gaa atc gaa cgc ttc ttt gag caa     288
Lys Leu Glu Thr Ser Ser Lys Ala Glu Ile Glu Arg Phe Phe Glu Gln
85          90          95

tat ccg caa gta cta aac cga aca gat gtc agc tgc att cac aat atg     336
Tyr Pro Gln Val Leu Asn Arg Thr Asp Val Ser Cys Ile His Asn Met
100         105         110

gcg ttc gct ttc tgc ggg tta act tta gat aaa aaa acc gat tat gtg     384
Ala Phe Ala Phe Cys Gly Leu Thr Leu Asp Lys Lys Thr Asp Tyr Val
115         120         125

atg gtc gca tta gtg acc aat ccg cca caa gtc aca tcg tat             426
Met Val Ala Leu Val Thr Asn Pro Pro Gln Val Thr Ser Tyr
130         135         140

```

```

<210> SEQ ID NO 148
<211> LENGTH: 142
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 148

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

Leu Thr Asn Ala Glu Thr Leu Ser Asp Gly Leu Pro Pro Gln Ala Ala
20          25          30

Gly Asp Tyr Val Phe Leu Asp Pro His Gln Asn Asn Thr Asp Ile Gln
35          40          45

Phe Arg Leu Lys Leu Lys Gly Lys Gln Trp Leu Ala Asp Gly Ser Gln
50          55          60

Asn Ala Gly Lys Ser Trp Ser Pro Val Cys Glu Val Ser Gly Glu Cys
65          70          75          80

Lys Leu Glu Thr Ser Ser Lys Ala Glu Ile Glu Arg Phe Phe Glu Gln
85          90          95

Tyr Pro Gln Val Leu Asn Arg Thr Asp Val Ser Cys Ile His Asn Met
100         105         110

```

-continued

---

Ala Phe Ala Phe Cys Gly Leu Thr Leu Asp Lys Lys Thr Asp Tyr Val  
 115 120 125

Met Val Ala Leu Val Thr Asn Pro Pro Gln Val Thr Ser Tyr  
 130 135 140

<210> SEQ ID NO 149  
 <211> LENGTH: 679  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(678)

<400> SEQUENCE: 149

cgc cga att att ggc aca acg aca aca gga tat tca cta atg cgc gca 48  
 Arg Arg Ile Ile Gly Thr Thr Thr Thr Gly Tyr Ser Leu Met Arg Ala  
 1 5 10 15

tta ttg cct ttt ctt cgt tta ttt aaa ttc gcc aaa ctg ccg tta att 96  
 Leu Leu Pro Phe Leu Arg Leu Phe Lys Phe Ala Lys Leu Pro Leu Ile  
 20 25 30

tta ggc ggc ttg ctg atg att tta ggg ctg gcg tcc agt atc ggg ttg 144  
 Leu Gly Gly Leu Leu Met Ile Leu Gly Leu Ala Ser Ser Ile Gly Leu  
 35 40 45

ctc acc ctt tcc ggc tgg ttt ctt gcc gcc acc gcc atc gcc ggt ttc 192  
 Leu Thr Leu Ser Gly Trp Phe Leu Ala Ala Thr Ala Ile Ala Gly Phe  
 50 55 60

ggc tcg cta ttt aac ttt ttc tac cca tcc gcc agc gta cgc ggt ttg 240  
 Gly Ser Leu Phe Asn Phe Phe Tyr Pro Ser Ala Ser Val Arg Gly Leu  
 65 70 75 80

gca atc ggg cgt acc gtg gcg cgc tac ctt gaa aaa gtg gtc acc cat 288  
 Ala Ile Gly Arg Thr Val Ala Arg Tyr Leu Glu Lys Val Val Thr His  
 85 90 95

gac gcc acc ttc cgc gta ttg gca aaa ctg cgt gtg cag gtg ttt gac 336  
 Asp Ala Thr Phe Arg Val Leu Ala Lys Leu Arg Val Gln Val Phe Asp  
 100 105 110

aaa atc att ccg tta agc cct gcg ctg ctc aac cgt tat cgt aac agc 384  
 Lys Ile Ile Pro Leu Ser Pro Ala Leu Leu Asn Arg Tyr Arg Asn Ser  
 115 120 125

gat tta tta aac cgc ttg gtt gcc gat gtg gac acc ctc gac agc cta 432  
 Asp Leu Leu Asn Arg Leu Val Ala Asp Val Asp Thr Leu Asp Ser Leu  
 130 135 140

tat ctt cgc ctc att gcg ccc ttt atc agc gcc ata gtg gtg att gcg 480  
 Tyr Leu Arg Leu Ile Ala Pro Phe Ile Ser Ala Ile Val Val Ile Ala  
 145 150 155 160

ttc att acc ttt ggc ttg agt ttt att aat gcc ccg ctc gcg ctg ttt 528  
 Phe Ile Thr Phe Gly Leu Ser Phe Ile Asn Ala Pro Leu Ala Leu Phe  
 165 170 175

atc ggt ttc aca tta ctg gcg ctc ttg ctg gtt atc ccg acg att ttt 576  
 Ile Gly Phe Thr Leu Leu Ala Leu Leu Leu Val Ile Pro Thr Ile Phe  
 180 185 190

tac cat ttg ggt aac aaa ttc ggc gcc aaa ctt acc caa tcc cgc gcc 624  
 Tyr His Leu Gly Asn Lys Phe Gly Ala Lys Leu Thr Gln Ser Arg Ala  
 195 200 205

ctt tac cgc acg caa ttt atc gaa ttt att cag gcg caa gcg gaa tta 672  
 Leu Tyr Arg Thr Gln Phe Ile Glu Phe Ile Gln Ala Gln Ala Glu Leu  
 210 215 220

ttg ctg t 679  
 Leu Leu  
 225

-continued

```

<210> SEQ ID NO 150
<211> LENGTH: 226
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<400> SEQUENCE: 150
Arg Arg Ile Ile Gly Thr Thr Thr Thr Gly Tyr Ser Leu Met Arg Ala
1          5          10          15
Leu Leu Pro Phe Leu Arg Leu Phe Lys Phe Ala Lys Leu Pro Leu Ile
20          25          30
Leu Gly Gly Leu Leu Met Ile Leu Gly Leu Ala Ser Ser Ile Gly Leu
35          40          45
Leu Thr Leu Ser Gly Trp Phe Leu Ala Ala Thr Ala Ile Ala Gly Phe
50          55          60
Gly Ser Leu Phe Asn Phe Phe Tyr Pro Ser Ala Ser Val Arg Gly Leu
65          70          75          80
Ala Ile Gly Arg Thr Val Ala Arg Tyr Leu Glu Lys Val Val Thr His
85          90          95
Asp Ala Thr Phe Arg Val Leu Ala Lys Leu Arg Val Gln Val Phe Asp
100         105         110
Lys Ile Ile Pro Leu Ser Pro Ala Leu Leu Asn Arg Tyr Arg Asn Ser
115         120         125
Asp Leu Leu Asn Arg Leu Val Ala Asp Val Asp Thr Leu Asp Ser Leu
130         135         140
Tyr Leu Arg Leu Ile Ala Pro Phe Ile Ser Ala Ile Val Val Ile Ala
145         150         155         160
Phe Ile Thr Phe Gly Leu Ser Phe Ile Asn Ala Pro Leu Ala Leu Phe
165         170         175
Ile Gly Phe Thr Leu Leu Ala Leu Leu Leu Val Ile Pro Thr Ile Phe
180         185         190
Tyr His Leu Gly Asn Lys Phe Gly Ala Lys Leu Thr Gln Ser Arg Ala
195         200         205
Leu Tyr Arg Thr Gln Phe Ile Glu Phe Ile Gln Ala Gln Ala Glu Leu
210         215         220
Leu Leu
225

```

```

<210> SEQ ID NO 151
<211> LENGTH: 323
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(321)
<400> SEQUENCE: 151
cct tcc aaa ttg acg tta gct ctt gct att gca agt ggc tta agt gta      48
Pro Ser Lys Leu Thr Leu Ala Leu Ala Ile Ala Ser Gly Leu Ser Val
1          5          10          15
aca aat tta agc tat gcc act aac gat act att caa gcg ggc aac ggc      96
Thr Asn Leu Ser Tyr Ala Thr Asn Asp Thr Ile Gln Ala Gly Asn Gly
20          25          30
att gcc gtg gta caa acc caa tcg ggt gaa atc caa ggt tat att cat      144
Ile Ala Val Val Gln Thr Gln Ser Gly Glu Ile Gln Gly Tyr Ile His
35          40          45

```

-continued

aac gat att ttg acc tat aaa ggc att ccg tat gcc aca gca gaa cgt 192  
 Asn Asp Ile Leu Thr Tyr Lys Gly Ile Pro Tyr Ala Thr Ala Glu Arg  
 50 55 60

ttt atg cca cca aaa ccg gtg gag aat tgg caa ggg aca aaa atg gcg 240  
 Phe Met Pro Pro Lys Pro Val Glu Asn Trp Gln Gly Thr Lys Met Ala  
 65 70 75 80

ttg act tat ggc gat gtc tgc ccg caa gtg ccg atg ggc ggt cgt agt 288  
 Leu Thr Tyr Gly Asp Val Cys Pro Gln Val Pro Met Gly Gly Arg Ser  
 85 90 95

ttc ttc ttt acc gga cct gaa atg acg gaa agt ga 323  
 Phe Phe Phe Thr Gly Pro Glu Met Thr Glu Ser  
 100 105

&lt;210&gt; SEQ ID NO 152

&lt;211&gt; LENGTH: 107

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 152

Pro Ser Lys Leu Thr Leu Ala Leu Ala Ile Ala Ser Gly Leu Ser Val  
 1 5 10 15

Thr Asn Leu Ser Tyr Ala Thr Asn Asp Thr Ile Gln Ala Gly Asn Gly  
 20 25 30

Ile Ala Val Val Gln Thr Gln Ser Gly Glu Ile Gln Gly Tyr Ile His  
 35 40 45

Asn Asp Ile Leu Thr Tyr Lys Gly Ile Pro Tyr Ala Thr Ala Glu Arg  
 50 55 60

Phe Met Pro Pro Lys Pro Val Glu Asn Trp Gln Gly Thr Lys Met Ala  
 65 70 75 80

Leu Thr Tyr Gly Asp Val Cys Pro Gln Val Pro Met Gly Gly Arg Ser  
 85 90 95

Phe Phe Phe Thr Gly Pro Glu Met Thr Glu Ser  
 100 105

&lt;210&gt; SEQ ID NO 153

&lt;211&gt; LENGTH: 177

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(177)

&lt;400&gt; SEQUENCE: 153

ggc ggc ggt gcc tgg gtt cag gcg gat ttg aag atg ttc caa atg cac 48  
 Gly Gly Gly Ala Trp Val Gln Ala Asp Leu Lys Met Phe Gln Met His  
 1 5 10 15

agg atg tcg ttt ggt tca tcg gtg gcc gcg caa aat acc ttg aac gtg 96  
 Arg Met Ser Phe Gly Ser Ser Val Ala Ala Gln Asn Thr Leu Asn Val  
 20 25 30

ggt gat att tac gcc gtg tca ctc aaa acc atc caa tgt cag ctg aaa 144  
 Val Asp Ile Tyr Ala Val Ser Leu Lys Thr Ile Gln Cys Gln Leu Lys  
 35 40 45

gcc att gtg aca gat ttt gat att tcg cac ctt 177  
 Ala Ile Val Thr Asp Phe Asp Ile Ser His Leu  
 50 55

&lt;210&gt; SEQ ID NO 154

&lt;211&gt; LENGTH: 59

-continued

---

```

<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 154
Gly Gly Gly Ala Trp Val Gln Ala Asp Leu Lys Met Phe Gln Met His
1      5      10      15
Arg Met Ser Phe Gly Ser Ser Val Ala Ala Gln Asn Thr Leu Asn Val
20     25     30
Val Asp Ile Tyr Ala Val Ser Leu Lys Thr Ile Gln Cys Gln Leu Lys
35     40     45
Ala Ile Val Thr Asp Phe Asp Ile Ser His Leu
50     55

<210> SEQ ID NO 155
<211> LENGTH: 469
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(468)

<400> SEQUENCE: 155
atg gag aaa aaa caa acc tca cgg gta caa aaa ctg gaa ttt ttg ctc      48
Met Glu Lys Lys Gln Thr Ser Arg Val Gln Lys Leu Glu Phe Leu Leu
1      5      10     15
aaa caa aca gat aaa atc cat ctg cgc gac gcg gca caa atg ctt gat      96
Lys Gln Thr Asp Lys Ile His Leu Arg Asp Ala Ala Gln Met Leu Asp
20     25     30
gtg tcg gaa atg act tta cgt cgg gat tta agt tcc gac agc ggc aat      144
Val Ser Glu Met Thr Leu Arg Arg Asp Leu Ser Ser Asp Ser Gly Asn
35     40     45
gtg gtg tta ttg ggc ggc tat atc gtg atg aac cca caa aaa agc ggc      192
Val Val Leu Leu Gly Gly Tyr Ile Val Met Asn Pro Gln Lys Ser Gly
50     55     60
aat cat tat cag att ttt gac caa caa acg cgc cac att acg gaa aaa      240
Asn His Tyr Gln Ile Phe Asp Gln Gln Thr Arg His Ile Thr Glu Lys
65     70     75     80
atg tgg ctc ggt aaa ctc gcc gcc aat ctc gtc aag gac gga gat acc      288
Met Trp Leu Gly Lys Leu Ala Ala Asn Leu Val Lys Asp Gly Asp Thr
85     90     95
gtg ttc ttc gat tgc ggt agc acc att ccg ttt atc att tcg caa atc      336
Val Phe Phe Asp Cys Gly Ser Thr Ile Pro Phe Ile Ile Ser Gln Ile
100    105    110
gat ccg cag ata aaa ttc acc gca ctt ttt tgc tcc atc aat agt ttt      384
Asp Pro Gln Ile Lys Phe Thr Ala Leu Phe Cys Ser Ile Asn Ser Phe
115    120    125
atg gcg ttg cag gac aaa ccg cac tgc gaa gtg att ctg tgc ggc gga      432
Met Ala Leu Gln Asp Lys Pro His Cys Glu Val Ile Leu Cys Gly Gly
130    135    140
cat tat tcg cgc cac aat tct ttc ctg act tcc gtg c      469
His Tyr Ser Arg His Asn Ser Phe Leu Thr Ser Val
145    150    155

<210> SEQ ID NO 156
<211> LENGTH: 156
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 156

```

-continued

```

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

```

```

<210> SEQ ID NO 157
<211> LENGTH: 340
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(339)

```

```

<400> SEQUENCE: 157
atg aca tat cca ggt gga aaa ggt aaa tgt ttc caa aaa atc att aat      48
Met Thr Tyr Pro Gly Gly Lys Gly Lys Cys Phe Gln Lys Ile Ile Asn
1      5      10      15
tta atg cct ccg cat gac gta tat att gaa act cat ctt ggt agt ggt      96
Leu Met Pro Pro His Asp Val Tyr Ile Glu Thr His Leu Gly Ser Gly
20     25     30
gca gta cta cga aat aaa aaa cca gca cta aaa aat att gga ata gat      144
Ala Val Leu Arg Asn Lys Lys Pro Ala Leu Lys Asn Ile Gly Ile Asp
35     40     45
cta gat ttt gat gtt att caa tca tgg att ggt tat tct cct gaa aat      192
Leu Asp Phe Asp Val Ile Gln Ser Trp Ile Gly Tyr Ser Pro Glu Asn
50     55     60
cat aag ttt ttt aat aat gat gca ttg gcg ttt cta act aag tac ctg      240
His Lys Phe Phe Asn Asn Asp Ala Leu Ala Phe Leu Thr Lys Tyr Leu
65     70     75     80
ttt act ggg aaa gag tta gta tat tgt gat cct cca tat gtt ctt tca      288
Phe Thr Gly Lys Glu Leu Val Tyr Cys Asp Pro Pro Tyr Val Leu Ser
85     90     95
act aga aga aga caa aaa ata tat aaa tat gaa tac act gat gag cag      336
Thr Arg Arg Arg Gln Lys Ile Tyr Lys Tyr Glu Tyr Thr Asp Glu Gln
100    105    110
cat g
His
340

```

```

<210> SEQ ID NO 158
<211> LENGTH: 113
<212> TYPE: PRT

```

-continued

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 158

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

His

&lt;210&gt; SEQ ID NO 159

&lt;211&gt; LENGTH: 771

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(771)

&lt;400&gt; SEQUENCE: 159

atc gac gct ttt ttc tct cgc caa aac aat caa ttt cac ttg gaa caa 48  
 Ile Asp Ala Phe Phe Ser Arg Gln Asn Asn Gln Phe His Leu Glu Gln  
 1 5 10 15  
 caa agc cat tgc gtt aac caa att atc gag caa tgg cgt tat aac ggg 96  
 Gln Ser His Cys Val Asn Gln Ile Ile Glu Gln Trp Arg Tyr Asn Gly  
 20 25 30  
 caa att atc ggg cgt gaa att ccg caa ttt gtc gcc gaa cag aaa aac 144  
 Gln Ile Ile Gly Arg Glu Ile Pro Gln Phe Val Ala Glu Gln Lys Asn  
 35 40 45  
 caa caa ggc ttg gca gtg cgt gtc acc tgc ccc gag caa acc tct ctt 192  
 Gln Gln Gly Leu Ala Val Arg Val Thr Cys Pro Glu Gln Thr Ser Leu  
 50 55 60  
 tta gcg gaa ttt aac aat caa ccg gtg aac gat gcc ctt caa acg gca 240  
 Leu Ala Glu Phe Asn Asn Gln Pro Val Asn Asp Ala Leu Gln Thr Ala  
 65 70 75 80  
 gaa aag tgc ggt gta tct ttt gag agt ttt cat att gtg gcg gaa gat 288  
 Glu Lys Cys Gly Val Ser Phe Glu Ser Phe His Ile Val Ala Glu Asp  
 85 90 95  
 ctc aat tct gaa atc acc gcc acg gaa aca ccc gct tgg caa ctg ctc 336  
 Leu Asn Ser Glu Ile Thr Ala Thr Glu Thr Pro Ala Trp Gln Leu Leu  
 100 105 110  
 tac acc acc tat ttg cag tct tgt tct ccc ctg caa agc ggt gaa tcc 384  
 Tyr Thr Thr Tyr Leu Gln Ser Cys Ser Pro Leu Gln Ser Gly Glu Ser  
 115 120 125  
 ctg caa ccg att ccg ctg tat aaa caa ctg aaa aac ata ccg cac tta 432  
 Leu Gln Pro Ile Pro Leu Tyr Lys Gln Leu Lys Asn Ile Pro His Leu  
 130 135 140  
 gca atg gat ttg gtt aaa tgg cag gaa aat tgg cag gcg tgc gat caa 480  
 Ala Met Asp Leu Val Lys Trp Gln Glu Asn Trp Gln Ala Cys Asp Gln

-continued

145	150	155	160	
ttg caa atg aac ggt tcc gtg ttg gaa caa cag gct ttg gtg caa att				528
Leu Gln Met Asn Gly Ser Val Leu Glu Gln Gln Ala Leu Val Gln Ile	165	170	175	
tca gac acc caa agc acg ctg ttt aag cat ggt tac cat cta acg cag				576
Ser Asp Thr Gln Ser Thr Leu Phe Lys His Gly Tyr His Leu Thr Gln	180	185	190	
gaa att gag cga cac agc ggc att cct act tac tat tat tta tac cgc				624
Glu Ile Glu Arg His Ser Gly Ile Pro Thr Tyr Tyr Tyr Leu Tyr Arg	195	200	205	
atc ggt gga aaa agc tgt gaa gcg gag ctg caa tca cgc tgt ccg tta				672
Ile Gly Gly Lys Ser Cys Glu Ala Glu Leu Gln Ser Arg Cys Pro Leu	210	215	220	
tgt aaa aga aaa tgg acg tta agc cac ccg ctt ttt gac ttc tta tat				720
Cys Lys Arg Lys Trp Thr Leu Ser His Pro Leu Phe Asp Phe Leu Tyr	225	230	235	240
ttt aaa tgt gat cat tgt cgc ctc gtt tca aac ctc tca tgg cat tgg				768
Phe Lys Cys Asp His Cys Arg Leu Val Ser Asn Leu Ser Trp His Trp	245	250	255	
caa				771
Gln				
<210> SEQ ID NO 160				
<211> LENGTH: 257				
<212> TYPE: PRT				
<213> ORGANISM: Actinobacillus actinomycetemcomitans				
<400> SEQUENCE: 160				
Ile Asp Ala Phe Phe Ser Arg Gln Asn Asn Gln Phe His Leu Glu Gln				
1	5	10	15	
Gln Ser His Cys Val Asn Gln Ile Ile Glu Gln Trp Arg Tyr Asn Gly				
	20	25	30	
Gln Ile Ile Gly Arg Glu Ile Pro Gln Phe Val Ala Glu Gln Lys Asn				
	35	40	45	
Gln Gln Gly Leu Ala Val Arg Val Thr Cys Pro Glu Gln Thr Ser Leu				
	50	55	60	
Leu Ala Glu Phe Asn Asn Gln Pro Val Asn Asp Ala Leu Gln Thr Ala				
65	70	75	80	
Glu Lys Cys Gly Val Ser Phe Glu Ser Phe His Ile Val Ala Glu Asp				
	85	90	95	
Leu Asn Ser Glu Ile Thr Ala Thr Glu Thr Pro Ala Trp Gln Leu Leu				
	100	105	110	
Tyr Thr Thr Tyr Leu Gln Ser Cys Ser Pro Leu Gln Ser Gly Glu Ser				
	115	120	125	
Leu Gln Pro Ile Pro Leu Tyr Lys Gln Leu Lys Asn Ile Pro His Leu				
	130	135	140	
Ala Met Asp Leu Val Lys Trp Gln Glu Asn Trp Gln Ala Cys Asp Gln				
145	150	155	160	
Leu Gln Met Asn Gly Ser Val Leu Glu Gln Gln Ala Leu Val Gln Ile				
	165	170	175	
Ser Asp Thr Gln Ser Thr Leu Phe Lys His Gly Tyr His Leu Thr Gln				
	180	185	190	
Glu Ile Glu Arg His Ser Gly Ile Pro Thr Tyr Tyr Tyr Leu Tyr Arg				
	195	200	205	

-continued

---

```

Ile Gly Gly Lys Ser Cys Glu Ala Glu Leu Gln Ser Arg Cys Pro Leu
 210                215                220

Cys Lys Arg Lys Trp Thr Leu Ser His Pro Leu Phe Asp Phe Leu Tyr
225                230                235                240

Phe Lys Cys Asp His Cys Arg Leu Val Ser Asn Leu Ser Trp His Trp
                245                250                255

```

Gln

```

<210> SEQ ID NO 161
<211> LENGTH: 330
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(330)

```

&lt;400&gt; SEQUENCE: 161

```

gag gcg gat aaa ttt aaa gtg gat att ccg tct atg gca aga ctg aga      48
Glu Ala Asp Lys Phe Lys Val Asp Ile Pro Ser Met Ala Arg Leu Arg
1                    5                    10                    15

atc agc ccg aat atc gac atc agt gcg aca ccg aag ctg ttg gaa ctt      96
Ile Ser Pro Asn Ile Asp Ile Ser Ala Thr Pro Lys Leu Leu Glu Leu
                20                    25                    30

tcc ggc aat att gat att ccc tgg gcg cgc att gcc att gaa aac ctg     144
Ser Gly Asn Ile Asp Ile Pro Trp Ala Arg Ile Ala Ile Glu Asn Leu
                35                    40                    45

ccg gac agt gca gtg gcg gtc agc tcc gat gaa gtg att tta aat ggc     192
Pro Asp Ser Ala Val Ala Val Ser Ser Asp Glu Val Ile Leu Asn Gly
                50                    55                    60

aat aag aag agt act ctg ccg aaa aca ttg ccg agc gaa acc caa agc     240
Asn Lys Lys Ser Thr Leu Pro Lys Thr Leu Pro Ser Glu Thr Gln Ser
65                70                    75                    80

ggc atg gca att cgt tct gat tta aga atc aat atc ggc gat gat gtc     288
Gly Met Ala Ile Arg Ser Asp Leu Arg Ile Asn Ile Gly Asp Asp Val
                85                    90                    95

agt tta aat gcc tat ggc ttg aaa acc cat ctc cac ggg ttg           330
Ser Leu Asn Ala Tyr Gly Leu Lys Thr His Leu His Gly Leu
                100                105                110

```

```

<210> SEQ ID NO 162
<211> LENGTH: 110
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

&lt;400&gt; SEQUENCE: 162

```

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

Ile Ser Pro Asn Ile Asp Ile Ser Ala Thr Pro Lys Leu Leu Glu Leu
                20                    25                    30

Ser Gly Asn Ile Asp Ile Pro Trp Ala Arg Ile Ala Ile Glu Asn Leu
                35                    40                    45

Pro Asp Ser Ala Val Ala Val Ser Ser Asp Glu Val Ile Leu Asn Gly
                50                    55                    60

Asn Lys Lys Ser Thr Leu Pro Lys Thr Leu Pro Ser Glu Thr Gln Ser
65                70                    75                    80

Gly Met Ala Ile Arg Ser Asp Leu Arg Ile Asn Ile Gly Asp Asp Val
                85                    90                    95

```

-continued

---

Ser Leu Asn Ala Tyr Gly Leu Lys Thr His Leu His Gly Leu  
 100 105 110

<210> SEQ ID NO 163  
 <211> LENGTH: 625  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(624)

<400> SEQUENCE: 163

gat aag aca gaa acg atg caa caa aat gaa gaa aaa atc acg ccg tca 48  
 Asp Lys Thr Glu Thr Met Gln Gln Asn Glu Glu Lys Ile Thr Pro Ser  
 1 5 10 15

gag caa aaa ccg atc gtg cat gaa acc gtt gtg gtg aag aaa acc ggt 96  
 Glu Gln Lys Pro Ile Val His Glu Thr Val Val Val Lys Lys Thr Gly  
 20 25 30

tcc gcg tta ggt ttg ctg gca ctt tta att gcg ttg ggt tta ggc ggc 144  
 Ser Ala Leu Gly Leu Leu Ala Leu Leu Ile Ala Leu Gly Leu Gly Gly  
 35 40 45

gcg ggc tat tat ttc ggt cag cta cag gtt gac gaa ata cag caa aaa 192  
 Ala Gly Tyr Tyr Phe Gly Gln Leu Gln Val Asp Glu Ile Gln Gln Lys  
 50 55 60

ctg acc gca ctt gaa aac caa ttg caa caa aaa ggc act tcc gcc gat 240  
 Leu Thr Ala Leu Glu Asn Gln Leu Gln Gln Lys Gly Thr Ser Ala Asp  
 65 70 75 80

gtt gcc ggc atg ccg gat ttt agt gca gag aaa aat cag ctg gcg aaa 288  
 Val Ala Gly Met Pro Asp Phe Ser Ala Glu Lys Asn Gln Leu Ala Lys  
 85 90 95

tta acg gaa ttt tcc caa gtg gca agt gat caa atc agc gcc ttg aat 336  
 Leu Thr Glu Phe Ser Gln Val Ala Ser Asp Gln Ile Ser Ala Leu Asn  
 100 105 110

cag aat ttg tcc gcc aaa gaa caa agc ctg tcg gca ttg caa caa cag 384  
 Gln Asn Leu Ser Ala Lys Glu Gln Ser Leu Ser Ala Leu Gln Gln Gln  
 115 120 125

gtg caa cgt ttg tcc aat caa gcc aaa gcg gag cag ccg aat gac tgg 432  
 Val Gln Arg Leu Ser Asn Gln Ala Lys Ala Glu Gln Pro Asn Asp Trp  
 130 135 140

tta ctg acc gaa gcg gat ttt ctg tta aat aac gct ttg cgc aaa ctg 480  
 Leu Leu Thr Glu Ala Asp Phe Leu Leu Asn Asn Ala Leu Arg Lys Leu  
 145 150 155 160

gtg ttg gat aac gac gtg gat acc agt gtg tcc ttg ttg aaa gtt gcc 528  
 Val Leu Asp Asn Asp Val Asp Thr Ser Val Ser Leu Leu Lys Val Ala  
 165 170 175

gat gaa acc ctt tcc aaa gtc gcc atg cca caa gtg gcg cag gtg cgt 576  
 Asp Glu Thr Leu Ser Lys Val Ala Met Pro Gln Val Ala Gln Val Arg  
 180 185 190

agc gcc att aac gcc gat tta aaa cag ttg ttg tcc ctg aac aat gtg g 625  
 Ser Ala Ile Asn Ala Asp Leu Lys Gln Leu Leu Ser Leu Asn Asn Val  
 195 200 205

SEQ ID NO 164

<211> LENGTH: 208  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 164

Asp Lys Thr Glu Thr Met Gln Gln Asn Glu Glu Lys Ile Thr Pro Ser

-continued

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

<210> SEQ ID NO 165  
 <211> LENGTH: 684  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(684)

<400> SEQUENCE: 165

atg	acg	att	tta	gtt	ctg	ggt	atc	aat	cac	aaa	act	gct	tcc	gtg	gca	48
Met	Thr	Ile	Leu	Val	Leu	Gly	Ile	Asn	His	Lys	Thr	Ala	Ser	Val	Ala	
1			5					10						15		
ttg	cgg	gaa	aag	gtg	gcg	ttt	tcc	gac	gaa	aag	cgc	act	ttt	gct	ttg	96
Leu	Arg	Glu	Lys	Val	Ala	Phe	Ser	Asp	Glu	Lys	Arg	Thr	Phe	Ala	Leu	
		20						25					30			
cgt	cac	att	caa	caa	acg	cag	ttg	gcg	gaa	agt	gcg	gtg	att	tta	tcc	144
Arg	His	Ile	Gln	Gln	Thr	Gln	Leu	Ala	Glu	Ser	Ala	Val	Ile	Leu	Ser	
		35				40						45				
acc	tgt	aat	cgc	acg	gaa	ggt	tat	ctg	cac	aat	aaa	agc	ggt	ccg	ccg	192
Thr	Cys	Asn	Arg	Thr	Glu	Val	Tyr	Leu	His	Asn	Lys	Ser	Val	Pro	Pro	
	50					55					60					
caa	gag	acg	caa	acc	tgg	atc	aca	ctg	gcg	gtg	cag	tgg	ttt	gcc	ggc	240
Gln	Glu	Thr	Gln	Thr	Trp	Ile	Thr	Leu	Ala	Val	Gln	Trp	Phe	Ala	Gly	
65				70						75					80	
att	cat	caa	cta	gcg	ttg	gcg	gag	ctg	cag	cac	tgt	ggt	tat	act	cac	288
Ile	His	Gln	Leu	Ala	Leu	Ala	Glu	Leu	Gln	His	Cys	Val	Tyr	Thr	His	
			85					90						95		
gaa	aat	ctt	cag	gcg	gcg	aat	cat	tta	atg	gaa	gtg	gcg	tgc	ggt	ttg	336
Glu	Asn	Leu	Gln	Ala	Ala	Asn	His	Leu	Met	Glu	Val	Ala	Cys	Gly	Leu	
		100						105						110		

-continued

```

gat tcg ctg att tta ggc gaa ccg cag att ttg ggg cag gtg aag caa      384
Asp Ser Leu Ile Leu Gly Glu Pro Gln Ile Leu Gly Gln Val Lys Gln
      115                      120                      125

gcc tac cac atg agc gag cag cat tat caa cag gaa ggg caa acc att      432
Ala Tyr His Met Ser Glu Gln His Tyr Gln Gln Glu Gly Gln Thr Ile
      130                      135                      140

tcc ggc gaa cta tcc cgt tta ttc caa aaa acc ttt gct acc gct aaa      480
Ser Gly Glu Leu Ser Arg Leu Phe Gln Lys Thr Phe Ala Thr Ala Lys
      145                      150                      155                      160

cgg gtg cgc acc gaa acc aac atc ggc gag agt gcg gtg tcc gtt gcc      528
Arg Val Arg Thr Glu Thr Asn Ile Gly Glu Ser Ala Val Ser Val Ala
      165                      170                      175

tat gcc gcc tgt agc cta gca cgt cag att ttt gaa tcc ctg cgt gac      576
Tyr Ala Ala Cys Ser Leu Ala Arg Gln Ile Phe Glu Ser Leu Arg Asp
      180                      185                      190

ttg acg att tta tta gtg ggc gca ggt gaa acc att gaa ctg gtg aac      624
Leu Thr Ile Leu Leu Val Gly Ala Gly Glu Thr Ile Glu Leu Val Asn
      195                      200                      205

cgc cat ttg tta cgt cac ggc gtg aaa aac tta ttt atc gcc aac cgt      672
Arg His Leu Leu Arg His Gly Val Lys Asn Leu Phe Ile Ala Asn Arg
      210                      215                      220

aca ttg gcg cgc      684
Thr Leu Ala Arg
225

<210> SEQ ID NO 166
<211> LENGTH: 228
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 166

Met Thr Ile Leu Val Leu Gly Ile Asn His Lys Thr Ala Ser Val Ala
1      5      10      15

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

Arg His Ile Gln Gln Thr Gln Leu Ala Glu Ser Ala Val Ile Leu Ser
35     40     45

Thr Cys Asn Arg Thr Glu Val Tyr Leu His Asn Lys Ser Val Pro Pro
50     55     60

Gln Glu Thr Gln Thr Trp Ile Thr Leu Ala Val Gln Trp Phe Ala Gly
65     70     75     80

Ile His Gln Leu Ala Leu Ala Glu Leu Gln His Cys Val Tyr Thr His
85     90     95

Glu Asn Leu Gln Ala Ala Asn His Leu Met Glu Val Ala Cys Gly Leu
100    105    110

Asp Ser Leu Ile Leu Gly Glu Pro Gln Ile Leu Gly Gln Val Lys Gln
115    120    125

Ala Tyr His Met Ser Glu Gln His Tyr Gln Gln Glu Gly Gln Thr Ile
130    135    140

Ser Gly Glu Leu Ser Arg Leu Phe Gln Lys Thr Phe Ala Thr Ala Lys
145    150    155    160

Arg Val Arg Thr Glu Thr Asn Ile Gly Glu Ser Ala Val Ser Val Ala
165    170    175

Tyr Ala Ala Cys Ser Leu Ala Arg Gln Ile Phe Glu Ser Leu Arg Asp
180    185    190

```

-continued

Leu Thr Ile Leu Leu Val Gly Ala Gly Glu Thr Ile Glu Leu Val Asn  
 195 200 205  
 Arg His Leu Leu Arg His Gly Val Lys Asn Leu Phe Ile Ala Asn Arg  
 210 215 220  
 Thr Leu Ala Arg  
 225

<210> SEQ ID NO 167  
 <211> LENGTH: 138  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(138)

<400> SEQUENCE: 167

atg cgc cgt tgg aag ctg aaa atc ttc cgc aaa atg aac cgc act ttg 48  
 Met Arg Arg Trp Lys Leu Lys Ile Phe Arg Lys Met Asn Arg Thr Leu  
 1 5 10 15  
 cgc gtt cgc ctt tcg ttc cca atg cac cga ttc gtg ccg gac ctt aat 96  
 Arg Val Arg Leu Ser Phe Pro Met His Arg Phe Val Pro Asp Leu Asn  
 20 25 30  
 tta ttt aac ttc gat ctt tgt ata ttc cgt cgt tta att cgt 138  
 Leu Phe Asn Phe Asp Leu Cys Ile Phe Arg Arg Leu Ile Arg  
 35 40 45

SEQ ID NO 168

<211> LENGTH: 46  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 168

Met Arg Arg Trp Lys Leu Lys Ile Phe Arg Lys Met Asn Arg Thr Leu  
 1 5 10 15  
 Arg Val Arg Leu Ser Phe Pro Met His Arg Phe Val Pro Asp Leu Asn  
 20 25 30  
 Leu Phe Asn Phe Asp Leu Cys Ile Phe Arg Arg Leu Ile Arg  
 35 40 45

<210> SEQ ID NO 169  
 <211> LENGTH: 1950  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(1950)

<400> SEQUENCE: 169

atg gct gat gta tta acc cgt ttc aac agt ggc aag ctt tgg gaa ttc 48  
 Met Ala Asp Val Leu Thr Arg Phe Asn Ser Gly Lys Leu Trp Glu Phe  
 1 5 10 15  
 gat ggc ggc att cat ccg ccc gac atg aaa tcc caa tcc aac cgc gcg 96  
 Asp Gly Gly Ile His Pro Pro Asp Met Lys Ser Gln Ser Asn Arg Ala  
 20 25 30  
 cct att cgt acc ttg ccg ttg ccc gat aat ttc tac gtt ctt ctg aaa 144  
 Pro Ile Arg Thr Leu Pro Leu Pro Asp Asn Phe Tyr Val Leu Leu Lys  
 35 40 45  
 caa cac gcc ggc aca gcg ggc aat tta ttg gta aaa tgc gcc gat cat 192  
 Gln His Ala Gly Thr Ala Gly Asn Leu Leu Val Lys Cys Gly Asp His

-continued

50	55	60	
ggt ttg aaa ggt caa cgc ctc acc cag ggg gac ggt ttg cgt tcg ctg Val Leu Lys Gly Gln Pro Leu Thr Gln Gly Asp Gly Leu Arg Ser Leu 65 70 75 80			240
ccg gtt cat gcg cct act tca ggc acg gtc att gat gtg atg cct tat Pro Val His Ala Pro Thr Ser Gly Thr Val Ile Asp Val Met Pro Tyr 85 90 95			288
gtc acc gcc cat cct tcc ggt cta ccg gaa acc tgt gtg cat att aaa Val Thr Ala His Pro Ser Gly Leu Pro Glu Thr Cys Val His Ile Lys 100 105 110			336
gcg gat gga tta gat caa tgg cgc gag caa acc ccg ttg gag gat ttc Ala Asp Gly Leu Asp Gln Trp Arg Glu Gln Thr Pro Leu Glu Asp Phe 115 120 125			384
ctt agc caa acg ccg gaa cag tta atc gaa aaa att tat cag gcg ggc Leu Ser Gln Thr Pro Glu Gln Leu Ile Glu Lys Ile Tyr Gln Ala Gly 130 135 140			432
att gcc ggt ctg ggt ggc gcg gta ttc ccg acc gcg gca aaa att cat Ile Ala Gly Leu Gly Gln Ala Val Phe Pro Thr Ala Ala Lys Ile His 145 150 155 160			480
tcc gcc gag aaa cag gtg aaa tta ctg att att aac gcc gcg gaa tgt Ser Ala Glu Lys Gln Val Lys Leu Leu Ile Ile Asn Gly Ala Glu Cys 165 170 175			528
gaa cct tac att acc tgc gac gat cgc tta atg cat gat tat gct gat Glu Pro Tyr Ile Thr Cys Asp Asp Arg Leu Met His Asp Tyr Ala Asp 180 185 190			576
gaa att atc gaa gcc gtg cgt att ttg cgc tac att tta cgc cct gag Glu Ile Ile Glu Gly Val Arg Ile Leu Arg Tyr Ile Leu Arg Pro Glu 195 200 205			624
aaa gtg gtg atc gcc gtt gaa gat aat aaa cca aaa gcg gtg aaa tcc Lys Val Val Ile Ala Val Glu Asp Asn Lys Pro Lys Ala Val Lys Ser 210 215 220			672
ttg gaa cgc gcc tta cac ggc gcc aac gat att gaa atc cga gtg att Leu Glu Arg Ala Leu His Gly Ala Asn Asp Ile Glu Ile Arg Val Ile 225 230 235 240			720
ccg acc aaa tac cct tcc ggc gcg gca aaa cag tta att caa gtg ctg Pro Thr Lys Tyr Pro Ser Gly Ala Ala Lys Gln Leu Ile Gln Val Leu 245 250 255			768
acc gcc atg gag gta cct agc ggt caa cgc tcc tcc ggt atc gcc gtg Thr Gly Met Glu Val Pro Ser Gly Gln Arg Ser Ser Gly Ile Gly Val 260 265 270			816
ctg atg caa aac atc gcc acc gct ttt gct att aaa cgc gca gtg atg Leu Met Gln Asn Ile Gly Thr Ala Phe Ala Ile Lys Arg Ala Val Met 275 280 285			864
gat gat gaa ccg ctg att gag cgc gtc gtc acc ctc acc ggt gat aaa Asp Asp Glu Pro Leu Ile Glu Arg Val Val Thr Leu Thr Gly Asp Lys 290 295 300			912
atc gcc gat aaa gcc aac tat tgg gcg cgt ttt gga acg ccg att tat Ile Ala Asp Lys Gly Asn Tyr Trp Ala Arg Phe Gly Thr Pro Ile Tyr 305 310 315 320			960
cac ttg ttg cgc gaa acg ggc tat caa tac gac gat cgt ttc ccg gtc His Leu Leu Arg Glu Thr Gly Tyr Gln Tyr Asp Asp Arg Phe Pro Val 325 330 335			1008
ttc atg gcc ggt ccg atg atg ggc ttt att ctg ccc gat tta aat gcg Phe Met Gly Gly Pro Met Met Gly Phe Ile Leu Pro Asp Leu Asn Ala 340 345 350			1056
ccg atg acc aaa gtg acc aac tgc ctg ttg gcg ccg gat cat ttt gaa Pro Met Thr Lys Val Thr Asn Cys Leu Leu Ala Pro Asp His Phe Glu			1104

-continued

355		360		365												
tac	gcc	ccg	ccg	gaa	gaa	gaa	aaa	aat	tgt	att	cgc	tgt	tct	gcc	tgt	1152
Tyr	Ala	Pro	Pro	Glu	Glu	Glu	Lys	Asn	Cys	Ile	Arg	Cys	Ser	Ala	Cys	
	370						375					380				
tcc	gat	gcc	tgc	ccg	gtg	aaa	ctc	atg	ccg	cag	caa	ttg	tat	tgg	ttt	1200
Ser	Asp	Ala	Cys	Pro	Val	Lys	Leu	Met	Pro	Gln	Gln	Leu	Tyr	Trp	Phe	
	385				390					395					400	
gca	cgc	agc	gaa	gat	cac	gaa	aaa	tcg	gaa	gaa	tat	tcc	ctc	aaa	gat	1248
Ala	Arg	Ser	Glu	Asp	His	Glu	Lys	Ser	Glu	Glu	Tyr	Ser	Leu	Lys	Asp	
			405					410						415		
tgt	att	gaa	tgc	ggc	gtg	tgc	gct	tat	ggt	tgc	cca	agt	cac	att	ccg	1296
Cys	Ile	Glu	Cys	Gly	Val	Cys	Ala	Tyr	Val	Cys	Pro	Ser	His	Ile	Pro	
			420					425					430			
tta	att	caa	tat	ttc	cgc	cgg	gaa	aaa	gct	aaa	atc	tgg	gaa	atc	aaa	1344
Leu	Ile	Gln	Tyr	Phe	Arg	Arg	Glu	Lys	Ala	Lys	Ile	Trp	Glu	Ile	Lys	
			435				440					445				
cac	aaa	gcc	aaa	ttg	gcg	gaa	gaa	gct	aaa	ata	cgt	ttt	gaa	caa	cgc	1392
His	Lys	Ala	Lys	Leu	Ala	Glu	Glu	Ala	Lys	Ile	Arg	Phe	Glu	Gln	Arg	
	450					455					460					
caa	gcc	cgt	ttg	gaa	cgg	gaa	gaa	cag	gaa	cgc	aaa	gat	cgc	tca	caa	1440
Gln	Ala	Arg	Leu	Glu	Arg	Glu	Glu	Gln	Glu	Arg	Lys	Asp	Arg	Ser	Gln	
	465				470					475					480	
cgt	gct	gca	gcc	gcc	cgt	cgt	gaa	gaa	ttg	gcg	caa	caa	aaa	ggc	gtg	1488
Arg	Ala	Ala	Ala	Ala	Arg	Arg	Glu	Glu	Leu	Ala	Gln	Gln	Lys	Gly	Val	
					485				490					495		
gat	ccg	gtg	gct	gcc	gcc	tta	gcg	cgc	tta	aaa	gcg	aaa	aaa	gcc	gaa	1536
Asp	Pro	Val	Ala	Ala	Ala	Leu	Ala	Arg	Leu	Lys	Ala	Lys	Lys	Ala	Glu	
			500					505					510			
acg	acg	gaa	gct	acg	cag	gca	gaa	cag	aaa	acc	att	ggt	gac	gaa	aaa	1584
Thr	Thr	Glu	Ala	Thr	Gln	Ala	Glu	Gln	Lys	Thr	Ile	Val	Asp	Glu	Lys	
		515				520						525				
ggt	cat	atc	ctg	cct	gac	aac	agc	gac	atc	atg	gca	caa	cgc	aaa	gcc	1632
Gly	His	Ile	Leu	Pro	Asp	Asn	Ser	Asp	Ile	Met	Ala	Gln	Arg	Lys	Ala	
	530					535					540					
cgt	cgt	tta	gcc	cgt	cag	gcg	gaa	gcg	gca	cac	tcg	ccg	tcg	cag	aaa	1680
Arg	Arg	Leu	Ala	Arg	Gln	Ala	Glu	Ala	Ala	His	Ser	Pro	Ser	Gln	Lys	
	545				550					555					560	
aca	gaa	aaa	acg	cta	gaa	aaa	acg	cta	gaa	aaa	acc	acc	gca	ctt	gag	1728
Thr	Glu	Lys	Thr	Leu	Glu	Lys	Thr	Leu	Glu	Lys	Thr	Thr	Ala	Leu	Glu	
				565					570					575		
gat	aaa	aaa	tct	acc	ggt	gcc	gcc	gcc	att	gcc	cgt	gcg	aaa	gcc	aag	1776
Asp	Lys	Lys	Ser	Thr	Val	Ala	Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Lys	
			580					585					590			
aaa	gcg	gcg	cag	caa	acg	gaa	gcc	gtc	gaa	gca	aac	gaa	cct	gaa	acg	1824
Lys	Ala	Ala	Gln	Gln	Thr	Glu	Ala	Val	Glu	Ala	Asn	Glu	Pro	Glu	Thr	
			595				600					605				
gca	aaa	agt	gcg	gtc	aat	att	tcc	ggt	gaa	aat	ggc	gca	gag	aac	gat	1872
Ala	Lys	Ser	Ala	Val	Asn	Ile	Ser	Gly	Glu	Asn	Gly	Ala	Glu	Asn	Asp	
	610					615					620					
ccg	cgc	aaa	gcc	gct	ggt	gcc	gcc	gct	att	gcc	cgt	gcg	aaa	gcg	aag	1920
Pro	Arg	Lys	Ala	Ala	Val	Ala	Ala	Ala	Ile	Ala	Arg	Ala	Lys	Ala	Lys	
	625				630					635					640	
aaa	gcc	caa	cgt	gaa	aac	acg	caa	caa	gat							1950
Lys	Ala	Gln	Arg	Glu	Asn	Thr	Gln	Gln	Asp							
				645					650							

-continued

---

```

<211> LENGTH: 650
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 170

Met Ala Asp Val Leu Thr Arg Phe Asn Ser Gly Lys Leu Trp Glu Phe
1          5          10          15
Asp Gly Gly Ile His Pro Pro Asp Met Lys Ser Gln Ser Asn Arg Ala
20          25          30
Pro Ile Arg Thr Leu Pro Leu Pro Asp Asn Phe Tyr Val Leu Leu Lys
35          40          45
Gln His Ala Gly Thr Ala Gly Asn Leu Leu Val Lys Cys Gly Asp His
50          55          60
Val Leu Lys Gly Gln Pro Leu Thr Gln Gly Asp Gly Leu Arg Ser Leu
65          70          75          80
Pro Val His Ala Pro Thr Ser Gly Thr Val Ile Asp Val Met Pro Tyr
85          90          95
Val Thr Ala His Pro Ser Gly Leu Pro Glu Thr Cys Val His Ile Lys
100         105         110
Ala Asp Gly Leu Asp Gln Trp Arg Glu Gln Thr Pro Leu Glu Asp Phe
115         120         125
Leu Ser Gln Thr Pro Glu Gln Leu Ile Glu Lys Ile Tyr Gln Ala Gly
130         135         140
Ile Ala Gly Leu Gly Gly Ala Val Phe Pro Thr Ala Ala Lys Ile His
145         150         155         160
Ser Ala Glu Lys Gln Val Lys Leu Leu Ile Ile Asn Gly Ala Glu Cys
165         170         175
Glu Pro Tyr Ile Thr Cys Asp Asp Arg Leu Met His Asp Tyr Ala Asp
180         185         190
Glu Ile Ile Glu Gly Val Arg Ile Leu Arg Tyr Ile Leu Arg Pro Glu
195         200         205
Lys Val Val Ile Ala Val Glu Asp Asn Lys Pro Lys Ala Val Lys Ser
210         215         220
Leu Glu Arg Ala Leu His Gly Ala Asn Asp Ile Glu Ile Arg Val Ile
225         230         235         240
Pro Thr Lys Tyr Pro Ser Gly Ala Ala Lys Gln Leu Ile Gln Val Leu
245         250         255
Thr Gly Met Glu Val Pro Ser Gly Gln Arg Ser Ser Gly Ile Gly Val
260         265         270
Leu Met Gln Asn Ile Gly Thr Ala Phe Ala Ile Lys Arg Ala Val Met
275         280         285
Asp Asp Glu Pro Leu Ile Glu Arg Val Val Thr Leu Thr Gly Asp Lys
290         295         300
Ile Ala Asp Lys Gly Asn Tyr Trp Ala Arg Phe Gly Thr Pro Ile Tyr
305         310         315         320
His Leu Leu Arg Glu Thr Gly Tyr Gln Tyr Asp Asp Arg Phe Pro Val
325         330         335
Phe Met Gly Gly Pro Met Met Gly Phe Ile Leu Pro Asp Leu Asn Ala
340         345         350
Pro Met Thr Lys Val Thr Asn Cys Leu Leu Ala Pro Asp His Phe Glu
355         360         365
Tyr Ala Pro Pro Glu Glu Glu Lys Asn Cys Ile Arg Cys Ser Ala Cys

```



-continued

```

acc tta aat ctc gcg gtg caa ctg gat gcc acc aaa caa att gcg ggc      192
Thr Leu Asn Leu Ala Val Gln Leu Asp Ala Thr Lys Gln Ile Ala Gly
   50                               55                               60

gtg ctt tcc aac tgg caa aaa cag ctg ggc aaa gac ttc gtg cgc ctt      240
Val Leu Ser Asn Trp Gln Lys Gln Leu Gly Lys Asp Phe Val Arg Leu
   65                               70                               75                               80

gcg ccg gaa ttg gca aat tta ccg atg ccc ggt gat ttg aat acg gtc      288
Ala Pro Glu Leu Ala Asn Leu Pro Met Pro Gly Asp Leu Asn Thr Val
   85                               90                               95

aat att gaa agc cta atg gaa atc aaa ccg gat gtt gtt ttc gtg acc      336
Asn Ile Glu Ser Leu Met Glu Ile Lys Pro Asp Val Val Phe Val Thr
   100                              105                              110

aat tac gcg ccg aaa gaa atg att gaa aaa atc agc caa atg aac gtg      384
Asn Tyr Ala Pro Lys Glu Met Ile Glu Lys Ile Ser Gln Met Asn Val
   115                              120                              125

ccg gtg att gcc att tcg tta cgc agc ggc gat aaa acc gaa caa agc      432
Pro Val Ile Ala Ile Ser Leu Arg Ser Gly Asp Lys Thr Glu Gln Ser
   130                              135                              140

aaa ctc aac ccg acc ctt gcc gat gaa aac aat gcc tac aac gaa ggg      480
Lys Leu Asn Pro Thr Leu Ala Asp Glu Asn Asn Ala Tyr Asn Glu Gly
   145                              150                              155                              160

tta aaa cgc ggg att gaa att att gcc gat gtt ttt gat aaa aaa      525
Leu Lys Arg Gly Ile Glu Ile Ile Ala Asp Val Phe Asp Lys Lys
   165                              170                              175

```

&lt;210&gt; SEQ ID NO 172

&lt;211&gt; LENGTH: 175

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 172

```

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

Thr Ser Val Trp Ala Asp Arg Val Ile Thr Asp Gln Leu Asp Arg Gln
 20                              25                              30

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

Thr Leu Asn Leu Ala Val Gln Leu Asp Ala Thr Lys Gln Ile Ala Gly
 50                              55                              60

Val Leu Ser Asn Trp Gln Lys Gln Leu Gly Lys Asp Phe Val Arg Leu
 65                              70                              75                              80

Ala Pro Glu Leu Ala Asn Leu Pro Met Pro Gly Asp Leu Asn Thr Val
 85                              90                              95

Asn Ile Glu Ser Leu Met Glu Ile Lys Pro Asp Val Val Phe Val Thr
100                              105                              110

Asn Tyr Ala Pro Lys Glu Met Ile Glu Lys Ile Ser Gln Met Asn Val
115                              120                              125

Pro Val Ile Ala Ile Ser Leu Arg Ser Gly Asp Lys Thr Glu Gln Ser
130                              135                              140

Lys Leu Asn Pro Thr Leu Ala Asp Glu Asn Asn Ala Tyr Asn Glu Gly
145                              150                              155                              160

Leu Lys Arg Gly Ile Glu Ile Ile Ala Asp Val Phe Asp Lys Lys
165                              170                              175

```

&lt;210&gt; SEQ ID NO 173

&lt;211&gt; LENGTH: 391

-continued

```

<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(390)

<400> SEQUENCE: 173

atg  cgc  gag  ttg  gtg  tat  aaa  ccg  ctt  gag  caa  cct  gtg  gaa  gca  cca      48
Met Ala Glu Leu Val Tyr Lys Pro Leu Glu Gln Pro Val Glu Ala Pro
1          5          10          15

aat  ccg  aat  cta  aaa  att  gaa  cgc  gta  aac  gaa  cag  ttt  gcg  gca  aaa      96
Asn Pro Asn Leu Lys Ile Glu Ala Val Asn Glu Gln Phe Ala Ala Lys
          20          25          30

tac  ccg  aaa  caa  ttt  gcg  tct  tgg  aaa  gcc  acc  gaa  aaa  ggc  gac  aag      144
Tyr Pro Lys Gln Phe Ala Ser Trp Lys Ala Thr Glu Lys Gly Asp Lys
          35          40          45

att  att  tat  gca  gat  gag  gaa  aat  cca  cgt  tta  atc  ata  tta  tgg  ggc      192
Ile Ile Tyr Ala Asp Glu Glu Asn Pro Arg Leu Ile Ile Leu Trp Gly
          50          55          60

ggt  tat  gcc  ttt  gcg  aaa  gaa  tat  aac  gca  ccg  cgc  gga  cac  att  tat      240
Gly Tyr Ala Phe Ala Lys Glu Tyr Asn Ala Pro Arg Gly His Ile Tyr
65          70          75          80

gcc  att  aaa  gat  tta  cgc  aat  att  ttg  cgt  acc  ggt  gcg  ccg  aaa  acc      288
Ala Ile Lys Asp Leu Arg Asn Ile Leu Arg Thr Gly Ala Pro Lys Thr
          85          90          95

gct  aac  gac  ggt  cca  caa  ccg  atg  gcg  tgt  tgg  acc  tgt  aaa  ggt  ccg      336
Ala Asn Asp Gly Pro Gln Pro Met Ala Cys Trp Thr Cys Lys Gly Pro
          100          105          110

gat  gtg  ccg  cgt  tta  atc  gcc  gaa  tgg  gga  gaa  gaa  ggc  tat  ttc  aat      384
Asp Val Pro Arg Leu Ile Ala Glu Trp Gly Glu Glu Gly Tyr Phe Asn
          115          120          125

ggt  aaa  t
Gly Lys
130

```

```

<210> SEQ ID NO 174
<211> LENGTH: 130
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 174

Met Ala Glu Leu Val Tyr Lys Pro Leu Glu Gln Pro Val Glu Ala Pro
1          5          10          15

Asn Pro Asn Leu Lys Ile Glu Ala Val Asn Glu Gln Phe Ala Ala Lys
          20          25          30

Tyr Pro Lys Gln Phe Ala Ser Trp Lys Ala Thr Glu Lys Gly Asp Lys
          35          40          45

Ile Ile Tyr Ala Asp Glu Glu Asn Pro Arg Leu Ile Ile Leu Trp Gly
          50          55          60

Gly Tyr Ala Phe Ala Lys Glu Tyr Asn Ala Pro Arg Gly His Ile Tyr
65          70          75          80

Ala Ile Lys Asp Leu Arg Asn Ile Leu Arg Thr Gly Ala Pro Lys Thr
          85          90          95

Ala Asn Asp Gly Pro Gln Pro Met Ala Cys Trp Thr Cys Lys Gly Pro
          100          105          110

Asp Val Pro Arg Leu Ile Ala Glu Trp Gly Glu Glu Gly Tyr Phe Asn
          115          120          125

```

-continued

Gly Lys  
130

&lt;210&gt; SEQ ID NO 175

&lt;211&gt; LENGTH: 540

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(540)

&lt;400&gt; SEQUENCE: 175

```

aaa gcc atg ccg gca tta gac tta aat aaa gac ggc aaa atc caa tat      48
Lys Ala Met Pro Ala Leu Asp Leu Asn Lys Asp Gly Lys Ile Gln Tyr
1          5          10          15

gtg tta tta aaa ggc gaa ccg ggc cac cct gat gcg gaa gca cgt acc      96
Val Leu Leu Lys Gly Glu Pro Gly His Pro Asp Ala Glu Ala Arg Thr
          20          25          30

aag tat gtg att gag caa cta aac gcg caa ggc att cca acg gaa caa      144
Lys Tyr Val Ile Glu Gln Leu Asn Ala Gln Gly Ile Pro Thr Glu Gln
          35          40          45

ctc ttt atc gac acc ggg atg tgg gat gcg gca ctg gca aaa gac aaa      192
Leu Phe Ile Asp Thr Gly Met Trp Asp Ala Ala Leu Ala Lys Asp Lys
          50          55          60

atg gat gcg tgg tta tcc agc tct aaa gcc aat gac att gaa gtc att      240
Met Asp Ala Trp Leu Ser Ser Ser Lys Ala Asn Asp Ile Glu Val Ile
65          70          75          80

att tcc aac aac gac ggc atg gcg atg ggc gca ttg gaa gca acc aaa      288
Ile Ser Asn Asn Asp Gly Met Ala Met Gly Ala Leu Glu Ala Thr Lys
          85          90          95

gca cac ggc aaa aaa tta ccg att ttc ggg gta gat gcg ttg cct gaa      336
Ala His Gly Lys Lys Leu Pro Ile Phe Gly Val Asp Ala Leu Pro Glu
100          105          110

gta tta caa ctc atc aag aaa ggc gac att gca ggt acc gta ttg aat      384
Val Leu Gln Leu Ile Lys Lys Gly Asp Ile Ala Gly Thr Val Leu Asn
115          120          125

gac ggc gcg act caa ggt aaa gcg att gtg gat tta tcc aac aac ctg      432
Asp Gly Ala Thr Gln Gly Lys Ala Ile Val Asp Leu Ser Asn Asn Leu
130          135          140

gca aac ggc aaa ccg gct acc gaa ggc acc aaa tgg gag ctt aaa gat      480
Ala Asn Gly Lys Pro Ala Thr Glu Gly Thr Lys Trp Glu Leu Lys Asp
145          150          155          160

cgc gtt gtg cgc att cct tat gtt ggc gta gat aaa gac aac ttg tct      528
Arg Val Val Arg Ile Pro Tyr Val Gly Val Asp Lys Asp Asn Leu Ser
165          170          175

caa ttc tta aaa      540
Gln Phe Leu Lys
180

```

&lt;210&gt; SEQ ID NO 176

&lt;211&gt; LENGTH: 180

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 176

```

Lys Ala Met Pro Ala Leu Asp Leu Asn Lys Asp Gly Lys Ile Gln Tyr
1          5          10          15

Val Leu Leu Lys Gly Glu Pro Gly His Pro Asp Ala Glu Ala Arg Thr
20          25          30

```

-continued

```

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

```

<210> SEQ ID NO 177
<211> LENGTH: 1071
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1071)
    
```

<400> SEQUENCE: 177

```

atg gca gga aat acc atc gga caa tta ttt cgc gtc acc acc ttc ggc      48
Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly
 1                               5                               10                               15
gag tcc cac ggc att gcc ttg ggt tgc att gtg gac ggc gta ccg ccg      96
Glu Ser His Gly Ile Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro
 20                               25                               30
aac atg gca tta tcg gaa gcg gat att caa ccg gat ttg gat cgt cgt      144
Asn Met Ala Leu Ser Glu Ala Asp Ile Gln Pro Asp Leu Asp Arg Arg
 35                               40                               45
aaa ccc ggc acc tcg cgc tat acc aca ccg cgc cgc gaa gac gat gaa      192
Lys Pro Gly Thr Ser Arg Tyr Thr Thr Pro Arg Arg Glu Asp Asp Glu
 50                               55                               60
gtg cag att tta tcc ggt gtc ttt gaa gga aaa acc acc ggc acc agt      240
Val Gln Ile Leu Ser Gly Val Phe Glu Gly Lys Thr Thr Gly Thr Ser
 65                               70                               75                               80
att ggc ata atc att aag aac ggc gat caa cgc tcg cag gac tat ggc      288
Ile Gly Ile Ile Ile Lys Asn Gly Asp Gln Arg Ser Gln Asp Tyr Gly
 85                               90                               95
gaa att aaa gat cgc ttc cgt ccg gga cat gca gat ttt act tat caa      336
Glu Ile Lys Asp Arg Phe Arg Pro Gly His Ala Asp Phe Thr Tyr Gln
 100                              105                              110
caa aaa tac ggc att cgt gat tat cgc ggc ggc ggt cgt tct tcc gcc      384
Gln Lys Tyr Gly Ile Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala
 115                              120                              125
cgc gaa act gcc atg cgc gtg gcg gcg ggt gcc atc gcg aaa aaa tat      432
Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr
 130                              135                              140
    
```

-continued

```

tta cgc gaa caa ttc ggc att gaa gtg cgt ggt ttc tta agc caa atc      480
Leu Arg Glu Gln Phe Gly Ile Glu Val Arg Gly Phe Leu Ser Gln Ile
145                150                155                160

ggc gat gtc aaa att gcg ccg caa tcc gtg gaa cat att gat tgg gca      528
Gly Asp Val Lys Ile Ala Pro Gln Ser Val Glu His Ile Asp Trp Ala
165                170                175

gaa gta aat agc aat ctg ttt ttc tgc ccc gat aaa agt gcg gtg gaa      576
Glu Val Asn Ser Asn Leu Phe Phe Cys Pro Asp Lys Ser Ala Val Glu
180                185                190

aaa ttc gat gaa tta att ctg gat ctg aaa aaa caa ggg gat tct atc      624
Lys Phe Asp Glu Leu Ile Arg Asp Leu Lys Lys Gln Gly Asp Ser Ile
195                200                205

ggg gct aaa ttg acc gtg gtg gcg gaa aac gtc ccc gtc ggg ttg ggc      672
Gly Ala Lys Leu Thr Val Val Ala Glu Asn Val Pro Val Gly Leu Gly
210                215                220

gaa ccg gtg ttt gat cgt ttg gat gcg gat tta gcc cac gca tta atg      720
Glu Pro Val Phe Asp Arg Leu Asp Ala Asp Leu Ala His Ala Leu Met
225                230                235                240

agc att aat gcg gta aaa ggc gtg gaa att ggt gac ggt ttc gct gtg      768
Ser Ile Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Ala Val
245                250                255

gta gaa caa aaa ggt agc caa cat cgt gac gaa atg atc ccg caa gga      816
Val Glu Gln Lys Gly Ser Gln His Arg Asp Glu Met Ile Pro Gln Gly
260                265                270

ttt ctt tcc aac tat gcc ggc ggg att ttg ggc ggc atc agt tca gga      864
Phe Leu Ser Asn Tyr Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly
275                280                285

caa ccg att atc gcc acg att gcc ctc aaa ccc act tcc agc att acc      912
Gln Pro Ile Ile Ala Thr Ile Ala Leu Lys Pro Thr Ser Ser Ile Thr
290                295                300

att ccg ggg cgc tcg gtg aat ctc gac aat gaa tct gtc gaa gtt gtt      960
Ile Pro Gly Arg Ser Val Asn Leu Asp Asn Glu Ser Val Glu Val Val
305                310                315                320

act aaa ggt cgc cac gat cct tgt gtc ggc atc cgc gcc gtg ccg att      1008
Thr Lys Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile
325                330                335

gcg gaa gct atg acg gcg att gta ttg ttg gat cat ttg ttg cgt ttt      1056
Ala Glu Ala Met Thr Ala Ile Val Leu Leu Asp His Leu Leu Arg Phe
340                345                350

aaa gcg caa tgc cga
Lys Ala Gln Cys Arg
355

```

&lt;210&gt; SEQ ID NO 178

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 178

```

Met Ala Gly Asn Thr Ile Gly Gln Leu Phe Arg Val Thr Thr Phe Gly
1                5                10                15

Glu Ser His Gly Ile Ala Leu Gly Cys Ile Val Asp Gly Val Pro Pro
20                25                30

Asn Met Ala Leu Ser Glu Ala Asp Ile Gln Pro Asp Leu Asp Arg Arg
35                40                45

Lys Pro Gly Thr Ser Arg Tyr Thr Thr Pro Arg Arg Glu Asp Asp Glu
50                55                60

```

-continued

Val Gln Ile Leu Ser Gly Val Phe Glu Gly Lys Thr Thr Gly Thr Ser  
65 70 75 80

Ile Gly Ile Ile Ile Lys Asn Gly Asp Gln Arg Ser Gln Asp Tyr Gly  
85 90 95

Glu Ile Lys Asp Arg Phe Arg Pro Gly His Ala Asp Phe Thr Tyr Gln  
100 105 110

Gln Lys Tyr Gly Ile Arg Asp Tyr Arg Gly Gly Gly Arg Ser Ser Ala  
115 120 125

Arg Glu Thr Ala Met Arg Val Ala Ala Gly Ala Ile Ala Lys Lys Tyr  
130 135 140

Leu Arg Glu Gln Phe Gly Ile Glu Val Arg Gly Phe Leu Ser Gln Ile  
145 150 155 160

Gly Asp Val Lys Ile Ala Pro Gln Ser Val Glu His Ile Asp Trp Ala  
165 170 175

Glu Val Asn Ser Asn Leu Phe Phe Cys Pro Asp Lys Ser Ala Val Glu  
180 185 190

Lys Phe Asp Glu Leu Ile Arg Asp Leu Lys Lys Gln Gly Asp Ser Ile  
195 200 205

Gly Ala Lys Leu Thr Val Val Ala Glu Asn Val Pro Val Gly Leu Gly  
210 215 220

Glu Pro Val Phe Asp Arg Leu Asp Ala Asp Leu Ala His Ala Leu Met  
225 230 235 240

Ser Ile Asn Ala Val Lys Gly Val Glu Ile Gly Asp Gly Phe Ala Val  
245 250 255

Val Glu Gln Lys Gly Ser Gln His Arg Asp Glu Met Ile Pro Gln Gly  
260 265 270

Phe Leu Ser Asn Tyr Ala Gly Gly Ile Leu Gly Gly Ile Ser Ser Gly  
275 280 285

Gln Pro Ile Ile Ala Thr Ile Ala Leu Lys Pro Thr Ser Ser Ile Thr  
290 295 300

Ile Pro Gly Arg Ser Val Asn Leu Asp Asn Glu Ser Val Glu Val Val  
305 310 315 320

Thr Lys Gly Arg His Asp Pro Cys Val Gly Ile Arg Ala Val Pro Ile  
325 330 335

Ala Glu Ala Met Thr Ala Ile Val Leu Leu Asp His Leu Leu Arg Phe  
340 345 350

Lys Ala Gln Cys Arg  
355

<210> SEQ ID NO 179  
 <211> LENGTH: 633  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(633)

<400> SEQUENCE: 179

gac ctc ttg gtg gat tcc tac gtg aaa tgg cgt atc aat gat tta ggt 48  
 Asp Leu Leu Val Asp Ser Tyr Val Lys Trp Arg Ile Asn Asp Leu Gly  
 1 5 10 15

cgt ttc ttc acc acg acc ggt ggt ggc gat tat gca caa gca gcc aac 96  
 Arg Phe Phe Thr Thr Thr Gly Gly Asp Tyr Ala Gln Ala Ala Asn  
 20 25 30

-continued

```

tta tta cgt cgt aaa gtc aat gac cgt ttg cgt tcc gaa atc ggt tcc      144
Leu Leu Arg Arg Lys Val Asn Asp Arg Leu Arg Ser Glu Ile Gly Ser
      35                40                45

cgc acc att aaa gac atc gtt tcc ggt aca cga ggc gaa ctc atg gta      192
Arg Thr Ile Lys Asp Ile Val Ser Gly Thr Arg Gly Glu Leu Met Val
      50                55                60

ggc acg aaa aaa gcg ctc aac agt ggg caa gac agc acc gcc gaa ctg      240
Gly Thr Lys Lys Ala Leu Asn Ser Gly Gln Asp Ser Thr Ala Glu Leu
      65                70                75                80

ggg att gaa gtg ctc gac gta cgg att aaa caa att aac ttg ccg gat      288
Gly Ile Glu Val Leu Asp Val Arg Ile Lys Gln Ile Asn Leu Pro Asp
      85                90                95

gaa gtg tct tcc tcc att tac cag cgt atg cgc gcc gaa cgg gat gcg      336
Glu Val Ser Ser Ser Ile Tyr Gln Arg Met Arg Ala Glu Arg Asp Ala
      100               105               110

gta gcc cgt gaa cac cgc tct caa ggt aaa gaa aaa gcg gca ttt att      384
Val Ala Arg Glu His Arg Ser Gln Gly Lys Glu Lys Ala Ala Phe Ile
      115               120               125

cag gcg gat gta gat cgt aaa gtc acc tta att atc gcc aat gcg gaa      432
Gln Ala Asp Val Asp Arg Lys Val Thr Leu Ile Ile Ala Asn Ala Glu
      130               135               140

aaa acc gca cag gaa tta cgc ggt gac ggc gac gcg acc gca gcc aaa      480
Lys Thr Ala Gln Glu Leu Arg Gly Asp Gly Asp Ala Thr Ala Ala Lys
      145               150               155               160

atc ttt gcc gat gcc ttt ggt aaa gag cct gaa ttt tac agc ttc att      528
Ile Phe Ala Asp Ala Phe Gly Lys Glu Pro Glu Phe Tyr Ser Phe Ile
      165               170               175

cgt agc ctg aaa gcc tat gaa agc agc ttc gcc gac tcg gac aat ttg      576
Arg Ser Leu Lys Ala Tyr Glu Ser Ser Phe Ala Asp Ser Asp Asn Leu
      180               185               190

ttg att tta aaa ccg gac agt gac ttc ttc cgt ttt atg caa tca cca      624
Leu Ile Leu Lys Pro Asp Ser Asp Phe Phe Arg Phe Met Gln Ser Pro
      195               200               205

agt aaa taa
Ser Lys
      210

```

&lt;210&gt; SEQ ID NO 180

&lt;211&gt; LENGTH: 210

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 180

```

Asp Leu Leu Val Asp Ser Tyr Val Lys Trp Arg Ile Asn Asp Leu Gly
1                5                10                15

Arg Phe Phe Thr Thr Thr Gly Gly Gly Asp Tyr Ala Gln Ala Ala Asn
20               25               30

Leu Leu Arg Arg Lys Val Asn Asp Arg Leu Arg Ser Glu Ile Gly Ser
35               40               45

Arg Thr Ile Lys Asp Ile Val Ser Gly Thr Arg Gly Glu Leu Met Val
50               55               60

Gly Thr Lys Lys Ala Leu Asn Ser Gly Gln Asp Ser Thr Ala Glu Leu
65               70               75                80

Gly Ile Glu Val Leu Asp Val Arg Ile Lys Gln Ile Asn Leu Pro Asp
85               90                95

Glu Val Ser Ser Ser Ile Tyr Gln Arg Met Arg Ala Glu Arg Asp Ala

```

-continued

100	105	110	
Val Ala Arg Glu His Arg Ser Gln Gly Lys Glu Lys Ala Ala Phe Ile 115 120 125			
Gln Ala Asp Val Asp Arg Lys Val Thr Leu Ile Ile Ala Asn Ala Glu 130 135 140			
Lys Thr Ala Gln Glu Leu Arg Gly Asp Gly Asp Ala Thr Ala Ala Lys 145 150 155 160			
Ile Phe Ala Asp Ala Phe Gly Lys Glu Pro Glu Phe Tyr Ser Phe Ile 165 170 175			
Arg Ser Leu Lys Ala Tyr Glu Ser Ser Phe Ala Asp Ser Asp Asn Leu 180 185 190			
Leu Ile Leu Lys Pro Asp Ser Asp Phe Phe Arg Phe Met Gln Ser Pro 195 200 205			
Ser Lys 210			
<210> SEQ ID NO 181			
<211> LENGTH: 582			
<212> TYPE: DNA			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(582)			
<400> SEQUENCE: 181			
atg atc gac aac atc aac gaa ctt cgc acc ttt atc acc gcg gcg caa Met Ile Asp Asn Ile Asn Glu Leu Arg Thr Phe Ile Thr Ala Ala Gln 1 5 10 15			48
gaa ggc agt ttc acc aaa gcc gcc gca aaa tta aac gtt tcc acc tcc Glu Gly Ser Phe Thr Lys Ala Ala Ala Lys Leu Asn Val Ser Thr Ser 20 25 30			96
gca tta agc cat tcc att cgc aag ctg gaa gaa cag ctc aac atc aaa Ala Leu Ser His Ser Ile Arg Lys Leu Glu Glu Gln Leu Asn Ile Lys 35 40 45			144
ctg ttc aac cgc acc aca cgc agc att gcc acc acg gag gcg ggc gag Leu Phe Asn Arg Thr Thr Arg Ser Ile Ala Thr Thr Glu Ala Gly Glu 50 55 60			192
cag ttg ttt caa aat ctc ttg ccg ttg ttt gaa agt att gaa gat aat Gln Leu Phe Gln Asn Leu Leu Pro Leu Phe Glu Ser Ile Glu Asp Asn 65 70 75 80			240
ctc aac gca tta agc acc ttt cgc aac acg ttg aaa ggg aaa tta tgc Leu Asn Ala Leu Ser Thr Phe Arg Asn Thr Leu Lys Gly Lys Leu Cys 85 90 95			288
att aac ggt aac gat cat gtt ttt tta tcc att ttg tgg gat aaa ttg Ile Asn Gly Asn Asp His Val Phe Leu Ser Ile Leu Trp Asp Lys Leu 100 105 110			336
atg gcg ttc gcg gaa caa tac ccc gaa atg gaa ttg gaa ttg acc agt Met Ala Phe Ala Glu Gln Tyr Pro Glu Met Glu Leu Glu Leu Thr Ser 115 120 125			384
gac acc aaa ttt gtg gat atc gtg gcg ggg cgg ttt gat gcg ggt att Asp Thr Lys Phe Val Asp Ile Val Ala Gly Arg Phe Asp Ala Gly Ile 130 135 140			432
cgc tta gga tcg gac gtg gca caa gat atg atc gcc gtg aga tta agc Arg Leu Gly Ser Asp Val Ala Gln Asp Met Ile Ala Val Arg Leu Ser 145 150 155 160			480
gac aaa atg caa atg gcg gtg gtc ggc acg cca gag tat ttc gcc aaa Asp Lys Met Gln Met Ala Val Val Gly Thr Pro Glu Tyr Phe Ala Lys			528

-continued

---

165	170	175	
aaa gcc aca ccg aag aaa gta gaa gac ttg ggc gaa cac gag tgc ttg			576
Lys Ala Thr Pro Lys Lys Val Glu Asp Leu Gly Glu His Glu Cys Leu			
180	185	190	
ctg gtg			582
Leu Val			
<210> SEQ ID NO 182			
<211> LENGTH: 194			
<212> TYPE: PRT			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<400> SEQUENCE: 182			
Met Ile Asp Asn Ile Asn Glu Leu Arg Thr Phe Ile Thr Ala Ala Gln			
1	5	10	15
Glu Gly Ser Phe Thr Lys Ala Ala Ala Lys Leu Asn Val Ser Thr Ser			
20	25	30	
Ala Leu Ser His Ser Ile Arg Lys Leu Glu Glu Gln Leu Asn Ile Lys			
35	40	45	
Leu Phe Asn Arg Thr Thr Arg Ser Ile Ala Thr Thr Glu Ala Gly Glu			
50	55	60	
Gln Leu Phe Gln Asn Leu Leu Pro Leu Phe Glu Ser Ile Glu Asp Asn			
65	70	75	80
Leu Asn Ala Leu Ser Thr Phe Arg Asn Thr Leu Lys Gly Lys Leu Cys			
85	90	95	
Ile Asn Gly Asn Asp His Val Phe Leu Ser Ile Leu Trp Asp Lys Leu			
100	105	110	
Met Ala Phe Ala Glu Gln Tyr Pro Glu Met Glu Leu Glu Leu Thr Ser			
115	120	125	
Asp Thr Lys Phe Val Asp Ile Val Ala Gly Arg Phe Asp Ala Gly Ile			
130	135	140	
Arg Leu Gly Ser Asp Val Ala Gln Asp Met Ile Ala Val Arg Leu Ser			
145	150	155	160
Asp Lys Met Gln Met Ala Val Val Gly Thr Pro Glu Tyr Phe Ala Lys			
165	170	175	
Lys Ala Thr Pro Lys Lys Val Glu Asp Leu Gly Glu His Glu Cys Leu			
180	185	190	
Leu Val			
<210> SEQ ID NO 183			
<211> LENGTH: 662			
<212> TYPE: DNA			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(660)			
<400> SEQUENCE: 183			
taa tct cgg caa tgt tcg cca cct tgc ttt ttt tgc ctg cat tat ttc			48
Ser Arg Gln Cys Ser Pro Pro Cys Phe Phe Cys Leu His Tyr Phe			
1	5	10	15
gcc gtt atc aaa aca aac cgc gca ccc cga acc caa aag tgc ggt gga			96
Ala Val Ile Lys Thr Asn Arg Ala Pro Arg Thr Gln Lys Cys Gly Gly			
20	25	30	
ttt tgg atg cgt ttt tta cgc atg ggc gtg gtt tca atc ctg tta ggg			144
Phe Trp Met Arg Phe Leu Arg Met Gly Val Val Ser Ile Leu Leu Gly			

-continued

35		40		45		
ggg	att ttt atc gtc ggc ggt ttg tat cgt tcc gaa tgg cgt gat gat					192
Gly	Ile Phe Ile Val Gly Gly Leu Tyr Arg Ser Glu Trp Arg Asp Asp					
	50		55		60	
att	cgt caa tgg gtt tct atg ccg cag gtg atg tta gac gag gcg aag					240
Ile	Arg Gln Trp Val Ser Met Pro Gln Val Met Leu Asp Glu Ala Lys					
	65		70		75	
caa	atc gct gac ttg acc ggc gtg gat ttg ggc aac cgt tat ttc ctg					288
Gln	Ile Ala Asp Leu Thr Gly Val Asp Leu Gly Asn Arg Tyr Phe Leu					
	80		85		90	95
gtg	ctt gcc gac aac gac gat gcc tta ctg gaa aaa gaa cgg gcg ctg					336
Val	Leu Ala Asp Asn Asp Asp Ala Leu Leu Glu Lys Glu Arg Ala Leu					
		100		105		110
aca	aca aaa ctg gat gaa cag cac atc cct tat cgc gcc ctt tcc caa					384
Thr	Thr Lys Leu Asp Glu Gln His Ile Pro Tyr Arg Ala Leu Ser Gln					
		115		120		125
tgg	atg atg tcg gaa gcg caa cag cgg caa ttt ata gtg gaa ttg cag					432
Trp	Met Met Ser Glu Ala Gln Gln Arg Gln Phe Ile Val Glu Leu Gln					
		130		135		140
gca	aaa ctc aaa ccg cag gat tat gcc gta ttg gat gag att ggc gtg					480
Ala	Lys Leu Lys Pro Gln Asp Tyr Ala Val Leu Asp Glu Ile Gly Val					
		145		150		155
ccg	tcg gaa aga tta caa cag gca ctg cgg gaa ttg aac acg cag ccg					528
Pro	Ser Glu Arg Leu Gln Gln Ala Leu Arg Glu Leu Asn Thr Gln Pro					
		160		165		170
ccg	tta tcc ttg cag cag gcg ttg caa tct acc gtc ggg caa gca tgg					576
Pro	Leu Ser Leu Gln Gln Ala Leu Gln Ser Thr Val Gly Gln Ala Trp					
		180		185		190
ctg	ccg ctc tat tta ggc aaa tta gcg gaa aat cag gtg gct ggc atc					624
Leu	Pro Leu Tyr Leu Gly Lys Leu Ala Glu Asn Gln Val Ala Gly Ile					
		195		200		205
gtg	cag gta agc gga cac agt gcc gtt tcc ctt gcg ca					662
Val	Gln Val Ser Gly His Ser Ala Val Ser Leu Ala					
		210		215		
<210> SEQ ID NO 184						
<211> LENGTH: 219						
<212> TYPE: PRT						
<213> ORGANISM: Actinobacillus actinomycetemcomitans						
<400> SEQUENCE: 184						
Ser	Arg Gln Cys Ser Pro Pro Cys Phe Phe Cys Leu His Tyr Phe Ala					
1		5		10		15
Val	Ile Lys Thr Asn Arg Ala Pro Arg Thr Gln Lys Cys Gly Gly Phe					
		20		25		30
Trp	Met Arg Phe Leu Arg Met Gly Val Val Ser Ile Leu Leu Gly Gly					
		35		40		45
Ile	Phe Ile Val Gly Gly Leu Tyr Arg Ser Glu Trp Arg Asp Asp Ile					
		50		55		60
Arg	Gln Trp Val Ser Met Pro Gln Val Met Leu Asp Glu Ala Lys Gln					
		65		70		75
Ile	Ala Asp Leu Thr Gly Val Asp Leu Gly Asn Arg Tyr Phe Leu Val					
		85		90		95
Leu	Ala Asp Asn Asp Asp Ala Leu Leu Glu Lys Glu Arg Ala Leu Thr					
		100		105		110
Thr	Lys Leu Asp Glu Gln His Ile Pro Tyr Arg Ala Leu Ser Gln Trp					

-continued

115	120	125
Met Met Ser Glu Ala Gln Gln Arg Gln Phe Ile Val Glu Leu Gln Ala		
130	135	140
Lys Leu Lys Pro Gln Asp Tyr Ala Val Leu Asp Glu Ile Gly Val Pro		
145	150	155
Ser Glu Arg Leu Gln Gln Ala Leu Arg Glu Leu Asn Thr Gln Pro Pro		
	165	170
Leu Ser Leu Gln Gln Ala Leu Gln Ser Thr Val Gly Gln Ala Trp Leu		
	180	185
Pro Leu Tyr Leu Gly Lys Leu Ala Glu Asn Gln Val Ala Gly Ile Val		
	195	200
Gln Val Ser Gly His Ser Ala Val Ser Leu Ala		
210	215	

<210> SEQ ID NO 185  
 <211> LENGTH: 247  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(246)

<400> SEQUENCE: 185

ggg gtg ttt atg tcc gcg cat aat ttc ccg aaa tcc cgt gaa acc cgt	48
Gly Val Phe Met Ser Ala His Asn Phe Pro Lys Ser Arg Glu Thr Arg	
1	15
gca cct aaa gtg gcg gaa ttg gcg tta tat cgt gag cgg ctg ccg gaa	96
Ala Pro Lys Val Ala Glu Leu Ala Leu Tyr Arg Glu Arg Leu Pro Glu	
	30
aaa tta agc tat ctg gct gac gca cca caa acg gat ccg gaa ggc agt	144
Lys Leu Ser Tyr Leu Ala Asp Ala Pro Gln Thr Asp Pro Glu Gly Ser	
	45
gaa gcc atc att cgc ttt agt cgt aaa gaa aaa cgt caa tat gtc acc	192
Glu Ala Ile Ile Arg Phe Ser Arg Lys Glu Lys Arg Gln Tyr Val Thr	
	60
tcc gaa aag aat ggc aag gcg aca aaa tgg ata gtg gat ttt gtt gat	240
Ser Glu Lys Asn Gly Lys Ala Thr Lys Trp Ile Val Asp Phe Val Asp	
65	70
ggg aag t	247
Gly Lys	

<210> SEQ ID NO 186  
 <211> LENGTH: 82  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 186

Gly Val Phe Met Ser Ala His Asn Phe Pro Lys Ser Arg Glu Thr Arg	
1	15
Ala Pro Lys Val Ala Glu Leu Ala Leu Tyr Arg Glu Arg Leu Pro Glu	
	30
Lys Leu Ser Tyr Leu Ala Asp Ala Pro Gln Thr Asp Pro Glu Gly Ser	
	45
Glu Ala Ile Ile Arg Phe Ser Arg Lys Glu Lys Arg Gln Tyr Val Thr	
	60
Ser Glu Lys Asn Gly Lys Ala Thr Lys Trp Ile Val Asp Phe Val Asp	
65	70
	75
	80



-continued

115

```

<210> SEQ ID NO 189
<211> LENGTH: 222
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(222)

<400> SEQUENCE: 189

gaa acc gtg tgc tat gaa atc atg cgc gaa atc att cgc gta cac cat      48
Glu Thr Val Cys Tyr Glu Ile Met Arg Glu Ile Ile Arg Val His His
1                               5                10                15

gta ttt gcc agc gaa caa ttc gtg gtt tat gcc tct cac gcc gtc gcc      96
Val Phe Ala Ser Glu Gln Phe Val Val Tyr Ala Ser His Ala Val Ala
                20                25                30

gat tat ctg att aac gaa gaa tcc cac ggc tta ctg gct gaa ctg gaa     144
Asp Tyr Leu Ile Asn Glu Glu Ser His Gly Leu Leu Ala Glu Leu Glu
                35                40                45

gtg ttc atc ggc aaa caa atc caa gta aaa act gaa gtg ttt tat act     192
Val Phe Ile Gly Lys Gln Ile Gln Val Lys Thr Glu Val Phe Tyr Thr
                50                55                60

cag gaa cag ttt gat gtg gtg atg tag                                  222
Gln Glu Gln Phe Asp Val Val Val Met
65                               70

```

```

<210> SEQ ID NO 190
<211> LENGTH: 73
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 190

Glu Thr Val Cys Tyr Glu Ile Met Arg Glu Ile Ile Arg Val His His
1                               5                10                15

Val Phe Ala Ser Glu Gln Phe Val Val Tyr Ala Ser His Ala Val Ala
                20                25                30

Asp Tyr Leu Ile Asn Glu Glu Ser His Gly Leu Leu Ala Glu Leu Glu
                35                40                45

Val Phe Ile Gly Lys Gln Ile Gln Val Lys Thr Glu Val Phe Tyr Thr
                50                55                60

Gln Glu Gln Phe Asp Val Val Val Met
65                               70

```

```

<210> SEQ ID NO 191
<211> LENGTH: 1670
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1668)

<400> SEQUENCE: 191

atc gaa cgt tat caa cgt tat aac aac acc tca tac aat ctt gag ccg      48
Ile Glu Arg Tyr Gln Arg Tyr Asn Asn Thr Ser Tyr Asn Leu Glu Pro
1                               5                10                15

gac atc aaa tac agt ccg ggc ggg ttg cgc gat ttg cat ttg ttg tat     96
Asp Ile Lys Tyr Ser Pro Gly Gly Leu Arg Asp Leu His Leu Leu Tyr
                20                25                30

tgg atc gcg ttg cgc cat aac ggg gct aaa aat tta cag gaa att tta     144

```



-continued

His	Gly	Phe	Asp	Gln	Arg	Glu	Thr	Glu	Thr	Met	Val	Trp	Leu	Val	Glu	
			340					345					350			
cag	cat	ttg	ctt	atg	tcg	gtc	acg	gca	caa	cgg	cgg	gat	att	cat	gat	1104
Gln	His	Leu	Leu	Met	Ser	Val	Thr	Ala	Gln	Arg	Arg	Asp	Ile	His	Asp	
		355				360						365				
cag	gaa	att	gta	ctg	aat	ttc	gcc	gaa	ctg	gtg	cgt	aat	cag	gtg	cgt	1152
Pro	Glu	Ile	Val	Leu	Asn	Phe	Ala	Glu	Leu	Val	Arg	Asn	Gln	Val	Arg	
	370				375						380					
ttg	gat	tat	tta	acc	tgc	ctg	acc	gtc	gcc	gat	att	gtg	gcg	acc	aat	1200
Leu	Asp	Tyr	Leu	Thr	Cys	Leu	Thr	Val	Ala	Asp	Ile	Val	Ala	Thr	Asn	
	385				390					395					400	
gaa	act	ttg	tgg	aat	agc	tgg	aag	cgt	tct	ttg	ctg	gcg	act	ttg	tac	1248
Glu	Thr	Leu	Trp	Asn	Ser	Trp	Lys	Arg	Ser	Leu	Leu	Ala	Thr	Leu	Tyr	
				405				410						415		
gat	tac	gcc	acc	caa	caa	ttc	gcc	caa	ggg	ctg	gaa	agt	atc	ttg	gat	1296
Asp	Tyr	Ala	Thr	Gln	Gln	Phe	Ala	Gln	Gly	Leu	Glu	Ser	Ile	Leu	Asp	
			420					425						430		
aat	caa	gcg	aaa	gcg	aaa	gga	cac	cgc	cga	tta	gca	ctg	cag	gaa	ata	1344
Asn	Gln	Ala	Lys	Ala	Lys	Gly	His	Arg	Arg	Leu	Ala	Leu	Gln	Glu	Ile	
			435				440							445		
cgt	gaa	aaa	acc	acc	gca	ctt	tcc	gac	aaa	cac	atc	gaa	aaa	ttg	tgg	1392
Arg	Glu	Lys	Thr	Thr	Ala	Leu	Ser	Asp	Lys	His	Ile	Glu	Lys	Leu	Trp	
	450					455					460					
cag	cgt	ttt	ccg	ata	gat	tat	ttc	ttg	cgc	aat	tcg	cca	caa	caa	att	1440
Gln	Arg	Phe	Pro	Ile	Asp	Tyr	Phe	Leu	Arg	Asn	Ser	Pro	Gln	Gln	Ile	
	465				470					475					480	
ggt	tgg	cat	acc	cgt	ttg	ctt	gcc	gaa	ttt	gaa	ggg	gaa	ttg	ttg	gtg	1488
Gly	Trp	His	Thr	Arg	Leu	Leu	Ala	Glu	Phe	Glu	Gly	Glu	Leu	Leu	Val	
				485				490							495	
aaa	gtc	agt	aac	cgg	ttt	tct	gcc	ggc	ggc	acg	gaa	att	ttc	att	tat	1536
Lys	Val	Ser	Asn	Arg	Phe	Ser	Ala	Gly	Gly	Thr	Glu	Ile	Phe	Ile	Tyr	
			500					505						510		
acc	aaa	gac	cga	ccg	aac	ctg	ttt	cac	aaa	gtg	gta	agt	act	atc	ggc	1584
Thr	Lys	Asp	Arg	Pro	Asn	Leu	Phe	His	Lys	Val	Val	Ser	Thr	Ile	Gly	
		515				520								525		
gcg	aaa	aaa	ctc	agt	atc	cat	gat	gcg	caa	att	atc	acc	gcc	aaa	gac	1632
Ala	Lys	Lys	Leu	Ser	Ile	His	Asp	Ala	Gln	Ile	Ile	Thr	Ala	Lys	Asp	
		530				535					540					
ggc	tat	gtg	ttg	gac	agt	ttt	att	gtg	acg	gaa	tta	ga				1670
Gly	Tyr	Val	Leu	Asp	Ser	Phe	Ile	Val	Thr	Glu	Leu					
	545				550					555						

<210> SEQ ID NO 192

<211> LENGTH: 556

<212> TYPE: PRT

<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 192

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

-continued

50	55	60
Gln Gln Phe Leu Phe Lys Val Arg Tyr Ala Leu His Leu Ile Leu Lys		
65	70	75 80
Arg Tyr Asp Asn Arg Leu Leu Phe Asp Arg Gln Leu Lys Val Ser Glu		
	85	90 95
Leu Leu Gly Phe Gln Gly Glu Gly Asn Gln Gly Val Glu Ala Met Met		
	100	105 110
Lys Arg Phe Phe Gln Ala Leu His Ser Ile Ser Leu Leu Ser Glu Leu		
	115	120 125
Leu Val Lys His Tyr Gln Glu His Phe Leu Thr Arg His Ala Val Val		
	130	135 140
Ser Glu Gln Ile Leu Asp Asp Asn Phe Ser Leu Ile Asn Gln Ser Ile		
145	150	155 160
Cys Leu Arg Asn His Gln Cys Phe Glu Gln Gln Pro Glu Ser Ile Leu		
	165	170 175
Asp Leu Phe Tyr His Leu Thr Gln Tyr Pro Gln Ala Glu Ile His Ser		
	180	185 190
Phe Val Leu Arg Glu Leu Tyr Leu Ala Leu Glu Gln Arg Gln Gly Tyr		
	195	200 205
Leu Cys Asp Leu Pro Ala Ala Arg Glu Lys Phe Val Arg Leu Phe Asn		
	210	215 220
Gln Pro Asn Ala Ile Lys Arg Ala Phe Phe Pro Met His Gln Tyr Gly		
225	230	235 240
Val Leu Thr Ala Tyr Leu Pro Gln Trp Gly Asn Val Val Gly Leu Met		
	245	250 255
Gln Phe Asp Leu Phe His Cys Tyr Thr Val Asp Glu His Ile Leu Arg		
	260	265 270
Val Met Leu Lys Leu Glu Ser Phe Leu Glu Gly Ala Ser Ala Gln Ser		
	275	280 285
His Pro Ile Cys His Gln Ile Phe Ser Arg Ile Ser Asp Arg Thr Leu		
	290	295 300
Leu Tyr Ile Ala Ala Leu Phe His Asp Ile Ala Lys Gly Arg Gly Gly		
305	310	315 320
Ser His Glu Leu Leu Gly Ala Val Asp Val Arg Glu Phe Ala Val Arg		
	325	330 335
His Gly Phe Asp Gln Arg Glu Thr Glu Thr Met Val Trp Leu Val Glu		
	340	345 350
Gln His Leu Leu Met Ser Val Thr Ala Gln Arg Arg Asp Ile His Asp		

-continued

355	360	365	
Pro Glu Ile Val Leu Asn Phe Ala Glu Leu Val Arg Asn Gln Val Arg			
370	375	380	
Leu Asp Tyr Leu Thr Cys Leu Thr Val Ala Asp Ile Val Ala Thr Asn			
385	390	395	400
Glu Thr Leu Trp Asn Ser Trp Lys Arg Ser Leu Leu Ala Thr Leu Tyr			
	405	410	415
Asp Tyr Ala Thr Gln Gln Phe Ala Gln Gly Leu Glu Ser Ile Leu Asp			
	420	425	430
Asn Gln Ala Lys Ala Lys Gly His Arg Arg Leu Ala Leu Gln Glu Ile			
	435	440	445
Arg Glu Lys Thr Thr Ala Leu Ser Asp Lys His Ile Glu Lys Leu Trp			
	450	455	460
Gln Arg Phe Pro Ile Asp Tyr Phe Leu Arg Asn Ser Pro Gln Gln Ile			
465	470	475	480
Gly Trp His Thr Arg Leu Leu Ala Glu Phe Glu Gly Glu Leu Leu Val			
	485	490	495
Lys Val Ser Asn Arg Phe Ser Ala Gly Gly Thr Glu Ile Phe Ile Tyr			
	500	505	510
Thr Lys Asp Arg Pro Asn Leu Phe His Lys Val Val Ser Thr Ile Gly			
	515	520	525
Ala Lys Lys Leu Ser Ile His Asp Ala Gln Ile Ile Thr Ala Lys Asp			
	530	535	540
Gly Tyr Val Leu Asp Ser Phe Ile Val Thr Glu Leu			
545	550	555	

<210> SEQ ID NO 193  
 <211> LENGTH: 567  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(567)

<400> SEQUENCE: 193

gtc aac cat tcg ctt tat tcc gta ttg aga ccg att aat ggc gaa agc	48
Val Asn His Ser Leu Tyr Ser Val Leu Arg Pro Ile Asn Gly Glu Ser	
1 5 10 15	
acc ctt att aaa ggt caa gcg aag tgg gtg att tca aga ggt tcg cgt	96
Thr Leu Ile Lys Gly Gln Ala Lys Trp Val Ile Ser Arg Gly Ser Arg	
20 25 30	
aat cgc act ttt cgt gtc ggt caa tct tat tgt cct tgt tgt tta ggg	144
Asn Arg Thr Phe Arg Val Gly Gln Ser Tyr Cys Pro Cys Cys Leu Gly	
35 40 45	
gaa aca cct tat ttg cgt aat gaa tgg cgt ttt gcg tgg cat ttt ggt	192
Glu Thr Pro Tyr Leu Arg Asn Glu Trp Arg Phe Ala Trp His Phe Gly	
50 55 60	

-continued

```

tgt tgc aaa cat caa gtt tta ctt gaa tct aaa tgc cct tgt tgt ggc      240
Cys Ser Lys His Gln Val Leu Leu Glu Ser Lys Cys Pro Cys Cys Gly
65              70              75              80

gaa ctg tat caa cct cat ttg ctt tcc gca gaa aaa cga cac tta aat      288
Glu Leu Tyr Gln Pro His Leu Leu Ser Ala Glu Lys Arg His Leu Asn
85              90              95

tac tgt cat caa tgt ggt gag aaa tta cag gtt gtt aca aca ccg ctt      336
Tyr Cys His Gln Cys Gly Glu Lys Leu Gln Val Val Thr Thr Pro Leu
100              105              110

aat gaa gta gaa att gca aca atg gaa aca ctt aat aac gta ttt atg      384
Asn Glu Val Glu Ile Ala Thr Met Glu Thr Leu Asn Asn Val Phe Met
115              120              125

act aac tca ggt gaa tgt ttc agg aaa cgt gtg aat gca caa gtg tac      432
Thr Asn Ser Gly Glu Cys Phe Arg Lys Arg Val Asn Ala Gln Val Tyr
130              135              140

ttt gct ata ttg cgt tac ttc atc aat ctt att cgg cgt gct acg gtc      480
Phe Ala Ile Leu Arg Tyr Phe Ile Asn Leu Ile Arg Arg Ala Thr Val
145              150              155              160

gta aaa tct act cac gct ttt gca aaa ttt gtg gaa gaa tgt ggt att      528
Val Lys Ser Thr His Ala Phe Ala Lys Phe Val Glu Glu Cys Gly Ile
165              170              175

tct caa gcg gaa ata tgc caa acc aaa acc gcc ctt gca      567
Ser Gln Ala Glu Ile Cys Gln Thr Lys Thr Ala Leu Ala
180              185

```

&lt;210&gt; SEQ ID NO 194

&lt;211&gt; LENGTH: 189

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 194

```

Val Asn His Ser Leu Tyr Ser Val Leu Arg Pro Ile Asn Gly Glu Ser
1              5              10              15

Thr Leu Ile Lys Gly Gln Ala Lys Trp Val Ile Ser Arg Gly Ser Arg
20              25              30

Asn Arg Thr Phe Arg Val Gly Gln Ser Tyr Cys Pro Cys Cys Leu Gly
35              40              45

Glu Thr Pro Tyr Leu Arg Asn Glu Trp Arg Phe Ala Trp His Phe Gly
50              55              60

Cys Ser Lys His Gln Val Leu Leu Glu Ser Lys Cys Pro Cys Cys Gly
65              70              75              80

Glu Leu Tyr Gln Pro His Leu Leu Ser Ala Glu Lys Arg His Leu Asn
85              90              95

Tyr Cys His Gln Cys Gly Glu Lys Leu Gln Val Val Thr Thr Pro Leu
100              105              110

Asn Glu Val Glu Ile Ala Thr Met Glu Thr Leu Asn Asn Val Phe Met
115              120              125

Thr Asn Ser Gly Glu Cys Phe Arg Lys Arg Val Asn Ala Gln Val Tyr
130              135              140

Phe Ala Ile Leu Arg Tyr Phe Ile Asn Leu Ile Arg Arg Ala Thr Val
145              150              155              160

Val Lys Ser Thr His Ala Phe Ala Lys Phe Val Glu Glu Cys Gly Ile
165              170              175

Ser Gln Ala Glu Ile Cys Gln Thr Lys Thr Ala Leu Ala
180              185

```

-continued

```

<210> SEQ ID NO 195
<211> LENGTH: 492
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(492)

<400> SEQUENCE: 195

acc ttg gat gtg ctt cgt tcc gaa act ttc gtt tcc gaa tta aaa ggc      48
Thr Leu Asp Val Leu Arg Ser Glu Thr Phe Val Ser Glu Leu Lys Gly
1           5           10           15

tta aat gct tat cgc acc acc gtg cct gtc atc ggc gga cac tcc ggt      96
Leu Asn Ala Tyr Arg Thr Thr Val Pro Val Ile Gly Gly His Ser Gly
           20           25           30

gtg act att ctt ccg tta tta tct caa gtg caa tac gtt gaa tgg aaa      144
Val Thr Ile Leu Pro Leu Leu Ser Gln Val Gln Tyr Val Glu Trp Lys
           35           40           45

gag gac gaa att gaa ccg tta acc aaa cgc att caa aat gcc ggc acc      192
Glu Asp Glu Ile Glu Pro Leu Thr Lys Arg Ile Gln Asn Ala Gly Thr
           50           55           60

gaa gta gta aac gcg aaa gcc ggc ggc ggt tcc gca acc tta tcc atg      240
Glu Val Val Asn Ala Lys Ala Gly Gly Gly Ser Ala Thr Leu Ser Met
           65           70           75           80

gcg cag gcg gca gcc cgt ttt gct aat gct gta gtc cgc ggt tta caa      288
Ala Gln Ala Ala Ala Arg Phe Ala Asn Ala Val Val Arg Gly Leu Gln
           85           90           95

ggg gaa acc gtc gta gaa tgc agc tat gtg gaa ggc gac gcc aaa tac      336
Gly Glu Thr Val Val Glu Cys Ser Tyr Val Glu Gly Asp Gly Lys Tyr
           100          105          110

gcc cgc ttc ttc gca caa ccg gtt cgc ttc ggc aag gaa ggt gtg gaa      384
Ala Arg Phe Phe Ala Gln Pro Val Arg Phe Gly Lys Glu Gly Val Glu
           115          120          125

gaa atc cta cca atc ggt aaa ctc agc gcc ttg gaa caa cag gct tta      432
Glu Ile Leu Pro Ile Gly Lys Leu Ser Ala Leu Glu Gln Gln Ala Leu
           130          135          140

gaa acc atg tta ccg aca ttg cgt gca gat att gaa tta ggt gag aag      480
Glu Thr Met Leu Pro Thr Leu Arg Ala Asp Ile Glu Leu Gly Glu Lys
           145          150          155          160

ttt att aat cca      492
Phe Ile Asn Pro

```

```

<210> SEQ ID NO 196
<211> LENGTH: 164
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 196

Thr Leu Asp Val Leu Arg Ser Glu Thr Phe Val Ser Glu Leu Lys Gly
1           5           10           15

Leu Asn Ala Tyr Arg Thr Thr Val Pro Val Ile Gly Gly His Ser Gly
           20           25           30

Val Thr Ile Leu Pro Leu Leu Ser Gln Val Gln Tyr Val Glu Trp Lys
           35           40           45

Glu Asp Glu Ile Glu Pro Leu Thr Lys Arg Ile Gln Asn Ala Gly Thr
           50           55           60

Glu Val Val Asn Ala Lys Ala Gly Gly Gly Ser Ala Thr Leu Ser Met

```

-continued

65	70	75	80	
Ala Gln Ala Ala	Ala Arg Phe Ala	Asn Ala Val Val	Arg Gly Leu Gln	
	85	90	95	
Gly Glu Thr Val	Val Glu Cys Ser	Tyr Val Glu Gly	Asp Gly Lys Tyr	
	100	105	110	
Ala Arg Phe Phe	Ala Gln Pro Val	Arg Phe Gly Lys	Glu Gly Val Glu	
	115	120	125	
Glu Ile Leu Pro	Ile Gly Lys Leu	Ser Ala Leu Glu	Gln Gln Ala Leu	
	130	135	140	
Glu Thr Met Leu	Pro Thr Leu Arg	Ala Asp Ile Glu	Leu Gly Glu Lys	
	145	150	155	160
Phe Ile Asn Pro				
<210> SEQ ID NO 197				
<211> LENGTH: 667				
<212> TYPE: DNA				
<213> ORGANISM: Actinobacillus actinomycetemcomitans				
<220> FEATURE:				
<221> NAME/KEY: CDS				
<222> LOCATION: (1)..(666)				
<400> SEQUENCE: 197				
gca tta agc ctg	caa agt ttc aac	ctt gaa gtg ccg	gtt gat gat aaa	48
Ala Leu Ser Leu	Gln Ser Phe Asn	Leu Glu Val Pro	Val Asp Asp Lys	
1	5	10	15	
gaa cgt atc gaa	aac atc aaa cgt	tac acc ggt gaa	aaa tta gat acg	96
Glu Arg Ile Glu	Asn Ile Lys Arg	Tyr Thr Gly Glu	Lys Leu Asp Thr	
	20	25	30	
gcg ttt gtc aac	gga tta gtg gaa	gcc tcg agc cgt	tta cgt cgc tta	144
Ala Phe Val Asn	Gly Leu Val Glu	Ala Ser Ser Arg	Leu Arg Arg Leu	
	35	40	45	
tcc ccg ccg gca	ttc cgt ttc caa	tta acc gaa tta	gcc cgc gcc gcc	192
Ser Pro Pro Ala	Phe Arg Phe Gln	Leu Thr Glu Leu	Ala Arg Ala Ala	
	50	55	60	
caa aaa cgc atc	gtc tta ccg gaa	ggc gac gaa ccg	cgc acc att aaa	240
Gln Lys Arg Ile	Val Leu Pro Glu	Gly Asp Glu Pro	Arg Thr Ile Lys	
	65	70	80	
gcg gcg att tta	tgt gcc gaa cgc	ggt atc gca gaa	tgt gtg ctg tta	288
Ala Ala Ile Leu	Cys Ala Glu Arg	Gly Ile Ala Glu	Cys Val Leu Leu	
	85	90	95	
gcc aaa ccg gaa	gac gta caa cgc	gtg gcg gaa tcc	caa gcc gtt aag	336
Ala Lys Pro Glu	Asp Val Gln Arg	Val Ala Glu Ser	Gln Gly Val Lys	
	100	105	110	
ttg gta aac ggc	att acc gtt atc	gac ccg gcg agc	gtg cgt gaa aac	384
Leu Val Asn Gly	Ile Thr Val Ile	Asp Pro Ala Ser	Val Arg Glu Asn	
	115	120	125	
tat gtg gca cgt	ttg gtt gag cta	cgc aaa gcc aaa	ggc atg acc gaa	432
Tyr Val Ala Arg	Leu Val Glu Leu	Arg Lys Ala Lys	Gly Met Thr Glu	
	130	135	140	
acc atg gcg cgt	gaa caa ttg gaa	gac aat gtt gtg	ctc ggt acc atg	480
Thr Met Ala Arg	Glu Gln Leu Glu	Asp Asn Val Val	Leu Gly Thr Met	
	145	150	160	
atg ttg gaa gcc	aac caa gta gac	ggt ttg gta tcc	ggc gcc gta cac	528
Met Leu Glu Ala	Asn Gln Val Asp	Gly Leu Val Ser	Gly Ala Val His	
	165	170	175	
acc acc gcc aac	acc att cgc ccg	cca atg caa atc	atc aaa acc gca	576
Thr Thr Ala Asn	Thr Ile Arg Pro	Pro Met Gln Ile	Ile Lys Thr Ala	

-continued

180	185	190	
ccg ggc agc tcc att att tct tcc atc ttc ttc atg ttg cta ccg gat			624
Pro Gly Ser Ser Ile Ile Ser Ser Ile Phe Phe Met Leu Leu Pro Asp			
195	200	205	
caa gta ttg gtc tat ggc gat tgc gca gtg aac ccg gat ccg a			667
Gln Val Leu Val Tyr Gly Asp Cys Ala Val Asn Pro Asp Pro			
210	215	220	

<210> SEQ ID NO 198  
 <211> LENGTH: 222  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 198

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

<210> SEQ ID NO 199  
 <211> LENGTH: 267  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(267)

<400> SEQUENCE: 199

ggt ata cgc cct gag cat tta att ccg tct gat gag gca gaa gtt acg			48
Gly Ile Arg Pro Glu His Leu Ile Pro Ser Asp Glu Ala Glu Val Thr			
1	5	10	15
ttg cgc agc aat gtg cag gtg gtg gaa ttg ctt ggt aac gaa acg caa			96

-continued

```

Leu Arg Ser Asn Val Gln Val Val Glu Leu Leu Gly Asn Glu Thr Gln
      20      25      30
att cac ctt gaa atc cct gaa att aaa caa ccg acc tta att tat cgc      144
Ile His Leu Glu Ile Pro Glu Ile Lys Gln Pro Thr Leu Ile Tyr Arg
      35      40      45
caa aat gat gtg gtg ttg gtg aag gag ggg gaa acg atg gac atc ggc      192
Gln Asn Asp Val Val Leu Val Lys Glu Gly Glu Thr Met Asp Ile Gly
      50      55      60
atc att ccg gaa cgt tgc cat ctg ttt aaa gaa gac ggc acc gcc tgc      240
Ile Ile Pro Glu Arg Cys His Leu Phe Lys Glu Asp Gly Thr Ala Cys
      65      70      75      80
caa cgt ttg tat aaa gaa aaa ggc gtt      267
Gln Arg Leu Tyr Lys Glu Lys Gly Val
      85

<210> SEQ ID NO 200
<211> LENGTH: 89
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 200
Gly Ile Arg Pro Glu His Leu Ile Pro Ser Asp Glu Ala Glu Val Thr
 1      5      10      15
Leu Arg Ser Asn Val Gln Val Val Glu Leu Leu Gly Asn Glu Thr Gln
      20      25      30
Ile His Leu Glu Ile Pro Glu Ile Lys Gln Pro Thr Leu Ile Tyr Arg
      35      40      45
Gln Asn Asp Val Val Leu Val Lys Glu Gly Glu Thr Met Asp Ile Gly
      50      55      60
Ile Ile Pro Glu Arg Cys His Leu Phe Lys Glu Asp Gly Thr Ala Cys
      65      70      75      80
Gln Arg Leu Tyr Lys Glu Lys Gly Val
      85

<210> SEQ ID NO 201
<211> LENGTH: 219
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(219)

<400> SEQUENCE: 201
tac atc gtc atc gcc ttt gtg gtg tca cag tta ttg gac gga aat ctg      48
Tyr Ile Val Ile Ala Phe Val Val Ser Gln Leu Leu Asp Gly Asn Leu
 1      5      10      15
ctg gtg ccg ttt ttg ttc tcc gaa gcg gtc aat ctg cac ccg ttg gtg      96
Leu Val Pro Phe Leu Phe Ser Glu Ala Val Asn Leu His Pro Leu Val
      20      25      30
atc atc att gcc gtt ttg att ttc ggt ggc ttg tgg gga ttc tgg ggc      144
Ile Ile Ile Ala Val Leu Ile Phe Gly Gly Leu Trp Gly Phe Trp Gly
      35      40      45
gta ttt ttt gcc att ccg ctg gcg act ttg gtg aaa gcg gtg gtg aac      192
Val Phe Phe Ala Ile Pro Leu Ala Thr Leu Val Lys Ala Val Val Asn
      50      55      60
gct tgg cct tcc aat gaa gcg gtg gaa      219
Ala Trp Pro Ser Asn Glu Ala Val Glu
      65      70

```

-continued

```

<210> SEQ ID NO 202
<211> LENGTH: 73
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 202
Tyr Ile Val Ile Ala Phe Val Val Ser Gln Leu Leu Asp Gly Asn Leu
1      5      10      15
Leu Val Pro Phe Leu Phe Ser Glu Ala Val Asn Leu His Pro Leu Val
20     25     30
Ile Ile Ile Ala Val Leu Ile Phe Gly Gly Leu Trp Gly Phe Trp Gly
35     40     45
Val Phe Phe Ala Ile Pro Leu Ala Thr Leu Val Lys Ala Val Val Asn
50     55     60
Ala Trp Pro Ser Asn Glu Ala Val Glu
65     70

<210> SEQ ID NO 203
<211> LENGTH: 631
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(630)

<400> SEQUENCE: 203
cct ttc gcc atc gaa agt gac gag aaa ttt gcc tcc gcc tgc att cgt      48
Pro Phe Ala Ile Glu Ser Asp Glu Lys Phe Ala Ser Ala Cys Ile Arg
1      5      10     15
tgc ggt cag tgc gtg caa gcc tgc cct tat gat atg ttg cat ttg gca      96
Cys Gly Gln Cys Val Gln Ala Cys Pro Tyr Asp Met Leu His Leu Ala
20     25     30
tcg ttg cta tca cca atg gaa gcg ggg acg ccg tat ttt atc gcg cgc      144
Ser Leu Leu Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg
35     40     45
gat aaa cct tgc gaa atg tgt ccg gat att cct tgc gcc cat gcg tgt      192
Asp Lys Pro Cys Glu Met Cys Pro Asp Ile Pro Cys Ala His Ala Cys
50     55     60
ccg agc ggt gcg tta gat cgt gag gcg cag gat att aat caa tcc cgt      240
Pro Ser Gly Ala Leu Asp Arg Glu Ala Gln Asp Ile Asn Gln Ser Arg
65     70     75     80
atg ggg ctg gcg gtg ttg ctg gat cat gaa acc tgc ttg aac tgg caa      288
Met Gly Leu Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln
85     90     95
ggc ttg cgt tgc gat gtg tgt tat ccg gtt tgt ccg ttg att gat aaa      336
Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asp Lys
100    105    110
gcc att acg ctg gaa agc cat cgt aat gag cgc acc ggc aag cac gcg      384
Ala Ile Thr Leu Glu Ser His Arg Asn Glu Arg Thr Gly Lys His Ala
115    120    125
gtg ttt att ccg acg gtg cat tcc gat ggc tgt acc ggc tgt ggc aaa      432
Val Phe Ile Pro Thr Val His Ser Asp Gly Cys Thr Gly Cys Gly Lys
130    135    140
tgc gaa caa gcg tgt gtc ttg gaa gaa gcg gca atc aaa gta tta ccg      480
Cys Glu Gln Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
145    150    155    160
atg cat ttg gcg aaa ggc atg tta ggc aaa cat tat cgt ttg ggt tgg      528
Met His Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp

```

-continued

165	170	175	
gaa gaa aag gcg aaa gcc gga cat tcc ttg gcg ccg aaa gat ttg att			576
Glu Glu Lys Ala Lys Ala Gly His Ser Leu Ala Pro Lys Asp Leu Ile			
180	185	190	
tcg atg ccg acc cgt atg ccg gaa gcc aca atg ccg gta atg ggc gca			624
Ser Met Pro Thr Arg Met Pro Glu Ala Thr Met Pro Val Met Gly Ala			
195	200	205	
gaa gac a			631
Glu Asp			
210			

<210> SEQ ID NO 204  
 <211> LENGTH: 210  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 204

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

<210> SEQ ID NO 205  
 <211> LENGTH: 354  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(354)

<400> SEQUENCE: 205

tgc ctg gaa cgg gtg aaa cgg ttg gag aag caa ggg gtg att atg ggg 48

-continued

Cys	Leu	Glu	Arg	Val	Lys	Arg	Leu	Glu	Lys	Gln	Gly	Val	Ile	Met	Gly	
1				5					10					15		
tat	cgt	gct	ttg	ctg	aat	ccc	gca	tta	ttg	gat	tcg	ccg	ttg	ttg	gtg	96
Tyr	Arg	Ala	Leu	Leu	Asn	Pro	Ala	Leu	Leu	Asp	Ser	Pro	Leu	Leu	Val	
			20					25					30			
atc	gtg	gaa	att	acg	ctg	gta	cgt	ggc	aag	ccc	gat	gtg	ttt	gaa	gaa	144
Ile	Val	Glu	Ile	Thr	Leu	Val	Arg	Gly	Lys	Pro	Asp	Val	Phe	Glu	Glu	
		35					40					45				
ttt	aac	gcg	gcg	gtg	cag	cag	tta	gat	gaa	att	cag	gaa	tgc	cat	ttg	192
Phe	Asn	Ala	Ala	Val	Gln	Gln	Leu	Asp	Glu	Ile	Gln	Glu	Cys	His	Leu	
	50					55					60					
gtt	tcc	ggt	gat	ttc	gat	tat	tta	ttg	aaa	aca	cgg	gtg	gcg	gat	atg	240
Val	Ser	Gly	Asp	Phe	Asp	Tyr	Leu	Leu	Lys	Thr	Arg	Val	Ala	Asp	Met	
65					70					75				80		
gcg	gcg	tat	cgt	aaa	ttg	ctg	ggg	acc	acc	ttg	ctg	cgc	ctg	ccc	ggg	288
Ala	Ala	Tyr	Arg	Lys	Leu	Leu	Gly	Thr	Thr	Leu	Leu	Arg	Leu	Pro	Gly	
				85					90					95		
gtg	aac	gac	acg	cgc	act	tat	gtg	gtg	atg	gaa	gaa	gtg	aaa	caa	acg	336
Val	Asn	Asp	Thr	Arg	Thr	Tyr	Val	Val	Met	Glu	Glu	Val	Lys	Gln	Thr	
			100					105					110			
aat	ttt	tta	cag	tta	aaa											354
Asn	Phe	Leu	Gln	Leu	Lys											
			115													

&lt;210&gt; SEQ ID NO 206

&lt;211&gt; LENGTH: 118

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 206

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

&lt;210&gt; SEQ ID NO 207

&lt;211&gt; LENGTH: 613

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;220&gt; FEATURE:

&lt;221&gt; NAME/KEY: CDS

&lt;222&gt; LOCATION: (1)..(612)

&lt;400&gt; SEQUENCE: 207

atg	agt	tta	aaa	ata	tta	tta	aat	cag	ccg	caa	tac	gat	ccg	att	cgt	48
Met	Ser	Leu	Lys	Ile	Leu	Leu	Asn	Gln	Pro	Gln	Tyr	Asp	Pro	Ile	Arg	

-continued

1	5	10	15	
gac aaa aaa gcc gag cgc aac tta ttt gcc cgt cgc gct ttg gtg tca				96
Asp Lys Lys Ala Glu Arg Asn Leu Phe Ala Arg Arg Ala Leu Val Ser	20	25	30	
ttt atc gcc gtg ttg gtg ttg tcg gtg gtg tta att tta aac ttg tat				144
Phe Ile Gly Val Leu Val Leu Ser Val Val Leu Ile Leu Asn Leu Tyr	35	40	45	
gat ttg cag gtg gtc aat tat gac ggt tat caa acc cgt tcc aac gcc				192
Asp Leu Gln Val Val Asn Tyr Asp Gly Tyr Gln Thr Arg Ser Asn Gly	50	55	60	
aat cgt att aag ttg ttg ccg ctg ccg ccg act cgc ggg ttg att tat				240
Asn Arg Ile Lys Leu Leu Pro Leu Pro Pro Thr Arg Gly Leu Ile Tyr	65	70	80	
gat cgc aac gcc aaa ctg ctg gcg gaa aat ctg acc ttt ttc ggg ctt				288
Asp Arg Asn Gly Lys Leu Leu Ala Glu Asn Leu Thr Phe Phe Gly Leu	85	90	95	
tat atc gtg cct gaa aag gtg gaa aat tta gac cgc act ttt gag gag				336
Tyr Ile Val Pro Glu Lys Val Glu Asn Leu Asp Arg Thr Phe Glu Glu	100	105	110	
ctg agg gtg ttg gta gcc tta act gat gaa gat att gcg aat ttt aac				384
Leu Arg Val Leu Val Gly Leu Thr Asp Glu Asp Ile Ala Asn Phe Asn	115	120	125	
aag gaa cgg cgt cgc tcc tcc cgt tat atg ccg att atg ctg aaa cga				432
Lys Glu Arg Arg Arg Ser Ser Arg Tyr Met Pro Ile Met Leu Lys Arg	130	135	140	
aat cta acg gaa gag caa att gcc cgt ttt gcg gtg aat caa tac aat				480
Asn Leu Thr Glu Glu Gln Ile Ala Arg Phe Ala Val Asn Gln Tyr Asn	145	150	160	
ttc cag agt ttg gat gtg aaa ccc tac ttt aag cgc cat tat tta tac				528
Phe Gln Ser Leu Asp Val Lys Pro Tyr Phe Lys Arg His Tyr Leu Tyr	165	170	175	
ggc gaa ccg ctg acc cat gtt ttg gcc tat gtg tca aaa att aac gat				576
Gly Glu Pro Leu Thr His Val Leu Gly Tyr Val Ser Lys Ile Asn Asp	180	185	190	
cgt gat gta gaa cgc ttg aaa aaa gag gaa aag tac g				613
Arg Asp Val Glu Arg Leu Lys Lys Glu Glu Lys Tyr	195	200		

<210> SEQ ID NO 208  
 <211> LENGTH: 204  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <400> SEQUENCE: 208

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

-continued

---

Tyr Ile Val Pro Glu Lys Val Glu Asn Leu Asp Arg Thr Phe Glu Glu  
 100 105 110  
 Leu Arg Val Leu Val Gly Leu Thr Asp Glu Asp Ile Ala Asn Phe Asn  
 115 120 125  
 Lys Glu Arg Arg Arg Ser Ser Arg Tyr Met Pro Ile Met Leu Lys Arg  
 130 135 140  
 Asn Leu Thr Glu Glu Gln Ile Ala Arg Phe Ala Val Asn Gln Tyr Asn  
 145 150 155 160  
 Phe Gln Ser Leu Asp Val Lys Pro Tyr Phe Lys Arg His Tyr Leu Tyr  
 165 170 175  
 Gly Glu Pro Leu Thr His Val Leu Gly Tyr Val Ser Lys Ile Asn Asp  
 180 185 190  
 Arg Asp Val Glu Arg Leu Lys Lys Glu Glu Lys Tyr  
 195 200

<210> SEQ ID NO 209  
 <211> LENGTH: 631  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(630)

<400> SEQUENCE: 209

cgc tta gca caa cat tca tcg gaa aaa ctg acc gca ctt tcc cat gca	48
Arg Leu Ala Gln His Ser Ser Glu Lys Leu Thr Ala Leu Ser His Ala	
1 5 10 15	
acc acg cat tct gac gcc caa agt gcg gta gaa aat cag agt gaa tct	96
Thr Thr His Ser Asp Ala Gln Ser Ala Val Glu Asn Gln Ser Glu Ser	
20 25 30	
gat agc gac gaa act gat gcg gat gtg ttg tta ggc gag gat tat cgt	144
Asp Ser Asp Glu Thr Asp Ala Asp Val Leu Leu Gly Glu Asp Tyr Arg	
35 40 45	
tgg gag tgg agc aac ccc gag ctt gcc aat att gag caa ggc cct aag	192
Trp Glu Trp Ser Asn Pro Glu Leu Ala Asn Ile Glu Gln Gly Pro Lys	
50 55 60	
ccc tcc gaa atc aaa gcc gcc att ttg cag gac atc act cct gaa tta	240
Pro Ser Glu Ile Lys Ala Ala Ile Leu Gln Asp Ile Thr Pro Glu Leu	
65 70 75 80	
cag caa aaa atc gtc aat tta act caa acg caa gat cgc tgg gcg cag	288
Gln Gln Lys Ile Val Asn Leu Thr Gln Thr Gln Asp Arg Trp Ala Gln	
85 90 95	
ctg att gag caa agc ggt gta gaa aat ctc acc aaa gag ttc gcc tta	336
Leu Ile Glu Gln Ser Gly Val Glu Asn Leu Thr Lys Glu Phe Ala Leu	
100 105 110	
aat acc ttc att tgg cag gaa aat gac gcg gag ttt aaa ctt ggt gtg	384
Asn Thr Phe Ile Trp Gln Glu Asn Asp Ala Glu Phe Lys Leu Gly Val	
115 120 125	
cgt tcc agc cac ggg cat tta aat cag gat aag cat cgg aag ctg tta	432
Arg Ser Ser His Gly His Leu Asn Gln Asp Lys His Arg Lys Leu Leu	
130 135 140	
caa cag gca ctt tca gtg gtg tta cag aaa gaa att gca ctg acc gtg	480
Gln Gln Ala Leu Ser Val Val Leu Gln Lys Glu Ile Ala Leu Thr Val	
145 150 155 160	
gaa att aac gac asp gaa caa tat ctg acg ccg acg gat tat cgc cgt	528
Glu Ile Asn Asp Asp Glu Gln Tyr Leu Thr Pro Thr Asp Tyr Arg Arg	
165 170 175	

## -continued

```

aaa acc tat gct caa ttg cgt gag cag gcg aaa cag gat ttg ttg caa 576
Lys Thr Tyr Ala Gln Leu Arg Glu Gln Ala Lys Gln Asp Leu Leu Gln
      180                      185                      190

gat gaa aag ttg caa cta ttg gag cgt gaa ttt gat tgt cag gtt gat 624
Asp Glu Lys Leu Gln Leu Leu Glu Arg Glu Phe Asp Cys Gln Val Asp
      195                      200                      205

gtg aaa a 631
Val Lys
    210

```

```

<210> SEQ ID NO 210
<211> LENGTH: 210
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```
<400> SEQUENCE: 210
```

```

Arg Leu Ala Gln His Ser Ser Glu Lys Leu Thr Ala Leu Ser His Ala
1                      5                      10                      15

Thr Thr His Ser Asp Ala Gln Ser Ala Val Glu Asn Gln Ser Glu Ser
20                      25                      30

Asp Ser Asp Glu Thr Asp Ala Asp Val Leu Leu Gly Glu Asp Tyr Arg
35                      40                      45

Trp Glu Trp Ser Asn Pro Glu Leu Ala Asn Ile Glu Gln Gly Pro Lys
50                      55                      60

Pro Ser Glu Ile Lys Ala Ala Ile Leu Gln Asp Ile Thr Pro Glu Leu
65                      70                      75                      80

Gln Gln Lys Ile Val Asn Leu Thr Gln Thr Gln Asp Arg Trp Ala Gln
85                      90                      95

Leu Ile Glu Gln Ser Gly Val Glu Asn Leu Thr Lys Glu Phe Ala Leu
100                     105                     110

Asn Thr Phe Ile Trp Gln Glu Asn Asp Ala Glu Phe Lys Leu Gly Val
115                     120                     125

Arg Ser Ser His Gly His Leu Asn Gln Asp Lys His Arg Lys Leu Leu
130                     135                     140

Gln Gln Ala Leu Ser Val Val Leu Gln Lys Glu Ile Ala Leu Thr Val
145                     150                     155                     160

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

Lys Thr Tyr Ala Gln Leu Arg Glu Gln Ala Lys Gln Asp Leu Leu Gln
180                     185                     190

Asp Glu Lys Leu Gln Leu Leu Glu Arg Glu Phe Asp Cys Gln Val Asp
195                     200                     205

Val Lys
210

```

```

<210> SEQ ID NO 211
<211> LENGTH: 1155
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1155)

```

```
<400> SEQUENCE: 211
```

```

ccc gaa cat ata aaa gac aag gta tcg aga ggt ttc att atg gca agt 48
Pro Glu His Ile Lys Asp Lys Val Ser Arg Gly Phe Ile Met Ala Ser
1                      5                      10                      15

```

-continued

gta aca ttg cgc aat gtg ggc aaa tct tac gga aac gta cat att tcc Val Thr Leu Arg Asn Val Gly Lys Ser Tyr Gly Asn Val His Ile Ser 20 25 30	96
aaa gat att aat ttg gat att gaa gaa ggc gaa ttt gtc gtc ttt gtc Lys Asp Ile Asn Leu Asp Ile Glu Glu Gly Glu Phe Val Val Phe Val 35 40 45	144
gga ccg tcc ggt tgc ggt aaa tcc aca tta ttg cga atg att gcc gga Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu Arg Met Ile Ala Gly 50 55 60	192
ctt gag gat att acc acc ggt gaa ctt tac atc ggt gaa aaa ccg atg Leu Glu Asp Ile Thr Thr Gly Glu Leu Tyr Ile Gly Glu Lys Arg Met 65 70 75 80	240
aac gat gtg ccg ccg gca aag cgc ggt atc ggt atg gtg ttc caa tct Asn Asp Val Pro Ala Lys Arg Gly Ile Gly Met Val Phe Gln Ser 85 90 95	288
tac gcc ctg tac ccg cac ttg gat gtg gca gaa aat atg tct ttc ggg Tyr Ala Leu Tyr Pro His Leu Asp Val Ala Glu Asn Met Ser Phe Gly 100 105 110	336
ctg aaa tta gcc ggt gta aat aaa acg gaa ccg gat cag cgc gtt aat Leu Lys Leu Ala Gly Val Asn Lys Thr Glu Arg Asp Gln Arg Val Asn 115 120 125	384
cag gtt gcc gaa att tta cag ctt gcc cat ttg ctt gaa cgt aaa ccg Gln Val Ala Glu Ile Leu Gln Leu Ala His Leu Leu Glu Arg Lys Pro 130 135 140	432
aaa gcc ttg tcg ggc ggt cag cgt caa cgt gtg gcg att ggg cga acc Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Ile Gly Arg Thr 145 150 155 160	480
ctt gtt tcc cag cca gaa gta ttc ttg ctg gac gaa ccg ctt tcc aac Leu Val Ser Gln Pro Glu Val Phe Leu Leu Asp Glu Pro Leu Ser Asn 165 170 175	528
tta gat gcc gcc ttg cgc gta caa atg ccg gtg gaa atc tcc aaa tta Leu Asp Ala Ala Leu Arg Val Gln Met Arg Val Glu Ile Ser Lys Leu 180 185 190	576
cac aaa aaa ctc aac cgc acc atg att tat gtt acc cat gac caa gtg His Lys Lys Leu Asn Arg Thr Met Ile Tyr Val Thr His Asp Gln Val 195 200 205	624
gaa gcc atg acc ctg gcg gac aaa atc gtg gtg ttg aat gcg ggc ggt Glu Ala Met Thr Leu Ala Asp Lys Ile Val Val Leu Asn Ala Gly Gly 210 215 220	672
att gcg cag gtg ggg aaa ccg ctg gaa ctt tac cat tat ccg caa aat Ile Ala Gln Val Gly Lys Pro Leu Glu Leu Tyr His Tyr Pro Gln Asn 225 230 235 240	720
cgt ttc gtg gcc ggt ttt atc ggt tca ccg aaa atg aat ttc ctg ccg Arg Phe Val Ala Gly Phe Ile Gly Ser Pro Lys Met Asn Phe Leu Pro 245 250 255	768
gtg aaa gtg act gct gtg gaa aaa gag ccg gtg caa atc gaa ttg ccc Val Lys Val Thr Ala Val Glu Lys Glu Arg Val Gln Ile Glu Leu Pro 260 265 270	816
gac gcc aac cat cat aac ttc tgg atc ccg gtt tcc ggt aat ggc gtg Asp Ala Asn His His Asn Phe Trp Ile Pro Val Ser Gly Asn Gly Val 275 280 285	864
aaa gtg ggt gaa aac ctt tca tta ggt ata cgc cct gag cat tta att Lys Val Gly Glu Asn Leu Ser Leu Gly Ile Arg Pro Glu His Leu Ile 290 295 300	912
ccg tct gat gag gca gaa gtt acg ttg cgc agc aat gtg cag gtg gtg Pro Ser Asp Glu Ala Glu Val Thr Leu Arg Ser Asn Val Gln Val Val 305 310 315 320	960

-continued

```

gaa ttg ctt ggt aac gaa acg caa att cac ctt gaa atc cct gaa att    1008
Glu Leu Leu Gly Asn Glu Thr Gln Ile His Leu Glu Ile Pro Glu Ile
                325                      330                      335

aaa caa ccg acc tta att tat cgc caa aat gat gtg gtg ttg gtg aag    1056
Lys Gln Pro Thr Leu Ile Tyr Arg Gln Asn Asp Val Val Leu Val Lys
                340                      345                      350

gag ggg gaa acg atg gac atc ggc atc att ccg gaa cgt tgc cat ctg    1104
Glu Gly Glu Thr Met Asp Ile Gly Ile Ile Pro Glu Arg Cys His Leu
                355                      360                      365

ttt aaa gaa gac ggc acc gcc tgc caa cgt ttg tat aaa gaa aaa ggc    1152
Phe Lys Glu Asp Gly Thr Ala Cys Gln Arg Leu Tyr Lys Glu Lys Gly
                370                      375                      380

gtt
Val
385

```

&lt;210&gt; SEQ ID NO 212

&lt;211&gt; LENGTH: 385

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 212

```

Pro Glu His Ile Lys Asp Lys Val Ser Arg Gly Phe Ile Met Ala Ser
1                    5                      10                      15

Val Thr Leu Arg Asn Val Gly Lys Ser Tyr Gly Asn Val His Ile Ser
                20                      25                      30

Lys Asp Ile Asn Leu Asp Ile Glu Glu Gly Glu Phe Val Val Phe Val
                35                      40                      45

Gly Pro Ser Gly Cys Gly Lys Ser Thr Leu Leu Arg Met Ile Ala Gly
                50                      55                      60

Leu Glu Asp Ile Thr Thr Gly Glu Leu Tyr Ile Gly Glu Lys Arg Met
65                      70                      75                      80

Asn Asp Val Pro Pro Ala Lys Arg Gly Ile Gly Met Val Phe Gln Ser
                85                      90                      95

Tyr Ala Leu Tyr Pro His Leu Asp Val Ala Glu Asn Met Ser Phe Gly
                100                     105                     110

Leu Lys Leu Ala Gly Val Asn Lys Thr Glu Arg Asp Gln Arg Val Asn
                115                     120                     125

Gln Val Ala Glu Ile Leu Gln Leu Ala His Leu Leu Glu Arg Lys Pro
                130                     135                     140

Lys Ala Leu Ser Gly Gly Gln Arg Gln Arg Val Ala Ile Gly Arg Thr
145                     150                     155                     160

Leu Val Ser Gln Pro Glu Val Phe Leu Leu Asp Glu Pro Leu Ser Asn
                165                     170                     175

Leu Asp Ala Ala Leu Arg Val Gln Met Arg Val Glu Ile Ser Lys Leu
                180                     185                     190

His Lys Lys Leu Asn Arg Thr Met Ile Tyr Val Thr His Asp Gln Val
                195                     200                     205

Glu Ala Met Thr Leu Ala Asp Lys Ile Val Val Leu Asn Ala Gly Gly
                210                     215                     220

Ile Ala Gln Val Gly Lys Pro Leu Glu Leu Tyr His Tyr Pro Gln Asn
225                     230                     235                     240

Arg Phe Val Ala Gly Phe Ile Gly Ser Pro Lys Met Asn Phe Leu Pro
                245                     250                     255

```

-continued

Val Lys Val Thr Ala Val Glu Lys Glu Arg Val Gln Ile Glu Leu Pro  
 260 265 270  
 Asp Ala Asn His His Asn Phe Trp Ile Pro Val Ser Gly Asn Gly Val  
 275 280 285  
 Lys Val Gly Glu Asn Leu Ser Leu Gly Ile Arg Pro Glu His Leu Ile  
 290 295 300  
 Pro Ser Asp Glu Ala Glu Val Thr Leu Arg Ser Asn Val Gln Val Val  
 305 310 315 320  
 Glu Leu Leu Gly Asn Glu Thr Gln Ile His Leu Glu Ile Pro Glu Ile  
 325 330 335  
 Lys Gln Pro Thr Leu Ile Tyr Arg Gln Asn Asp Val Val Leu Val Lys  
 340 345 350  
 Glu Gly Glu Thr Met Asp Ile Gly Ile Ile Pro Glu Arg Cys His Leu  
 355 360 365  
 Phe Lys Glu Asp Gly Thr Ala Cys Gln Arg Leu Tyr Lys Glu Lys Gly  
 370 375 380  
 Val  
 385

<210> SEQ ID NO 213  
 <211> LENGTH: 447  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(447)

<400> SEQUENCE: 213

atg cca aaa aat gcg caa ttc tac ctg ctt tcc gat gcc tct ccc gca	48
Met Pro Lys Asn Ala Gln Phe Tyr Leu Leu Ser Asp Ala Ser Pro Ala	
1 5 10 15	
cag acg aat ttg tct gcg gtg gaa agc ctt gcc tgc aat ttg gcg gcg	96
Gln Thr Asn Leu Ser Ala Val Glu Ser Leu Ala Cys Asn Leu Ala Ala	
20 25 30	
tcc gcc tgg cgt ttg gga aaa cgg gtt ctg ttg gcg tgt gaa aat gaa	144
Ser Ala Trp Arg Leu Gly Lys Arg Val Leu Leu Ala Cys Glu Asn Glu	
35 40 45	
gcg cag gcg ctc aat att gat gaa gcc ctt tgg caa cgg gaa ccg gac	192
Ala Gln Ala Leu Asn Ile Asp Glu Ala Leu Trp Gln Arg Glu Pro Asp	
50 55 60	
gaa ttc gtc ccg cac aac ctt tcc ggc gaa gcc acc acg tat gcc acg	240
Glu Phe Val Pro His Asn Leu Ser Gly Glu Ala Thr Thr Tyr Ala Thr	
65 70 75 80	
ccc atc gaa atc agc tgg acg ggc aaa cgc aac gca caa agc cgc gat	288
Pro Ile Glu Ile Ser Trp Thr Gly Lys Arg Asn Ala Gln Ser Arg Asp	
85 90 95	
ttg ctg att aat tta caa ccg cag ctg ccg gaa ttc atc aac agc ttt	336
Leu Leu Ile Asn Leu Gln Pro Gln Leu Pro Glu Phe Ile Asn Ser Phe	
100 105 110	
aac caa att atc gat ttc gta ccc gcc gaa gaa caa caa aaa gct tta	384
Asn Gln Ile Ile Asp Phe Val Pro Ala Glu Glu Gln Gln Lys Ala Leu	
115 120 125	
gcg cgg gaa cgt tat aaa caa ttg agg cag ttg ggc tgg gaa ttg agt	432
Ala Arg Glu Arg Tyr Lys Gln Leu Arg Gln Leu Gly Trp Glu Leu Ser	
130 135 140	
acg gag cag gcg ggg	447

-continued

Thr Glu Gln Ala Gly  
145

<210> SEQ ID NO 214  
<211> LENGTH: 149  
<212> TYPE: PRT  
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 214

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

<210> SEQ ID NO 215  
<211> LENGTH: 774  
<212> TYPE: DNA  
<213> ORGANISM: Actinobacillus actinomycetemcomitans  
<220> FEATURE:  
<221> NAME/KEY: CDS  
<222> LOCATION: (1)..(774)

<400> SEQUENCE: 215

aaa gac aac aaa atc tgg cac ttc acc tta cga aaa gaa gca ata tgg 48  
Lys Asp Asn Lys Ile Trp His Phe Thr Leu Arg Lys Glu Ala Ile Trp  
1 5 10 15  
tct aac ggc gaa ccg gtg act gcg cag caa ttt gtt gca agc tgg caa 96  
Ser Asn Gly Glu Pro Val Thr Ala Gln Gln Phe Val Ala Ser Trp Gln  
20 25 30  
cgg ctg gcg caa tcg gat tct cct tta aag cac tat tta cgc tac ctt 144  
Arg Leu Ala Gln Ser Asp Ser Pro Leu Lys His Tyr Leu Arg Tyr Leu  
35 40 45  
aac tta gtc aac gcg gag aaa gtg tta cag caa act ctg ctg cca gag 192  
Asn Leu Val Asn Ala Glu Lys Val Leu Gln Gln Thr Leu Leu Pro Glu  
50 55 60  
cag ttg gga att gtc gcg gaa aat gac cgc act tta cgc tta act tta 240  
Gln Leu Gly Ile Val Ala Glu Asn Asp Arg Thr Leu Arg Leu Thr Leu  
65 70 75 80  
gat aaa gcg acc cct tac ttg ccg caa atg ctg gcg cat atc agc ctg 288  
Asp Lys Ala Thr Pro Tyr Leu Pro Gln Met Leu Ala His Ile Ser Leu  
85 90 95

-continued

ttg cca caa tat ttg tcg cca cat gaa ggc att gtg acc aac ggg gcg	336
Leu Pro Gln Tyr Leu Ser Pro His Glu Gly Ile Val Thr Asn Gly Ala	
100 105 110	
tat caa gtg atg ggg cag caa ggc aat ctc atc cat ttg gaa aag aac	384
Tyr Gln Val Met Gly Gln Gln Gly Asn Leu Ile His Leu Glu Lys Asn	
115 120 125	
ccg caa tat tgg gcg aaa gaa aaa gtg gcg ttt aaa aat gtg gat tat	432
Pro Gln Tyr Trp Ala Lys Glu Lys Val Ala Phe Lys Asn Val Asp Tyr	
130 135 140	
cag aaa atc gca ctg caa cag gac gtc agc gcc tta gat gtg tgg	480
Gln Lys Ile Ala Leu Gln Gln Asp Val Ser Ala Leu Asp Val Val Trp	
145 150 155 160	
cag ccg cag caa caa acg gat caa acg caa tac ttc ccg caa ctt tgc	528
Gln Pro Gln Gln Thr Asp Gln Thr Gln Tyr Phe Pro Gln Leu Cys	
165 170 175	
acc tat ttt tac acc ttt aat ttt aac atg cca caa ctg gcg caa agc	576
Thr Tyr Phe Tyr Thr Phe Asn Phe Asn Met Pro Gln Leu Ala Gln Ser	
180 185 190	
ccg gtg cgt aag gca ttg gca atg atg aca tct gcc cgc agt tta ttg	624
Pro Val Arg Lys Ala Leu Ala Met Met Thr Ser Ala Arg Ser Leu Leu	
195 200 205	
ccg gaa agt aaa aac agg att cct tta acg gat aat ttt tta cca att	672
Pro Glu Ser Lys Asn Arg Ile Pro Leu Thr Asp Asn Phe Leu Pro Ile	
210 215 220	
tcc atg caa acc atc gat agc cgg tgg gag caa acg ccg gtt gaa caa	720
Ser Met Gln Thr Ile Asp Ser Arg Trp Glu Gln Thr Pro Val Glu Gln	
225 230 235 240	
tta tta agc caa gcg cga att gga gag aag gca ccg ctc aaa ctg acc	768
Leu Leu Ser Gln Ala Arg Ile Gly Glu Lys Ala Pro Leu Lys Leu Thr	
245 250 255	
cta agt	774
Leu Ser	

<210> SEQ ID NO 216  
 <211> LENGTH: 258  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <400> SEQUENCE: 216

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



-continued

---

```

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

```

```

<210> SEQ ID NO 219
<211> LENGTH: 159
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(159)

```

```

<400> SEQUENCE: 219

```

```

atg gca aca ggc aaa agc att att tta atg gga gtt tcc agt aca gga      48
Met Ala Thr Gly Lys Ser Ile Ile Leu Met Gly Val Ser Ser Thr Gly
1      5      10      15
aaa aca tca gtg ggg acg gaa gta gca cgt cgt ttg gag ata aaa ctg      96
Lys Thr Ser Val Gly Thr Glu Val Ala Arg Arg Leu Glu Ile Lys Leu
      20      25      30
att gat ggc gat gat ctg cac ccg cgc gcc aat atc ata aaa atg ggc      144
Ile Asp Gly Asp Asp Leu His Pro Arg Ala Asn Ile Ile Lys Met Gly
      35      40      45
gaa gga cat ccg ctc      159
Glu Gly His Pro Leu
      50

```

```

<210> SEQ ID NO 220
<211> LENGTH: 53
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 220

```

```

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

```

```

<210> SEQ ID NO 221
<211> LENGTH: 289
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

-continued

---

```

<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(288)

<400> SEQUENCE: 221
aac att gct tat gcg gcg aaa gac aaa tac agt cgt gaa gaa atc atc      48
Asn Ile Ala Tyr Ala Ala Lys Asp Lys Tyr Ser Arg Glu Glu Ile Ile
1           5           10           15

aaa gcg gca aaa gcg gcg cac gcc atg gaa ttt atc gag cat ttg gaa      96
Lys Ala Ala Lys Ala Ala His Ala Met Glu Phe Ile Glu His Leu Glu
          20           25           30

aac ggt ctg gat acg gtt atc ggc gaa aac ggc gcc agc tta tcc ggc      144
Asn Gly Leu Asp Thr Val Ile Gly Glu Asn Gly Ala Ser Leu Ser Gly
          35           40           45

ggt caa cgc cag cgt tta gcc atc gcc cgc gcc ttg ttg cgt aac tcg      192
Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Arg Asn Ser
          50           55           60

ccg gta ttg att tta gat gaa gcc acc tcg gca ttg gat acg gaa tcc      240
Pro Val Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
65           70           75           80

gaa cgc gca att caa gcg gca ttg gaa gaa atc caa aaa gat cgc acg g      289
Glu Arg Ala Ile Gln Ala Ala Leu Glu Glu Ile Gln Lys Asp Arg Thr
          85           90           95

<210> SEQ ID NO 222
<211> LENGTH: 96
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 222
Asn Ile Ala Tyr Ala Ala Lys Asp Lys Tyr Ser Arg Glu Glu Ile Ile
1           5           10           15

Lys Ala Ala Lys Ala Ala His Ala Met Glu Phe Ile Glu His Leu Glu
          20           25           30

Asn Gly Leu Asp Thr Val Ile Gly Glu Asn Gly Ala Ser Leu Ser Gly
          35           40           45

Gly Gln Arg Gln Arg Leu Ala Ile Ala Arg Ala Leu Leu Arg Asn Ser
          50           55           60

Pro Val Leu Ile Leu Asp Glu Ala Thr Ser Ala Leu Asp Thr Glu Ser
65           70           75           80

Glu Arg Ala Ile Gln Ala Ala Leu Glu Glu Ile Gln Lys Asp Arg Thr
          85           90           95

<210> SEQ ID NO 223
<211> LENGTH: 353
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(351)

<400> SEQUENCE: 223
tcg aac atc aac cct gat gat cca agt gcg att atc gaa ggc aac gaa      48
Ser Asn Ile Asn Pro Asp Asp Pro Ser Ala Ile Ile Glu Gly Asn Glu
1           5           10           15

aaa gtg gtt cgc cct cgt tta acc gac gcg gaa ttc ttc tcc aaa acc      96
Lys Val Val Arg Pro Arg Leu Thr Asp Ala Glu Phe Phe Ser Lys Thr
          20           25           30

gac tta aaa caa aaa tta gtg gat cgc tta ccg cgc ttg gaa act gtg      144

```

-continued

```

Asp Leu Lys Gln Lys Leu Val Asp Arg Leu Pro Arg Leu Glu Thr Val
   35          40          45
ttg ttc caa caa caa ctt ggc aca ttg cgt gat aaa acc gac cgc atc   192
Leu Phe Gln Gln Gln Leu Gly Thr Leu Arg Asp Lys Thr Asp Arg Ile
   50          55          60
gaa caa ctt gcg ggt gca atc gcc aaa caa atc ggt gcc gac gaa gcg   240
Glu Gln Leu Ala Gly Ala Ile Ala Lys Gln Ile Gly Ala Asp Glu Ala
   65          70          75
aaa gca aaa cgt gcg ggc ttg ctg tca aaa tgc gat ttg atg acc aat   288
Lys Ala Lys Arg Ala Gly Leu Leu Ser Lys Cys Asp Leu Met Thr Asn
   85          90          95
atg gtg ttt gaa ttc acc gac acc caa ggc gta atg ggt atg cac tat   336
Met Val Phe Glu Phe Thr Asp Thr Gln Gly Val Met Gly Met His Tyr
   100          105          110
gcc cgt cac gac ggc ga   353
Ala Arg His Asp Gly
   115

<210> SEQ ID NO 224
<211> LENGTH: 117
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 224
Ser Asn Ile Asn Pro Asp Asp Pro Ser Ala Ile Ile Glu Gly Asn Glu
 1          5          10          15
Lys Val Val Arg Pro Arg Leu Thr Asp Ala Glu Phe Phe Ser Lys Thr
 20          25          30
Asp Leu Lys Gln Lys Leu Val Asp Arg Leu Pro Arg Leu Glu Thr Val
 35          40          45
Leu Phe Gln Gln Gln Leu Gly Thr Leu Arg Asp Lys Thr Asp Arg Ile
 50          55          60
Glu Gln Leu Ala Gly Ala Ile Ala Lys Gln Ile Gly Ala Asp Glu Ala
 65          70          75
Lys Ala Lys Arg Ala Gly Leu Leu Ser Lys Cys Asp Leu Met Thr Asn
 85          90          95
Met Val Phe Glu Phe Thr Asp Thr Gln Gly Val Met Gly Met His Tyr
 100          105          110
Ala Arg His Asp Gly
 115

<210> SEQ ID NO 225
<211> LENGTH: 366
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(366)

<400> SEQUENCE: 225
cta ttg gaa aaa caa ggg tta att aaa tta aaa gat ccg acc aac ctg   48
Leu Leu Glu Lys Gln Gly Leu Ile Lys Leu Lys Asp Pro Thr Asn Leu
 1          5          10          15
ttc tcc act tct ata gat atc att gaa aat ccg aaa aat tta caa atc   96
Phe Ser Thr Ser Ile Asp Ile Ile Glu Asn Pro Lys Asn Leu Gln Ile
 20          25          30
aaa gaa gtg gat acc tcc gtt gcg gca cgt gcc tta gat gac gtt gat   144
Lys Glu Val Asp Thr Ser Val Ala Ala Arg Ala Leu Asp Asp Val Asp

```

-continued

35	40	45	
ttg gcg gta gtg aat aac aac tac gcc ggt caa gta ggc tta aat gcg			192
Leu Ala Val Val Asn Asn Asn Tyr Ala Gly Gln Val Gly Leu Asn Ala			
50	55	60	
caa gat cac ggc gta ttt gtg gaa gat aaa gat tca ccg tat gta aat			240
Gln Asp His Gly Val Phe Val Glu Asp Lys Asp Ser Pro Tyr Val Asn			
65	70	75	80
att atc gtg gca cgg acc gat aac aaa gac agc aaa gcc gta cag act			288
Ile Ile Val Ala Arg Thr Asp Asn Lys Asp Ser Lys Ala Val Gln Thr			
85	90	95	
ttc gtg aaa gcc tac caa acc ccg gaa gtg gaa caa gaa gcg aaa aaa			336
Phe Val Lys Ala Tyr Gln Thr Pro Glu Val Glu Gln Glu Ala Lys Lys			
100	105	110	
cac ttt aaa gac ggc gtg gta aaa ggc tgg			366
His Phe Lys Asp Gly Val Val Lys Gly Trp			
115	120		
<210> SEQ ID NO 226			
<211> LENGTH: 122			
<212> TYPE: PRT			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<400> SEQUENCE: 226			
Leu Leu Glu Lys Gln Gly Leu Ile Lys Leu Lys Asp Pro Thr Asn Leu			
1	5	10	15
Phe Ser Thr Ser Ile Asp Ile Ile Glu Asn Pro Lys Asn Leu Gln Ile			
20	25	30	
Lys Glu Val Asp Thr Ser Val Ala Ala Arg Ala Leu Asp Asp Val Asp			
35	40	45	
Leu Ala Val Val Asn Asn Asn Tyr Ala Gly Gln Val Gly Leu Asn Ala			
50	55	60	
Gln Asp His Gly Val Phe Val Glu Asp Lys Asp Ser Pro Tyr Val Asn			
65	70	75	80
Ile Ile Val Ala Arg Thr Asp Asn Lys Asp Ser Lys Ala Val Gln Thr			
85	90	95	
Phe Val Lys Ala Tyr Gln Thr Pro Glu Val Glu Gln Glu Ala Lys Lys			
100	105	110	
His Phe Lys Asp Gly Val Val Lys Gly Trp			
115	120		
<210> SEQ ID NO 227			
<211> LENGTH: 465			
<212> TYPE: DNA			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
<220> FEATURE:			
<221> NAME/KEY: CDS			
<222> LOCATION: (1)..(465)			
<400> SEQUENCE: 227			
atg act tgg caa aac gtg tcg atc atc gtt agt tat cct caa act gac			48
Met Thr Trp Gln Asn Val Ser Ile Ile Val Ser Tyr Pro Gln Thr Asp			
1	5	10	15
ata aaa agg gga tct ttt atg aac ttg aaa aaa tta tta ggc gtc gca			96
Ile Lys Arg Gly Ser Phe Met Asn Leu Lys Lys Leu Leu Gly Val Ala			
20	25	30	
aca tta gcc tcc gta ttc gcc tta acg gct tgt aat gaa gag aaa aaa			144
Thr Leu Ala Ser Val Phe Ala Leu Thr Ala Cys Asn Glu Glu Lys Lys			
35	40	45	

-continued

```

ccg gaa gcc gca ccg gca gac aaa ccg gcg gca gaa gcc ccg gca aca    192
Pro Glu Ala Ala Pro Ala Asp Lys Pro Ala Ala Glu Ala Pro Ala Thr
   50                               55                               60

atc aaa gtg ggc gtg atg gca gga ccg gaa cac caa gtg gct gaa atc    240
Ile Lys Val Gly Val Met Ala Gly Pro Glu His Gln Val Ala Glu Ile
   65                               70                               75                               80

gca gcg aaa gtg gca aaa gaa aaa tac aac tta gac gta gaa tac gtt    288
Ala Ala Lys Val Ala Lys Glu Lys Tyr Asn Leu Asp Val Glu Tyr Val
                               85                               90                               95

tta ttc aat gac tac gcc ttg cca aac act gca gtg tct aaa ggt gat    336
Leu Phe Asn Asp Tyr Ala Leu Pro Asn Thr Ala Val Ser Lys Gly Asp
                               100                              105                              110

tta gac gtt aac gca atg caa cat aaa ccg tat tta gac aaa gat tcc    384
Leu Asp Val Asn Ala Met Gln His Lys Pro Tyr Leu Asp Lys Asp Ser
                               115                              120                              125

caa gcg aaa gga ttg aac aac tta gtg atc gtg ggt aat acc ttc gtt    432
Gln Ala Lys Gly Leu Asn Asn Leu Val Ile Val Gly Asn Thr Phe Val
                               130                              135                              140

tac ccg tta gcc ggc tat tca aaa aaa atc aaa    465
Tyr Pro Leu Ala Gly Tyr Ser Lys Lys Ile Lys
   145                               150                               155

```

```

<210> SEQ ID NO 228
<211> LENGTH: 155
<212> TYPE: PRT
<213> ORGANISM: Actinobacillus actinomycetemcomitans

```

```

<400> SEQUENCE: 228

```

```

Met Thr Trp Gln Asn Val Ser Ile Ile Val Ser Tyr Pro Gln Thr Asp
 1                               5                               10                               15

Ile Lys Arg Gly Ser Phe Met Asn Leu Lys Lys Leu Leu Gly Val Ala
 20                               25                               30

Thr Leu Ala Ser Val Phe Ala Leu Thr Ala Cys Asn Glu Glu Lys Lys
 35                               40                               45

Pro Glu Ala Ala Pro Ala Asp Lys Pro Ala Ala Glu Ala Pro Ala Thr
 50                               55                               60

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

Ala Ala Lys Val Ala Lys Glu Lys Tyr Asn Leu Asp Val Glu Tyr Val
 85                               90                               95

Leu Phe Asn Asp Tyr Ala Leu Pro Asn Thr Ala Val Ser Lys Gly Asp
 100                              105                              110

Leu Asp Val Asn Ala Met Gln His Lys Pro Tyr Leu Asp Lys Asp Ser
 115                              120                              125

Gln Ala Lys Gly Leu Asn Asn Leu Val Ile Val Gly Asn Thr Phe Val
 130                              135                              140

Tyr Pro Leu Ala Gly Tyr Ser Lys Lys Ile Lys
 145                               150                               155

```

```

<210> SEQ ID NO 229
<211> LENGTH: 1008
<212> TYPE: DNA
<213> ORGANISM: Actinobacillus actinomycetemcomitans
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1008)

```

-continued

&lt;400&gt; SEQUENCE: 229

atg atg gaa ctc gcc tat ttg caa aaa acg ccg cca aaa cag acc gca Met Met Glu Leu Ala Tyr Leu Gln Lys Thr Pro Pro Lys Gln Thr Ala 1 5 10 15	48
ctt tta aaa gcg gaa tgc gcg gat ttt gtc gtc aaa gag caa ctg ggc Leu Leu Lys Ala Glu Cys Ala Asp Phe Val Val Lys Glu Gln Leu Gly 20 25 30	96
tac gac atg agc ggc gac ggc gaa ttc gtg gcg gtg aaa ata cgc aaa Tyr Asp Met Ser Gly Asp Gly Glu Phe Val Ala Val Lys Ile Arg Lys 35 40 45	144
acc gat tgc aac acc ttg ttt gta ggc gag caa ctg gcg aaa ttc gcc Thr Asp Cys Asn Thr Leu Phe Val Gly Glu Gln Leu Ala Lys Phe Ala 50 55 60	192
ggc att tcg gca cgc aac atg agt tat gcc ggt ttg aaa gat cgc aaa Gly Ile Ser Ala Arg Asn Met Ser Tyr Ala Gly Leu Lys Asp Arg Lys 65 70 75 80	240
gct gtc acc gaa caa tgg ttc agc ctg caa atg ccc ggg caa ccg acg Ala Val Thr Glu Gln Trp Phe Ser Leu Gln Met Pro Gly Gln Pro Thr 85 90 95	288
ccg gat ttc agc caa ttt cac ctt gac ggc gtg gat att ctt gaa gtg Pro Asp Phe Ser Gln Phe His Leu Asp Gly Val Asp Ile Leu Glu Val 100 105 110	336
acc cgc cac caa cgc aaa atc cgt atc ggc agc ctg caa ggc aat cat Thr Arg His Gln Arg Lys Ile Arg Ile Gly Ser Leu Gln Gly Asn His 115 120 125	384
ttt gag att ttg ctg cgc cac gcg gaa gaa acc gac gag ctc aaa gtg Phe Glu Ile Leu Leu Arg His Ala Glu Glu Thr Asp Glu Leu Lys Val 130 135 140	432
cgg ttg gat ttt ctg gca aaa aac ggc ttc ccc aat tat ttc acc gaa Arg Leu Asp Phe Leu Ala Lys Asn Gly Phe Pro Asn Tyr Phe Thr Glu 145 150 155 160	480
cag cgt ttc ggg cgc gac ggc aac aat ctc acc caa gcc cta cgc tgg Gln Arg Phe Gly Arg Asp Gly Asn Asn Leu Thr Gln Ala Leu Arg Trp 165 170 175	528
gcg gcg ggc gaa atc aaa gtg aaa gat cgc aac aag cgc agt ttc tat Ala Ala Gly Glu Ile Lys Val Lys Asp Arg Asn Lys Arg Ser Phe Tyr 180 185 190	576
att tcc gcc gcc cgc agt gag att ttc aat tta atc gtt gcc aaa cgt Ile Ser Ala Ala Arg Ser Glu Ile Phe Asn Leu Ile Val Ala Lys Arg 195 200 205	624
att gaa ctc agt ctg gcg cag cag gtc tta aat gga gac gtt ttg caa Ile Glu Leu Ser Leu Ala Gln Gln Val Leu Asn Gly Asp Val Leu Gln 210 215 220	672
ctg aac ggt tcg cac agt tgg ttt gtg gcg gac gca tcg gaa gat ttg Leu Asn Gly Ser His Ser Trp Phe Val Ala Asp Ala Ser Glu Asp Leu 225 230 235 240	720
acg caa ctg caa caa cgc ttg gca caa cgg gat att ttg ctt acc gca Thr Gln Leu Gln Gln Arg Leu Ala Gln Arg Asp Ile Leu Leu Thr Ala 245 250 255	768
ccg ctt atc ggc gaa gag gac aaa agt gcg gtg gat ttt gag aat gaa Pro Leu Ile Gly Glu Glu Asp Lys Ser Ala Val Asp Phe Glu Asn Glu 260 265 270	816
att ttt gtc gcg cac caa gcc ttg ttc cat ttg atg cgg caa gaa cgc Ile Phe Val Ala His Gln Ala Leu Phe His Leu Met Arg Gln Glu Arg 275 280 285	864
gtg aaa gcc gcc cgc cgt ccg att tta atg cag gcg caa cag ttt caa Val Lys Ala Ala Arg Arg Pro Ile Leu Met Gln Ala Gln Gln Phe Gln 290 295 300	912

-continued

290	295	300	
tgg caa ttt gaa ccg aac ggt ttg cgc ctt aaa ttt tat ttg ccg gca			960
Trp Gln Phe Glu Pro Asn Gly Leu Arg Leu Lys Phe Tyr Leu Pro Ala			
305	310	315	320
ggc agt tac gcc acg gcg ttg gta cgc gag ctg gtg aat gtt gaa aac			1008
Gly Ser Tyr Ala Thr Ala Leu Val Arg Glu Leu Val Asn Val Glu Asn			
325	330	335	
 <210> SEQ ID NO 230			
<211> LENGTH: 336			
<212> TYPE: PRT			
<213> ORGANISM: Actinobacillus actinomycetemcomitans			
 <400> SEQUENCE: 230			
Met Met Glu Leu Ala Tyr Leu Gln Lys Thr Pro Pro Lys Gln Thr Ala			
1	5	10	15
Leu Leu Lys Ala Glu Cys Ala Asp Phe Val Val Lys Glu Gln Leu Gly			
	20	25	30
Tyr Asp Met Ser Gly Asp Gly Glu Phe Val Ala Val Lys Ile Arg Lys			
	35	40	45
Thr Asp Cys Asn Thr Leu Phe Val Gly Glu Gln Leu Ala Lys Phe Ala			
	50	55	60
Gly Ile Ser Ala Arg Asn Met Ser Tyr Ala Gly Leu Lys Asp Arg Lys			
65	70	75	80
Ala Val Thr Glu Gln Trp Phe Ser Leu Gln Met Pro Gly Gln Pro Thr			
	85	90	95
Pro Asp Phe Ser Gln Phe His Leu Asp Gly Val Asp Ile Leu Glu Val			
	100	105	110
Thr Arg His Gln Arg Lys Ile Arg Ile Gly Ser Leu Gln Gly Asn His			
	115	120	125
Phe Glu Ile Leu Leu Arg His Ala Glu Glu Thr Asp Glu Leu Lys Val			
	130	135	140
Arg Leu Asp Phe Leu Ala Lys Asn Gly Phe Pro Asn Tyr Phe Thr Glu			
145	150	155	160
Gln Arg Phe Gly Arg Asp Gly Asn Asn Leu Thr Gln Ala Leu Arg Trp			
	165	170	175
Ala Ala Gly Glu Ile Lys Val Lys Asp Arg Asn Lys Arg Ser Phe Tyr			
	180	185	190
Ile Ser Ala Ala Arg Ser Glu Ile Phe Asn Leu Ile Val Ala Lys Arg			
	195	200	205
Ile Glu Leu Ser Leu Ala Gln Gln Val Leu Asn Gly Asp Val Leu Gln			
	210	215	220
Leu Asn Gly Ser His Ser Trp Phe Val Ala Asp Ala Ser Glu Asp Leu			
225	230	235	240
Thr Gln Leu Gln Gln Arg Leu Ala Gln Arg Asp Ile Leu Leu Thr Ala			
	245	250	255
Pro Leu Ile Gly Glu Glu Asp Lys Ser Ala Val Asp Phe Glu Asn Glu			
	260	265	270
Ile Phe Val Ala His Gln Ala Leu Phe His Leu Met Arg Gln Glu Arg			
	275	280	285
Val Lys Ala Ala Arg Arg Pro Ile Leu Met Gln Ala Gln Gln Phe Gln			
290	295	300	
Trp Gln Phe Glu Pro Asn Gly Leu Arg Leu Lys Phe Tyr Leu Pro Ala			

-continued

305	310	315	320	
Gly Ser Tyr Ala Thr Ala Leu Val Arg Glu Leu Val Asn Val Glu Asn				
	325	330	335	
<210> SEQ ID NO 231 <211> LENGTH: 738 <212> TYPE: DNA <213> ORGANISM: Actinobacillus actinomycetemcomitans <220> FEATURE: <221> NAME/KEY: CDS <222> LOCATION: (1)..(738)				
<400> SEQUENCE: 231				
atg aat att tta tta agt aac gat gac ggc att cac gcg ccg ggc att				48
Met Asn Ile Leu Leu Ser Asn Asp Asp Gly Ile His Ala Pro Gly Ile				
1	5	10	15	
cgt gtg atg gca gaa gca ttg cgt aag att gcc aat gtg acc atc gtc				96
Arg Val Met Ala Glu Ala Leu Arg Lys Ile Ala Asn Val Thr Ile Val				
	20	25	30	
gcg ccg gac agc aac cgc agc gcc gcc tcc agt tcc tta acc ttg gtg				144
Ala Pro Asp Ser Asn Arg Ser Ala Ala Ser Ser Ser Leu Thr Leu Val				
	35	40	45	
aag ccg ttg tat ccg tta cat ttg gaa agc ggt gat tat tgc gtc aac				192
Lys Pro Leu Tyr Pro Leu His Leu Glu Ser Gly Asp Tyr Cys Val Asn				
	50	55	60	
ggc acg ccg gcg gat tgc gtg cat att gcg ctg aac ggt ttt ctt tcc				240
Gly Thr Pro Ala Asp Cys Val His Ile Ala Leu Asn Gly Phe Leu Ser				
	65	70	75	80
ggg cgc atc gat ttg gtg att tcc ggc atc aac gcc ggg gcg aac ctg				288
Gly Arg Ile Asp Leu Val Ile Ser Gly Ile Asn Ala Gly Ala Asn Leu				
	85	90	95	
ggc gat gat gtg cta tat tcc ggc acg gtc gcg gca gca ttt gaa ggg				336
Gly Asp Asp Val Leu Tyr Ser Gly Thr Val Ala Ala Ala Phe Glu Gly				
	100	105	110	
cgt cat ctg ggc ttg ccg tct att gcg gta tcg ctc gat ggt cgt caa				384
Arg His Leu Gly Leu Pro Ser Ile Ala Val Ser Leu Asp Gly Arg Gln				
	115	120	125	
cat ttt gaa acg gcg gcg cgc gtg gta tgc gat ttg gtg ccg aaa tta				432
His Phe Glu Thr Ala Ala Arg Val Val Cys Asp Leu Val Pro Lys Leu				
	130	135	140	
cac gcc caa tta tta ggc aaa cac gaa att ctg aat att aac gtg ccc				480
His Ala Gln Leu Leu Gly Lys His Glu Ile Leu Asn Ile Asn Val Pro				
	145	150	155	160
gat gtg cct tac gaa gaa ctg aaa ggc att aaa gtg tgc cat ttg ggc				528
Asp Val Pro Tyr Glu Glu Leu Lys Gly Ile Lys Val Cys His Leu Gly				
	165	170	175	
tac cgt tct tcc gct tct gaa gtg att aaa cag caa agc ccg cgt ggc				576
Tyr Arg Ser Ser Ala Ser Glu Val Ile Lys Gln Gln Ser Pro Arg Gly				
	180	185	190	
gaa gac atg tat tgg atc ggg ctc agc ggc ttg ccg gaa tat gaa agc				624
Glu Asp Met Tyr Trp Ile Gly Leu Ser Gly Leu Pro Glu Tyr Glu Ser				
	195	200	205	
gaa ggc acc gat ttc cac gcg gtg aaa aac ggc tat gtt tcc att acg				672
Glu Gly Thr Asp Phe His Ala Val Lys Asn Gly Tyr Val Ser Ile Thr				
	210	215	220	
ccg att cag gtg gac atg acc gcg cac cac tca atc aac gct tta caa				720
Pro Ile Gln Val Asp Met Thr Ala His His Ser Ile Asn Ala Leu Gln				
	225	230	235	240

-continued

cgt tgg tta gaa agt gaa 738  
 Arg Trp Leu Glu Ser Glu  
 245

<210> SEQ ID NO 232  
 <211> LENGTH: 246  
 <212> TYPE: PRT  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans

<400> SEQUENCE: 232

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

<210> SEQ ID NO 233  
 <211> LENGTH: 426  
 <212> TYPE: DNA  
 <213> ORGANISM: Actinobacillus actinomycetemcomitans  
 <220> FEATURE:  
 <221> NAME/KEY: CDS  
 <222> LOCATION: (1)..(426)

<400> SEQUENCE: 233

gat ctg ccg ttg gcg aac cct tac gaa atg ctg atc ctc gcg tcc atc 48  
 Asp Leu Pro Leu Ala Asn Pro Tyr Glu Met Leu Ile Leu Ala Ser Ile  
 1 5 10 15  
 gtg gaa aaa gaa acc ggc att gct gca gaa cgc cca caa gtg gcg tcg 96

-continued

---

Val	Glu	Lys	Glu	Thr	Gly	Ile	Ala	Ala	Glu	Arg	Pro	Gln	Val	Ala	Ser		
			20					25					30				
gta	ttc	att	aat	cgg	tta	aaa	gcc	aaa	atg	aag	ctg	caa	acc	gat	ccg		144
Val	Phe	Ile	Asn	Arg	Leu	Lys	Ala	Lys	Met	Lys	Leu	Gln	Thr	Asp	Pro		
		35					40					45					
acc	gtc	att	tac	ggc	atg	ggc	gac	gac	tac	aac	ggc	aat	att	cgc	aaa		192
Thr	Val	Ile	Tyr	Gly	Met	Gly	Asp	Asp	Tyr	Asn	Gly	Asn	Ile	Arg	Lys		
	50					55					60						
aaa	gat	ttg	gaa	acg	cca	acg	cct	tat	aac	acc	tat	gtg	att	gac	ggc		240
Lys	Asp	Leu	Glu	Thr	Pro	Thr	Pro	Tyr	Asn	Thr	Tyr	Val	Ile	Asp	Gly		
65					70					75					80		
ttg	ccg	ccg	aca	ccg	att	gcg	atg	ccg	agt	gaa	gag	gcg	tta	cag	gcg		288
Leu	Pro	Pro	Thr	Pro	Ile	Ala	Met	Pro	Ser	Glu	Glu	Ala	Leu	Gln	Ala		
				85				90						95			
gtg	gca	cat	ccg	gcg	caa	acg	gcg	ttt	tat	tat	ttc	gtg	gca	gac	ggc		336
Val	Ala	His	Pro	Ala	Gln	Thr	Ala	Phe	Tyr	Tyr	Phe	Val	Ala	Asp	Gly		
			100					105					110				
acg	ggg	gga	cac	aaa	ttc	agt	cgt	aat	tta	aac	gaa	cat	aac	aaa	gcg		384
Thr	Gly	Gly	His	Lys	Phe	Ser	Arg	Asn	Leu	Asn	Glu	His	Asn	Lys	Ala		
	115						120					125					
gtg	cag	caa	tat	ttg	cgc	tgg	tac	cgc	gaa	caa	aac	gga	aaa				426
Val	Gln	Gln	Tyr	Leu	Arg	Trp	Tyr	Arg	Glu	Gln	Asn	Gly	Lys				
	130					135					140						

&lt;210&gt; SEQ ID NO 234

&lt;211&gt; LENGTH: 142

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Actinobacillus actinomycetemcomitans

&lt;400&gt; SEQUENCE: 234

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

---

We claim:

1. A method of detecting the presence or absence of *A. actinomycetemcomitans* or an *A. actinomycetemcomitans* antigen in a test sample comprising contacting the test sample with an antibody or a fragment thereof that specifically binds to a polypeptide consisting of SEQ ID NO:146, and detecting an immunocomplex comprising *A. actinomycetemcomitans* or an *A. actinomycetemcomitans* antigen and the antibody or fragment thereof, wherein detection of the immunocomplex indicates the presence of *A. actinomycetemcomitans* or an *A. actinomycetemcomitans* antigen in the test sample.

2. The method of claim 1, wherein the test sample is plaque, saliva, crevicular fluid, sputum, blood, serum, plasma, urine, feces, cerebrospinal fluid, amniotic fluid, wound exudate, or tissue.

3. The method of claim 1, wherein the antibody or fragment thereof is bound to a solid substrate.

4. The method of claim 1, wherein the method is an enzyme-linked immunosorbant assay (ELISA), a radioimmunoassay (RIA), or a western blot assay.

5. A method for detecting an antibody specific for *A. actinomycetemcomitans* in a test sample comprising contacting the test sample with a purified polypeptide comprising SEQ ID NO:146 and detecting formation of an immunocomplex comprising the polypeptide of SEQ ID NO:146 and the antibody specific for *A. actinomycetemcomitans*, wherein detection of the immunocomplex indicates the presence of an antibody specific for *A. actinomycetemcomitans* in the test sample.

6. The method of claim 5, wherein the test sample is plaque, saliva, crevicular fluid, sputum, blood, serum, plasma, urine, feces, cerebrospinal fluid, amniotic fluid, wound exudate, or tissue.

7. The method of claim 5, wherein the polypeptide is bound to a solid substrate.

8. The method of to claim 5, wherein the method is an enzyme-linked immunosorbant assay (ELISA), a radioimmunoassay (RIA), or a western blot assay.

\* \* \* \* \*

专利名称(译)	放线杆菌放线杆菌抗原的鉴定用于牙周病的诊断，治疗和监测		
公开(公告)号	<a href="#">US20060160159A1</a>	公开(公告)日	2006-07-20
申请号	US11/333747	申请日	2006-01-17
[标]申请(专利权)人(译)	佛罗里达大学研究基金会有限公司		
申请(专利权)人(译)	佛罗里达州研究基金会大学		
当前申请(专利权)人(译)	佛罗里达州研究基金会大学		
[标]发明人	HANDFIELD MARTIN HILLMAN JEFFREY DANIEL PROGULSKE FOX ANN		
发明人	HANDFIELD, MARTIN HILLMAN, JEFFREY DANIEL PROGULSKE-FOX, ANN		
IPC分类号	G01N33/554 G01N33/569 G01N33/53 A61K31/7088 A61K38/00 A61K39/00 A61K39/395 A61P1/02 A61P3/10 A61P13/02 A61P19/08 A61P29/00 A61P31/04 A61P35/02 A61P37/02 A61P43/00 C07K14 /195 C07K14/32 C07K16/12 C12N1/15 C12N1/19 C12N1/21 C12N5/10 C12N15/09 C12N15/31 C12P21 /08 C12Q1/68		
CPC分类号	A61K39/00 A61K2039/53 C07K14/285 G01N33/56911 Y10S435/81 A61P1/02 A61P3/10 A61P13/02 A61P19/08 A61P29/00 A61P31/04 A61P35/02 A61P37/02 A61P43/00		
优先权	09/995493 2001-11-28 US PCT/US2002/037235 2002-11-20 WO PCT/US2003/032645 2003-10-15 WO		
其他公开文献	US7498143		
外部链接	<a href="#">Espacenet</a> <a href="#">USPTO</a>		

#### 摘要(译)

提供抗体，多肽和多核苷酸用于检测，预防，改善和治疗由 Actinobacillus actinomycetemcomitans 引起的疾病。