

(19) World Intellectual Property Organization
International Bureau



(43) International Publication Date
26 September 2002 (26.09.2002)

PCT

(10) International Publication Number
WO 02/075507 A2

(51) International Patent Classification⁷: **G06F 1/00**

(21) International Application Number: PCT/US02/01971

(22) International Filing Date: 17 January 2002 (17.01.2002)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
09/809,665 15 March 2001 (15.03.2001) US

(71) Applicant (*for all designated States except US*): **PHARMACIA & UPJOHN COMPANY** [US/US]; 301 Henrietta Street, Kalamazoo, MI 49007 (US).

(72) Inventors; and

(75) Inventors/Applicants (*for US only*): **LOWERY, David, E.** [US/US]; 1207 Woodland Drive, Portage, MI 49024 (US). **FULLER, Troy, E.** [US/US]; 111 Dreamfield Drive, Battle Creek, MI 49014 (US). **KENNEDY, Michael, J.** [US/US]; 2364 Quincy Avenue, Portage, MI 49024 (US).

(74) Agent: **WILLIAMS, Joseph, A., Jr.**; Marshall, Gerstein & Borun, 6300 Sears Tower, 233 South Wacker Drive, Chicago, IL 60606 (US).

(81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, OM, PH, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VN, YU, ZA, ZW.

(84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Published:

— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: ANTI-BACTERIAL VACCINE COMPOSITIONS

(57) Abstract: Gram negative bacterial virulence genes are identified, thereby allowing the identification of novel anti-bacterial agents that target these virulence genes and their products, and the provision of novel gram negative bacterial mutants useful in vaccines.



WO 02/075507 A2

ANTI-BACTERIAL VACCINE COMPOSITIONS

This application is a continuation-in-part of U.S. Patent Application Serial No: 09/545,199, filed April 6, 2000, which claims benefit of U.S. Provisional Patent Application Serial Nos. 60/153,453, filed September 10, 1999 and 60/128,689, filed April 9, 1999.

FIELD OF THE INVENTION

The present invention relates generally to the identification of genes responsible for virulence of *Pasteurellaceae* bacteria, thereby allowing for production of novel attenuated mutant strains useful in vaccines and identification of new anti-bacterial agents that target the virulence genes and their products.

BACKGROUND OF THE INVENTION

The family *Pasteurellaceae* encompasses several significant pathogens that infect a wide variety of animals. In addition to *P. multocida*, prominent members of the family include *Pasteurella (Mannheimia) haemolytica*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*. *P. multocida* is a gram-negative, nonmotile coccobacillus which is found in the normal flora of many wild and domestic animals and is known to cause disease in numerous animal species worldwide [Biberstein, In M. Kilian, W. Frederickson, and E. L. Biberstein (ed.), *Haemophilus, Pasteurella, and Actinobacillus*. Academic Press, London, p. 61-73 (1981)]. The disease manifestations following infection include septicemias, bronchopneumonias, rhinitis, and wound infections [Reviewed in Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993), incorporated herein by reference].

Infection by *P. multocida* generally results from invasion during periods of stress, but transmission may also occur by aerosol or contact exposure, or via flea and tick vectors. In fowl, *P. multocida* infection gives rise to acute to peracute septicemia, particularly prevalent in domestic turkeys and wild waterfowl under stress conditions associated with overcrowding, laying, molting, or severe

climatic change. In cattle, a similar hemorrhagic septicemia follows infection and manifests conditions including high fever and depression, generally followed by quick death. Transmission is most likely through aerosol contact, but infection can also arise during periods of significant climatic change. In rabbits, infection gives rise to recurring purulent rhinitis, generally followed by conjunctivitis, otitis media, sinusitis, subcutaneous abscesses, and chronic bronchopneumonia. In severe infections, rabbit mortality arises from acute fibrinous bronchopneumonia, septicemia, or endotoxemia. Disease states normally arise during periods of stress. In pigs, common *P. multocida* disease states include atrophic rhinitis and bacterial pneumonia. Similar pneumonia conditions are also detected in dogs, cats, goats, and sheep. *P. multocida* is commonly detected in oral flora of many animals and is therefore a common contaminant in bite and scratch wounds.

P. multocida strains are normally designated by capsular serogroup and somatic serotype. Five capsular serogroups (A, B, D, E, and F) and 16 somatic serotypes are distinguished by expression of characteristic heat-stable antigens. Most strains are host specific and rarely infect more than one or two animals. The existence of different serotypes presents a problem for vaccination because traditional killed whole cell bacteria normally provide only serotype-specific protection. However, it has been demonstrated that natural infection with one serotype can lead to immunological protection against multiple serotypes [Shewen, *et al.*, In C. L. Gyles and C. O. Thoen (Ed.), Pathogenesis of Bacterial Infections in Animals. Iowa State University Press, Ames, p. 216-225 (1993)] and cross protection can also be stimulated by using inactivated bacteria grown *in vivo* [Rimler, *et al.*, *Am J Vet Res.* 42:2117-2121 (1981)]. One live spontaneous mutant *P. multocida* strain has been utilized as a vaccine and has been shown to stimulate a strong immune response [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)]. This attenuated strain, however, has been shown to revert to a virulent state or cause mortality if the vaccine recipient is stressed [Davis, *Poultry Digest.* 20:430-434 (1987), Schlink, *et al.*, *Avian Dis.* 31(1):13-21 (1987)].

Another member of the *Pasteurella* family, *A. pleuropneumoniae* exhibits strict host specificity for swine and is the causative agent of highly contagious porcine pleuropneumonia. Infection normally arises in intensive breeding conditions, and is believed to occur by a direct mode of transmission. The disease is often fatal and, as a result, leads to severe economic loss in the swine producing industry. *A. pleuropneumoniae* infection may be chronic or acute, and infection is characterized by a hemorrhagic, necrotic bronchopneumonia with accompanying fibrinous pleuritis. To date, bacterial virulence has been attributed to structural proteins, including serotype-specific capsular polysaccharides, lipopolysaccharides, and surface proteins, as well as extracellular cytolytic toxins. Despite purification and, in some instances cloning, of these virulence factors, the exact role of these virulence factors in *A. pleuropneumoniae* infection is poorly understood.

Twelve serotypes of *A. pleuropneumoniae* have been identified based on antigenic differences in capsular polysaccharides and production of extracellular toxins. Serotypes 1, 5, and 7 are most relevant to *A. pleuropneumoniae* infection in the United States, while serotypes 1, 2, 5, 7, and 9 are predominant in Europe. There are at least three significant extracellular toxins of *A. pleuropneumoniae* that are members of the haemolysin family and are referred to as RTX toxins. RTX toxins are produced by many Gram negative bacteria, including *E. coli*, *Proteus vulgaris*, and *Pasteurella haemolytica*, and the proteins generally share structural and functional characteristics. Toxins from the various serotypes differ, however, in host specificity, target cells, and biological activities.

The major *A. pleuropneumoniae* RTX toxins include ApxI, ApxII, and ApxIII. ApxI and ApxII have haemolytic activity, with ApxI being more potent. ApxIII shows no haemolytic activity, but is cytotoxic for alveolar macrophages and neutrophils. Most *A. pleuropneumoniae* serotypes produce two of these three toxins. For example, serotypes 1, 5, 9, and 11 express ApxI and ApxII, and serotypes 2, 3, 4, 6, and 8 express ApxII and ApxIII. Serotype 10, however, produces only ApxI, and serotypes 7 and 12 express only ApxII. Those *A. pleuropneumoniae* serotypes that produce both ApxI and ApxII are the most virulent strains of the bacteria.

The Apx toxins were demonstrated to be virulence factors in murine models and swine infection using randomly mutated wild type bacteria [Tascon, *et al.*, *Mol. Microbiol.* 14:207-216 (1994)]. Other *A. pleuropneumoniae* mutants have also been generated with targeted mutagenesis to inactivate the gene encoding the AopA outer membrane virulence protein [Mulks and Buysee, *Gene* 165:61-66 (1995)].

At least eleven serotypes (1, 2, 5-9, 12-14 and 16) have been demonstrated within *Mannheimia* [*Pasteurella*] *haemolytica* [Angen, *et al.*, *Vet Microbiol* 65(4):283-90 (1999)], a *Pasteurellaceae* species which is responsible for serious outbreaks of acute pneumonia in neonatal, weaned, growing and adult lambs, calves, and goats [Ackermann, *et al.*, *Microbes Infect* 2(9):1079-88 (2000)]. Transportation, viral infections, overcrowding, and other stressful conditions predispose animals to *M. haemolytica* infection [Ackermann, *et al.*, *supra.*] The leukotoxin (Lkt) of *M. haemolytica* is believed to play a significant role in pathogenesis, causing cell lysis and apoptosis that lead to the lung pathology characteristic of bovine shipping fever [Highlander, *et al.*, *Infect Immun* 68(7):3916-22 (2000)] as well as lung injury in bovine pneumonic pasteurellosis [Jeyaseelan, *et al.*, *Microb Pathog* 30(2):59-69 (2001)]. Lkt is a pore-forming exotoxin that has the unique property of inducing cytolysis only in ruminant leukocytes and platelets [Jeyaseelan, *et al.*, (2001), *supra.*]. Cytolysis of many cell types is mediated by arachidonic acid (AA) and its generation by phospholipases is regulated by G-protein-coupled receptors [Jeyaseelan, *et al.*, (2001) *supra*] Recent studies indicate that *M. haemolytica* Lkt binds to bovine CD18, the common subunit of all beta2 integrins [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)]. It has also been shown that LFA-1 is a Lkt receptor, Lkt binding to LFA-1 is not target cell specific, Lkt binding to bovine LFA-1 correlates with calcium elevation and cytolysis, and bovine LFA-1 expression correlates with the magnitude of Lkt-induced target cell cytolysis [Jeyaseelan, *et al.*, *Infect Immun* 68(1):72-9 (2000)].

In attempts to produce vaccine compositions, traditional killed whole cell bacteria have provided only serotype-specific protection [MacInnes and Smart, *supra*], however, it has been demonstrated that natural infection with a highly virulent

serotype can stimulate strong protective immunity against multiple serotypes [Nielsen, *Nord Vet Med.* 31:407-13 (1979), Nielsen, *Nord Vet Med.* 36:221-234 (1984), Nielsen, *Can J Vet Res.* 29:580-582 (1988), Nielsen, *ACTA Vet Scand.* 15:80-89 (1994)]. One defined live-attenuated vaccine strain producing an inactive form of the ApxII toxin has shown promise for cross protection in swine [Prideaux, *et al.*, *Infection & Immunity* 67:1962-1966 (1999)], while other undefined live-attenuated mutants have also shown promise [Inzana, *et al.*, *Infect Immun.* 61:1682-6, (1993), Paltineanu, *et al.*, *In International Pig Veterinary Society*, 1992, p. 214, Utrera, *et al.*, *In International Pig Veterinary Society*, 1992, p. 213].

Because of the problems associated with vaccine formulations comprising bacterial strains with undefined, spontaneous mutations, there exists a need in the art for rational construction of live attenuated bacterial strains for use in vaccines that will safely stimulate protective immunity against homologous and heterologous *Pasteurellaceae* serotypes. There further exists a need to identify attenuated bacterial strains and genes required for bacterial virulence, thereby facilitating development of methods to identify anti-bacterial agents.

SUMMARY OF THE INVENTION

In general, the present invention provides materials and methods for production and use of vaccine compositions comprising attenuated gram negative bacteria. In one aspect, vaccine compositions of the invention comprise attenuated species in the *Pasteurellaceae* family of bacteria, which is known in the art and described, in part, in Dewhirst, *et al.*, *J. Bacteriol.* 174:2002-2013 (1992), incorporated herein by reference in its entirety. Species in the family include, but are not limited to, *A. actinomycetemcomitans*, *A. capsulatus*, *A. equuli*, *A. lignieresii*, *A. pleuropneumoniae* (*H. pleuropneumoniae*), *A. seminis*, *A. suis* (*H. suis*), *A. ureae* (*p. ureae*), *A. capsulatus*, Bisgaard taxon 11, *H. aegyptius*, *H. aphrophilus*, *H. aphrophilus* (*H. parainfluenzae*), *H. ducreyi*, *H. haemoglobinophilus*, *H. haemolyticus*, *H. influenzae*, *H. paracuniculus*, *H. paragallinarum*, *H. parahaemolyticus*, *H. parainfluenzae*, (*H. paraphrophilus*), *H.*

paraphrohaemolyticus, *H. paraphrophilus*, *H. parasuis*, *H. parasuis* type 5, *H. segnis*,
H. somnus, *Haemophilus* minor group, *Haemophilus* taxon C, *P. aerogenes*, *P. anatis*,
P. avium (*H. avium*), *P. canis*, *P. dagmatis*, *P. gallinarum*, *P. (Mannheimia)*
haemolytica, *P. trehalosi* (*P. haemolytica* biotype T), *P. langaa*, *P. multocida*, *P.*
5 *pneumotropica*, *P. stomatis*, *P. volantium* (*H. parainfluenzae*), *P. volantium*,
Pasteurella species A, *Pasteurella* species B, and *Haemophilus*
paraphrohaemolyticus. Preferably, vaccine compositions comprise attenuated
Pasteurella (Mannheimia) haemolytica, *Actinobacillus pleuropneumoniae*,
Haemophilus somnus, or *Pasteurella multocida* bacteria. In a most preferred
10 embodiment, vaccine compositions of the invention comprise attenuated *Pasteurella*
multocida and *A. plueropneumoniae* bacterial strains.

One aspect of the invention provides gram negative bacterial
 organisms containing a functional mutation in a gene sequence represented by any one
 of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51,
 15 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110,
 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142,
 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and
 174, or species homologs thereof, wherein the mutation inhibits or abolishes
 expression and/or biological activity of an encoded gene product (*i.e.*, the polypeptide
 20 encoded by a gene); said functional mutation resulting in attenuated virulence of the
 bacterial strain. Functional mutations that modulate (*i.e.*, increase or decrease)
 expression and/or biological activity of a gene product include insertions or deletions
 in the protein coding region of the gene itself or in sequences responsible for, or
 involved in, control of gene expression. Deletion mutants include those wherein all or
 25 part of a specific gene sequence is deleted. Also contemplated are compositions, and
 preferably vaccine compositions, comprising mutated and attenuated gram negative
 bacterial organisms, optionally comprising a suitable adjuvant and/or a
 pharmaceutically acceptable diluent or carrier. In order for a modified strain to be
 effective in a vaccine formulation, the attenuation must be significant enough to

prevent the pathogen from evoking severe clinical symptoms, but also insignificant enough to allow limited replication and growth of the bacteria in the host.

The invention also provides polynucleotides encoding gene products that are required for virulence in gram negative bacteria. Polynucleotides of the invention include DNA, such as complementary DNA, genomic DNA including
5 complementary or anti-sense DNA, and wholly or partially synthesized DNA; RNA, including sense and antisense strands; and peptide nucleic acids as described, for example in Corey, *TIBTECH* 15:224-229 (1997). Virulence gene polynucleotides of the invention include those set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21,
10 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, polynucleotides encoding a virulence gene product encoded by a polynucleotide of SEQ ID NOs: 1, 3,
15 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or a species homolog thereof, and polynucleotide that hybridize, under moderately to highly stringent
20 conditions, to the noncoding strand (or complement) of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and
25 174, or species homologs thereof. The invention therefore comprehends gene sequences from *Pasteurellaceae* set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162,
30 163, 164, 166, 168, 170, 172, and 174, as well as related gene sequences from other

gram negative bacterial organisms, including naturally occurring (*i.e.*, species homologs) and artificially induced variants thereof. The invention also comprehends polynucleotides which encode polypeptides deduced from any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof. Knowledge of the sequence of a polynucleotide of the invention makes readily available every possible fragment of that polynucleotide. The invention therefore provides fragments of a polynucleotide of the invention.

The invention further embraces expression constructs comprising polynucleotides of the invention. Host cells transformed, transfected or electroporated with a polynucleotide of the invention are also contemplated. The invention provides methods to produce a polypeptide encoded by a polynucleotide of the invention comprising the steps of growing a host cell of the invention under conditions that permit, and preferably promote, expression of a gene product encoded by the polynucleotide, and isolating the gene product from the host cell or the medium of its growth.

Identification of polynucleotides of the invention makes available the encoded polypeptides. Polypeptides of the invention include full length and fragment, or truncated, proteins; variants thereof; fusion, or chimeric proteins; and analogs, including those wherein conservative amino acid substitutions have been introduced into wild-type polypeptides. Antibodies that specifically recognize polypeptides of the invention are also provided, and include monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized antibodies, human antibodies, and complementary determining region (CDR)-grafted antibodies, as well as compounds that include CDR sequences which specifically recognize a polypeptide of the invention. The invention also provides anti-idiotypic antibodies immunospecific for antibodies of the invention.

According to another aspect of the invention, methods are provided for identifying novel anti-bacterial agents that modulate the function of gram negative bacteria virulence genes or gene products. Methods of the invention include screening potential agents for the ability to interfere with expression of virulence gene products encoded by the DNA sequences set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, or species homologs thereof, or screening potential agents for the ability to interfere with biological function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that provide positive results in such screening assays. In particular, agents that interfere with the expression of virulence gene products include anti-sense polynucleotides and ribozymes that are complementary to the virulence gene sequences. The invention further embraces methods to modulate transcription of gene products of the invention through use of oligonucleotide-directed triplet helix formation.

Agents that interfere with the function of virulence gene products include variants of virulence gene products, binding partners of the virulence gene products and variants of such binding partners, and enzyme inhibitors (where the product is an enzyme).

Novel anti-bacterial agents identified by the methods described herein are provided, as well as methods for treating a subject suffering from infection with gram negative bacteria involving administration of such novel anti-bacterial agents in an amount effective to reduce bacterial presence.

Numerous additional aspects and advantages of the invention will become apparent to those skilled in the art upon consideration of the following detailed description of the invention which describes presently prepared embodiments thereof.

5

DETAILED DESCRIPTION OF THE INVENTION

"Virulence genes," as used herein, are genes whose function or products are required for successful establishment and/or maintenance of bacterial infection in a host animal. Thus, virulence genes and/or the proteins encoded thereby are involved in pathogenesis in the host organism, but may not be necessary for growth.

"Signature-tagged mutagenesis (STM)," as used herein, is a method generally described in International Patent Publication No. WO 96/17951, incorporated herein by reference, and includes, for example, a method for identifying bacterial genes required for virulence in a murine model of bacteremia. In this method, bacterial strains that each have a random mutation in the genome are produced using transposon integration; each insertional mutation carries a different DNA signature tag which allows mutants to be differentiated from each other. The tags comprise 40 bp variable central regions flanked by invariant "arms" of 20 bp which allow the central portions to be co-amplified by polymerase chain reaction (PCR). Tagged mutant strains are assembled in microtiter dishes, then combined to form the "inoculum pool" for infection studies. At an appropriate time after inoculation, bacteria are isolated from the animal and pooled to form the "recovered pool." The tags in the recovered pool and the tags in the inoculum pool are separately amplified, labeled, and then used to probe filters arrayed with all of the different tags representing the mutants in the inoculum. Mutant strains with attenuated virulence are those which cannot be recovered from the infected animal, *i.e.*, strains with tags that give hybridization signals when probed with tags from the inoculum pool but not when probed with tags from the recovered pool. In a variation of this method, non-radioactive detection methods such as chemiluminescence can be used

Signature-tagged mutagenesis allows a large number of insertional mutant strains to be screened simultaneously in a single animal for loss of virulence. Screening nineteen pools of mutant *P. multocida* strains resulted in the identification of more than 60 strains with reduced virulence, many of which were confirmed to be attenuated in virulence by subsequent determination of an approximate LD₅₀ for the individual mutants. Screening of *A. pleuropneumoniae* mutants resulted in identification of more than 100 strains having mutations in 35 different genes. Of these, mutations in 22 genes results in significantly attenuated *A. pleuropneumoniae* strains. The nucleotide sequence of the open reading frame disrupted by the transposon insertion was determined by sequencing both strands and an encoded amino acid sequence was deduced. Novelty of both the polynucleotide and amino acid sequences was determined by comparison of the sequences with DNA and protein database sequences. Knowledge of the virulence genes in these species permitted identification of species homologs in *P. (Mannheimia) haemolytica*.

The identification of bacterial, and more particularly *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes provides for microorganisms exhibiting reduced virulence (*i.e.*, attenuated strains), which are useful in vaccines. Such microorganisms include *Pasteurellaceae* mutants containing at least one functional mutation inactivating a gene represented by any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174. The worker of ordinary skill in the art will realize that a "functional mutation" may occur in protein coding regions of a gene of the invention, as well as in regulatory regions that modulate transcription of the virulence gene RNA.

The worker of ordinary skill will also appreciate that attenuated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* strains of the invention include those bearing more than one functional mutation. More than one mutation may result in additive or synergistic degrees of attenuation. Multiple

mutations can be prepared by design or may fortuitously arise from a deletion event originally intended to introduce a single mutation. An example of an attenuated strain with multiple deletions is a *Salmonella typhimurium* strain wherein the *cya* and *crp* genes are functionally deleted. This mutant *S. typhimurium* strain has shown promise as a live vaccine.

Identification of virulence genes in *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* can provide information regarding similar genes in other pathogenic species. As an example, identification of the *aroA* gene led to identification of conserved genes in a diverse number of pathogens, including *Aeromonas hydrophila*, *Aeromonas salmonicida*, *Salmonella typhimurium*, *Salmonella enteritidis*, *Salmonella dublin*, *Salmonella gallinarum*, *Bordetella pertussis*, *Yersinia enterocolitica*, *Neisseria gonorrhoeae*, and *Bacillus anthracis*. In many of these species, attenuated bacterial strains bearing mutations in the *aroA* gene have proven to be effective in vaccine formulations. Using the virulence genes sequences identified in *P. multocida*, similar or homologous genes can be identified in other organisms, particularly within the *Pasteurella* family, as well as *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica*, and *Haemophilus somnus*. Likewise, identification of *A. pleuropneumoniae* virulence genes can permit identification of related genes in other organisms. Southern hybridization using the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* genes as probes can identify these related genes in chromosomal libraries derived from other organisms. Alternatively, PCR can be equally effective in gene identification across species boundaries. As still another alternative, complementation of, for example, a *P. multocida* mutant with a chromosomal library from other species can also be used to identify genes having the same or related virulence activity. Identification of related virulence genes can therefore lead to production of an attenuated strain of the other organism which can be useful as still another vaccine formulation. Examples of *P. multocida* genes that have been demonstrated to exist in other species (e.g. *P. (Mannheimia) haemolytica*, *A. pleuropneumoniae* and *H. somnus*) include genes *exxB*, *atpG*, *pnp*, *guaB* and *yjgF*.

Attenuated *P. multocida* strains identified using STM are insertional mutants wherein a virulence gene has been rendered non-functional through insertion of transposon sequences in either the open reading frame or regulatory DNA sequences. These insertional mutants still contain all of the genetic information required for bacterial virulence and can possibly revert to a pathogenic state by deletion of the inserted transposon. Therefore, in preparing a vaccine formulation, it is desirable to take the information gleaned from the attenuated strain and create a deletion mutant strain wherein some, most, or all of the virulence gene sequence is removed, thereby precluding the possibility that the bacteria will revert to a virulent state.

The vaccine properties of an attenuated insertional mutant identified using STM are expected to be the same or similar to those of a bacteria bearing a deletion in the same gene. However, it is possible that an insertion mutation may exert "polar" effects on adjoining gene sequences, and as a result, the insertion mutant may possess characteristic distinct from a mutant strain with a deletion in the same gene sequence. Deletion mutants can be constructed using any of a number of techniques well known and routinely practiced in the art.

In one example, a strategy using counterselectable markers can be employed which has commonly been utilized to delete genes in many bacteria. For a review, see, for example, Reyrat, *et al.*, *Infection and Immunity* 66:4011-4017 (1998), incorporated herein by reference. In this technique, a double selection strategy is often employed wherein a plasmid is constructed encoding both a selectable and counterselectable marker, with flanking DNA sequences derived from both sides of the desired deletion. The selectable marker is used to select for bacteria in which the plasmid has integrated into the genome in the appropriate location and manner. The counterselectable marker is used to select for the very small percentage of bacteria that have spontaneously eliminated the integrated plasmid. A fraction of these bacteria will then contain only the desired deletion with no other foreign DNA present. The key to the use of this technique is the availability of a suitable counterselectable marker.

In another technique, the *cre-lox* system is used for site specific recombination of DNA. The system consists of 34 base pair *lox* sequences that are recognized by the bacterial *cre* recombinase gene. If the *lox* sites are present in the DNA in an appropriate orientation, DNA flanked by the *lox* sites will be excised by the *cre* recombinase, resulting in the deletion of all sequences except for one remaining copy of the *lox* sequence. Using standard recombination techniques, it is possible to delete the targeted gene of interest in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome and to replace it with a selectable marker (e.g., a gene coding for kanamycin resistance) that is flanked by the *lox* sites. Transient expression (by electroporation of a suicide plasmid containing the *cre* gene under control of a promoter that functions in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*) of the *cre* recombinase should result in efficient elimination of the *lox* flanked marker. This process would result in a mutant containing the desired deletion mutation and one copy of the *lox* sequences.

In another approach, it is possible to directly replace a desired deleted sequence in the *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* genome with a marker gene, such as green fluorescent protein (GFP), β -galactosidase, or luciferase. In this technique, DNA segments flanking a desired deletion are prepared by PCR and cloned into a suicide (non-replicating) vector for *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica*. An expression cassette, containing a promoter active in *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* and the appropriate marker gene, is cloned between the flanking sequences. The plasmid is introduced into wild-type *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. Bacteria that incorporate and express the marker gene (probably at a very low frequency) are isolated and examined for the appropriate recombination event (i.e., replacement of the wild type gene with the marker gene).

The reduced virulence of these organisms and their immunogenicity may be confirmed by administration to a subject animal. While it is possible for an avirulent microorganism of the invention to be administered alone, one or more of

such mutant microorganisms are preferably administered in a vaccine composition containing suitable adjuvant(s) and pharmaceutically acceptable diluent(s) or carrier(s). The carrier(s) must be "acceptable" in the sense of being compatible with the avirulent microorganism of the invention and not deleterious to the subject to be immunized. Typically, the carriers will be water or saline which will be sterile and pyrogen free. The subject to be immunized is a subject needing protection from a disease caused by a virulent form of *P. multocida*, *A. pleuropneumoniae*, *P. (Mannheimia) haemolytica* or other pathogenic microorganisms.

It will be appreciated that the vaccine of the invention may be useful in the fields of human medicine and veterinary medicine. Thus, the subject to be immunized may be a human or other animal, for example, farm animals including cows, sheep, pigs, horses, goats and poultry (e.g., chickens, turkeys, ducks and geese) companion animals such as dogs and cats; exotic and/or zoo animals; and laboratory animals including mice, rats, rabbits, guinea pigs, and hamsters.

The invention also provides polypeptides and corresponding polynucleotides required for *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica* virulence. The invention includes both naturally occurring and non-naturally occurring polynucleotides and polypeptide products thereof. Naturally occurring virulence products include distinct gene and polypeptide species as well as corresponding species homologs expressed in organisms other than *P. multocida*, *A. pleuropneumoniae*, or *P. (Mannheimia) haemolytica* strains. Non-naturally occurring virulence products include variants of the naturally occurring products such as analogs and virulence products which include covalent modifications. In a preferred embodiment, the invention provides virulence polynucleotides comprising the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, and polypeptides having amino acids sequences encoded by the polynucleotides.

The present invention provides novel purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* polynucleotides (e.g., DNA sequences and RNA transcripts, both sense and complementary antisense strands) encoding the bacterial virulence gene products. DNA sequences of the invention include genomic and cDNA sequences as well as wholly or partially chemically synthesized DNA sequences. Genomic DNA of the invention comprises the protein coding region for a polypeptide of the invention and includes variants that may be found in other bacterial strains of the same species. "Synthesized," as used herein and is understood in the art, refers to purely chemical, as opposed to enzymatic, methods for producing polynucleotides. "Wholly" synthesized DNA sequences are therefore produced entirely by chemical means, and "partially" synthesized DNAs embrace those wherein only portions of the resulting DNA were produced by chemical means. Preferred DNA sequences encoding *P. multocida* virulence gene products are set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, and species homologs thereof. Preferred *A. pleuropneumoniae* DNA sequences encoding virulence gene products are set out in SEQ ID NOs: 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, and species homologs thereof. Preferred *P. (Mannheimia) haemolytica* virulence gene products are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, and species homologs thereof. The worker of skill in the art will readily appreciate that the preferred DNA of the invention comprises a double stranded molecule, for example, molecules having the sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof, along with the complementary molecule (the "non-coding strand" or "complement") having a sequence deducible from the sequence of SEQ ID NO: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53,

55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, according to Watson-Crick base pairing rules for DNA. Also preferred are

5 polynucleotides encoding the gene products encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166,

10 168, 170, 172, and 174 and species homologs thereof. The invention further embraces species, preferably bacterial, homologs of the *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* DNA.

The polynucleotide sequence information provided by the invention makes possible the identification and isolation of polynucleotides encoding related

15 bacterial virulence molecules by well known techniques including Southern and/or Northern hybridization, and polymerase chain reaction (PCR). Examples of related polynucleotides include polynucleotides encoding polypeptides homologous to a virulence gene product encoded by any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57,

20 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, and species homologs thereof, and structurally related polypeptides sharing one or more biological and/or physical properties of a virulence gene product of the invention.

25 The invention also embraces DNA sequences encoding bacterial gene products which hybridize under moderately to highly stringent conditions to the non-coding strand, or complement, of any one of the polynucleotides set out in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116,

30 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146,

148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174, and species homologs thereof. DNA sequences encoding virulence polypeptides which would hybridize thereto but for the degeneracy of the genetic code are contemplated by the invention. Exemplary high stringency conditions include a final wash in buffer comprising 0.2X SSC/0.1% SDS, at 65°C to 75°C, while exemplary moderate stringency conditions include a final wash in buffer comprising 2X SSC/0.1% SDS, at 35°C to 45°C. It is understood in the art that conditions of equivalent stringency can be achieved through variation of temperature and buffer, or salt concentration as described in Ausubel, *et al.* (Eds.), Protocols in Molecular Biology, John Wiley & Sons (1994), pp. 6.0.3 to 6.4.10. Modifications in hybridization conditions can be empirically determined or precisely calculated based on the length and the percentage of guanosine/cytosine (GC) base pairing of the probe. The hybridization conditions can be calculated as described in Sambrook, *et al.*, (Eds.), Molecular Cloning: A Laboratory Manual, Cold Spring Harbor Laboratory Press: Cold Spring Harbor, New York (1989), pp. 9.47 to 9.51.

Autonomously replicating recombinant expression constructions such as plasmid and viral DNA vectors incorporating virulence gene sequences are also provided. Expression constructs wherein virulence polypeptide-encoding polynucleotides are operatively linked to an endogenous or exogenous expression control DNA sequence and a transcription terminator are also provided. The virulence genes may be cloned by PCR, using *P. multocida* genomic DNA as the template. For ease of inserting the gene into expression vectors, PCR primers are chosen so that the PCR-amplified gene has a restriction enzyme site at the 5' end preceding the initiation codon ATG, and a restriction enzyme site at the 3' end after the termination codon TAG, TGA or TAA. If desirable, the codons in the gene are changed, without changing the amino acids, according to *E. coli* codon preference described by Grosjean and Fiers, *Gene*, 18:199-209 (1982), and Konigsberg and Godson, *Proc. Natl. Acad. Sci. (USA)*, 80:687-691 (1983). Optimization of codon usage may lead to an increase in the expression of the gene product when produced in *E. coli*. If the gene product is to be produced extracellularly, either in the periplasm of

E. coli or other bacteria, or into the cell culture medium, the gene is cloned without its initiation codon and placed into an expression vector behind a signal sequence.

According to another aspect of the invention, host cells are provided, including procaryotic and eukaryotic cells, either stably or transiently transformed, transfected, or electroporated with polynucleotide sequences of the invention in a manner which permits expression of virulence polypeptides of the invention.

Expression systems of the invention include bacterial, yeast, fungal, viral, invertebrate, and mammalian cells systems. Host cells of the invention are a valuable source of immunogen for development of antibodies specifically immunoreactive with the virulence gene product. Host cells of the invention are conspicuously useful in methods for large scale production of virulence polypeptides wherein the cells are grown in a suitable culture medium and the desired polypeptide products are isolated from the cells or from the medium in which the cells are grown by, for example, immunoaffinity purification or any of the multitude of purification techniques well known and routinely practiced in the art. Any suitable host cell may be used for expression of the gene product, such as *E. coli*, other bacteria, including *P. multocida*, *Bacillus* and *S. aureus*, yeast, including *Pichia pastoris* and *Saccharomyces cerevisiae*, insect cells, or mammalian cells, including CHO cells, utilizing suitable vectors known in the art. Proteins may be produced directly or fused to a peptide or polypeptide, and either intracellularly or extracellularly by secretion into the periplasmic space of a bacterial cell or into the cell culture medium. Secretion of a protein requires a signal peptide (also known as pre-sequence); a number of signal sequences from prokaryotes and eukaryotes are known to function for the secretion of recombinant proteins. During the protein secretion process, the signal peptide is removed by signal peptidase to yield the mature protein.

To simplify the protein purification process, a purification tag may be added either at the 5' or 3' end of the gene coding sequence. Commonly used purification tags include a stretch of six histidine residues (U.S. Patent Nos. 5,284,933 and 5,310,663), a streptavidin-affinity tag described by Schmidt and Skerra, *Protein Engineering*, 6:109-122 (1993), a FLAG peptide [Hopp *et al.*, *Biotechnology*, 6:1205-

1210 (1988)], glutathione S-transferase [Smith and Johnson, *Gene*, 67:31-40 (1988)], and thioredoxin [LaVallie *et al.*, *Bio/Technology*, 11:187-193 (1993)]. To remove these peptide or polypeptides, a proteolytic cleavage recognition site may be inserted at the fusion junction. Commonly used proteases are factor Xa, thrombin, and enterokinase.

The invention also provides purified and isolated *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence polypeptides encoded by a polynucleotide of the invention. Presently preferred are polypeptides comprising the amino acid sequences encoded by any one of the polynucleotides set out in SEQ ID NOs : 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172 and 174, and species homologs thereof. The invention embraces virulence polypeptides encoded by a DNA selected from the group consisting of : a) the DNA sequence set out in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174 and species homologs thereof; b) DNA molecules encoding *P. multocida*, *A. pleuropneumoniae* or *P. (Mannheimia) haemolytica*. polypeptides encoded by any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 164, 166, 168, 170, 172, and 174, and species homologs thereof; and c) a DNA molecule, encoding a virulence gene product, that hybridizes under moderately stringent conditions to the DNA of (a) or (b).

The invention also embraces polypeptides that have at least about 99%, at least about 95%, at least about 90%, at least about 85%, at least about 80%, at least about 75%, at least about 70%, at least about 65%, at least about 60%, at least

about 55%, and at least about 50% identity and/or homology to the preferred polypeptides of the invention. Percent amino acid sequence "identity" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in the virulence gene product sequence after aligning both sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Percent sequence "homology" with respect to the preferred polypeptides of the invention is defined herein as the percentage of amino acid residues in the candidate sequence that are identical with the residues in one of the virulence polypeptide sequences after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and also considering any conservative substitutions as part of the sequence identity. Conservative substitutions can be defined as set out in Tables A and B.

Table A
Conservative Substitutions I

	<u>SIDE CHAIN CHARACTERISTIC</u>		<u>AMINO ACID</u>
	Aliphatic	Non-polar	G A P I L V
		Polar - uncharged	C S T M N Q
		Polar - charged	D E K R
	Aromatic		H F W Y
	Other		N Q D E

Polypeptides of the invention may be isolated from natural bacterial cell sources or may be chemically synthesized, but are preferably produced by recombinant procedures involving host cells of the invention. Virulence gene products of the invention may be full length polypeptides, biologically active fragments, or variants thereof which retain specific biological or immunological activity. Variants may comprise virulence polypeptide analogs wherein one or more

of the specified (*i.e.*, naturally encoded) amino acids is deleted or replaced or wherein one or more non-specified amino acids are added: (1) without loss of one or more of the biological activities or immunological characteristics specific for the virulence gene product; or (2) with specific disablement of a particular biological activity of the virulence gene product. Deletion variants contemplated also include fragments lacking portions of the polypeptide not essential for biological activity, and insertion variants include fusion polypeptides in which the wild-type polypeptide or fragment thereof have been fused to another polypeptide.

Variant virulence polypeptides include those wherein conservative substitutions have been introduced by modification of polynucleotides encoding polypeptides of the invention. Conservative substitutions are recognized in the art to classify amino acids according to their related physical properties and can be defined as set out in Table A (from WO 97/09433, page 10, published March 13, 1997 (PCT/GB96/02197, filed 9/6/96). Alternatively, conservative amino acids can be grouped as defined in Lehninger, [*Biochemistry*, Second Edition; Worth Publishers, Inc. NY:NY (1975), pp.71-77] as set out in Table B.

Table B
Conservative Substitutions II

	<u>SIDE CHAIN</u> <u>CHARACTERISTIC</u>	<u>AMINO ACID</u>
	Non-polar (hydrophobic)	
	A. Aliphatic:	A L I V P
	B. Aromatic:	F W
	C. Sulfur-containing:	M
	D. Borderline:	G
	Uncharged-polar	
	A. Hydroxyl:	S T Y
	B. Amides:	N Q
	C. Sulfhydryl:	C
	D. Borderline:	G
	Positively Charged (Basic):	K R H
	Negatively Charged (Acidic):	D E

Variant virulence products of the invention include mature virulence gene products, *i.e.*, wherein leader or signal sequences are removed, having additional amino terminal residues. Virulence gene products having an additional methionine residue at position -1 are contemplated, as are virulence products having additional methionine and lysine residues at positions -2 and -1. Variants of these types are particularly useful for recombinant protein production in bacterial cell types. Variants of the invention also include gene products wherein amino terminal sequences derived from other proteins have been introduced, as well as variants comprising amino terminal sequences that are not found in naturally occurring proteins.

The invention also embraces variant polypeptides having additional amino acid residues which result from use of specific expression systems. For example, use of commercially available vectors that express a desired polypeptide as a fusion protein with glutathione-S-transferase (GST) provide the desired polypeptide having an additional glycine residue at position -1 following cleavage of the GST component from the desired polypeptide. Variants which result from expression using other vector systems are also contemplated.

Also comprehended by the present invention are antibodies (*e.g.*, monoclonal and polyclonal antibodies, single chain antibodies, chimeric antibodies, humanized, human, and CDR-grafted antibodies, including compounds which include CDR sequences which specifically recognize a polypeptide of the invention) and other binding proteins specific for virulence gene products or fragments thereof. The term "specific for" indicates that the variable regions of the antibodies of the invention recognize and bind a virulence polypeptide exclusively (*i.e.*, are able to distinguish a single virulence polypeptides from related virulence polypeptides despite sequence identity, homology, or similarity found in the family of polypeptides), but may also interact with other proteins (for example, *S. aureus* protein A or other antibodies in ELISA techniques) through interactions with sequences outside the variable region of the antibodies, and in particular, in the constant region of the molecule. Screening assays to determine binding specificity of an antibody of the invention are well known and routinely practiced in the art. For a comprehensive discussion of such assays, see

Harlow *et al.* (Eds), Antibodies A Laboratory Manual; Cold Spring Harbor Laboratory; Cold Spring Harbor, NY (1988), Chapter 6. Antibodies that recognize and bind fragments of the virulence polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, a virulence polypeptide of the invention from which the fragment was derived.

The DNA and amino acid sequence information provided by the present invention also makes possible the systematic analysis of the structure and function of the virulence genes and their encoded gene products. Knowledge of a polynucleotide encoding a virulence gene product of the invention also makes available anti-sense polynucleotides which recognize and hybridize to polynucleotides encoding a virulence polypeptide of the invention. Full length and fragment anti-sense polynucleotides are provided. The worker of ordinary skill will appreciate that fragment anti-sense molecules of the invention include (i) those which specifically recognize and hybridize to a specific RNA (as determined by sequence comparison of DNA encoding a virulence polypeptide of the invention to DNA encoding other known molecules) as well as (ii) those which recognize and hybridize to RNA encoding variants of the family of virulence proteins. Antisense polynucleotides that hybridize to RNA encoding other members of the virulence family of proteins are also identifiable through sequence comparison to identify characteristic, or signature, sequences for the family of molecules.

The invention further contemplates methods to modulate gene expression through use of ribozymes. For a review, see Gibson and Shillito, *Mol. Biotech.* 7:125-137 (1997). Ribozyme technology can be utilized to inhibit translation of mRNA in a sequence specific manner through (i) the hybridization of a complementary RNA to a target mRNA and (ii) cleavage of the hybridized mRNA through nuclease activity inherent to the complementary strand. Ribozymes can be identified by empirical methods but more preferably are specifically designed based on accessible sites on the target mRNA [Bramlage, *et al.*, *Trends in Biotech* 16:434-438 (1998)]. Delivery of ribozymes to target cells can be accomplished using either

exogenous or endogenous delivery techniques well known and routinely practiced in the art. Exogenous delivery methods can include use of targeting liposomes or direct local injection. Endogenous methods include use of viral vectors and non-viral plasmids.

5 Ribozymes can specifically modulate expression of virulence genes when designed to be complementary to regions unique to a polynucleotide encoding a virulence gene product. "Specifically modulate" therefore is intended to mean that ribozymes of the invention recognizes only a single polynucleotide. Similarly, ribozymes can be designed to modulate expression of all or some of a family of
10 proteins. Ribozymes of this type are designed to recognize polynucleotide sequences conserved in all or some of the polynucleotides which encode the family of proteins.

 The invention further embraces methods to modulate transcription of a virulence gene of the invention through use of oligonucleotide-directed triplet helix formation. For a review, see Lavrovsky, *et al.*, *Biochem. Mol. Med.* 62:11-22 (1997).
15 Triplet helix formation is accomplished using sequence specific oligonucleotides which hybridize to double stranded DNA in the major groove as defined in the Watson-Crick model. Hybridization of a sequence specific oligonucleotide can thereafter modulate activity of DNA-binding proteins, including, for example, transcription factors and polymerases. Preferred target sequences for hybridization
20 include transcriptional regulatory regions that modulate virulence gene product expression. Oligonucleotides which are capable of triplet helix formation are also useful for site-specific covalent modification of target DNA sequences. Oligonucleotides useful for covalent modification are coupled to various DNA damaging agents as described in Lavrovsky, *et al.* [*supra*].

25 The identification of *P. multocida*, *A. pleuropneumoniae* and *P. (Mannheimia) haemolytica* virulence genes renders the genes and gene products useful in methods for identifying anti-bacterial agents. Such methods include assaying potential agents for the ability to interfere with expression of virulence gene products represented by the DNA sequences set forth in any one of SEQ ID NOS: 1,
30 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68,

70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 and species homologs thereof (*i.e.*, the genes represented by DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 encode the virulence gene product, or the DNA sequences of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 are adjacent the gene encoding the virulence gene product, or are involved in regulation of expression of the virulence gene product), or assaying potential agents for the ability to interfere with the function of a bacterial gene product encoded in whole or in part by a DNA sequence set forth in any one of SEQ ID NOS: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174, species homologs thereof, or the complementary strand thereof, followed by identifying agents that are positive in such assays. Polynucleotides and polypeptides useful in these assays include not only the genes and encoded polypeptides as disclosed herein, but also variants thereof that have substantially the same activity as the wild-type genes and polypeptides.

The virulence gene products produced by the methods described above are used in high throughput assays to screen for inhibitory agents. The sources for potential agents to be screened are chemical compound libraries, fermentation media of *Streptomyces*, other bacteria and fungi, and cell extracts of plants and other vegetations. For proteins with known enzymatic activity, assays are established based

on the activity, and a large number of potential agents are screened for ability to inhibit the activity. For proteins that interact with another protein or nucleic acid, binding assays are established to measure such interaction directly, and the potential agents are screened for ability to inhibit the binding interaction.

5 The use of different assays known in the art is contemplated according to this aspect of the invention. When the function of the virulence gene product is known or predicted by sequence similarity to a known gene product, potential inhibitors can be screened in enzymatic or other types of biological and/or biochemical assays keyed to the function and/or properties of the gene product. When
10 the virulence gene product is known or predicted by sequence similarity to a known gene product to interact with another protein or nucleic acid, inhibitors of the interaction can be screened directly in binding assays. The invention contemplates a multitude of assays to screen and identify inhibitors of binding by the virulence gene product. In one example, the virulence gene product is immobilized and interaction
15 with a binding partner is assessed in the presence and absence of a putative inhibitor compound. In another example, interaction between the virulence gene product and its binding partner is assessed in a solution assay, both in the presence and absence of a putative inhibitor compound. In both assays, an inhibitor is identified as a compound that decreases binding between the virulence gene product and its binding
20 partner. Other assays are also contemplated in those instances wherein the virulence gene product binding partner is a protein. For example, variations of the di-hybrid assay are contemplated wherein an inhibitor of protein/protein interactions is identified by detection of a positive signal in a transformed or transfected host cell as described in PCT publication number WO 95/20652, published August 3, 1995.

25 Candidate inhibitors contemplated by the invention include compounds selected from libraries of potential inhibitors. There are a number of different libraries used for the identification of small molecule modulators, including: (1) chemical libraries, (2) natural product libraries, and (3) combinatorial libraries comprised of random peptides, oligonucleotides or organic molecules. Chemical
30 libraries consist of structural analogs of known compounds or compounds that are

identified as "hits" or "leads" via natural product screening. Natural product libraries are collections of microorganisms, animals, plants, or marine organisms which are used to create mixtures for screening by: (1) fermentation and extraction of broths from soil, plant or marine microorganisms or (2) extraction of plants or marine organisms. Natural product libraries include polyketides, non-ribosomal peptides, and variants (non-naturally occurring) thereof. For a review, see *Science* 282:63-68 (1998). Combinatorial libraries are composed of large numbers of peptides, oligonucleotides, or organic compounds as a mixture. They are relatively easy to prepare by traditional automated synthesis methods, PCR, cloning, or proprietary synthetic methods. Of particular interest are peptide and oligonucleotide combinatorial libraries. Still other libraries of interest include peptide, protein, peptidomimetic, multiparallel synthetic collection, recombinatorial, and polypeptide libraries. For a review of combinatorial chemistry and libraries created therefrom, see Myers, *Curr. Opin. Biotechnol.* 8:701-707 (1997). Identification of modulators through use of the various libraries described herein permits modification of the candidate "hit" (or "lead") to optimize the capacity of the "hit" to modulate activity.

Still other candidate inhibitors contemplated by the invention can be designed and include soluble forms of binding partners, as well as binding partners as chimeric, or fusion, proteins. Binding partners as used herein broadly encompasses antibodies, antibody fragments, and modified compounds comprising antibody domains that are immunospecific for the expression product of the identified virulence gene.

Other assays may be used when a binding partner (*i.e.*, ligand) for the virulence gene product is not known, including assays that identify binding partners of the target protein through measuring direct binding of test binding partner to the target protein, and assays that identify binding partners of target proteins through affinity ultrafiltration with ion spray mass spectroscopy/HPLC methods or other physical and analytical methods. Alternatively, such binding interactions are evaluated indirectly using the yeast two-hybrid system described in Fields and Song, *Nature*, 340:245-246 (1989), and Fields and Sternglanz, *Trends in Genetics*, 10:286-292 (1994), both of

which are incorporated herein by reference. The two-hybrid system is a genetic assay for detecting interactions between two proteins or polypeptides. It can be used to identify proteins that bind to a known protein of interest, or to delineate domains or residues critical for an interaction. Variations on this methodology have been developed to clone genes that encode DNA-binding proteins, to identify peptides that bind to a protein, and to screen for drugs. The two-hybrid system exploits the ability of a pair of interacting proteins to bring a transcription activation domain into close proximity with a DNA-binding domain that binds to an upstream activation sequence (UAS) of a reporter gene, and is generally performed in yeast. The assay requires the construction of two hybrid genes encoding (1) a DNA-binding domain that is fused to a first protein and (2) an activation domain fused to a second protein. The DNA-binding domain targets the first hybrid protein to the UAS of the reporter gene; however, because most proteins lack an activation domain, this DNA-binding hybrid protein does not activate transcription of the reporter gene. The second hybrid protein, which contains the activation domain, cannot by itself activate expression of the reporter gene because it does not bind the UAS. However, when both hybrid proteins are present, the noncovalent interaction of the first and second proteins tethers the activation domain to the UAS, activating transcription of the reporter gene. When the virulence gene product (the first protein, for example) is already known to interact with another protein or nucleic acid, this assay can be used to detect agents that interfere with the binding interaction. Expression of the reporter gene is monitored as different test agents are added to the system; the presence of an inhibitory agent results in lack of a reporter signal.

When the function of the virulence gene product is unknown and no ligands are known to bind the gene product, the yeast two-hybrid assay can also be used to identify proteins that bind to the gene product. In an assay to identify proteins that bind to the first protein (the target protein), a large number of hybrid genes each encoding different second proteins are produced and screened in the assay. Typically, the second protein is encoded by a pool of plasmids in which total cDNA or genomic DNA is ligated to the activation domain. This system is applicable to a wide variety

of proteins, and it is not even necessary to know the identity or function of the second binding protein. The system is highly sensitive and can detect interactions not revealed by other methods; even transient interactions may trigger transcription to produce a stable mRNA that can be repeatedly translated to yield the reporter protein.

5 Other assays may be used to search for agents that bind to the target protein. One such screening method to identify direct binding of test ligands to a target protein is described in U.S. Patent No. 5,585,277, incorporated herein by reference. This method relies on the principle that proteins generally exist as a mixture of folded and unfolded states, and continually alternate between the two
10 states. When a test ligand binds to the folded form of a target protein (i.e., when the test ligand is a ligand of the target protein), the target protein molecule bound by the ligand remains in its folded state. Thus, the folded target protein is present to a greater extent in the presence of a test ligand which binds the target protein, than in the absence of a ligand. Binding of the ligand to the target protein can be determined
15 by any method which distinguishes between the folded and unfolded states of the target protein. The function of the target protein need not be known in order for this assay to be performed. Virtually any agent can be assessed by this method as a test ligand, including, but not limited to, metals, polypeptides, proteins, lipids, polysaccharides, polynucleotides and small organic molecules.

20 Another method for identifying ligands for a target protein is described in Wieboldt *et al.*, *Anal. Chem.*, 69:1683-1691 (1997), incorporated herein by reference. This technique screens combinatorial libraries of 20-30 agents at a time in solution phase for binding to the target protein. Agents that bind to the target protein are separated from other library components by centrifugal ultrafiltration. The
25 specifically selected molecules that are retained on the filter are subsequently liberated from the target protein and analyzed by HPLC and pneumatically assisted electrospray (ion spray) ionization mass spectroscopy. This procedure selects library components with the greatest affinity for the target protein, and is particularly useful for small molecule libraries.

The inhibitors/binders identified by the initial screens are evaluated for their effect on virulence in *in vivo* mouse models of *P. multocida* infections. Models of bacteremia, endocarditis, septic arthritis, soft tissue abscess, or pneumonia may be utilized. Models involving use of other animals are also comprehended by the invention. For example, rabbits can be challenged with a wild type *P. multocida* strain before or after administration of varying amounts of a putative inhibitor/binder compound. Control animals, administered only saline instead of putative inhibitor/binder compound provide a standard by which deterioration of the test animal can be determined. Other animal models include those described in the Animal and Plant Health Inspection Service, USDA, January 1, 1994 Edition, §§113.69-113.70; Panciera and Corstvet, *Am. J. Vet. Res.* 45:2532-2537; Ames, *et al.*, *Can. J. Comp. Med.* 49:395-400 (1984); and Mukkur, *Infection and Immunity* 18:583-585 (1977). Inhibitors/binders that interfere with bacterial virulence are can prevent the establishment of an infection or reverse the outcome of an infection once it is established.

Any adjuvant known in the art may be used in the vaccine composition, including oil-based adjuvants such as Freund's Complete Adjuvant and Freund's Incomplete Adjuvant, mycolate-based adjuvants (*e.g.*, trehalose dimycolate), bacterial lipopolysaccharide (LPS), peptidoglycans (*i.e.*, mureins, mucopeptides, or glycoproteins such as N-Opaca, muramyl dipeptide [MDP], or MDP analogs), proteoglycans (*e.g.*, extracted from *Klebsiella pneumoniae*), streptococcal preparations (*e.g.*, OK432), Biostim™ (*e.g.*, 01K2), the "Iscoms" of EP 109 942, EP 180 564 and EP 231 039, aluminum hydroxide, saponin, DEAE-dextran, neutral oils (such as miglyol), vegetable oils (such as arachis oil), liposomes, Pluronic® polyols, the Ribí adjuvant system (see, for example GB-A-2 189 141), or interleukins, particularly those that stimulate cell mediated immunity. An alternative adjuvant consisting of extracts of *Amycolata*, a bacterial genus in the order Actinomycetales, has been described in U.S. Patent No. 4,877,612. Additionally, proprietary adjuvant mixtures are commercially available. The adjuvant used will depend, in part, on the

recipient organism. The amount of adjuvant to administer will depend on the type and size of animal. Optimal dosages may be readily determined by routine methods.

The vaccine compositions optionally may include vaccine-compatible pharmaceutically acceptable (*i.e.*, sterile and non-toxic) liquid, semisolid, or solid
5 diluents that serve as pharmaceutical vehicles, excipients, or media. Any diluent known in the art may be used. Exemplary diluents include, but are not limited to, polyoxyethylene sorbitan monolaurate, magnesium stearate, methyl- and propylhydroxybenzoate, talc, alginates, starches, lactose, sucrose, dextrose, sorbitol, mannitol, gum acacia, calcium phosphate, mineral oil, cocoa butter, and oil of
10 theobroma.

The vaccine compositions can be packaged in forms convenient for delivery. The compositions can be enclosed within a capsule, caplet, sachet, cachet, gelatin, paper, or other container. These delivery forms are preferred when compatible with entry of the immunogenic composition into the recipient organism
15 and, particularly, when the immunogenic composition is being delivered in unit dose form. The dosage units can be packaged, *e.g.*, in tablets, capsules, suppositories or cachets.

The vaccine compositions may be introduced into the subject to be immunized by any conventional method including, *e.g.*, by intravenous, intradermal,
20 intramuscular, intramammary, intraperitoneal, or subcutaneous injection; by oral, sublingual, nasal, anal, or vaginal, delivery. The treatment may consist of a single dose or a plurality of doses over a period of time.

The invention also comprehends use of an attenuated bacterial strain of the invention for manufacture of a vaccine medicament to prevent or alleviate
25 bacterial infection and/or symptoms associated therewith. The invention also provides use of inhibitors of the invention for manufacture of a medicament to prevent or alleviate bacterial infection and/or symptoms associated therewith.

The present invention is illustrated by the following examples.
Example 1 describes constructions of *P. multocida* mutants. Example 2 relates to
30 screening for *P. multocida* mutants. Example 3 addresses methods to determine

virulence of the *P. multocida* mutants. Example 4 describes cloning of *P. multocida* virulence genes. Example 5 addresses identification of genes in other species related to *P. multocida* virulence genes. Example 6 describes construction of *A. pleuropneumoniae* mutants. Example 7 addresses screening for attenuated *A. pleuropneumoniae* mutants. Example 8 relates to identification of *A. pleuropneumoniae* virulence genes. Example 9 describes competition challenge of *A. pleuropneumoniae* mutants and wild type bacteria. Example 10 characterizes *A. pleuropneumoniae* genes identified. Example 11 addresses efficacy of *A. pleuropneumoniae* mutant to protect against wild type bacterial challenge. Example 12 describes identification of species homolog virulence genes in *P. (Mannheimia) haemolytica*.

Example 1

Construction of a Library of Tagged-Transposon *P. multocida* Mutants

A library of tagged-transposon mutants was constructed in parental vector pLOF/Km [Herrero, *et al.*, *J Bacteriol.* 172:6557-67 (1990)] which has previously been demonstrated to be functional and random in *P. multocida* [Lee, *et al.*, *Vet Microbiol.* 50:143-8 (1996)]. Plasmid pLOF/Km was constructed as a modification of suicide vector pGP704 and included a transposase gene under control of the *Tac* promoter as well as the mini-Tn10 transposable element encoding kanamycin resistance. Plasmid pTEF-1 was constructed as described below by modifying pLOF/Km to accept sequence tags which contained a semi-random [NK]₃₅ sequence.

Plasmid pLOF/Km was first modified to eliminate the unique *Kpn*I restriction site in the multiple cloning region and then to introduce a new *Kpn*I site in the mini-Tn10 region. The plasmid was digested with *Kpn*I and the resulting overhanging ends were filled in with Klenow polymerase according to manufacturer's suggested protocol. Restriction digests and ligations described herein were performed according to manufacturer's suggested protocols (Gibco BRL, Gaithersburg, MD and Boehringer Mannheim, Indianapolis, IN). The blunt end product was self-ligated to

produce a plasmid designated pLOF/Km--*KpnI* which was transformed into *E.coli* DH5 α : λ pir for amplification. *E.coli* DH5 α : (λ pir ϕ 80dlacZ Δ M15, recA1, endA1, gyrA96, thi-1, hsdR17(r_k⁻, m_k⁻, supE44, relA1, deoR, Δ (lacZYA-argF)U169, was propagated at 37°C in Luria-Bertani (LB) medium. Plasmids were prepared using

5 QIAGEN SpinPreps from QIAGEN Inc. (Santa Clarita, CA) and digested with *SfiI* which cuts at a unique site within the mini-Tn10 transposable element. A *SfiI*-*KpnI*-*SfiI* adaptor was prepared by annealing oligonucleotides TEF1 (SEQ ID NO: 86) and TEF3 (SEQ ID NO: 87) and the resulting double-stranded adapter was ligated into the *SfiI* site to create plasmid pTEF-1. Oligonucleotides TEF1 and TEF3 (as well as all

10 other oligonucleotides described herein) were synthesized by Genosys Biotechnologies (The Woodlands, TX).

TEF1 5'-AGGCCGGTACCGGCCGCCT SEQ ID NO: 86

15 TEF3 5'-CGGCCGGTACCGGCCTAGG SEQ ID NO: 87

Unique sequence tags for insertion into the *KpnI* site of pTEF-1 were prepared as follows. PCR was carried out to generate double stranded DNA tags using a GeneAmp XL PCR Kit (PE Applied Biosystems, Foster City, CA) under

20 conditions including 250 μ M each dNTP, 1.5 mM Mg(OAc)₂, 100 pmol each primer TEF14 (SEQ ID NO: 88) and TEF15 (SEQ ID NO: 89), 1 ng TEF26 (SEQ ID NO: 90) as template DNA and 2.5 units recombinant *Tth* DNA Polymerase XL.

25 TEF14 5'-CATGGTACCCATTCTAAC SEQ ID NO: 88

TEF15 5'-CTAGGTACCTACAACCTC SEQ ID NO: 89

TEF26 SEQ ID NO: 90

5'-CTAGGTACCTACAACCTCAAGCTT-[NK]₃₅-
 30 AAGCTTGGTTAGAATGGGTACCATG

Reaction conditions included an initial incubation at 95°C for one minute, followed by thirty cycles of 30 seconds at 95°C, 45 seconds at 45°C, and 15 seconds at 72°C, followed by a final incubation at 72°C for two minutes. The PCR products were digested with *KpnI* and purified using a QIAGEN Nucleotide Removal Kit (QIAGEN, Inc., Chatsworth, GA) according to the manufacturer's suggested protocol. The unique tag sequences were ligated into the mini-Tn10 element of linearized pTEF-1, previously digested with *KpnI* and dephosphorylated with calf intestinal alkaline phosphatase (Boehringer Mannheim) using standard procedures. The resulting plasmid library was transformed into *E.coli* DH5 α : λ pir. Colony blot analysis was performed according to the DIG User's Guide (Boehringer-Mannheim) with hybridization and detection performed as follows.

Hybridizations were essentially performed according to the Genius Non-Radioactive User's Guide (Boehringer Mannheim Biochemicals), the product sheet for the DIG-PCR labeling kit (Boehringer Mannheim Biochemicals), and the product sheet for CSPD (Boehringer Mannheim Biochemicals). For preparation of probes, a 100 μ l primary PCR reaction was set up using Amplitaq PCR buffer (PE Applied Biosystems), 200 μ M dNTPs, 140 pmol each of primers TEF5 (SEQ ID NO: 91) and TEF6 (SEQ ID NO: 92), 2 mM MgCl₂, 2.5 units Amplitaq (PE Applied Biosystems) and 1 ng of plasmid DNA.

TEF5 5'-TACCTACAACCTCAAGCT SEQ ID NO: 91

TEF6 5'-TACCCATTCTAACCAAGC SEQ ID NO: 92

Cycle conditions included an initial incubation at 95°C for two minutes, followed by 35 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The amplification products were separated using electrophoresis on a 2% - 3:1 NuSieve GTG (FMC BioProducts, Rockland, ME, USA):Agarose gel and the 109 bp product was excised and purified. Gel extractions were carried out using a QIAGEN Gel Extraction kit (QIAGEN).

Approximately 15 ng of the primary product was labeled in a 50 µl PCR reaction using the DIG PCR Kit, 50 pmol each of primers TEF24 and TEF25, and a 1:1 mix of DIG Probe Synthesis Mix with 2 mM dNTP stock solution.

5 TEF24 5'-TACCTACAACCTCAAGCTT SEQ ID NO: 93

 TEF25 5'-TACCCATTCTAACCAAGCTT SEQ ID NO: 94

10 PCR conditions included an initial incubation at 95°C for four minutes, followed by 25 cycles of 95°C for 30 seconds, 50°C for 45 seconds, 72°C for 15 seconds and a final incubation at 72°C for three minutes. The labeled PCR product was digested with *Hind*III in a total reaction volume of 90 µl and purified from the constant primer arms using a 2% - 3:1 NuSieve GTG (FMC BioProducts):Agarose gel. The region containing the labeled variable tag was excised and the entire gel slice was dissolved and denatured in 10 ml of DIG EasyHyb at 95°C for ten minutes.

15 Dot blots were prepared using a Hybond[®]-N⁺ membrane (Amersham-Pharmacia Biotech). Target DNA for each tag was prepared in 96 well plates using approximately 30 ng of PCR product. An equal volume of 0.1 N NaOH was added to denature the sample and each sample was applied to the membrane with minimal vacuum using a Minifold I[™] Dot-Blot Apparatus from Schleicher and Schuell (Keene, NH, USA). Each well was washed with 150 µl of Neutralization Solution (0.5 M Tris /3 M NaCl, pH 7.5) and 150 µl of 2X SSC. Membranes were UV-crosslinked in a Stratalinker (Stratagene, La Jolla, CA, USA) and prehybridized for one hour in 20 mls DIG EasyHyb Buffer at 42°C. The denatured probe was added and hybridization carried out overnight at 42°C. The membrane was washed two times in 2X SSC containing 0.1% SDS for five minutes each wash. Two high stringency washes were performed in 50 ml of pre-warmed 0.1X SSC buffer containing 0.1% SDS at 68°C for 15 minutes before proceeding with standard Genius Detection protocols (Genius Manual).

It is desirable to use a non-radioactive detection system for safety, lower cost, ease of use, and reduction of hazardous materials. In initial experiments using similar procedures previously described [Mei, *et al.*, *Mol Microbiol.* 26:399-407 (1997)], unacceptable background levels of hybridization were obtained in
5 negative controls. In order to decrease background, tag length was increased by 30 bp to a total of 70, amplification primers were lengthened to include all sequence flanking the variable region, a lower concentration of dig-dUTP was used, and the conserved sequences flanking the sequence tag region were removed by gel
10 purification. Most significantly, PCR was used to generate [NK]₃₅ sequence tags as the target DNA in dot blots rather than the entire plasmids containing the tagged transposons after detecting background hybridization from the transposon itself. Using these modifications background was eliminated making chemiluminescent/non-radioactive screening more effective.

Approximately four hundred different transformants resulting from the
15 ligation of pTEF-1 with the PCR generated sequence tags were screened by colony blot and the 96 strongest hybridizing colonies were assembled into microtiter plates for further use. Even though the likelihood of duplicated tags was very low, half of the plate of master tags was probed against the other to confirm that no tags were duplicated. The plasmids containing these tags were purified and transformed into
20 *E.coli* S17-1:λpir (pir, *recA*, *thi*, *pro*, *hsd*, (r-m+), RP4-2, (Tc::Mu), (Km::Tn7), [TnpR], [SmR]), and the transformed bacteria propagated at 37°C in Luria-Bertani (LB) medium. Each of the 96 *E.coli* S17-1:λpir transformants containing the tagged plasmid pTEF-1 was used in conjugative matings to generate transposon mutants of *P. multocida*. *P. multocida* strain TF5 is a spontaneous nalidixic acid resistant mutant
25 derived from UC6731, a bovine clinical isolate. *P. multocida* strains were grown on brain heart infusion (BHI) media (Difco Laboratories, Detroit, MI, USA) at 37°C and in 5% CO₂ when grown on plates. Matings were set up by growing each *E.coli* S17-1:λpir /pTEF1:[NK]₃₅ clone and the TF5 strain to late log phase. Fifty µl of culture for each tagged-pTEF-1 clone was mixed with 200 µl of the TF5 culture and 50 µl of
30 each mating mixture was spotted onto 0.22 TM filters previously placed on BHI plates

containing 100 mM IPTG and 10 mM MgSO₄. Following overnight incubation at 37°C with 5% CO₂, mating mixtures were washed off of each filter into 3 ml of PBS and 25 µl of each was plated onto BHIN⁵⁰K¹⁰⁰ plates. Following selective overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 µl BHIN⁵⁰K⁵⁰ making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 µl of 75% glycerol was added to each well and plates were stored frozen at -80°C.

Nineteen pools were assembled by transferring the transposon mutants to microtiter plates making sure that each well contained a transposon mutant with the appropriate tag for that well. In other words, a specific well in each microtiter plate always contained a transposon mutant with the same sequence tag even though the location of the transposon within those mutants may be different.

Example 2

Murine Screening for Attenuated *P. multocida* Mutants

Nineteen pools of *Pasteurella multocida* transposon mutants were screened using a murine model of septicemia. Frozen plates of pooled *P. multocida* transposon mutants were removed from -80°C storage and subcultured by transferring 10 µl from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 200 µl of brain heart infusion (DIFCO) with 50 µg/ml nalidixic acid (Sigma) and 50 µg/ml kanamycin (Sigma) (BHIN⁵⁰K⁵⁰). Plates were incubated without shaking overnight at 37°C in 5% CO₂. Overnight plates were subcultured by transferring 10 µl from each well to a new flat bottomed 96-well plate (Corning Costar) containing 100 µl of BHI per well and incubating at 37°C with shaking at approximately 150 rpm. The OD₅₄₀ was monitored using a micro-titer plate reader. At an OD₅₄₀ of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 µl from each of the wells of the micro-titer plate. The culture was diluted appropriately in BHI to doses of approximately 10⁴, 10⁵, 10⁶ CFU/ml and 0.2 ml of each dilution was used to infect female 14-16 g BALB/c mice by intraperitoneal administration. At two days post-infection, one or two surviving mice were euthanized and the spleens harvested. The entire spleen was homogenized

in 1.0 ml sterile 0.9 % saline. Dilutions of the homogenate from 10^{-2} to 10^{-5} were prepared and plated onto BHIN⁵⁰K⁵⁰ plates. Following overnight growth, at least 20,000 colonies were pooled in 10 mls BHI broth to form the "recovered pool" and 0.5 ml of the recovered pool was centrifuged at 3,500 X g and the pellet used to
5 prepare genomic DNA according to a previously described protocol [Wilson, *In F. M. Ausubel, et al.*, (ed.), Current Protocols in Molecular Biology, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5. (1997)].

Initial experiments with virulent wild-type *P. multocida* indicated that organisms could be recovered from the spleen, lungs, kidneys, and liver indicating a
10 truly septicemic model of infection. Dot blots for both the "input" and "recovered" pools were performed as described in Example 1 and evaluated both by visual inspection and by semi-quantitative analysis. Hybridization was carried out as described in Example 1 except that 5 µg of genomic DNA from input and recovered
15 pools was used as template. Semi-quantitative analysis indicates whether a significant reduction in a single clone has occurred. If a mutant is unable to survive within the host, then the recovered signal should be very low compared to the input signal yielding a high input/recovered ratio. Most mutants will grow as well *in vivo* as *in vitro* and therefore a ratio of their signals should be approximately equal to 1. Clones selected by quantitative analysis as being highly reduced in the recovered pool were
20 selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots.

Example 3 Determination of Virulence for *P. multocida* Candidate Mutants

25 Each potential mutant which exhibited reduced recovery from splenic tissue was isolated from the original pool plate and used individually in a challenge experiment to verify and roughly estimate the attenuation caused by the transposon mutation. Individual candidate mutants from *in vivo* screens were grown on Sheep Blood Agar plates overnight in 5% CO₂ at 37°C. Approximately six colonies of each
30 mutant were inoculated into BHI broth and allowed to grow for six hours. Dilutions were prepared and five mice each were infected as described above with 10^2 , 10^3 , 10^4

and 10^5 CFU each. Attenuation was determined by comparing mortality after six days relative to the wild type. Surviving mice were presumed to be protected and then challenged with a dose of wild type *P. multocida* at a concentration approximately 200-fold greater than the LD_{50} for the wild type strain. Survival rate was then determined for each challenged group of mice.

Results indicated that 62 of 120 potential transposon mutants were attenuated, having an approximate LD_{50} of at least 10 fold higher than the wild type strain. The clones and their approximate LD_{50} values are listed in Table 1. A control experiment with the wild type strain was run in parallel with each set of challenges and in all cases mortality in wild type-challenged groups was 100%.

In addition to LD_{50} values, Table 1 also provides data from vaccination and challenge experiments. Briefly, groups of mice ($n = 5$ to 10) were vaccinated by intraperitoneal injection with the individual *P. multocida* strains shown in Table 1 at a dose that was approximately 200 times greater than the LD_{50} of the virulent, wild type strain. Animals were observed for 28 days after which mortality figures were calculated.

Table 1
***P. multocida* Virulence Genes**

Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	LD_{50}
—	wild type	-	0/10	-	<10
23	PM1B1	guaB	10/10, 10/10, 10/10	9/10, 9/10	4.3×10^6
11	PM1D1	dsbB	10/10, 5/10	10/10, 5/5	8.4×10^4
3	PM1BD7	atpG	5/5, 10/10	10/10	$>3 \times 10^5$
74	PM1BE11	yhcJ (HI0145)	10/10	5/10	$>2 \times 10^5$
70	PM1BF6	yabK (HI1020)	3/5, 8/10	9/9	$>2 \times 10^5$
19	PM2G8	fhaC	4/5, 9/10	9/9	$>4 \times 10^5$
76	PM3C9	yiaO (HI0146)	3/5		$>6 \times 10^5$
118	PM3G11	UnkO	4/5, 10/10	10/10	$>3 \times 10^5$
31	PM7B4	iroA (UnkB)	0/5		
17	PM4C6	fhaB (fhaB2)	2/5, 10/10, 9/10	10/10, 9/9	$>3 \times 10^6$
9	PM4G10-T9	dnaA	4/5		$>5 \times 10^5$
1	PM4D5-T5	atpB	5/5		$>4 \times 10^5$
53	PM4D5-T1	UnkC2	5/5		$>4 \times 10^5$
15	PM4F2	fhaB (fhaB1)	3/5, 6/10, 10/10	6/6, 10/10	$>3 \times 10^5$
41	PM5F7	mreB	4/5		1×10^3
7	PM5E2	devB	0/5, 3/10	2/3	ND
68	PM6H5-T1	xylA	5/5		$>3 \times 10^5$
78	PM6H8	yigF (HI0719)	5/5, 9/10	9/9	$>3 \times 10^5$
108	PM7D12	pnp	5/5, 9/10	9/9	
51	PM8C1R1-T2	UnkC1	5/5		$\sim 6 \times 10^5$

Nucleotide SEQ ID NO:	Representative Isolate	Possible Gene Function	Vaccination # survivors/total	Challenge # survivors/total	LD ₅₀
37	PM8C1-T3	mgIB	5/5		-6 x 10 ⁵
58	PM8C1R1-T6	UnkD1	5/5		-6 x 10 ⁵
45	PM10H7	purF (HI1707)	3/5, 8/10, 8/10	8/8, 8/8	>3 x 10 ⁵
25	PM10H10-T2	HI1501	5/5		>1 x 10 ⁴
72	PM11G8-T2	ygiK	5/5		>2.4 x 10 ³
21	PM11G8-T4	greA	5/5		>2.4 x 10 ³
84	PM12H6	yyam (HI0687)	3/5, 0/10		-2.2 x 10 ³
33	PM15G8-T2	kdtB	5/5		>1.2 x 10 ⁵
116	PM15G8-T1	UnkK	5/5		>1.2 x 10 ⁵
104	PM16G11-T1	hmbR	3/5		>1.9 x 10 ⁵
29	PM16G11-T2	hxC	3/5		>1.9 x 10 ⁵
35	PM16H8	lgtC	5/5, 10/10	10/10	>2.4 x 10 ⁵
80	PM16H3	yleA (HI0019)	5/5, 10/10		>2.0 x 10 ⁵
49	PM17H6-T1	sopE	4/5		-6 x 10 ⁵
120	PM17H6	UnkP	4/5		-6 x 10 ⁵
5	PM18F5-T8	cap5E	5/5		>2.4 x 10 ⁵
82	PM18F5-T10	yoyB (HI0345)	5/5		>2.4 x 10 ⁵
13	PM19A1	exbB	5/5, 10/10	10/10	>1.2 x 10 ⁵
112	PM19D4	rci	5/5, 8/10	8/8	-1.6 x 10 ⁵
39	PM20A12	mioC (HI0669)	3/5, 8/10	8/8	-2 x 10 ⁴
60	PM20C2	UnkD2	5/5, 10/10	10/10	>8.2 x 10 ⁶

Example 4 Cloning and Identification of Genes Required for *P. multocida* Virulence

Each transposon mutant which was verified to be attenuated was analyzed further to determine the identity of the disrupted open reading frame. DNA from each mutant was amplified, purified, and digested with restriction enzymes that were known not to cut within the transposon and generally produced 4-8 kb fragments that hybridized with the transposon. Using selection for kanamycin resistance encoded by the transposon, at least one fragment for each transposon mutant was cloned.

Southern hybridization with multiple restriction enzymes was performed for each attenuated mutant using a labeled 1.8 kb *Mlu*I fragment from pLOF/Km as a probe to identify a suitably sized fragment for cloning. The mini-Tn10 element and flanking DNA from each mutant was cloned into pUC19 and the flanking sequence determined using internal primers TEF32 and TEF40, primer walking and in some cases universal pUC-19 primers.

TEF-32 GGCAGAGCATTACGCTGAC SEQ ID NO: 95
TEF-40 GTACCGGCCAGGCGGCCACGCGTATTC SEQ ID NO:96

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry
5 kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377
DNA Sequencer. Double stranded sequence for putative interrupted open reading
frames was obtained for each clone. Sequencer 3.0 software (Genecodes, Corp., Ann
Arbor, MI) was used to assemble and analyze sequence data. GCG programs
[Devereux, *et al.*, 1997. Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer
10 Group, Inc., Madison] were used to search for homologous sequences in currently
available databases.

In 37% of the clones that were identified as being attenuated, there
were multiple insertions of the mini-Tn10 transposable element. Each insertion
including its flanking sequence was cloned individually into pGP704 and mated into
15 the wild-type strain to produce new mutants of *P. multocida*, each carrying only one
of the multiple original insertions. Individual mutants were retested individually to
determine the insertion responsible for the attenuated phenotype. The nucleotide
sequence of the disrupted, predicted open reading frame was determined by
sequencing both strands, and the predicted amino acid sequence was used to search
20 currently available databases for similar sequences. Sequences either matched known
genes, unknown genes, and hypothetical open reading frames previously sequenced or
did not match any previously identified sequence. For those genes having homology
to previously identified sequences, potential functions were assigned as set out in
Table 1.

25

Example 5 **Identification of Related Genes in Other Species**

In separate experiments, STM was also performed using *Actinobacillus*
pleuropneumoniae (App). One of the App strains contained an insertion in a gene that
30 was sequenced (SEQ ID NO: 97) and identified as a species homolog of the *P.*
multocida *atpG* gene. This result suggested the presence in other bacterial species of

homologs to previously unknown *P. multocida* genes that can also be mutated to produce attenuated strains of the other bacterial species for use in vaccine compositions. In order to determine if homologs of other *P. multocida* genes exists in other bacterial species, Southern hybridization was performed on genomic DNA from other species using the *A. pleuropneumoniae atpG* gene as a probe.

Actinobacillus pleuropneumoniae, *Pasteurella haemolytica* (Ph), *P. multocida*, and *Haemophilus somnus* (Hs) genomic DNA was isolated using the CTAB method and digested with *EcoRI* and *HindIII* for two hours at 37°C. Digested DNA was separated on a 0.7% agarose gel at 40V in TAE buffer overnight. The gel was immersed sequentially in 0.1 M HCL for 30 minutes, twice in 0.5 M NaOH/1.5 M NaCl for 15 minutes each, and twice in 2.5 M NaCl/1 M Tris, pH 7.5. The DNA was transferred to nitrocellulose membranes (Amersham Hybond N⁺) overnight using 20X SSC buffer (3 M NaCl/0.3 M sodium citrate). The DNA was crosslinked to the membrane using a UV Stratalinker on autocrosslink setting (120 millijoules). The membrane was prehybridized in 5X SSC/ 1% blocking solution/0.1% sodium lauroyl sarcosine/0.02% SDS at 50°C for approximately seven hours and hybridized overnight at 50°C in the same solution containing a PCR generated atgG probe.

The probe was prepared using primers DEL-1389 (SEQ ID NO: 98) and TEF-46 (SEQ ID NO: 99) in a with a GeneAmp XL PCR kit in a GeneAmp PCR System 2400. Template was genomic *A. pleuropneumoniae* DNA.

DEL-1389	TCTCCATTCCCTTGCTGCGGCAGGG	SEQ ID NO: 98
TEF-46	GGAATTACAGCCGGATCCGGG	SEQ ID NO: 99

The PCR was performed with an initial heating step at 94°C for five minutes, 30 cycles of denaturation t 94°C for 30 sec, annealing at 50°C for 30 sec, and elongation at 72°C for three minutes, and a final extension step at 72°C for five minutes. The amplification products were separated on an agarose gel, purified using a QIAquick gel purification kit (QIAGEN), and labeled using a DIG-High Primer kit (Boehringer Mannheim). The blot was removed from the hybridization solution and rinsed in 2X

SSC and washed two times for five minutes each wash in the same buffer. The blot was then washed two times for 15 minutes each in 0.5X SSC at 60°C. Homologous bands were visualized using a DIG Nucleic Acid Detection Kit (Boehringer Mannheim).

Single bands were detected in *Pasteurella haemolytica*, *Haemophilus somnus* and *A. pleuropneumoniae* using *EcoRI* digested DNA. Two bands were detected using *EcoRI* digested DNA from *Pasteurella multocida*.

Example 6

10 Construction of a Library of Tagged-Transposon *P. multocida* Mutants

Transposon mutagenesis using pLOF/Km has previously been reported to be functional and random in *A. pleuropneumoniae* [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. To construct tagged transposon mutants of *A. pleuropneumoniae*, each of 96 *E. coli* S17-1: λ pir transformants containing pre-selected tagged plasmids (pTEF-1:[NK]₃₅) was used in conjugative matings to generate transposon mutants of *A. pleuropneumoniae* strain AP225, a serotype 1 spontaneous nalidixic acid resistant mutant derived from an in vivo passaged ATCC 27088 strain. *A. pleuropneumoniae* strains were grown on Brain Heart Infusion (BHI) (Difco Laboratories, Detroit, MI) media with 10 μ g/ml B-nicotinamide adenine dinucleotide (V¹⁰), (Sigma, St. Louis, Missouri) at 37°C and in 5% CO₂ when grown on plates. *E. coli* S17-1: λ pir (λ pir, *recA*, *thi*, *pro*, *hsdR*(r_k⁻,m_k⁺), RP4-2, (Tc^R::Mu), (Km^R::Tn7), [Tnp^R], [Sm^R]) was propagated at 37°C in Luria-Bertani (LB) medium. Antibiotics when necessary were used at 100 μ g/ml ampicillin (Sigma), 50 μ g/ml nalidixic acid (N⁵⁰)(Sigma), and 50 (K⁵⁰) or 100 (K¹⁰⁰) μ g/ml of kanamycin (Sigma).

25 Matings were set up by growing each *E. coli* S17-1: λ pir/pTEF1:[NK]₃₅ clone and the AP225 strain to late log phase. A 50 μ l aliquot of culture for each tagged-pTEF-1 clone was mixed with 150 μ l of the APP225 culture, and then 50 μ l of each mating mixture was spotted onto 0.22 μ M filters previously placed onto BHIV¹⁰ plates containing 100 μ M IPTG and 10 mM MgSO₄. Following overnight incubation
30 at 37°C with 5% CO₂, mating mixtures were washed off of each filter into 2 ml of PBS and 200 μ l of each was plated onto BHIV¹⁰N⁵⁰K¹⁰⁰ plates. After selective

overnight growth, colonies were assembled into microtiter plates by toothpick transfer into 200 μ l BHIV¹⁰N⁵⁰K⁵⁰ making sure that each well in a microtiter plate always contained a transposon mutant with the same sequence tag. Following overnight growth, 50 μ l of 75% glycerol was added to each well and plates were stored frozen at -80°C.

APP does not appear to have as much bias towards multiple insertions of the mini-Tn10 element as did *P. multocida*. Only approximately 3% of the mutants were determined to contain multiple insertions, which is in agreement with the 4% previously reported [Tascon, *et al.*, *J Bacteriol.* 175:5717-22 (1993)]. A problem in APP consisted of identifying numerous mutants (discussed below) containing insertions into 23S RNA regions: 28 total mutants with insertions into 13 unique sites. This may indicate that 23S RNA contains preferential insertion sites and that the growth of APP is affected by these insertions enough to result in differential survival within the host. Southern blot analysis using an APP 23S RNA probe suggests that APP may contain only three ribosomal operons as compared to five in *H. influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)] and seven complete operons in *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. This site preference and its effect on growth rate may be a significant barrier to "saturation mutagenesis" since a significant number of clones will contain insertions into these rRNAs and large volume screening will be necessary to obtain additional unique attenuating mutations.

Example 7

Porcine Screening for Attenuated *A. pleuropneumoniae* Mutants

Twenty pools of *A. pleuropneumoniae* transposon mutants, containing a total of approximately 800 mutants, were screened using a porcine intratracheal infection model. Each pool was screened in two separate animals.

Frozen plates of pooled *A. pleuropneumoniae* transposon mutants were removed from -80°C storage and subcultured by transferring 20 μ l from each well to a new 96 well round bottom plate (Corning Costar, Cambridge, MA, USA) containing 180 μ l of BHIV¹⁰N⁵⁰K⁵⁰. Plates were incubated without shaking overnight at 37°C in

5% CO₂. Overnight plates were then subcultured by transferring 10 µl from each well to a new flat bottomed 96 well plate (Corning Costar) containing 100 µl of BHIV¹⁰ per well and incubating at 37°C with shaking at 150 rpm. The OD₅₆₂ was monitored using a microtiter plate reader. At an OD₅₆₂ of approximately 0.2 to 0.25, each plate was pooled to form the "input pool" by combining 100 µl from each of the wells of the microtiter plate. The culture was diluted appropriately in BHI to approximately 2 X 10⁶ CFU/ml. For each diluted pool, 4.0 ml was used to infect 10-20 kg SPF pigs (Whiteshire-Hamroc, Albion, IN) by intratracheal administration using a tracheal tube. At approximately 20 hours post-infection, all surviving animals were euthanized and the lungs removed. Lavage was performed to recover surviving bacteria by infusing 150 mls of sterile PBS into the lungs, which were then massaged to distribute the fluid. The lavage fluid was recovered, and the process was repeated a second time. The lavage fluid was centrifuged at 450 x g for 10 minutes to separate out large debris. Supernatants were then centrifuged at 2,800 x g to pellet the bacteria. Pellets were resuspended in 5 mls BHI and plated in dilutions ranging from 10⁻² to 10⁻⁵ onto BHIV¹⁰N⁵⁰K⁵⁰ plates. Following overnight growth, at least 100,000 colonies were pooled in 10 mls BHI broth to form the "recovered pools". A 0.7 ml portion of each recovered pool was used to prepare genomic DNA by the CTAB method [Wilson, *In Ausubel, et al.*, (eds.), *Current Protocols in Molecular Biology*, vol. 1. John Wiley and Sons, New York, p. 2.4.1-2.4.5 (1997)].

Recovery from the animals routinely was in the 10⁸ CFU range from lung lavage.

Dot blots were performed and evaluated both by visual inspection and by semi-quantitative analysis as described previously. All hybridizations and detections were performed as described. Briefly, probes were prepared by a primary PCR amplification, followed by agarose gel purification of the desired product and secondary PCR amplification incorporating dig-dUTP. Oligonucleotides including TEF5, TEF6, TEF24, TEF25, TEF48 and TEF62, were synthesized by Genosys Biotechnologies (The Woodlands, TX). Primers TEF69, TEF65, and TEF66 were also used for inverse PCR reactions and sequencing.

TEF69	GACGTTTCCCGTTGAATATGGCTC	SEQ ID NO: 166
TEF65	GCCGGATCCGGGATCATATGACAAGA	SEQ ID NO: 167
TEF66	GACAAGATGTGTATCCACCTTAAC	SEQ ID NO: 168

5

The labeled PCR product was then digested with *Hind*III to separate the constant primer arms from the unique tag region. The region containing the labeled variable tag was excised and the entire gel slice was then dissolved and denatured in DIG EasyHyb. Dot blots were prepared and detected using the standard CSPD detection protocol. Film exposures were made for visual evaluation, and luminescent counts per second (LCPS) were determined for each dot blot sample. The $LCPS_{input} / LCPS_{recovered}$ ratio for each mutant was used to determine mutants likely to be attenuated.

Clones selected as being present in the input pool but highly reduced in the recovered pool were selected for further study. Additional clones with questionable input/recovered ratios were also selected after visually evaluating films made from the dot blots. A total of 110 clones were selected.

Example 8

Identification of *A. pleuropneumoniae* Virulence Genes

A partial flanking sequence was determined for each of the 110 mutants by inverse PCR and direct product sequencing. Inverse PCR was used to generate flanking DNA products for direct sequencing as described above. Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs [Devereux and Haeberli, Wisconsin Package Version 9.0, 9.0 ed. Genetics Computer Group, Inc., Madison (1997)] were used to search for homologous sequences in currently available databases.

Table 2 shows the *A. pleuropneumoniae* genes identified and extent to which open reading frames were determinable. Sequence identification numbers are provided for nucleotide sequences as well as deduced amino acid sequences where located.

5

Table 2
***A. pleuropneumoniae* Open Reading Frames**

	<u>Complete Open Reading Frame</u>		<u>NO Start Codon - Stop Codon</u>	
10	atpH	SEQ ID NO: 134	dkSA	SEQ ID NO: 136
	aptG	SEQ ID NO: 132	dnaK	SEQ ID NO: 138
	exbB	SEQ ID NO: 140	HI0379	SEQ ID NO: 144
	OmpP5	SEQ ID NO: 152		
	OmpP5-2	SEQ ID NO: 150	<u>NO Start Codon - NO Stop Codon</u>	
15	tig	SEQ ID NO: 160	pnp	SEQ ID NO: 154
	fkpA	SEQ ID NO: 142	apvA-or 1	SEQ ID NO: 122
	hupA	SEQ ID NO: 146	apvA-or 2	SEQ ID NO: 124
	rpmF	SEQ ID NO: 158	apvB	SEQ ID NO: 126
			apvD	SEQ ID NO: 130
20	<u>Start Codon - NO Stop Codon</u>		<u>RNA or Noncoding Sequences</u>	
	lpdA	SEQ ID NO: 148	tRNA-leu	SEQ ID NO: 162
	potD	SEQ ID NO: 156	tRNA-glu	SEQ ID NO: 163
	yaeE	SEQ ID NO: 164		
	apvC	SEQ ID NO: 128		

25

The putative identities listed in Table 3 (below, Example 9) were assigned by comparison with bacterial databases. The 110 mutants represented 35 groups of unique transposon insertions. The number of different mutations per loci varied, with some clones always containing an insertion at a single site within an ORF to clones containing insertions within different sites of the same ORF. Three multiple

30 insertions were detected in the 110 mutants screened as determined by production of multiple PCR bands and generation of multiple sequence electropherograms.

Example 9
Competition Challenge of *A. pleuropneumoniae*
Mutants with Wild Type APP225

A representative clone from each of the unique attenuated mutant
 5 groups identified above that was absent or highly reduced in the recovered population
 was isolated from the original pool plate and used in a competition challenge
 experiment with the wild type strain (AP225) to verify the relative attenuation caused
 by the transposon mutation. Mutant and wild type strains were grown in BHIV¹⁰ to an
 OD₅₉₀ of 0.6 – 0.9. Approximately 5.0×10^6 CFU each of the wild type and mutant
 10 strains were added to 4 mls BHI. The total 4 ml dose was used infect a 10-20 kg SPF
 pig by intratracheal administration with a tracheal tube. At approximately 20 hours
 post-infection, all surviving animals were euthanized and the lungs removed. Lung
 lavages were performed as described above. Plate counts were carried out on
 BHIV¹⁰N⁵⁰ and BHIV¹⁰N⁵⁰K¹⁰⁰ to determine the relative numbers of wild type to
 15 mutant in both the input cultures and in the lung lavage samples. A Competitive
 Index (CI) was calculated as the $[\text{mutant CFU} / \text{wild type CFU}]_{\text{input}} / [\text{mutant CFU} / \text{wild type CFU}]_{\text{recovered}}$.

Of the 35 potential transposon mutants, 22 were significantly
 attenuated, having a competitive index (CI) of less than 0.2. A transposon mutant that
 20 did not seem to be attenuated based on the STM screening results was chosen from
 one of the pools as a positive control. This mutant had a CI in vivo of approximately
 0.6. An in vitro competition was also done for this mutant resulting in a CI of 0.8.
 The mutant was subsequently determined to contain an insertion between 2
 phenylalanine tRNA's.

25 Competitive indices for unique attenuated single-insertion mutants are
 listed in Table 3. Competitive indices for *atpG*, *pnp*, and *exbB* App mutants indicated
 that the mutants were unable to compete effectively with the wild type strains and
 were therefore attenuated.

Table 3
Virulence and Proposed Function of *A. pleuropneumoniae* Mutants

Mutant	Similarity	Putative or Known Functions	C.I.
AP20A6	<i>atpH</i>	ATP synthase	.009
AP7F10	<i>atpG</i>	ATP synthase	.013
AP17C6	<i>lpdA</i>	dihydrolipoamide dehydrogenase	.039
AP11E7	<i>exbB</i>	transport of iron compounds	.003,.003,.006
AP3H7	<i>potD</i>	Spermidine/putrescine transport	.308
AP8H6	<i>OmpP5</i>	Adhesin / OmpA homolog	.184
AP18H8	<i>OmpP5-2</i>	Adhesin / OmpA homolog	.552
AP13E9	<i>tig</i>	Peptidyl-prolyl isomerase	.050
AP13C2	<i>fkpA</i>	Peptidyl-prolyl isomerase	<.001
AP15C11	<i>pnp</i>	Polynucleotide phosphorylase	.032
AP18F12	<i>hupA</i>	Histone – like protein	.001
AP20F8	<i>dksA</i>	Dosage dependent suppressor of <i>dnaK</i> mutations	.075
AP5G4	<i>dnaK</i>	Heat shock protein – molecular chaperone	.376
AP17C9	<i>tRNA-leu</i>	Protein Synthesis	.059
AP5D6	<i>tRNA-glu</i>	Protein Synthesis	.055
AP18B2	<i>rpmF</i>	Protein Synthesis	.112
AP10E7	<i>yaeA</i>	Unknown	.001
AP19A5	HI0379	Unknown	.061
AP10C10	<i>apvA</i>	Unknown	.157
AP18F5	<i>apvB</i>	Unknown	.103
AP2A6	<i>apvC</i>	Unknown	.091
AP2C11	<i>apvD</i>	Unknown	.014

Accuracy of the CI appeared to be very good as the *exbB* mutant was competed within three different animals yielding CI's of 0.003, 0.003 and 0.006. The use of a Competitive Index number to assign attenuation based upon one competition in a large animal study was further confirmed based on preliminary vaccination results in pigs with 7 mutants (n=8) described below in Example 11.

Example 10

Characterization of Attenuated *A. pleuropneumoniae* Virulence Genes

The *A. pleuropneumoniae* genes identified represent four broad functional classes: biosynthetic enzymes, cellular transport components, cellular regulation components and unknowns.

The *atpG* gene, encoding the F₁-γ subunit of the F₀F₁ H⁺-ATPase complex, can function in production of ATP or in the transport of protons by hydrolyzing ATP. A related *atpG* attenuated mutant was also identified in *P. multocida*. Another *atp* gene, *atpH*, that encodes the F₁ δ subunit was also identified. Phenotypes of *atp* mutants include non-adaptable acid-sensitivity phenotype [Foster, *J Bacteriol.* 173:6896-6902 (1991)], loss of virulence in *Salmonella typhimurium* [Garcia del Portillo, *et al.*, *Infect Immun.* 61:4489-4492 (1993)] and *P. multocida* (above) and a reduction in both transformation frequencies and induction of competence regulatory genes in *Haemophilus influenzae* Rd [Gwinn, *et al.*, *J Bacteriol.* 179:7315-20 (1997)].

LpdA is a dihydrolipoamide dehydrogenase that is a component of two enzymatic complexes: pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase. While the relationship to virulence is unknown, production of LpdA is induced in *Salmonella typhimurium* when exposed to a bactericidal protein from human which may suggest that this induction may be involved in attempts to repair the outer membrane [Qi, *et al.*, *Mol Microbiol.* 17:523-31 (1995)].

Transport of scarce compounds necessary for growth and survival are critical in vivo. ExbB is a part of the TonB transport complex [Hantke, and Zimmerman, *Microbiology Letters.* 49:31-35 (1981)], interacting with TonB in at least two distinct ways [Karlsson, *et al.*, *Mol Microbiol.* 8:389-96 (1993), Karlsson, *et al.*, *Mol Microbiol.* 8:379-88 (1993)]. Iron acquisition is essential for pathogens. In this work, attenuated *exbB* mutants in both APP and *P. multocida* have been identified. Several TonB-dependent iron receptors have been identified in other bacteria [Biswas, *et al.*, *Mol. Microbiol.* 24:169-179 (1997), Braun, *FEMS Microbiol Rev.* 16:295-307 (1995), Elkins, *et al.*, *Infect Immun.* 66:151-160 (1998), Occhino, *et*

al., *Mol Microbiol.* 29:1493-507 (1998), Stojiljkovic and Srinivasan, *J Bacteriol.* 179:805-12 (1997)]. *A. pleuropneumoniae* produces 2 transferrin-binding proteins, which likely depend on the ExbB/ExbD/TonB system, for acquisition of iron. PotD is a periplasmic binding protein that is required for spermidine (a polyamine) transport [Kashiwagi, et al., *J Biol Chem.* 268:19358-63 (1993)]. Another member of the *Pasteurellaceae* family, *Pasteurella haemolytica*, contains a homologue of *potD* (Lpp38) that is a major immunogen in convalescent or outer membrane protein vaccinated calves [Pandher and Murphy, *Vet Microbiol.* 51:331-41 (1996)]. In *P. haemolytica*, PotD appeared to be associated with both the inner and outer membranes. The role of PotD in virulence or in relationship to protective antibodies is unknown although previous work has shown *potD* mutants of *Streptococcus pneumoniae* to be attenuated [Polissi, et al., *Infect. Immun.* 66:5620-9 (1998)].

Relatively few "classical virulence factors," such as adhesins or toxins with the exception of homologues to OMP P5 of *Haemophilus influenzae*, were identified. *H. influenzae* OMP P5 is a major outer membrane protein that is related to the OmpA porin family of proteins [Munson, et al., *M Infect Immun.* 61:4017-20 (1993)]. OMP P5 in nontypeable *Haemophilus influenzae* has been shown to encode a fimbrial subunit protein expressed as a filamentous structure [Sirakova, et al., *Infect Immun.* 62:2002-20 (1994)] that contributes to virulence and binding of both mucin and epithelial cells [Miyamoto and Bakaletz, *Microb Pathog.* 21:343-56 (1996), Reddy, et al., *Infect Immun.* 64:1477-9 (1996), Sirakova, et al., *Infect Immun.* 62:2002-20 (1994)]. A significant finding was identification of two distinct ORF's that appear to encode OMP P5 homologues. This is also the case with two very similar proteins, MOMP and OmpA2 from *Haemophilus ducreyi*. It remains to be determined whether both are functionally involved in the production of fimbriae and whether the presence of two such ORFs represents a divergent duplication with redundant or complementing functions. Interestingly, the two OMP P5 mutants seem to have disparate CI values, suggesting a difference in essentiality or functionality for only one copy. OMP P5 has been shown to undergo molecular variation during chronic infections [Duim, et al., *Infect Immun.* 65:1351-1356 (1997)], however, this

appears to be restricted to a single gene undergoing point mutations resulting in amino acid changes rather than "type switching" due to differential expression of multiple genes.

Protein folding enzymes are important accessories for the efficient folding of periplasmic and extracellular proteins, and two genes were identified whose products have peptidyl-prolyl isomerase activity: *fkpA* and *tig* (trigger factor). FkpA is a periplasmic protein that is a member of the FK506-binding protein family [Horne and Young, *Arch Microbiol.* 163:357-65 (1995); Missiakas, *et al.*, *Mol Microbiol.* 21:871-84 (1996)]. FkpA has been shown to contribute to intracellular survival of *Salmonella typhimurium* [Horne, *et al.*, *Infect Immun.* 65:806-10 (1997)] and a *Legionella pneumophila* homolog, *mip* [Engleberg, *et al.*, *Infect Immun.* 57:1263-1270 (1989)], is responsible for virulence and infection of macrophages [Cianciotto, *et al.*, *J. Infect. Dis.* 162:121-6 (1990); Cianciotto, *et al.*, *Infect. Immun.* 57:1255-1262 (1989)]. Tig, or trigger factor [Crooke and Wickner, *Proc. Natl. Acad. Sci. USA.* 84:5216-20 (1987), Guthrie, and Wickner, *J Bacteriol.* 172:5555-62 (1990), reviewed in Hesterkamp, and Bukau., *FEBS Lett.* 389:32-4 (1996)], is a peptidyl prolyl isomerase containing a typical FKBP region [Callebaut and Mornon, *FEBS Lett.* 374:211-215 (1995)], but is unaffected by FK506 [Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Tig has been shown to associate with the ribosomes and nascent polypeptide chains [Hesterkamp, *et al.*, *Proc Natl Acad Sci USA* 93:4437-41 (1996), Stoller, *et al.*, *EMBO J.* 14:4939-48 (1995)]. Possible roles include an unknown influence on cell division [Guthrie, and Wickner, *J Bacteriol.* 172:5555-62 (1990)] in *E. coli*, a role in the secretion and activation of the *Streptococcus pyogenes* cysteine proteinase [Lyon, *et al.*, *EMBO J.* 17:6263-75 (1998)] and survival under starvation conditions in *Bacillus subtilis* [Gothel, *et al.*, *Biochemistry* 37:13392-9 (1998)].

Bacterial pathogens employ many mechanisms to coordinately regulate gene expression in order to survive a wide variety of environmental conditions within the host. Differences in mRNA stability can modulate gene expression in prokaryotes [Belasco and Higgins, *Gene* 72:15-23 (1988)]. For example, *rnr* (*vacB*) is required for expression of plasmid borne virulence genes in *Shigella flexneri* [Tobe, *et al.*, *J*

Bacteriol. 174:6359-67 (1992)] and encodes the RnaseR ribonuclease [Cheng, *et al.*, *J. Biol. Chem.* 273:14077-14080 (1998)]. PNP is a polynucleotide phosphorylase that is involved in the degradation of mRNA. Null *pnp* / *rnr* mutants are lethal, suggesting a probable overlap of function. It therefore is possible that both *rnr* and *pnp* are
5 involved in the regulation of virulence gene expression. A *pnp* mutant of *P. multocida* is avirulent in a mouse septicemic model (Example 2)]. Other *pnp*-associated phenotypes include competence deficiency and cold sensitivity in *Bacillus subtilis* [Wang and Bechhofer, *J Bacteriol.* 178:2375-82 (1996)].

HupA is a bacterial histone-like protein, which in combination with
10 HupB constitute the HU protein in *E. coli*. Reports have suggested that *hupA* and *hupB* single mutants do not demonstrate any observable phenotype [Huisman, *et al.*, *J Bacteriol.* 171:3704-12 (1989), Wada, *et al.*, *J Mol Biol.* 204:581-91 (1988)], however, *hupA-hupB* double mutants have been shown to be cold sensitive, sensitive to heat shock and blocked in many forms of site-specific DNA recombination [Wada,
15 *et al.*, *J Mol Biol.* 204:581-91 (1988), Wada, *et al.*, *Gene.* 76:345-52 (1989)]. One limited data previously indicated that *hupA* is directly involved in virulence [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. The mechanism of *hupA* attenuation remains unknown.

DnaK is a well known and highly conserved heat shock protein
20 involved in regulatory responses to various stressful environmental changes [reviewed in Lindquist and Craig, *Annu Rev Genet.* 22:631-77 (1988)]. DnaK is also one of the most significantly induced stress proteins in *Yersinia enterocolitica* after being phagocytosed by macrophages [Yamamoto, *et al.*, *Microbiol Immunol.* 38:295-300 (1994)] and a *Brucella suis dnaK* mutant failed to multiply within human
25 macrophage-like cells [Kohler, *et al.*, *Mol Microbiol.* 20:701-12 (1996)]. In contrast, another intracellular pathogen, *Listeria monocytogenes*, did not show induction of *dnaK* after phagocytosis [Hanawa, *et al.*, *Infect Immun.* 63:4595-9 (1995)]. A *dnaK* mutant of *Vibrio cholera* affected the production of ToxR and its regulated virulence factors in vitro but similar results were not obtained from in vivo grown cells
30 [Chakrabarti, *et al.*, *Infect Immun.* 67:1025-1033 (1999)]. The CI of *A.*

pleuropneumonia dnaK mutant was higher than most of the attenuated mutants although still approximately half of the positive control strain.

DksA is a dosage dependent suppressor of filamentous and temperature-sensitive growth in a *dnaK* mutant of *E. coli* [Kang and Craig, *J Bacteriol.* 172:2055-64 (1990)]. There is currently no defined molecular function for DksA, but the gene has been identified as being critical for the virulence of *Salmonella typhimurium* in chickens and newly hatched chicks [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)]. In that work, it was noted that the *dksA* mutant did not grow well with glucose or histidine but did grow well with glutamine or glutamate as the sole carbon source. This observation may indicate that the *dksA* mutant is somehow impaired in the biosynthesis of glutamate [Turner, *et al.*, *Infect Immun.* 66:2099-106 (1998)].

Three genes were identified that have roles in protein synthesis: tRNA-leu, tRNA-glu and *rpmF*. Excluding protein synthesis, tRNA's also have a wide variety of functional roles in peptidoglycan synthesis [Stewart, *et al.*, *Nature* 230:36-38 (1971)], porphyrin ring synthesis [Jahn, *et al.*, *Trends Biochem Sci.* 17:215-8 (1992)], targeting of proteins for degradation [Tobias, *et al.*, *Science* 254:1374-7 (1991)], post-translational addition of amino acids to proteins [Leibowitz and Soffer, *B.B.R.C.* 36:47-53 (1969)] and mediation of bacterial-eukaryotic interactions [Gray, *et al.*, *J Bacteriol.* 174:1086-98 (1992), Hromockyj, *et al.*, *Mol Microbiol.* 6:2113-24 (1992)]. More specifically, tRNA-leu is implicated in transcription attenuation [Carter, *et al.*, *Proc. Natl. Acad. Sci. USA* 83:8127-8131 (1986)], lesion formation by *Pseudomonas syringae* [Rich and Willis, *J Bacteriol.* 179:2247-58 (1997)] and virulence of uropathogenic *E. coli* [Dobrindt, *et al.*, *FEMS Microbiol Lett.* 162:135-141 (1998), Ritter, *et al.*, *Mol Microbiol.* 17:109-21 (1995)]. It is unknown whether the tRNA that we have identified represents a minor species of tRNA-leu in *A. pleuropneumoniae*. Regardless, it is possible that tRNA-leu may have any one of a wide range of functions. RpmF is a ribosomal protein whose gene is also part of an operon containing fatty acid biosynthesis enzymes in *E. coli*. Further work will be required to indicate if this is the case in *A. pleuropneumoniae*, although the same

clustering of *fab* genes and *rpmF* occurs in *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)]. The expression of the *fab* genes is not necessarily dependent on transcripts originating upstream of *rpmF* as there has been a secondary promoter identified within *rpmF* [Zhang and Cronan, Jr., *J Bacteriol.* 180:3295-303 (1998)].

The final class of attenuated mutants includes mutations within genes of unknown function or genes that have not been previously identified. Homologs of *yaeA* and HI0379 have previously been identified in *Escherichia coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)] and *Haemophilus influenzae* [Fleischmann, *et al.*, *Science* 269:496-512 (1995)], respectively. The remaining unknowns have been designated *Actinobacillus pleuropneumoniae* virulence genes (*apv*). The *apvC* gene shows significant similarity to HI0893, however, the proposed similarity of HI0893 as a transcriptional repressor similar to the fatty acid response regulator Bm3R1 [Palmer, *J Biol Chem.* 273:18109-16 (1998)] is doubtful. The *apvD* gene is also most similar to a putative membrane protein (b0878) with unknown function from *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. Two other unknowns, *apvA* and *apvB* had no significant matches in the public databases.

Example 11

Safety and Efficacy of *A. pleuropneumoniae* Mutants

Nine groups (n=8) of SPF pigs (4-5 weeks old, 3-10 kg) were used to determine the safety and efficacy of seven *A. pleuropneumoniae* mutants as live attenuated vaccine strains. Seven groups were infected intranasally with 10^{10} CFU of each mutant on day 1. One group was vaccinated on days 1 and 15 with the commercially available vaccine Pleuromune (Bayer), and one naive group was not vaccinated. On day 29, all groups were challenged intranasally with $1-5 \times 10^5$ CFU per pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. Results are shown in Table 4.

Table 4
Efficacy of *A. pleuropneumoniae* Mutants

	<u>Vaccine</u>	% Mortality following intranasal challenge	
		<u>Vaccination</u>	<u>Challenge</u>
5	Pleuromune	0	37.5
	exbB	0	0
	tig	12.5	0
	fkpA	12.5	0
	HI0385	50.0	0
10	pnp	0	0
	yaeE	0	0
	atpG	0	0
	None	N/A	50.0

15 The *exbB*, *atpG*, *pnp*, and *yaeA* mutants caused no mortality when administered at a dosage of 10^{10} CFU intranasally. The *fkpA* and *tig* mutant groups had one death each and the HI0379 group (highest CI of the 7 mutants tested shown in Example 9) had four deaths. Wildtype LD₅₀ using this model was generally 1×10^7 CFU, indicating that each of these mutants is at least 100 fold attenuated and that

20 there is a reasonable correlation between CI and attenuation.

Example 12
Identification of *P.(Mannheimia) haemolytica* Species Homologs

25 Based on the sequences of virulence genes identified in *P. multocida* and *A. pleuropneumoniae*, attempt were made to identify related genes, *i.e.*, species homologs, in *P. (Mannheimia) haemolytica*. PCR was utilized with the degenerate primers shown below to attempt amplification of the *P. (Mannheimia) haemolytica* genes as indicated. Primer sequences, synthesized by Sigma-Genosys (The Woodlands, TX), include standard single letter designations, wherein B indicates

either (C,G or T), D indicates either (G,A or T), H indicates either (A,C or T), K indicates either (G or T), M indicates either (A or C), N indicates either (A,G,C or T), R indicates either (A or G), S indicates either (G or C), V indicates either (G, A, or C), W indicates either (A or T), and Y indicates either (C or T).

5

atpG	TEF146	ATG GCN GGN GCN AAR GAR AT	SEQ ID NO: 176
	TEF148	GCN GCY TTC ATN GCN ACC AT	SEQ ID NO: 177

10

guaB	TEF240	GGN TTY ATY CAY AAA AAY ATG	SEQ ID NO: 178
	TEF243	TCT TTN GTR ATN GTN ACA TCR TG	SEQ ID NO: 179

pnp	TEF141	GCS GGY AAA CCR CGT TGG GAT TGG	SEQ ID NO: 180
	TEF142	CRC CTA ARA TRT CTG AAA GCA CCA C	SEQ ID NO: 181

15

purF	TEF244	ATG TGY GGN ATY GTN GGN AT	SEQ ID NO: 182
	TEF247	CAT ATC AAT ACC ATA CAC ATT	SEQ ID NO: 183

yjgF	TEF162	GGN CCN TAY GTN CAR G	SEQ ID NO: 184
	TEF163	NGC NAC YTC NAC RCA	SEQ ID NO: 185

20

For amplification of initial degenerate PCR products, a 50 µl reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 µM dNTPs, 25 pmol each of the appropriate primers, 0.8 mM MgCl₂, 0.5 U *rTth* DNA polymerase, XL (PE Applied Biosystems) and approximately 1 µg of TF1 DNA.

25

Cycle conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 15 s, 40-60°C for 60 s, 72°C for 1.5 min; and a final hold at 72°C for 5 min. Each PCR product was band purified from an agarose gel using the QIAGEN Gel Extraction Kit (QIAGEN, Valencia CA).

30

Sequencing reactions were performed using the BigDye™ Dye Terminator Chemistry kit from PE Applied Biosystems (Foster City, CA) and run on an ABI Prism 377 DNA Sequencer. Double stranded sequence for the open reading frame (ORF) for each clone was obtained. Sequencher 3.0 software (Genecodes, Corp., Ann Arbor, MI) was used to assemble and analyze sequence data. GCG programs were used to confirm the identity of the ORF by searching for homologous sequences in currently available databases.

35

The Vectorette Kit (Genosys Biotechnologies, The Woodlands, TX) was used to obtain additional flanking sequence for each of the genes. Vectorette libraries were prepared according to the manufacturer's suggested protocol. Perkin Elmer Applied Biosystems GeneAmp XL PCR Kit components were used to create the

5 Vectorette PCR products with the following reaction conditions. A 50 μ l reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 μ M dNTPs, 25 pmol each of the appropriate primers(shown below), 0.8 mM MgCl₂, 0.5 U *rTth* DNA polymerase, XL (PE Applied Biosystems) and 1 μ l of the appropriate vectorette library. Cycle

10 conditions were 94°C for 1.5 min; followed by 35 cycles of 94°C for 20 s, 60°C for 45s, 72°C for 4 min; and a final hold of 72°C for 7 min. The second primer for each library was the manufacturer's vectorette primer.

Table 5

Gene	Vectorette library	Primer(s)
atpG	BglII, HindIII	TEF217 GAAGCCGCCATACGCTCTTGGG SEQ ID NO: 186
	ClaI	TEF218 GTTGCTTCCTTTGCCTGCACTGG SEQ ID NO: 187
guaB	EcoRI	TEF265 GGCTCAGAAACAATACCACTTTCA SEQ ID NO: 188
	HindIII, TaqI	TEF268 GCACCAAAGCAGAATTTGTCC SEQ ID NO: 189
pnp	ClaI, HincII	TEF219 GGTGATGATGTCGATGATAGTCCC SEQ ID NO: 190
	TaqI,	TEF220 GGCGTATTAGCCGTGATGCCAACC SEQ ID NO: 191
	BamHI	TEF286 GACCACTTAGGCGATATGGACTT SEQ ID NO: 192
purF	TaqI	TEF271 ACCATCATAAATCGCCTGATTC SEQ ID NO: 193
		TEF292 ACCTGCGGCATCTTGTCTC SEQ ID NO: 194
	HincII	TEF274 ACGGGTTTATTTTGCCTCTG SEQ ID NO: 195
yjgF	ClaI	TEF221 CGCCGGTTTCAGGATTCACGGG SEQ ID NO: 196
	EcorV	TEF281 CTGAACAACGTGAAAGCCAT SEQ ID NO: 197

Vectorette PCR products were band purified and sequenced as described above.

Polynucleotide sequences for the atpG, guaB, pnp, purF, and yjgF genes are set out in SEQ ID NOs: 166, 168, 170, 172 and 174, respectively. Polypeptides encoded by these genes are set out in SEQ ID NOs: 167, 169, 171, 173, and 175, respectively.

;

Numerous modifications and variations in the invention as set forth in the above illustrative examples are expected to occur to those skilled in the art. Consequently only such limitations as appear in the appended claims should be placed on the invention.

WHAT IS CLAIMED IS:

1. A gram-negative bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130, or species homologs thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
2. The gram-negative bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
3. The gram-negative bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
5. An attenuated *Pasteurellaceae* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
6. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
7. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

8. The *Pasteurellaceae* bacteria of claim 5 wherein said mutation results in deletion of all or part of said gene.

9. The *Pasteurellaceae* bacteria of claim 5 selected from the group consisting of *Pasteurella (Mannheimia) haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*.

10. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

11. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

12. The *Pasteurellaceae* bacteria of claim 9 wherein said mutation results in deletion of all or part of said gene.

13. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *P. multocida* bacteria.

14. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

15. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

16. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of all or part of said gene.

17. The attenuated *Pasteurellaceae* bacteria of claim 9 that is a *A. pleuropneumoniae* bacteria.

18. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

19. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

20. The *Pasteurellaceae* bacteria of claim 17 wherein said mutation results in deletion of all or part of said gene.

21. An immunogenic composition comprising the bacteria according to any one of claims 1 through 20.

22. A vaccine composition comprising the immunogenic composition according to claim 21 and a pharmaceutically acceptable carrier.

23. The vaccine composition according to claim 22 further comprising an adjuvant.

24. A method for producing a gram-negative bacteria mutant comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

25. A method for producing an attenuated *Pasteurellaceae* bacteria comprising the step of introducing a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29,

31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172, and 174 or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

26. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, 164, 166, 168, 170, 172 and 174.

27. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130.

28. A purified and isolated polynucleotide encoding a *Pasteurellaceae* virulence gene product, or species homolog thereof, selected from the group consisting of:

- a) the polynucleotide according to claim 27,
- b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a), and
- c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

29. A purified and isolated *Pasteurellaceae* polynucleotide encoding a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109,

111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

30. The polynucleotide of claim 29 which is a DNA.

31. A vector comprising the DNA of claim 30.

32. The vector of claim 31 that is an expression vector, wherein the DNA is operatively linked to an expression control DNA sequence.

33. A host cell stably transformed or transfected with the DNA of claim 30 in a manner allowing the expression of the encoded polypeptide in said host cell.

34. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 33 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

35. A purified polypeptide produced by the method of claim 34.

36. A purified polypeptide comprising a polypeptide selected from the group consisting of polypeptides having amino acid sequences set forth in SEQ ID NOs: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175.

37. An antibody that is specifically reactive with the polypeptide of claim 36.

38. The antibody of claim 33 that is a monoclonal antibody.

39. A method of using the monoclonal antibody of claim 39 for identifying a bacteria of claim 1, 5, 9, or 13 comprising the step of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

40. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175 and identifying an agent that interferes with expression or activity of said gene products.

41. A method of identifying an anti-bacterial agent comprising the steps of:

- a) measuring expression or activity of a gene product as set out in SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 165, 167, 169, 171, 173, and 175;
- b) contacting the gene product in (a) with a test compound
- c) measuring expression or activity of the gene product in the presence of the test compound; and
- d) identifying the test compound as an antibacterial agent when expression or activity of the gene product is decreased in the presence of the test compound as compared to expression or activity in the presence of the test compound.

SEQUENCE LISTING

<110> Lowery E., David, et al.

<120> Anti-Bacterial Vaccine Compositions

<130> 28341/00435

<140> 09/809,665

<141> 2001-03-15

<150> 60/153,453

<151> 1999-09-10

<150> 60/128,689

<151> 1999-04-09

<150> 09/545,199

<151> 2000-04-06

<160> 197

<170> PatentIn Ver. 2.0

<210> 1

<211> 1112

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (210)..(1001)

<220>

<223> atpB

<220>

<221> misc_feature

<222> 1099

<223> n = A or T or G or C

<220>

<221> misc_feature

<222> 1104

<223> n = A or T or G or C

<400> 1

```

gtcaacaaca ttttatggtg gagaggccgt taaatttata tccacaattt ttttgattgt 60
acttgctttt aaactgttca attcaatgca ttttattgca ttttttgttg gatattttat 120
aacaatagtt ttaaacaata ttcttccatt ttttataagt aagtacttaa atataaagca 180
ttttcataaa tatcaataaa ggattagtt atg gca gca gag ctt aca aca gcg 233
                               Met Ala Ala Glu Leu Thr Thr Ala
                               1           5

gga tat att ggg cac cat tta gca ttc ttg aaa aca ggg gat tct ttc 281
Gly Tyr Ile Gly His His Leu Ala Phe Leu Lys Thr Gly Asp Ser Phe
10           15           20

```

tgg cat gtt cat tta gat acc ctt cta ttt tca att att tca ggt gca	329
Trp His Val His Leu Asp Thr Leu Leu Phe Ser Ile Ile Ser Gly Ala	
25 30 35 40	
att ttt ctt ttt gtt ttt tca aaa gtt gca aaa aaa gca acg ccg ggt	377
Ile Phe Leu Phe Val Phe Ser Lys Val Ala Lys Lys Ala Thr Pro Gly	
45 50 55	
gtg cct agc aag atg caa tgt ttt gtt gag ata atg gtt gat tgg att	425
Val Pro Ser Lys Met Gln Cys Phe Val Glu Ile Met Val Asp Trp Ile	
60 65 70	
gat ggg atc gta aaa gaa aat ttc cat ggt cct cgt cat gct gtt gga	473
Asp Gly Ile Val Lys Glu Asn Phe His Gly Pro Arg His Ala Val Gly	
75 80 85	
cca tta gca tta act att ttc tgc tgg gta ttc att atg aat gct atc	521
Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile	
90 95 100	
gat ttg atc cca gta gat ttc cta cct caa tta gcc cat tta ttt ggt	569
Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly	
105 110 115 120	
att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta	617
Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu	
125 130 135	
ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa	665
Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys	
140 145 150	
tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt	713
Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe	
155 160 165	
aat cat cct ttg tta att ccg gtt aac tta gcg ctt gaa tca gtc aca	761
Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr	
170 175 180	
tta tta gca aaa cct gtt tct ttg gcg ttc cgt ctt ttc ggg aat atg	809
Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met	
185 190 195 200	
tat gca ggt gaa ctt atc ttt att ctt att gca gtg atg tac atg gca	857
Tyr Ala Gly Glu Leu Ile Phe Ile Leu Ile Ala Val Met Tyr Met Ala	
205 210 215	
aat aat ttt gca ctt aat tca atg ggt att ttc atg cat ttg gct tgg	905
Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp	
220 225 230	
gct att ttc cat att ctt gtg att acc tta caa gca ttt att ttt atg	953
Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met	
235 240 245	
atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac	1001
Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His	
250 255 260	
taatttttta taaacaaaac cagaccttgg gtctaaattt caatcttatg gagaacatta	1061
tggaacactg taattactac aacaatcatc gcactctgnaa ttnttcttgc t	1112

<210> 2
 <211> 264
 <212> PRT
 <213> Pasteurella multocida

<400> 2
 Met Ala Ala Glu Leu Thr Thr Ala Gly Tyr Ile Gly His His Leu Ala
 1 5 10 15
 Phe Leu Lys Thr Gly Asp Ser Phe Trp His Val His Leu Asp Thr Leu
 20 25 30
 Leu Phe Ser Ile Ile Ser Gly Ala Ile Phe Leu Phe Val Phe Ser Lys
 35 40 45
 Val Ala Lys Lys Ala Thr Pro Gly Val Pro Ser Lys Met Gln Cys Phe
 50 55 60
 Val Glu Ile Met Val Asp Trp Ile Asp Gly Ile Val Lys Glu Asn Phe
 65 70 75 80
 His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys
 85 90 95
 Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu
 100 105 110
 Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro
 115 120 125
 Thr Ala Asp Ile Ser Gly Thr Leu Gly Leu Ser Ile Gly Val Phe Phe
 130 135 140
 Leu Ile Ile Phe Tyr Thr Ile Lys Ser Lys Gly Met Ser Gly Phe Val
 145 150 155 160
 Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val
 165 170 175
 Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu
 180 185 190
 Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile
 195 200 205
 Leu Ile Ala Val Met Tyr Met Ala Asn Asn Phe Ala Leu Asn Ser Met
 210 215 220
 Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile
 225 230 235 240
 Thr Leu Gln Ala Phe Ile Phe Met Met Leu Thr Val Val Tyr Leu Ser
 245 250 255
 Met Gly Tyr Asn Lys Ala Glu His
 260

<210> 3
 <211> 1972
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (364) .. (1230)

<220>
 <223> atpG

<400> 3
 agcgggccat ttggctcagt tcggcttcgg attcttatga tgcacacgta agcaattatc 60
 acatgggtcaa aaagtaactg aattattgaa acaaaaccaa tactctccgt tatctgtagc 120
 acaacaagca ttagtggttat ttgcagtaga gtttggttac ttagaagaag tggacttaga 180
 tcgtattggg tcatattgaat cagcactttt agagtatgct aaccataact atgctgattt 240
 tatgcgtagg ttaaccaat ctggcaatta caatgatgaa attaaagagt cattaaaagg 300
 cattttggat agcttcaaag caaacagtgc gtggtaagtt aacactttaa atggagagac 360
 aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa 408
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys
 1 5 10 15
 agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tcg aaa 456
 Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys
 20 25 30
 atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa 504
 Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
 35 40 45
 aca ata cgt aac gtg att agc cac gtt tcc aaa gca acg att ggt tac 552
 Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr
 50 55 60
 aag cat cca ttt tta gtg gat cgc gaa gta aaa aaa gtg ggc atg att 600
 Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
 65 70 75
 gtt gtg tcc aca gat cgt ggt ctt tgt ggt ggc tta aac gtg aac ttg 648
 Val Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu
 80 85 90 95
 ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt 696
 Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
 100 105 110
 tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa 744
 Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln
 115 120 125
 tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act 792
 Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr
 130 135 140
 ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840
 Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala
 145 150 155
 tat aaa aaa ggg gaa gta gat gtt gtg tat tta gtt tat aac aaa ttt 888
 Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
 160 165 170 175

```

att aac acg atg tcg caa aag cca gta ttg gaa aaa tta att cca tta 936
Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu
180 185 190

cca gaa tta gat aat gat gaa tta ggc gaa aga aaa caa gtt tgg gat 984
Pro Glu Leu Asp Asn Asp Glu Leu Gly Glu Arg Lys Gln Val Trp Asp
195 200 205

tat att tac gaa cct gat gcg aaa gta tta tta gat aat tta ttg gtt 1032
Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val
210 215 220

cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct 1080
Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala
225 230 235

tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac 1128
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn
240 245 250 255

gca ggt aac tta att aat gag tta cag tta gtc tat aac aaa gct cgt 1176
Ala Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg
260 265 270

caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca 1224
Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala
275 280 285

gca att taacaaatag aggatcggta atggcaactg gaaaaattgt acaaatcatc 1280
Ala Ile

ggtgcgggtta ttgacgttga attcccacaa gatgcagtac caaaagtata tgatgcctta 1340

aatggttga aa caggttttagt acttgaagtt caacaacaat taggtggtgg tgtagttcgc 1400

tgtatcgcaa tgggatcatc tgatggatta aaacgcggtt taagcgtaac aaatacgaat 1460

aacccaatct ctgttccagt gggaacgaaa acattgggtc gtatcatgaa cgtattgggt 1520

gaaccaatcg atgagcaagg tgaaatcggg gcagaagaga attggtctat tcaccgtgcg 1580

ccaccaagtt atgaagaaca atctaacagt actgaacttt tagaaacggg aattaaagtt 1640

atcgacttag tttgtccgtt tgcgaaaggg ggtaaagtag gtttattcgg tgggtcgggt 1700

gtcggtaaaa ccgtcaatat gatggaatta atccgtaaca tcgcaattga gcaactcaggt 1760

tactctgtct ttgcgggggt aggtgagcgt acgcgtgaag gtaacgactt ctatcatgag 1820

atgaaagact ctaacgtatt agataaagtg tctcttgttt atgggtcaaat gaacgagcca 1880

ccaggttaacc gtttacgtgt ggcattaaca ggcttaacta tggcggaata attccgtgat 1940

gaaggtcgtg atgtcttatt ctctgttgat aa 1972

```

<210> 4

<211> 289

<212> PRT

<213> Pasteurella multocida

<400> 4

Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Ser

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

Ile

<210> 5
 <211> 1357
 <212> DNA
 <213> Pasteurella multocida
 <220>

<221> CDS

<222> (1)..(813)

<220>

<223> cap5E

<400> 5

```

gtc gac tat att tat cat gct gcc gca tta aag caa gtg cct tca tgc 48
Val Asp Tyr Ile Tyr His Ala Ala Ala Leu Lys Gln Val Pro Ser Cys
1 5 10 15

gag ttt tat ccg tta gag gca gtg aaa acc aat att tta ggt acg gca 96
Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala
20 25 30

aat gtc tta gaa gcc gcc atc caa aac cag ata aaa cgc gtc gtc tgt 144
Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
35 40 45

ctt agc aca gat aaa gcg gtg tac cca att aat gcg atg ggc att tct 192
Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
50 55 60

aaa gca atg atg gaa aaa gtc atc atc gca aaa tcg cgt aac cta gaa 240
Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
65 70 75 80

ggc aca cca acg aca atc tgt tgt act cgc tat ggc aat gtc atg gca 288
Gly Thr Pro Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
85 90 95

tcg cgt ggt tcg gtt atc cca tta ttt gtc gat caa ata cgt caa ggc 336
Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
100 105 110

aag cct ttt act att act gat cct gag atg aca cgc ttt atg atg aca 384
Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
115 120 125

ttg gaa gat gct gtg gat tta gtc cta tat gca ttt aaa aat ggt caa 432
Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln
130 135 140

aat ggt gat gtt ttt gta caa aaa gcc ccc gca gca acc att ggt acc 480
Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
145 150 155 160

ctt gcc aaa gca att acc gaa tta tta tct gtc cca aat cac cct att 528
Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile
165 170 175

tcc att ata ggt acg cgt cat gga gag aaa gca ttc gaa gct tta tta 576
Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
180 185 190

agc cgt gaa gaa atg gtt cat gca att aat gaa ggt aat tat tat cgc 624
Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
195 200 205

atc cca gcc gat caa cgc agt tta aat tac agt aaa tat gtc gaa aaa 672
Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
210 215 220

```

```

ggg gaa cca aaa att acc gaa gtc acc gac tac aac tca cat aat act 720
Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
225                230                235                240

gag cgt ttg act gtc aag gaa atg aag cag tta ctg ctt aaa ctt gaa 768
Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
                245                250                255

ttc ata cag aaa atg att gag ggt gaa tac atc tca ccg gag gta 813
Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val
                260                265                270

taaaaatgaa agtcttagta actggttcaa atgggttttat tgcgaaaaat ctgattcagt 873

ctttatctga ggaacaagat attgagattt tatgttatca ccgtcaatcc tctgagaaaa 933

cgcttattca tcatgtattg agtgctgatt ggattattca tcttgccgggt gcgaatcgtc 993

cacctgaaga acaagaattt atgacatcaa atacacaatt gacggaaaaa atttgccgta 1053

ttttacagcg tcatcagaaa aaaacgcctt tgttatatcc ctctagcatt caagtagaaa 1113

gtcccaaaat aagtacttat tcgcaaacca aattagaaag tgaatatcat gttcatcaat 1173

tacataaaga aaatggtaat ccgatttata tctgccgttt agctaattgct tttggcaaatt 1233

ggtcacgacc tcactataac tcggtagtcg ccacattttg ccataactta attcatgatt 1293

taccocatga aattcatgat catactgcag aaataaggct catttatatt gatgatgtcg 1353

ttga 1357

```

```

<210> 6
<211> 271
<212> PRT
<213> Pasteurella multocida

```

```

<400> 6
Val Asp Tyr Ile Tyr His Ala Ala Ala Leu Lys Gln Val Pro Ser Cys
 1                5                10                15

Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala
 20                25                30

Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys
 35                40                45

Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
 50                55                60

Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
 65                70                75                80

Gly Thr Pro Thr Thr Ile Cys Cys Thr Arg Tyr Gly Asn Val Met Ala
 85                90                95

Ser Arg Gly Ser Val Ile Pro Leu Phe Val Asp Gln Ile Arg Gln Gly
100                105                110

Lys Pro Phe Thr Ile Thr Asp Pro Glu Met Thr Arg Phe Met Met Thr
115                120                125

```


Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln
 130 135 140
 Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
 145 150 155 160
 Leu Ala Lys Ala Ile Thr Glu Leu Leu Ser Val Pro Asn His Pro Ile
 165 170 175
 Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
 180 185 190
 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
 195 200 205
 Ile Pro Ala Asp Gln Arg Ser Leu Asn Tyr Ser Lys Tyr Val Glu Lys
 210 215 220
 Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr
 225 230 235 240
 Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
 245 250 255
 Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val
 260 265 270

<210> 7
 <211> 6132
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (4032)..(4727)

<220>
 <223> devB

<400> 7
 gtcaacaatt accgcacttt agtggagtaa ataacaatgg cgaaaaagaa taacgggcat 60
 gaaaaagagg atgatgttcg cctagataaa tggctttggg ctgcccgttt ttataaaaca 120
 cgtacttttag caaaagacat gattgatggc ggtaaagtgc attataatgg gcagcgcacg 180
 aaacccaata aaacggttga aattggtggt gtgatcaaac ttcgtcaagg taatgacgaa 240
 aaagaagtgg aagtgcttgc gctttctacg caacgtcgtg gggcgccaga agcacaattg 300
 ttgtatcaag aaacagaaaa aagccttgaa caacgtgcga aaatggcgat tgcacgtaag 360
 attaatgcat taacgatgcc gcacctgat cgtcgcccga ataaaaaaga gcggcgatgat 420
 ttattgaaat ttaaacaatca agatagcttt tcatcttgat gatgtgattt acctactttt 480
 cttattaaag aaaggaatat ggggaagctg tgtgcttgcc cttaacctga ataaaggctt 540
 tttatgacag acaacacaga caatgacaaa ctgtatcgct accttttcca agatcgcgcg 600
 gtgcgcggtg aatgggtacg gttaaaccac acgtttactg atacgttaaa tacacatcaa 660

tatccgaaaag tcatccaaaa cttgctcggt gaaatgatgg tggcgaccag tttattgacg 720
gcgacgttaa aatttgaagg ggatattact gttcaagtac aaggtgatgg accattaaaa 780
ttagcattag ttaatggcaa tcatcagcag caaattcgcg cattagcgcg tttacaagcg 840
gatgtcagtg atgatatgag tttggcgcaa ttagtcggga aaggggtatt agtgattacg 900
attgcaccga cagaaggcga gcgttaccaa ggcgtgattg cgtagataa gccaaaccatt 960
actgcctgtc ttgaagatta ttttgtcggt tcagaacaat tgcaaacca gcttattatt 1020
cgtgctggcg aatttgaagg acaacctgtg gcagccggtg tgttggtaca aattatgccg 1080
gacggttcag gttctccaga ggattttgaa cacttagcaa cattggcagc gacggtgaaa 1140
gaggaagaac tatttggttt aacagcagaa gaattattgt accgtttata tcatgaagag 1200
cgtgttgaaa ttttcccttc acagccgacg tcatttttct gtggctgctc acaagaacgt 1260
tctggtgccg cattgttggt gatttctgat gaagaattgg atgaagtctt ggcagagcat 1320
aacggtacca ttgatatgca gtgtgaatgt tgtgggacgc attatttctt caataaagca 1380
gcgattatgc aattgaaagt agaaaaataa gtcttggtat tatggatttt gttgcaggct 1440
atcaagatat ttgatagcct gtttttcctt tgcagcaaac gattttatga gaaaaacgcc 1500
gtcttctcac acagtagttt aggtattgca tagcatgaag cgggaaacta tgtttggcg 1560
ttgtctgttt aaaaaggtta tctatgttag cactttcacc atcattactt gaaaaaacac 1620
ttgaaatcgc ggatcaagca ggagattttt taacgcgatt ttataccgac tcagggcaaa 1680
atgcgttagc aattcaaacc aaacaagata acacgccagt gactgccgtg gatttatttt 1740
tgagtcaatt ttttaattgaa aaattgaccg cactgacacc tgagggtccc attctttccg 1800
aagagagttg taaaatcccc ttacaagatc gtgcacattg ggcagaatat tgggttaattg 1860
accactcga tggaaccaa caatttatta atcgacccga tcaattttcc attttgatta 1920
cacttgcca acacaatcaa cccgtcttaa gcattacca tgcccctatt ttacaaacga 1980
cctattatgc tatgcagggc tttggtgctt acagaaggca gggcaatcaa caagaaaagc 2040
taaacaacca agcgcgacct gagcagcgaa aatcaaaat tgctgtggga gtcggggggcg 2100
ttgaacggaa aattcagccc ttgttaaatac cagcttatca atatgaattt ttggtttatg 2160
gttcaagtgg cttaaaaggc ggcttagtgg ccgatggcac ttgtgattgc tatattcgag 2220
taggaaaaac gggatgaatg gatacggggg cggctgaaat cctcttacgt gaaatgggag 2280
gtgctgtgtt tgactttgct tttcaaccgc ttagctataa tcagagagaa agttttatta 2340
atcccaattt tgtgatggta gcgaatacag aatttgattg gcagaaaatt tttcaatttc 2400
attcgacta ggcattattt attataagat gcgatatctt atgacctcta tttttaacaa 2460
acggatttca ggaaaaaaat gaaaattgaa gcagacaaca attgtattgt aatttttgg 2520
gcatcaggtg atttaactta tcgtaaattg attcctgcac tgtataactt atataaaatc 2580

```

ggtcgtttga ctgagcattt ctccgtgtta ggtgtggcaa gaacggaatt aagtgatgag 2640
ggtttccgtg aaaaaatgcg ccaagcgttg atcaaaagtg aaaaagcgaa tggcgaaaca 2700
ctcgatcaat tttgtagcca cttttattat caggcattaa ataccgcgga tgctgccgat 2760
tatggcaagt taattcctcg tcttgatgac ttacatgata aatatcaaac ttgtggtaac 2820
acactttact atttatctac gccgccaagc ctttatggcg tgattccaga atgccttgcg 2880
gcacatgggt taaatactga agagtttggc tggagcggt taattgtgga aaaaccgttt 2940
ggttatgata tacgcacggc aaaagaactc gatattcaaa ttcaccgttt ctttgatgaa 3000
caccaaattt atcgtattga ccactatctt ggtaaagaaa cggttcaaaa tctgcttggtg 3060
ttgcgttttt ctaatggatg gtttgaacca ctctggaacc gtaatttcat tgattatatt 3120
gaaatcacgg gcgcagaatc tatcgggtga gaagagcgtg gtggttatta cgatgattct 3180
ggcgcaatgc gtgatatggt ccaaaacat ttgttgcaag tgtagccat ggttgcgatg 3240
gagccaccag caattattaa tgccgactca atgcgtgatg aagtggcaaa agtcttgat 3300
tgtttacatc cattaagtga ggatgactta gaaaatcatt tagtcttagg gcaatatacg 3360
gcaggcacag ttgaaggtga agcgggttaag ggctacttac aggaaaaagg tgtgccggca 3420
gagtctaata cggaactta catggcatta cgttgtgaaa ttgacaactg gcgttggcg 3480
ggtgtgccat tttatgtgcg tactgggaaa cggttaccaa gtcgagtgc cgaaattgtg 3540
attcatttca aaaccacacc acatccggta ttagccaaa aagcaccaga aaacaaatta 3600
attatccgta ttcaaccgga tgaagcgatt tcgatgcgtt ttggtttgaa aaaaccggga 3660
gcagggtttg aagcaaaaga agtgtcgatg gatttccgtt atgcggatct tgcctcacca 3720
agcttactga ccgcttatga gcgtttatta ttggattcta tgaaaggcga tgccactttg 3780
tttgccgta ctgatgcggt acatgcctgt tggcagtttg tggagccgat tttacaatat 3840
aaagcacaaa atgggcgtgt ttatgagtat gaagccggta cttggggacc gacagaagcc 3900
gacaaactga tcgcgaaaac gggtcgtggt tggcgtaaac caagtggatt aatgaaaag 3960
aaagtgtaat gtccgcctct ttcgtaagaa atgcgagggg ctaatgtgag cagattgagt 4020
aaggaaagat c atg aat aca atc att ttt gac agt gca cag cat gcc gta 4070
          Met Asn Thr Ile Ile Phe Asp Ser Ala Gln His Ala Val
              1             5             10

gag aaa att gca caa gaa ttg tta gcg tat agc tta gaa ggt cgc cct 4118
Glu Lys Ile Ala Gln Glu Leu Leu Ala Tyr Ser Leu Glu Gly Arg Pro
      15             20             25

gtg cat att tcc tta tcc gga ggc tca acg ccg aaa ttg tta ttt aaa 4166
Val His Ile Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys
      30             35             40             45

act tta gct caa gca ccg tat aac acc gag att caa tgg aaa aat ttg 4214
Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu
              50             55             60

```

cat ttt tgg tgg ggc gat gat cgt atg gtg cca cca acc gat cca gaa 4262
 His Phe Trp Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu
 65 70 75
 agt aat tac ggc gag gtg caa aaa ttg tta ttc gat cat att cag atc 4310
 Ser Asn Tyr Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile
 80 85 90
 cct gca gaa aat att cac cgc att cgt ggt gaa gcc ccc gtt gag agt 4358
 Pro Ala Glu Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser
 95 100 105
 gaa ctt cac cgt ttt gaa caa gcg cta agt gcg gtc att cct ggg caa 4406
 Glu Leu His Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln
 110 115 120 125
 gtt ttt gat tgg att att ttg ggc atg gga acg gac ggg cac acg gcc 4454
 Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala
 130 135 140
 tca tta ttc ccg cat caa acc gat ttt gac gat cct cat ttc gcc gtg 4502
 Ser Leu Phe Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val
 145 150 155
 atc gcg aaa cac cct gaa aca ggg caa att cgt att tca aaa aca gcg 4550
 Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala
 160 165 170
 aaa ttg att gaa caa gca aag cgg gtg acc tat ttg gtg aca ggt agc 4598
 Lys Leu Ile Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser
 175 180 185
 agt aaa gcc gag atc tta aaa gaa att caa act act ccg gca gaa caa 4646
 Ser Lys Ala Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln
 190 195 200 205
 ctg cct tat cct gct gcg aaa atc aaa gcg aag cat ggg gtg acg gaa 4694
 Leu Pro Tyr Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu
 210 215 220
 tgg tat ttg gat aag gat gcg gca aaa tta ctg taatgcgtcg tgagattttt 4747
 Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu
 225 230
 caacattttt gcaaagagac ttgaaacaaa atagaccata gcgttcgttt tcaacgagtg 4807
 ctgaaaatga aggctctcgt tgaaaatggc gccatttagt gggtaagctt aaggttcgtc 4867
 cagacagcgc tatcaaaaagg gtaaaagaat gtatcaactc tattttaatc caccaaaatc 4927
 ttcatgggtca ttacgcgttt ggggtgttatt gaaagaactg gcaattcctt ttgagcctaa 4987
 aattgtacgt tatttgatg atttaagtga acaacgcaa caatttaagg cgttttcgcc 5047
 gacttcaaaa atcccagtat tgcgtgctga tgggtgtgtc atttgggaca gtttagcgat 5107
 tatcgagttt ttggcagaaa gttatccgca cgtgtgggag caagataagg cgacaagagc 5167
 gtggtcacgt tctgcttggt ctgaaatgca ctctggcttt gaaaatttgc gtgaaatgtg 5227
 tgatttcgcc cctttagctc gcaaaccggt acaagaaatg cccgctgtgt taagccaaga 5287
 gctaacaagg cttaatcaat tattagaaga agggttaaca aatcacactg ggcgatttaa 5347

tgcaaacctc cagtgcctttt ggtcgagtac aatcctcggt gtcttttttc cgtaattcct 5407
 atgatgactt tgccgcttat cgtgcggtgt taaatcgttt aactggcttt catagcgcga 5467
 ttaaagcggc taatcgccca agcaaattag tgctcacaga aagtcgtcat gatattggtt 5527
 ttcatgatct caacgtagag accccgcaag gaaaaacctt aattgacaag ctcaacctac 5587
 aatttcctct cgggtacatgg ttattaattc aaggacattc tgggtgtaggg aaaacaacct 5647
 tgtaagaac cattgcggga ctatggcctt atgctagtgg gacaattcaa cgccacaaac 5707
 aagatactct gtttctttct caaaaacctt atttgccaca aggtcgctta cttgatgccc 5767
 tattttatcc tgaactggcg cctgaagacg tgaatgagca acaagttata gacatactcg 5827
 cgaaagtaca actcgggcat ttaagcgata aactagaaca agaaaatgat tggacacggg 5887
 tactctcttt aggtgaacaa caacgtctgt cgtttgctcg cattttattg cataaaccta 5947
 ctgttggttt cttagatgaa gccactgccg gcatggatga aggactggaa gatgcatgt 6007
 accgcttact gaaagatgaa ctgcctcaga ttactgtgat cagtgttgga caccgttcga 6067
 cgtaattcc gcaccattca cagcaattac acattcaata acaagacagg gcgttggtga 6127
 gtcca 6132

<210> 8

<211> 232

<212> PRT

<213> Pasteurella multocida

<400> 8

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

145	150	155	160
His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile	165	170	175
Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser Ser Lys Ala	180	185	190
Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln Leu Pro Tyr	195	200	205
Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu Trp Tyr Leu	210	215	220
Asp Lys Asp Ala Ala Lys Leu Leu	225	230	

<210> 9
 <211> 2438
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1635) .. (2396)

<220>
 <223> dnaA

<400> 9
 gacccaatgc ttgccaccgg cggctctatg attgcgacaa tcgatcttct aaaagcgaaa 60
 ggctgtaaac acattaaagt gctcgtgtta gtcgccgcgc ctgaaggcat taaagcatta 120
 gaagctgcgc accctgatat cgaattatat accgcatcag ttgatagtca cttaaataaa 180
 caaggctata ttattccagg tcttggtgat gccggtgata aaatttttgg cactaaataa 240
 tcccaacaca agcggcatct tatgccgctt ttttcggtc aatttatagc gcttacaatc 300
 ttaacagctt gaacactata aaatgaaaag ttaattcaga cagagagttg aaacttaaca 360
 tgacaaatca aaatccccct gttcttctag aacaaaatca cgcaaaacaa gccttcggtg 420
 ggctacaaat gctttttggt gccttcggtg ctttagtcct tgttcccctg attacgggtt 480
 taaatgccaa tactgcctta ttgaccgcag ggattgggac actcttattc caactttgta 540
 ctggacgcca agtcccaatt ttcttagcct ctccctttgc ttttattgca ccaattcaat 600
 atggcgtggc aacatggggc attgctacta ctatgggggg gctgggtgtt actggactgg 660
 tttattttgc cctcagtacg ttagtcaaaa ttaaagggtg tgggtgctta caaaaagtct 720
 ttccgccagt agttgttggc cccgttatta tcatcatcgg tatgggactt gccctgttg 780
 ccgtggacat ggcattaggt aaaaacagca cttatcaata taacgatgcc gtattcggtt 840
 cgatggcaac attattgaca acgttaggtg ttgcggtgtt tgctaaaggc atgatgaaat 900
 taattcctat catgtttggt attgtcgtcg gctatatcct ctgcttattc ttaggcttaa 960

```

ttaatttcca acctgtcatt gatgcacctt ggttttagtgt gccagaaatt actacccttg 1020
aatttaaatt agaagctatt ctttatttat taccgattgc tatcgcccca gcagttgagc 1080
atgtcgggtgg gatcatggca atcagttcgg tgacagggaa agacttccta caaaaaccag 1140
gattacatcg cactttatta ggggatggta ttgcaacgag tgccgcctca ttcttaggag 1200
gaccacctaa tacaacttat gctgaagtca ctggtgctgt catgcttacg cgcaacttta 1260
accctaaaat catgacatgg gcagccgttt gggcaattgc gatttccttc tgtggtaaag 1320
tcggggcttt cctctctacc attccaacta ttgtcatggg tggcattatg atgttagtgt 1380
ttggctctat cgccgtagtc ggtatgagta cactgatccg tggtaaagtg gatgtaacag 1440
aagcgcgtaa tctgtgtatt atttccgttg tgatgacgtt tggcatcggg ggtatgtttg 1500
tgaactttgg agaagtctcc ttaaaaggga ttagtttatg cgccgttgct gcgattttac 1560
tcaacttaat cttacccaaa gccaaaaaca cccaataga agaaaatcga taagagaaaa 1620

ttaagggtta agtc ttg ctt aac cct tca ttt ttc gtt tat cct tat tct 1670
          Leu Leu Asn Pro Ser Phe Phe Val Tyr Pro Tyr Ser
              1              5              10

cct ttt ttc gat ttt gta ggt tgc ttt ttg tta gaa aat ttc caa tta 1718
Pro Phe Phe Asp Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu
          15              20              25

cct ttg cct att cat caa ctc gat gat gaa acg ctg gat aat ttc tat 1766
Pro Leu Pro Ile His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr
          30              35              40

ccc gac aat aat tta ttg ttg ctc aat tcg cta cgc aaa aat ttt act 1814
Pro Asp Asn Asn Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr
          45              50              55              60

tgt cta aca caa caa ttt ttt tat att tgg ggc gag caa agc agt ggt 1862
Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
          65              70              75

aaa agt cac ctc tta aaa ggc att act cat cat ttt ttc ctt tta cag 1910
Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
          80              85              90

cgc ccc gct atc tat gtg ccc tta gaa aaa tcc caa tat ttc tca ccg 1958
Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
          95              100              105

gcg gta ctc gaa aac tta gaa caa caa caa ttg gtt tgt tta gat aat 2006
Ala Val Leu Glu Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn
          110              115              120

tta cag gca att ata ggc aat act gaa tgg gaa tta gcg att ttt gat 2054
Leu Gln Ala Ile Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp
          125              130              135              140

tta ttt aat cgc ata aaa tct gtt gaa aat aca ctg ctt gtg atc agt 2102
Leu Phe Asn Arg Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser
          145              150              155

gca aat caa tcc cca act gca tta cct gta agt tta cct gac tta gct 2150

```

Ala Asn Gln Ser Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala
 160 165 170

tca cgt tta cgc tgg gga gaa agc tat cag ctg gtc ccc tta aat gat 2198
 Ser Arg Leu Arg Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp
 175 180 185

caa caa aaa atc cat gta ttg caa aaa aat gca cat caa cgt ggt atc 2246
 Gln Gln Lys Ile His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile
 190 195 200

gaa ctc ccc gat gaa gta gct aat ttt ctt ttg aaa cgc tta gag cgc 2294
 Glu Leu Pro Asp Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg
 205 210 215 220

gat atg aaa acg tta ttt gaa gca cta agt aaa tta gat aaa gca tca 2342
 Asp Met Lys Thr Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser
 225 230 235

tta caa gcc caa cgt aaa tta acg att ccc ttt gta aaa gaa att tta 2390
 Leu Gln Ala Gln Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu
 240 245 250

aag cta taaaaaaaga ccacctcttt atcagggtgat ctttcttgtc ga 2438
 Lys Leu

<210> 10

<211> 254

<212> PRT

<213> Pasteurella multocida

<400> 10

Leu Leu Asn Pro Ser Phe Phe Val Tyr Pro Tyr Ser Pro Phe Phe Asp
 1 5 10 15

Phe Val Gly Cys Phe Leu Leu Glu Asn Phe Gln Leu Pro Leu Pro Ile
 20 25 30

His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn
 35 40 45

Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln
 50 55 60

Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly Lys Ser His Leu
 65 70 75 80

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

Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu
 100 105 110

Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn Leu Gln Ala Ile
 115 120 125

Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg
 130 135 140

Ile Lys Ser Val Glu Asn Thr Leu Leu Val Ile Ser Ala Asn Gln Ser
 145 150 155 160

Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg
 165 170 175
 Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile
 180 185 190
 His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp
 195 200 205
 Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr
 210 215 220
 Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser Leu Gln Ala Gln
 225 230 235 240
 Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu Lys Leu
 245 250

<210> 11
 <211> 2060
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (856)..(1389)

<220>
 <223> dsbB

<400> 11
 gaattcttct tacgtatgct ccagtcacg ttgccagttc tcatttgtgg tttagtgtacc 60
 tgcttcttag tggaaaaatt tgggtgtattt ggctatggcg ccaaattgcc acgtaaagta 120
 tggggcatct tggcaaagtt tgatcgcaat aatcaacaaa aaatgtcacg acaagatcgt 180
 ttgaaacttt ttgtgcaagc tttaattgggt atttgggttg ttgttggact cgcattccat 240
 ctgcgcccg tcggtatcat tggtttaacg gtgattattt tggctacttc attttgtgggt 300
 gtcaccagcg agcatgctat tggtaaagcc ttccaggaat ccttaccctt cacagcattg 360
 ttagtggtgt tcttctcggt tgttgccgtc atcattgacc aacatctgtt tgcgccaatt 420
 attcagtttg tgctggctgc cagtgaacat actcagcttg ctcttttcta tatttttaac 480
 ggtttggtat ccgccatttc agataatgtg tttgtggcca cagtttatat caatgaaacc 540
 aaagcggcat tagaggctgg cttaattgct caaccacaat atgaattact ggcagtagca 600
 attaataccg gtaccaatct tccttctggt gcaaccccaa atgggtcaagc cgcattctta 660
 tttttattga cctcatcaact ggcaccatta attcgtcttt cttatggtag aatggtttat 720
 atggcattgc cttataccat cgtattatcc tgtattgggt tattgactgt ggaatatatt 780
 ttgctggcg caaccaatgt gtcattcaa attggtttat taaaaccaat gtaatgacaa 840
 gtaaaaggag gaaac atg cta agc ttt ttt aag aca ctc tca aca aaa cga 891
 Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg
 1 5 10

agt gca tgg ttt cta ttg ttt agc tca gct tta cta tta gag gct atc 939
 Ser Ala Trp Phe Leu Leu Phe Ser Ser Ala Leu Leu Leu Glu Ala Ile
 15 20 25

gct ctt tat ttt caa cat ggc atg ggg ctc gcc cct tgt gtc atg tgt 987
 Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys
 30 35 40

att tac gag agg gta gct att ctt ggc att gct ttc tcc ggt tta ttg 1035
 Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu
 45 50 55 60

ggg tta ctc tac ccg agt tcg atg ctt ttg cgc ctt gtg gcg tta tta 1083
 Gly Leu Leu Tyr Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu
 65 70 75

att ggt tta agc agt gca atc aaa ggc tta atg att agc atc acc cat 1131
 Ile Gly Leu Ser Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His
 80 85 90

tta gat cta caa ctt tac cct gca cct tgg aaa caa tgt tca gcg gtg 1179
 Leu Asp Leu Gln Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val
 95 100 105

gca gaa ttt ccc gag act tta ccc tta gat cag tgg ttt cct gca ctc 1227
 Ala Glu Phe Pro Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu
 110 115 120

ttc ctc cct tca ggc tca tgc agt gaa gta aca tgg caa ttt ctc ggc 1275
 Phe Leu Pro Ser Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly
 125 130 135 140

ttt tct atg gtg caa tgg atc gtc gtc att ttt gca ctc tat acc tta 1323
 Phe Ser Met Val Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu
 145 150 155

tta ctt gct ctc att ttc atc agc caa gtc aaa cgt cta aaa ccc aag 1371
 Leu Leu Ala Leu Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys
 160 165 170

cag cgc aga ctc ttt cat taagtcataa aaaatgggtgc gataaagcac 1419
 Gln Arg Arg Leu Phe His
 175

catttttcat ttctcgttcg gtatagatta aatttcttgc acgacaaact gcaggaatg 1479

tcttgctaata aatcttgctt tacgtgctt taagcgtttt aaacgtaatg cgcgtccttg 1539

tgataaacga tataattttt ttgtcggctt caaaaagctt ttacgtctcg ccatactctt 1599

cctcttattg tgctggtacg gttgtcgcta acgtatccgt ttctttcttg atttcgttga 1659

tgttttctat ttcggcggct tgtgtatcta atgtttcttc aatttgtgct tgctgtaccc 1719

gataataatg cacaatgctg ttcatataac gacggatatt ttccacatag tgatatgctt 1779

catagcctcg cgcatacccg tattttaacc ccgtgtaata gcgtttttct gctaatagtg 1839

gcaaattctt cttcacatct aaccaattat cgggatcacc acctaggctc ttggttaaac 1899

ggcgcgcac taacaaatgc cctaatacca tattatacgc cgctaaggca aaccaaatac 1959

gctcatcttc tttaatcgta tcaggcattt gcgtaataag ccaatgtaaa tattctgaac 2019

cggcctttaat actttgttcc ggatccgttc tgtcttgaat t

2060

<210> 12

<211> 178

<212> PRT

<213> Pasteurella multocida

<400> 12

Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg Ser Ala Trp Phe
1 5 10 15

Leu Leu Phe Ser Ser Ala Leu Leu Leu Glu Ala Ile Ala Leu Tyr Phe
20 25 30

Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys Ile Tyr Glu Arg
35 40 45

Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr
50 55 60

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

Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His Leu Asp Leu Gln
85 90 95

Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val Ala Glu Phe Pro
100 105 110

Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu Phe Leu Pro Ser
115 120 125

Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly Phe Ser Met Val
130 135 140

Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Leu Ala Leu
145 150 155 160

Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys Gln Arg Arg Leu
165 170 175

Phe His

<210> 13

<211> 4426

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (2756)..(3211)

<220>

<223> exbB

<400> 13

gaattcttga cctgggtgtga ggcttttatt gacttccacc ccaattgcgc gttctttcac 60

tttattaata aagtcacgta ccactggtaa cgccacatcc gcttctaata atgccatgcg 120

gacttcacgt agcgtttcct taatattgtc atcagttaaa cgtccacgtc cactaatgtt 180
 acgtagcgtt tttgacaagc gatccgacaa attctcaaac atgcaatctt cctattttaat 240
 ctcgaaaaaa ttgccctaata tatactgaaa tcccatagat tttcatcctt tgtaataaat 300
 ttatagcgat ttcacagtga gaaagttaga atggacggag aacaaagggtg agggaatttc 360
 aatgtggctt tcaatttttt ccgtgttttt ttatctattg agtgtcttac tcattacccc 420
 tatgttggtt aaaattcaag cgggcgaacc cgcacgtgtt cccaatagga tgcctttttt 480
 aacggcagca ttactcgcca ttcttctgca ctttatcaat cttattcctc tttttaccga 540
 ttttaaccagc ggtcaaaatt tctcggttat cgaaatcagt tccttaatca gtgttatgac 600
 agcaacgatc gccacattag cgttttttatt tcgcatacac actttatggt ttttattacc 660
 gattatttat tctttcgcca tcattaatct ggtcctcagt accttaatgc cggcgcattt 720
 tttatatcat cttaatcaag atatgggctt atttattcat gtaggcttat cactgttgac 780
 ttattcggtc tgttcgattg tcgcgttata ttccattcag ttagtttgga tcgatcgcgc 840
 cttaaaaaat aaaaaactgc ctttttcacc aatgattcca ccgttaatga ccgtagagcg 900
 ccattttttt cgtttaatgc tgatagggtga aatattactc acgattgtcc tcatttcagg 960
 gagctaccat ttatcgaaaa cctttgcccc acaagacatc cagaaagctg ttttttcttt 1020
 cttggcttgg atagtctttg ggagtgcact ggttggtcat tggaagctcc attggcgtgg 1080
 aaaaaaagtg gtgtattatg cgcttttagg tatcattctc ctgactatcg cctatttttg 1140
 tagtcgtgta atgcttgaaa tataaacaag atttatttat gctacgcat agtaaaagt 1200
 cggttcaaaa aacgaaaaaa tgaccgcact tttcgatttt tgattaactc gcaaaaggat 1260
 gcattttgga cagtattccc cttagtaccc tctttattac actcatcatc ttattgatca 1320
 tctctgctta tttttcaggc tctgaaaccg gtttggtgtc tgccaatcgt tatcgactac 1380
 gccatttagc cgaaaaagg catagagggtg cgaaaaaagc ggaaaaatta ctgaaaaaaa 1440
 cagatgtttt gcttagcctg attttaattt gtaataactt agtcaatatt actgcttctg 1500
 ccattaccac gattatcggc atgcgcttat atggcgatgc gggagtcgcc attgcaactg 1560
 gggcattaac ctttgtgatg cttatttttg ccgaaatttt gccgaaaact atcgccgccc 1620
 gttatccaga aaaagtggca ttcacgtcca gtcatttggt gtccgttttt ctgcgacttt 1680
 ttaccccgct ggtctattta atgaatttaa ttattcaggg gattttggca ctattacgtc 1740
 taaaatcaga taataaatca acctcattaa gccagagga attacgttcc atcgtaaatg 1800
 aatcaggtaa atttattcct tccgcccacc aagaaatgct gttatctatt ttggatttag 1860
 aaggggtcac cgtagatgac attatggtgc cacgtaatga cattgggggt attgatattg 1920
 acgatgattg gaaagccatt atgcgtcaac ttaaccatgc agcgcacggg cgtgttgtag 1980
 tgtataaagg aaatatggat gaaaatattt tggggatggt acgtgtacgt gaagcctatc 2040

```

gcttaatgct cgataaaaat gaatttaaca aagaaacttt aatccgtgcc gccgatgaag 2100
tgtattttat tcctgaaggt acgccactga atagccaatt attaaatttc cgcaacaata 2160
aagaaaggat tgggttagtt gtagatgaat atgggtgatat taaaggctta gtcaccttag 2220
aagatatctt agaagagatt gtcggtgaat ttaccacttc aacagcccca tcaattaacg 2280
atgaagttat ccacaaatca gacggttcgc ttatcattga gggatccgcc aatttacgtg 2340
atttgaataa attatttgac tggaatctcg ataccgaaga tgcacgtacc ttcaacggct 2400
taatttttaga gcatttagaa gaaattccag aagaaggaac ggtatgtgaa attaatgggc 2460
tacaatcac gattctagaa gtgaatgaca acatgattaa acaagccaaa gtcattaaac 2520
tttaattcaa catctggcta agcgatgtca tcaagacatc gcttttttat tccgtacatg 2580
aatgtttgat ccaacacaac atttattcaa cattggataa ataatcatcc taaatcgac 2640
gaattttcta ttaccaccgt ttttggcttt tgctagaatc ttgcaattga aattaattct 2700
caataccgta taatgttcaa cattattttg cgatacaaat taaaggatta ttaaa atg 2758
                                         Met
                                         1

cca caa tta ttc caa ttc tta caa caa tat att gat tac att att cta 2806
Pro Gln Leu Phe Gln Phe Leu Gln Gln Tyr Ile Asp Tyr Ile Ile Leu
          5                10                15

ggc tta ctt gcc ttc atg agc ttt att atg gtt tgg ctt gtg att gaa 2854
Gly Leu Leu Ala Phe Met Ser Phe Ile Met Val Trp Leu Val Ile Glu
          20                25                30

cgc ttt ctt ttc tta agt cgc gtc aac gtg gca tct tat gaa agc ata 2902
Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser Ile
          35                40                45

cat gaa tta gac att gac tta caa cgc cac ctc aca gct atc tct aca 2950
His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser Thr
          50                55                60                65

atc ggt tct aat gca cct tat gta ggt ttg ctt ggt acc gtc att ggt 2998
Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile Gly
          70                75                80

att ctc tta act ttc tat gaa tta ggt cac tcc ggt ggc gat att gat 3046
Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile Asp
          85                90                95

gcg gcg gcc att atg gtg cac tta tca tta gcc tta aaa gcc aca gca 3094
Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr Ala
          100                105                110

gta ggt att tta gtc gcc att cct gca atg gtg tgt tac aac ggt tta 3142
Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly Leu
          115                120                125

gga cgt aaa gtc gaa gtt aat cgt ttg aaa tgg ttt gcc tta aat gag 3190
Gly Arg Lys Val Glu Val Asn Arg Leu Lys Trp Phe Ala Leu Asn Glu
          130                135                140                145

aaa aaa gcc aaa caa caa gca tagggagccg tcatgaaaaa gtttgatgaa 3241

```

Lys Lys Ala Lys Gln Gln Ala
150

atcaacatta tcccttttat tgacatcatg ttggtactat tggctatcgt tctgattaca 3301
gcctctttta tttcacaagg taaaatccaa gtgaatgtac caaaagcaag ttcaacagtt 3361
gcgtttcggt cagatgattt agccaaattg ctgactatta cggaagcgg tgaaattttt 3421
tatcacgata aaccgattac gatagaggca ttggaacaag aaatcagtaa ttgggaaaaa 3481
gatcaaaaag tcaccttgaa ggtagatgca aaatccagtt tccaagattt cgtttctatc 3541
actgatatta tggctaaaaa tgaaattaaa aatgtcgcta tcgtgacggt taaagaaaag 3601
gcatctcaat gatagataaa agtcgttctt gcatcgggtt tgcaatttca ttgctttttc 3661
acgcaagttt tgtctctttc ctgtattgga ttgtacaaa agacgatgac agcgcgaaatg 3721
gatttgctgc cgatatcatc tcaactcata tttccatgga aatgctggcg gctaccgttt 3781
tagaagaacc agagccggaa ccagagccgg cgctccggt agtagaacct gaactgcaa 3841
aagaagtagt cgcagatccg acggtaaaac ctgagccacc aaaagaaccc gaaaaacaa 3901
aagagcctga aaagccaaaa gagaaaccga aagaaaaacc aaaagaaaag ccgaaaaaac 3961
cgaagaaaga acaacgtgat ttaccaaagt cagatcgcca aattgattct aattcatcga 4021
tcaatcaaca agcgaccaca acaggcaaca tcacaaccaa taatccgaat ctggtcggta 4081
aaggtaatag cacagatgaa gtcaatgctt atcgctcggc tttacgcaga gaaattgaaa 4141
aacataaacg ctatccaaac cgtgcacgca tgatgcgcaa acaagggtgtg gtaacaatca 4201
cgttccatct taataatgcc ggcgtaatta gtaatgcgcg aatcagcaaa tcttccggct 4261
cagaagaatt agataacgct gcaactggtag ctgtcaataa tgcccgtcca attggtccac 4321
tgctgttgg tatgccaaat gaagtgcgcg ttcctgtcag tttcagaatc acaaattaaa 4381
aaagtgcggt aaaatttacc gcactttttt ctctctatta gaatt 4426

<210> 14

<211> 152

<212> PRT

<213> Pasteurella multocida

<400> 14

Met Pro Gln Leu Phe Gln Phe Leu Gln Gln Tyr Ile Asp Tyr Ile Ile
1 5 10 15

Leu Gly Leu Leu Ala Phe Met Ser Phe Ile Met Val Trp Leu Val Ile
20 25 30

Glu Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser
35 40 45

Ile His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser
50 55 60

Thr Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile

65		70		75		80
Gly Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile						
		85		90		95
Asp Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr						
		100		105		110
Ala Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly						
		115		120		125
Leu Gly Arg Lys Val Glu Val Asn Arg Leu Lys Trp Phe Ala Leu Asn						
		130		135		140
Glu Lys Lys Ala Lys Gln Gln Ala						
145		150				

<210> 15
 <211> 6876
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (534)..(6863)

<220>
 <223> fhaB1

<400> 15
 agatgctgga tctgatcctt caactcagca aaagttcgat ttattcaaca aagccgccgt 60
 cccgtcaagt cagcgtaatg tctgccagtg ttacaccaat taaccaattc tgattagaaa 120
 aactcatcga gcatcaaatg aaactgcaat ttattcatat caggattatc aataccatat 180
 ttttgaaaaa gccgtttctg taatgaagga gaaaactcac cgaggcagtt ccataggatg 240
 gcaagatcct ggtatcggtc tgcgattccg actcgtccaa catcaatata acctattaat 300
 ttcccctcgt caaaaataag gttatcaagt gagaaatcac catgagtgac gactgaatcc 360
 ggtgagaatg gcaaaagctt atgcatttct ttccagactt gttcaacagg ccagccatta 420
 cgctcgtcat caaaatcact cgcatacaacc aaaccggtat tcattcgtga ttgcgcctga 480
 gcgagacgaa atacgcgatc gctgttaaaa ggacaattac aaacaggaat cga atg 536
 Met
 1
 caa ccg gcg cag gaa cac tgc cag cgc atc aac aat att gtt aac caa 584
 Gln Pro Ala Gln Glu His Cys Gln Arg Ile Asn Asn Ile Val Asn Gln
 5 10 15
 gaa aac ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag 632
 Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu
 20 25 30
 cgt tct gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca 680
 Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr
 35 40 45

gtt cat act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg	728
Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val	
50 55 60 65	
agt tat aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt	776
Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val	
70 75 80	
gcg gta cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg	824
Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu	
85 90 95	
caa gaa caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc	872
Gln Glu Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile	
100 105 110	
cgt tct gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca	920
Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser	
115 120 125	
gaa tca aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga	968
Glu Ser Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly	
130 135 140 145	
aca ttt aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt	1016
Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe	
150 155 160	
aac caa aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg	1064
Asn Gln Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr	
165 170 175	
atg tac tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt	1112
Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly	
180 185 190	
aat gca tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg	1160
Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu	
195 200 205	
ttt ggc tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat	1208
Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn	
210 215 220 225	
ttt agt gct tat cag ctt cta tct cat att cag cat tca cca atg tac	1256
Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr	
230 235 240	
caa aaa gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc	1304
Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser	
245 250 255	
tat gat gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca	1352
Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr	
260 265 270	
gat ttc att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa	1400
Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys	
275 280 285	
cta gaa ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt	1448
Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg	
290 295 300 305	

ggt aag ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta	1496
Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu	
310 315 320	
cca tca gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa	1544
Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu	
325 330 335	
gag gac ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca	1592
Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro	
340 345 350	
aac tta ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct	1640
Asn Leu Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser	
355 360 365	
cct att gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa	1688
Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu	
370 375 380 385	
gaa agc cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat	1736
Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp	
390 395 400	
gag tct gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa	1784
Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys	
405 410 415	
gag atg ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat	1832
Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn	
420 425 430	
aaa cca cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa	1880
Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu	
435 440 445	
ttc ttt gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga	1928
Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly	
450 455 460 465	
gaa gag ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc	1976
Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr	
470 475 480	
aat cta gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga	2024
Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg	
485 490 495	
gaa aaa gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg	2072
Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu	
500 505 510	
cag gag tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa	2120
Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys	
515 520 525	
gca aga ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa	2168
Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys	
530 535 540 545	
cgt gtt gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa	2216
Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys	
550 555 560	

att gct aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu 565 570 575	2264
att cgc cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu 580 585 590	2312
aag aaa caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala 595 600 605	2360
gaa cag aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp 610 615 620 625	2408
att gaa caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu 630 635 640	2456
gca tca aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys 645 650 655	2504
gtg gaa act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln 660 665 670	2552
gat gac tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn 675 680 685	2600
aca aaa ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp 690 695 700 705	2648
cat caa gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu 710 715 720	2696
aac caa aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met 725 730 735	2744
gac aat tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala 740 745 750	2792
gca tta act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp 755 760 765	2840
tat gtc aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val 770 775 780 785	2888
tat ttc gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta Tyr Phe Ala Ser Thr Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu 790 795 800	2936
ggc act ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat Gly Thr Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp 805 810 815	2984

gtg gtg aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg	3032
Val Val Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala	
820 825 830	
agt aat aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca	3080
Ser Asn Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr	
835 840 845	
cgt tta gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca	3128
Arg Leu Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala	
850 855 860 865	
aat gat gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa	3176
Asn Asp Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu	
870 875 880	
ggg cat tta cat ctt gaa aca gat aag gat tca act att gat gta caa	3224
Gly His Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln	
885 890 895	
gca tcg gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg	3272
Ala Ser Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val	
900 905 910	
aat ctc aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc	3320
Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe	
915 920 925	
tcg ccg agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa	3368
Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys	
930 935 940 945	
gtc cca ctt tta ggc gtg tcg tct cca tcc agt tat tca gag cat act	3416
Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His Thr	
950 955 960	
agt gag gca act tca gag gga tca atc ttc gaa gta ggg cac tta cat	3464
Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu His	
965 970 975	
ctt gcg gta gac aga gat gtg aac caa gcg ggg agt aaa att aag gct	3512
Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys Ala	
980 985 990	
aag tat acc act ggt gtt gtg aaa ggg aac ttt aat act gaa gcg ggc	3560
Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala Gly	
995 1000 1005	
aag aat att aaa cat gtc gaa aaa gaa gaa tat agt tca cag cta ttt	3608
Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu Phe	
1010 1015 1020 1025	
gct tca gca cac gcg agt ggt ggt ggc acc tca gtt cgt tat gac tat	3656
Ala Ser Ala His Ala Ser Gly Gly Gly Thr Ser Val Arg Tyr Asp Tyr	
1030 1035 1040	
aac agc caa gat ggt ggc aat gcc tct gtt ggt gtt ccg aca aac cat	3704
Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn His	
1045 1050 1055	
act gga gtt ggg gca gag gca gga atg tca ttc acc cat acc aaa gac	3752
Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys Asp	
1060 1065 1070	

aaa gaa aca ctg ctc act cac acc aat agt gaa tta caa gtc aaa cat Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys His 1075 1080 1085	3800
ggg aaa tta cat gtg ctt ggt tat gcc gat att ggt gga gta gat att Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp Ile 1090 1095 1100 1105	3848
aat act aaa cta cca gaa gat gca caa agc aaa gca cag aaa gag ata Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu Ile 1110 1115 1120	3896
gcg gct agc aag cca gag aag acc gag caa tct gca cag gat gtg gct Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val Ala 1125 1130 1135	3944
caa gct caa tca aat gcc aat aag gat aag gaa aat aaa gcc cca gaa Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro Glu 1140 1145 1150	3992
ata aaa gaa tta tca gag gct gaa atc gcg gat ctc atg tca gaa aaa Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu Lys 1155 1160 1165	4040
tca aaa gcg tat ttt gat gat ttt gca gag caa gcg aaa aaa gca cct Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala Pro 1170 1175 1180 1185	4088
gaa aac aat cga ttt gaa ttg tct gcg aaa gaa att aag tcg agc aaa Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser Lys 1190 1195 1200	4136
caa aaa gac caa tat gat cat gag tct gaa cgg acg act ttt aaa gtt Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys Val 1205 1210 1215	4184
gga cct gaa gcg gag gct cat tct gcg gtt gcc gat atg gtg agc cat Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser His 1220 1225 1230	4232
tta gtg aaa gaa tat aga gat gca caa aat ggg act aaa caa gac ggt Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp Gly 1235 1240 1245	4280
aca gta gca tta caa cat gct agt gat gtc tta aat att gtg acg ggg Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr Gly 1250 1255 1260 1265	4328
gat tta gcg ggg agt tca gct aaa ttg tct gtt gaa aga aca cat gag Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His Glu 1270 1275 1280	4376
aca aaa cga acg aca gaa acg ggg gat att gtt act aag att ggt ggc Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly Gly 1285 1290 1295	4424
aat gtc aca ctg tca gca cgc agt ggt agt gtg aac ctt aaa aat gta Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn Val 1300 1305 1310	4472
caa agt gat gaa caa gct aat ttg acc tta aga gca aaa gaa gat gtg Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp Val 1315 1320 1325	4520

aat gtg ctg tct ggt gaa aaa aca cga gaa acc aca gaa aca gta tca	4568
Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val Ser	
1330 1335 1340 1345	
aga cag aaa ctt tct cat ggt gtg aac gca ggt tgc agt atg atg agt	4616
Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met Ser	
1350 1355 1360	
ggc gcc tgt act gcc ggt gtt agc aca tca ctt gaa gga aat gaa agc	4664
Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu Ser	
1365 1370 1375	
tat acg tca gaa cgt gaa acg gct caa aat aac agt ttc tta aaa gca	4712
Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys Ala	
1380 1385 1390	
cgc aac atg aaa gtt gaa gca ggt cgc gat ttt aat gtt gtc agt tcg	4760
Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser Ser	
1395 1400 1405	
aat att gat gca gat aag ctc gat ctc cac gtt aaa gga aaa acg aat	4808
Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr Asn	
1410 1415 1420 1425	
gtg gta tcc aaa caa gat acg tta caa aaa gtg acg cat gga gtt gac	4856
Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val Asp	
1430 1435 1440	
tat aat ctt tcc gct ggc gtt gca ctt tct agt gca aca att gct acc	4904
Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala Thr	
1445 1450 1455	
cca acc ggt aat gtt ggt ttc ggt tat acc aat gag acc gaa agc aag	4952
Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser Lys	
1460 1465 1470	
cgg acg gtt aat caa caa gca ggg att aaa gcg aat aaa att aca ggg	5000
Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr Gly	
1475 1480 1485	
caa acg cat gac tta aat ctt gag ggg gga tat ctt gtc agc aac gat	5048
Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn Asp	
1490 1495 1500 1505	
aag gat aat cag ctg aaa gtt acc ggc gat gtc aca act aaa gcc ctt	5096
Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala Leu	
1510 1515 1520	
cac gat caa cat gat aaa gat ggt gga aca ttt ggt tta tct gtg ggt	5144
His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val Gly	
1525 1530 1535	
atc agt gaa cgt ggt act acc gcc ttt aat gta cga ggt ggg cga gct	5192
Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg Ala	
1540 1545 1550	
gaa cag aaa cac tat aat gca acg cag aaa tcc act ctt tct ggc gtg	5240
Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly Val	
1555 1560 1565	
gat acc tct caa gcg aat gta tca ggt caa gtg aat aca gat tta acc	5288
Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu Thr	
1570 1575 1580 1585	

aag gca aaa gct gtc aca cgt gat gat act tac gca agt acg caa ttt	5336
Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln Phe	
1590 1595 1600	
agt ttt gaa gtg gca gat att gtg gaa tta gga cag aga gcg aaa aac	5384
Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys Asn	
1605 1610 1615	
aag ctg tca gca cca aac aat gac acc gat atg gcg tca ggc tcc aca	5432
Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser Thr	
1620 1625 1630	
tta cgc tcg cgt tct act aca gaa gaa gca gat gta cca aca aca aga	5480
Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr Arg	
1635 1640 1645	
tcg cgt gta acg gat gag gcg gat tct gta tcc gtg aaa aat ccg att	5528
Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro Ile	
1650 1655 1660 1665	
tat gaa agt gca gat gct gtt gta cca aca cca cgt agt aga aat gtg	5576
Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn Val	
1670 1675 1680	
gac agt acc gat ctt gtg gac aat cca ctg tat gct agt gcc act aca	5624
Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr Thr	
1685 1690 1695	
aaa gca aac atc cat gat tat gaa gaa att cca gcc gtt tat agc aaa	5672
Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser Lys	
1700 1705 1710	
gtc ggt gat aac aat gct gat ctt gtt cgt cat aaa acg gca act agt	5720
Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr Ser	
1715 1720 1725	
gat gag cat ctt tat gca gag att aat gaa cca aca tat agc cgt gtt	5768
Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg Val	
1730 1735 1740 1745	
ggg gat aaa aat gca gat atg aga cgt cat aac gcg gca ggt aca aca	5816
Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr Thr	
1750 1755 1760	
gac tat gcc gat gtc gtg caa gca cat aca aga aag gca gat gat cca	5864
Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp Pro	
1765 1770 1775	
cta cca gca tta ccg aat cag ggt aaa gca aga acg gta aac gac ggt	5912
Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp Gly	
1780 1785 1790	
tca gag cat att tat act gat att agc gac gtg ggc act caa act aaa	5960
Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr Lys	
1795 1800 1805	
gct att gat agt act tat gca aca gta ggc atg ccg aaa gcg aat gcc	6008
Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn Ala	
1810 1815 1820 1825	
ggt aac ttg ata ggg caa aat ggc tta ggc agc att tat cac agc cca	6056
Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser Pro	
1830 1835 1840	

gac agt gct tat aaa aca tgg caa ttg ctt gat caa ttt gcc aac aaa	6104
Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn Lys	
1845 1850 1855	
ggc gga gat gcg gtc ttc tta cgc cct gca aca gaa atg aaa tgt gca	6152
Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys Ala	
1860 1865 1870	
ggg gca cct tta aaa tat acc ttt atc gtg cgt gat tat ttg ctc aga	6200
Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu Arg	
1875 1880 1885	
cgc cat acc tta gat aaa tca aga tta ttt tat aac gca cat aat aaa	6248
Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn Lys	
1890 1895 1900 1905	
acc tta ttt agc gtg cct atc gtt gat gca aaa gtc aaa atg ctg ttt	6296
Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu Phe	
1910 1915 1920	
gct gaa aaa aat atc caa gtc aat tac gat cgt agc ctt aca gcc att	6344
Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala Ile	
1925 1930 1935	
gat ctg agt aaa cgt att gcg acc ttt aat agc cca gaa gga gtt gta	6392
Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val Val	
1940 1945 1950	
gaa gtc cct tat gat ttt att aat gtg gta cct cca atg cga gca cct	6440
Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala Pro	
1955 1960 1965	
gat gcc gtt cgt caa tca gca ctc gcg tgg caa gaa gga aaa tgg gct	6488
Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp Ala	
1970 1975 1980 1985	
aac gat ggt tgg gtt gaa gta gaa aaa cat acc ttg cgt cac cgt cgt	6536
Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg Arg	
1990 1995 2000	
tat gcc aat gtg ttt gct gtg ggt gat gtg gca ggg gtc cca aaa ggc	6584
Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys Gly	
2005 2010 2015	
aaa acg gct gcc agt gtc aaa tgg caa gtt cct gtt gca gtg gca cat	6632
Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala His	
2020 2025 2030	
tta ctc gca gaa tta gag ggc aaa cct tgt gat gaa att tac aac ggt	6680
Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn Gly	
2035 2040 2045	
tat aca tct tgt cca tta att act caa tta gga aag ggg atg cta gta	6728
Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu Val	
2050 2055 2060 2065	
gaa ttt gat tat aac aac cac tta aca cct tct ttc ccc ggt gta ata	6776
Glu Phe Asp Tyr Asn Asn His Leu Thr Pro Ser Phe Pro Gly Val Ile	
2070 2075 2080	
gcg cca tta gaa gaa ctg tgg gca aca tgg gca att aaa aca tta ggt	6824
Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu Gly	
2085 2090 2095	

tta aaa ccc act tat tta ggt atg tta cgt gga tta gct taaggagcgt 6873
 Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala
 2100 2105 2110

tga 6876

<210> 16

<211> 2110

<212> PRT

<213> Pasteurella multocida

<400> 16

Met Gln Pro Ala Gln Glu His Cys Gln Arg Ile Asn Asn Ile Val Asn
 1 5 10 15

Gln Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala
 20 25 30

Glu Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu
 35 40 45

Thr Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn
 50 55 60

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

Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn
 85 90 95

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

Ile Arg Ser Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser
 115 120 125

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

Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala
 145 150 155 160

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

Thr Met Tyr Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser
 180 185 190

Gly Asn Ala Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala
 195 200 205

Leu Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu
 210 215 220

Asn Phe Ser Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met
 225 230 235 240

Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys
 245 250 255

Ser Tyr Asp Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro
 260 265 270

Thr Asp Phe Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly
 275 280 285
 Lys Leu Glu Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu
 290 295 300
 Arg Gly Lys Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser
 305 310 315 320
 Leu Pro Ser Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu
 325 330 335
 Glu Glu Asp Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met
 340 345 350
 Pro Asn Leu Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu
 355 360 365
 Ser Pro Ile Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile
 370 375 380
 Glu Glu Ser His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp
 385 390 395 400
 Asp Glu Ser Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu
 405 410 415
 Lys Glu Met Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly
 420 425 430
 Asn Lys Pro Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp
 435 440 445
 Glu Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu
 450 455 460
 Gly Glu Glu Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser
 465 470 475 480
 Thr Asn Leu Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys
 485 490 495
 Arg Glu Lys Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys
 500 505 510
 Leu Gln Glu Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln
 515 520 525
 Lys Ala Arg Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu
 530 535 540
 Lys Arg Val Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp
 545 550 555 560
 Lys Ile Ala Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu
 565 570 575
 Glu Ile Arg Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu
 580 585 590
 Glu Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln
 595 600 605

Ala Glu Gln Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu
 610 615 620
 Asp Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala
 625 630 635 640
 Glu Ala Ser Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro
 645 650 655
 Lys Val Glu Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn
 660 665 670
 Gln Asp Asp Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu
 675 680 685
 Asn Thr Lys Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe
 690 695 700
 Asp His Gln Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His
 705 710 715 720
 Leu Asn Gln Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu
 725 730 735
 Met Asp Asn Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly
 740 745 750
 Ala Ala Leu Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val
 755 760 765
 Trp Tyr Val Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys
 770 775 780
 Val Tyr Phe Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly
 785 790 795 800
 Leu Gly Thr Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys
 805 810 815
 Asp Val Val Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu
 820 825 830
 Ala Ser Asn Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu
 835 840 845
 Thr Arg Leu Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe
 850 855 860
 Ala Asn Asp Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr
 865 870 875 880
 Glu Gly His Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val
 885 890 895
 Gln Ala Ser Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp
 900 905 910
 Val Asn Leu Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys
 915 920 925
 Phe Ser Pro Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu
 930 935 940

Lys Val Pro Leu Leu Gly Val Ser Ser Pro Ser Ser Tyr Ser Glu His
 945 950 955 960
 Thr Ser Glu Ala Thr Ser Glu Gly Ser Ile Phe Glu Val Gly His Leu
 965 970 975
 His Leu Ala Val Asp Arg Asp Val Asn Gln Ala Gly Ser Lys Ile Lys
 980 985 990
 Ala Lys Tyr Thr Thr Gly Val Val Lys Gly Asn Phe Asn Thr Glu Ala
 995 1000 1005
 Gly Lys Asn Ile Lys His Val Glu Lys Glu Glu Tyr Ser Ser Gln Leu
 1010 1015 1020
 Phe Ala Ser Ala His Ala Ser Gly Gly Gly Thr Ser Val Arg Tyr Asp
 1025 1030 1035 1040
 Tyr Asn Ser Gln Asp Gly Gly Asn Ala Ser Val Gly Val Pro Thr Asn
 1045 1050 1055
 His Thr Gly Val Gly Ala Glu Ala Gly Met Ser Phe Thr His Thr Lys
 1060 1065 1070
 Asp Lys Glu Thr Leu Leu Thr His Thr Asn Ser Glu Leu Gln Val Lys
 1075 1080 1085
 His Gly Lys Leu His Val Leu Gly Tyr Ala Asp Ile Gly Gly Val Asp
 1090 1095 1100
 Ile Asn Thr Lys Leu Pro Glu Asp Ala Gln Ser Lys Ala Gln Lys Glu
 1105 1110 1115 1120
 Ile Ala Ala Ser Lys Pro Glu Lys Thr Glu Gln Ser Ala Gln Asp Val
 1125 1130 1135
 Ala Gln Ala Gln Ser Asn Ala Asn Lys Asp Lys Glu Asn Lys Ala Pro
 1140 1145 1150
 Glu Ile Lys Glu Leu Ser Glu Ala Glu Ile Ala Asp Leu Met Ser Glu
 1155 1160 1165
 Lys Ser Lys Ala Tyr Phe Asp Asp Phe Ala Glu Gln Ala Lys Lys Ala
 1170 1175 1180
 Pro Glu Asn Asn Arg Phe Glu Leu Ser Ala Lys Glu Ile Lys Ser Ser
 1185 1190 1195 1200
 Lys Gln Lys Asp Gln Tyr Asp His Glu Ser Glu Arg Thr Thr Phe Lys
 1205 1210 1215
 Val Gly Pro Glu Ala Glu Ala His Ser Ala Val Ala Asp Met Val Ser
 1220 1225 1230
 His Leu Val Lys Glu Tyr Arg Asp Ala Gln Asn Gly Thr Lys Gln Asp
 1235 1240 1245
 Gly Thr Val Ala Leu Gln His Ala Ser Asp Val Leu Asn Ile Val Thr
 1250 1255 1260
 Gly Asp Leu Ala Gly Ser Ser Ala Lys Leu Ser Val Glu Arg Thr His
 1265 1270 1275 1280

Glu Thr Lys Arg Thr Thr Glu Thr Gly Asp Ile Val Thr Lys Ile Gly
 1285 1290 1295
 Gly Asn Val Thr Leu Ser Ala Arg Ser Gly Ser Val Asn Leu Lys Asn
 1300 1305 1310
 Val Gln Ser Asp Glu Gln Ala Asn Leu Thr Leu Arg Ala Lys Glu Asp
 1315 1320 1325
 Val Asn Val Leu Ser Gly Glu Lys Thr Arg Glu Thr Thr Glu Thr Val
 1330 1335 1340
 Ser Arg Gln Lys Leu Ser His Gly Val Asn Ala Gly Cys Ser Met Met
 1345 1350 1355 1360
 Ser Gly Ala Cys Thr Ala Gly Val Ser Thr Ser Leu Glu Gly Asn Glu
 1365 1370 1375
 Ser Tyr Thr Ser Glu Arg Glu Thr Ala Gln Asn Asn Ser Phe Leu Lys
 1380 1385 1390
 Ala Arg Asn Met Lys Val Glu Ala Gly Arg Asp Phe Asn Val Val Ser
 1395 1400 1405
 Ser Asn Ile Asp Ala Asp Lys Leu Asp Leu His Val Lys Gly Lys Thr
 1410 1415 1420
 Asn Val Val Ser Lys Gln Asp Thr Leu Gln Lys Val Thr His Gly Val
 1425 1430 1435 1440
 Asp Tyr Asn Leu Ser Ala Gly Val Ala Leu Ser Ser Ala Thr Ile Ala
 1445 1450 1455
 Thr Pro Thr Gly Asn Val Gly Phe Gly Tyr Thr Asn Glu Thr Glu Ser
 1460 1465 1470
 Lys Arg Thr Val Asn Gln Gln Ala Gly Ile Lys Ala Asn Lys Ile Thr
 1475 1480 1485
 Gly Gln Thr His Asp Leu Asn Leu Glu Gly Gly Tyr Leu Val Ser Asn
 1490 1495 1500
 Asp Lys Asp Asn Gln Leu Lys Val Thr Gly Asp Val Thr Thr Lys Ala
 1505 1510 1515 1520
 Leu His Asp Gln His Asp Lys Asp Gly Gly Thr Phe Gly Leu Ser Val
 1525 1530 1535
 Gly Ile Ser Glu Arg Gly Thr Thr Ala Phe Asn Val Arg Gly Gly Arg
 1540 1545 1550
 Ala Glu Gln Lys His Tyr Asn Ala Thr Gln Lys Ser Thr Leu Ser Gly
 1555 1560 1565
 Val Asp Thr Ser Gln Ala Asn Val Ser Gly Gln Val Asn Thr Asp Leu
 1570 1575 1580
 Thr Lys Ala Lys Ala Val Thr Arg Asp Asp Thr Tyr Ala Ser Thr Gln
 1585 1590 1595 1600
 Phe Ser Phe Glu Val Ala Asp Ile Val Glu Leu Gly Gln Arg Ala Lys
 1605 1610 1615

Asn Lys Leu Ser Ala Pro Asn Asn Asp Thr Asp Met Ala Ser Gly Ser
 1620 1625 1630
 Thr Leu Arg Ser Arg Ser Thr Thr Glu Glu Ala Asp Val Pro Thr Thr
 1635 1640 1645
 Arg Ser Arg Val Thr Asp Glu Ala Asp Ser Val Ser Val Lys Asn Pro
 1650 1655 1660
 Ile Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn
 1665 1670 1675 1680
 Val Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr
 1685 1690 1695
 Thr Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser
 1700 1705 1710
 Lys Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr
 1715 1720 1725
 Ser Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg
 1730 1735 1740
 Val Gly Asp Lys Asn Ala Asp Met Arg Arg His Asn Ala Ala Gly Thr
 1745 1750 1755 1760
 Thr Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp
 1765 1770 1775
 Pro Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp
 1780 1785 1790
 Gly Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr
 1795 1800 1805
 Lys Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn
 1810 1815 1820
 Ala Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser
 1825 1830 1835 1840
 Pro Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn
 1845 1850 1855
 Lys Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys
 1860 1865 1870
 Ala Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu
 1875 1880 1885
 Arg Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn
 1890 1895 1900
 Lys Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu
 1905 1910 1915 1920
 Phe Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala
 1925 1930 1935
 Ile Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val
 1940 1945 1950

Val Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala
 1955 1960 1965

Pro Asp Ala Val Arg Gln Ser Ala Leu Ala Trp Gln Glu Gly Lys Trp
 1970 1975 1980

Ala Asn Asp Gly Trp Val Glu Val Glu Lys His Thr Leu Arg His Arg
 1985 1990 1995 2000

Arg Tyr Ala Asn Val Phe Ala Val Gly Asp Val Ala Gly Val Pro Lys
 2005 2010 2015

Gly Lys Thr Ala Ala Ser Val Lys Trp Gln Val Pro Val Ala Val Ala
 2020 2025 2030

His Leu Leu Ala Glu Leu Glu Gly Lys Pro Cys Asp Glu Ile Tyr Asn
 2035 2040 2045

Gly Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu
 2050 2055 2060

Val Glu Phe Asp Tyr Asn Asn His Leu Thr Pro Ser Phe Pro Gly Val
 2065 2070 2075 2080

Ile Ala Pro Leu Glu Glu Leu Trp Ala Thr Trp Ala Ile Lys Thr Leu
 2085 2090 2095

Gly Leu Lys Pro Thr Tyr Leu Gly Met Leu Arg Gly Leu Ala
 2100 2105 2110

<210> 17
 <211> 3247
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1479)..(3245)

<220>
 <223> fhaB2

<400> 17
 gtcgaccttg cgggtgaaaa ggtatctcta aattttggcg atatcattca tgcttaccaa 60
 aaccagcccc tatcaacaaa agttgttttt caattagtga aagatttgac ggaagtttta 120
 taccgttctg gctacgtgac aagtgcattt gggttaaaaa attcaaaaat cagcaatggc 180
 gatcttgaat ttattgtact gtggggaaga actcgcgatc tgtttgatga tggggagaaa 240
 ccaaccggtt ttagagataa aacaatgtta tcagtcctac ccaatttaat cggaaatcgc 300
 ttaagtattc acgacattga ccagttgatc gaaatcttaa atactacgaa taaaaaagcc 360
 acagtgaatg tggttgcaag tgaagaaaaa ggcagctcaa atctaaatat tgaagacaaa 420
 tatgatgttt ttccgcaagt gagtgcgga ttcaataatt caggtgctgg caataatgcc 480
 aatgggcgta atcaagctac attgaatatt gcttgagtg atctattagg cacgaatgat 540
 cgttggagtt tctcgagtag ttaccgttta tataaaaatc atcatgctaa ccagcaacgc 600

```

aattatactt tgtcttacag tcagcctata ggcttttcta cagtagaaat taaagcatcg 660
gaatctacgt atgaaaaaga acttcgcggt ataaatactc attcttctca tgggaaaacc 720
caaagcttag ctgtcaagct gatgcatgtg ttattgcgta ataaggagag tattttatct 780
acatataccg agttcgagtt taaaaaacgg attagttatt tttctgatat tttgattggg 840
aaatatcaca ataataaagt gagcgtaggg ttatcttaca tgactaattt tgcttacggg 900
aagctttaca gcgacattgc ttacgcgaat gggttgagat ggtttggggc gaattattca 960
gcatatgatg caaatcgtga aaaaacctta aaattattgt caggaagtat taattggcag 1020
cgtccaatat ccctgtttga acgtgcgatg aattatcaat tacgtattgg tgcccaatat 1080
ggttttgata gtttgatttc tgaaaatcaa ttttcaattg gtgatgaata tacagtaaga 1140
ggatttaaag gtggtgcggt ttctggtgat agtgggtgcgt atttatcaca aacactgacg 1200
gttccttttt atccacaaaa agcatattta tctcaggtat ccccttttat tggatttgat 1260
atgggtaaag tacatattaa atcaaagcat aaaacaacca ctttagtcgg ttttgcccta 1320
ggcttgaaaa cgcaaataaa gttattttca ttatcattaa cctatgcaca accaatgaat 1380
ggtgtgagtg gtgttacgca acatcgtaa aaaccgattt attatttctc aggatcactt 1440
tctttttaat ctcttttaag tttaaggatt aacttaat atg aac aaa aat cgt tac 1496
                               Met Asn Lys Asn Arg Tyr
                               1           5

aaa ctc att ttt agt caa gtc aaa ggt tgt ctc gtt cct gtg gca gaa 1544
Lys Leu Ile Phe Ser Gln Val Lys Gly Cys Leu Val Pro Val Ala Glu
              10              15              20

tgt att aac tca gct att agc aat ggt tca tct gat tca aca tcc aca 1592
Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser Ser Asp Ser Thr Ser Thr
              25              30              35

tca gaa caa gtt gaa gag gaa cct ttc ctt cta gaa caa tat tca ctt 1640
Ser Glu Gln Val Glu Glu Glu Pro Phe Leu Leu Glu Gln Tyr Ser Leu
              40              45              50

tcc tcc gtg tct tta tta gta aaa agc acg ttc aat cct gtt tcg tat 1688
Ser Ser Val Ser Leu Leu Val Lys Ser Thr Phe Asn Pro Val Ser Tyr
              55              60              65              70

gca atg caa ttg act tgg aaa cag ctt tct att tta ttt tta act gtg 1736
Ala Met Gln Leu Thr Trp Lys Gln Leu Ser Ile Leu Phe Leu Thr Val
              75              80              85

att tct gtt cct gtt ttg gct gag gga aaa ggg gat gaa aga aat caa 1784
Ile Ser Val Pro Val Leu Ala Glu Gly Lys Gly Asp Glu Arg Asn Gln
              90              95              100

tta aca gtg att gat aat agc gat cat att aaa tta gat gca tct aat 1832
Leu Thr Val Ile Asp Asn Ser Asp His Ile Lys Leu Asp Ala Ser Asn
              105              110              115

ctt gct ggt aat gat aaa aca aaa atc tat caa gca gaa aat aaa gtt 1880
Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr Gln Ala Glu Asn Lys Val
              120              125              130

```

ctg gtt att gat att gct aaa cca aat ggg aaa ggg att tca gat aac	1928
Leu Val Ile Asp Ile Ala Lys Pro Asn Gly Lys Gly Ile Ser Asp Asn	
135 140 145 150	
cgt ttt gaa aaa ttt aat att cca aat agc gcg gtg ttt aat aat aat	1976
Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser Ala Val Phe Asn Asn Asn	
155 160 165	
ggg act gaa gcg cag gca aga tca aca tta att ggt tac att ccg caa	2024
Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu Ile Gly Tyr Ile Pro Gln	
170 175 180	
aat caa aat tta agg gga ggg aaa gaa gct gat gtt ata tta aat caa	2072
Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala Asp Val Ile Leu Asn Gln	
185 190 195	
gtg aca ggt cct caa gaa agt aaa att gtt ggc gcg ctt gaa gta tta	2120
Val Thr Gly Pro Gln Glu Ser Lys Ile Val Gly Ala Leu Glu Val Leu	
200 205 210	
ggg aaa aaa gct gat atc gtc att gca aac caa aat ggt att acc tta	2168
Gly Lys Lys Ala Asp Ile Val Ile Ala Asn Gln Asn Gly Ile Thr Leu	
215 220 225 230	
aat ggt gta aga aca ata aat tca gat cgt ttt gtt gcc act acg agt	2216
Asn Gly Val Arg Thr Ile Asn Ser Asp Arg Phe Val Ala Thr Thr Ser	
235 240 245	
gag ctt ata gat ccg aat cag atg atg tta aag gtt aca aaa gga aat	2264
Glu Leu Ile Asp Pro Asn Gln Met Met Leu Lys Val Thr Lys Gly Asn	
250 255 260	
gtg atc att gat att gat ggt ttt tcg aca gat gga tta aag tat tta	2312
Val Ile Ile Asp Ile Asp Gly Phe Ser Thr Asp Gly Leu Lys Tyr Leu	
265 270 275	
gat att att gct aaa aaa att gaa caa aag caa tca att aca tca ggg	2360
Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys Gln Ser Ile Thr Ser Gly	
280 285 290	
gat aat tca gaa gca aaa aca gat gtc act ctt att gcg ggt tcc agt	2408
Asp Asn Ser Glu Ala Lys Thr Asp Val Thr Leu Ile Ala Gly Ser Ser	
295 300 305 310	
gaa tat gat tta agc aaa cat gag ctg aaa aaa acg agc ggt gaa aat	2456
Glu Tyr Asp Leu Ser Lys His Glu Leu Lys Lys Thr Ser Gly Glu Asn	
315 320 325	
gta tct aat gat gtt att gct atc acg gga tct agt aca ggc gca atg	2504
Val Ser Asn Asp Val Ile Ala Ile Thr Gly Ser Ser Thr Gly Ala Met	
330 335 340	
cat ggt aaa aat att aag ttg att gtg aca gat aaa ggt gca ggc gta	2552
His Gly Lys Asn Ile Lys Leu Ile Val Thr Asp Lys Gly Ala Gly Val	
345 350 355	
aaa cat gat gga att att ttg tct gaa aat gat att cag att gaa atg	2600
Lys His Asp Gly Ile Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met	
360 365 370	
aat gaa ggt gac tta gaa ctt ggc aat acg att cag caa aca gtg gta	2648
Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr Ile Gln Gln Thr Val Val	
375 380 385 390	


```

aaa aaa gac cga aat att cga gcc aag aaa aaa att gaa gtg aaa aac 2696
Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys Lys Ile Glu Val Lys Asn
395 400 405

gct aat cgt gtt ttt gtt ggt agt caa acg aaa tca gat gaa att tcg 2744
Ala Asn Arg Val Phe Val Gly Ser Gln Thr Lys Ser Asp Glu Ile Ser
410 415 420

tta gag gcg aaa caa gtt aaa atc aga aaa aac gca gag att agg agt 2792
Leu Glu Ala Lys Gln Val Lys Ile Arg Lys Asn Ala Glu Ile Arg Ser
425 430 435

acg aca caa gcc aaa atc gta gca aag ggt gcc ctg tct att gag caa 2840
Thr Thr Gln Ala Lys Ile Val Ala Lys Gly Ala Leu Ser Ile Glu Gln
440 445 450

aat gcg aag ctc gtc gct aaa aag ata gat gtg gca aca gaa act cta 2888
Asn Ala Lys Leu Val Ala Lys Lys Ile Asp Val Ala Thr Glu Thr Leu
455 460 465 470

act aat gct ggg cgt att tat ggt cga gag gtt aag ctt gac act aat 2936
Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu Val Lys Leu Asp Thr Asn
475 480 485

aat ttg att aat gat aaa gaa att tat gct gaa cgg aaa ttg agt att 2984
Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala Glu Arg Lys Leu Ser Ile
490 495 500

ttg acg aaa gga aaa gat ctt gaa att att caa gat aga tat ttg tct 3032
Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile Gln Asp Arg Tyr Leu Ser
505 510 515

cca ctg atg cgc gta aaa agt agt gtc cgc ttt tta ggc tct ccg ttt 3080
Pro Leu Met Arg Val Lys Ser Ser Val Arg Phe Leu Gly Ser Pro Phe
520 525 530

ttc tca ata tct ccg tcg atg ctc gca agc ctt agt gca cag ttt aag 3128
Phe Ser Ile Ser Pro Ser Met Leu Ala Ser Leu Ser Ala Gln Phe Lys
535 540 545 550

cct ggt ttt gtg aat aag gga ctc att gaa agt gcg ggg agt gca gaa 3176
Pro Gly Phe Val Asn Lys Gly Leu Ile Glu Ser Ala Gly Ser Ala Glu
555 560 565

tta act ttt aaa gaa aaa acc agt ttt tta aca gag ggc aat aat ttt 3224
Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu Thr Glu Gly Asn Asn Phe
570 575 580

att aga gct aaa gat gcg tta ac 3247
Ile Arg Ala Lys Asp Ala Leu
585

```

<210> 18

<211> 589

<212> PRT

<213> Pasteurella multocida

<400> 18

```

Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
1 5 10 15

```

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

Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
 355 360 365
 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
 370 375 380
 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
 385 390 395 400
 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
 405 410 415
 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
 420 425 430
 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
 435 440 445
 Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp
 450 455 460
 Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu
 465 470 475 480
 Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
 485 490 495
 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
 500 505 510
 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
 515 520 525
 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
 530 535 540
 Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
 545 550 555 560
 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
 565 570 575
 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu
 580 585

<210> 19
 <211> 3247
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(1446)

<220>
 <223> fhaC

<400> 19
 gtc gac ctt gcg ggt gaa aag gta tct cta aat ttt ggc gat atc att 48
 Val Asp Leu Ala Gly Glu Lys Val Ser Leu Asn Phe Gly Asp Ile Ile
 1 5 10 15

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

tat ttt tct gat att ttg att ggg aaa tat cac aat aat aaa gtg agc	864
Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser	
275 280 285	
gta ggg tta tct tac atg act aat ttt gct tac ggg aag ctt tac agc	912
Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser	
290 295 300	
gac att gct tac gcg aat ggg ttg aga tgg ttt ggg gcg aat tat tca	960
Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser	
305 310 315 320	
gca tat gat gca aat cgt gaa aaa acc tta aaa tta ttg tca gga agt	1008
Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser	
325 330 335	
att aat tgg cag cgt cca ata tcc ctg ttt gaa cgt gcg atg aat tat	1056
Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr	
340 345 350	
caa tta cgt att ggt gcc caa tat ggt ttt gat agt ttg tat tct gaa	1104
Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu	
355 360 365	
aat caa ttt tca att ggt gat gaa tat aca gta aga gga ttt aaa ggt	1152
Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly	
370 375 380	
ggt gcg gtt tct ggt gat agt ggt gcg tat tta tca caa aca ctg acg	1200
Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr	
385 390 395 400	
ggt cct ttt tat cca caa aaa gca tat tta tct cag gta tcc cct ttt	1248
Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe	
405 410 415	
att gga ttt gat atg ggt aaa gta cat att aaa tca aag cat aaa aca	1296
Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr	
420 425 430	
acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta	1344
Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu	
435 440 445	
ttt tca tta tca tta acc tat gca caa cca atg aat ggt gtg agt ggt	1392
Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly	
450 455 460	
ggt acg caa cat cgt caa aaa ccg att tat tat ttc tca gga tca ctt	1440
Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu	
465 470 475 480	
tct ttt taatctcttt taagttaaag gattaactta atatgaacaa aaatcggttac	1496
Ser Phe	
aaactcattt ttagtcaagt caaagggttg ctcgttcctg tggcagaatg tattaactca	1556
gctattagca atgggttcac tgattcaaca tccacatcag aacaagttga agaggaaacct	1616
ttccttctag aacaatattc actttcctcc gtgtctttat tagtaaaaag cacgttcaat	1676
cctgtttcgt atgcaatgca attgacttgg aaacagcttt ctattttatt ttttaactgtg	1736

```

atttctgttc ctgttttggc tgagggaataa ggggatgaaa gaaatcaatt aacagtgtatt 1796
gataatagcg atcatattaa attagatgca tctaattctg ctggtaatga taaaacaaaa 1856
atctatcaag cagaaaataa agttcttggtt attgatattg ctaaaccaaa tgggaaaggg 1916
atttcagata accgttttga aaaatttaatt attccaaata gcgcggtgtt taataataat 1976
gggactgaag cgcaggcaag atcaacatta attgggttaca ttccgcaaaa tcaaaattta 2036
aggggagggg aagaagctga tggtatatta aatcaagtga caggctctca agaaagtaaa 2096
attgttggcg cgcttgaagt attaggtaaa aaagctgata tcgtcattgc aaacccaaat 2156
ggattacct taaatggtgt aagaacaata aattcagatc gttttgttgc cactacgagt 2216
gagcttatag atccgaatca gatgatgtta aagggtacaa aaggaaatgt gatcattgat 2276
attgatgggt tttcgacaga tggattaaag tatttagata ttattgctaa aaaaattgaa 2336
caaaagcaat caattacatc aggggataat tcagaagcaa aaacagatgt cactcttatt 2396
gcgggttcca gtgaatatga tttaagcaaa catgagctga aaaaaacgag cggtgaaaat 2456
gtatctaatt atgttattgc tatcacggga tctagtagag gcgcaatgca tggtaaaaaat 2516
attaagttga ttgtgacaga taaaggtgca ggcgtaaaac atgatggaat tattttgtct 2576
gaaaatgata ttcagattga aatgaatgaa ggtgacttag aacttggcaa tacgattcag 2636
caaacagtgg taaaaaaaga ccgaaatatt cgagccaaga aaaaaattga agtgaaaaac 2696
gctaactcgt tttttgttgg tagtcaaacg aaatcagatg aaatttcgtt agaggcgaaa 2756
caagttaaaa tcagaaaaaa cgcagagatt aggagtacga cacaagccaa aatcgtagca 2816
aagggtgccc tgtctattga gcaaaatgcg aagctcgtcg ctaaaaagat agatgtggca 2876
acagaaactc taactaatgc tgggcgtatt tatggtcgag aggttaagct tgacactaat 2936
aatttgatta atgataaaga aatttatgct gaacggaaat tgagtatttt gacgaaagga 2996
aaagatcttg aaattattca agatagatat ttgtctccac tgatgcgcgt aaaaagtagt 3056
gtccgctttt taggctctcc gtttttctca atatctccgt cgatgctcgc aagccttagt 3116
gcacagttta agcctgggtt tgtgaataag ggactcattg aaagtgcggg gagtgcagaa 3176
ttaactttta aagaaaaaac cagtttttta acagagggca ataattttat tagagctaaa 3236
gatgcgttaa c 3247

```

<210> 20

<211> 482

<212> PRT

<213> Pasteurella multocida

<400> 20

Val Asp Leu Ala Gly Glu Lys Val Ser Leu Asn Phe Gly Asp Ile Ile

1

5

10

15

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

Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
 355 360 365
 Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
 370 375 380
 Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
 385 390 395 400
 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
 405 410 415
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
 420 425 430
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
 435 440 445
 Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
 450 455 460
 Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
 465 470 475 480

Ser Phe

<210> 21
 <211> 1170
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (639)..(1022)

<220>
 <223> greA

<400> 21
 gtcaacaaac ggcaaccact tcggcaaaaa gcgattgcgc ttgtgttctg ctctaagctc 60
 aagcgttggg atcgcgcgaa ttgcgttgac cactggtgag atcggggtca cctgtaaaac 120
 gtacgataag atcgccatgc atttcattgt tttttatttt tccattgggt aatagactgg 180
 tttcaaattg aaattggtca cttagtacga gtttggcggt taaggcgggt agcacttttt 240
 gtgtactggc gggtaacata aagggtactgg ctggtgagc tacaattttt tcattacgat 300
 ttaagttttt agccacaaaa cctaggctgg tcccttcggg taaatgagcg ttgatttcag 360
 caagatcaat ctgagcataa ctgaaatgac tgacgagtaa actacatata agtatcggtc 420
 gtttgaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tattttatac ataattggct 480
 cgagcagttg ctattttttt attgtcgaac aataatagta tttgaaccct cgagagtaaa 540
 tccttttctc gttaaact ttttttttta ttcaactacg gcattgtttt tacaatgttg 600


```
<210> 22
<211> 128
<212> PRT
<213> Pasteurella multocida
```

```

<400> 22
Met Lys Gln Ile Pro Met Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln
  1             5             10             15
Glu Leu Asp Phe Leu Lys Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala
          20             25             30
Ile Ala Glu Ala Arg Glu His Gly Asp Leu Lys Glu Asn Ala Glu Tyr
      35             40             45
His Ala Ala Arg Glu Gln Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu
      50             55             60
Ile Glu Gly Lys Leu Ala Asn Ser Gln Ile Ile Asp Val Thr Lys Ile
  65             70             75             80

```

Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
 85 90 95
 Ile Asp Thr Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
 100 105 110
 Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
 115 120 125

<210> 23
 <211> 4666
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (980)..(2440)

<220>
 <223> guaB

<400> 23
 aacacatgaa cctcttcccc aaaatacgca tccatatctc gccaatcttg gcgaaatgct 60
 tcatcaattc ctgcttggtc aaaatgttgt aaacgtgcaa tcaacttttt acctaattct 120
 gcgatcaatt tattccgata aatcggttgt aatacttcaa tcagctctgc ccaaggttga 180
 tcaatttgct gtgtttgttt tgggaaagac aaattaatgc caaagccaat cagcagatta 240
 tgttgattat tctgacgatt ggcgatttcg accaaaatcc ctgctaattt gcgcccattg 300
 aatagcacat catttggtcca ttttaatcca atgttcaaag cacctgcttg ctttagcggt 360
 tctgcgattg ccataccac tactaaactc aagccttcta aattgacctt ttggtcacat 420
 gcccaataca aactcataat cacttgcca gcaaaaggag aaagccattg acgaccacgt 480
 cgtccacgtc ccgcagtttg atattctgct aagcaaatac cgcccttttc caaatgtgca 540
 atattgtcaa gcaagaattg attggctgag ttaataatcg gcttaatata aagtgggtaa 600
 ggtgctaacg cttgcgtcaa ataagattca tttaagcgac ttaattgagg tatgagacga 660
 aaatggttga cttgctgttc tatttgatc ccttggtgtt tcaatttttc gatattgtgt 720
 aagatatctt gttctgaata acctaaaagt gcagtcaatt ctgctaaaga aagttgttga 780
 tagctagcga gtaatgcaag tacgttttgc ataaaaatcc ttatttatat aaccaaagag 840
 aggcaactta ttatagacaa tgattttctc gaaaatcgat aaaaaaatcc attttcaaac 900
 agcaacgaaa tctgtataat gcgaccgcaa tatttttttac ccttttattt ttcatatcaa 960
 cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
 Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
 1 5 10
 gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
 Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
 15 20 25

gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca	1108
Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro	
30 35 40	
atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc	1156
Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile	
45 50 55	
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct	1204
Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser	
60 65 70 75	
att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc	1252
Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser	
80 85 90	
ggg att gta tcc gat cct gtc acc gtt tca cca acc tta tct tta gca	1300
Gly Ile Val Ser Asp Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala	
95 100 105	
gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt	1348
Glu Leu Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val	
110 115 120	
gtt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca	1396
Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr	
125 130 135	
cgc ttt gtc acg gat tta aat aaa aca gtg gcg gac ttt atg acc cct	1444
Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro	
140 145 150 155	
aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att	1492
Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile	
160 165 170	
ttt ggt cta atg cat aca cac cgt gta gaa aaa gtc ctt gtt gtc agc	1540
Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser	
175 180 185	
gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa	1588
Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys	
190 195 200	
tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt	1636
Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg	
205 210 215	
gtc ggt gct gca gta gga gca gga cct ggt aat gaa gaa cgt att gat	1684
Val Gly Ala Ala Val Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp	
220 225 230 235	
gca tta gtg aaa gca ggg gtc gat gtg tta ttg att gac tca tca cac	1732
Ala Leu Val Lys Ala Gly Val Asp Val Leu Leu Ile Asp Ser Ser His	
240 245 250	
ggg cat tca gaa ggt gtg tta caa cgt gtg cgt gaa act cgt gcg aaa	1780
Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys	
255 260 265	
tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc	1828
Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly	
270 275 280	

gca att gcg ttg gct gat gca ggg gca agt gca gtg aaa gtg ggg att 1876
 Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile
 285 290 295

ggt cct ggt tca att tgt aca aca cgt att gtc aca ggc gtg ggc gtt 1924
 Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val
 300 305 310 315

cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg 1972
 Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg
 320 325 330

ggt att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att 2020
 Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile
 335 340 345

tcg aaa gcc att gcg gcg ggc gcc tct tgt gtt atg gtg ggt tcc atg 2068
 Ser Lys Ala Ile Ala Ala Gly Ala Ser Cys Val Met Val Gly Ser Met
 350 355 360

ttt gca ggt aca gaa gaa gca cca ggt gaa atc gaa ctt tat caa ggt 2116
 Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly
 365 370 375

cgt gcc ttt aaa tct tat cga ggt atg gga tcg tta ggt gcg atg agc 2164
 Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser
 380 385 390 395

aaa ggc tca agc gac cgc tat ttc cag tcc gat aat gca gct gac aaa 2212
 Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys
 400 405 410

tta gta cca gaa ggt att gaa gga cgt att cca tat aaa gga ttc tta 2260
 Leu Val Pro Glu Gly Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu
 415 420 425

aaa gaa att atc cat caa caa atg ggt gga ttg cgt tct tgt atg ggc 2308
 Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly
 430 435 440

tta acg ggt tgt gca acc att gat gaa ctc cgt acc aaa gcg cag ttt 2356
 Leu Thr Gly Cys Ala Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe
 445 450 455

gtg cgc att agt ggt gca ggg atc caa gaa agc cat gtg cat gat gtg 2404
 Val Arg Ile Ser Gly Ala Gly Ile Gln Glu Ser His Val His Asp Val
 460 465 470 475

act atc aca aaa gaa gcc cct aat tat cgt atg ggt taaacattgc 2450
 Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly
 480 485

ttaggtgggg attatcccca cctaagttaa ttttaaataa caacgttaat agagaagctt 2510
 atttttatgt atggcattaa aattaaat gttattaaac tttttctatt aaagttttta 2570
 agaaataaat atcgatataa aatcaatatt caacatcatc tcattagtat tgaaggaaaa 2630
 tgcggtgagt ttgatttaag ccagctaaac tatgtttatt tgggtgaaaga tcctgagata 2690
 agaaataatc gactgacact gtacttgaat gattttttca aaattggggg aaattatcat 2750
 ggattttactc aaatgtatca gacactatca tccaagtatg gttttgatga cgcaacgttt 2810

tttgaatatc tttgtaagaa agggcctttt tctattcaaa tttggcgtaa aaaacaaact 2870
caaaattatg tgattcttga tgaagcctat actgactata cacaaggttt tgaaattcaa 2930
tctcctgaaa aaatatttat tccttggggg actacttatg aagccttatt tcagcagaca 2990
caattttaaag aaaaaggaat ctcttatgac tttatcttcc ctattcggat agggcgttta 3050
ttactcaagg atgtgtggat cacaccaagt gtccgaaaag atgtaccgat tttagcgta 3110
tacactgagt gctatcatga atccgcgaca gaaaaaagtt atcaggaatt aaccgccgca 3170
ttacgtgaga accaacagtt aatcagatca tgtgttgaag aacgagccga tccgaaatta 3230
tataagtctg ttttacgcct taacgcgaca gaatttgaat tgcgttatta tcgacatata 3290
cgagacgatt ttgatagggg atacactaaa ttcagcatta gagatacgac agactattta 3350
gattatgtga tcaacgagcc ttatgaaaat caattagtga taacggatta tttagtgatt 3410
gaggcgcaaa atttaataaa aatggattat accgataatt ccattattaa acgccgacca 3470
ccaaaaataa aagaaaagtt tcgtgatgca caaagcctga tttggacaga tgatctcaat 3530
cataaaatcg gttttaccag tgatgaccgc gctatcgtct ttgataaagc ggacattgaa 3590
tcctttactc tggcaaatat agagacaacc cgaagacata atcgcagttc actcagcatc 3650
tgttttgtgg ataaaaataa ggaagccatc actgtatttc tagctgaaca tcattttctg 3710
ataccctatg tggataaaat aaaaacactg acacaaaaag aggtgttggt tcttgaagaa 3770
tatatagagg atgtttaaaa aaccgataac atcttgatgt catcgcaaat tcaaaactcct 3830
tttacacaat atatttaaac ttttaaccga tttaatattt acgtaaaaac aactaagaga 3890
acttaaatga acaacattca caaccataaa attttaattt tggacttcgg ttcacaatat 3950
accagttga ttgccgcgct gtacgtgaa attggcgtgt actgcgaact ttgggcatgg 4010
gatgtatccg aagccgatat tcgtgagttt aatccaactg ggattattct ttctgggtgg 4070
cctgaaagta ccactgaaga aaacagccca cgagctcccg aatacgtatt caacgccggt 4130
gtaccctgat tagggatctg ttatgggatg caaaccatgg cgatgcaact aggtggttta 4190
actgaaactt ctactcaccg agaatttggt tatgcatcag tgaatctaaa agccgcggac 4250
gcgttatattg ctcaattaaa tgatgatgtc gcaagttcac agcccaaatt agacgttttg 4310
atgagccatg gcgataaagt gacgcgtttg ccagatcatt tccaagtcac cgcaatgacc 4370
tcaacctgtc caatcgagc tatgtcggat gaacgtcgtc gtttttatgg tgtccaattc 4430
caccagaag tgactcatac aaaaagcggg cttgaattat taacgaattt tgtgggtgaag 4490
atctgtgggt gtgaacgtaa ctggacacca gaaaatatca ttgaagatgc cgttgctcgt 4550
cttaaagcac aagtgggcga tgatgaagtg attttaggct tatctgggtg cgttaactgc 4610
cgtataggca gcttagaaaa agtgtccgcg ctcacgttaa tccccgtaag cgttga 4666

<210> 24

<211> 487

<212> PRT

<213> Pasteurella multocida

<400> 24

```

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

Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
          20           25           30

Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
      35           40           45

Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
 50           55           60

Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
 65           70           75           80

Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp
          85           90           95

Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
      100           105           110

Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
      115           120           125

Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
 130           135           140

Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
 145           150           155           160

Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
          165           170           175

Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
          180           185           190

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

Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
      210           215           220

Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala
 225           230           235           240

Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly
          245           250           255

Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro
          260           265           270

Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
      275           280           285

Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
      290           295           300

```

Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
 305 310 315 320
 Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg Gly Ile Pro Val Ile
 325 330 335
 Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala
 340 345 350
 Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu
 355 360 365
 Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
 370 375 380
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
 385 390 395 400
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
 405 410 415
 Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His
 420 425 430
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
 435 440 445
 Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
 450 455 460
 Ala Gly Ile Gln Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
 465 470 475 480
 Ala Pro Asn Tyr Arg Met Gly
 485

<210> 25
 <211> 2364
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (191)..(1828)

<220>
 <223> Hi1501

<400> 25
 gtcaacactc atcgcacagc tgaggcattt cccgaaagct gatcatgatg atggacctga 60
 tgcgctagag atgctgtgga aaaatgcggt aagcagctct gccccgattg agttcatgac 120
 aattgacggc gatttagggc gtgatgaatt tgatgacggc gatttataca gtatttggcg 180
 gagataaaaa atg gcg aag aaa aag aaa aaa tta caa caa gcg aaa aaa 229
 Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys
 1 5 10
 gta caa gtt ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277
 Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu
 15 20 25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca	325
Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala	
30 35 40 45	
aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg	373
Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala	
50 55 60	
caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg	421
Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly	
65 70 75	
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc	469
Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg	
80 85 90	
att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc	517
Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Lys Leu Gln Val	
95 100 105	
gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg	565
Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met	
110 115 120 125	
gtg gat atg atg gat gcg gta gga cat ggt ttt tcg gcg tta gaa att	613
Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile	
130 135 140	
gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca	661
Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala	
145 150 155	
cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt	709
Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu	
160 165 170	
aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg	757
Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp	
175 180 185	
gta gtg cat acc cac aaa tca aga aca gta cag ctt gct cgt atg ggt	805
Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly	
190 195 200 205	
tta ttt aga acg ctc gca tgg ctt tat atg ttt aaa cac tac tcg gtg	853
Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val	
210 215 220	
cat gat ttt gcc gaa ttt cta gag ctt tat ggt atg ccg att cgt att	901
His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile	
225 230 235	
ggt aaa tac cca ttt ggg gca acg aat gac gaa aag cgc aca tta ttg	949
Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu	
240 245 250	
cgt gca ctt gct caa atc gga cat aac gca gca ggg att atg cca gaa	997
Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu	
255 260 265	
gga atg aat gtt gag ttg cat aat gtg aca aac act act ggc tcg gct	1045
Gly Met Asn Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala	
270 275 280 285	

gga agc aac ccg ttt ttg caa atg gtg gac tgg tgt gaa aag tcc gcc	1093
Gly Ser Asn Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala	
290 295 300	
gca cgt ttg att cta ggg caa aca tta aca agc ggt gca gat ggt aaa	1141
Ala Arg Leu Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys	
305 310 315	
act tca act aat gcc ctt gga caa gtg cat aat gaa gtc aga cgt gac	1189
Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp	
320 325 330	
ttg ctt gtg tct gat gct aaa cag att gca caa act att aca caa cag	1237
Leu Leu Val Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln	
335 340 345	
att att ctg cca tat ctt caa att aac att gat ccg aat att ttg cct	1285
Ile Ile Leu Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro	
350 355 360 365	
tct cgt gtg ccg tat ttc gag ttt gac acg aaa gaa tat gct gat tta	1333
Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu	
370 375 380	
agt gtc cta gcg gat gct att cct aag ctt gtg agc gta gga gtg cgc	1381
Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg	
385 390 395	
att cct gaa aat tgg gtg cgt gat aaa gcg ggc att cca gaa ccg cag	1429
Ile Pro Glu Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln	
400 405 410	
gaa aat gaa acg att tta agt gcg gtt caa cat gat ttt aaa aca gat	1477
Glu Asn Glu Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp	
415 420 425	
tta aac gat gtt gaa aat ccg aaa aaa cag acc gca ctt tct gta caa	1525
Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln	
430 435 440 445	
aat cac gtg aca ggt tgt cag tgt gat ggc tgt cgt ggt gtt gca tta	1573
Asn His Val Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu	
450 455 460	
tct gcg aat aat aac agt tct act gcg cag ggc gtg cta gat ggt gga	1621
Ser Ala Asn Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly	
465 470 475	
ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca	1669
Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro	
480 485 490	
atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat	1717
Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp	
495 500 505	
gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac	1765
Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His	
510 515 520 525	
gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt	1813
Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu	
530 535 540	

gga gga act aat gtc taaaccgctt agttttctat tcggacttga accaacgcaa 1868
 Gly Gly Thr Asn Val
 545

gccattgagt ttttacataa taaaaaatta cttgcaacga aagtgtttaa aaaatcactg 1928
 catgatagtg ccatcgcaag agctacaaca atcgcgagat tatctagtct tgagatgacg 1988
 aatgatattt ataaatcaat ggaagttgcc aaaaagagg gtaagagctt tacacaatgg 2048
 aaaaaagact tggttaagtga gtttgagaaa aaaggctggg tattcgggca tgataaatct 2108
 atcagtcgcg gtatcgacgg aaaactgttg gctgatccga aaacaggcga atattttggg 2168
 acaccgcgtc ggctgaatac aatttatcgt acaaacgtgc aagccgcata ttctgcggcg 2228
 cgctatcagc gcatgatgga taatattgat catcgccctt attggcaata ttccgctgtc 2288
 agcgatgagc gtacacgacc ctctcatctt gcactaaacg gtcgaattta tcgctatgat 2348
 gacccgtttt ggtcga 2364

<210> 26
 <211> 546
 <212> PRT
 <213> Pasteurella multocida

<400> 26
 Met Ala Lys Lys Lys Lys Lys Leu Gln Gln Ala Lys Lys Val Gln Val
 1 5 10 15
 Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu Thr Gly Arg
 20 25 30
 Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala Lys Leu Lys
 35 40 45
 Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala Gln His Glu
 50 55 60
 Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly Ala Asn Ile
 65 70 75 80
 Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg Ile Ala Glu
 85 90 95
 Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp
 100 105 110
 Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met Val Asp Met
 115 120 125
 Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile Glu Trp Lys
 130 135 140
 Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala Arg Pro Gln
 145 150 155 160
 Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu Lys Thr Pro
 165 170 175

Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp Val Val His
 180 185 190
 Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly Leu Phe Arg
 195 200 205
 Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe
 210 215 220
 Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile Gly Lys Tyr
 225 230 235 240
 Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu
 245 250 255
 Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn
 260 265 270
 Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala Gly Ser Asn
 275 280 285
 Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala Ala Arg Leu
 290 295 300
 Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys Thr Ser Thr
 305 310 315 320
 Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp Leu Leu Val
 325 330 335
 Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu
 340 345 350
 Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val
 355 360 365
 Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu Ser Val Leu
 370 375 380
 Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg Ile Pro Glu
 385 390 395 400
 Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln Glu Asn Glu
 405 410 415
 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp
 420 425 430
 Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val
 435 440 445
 Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn
 450 455 460
 Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly Leu Ala Gln
 465 470 475 480
 Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys
 485 490 495
 Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala
 500 505 510

Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu
 515 520 525

Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu Gly Gly Thr
 530 535 540

Asn Val
 545

<210> 27
 <211> 1353
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> hmbR

<220>
 <221> CDS
 <222> (2)..(1351)

<220>
 <221> misc_feature
 <222> 125
 <223> Xaa = any or unknown amino acid

<220>
 <221> misc_feature
 <222> 133
 <223> Xaa = any or unknown amino acid

<220>
 <221> misc_feature
 <222> 141
 <223> Xaa = any or unknown amino acid

<220>
 <221> misc_feature
 <222> 151
 <223> Xaa = any or unknown amino acid

<400> 27
 g tca acg aaa gtc ggt tac gat att aat aac act cat cgt ttt aca ctg 49
 Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu
 1 5 10 15

ttt tta gaa gat cgc cgt gaa aag aag ctt acc gaa gaa aaa aca tta 97
 Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
 20 25 30

ggg ctt agt gat gca gtg cgt ttt gct aat gat caa acc cct tat ctc 145
 Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
 35 40 45

cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193
 Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
 50 55 60

gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241
 Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
 65 70 75 80

caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg	289
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser	
85 90 95	
ttt gta tat tta caa aga cag aat ata gct cgg gga gaa ttt tca acg	337
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr	
100 105 110	
agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc	385
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe	
115 120 125	
gaa ttt cgt gat ang ttt tta gaa aat atg aat aag cnt ttt acg ttt	433
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe	
130 135 140	
cgg ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat	481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr	
145 150 155 160	
aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg	529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met	
165 170 175	
gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg	577
Asp Asp Ile Lys Ile Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg	
180 185 190	
tgg gat cac tat aac tat aag cca tta tta aat tct cag cat aat atc	625
Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile	
195 200 205	
aac agg aca cag aga tta cct tat cca aaa aca tca tcc aaa ttt tcg	673
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser	
210 215 220	
tat caa ttg agt tta gag tat caa tta cat cca tca cat caa att gca	721
Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala	
225 230 235 240	
tac cgt tta agt acc ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat	769
Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr	
245 250 255	
ttt gaa gac cga gga aaa agt tct tca caa ttt ctt cct aac ccc gat	817
Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp	
260 265 270	
cta caa ccg gaa act gca ctg aat cat gaa ata agt tac cgt ttc caa	865
Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln	
275 280 285	
aat caa tat gcc cat ttc agc gtc ggg ctt ttc cgt aca cgt tat cat	913
Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His	
290 295 300	
aac ttt att caa gaa cgt gag atg acc tgt gat aaa att cca tat gag	961
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu	
305 310 315 320	
tat aat agg act tat gga tat tgc acg cat aat act tat gta atg ttt	1009
Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe	
325 330 335	

```

gtt aat gaa cct gaa gcc gtg att aaa ggg gtt gaa gta agc ggt gct 1057
Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala
      340              345              350

tta aat ggg tcg gca ttc gga ctt tcc gac ggt tta act ttc cgt ctc 1105
Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
      355              360              365

aaa ggg agc tac agc aaa ggt caa aat cat gac ggc gat ccg tta aaa 1153
Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
      370              375              380

tct att caa cca tgg aca gtg gta acc ggt att gat tac gaa act gaa 1201
Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
      385              390              395              400

ggg tgg agc gtg agt ttg agc ggg cgt tat agt gcg gct aaa aaa gcc 1249
Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
      405              410              415

aaa gat gcg ata gaa acg gaa tac aca cat gat aaa aag gtt gtc aaa 1297
Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys
      420              425              430

caa tgg ccg cat tta agt cca tcc tac ttt gtt gtt gat ttt acg ggg 1345
Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly
      435              440              445

caa gtt ga
Gln Val
      450
1353

```

```

<210> 28
<211> 450
<212> PRT
<213> Pasteurella multocida

```

```

<220>
<221> misc_feature
<222> 125
<223> Xaa = any or unknown amino acid

```

```

<220>
<221> misc_feature
<222> 133
<223> Xaa = any or unknown amino acid

```

```

<220>
<221> misc_feature
<222> 141
<223> Xaa = any or unknown amino acid

```

```

<220>
<221> misc_feature
<222> 151
<223> Xaa = any or unknown amino acid

```

```

<400> 28
Ser Thr Lys Val Gly Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu
  1           5           10           15

```

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

Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu
 355 360 365
 Lys Gly Ser Tyr Ser Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys
 370 375 380
 Ser Ile Gln Pro Trp Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu
 385 390 395 400
 Gly Trp Ser Val Ser Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala
 405 410 415
 Lys Asp Ala Ile Glu Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys
 420 425 430
 Gln Trp Pro His Leu Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly
 435 440 445
 Gln Val
 450

<210> 29
 <211> 4936
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1078)..(2769)

<220>
 <223> hxuC

<400> 29
 gtcaacaaca aagcgcacag gcattacttc atgccacaca catcatcacag aaagtacgta 60
 ccgatttaac gcaaatatga gccgtcaaca ttcattctttt cctatcataa agcggtttcat 120
 catggctagc attctagcaa aaattagttg aggaaaatag cgggtcttggt ttgcttaaaa 180
 aacaaccac cccgtagggc acggctgttt ctttttgaga aattacgctt cttcatcttg 240
 atcttttttc aagatctcat cttcattgag ttttaaaaga cgggcaatcg cattgcggta 300
 ggagatttca aggctttctc gactagtagc aatgacacct tgatcgatta agaaaccgtc 360
 attgacatca taaacccaac catgtaatga gagttttttc ccatttttcc acgcggattt 420
 aatgattgac gagcgaccta agttataaac ttgctctgcg acgttaattt tcgtcagcat 480
 atcagcccggt ttttcaggcg gtaaattgcc aagtaaatga ctatgcttat accaaatatc 540
 gcgtaagtgg agtaaccagt tattaattaa acctaaatct tgatccgcca ttgcggcttt 600
 aattccacca cagtttgtat gtccacaaat aataatgtgt tcaatattta agacctcaac 660
 ggcatattgc acaacagata aacagtttaa atcgggtgtga atgacttgat ttgcaacatt 720
 acgatgcaca aacagctcac ccggtcctaa atttgtaaat ttttctgcag gaacacggct 780
 atccgagcaa ccaatccaaa gatagctcgg ggtttgatga tcagccaatt ctttaaagta 840


```

agaggagttt tcctctttca tccgtaacgc ccagctataa ttattggcaa aaagttgttc 900
aatttttttc attagagtga ttcctatacc gcaaaaataa gggggctagt atagcttaga 960
aatagacagt gggtaaagaa aggcaaaaaa ttgtatagga taacttggtt tttattgcca 1020
tttatttaga attagaatct ttaataataa aaataattat cattaagggtt aatagtt 1077

atg gat aaa aat tta atg aag gga tgt gta ttc tta tca ata gtc ggt 1125
Met Asp Lys Asn Leu Met Lys Gly Cys Val Phe Leu Ser Ile Val Gly
  1             5             10             15

tgc ggt atc caa ata ggg cta gca tca aat cca aat cct cca gat gtg 1173
Cys Gly Ile Gln Ile Gly Leu Ala Ser Asn Pro Asn Pro Pro Asp Val
             20             25             30

gat gag tta tta cct att att gtg aat gct gat gaa gat aat aaa tta 1221
Asp Glu Leu Leu Pro Ile Ile Val Asn Ala Asp Glu Asp Asn Lys Leu
             35             40             45

cca ggt cgt tct gta tta aaa cag aaa aat atc gat caa caa caa gca 1269
Pro Gly Arg Ser Val Leu Lys Gln Lys Asn Ile Asp Gln Gln Gln Ala
             50             55             60

gat aat gcc gct gac tta ata aat att tta cct ggg gta aat atg gcg 1317
Asp Asn Ala Ala Asp Leu Ile Asn Ile Leu Pro Gly Val Asn Met Ala
             65             70             75             80

gga gga ttt cgc cct ggt ggt caa aca tta aat att aat gga atg ggt 1365
Gly Gly Phe Arg Pro Gly Gly Gln Thr Leu Asn Ile Asn Gly Met Gly
             85             90             95

gat gct gaa gat gtt aga gtt caa cta gac ggc gca aca aaa agt ttc 1413
Asp Ala Glu Asp Val Arg Val Gln Leu Asp Gly Ala Thr Lys Ser Phe
             100             105             110

gaa aaa tat caa caa ggc tct att ttt att gaa cct gag tta tta aga 1461
Glu Lys Tyr Gln Gln Gly Ser Ile Phe Ile Glu Pro Glu Leu Leu Arg
             115             120             125

aag gtg aca gta gac aaa gga aat tat tct cct caa tat ggc aat ggt 1509
Lys Val Thr Val Asp Lys Gly Asn Tyr Ser Pro Gln Tyr Gly Asn Gly
             130             135             140

ggc ttt gct ggt act gta aaa ttt gaa aca aaa gat gca act gat ttt 1557
Gly Phe Ala Gly Thr Val Lys Phe Glu Thr Lys Asp Ala Thr Asp Phe
             145             150             155             160

ttg aaa gaa aat cag aaa ata ggt gga tta ttt aaa tat gga aat aat 1605
Leu Lys Glu Asn Gln Lys Ile Gly Gly Leu Phe Lys Tyr Gly Asn Asn
             165             170             175

agc aat aat aac caa aaa act tat agt aca gcc cta gtt tta cag aat 1653
Ser Asn Asn Asn Gln Lys Thr Tyr Ser Thr Ala Leu Val Leu Gln Asn
             180             185             190

gaa caa aaa aat att gat ttg tta tta ttt ggt tct gta aga aat gca 1701
Glu Gln Lys Asn Ile Asp Leu Leu Leu Phe Gly Ser Val Arg Asn Ala
             195             200             205

agc aat tat aca aga cct gat aaa agt aaa att ctt ttt tca aaa aac 1749
Ser Asn Tyr Thr Arg Pro Asp Lys Ser Lys Ile Leu Phe Ser Lys Asn
             210             215             220

```

aat caa aaa agt gga tta ata aaa gta aat tgg caa att act cct gaa	1797
Asn Gln Lys Ser Gly Leu Ile Lys Val Asn Trp Gln Ile Thr Pro Glu	
225 230 235 240	
cat tta tta act tta tcc agt gtt tat ggc att cat aaa ggg tgg gaa	1845
His Leu Leu Thr Leu Ser Ser Val Tyr Gly Ile His Lys Gly Trp Glu	
245 250 255	
cct tgg gca gca aaa aga gat gtg atg tgc aga cca aca gaa aca gaa	1893
Pro Trp Ala Ala Lys Arg Asp Val Met Ser Arg Pro Thr Glu Thr Glu	
260 265 270	
ata aaa cac tat ggg att gat gtt gcg tgg aaa cgt aaa ctt gtt tat	1941
Ile Lys His Tyr Gly Ile Asp Val Ala Trp Lys Arg Lys Leu Val Tyr	
275 280 285	
cga gat caa aaa gat gaa agt tat tca ttg aaa tat cgc tat tta cct	1989
Arg Asp Gln Lys Asp Glu Ser Tyr Ser Leu Lys Tyr Arg Tyr Leu Pro	
290 295 300	
gaa aat aat aag tgg att aat ttg tct gtt cag ctg agt tat agt aaa	2037
Glu Asn Asn Lys Trp Ile Asn Leu Ser Val Gln Leu Ser Tyr Ser Lys	
305 310 315 320	
aca gag cag aat gat act cgc cat gag aaa gtc act tct tca ttc cta	2085
Thr Glu Gln Asn Asp Thr Arg His Glu Lys Val Thr Ser Ser Phe Leu	
325 330 335	
ggt aca tta gga aat aaa agt tgg ata act tat tca gat ctt act ttt	2133
Gly Thr Leu Gly Asn Lys Ser Trp Ile Thr Tyr Ser Asp Leu Thr Phe	
340 345 350	
gat ata agt aac aca agt act cta aat att ggg cgt gct gag cat gaa	2181
Asp Ile Ser Asn Thr Ser Thr Leu Asn Ile Gly Arg Ala Glu His Glu	
355 360 365	
cta cta ttt ggt tta cag tgg tta aaa aat aaa aga aat acc ctt atg	2229
Leu Leu Phe Gly Leu Gln Trp Leu Lys Asn Lys Arg Asn Thr Leu Met	
370 375 380	
tat cat aaa ggg gga gtc aag aag gca gac tat aat tat ggc tat ttt	2277
Tyr His Lys Gly Gly Val Lys Lys Ala Asp Tyr Asn Tyr Gly Tyr Phe	
385 390 395 400	
cag cct tat tat atg cct tct gga cgc cag tat aca caa gca ttt tat	2325
Gln Pro Tyr Tyr Met Pro Ser Gly Arg Gln Tyr Thr Gln Ala Phe Tyr	
405 410 415	
tta caa gat caa ata aaa tgg cag aat ttc ctc ttt aca gga ggg ata	2373
Leu Gln Asp Gln Ile Lys Trp Gln Asn Phe Leu Phe Thr Gly Gly Ile	
420 425 430	
aga tat gac cat atc aat aat ata ggg cag aaa aat tta gcg cca cga	2421
Arg Tyr Asp His Ile Asn Asn Ile Gly Gln Lys Asn Leu Ala Pro Arg	
435 440 445	
tat aat gat atc tct gca gga cat gat tat agc cag aaa aat tat aat	2469
Tyr Asn Asp Ile Ser Ala Gly His Asp Tyr Ser Gln Lys Asn Tyr Asn	
450 455 460	
ggt tgg tct tat tat tta ggt ctt aag tat gat gta aat cat tat tta	2517
Gly Trp Ser Tyr Tyr Leu Gly Leu Lys Tyr Asp Val Asn His Tyr Leu	
465 470 475 480	

```

agt tta ttt acg aat ttt agt aaa act tgg cga gcc cct gtt att gat 2565
Ser Leu Phe Thr Asn Phe Ser Lys Thr Trp Arg Ala Pro Val Ile Asp
                        485                        490                        495

gaa cag tat gag aca caa tat agt caa gct tct gta tct gcg act tct 2613
Glu Gln Tyr Glu Thr Gln Tyr Ser Gln Ala Ser Val Ser Ala Thr Ser
                        500                        505                        510

tta aat tta gaa aaa gaa atg att aat caa acc aga gtg ggt gga att 2661
Leu Asn Leu Glu Lys Glu Met Ile Asn Gln Thr Arg Val Gly Gly Ile
                        515                        520                        525

att act ctc aat cat cta ttt cag gaa aat gat gct ttt caa ttt aga 2709
Ile Thr Leu Asn His Leu Phe Gln Glu Asn Asp Ala Phe Gln Phe Arg
                        530                        535                        540

act act tat ttt tac aat cgc ggc aag aat gaa atc ttc aaa acg aga 2757
Thr Thr Tyr Phe Tyr Asn Arg Gly Lys Asn Glu Ile Phe Lys Thr Arg
545                        550                        555                        560

ggg gtt aac cgt tagagttggg tgaaatgact gaaaaattag acctatacgt 2809
Gly Val Asn Arg

tactgttaaa ggtggcggtta tttctgggtca agcgggtgca atccggtcacg gtatcactcg 2869

tgcattaatc gaatatgatg agagttttacg ctctgtatta cgcgcagctg gtttcggttac 2929

tcgcatgca cgtcaagttg aacgtaaaaa agtgggttta cgcaaagcgc gtcgtcgtcc 2989

acaattctca aaacgttaat ttttctttta cgttttatat tcagattgca agcccaaaag 3049

gcttgcaatt tttttatctc aataaaattht acgataatct ttggaaatca gtgggcgatt 3109

tgtggtagaa taaacgcccc ttttttatat aaaatcatgc cagaatcagg caaagttaa 3169

taaattttta ttcatttttag agctgtcgga ggaatagatg acaagcgctg caaataaacg 3229

ttcaataatg acactttttt cagataaaaac agatatttat tgccaccaag taaggattgt 3289

tttggtgaa aagggtgttg cttatgaaac ggaagttgta gatcctcaag tcgtatcaga 3349

agatttaatg gaattaaatc cgtatggcac gttgccgaca ttagttgatc gtgatttagt 3409

gttatttaat tcacgtatta ttatggaata tcttgatgag cgtttccctc atccaccttt 3469

gatgcctgtt tatccagtgg cacgtgggaa aagccgttta ttaatgttac gtattgagca 3529

agattggtac ccagtattag caaaagctga aaaaggcacg gacgcagaac gtgctgtcgc 3589

attaaaacaa ttaagagaag agatttttagc gattgagcct attttcacgc agatgcctta 3649

ttttatgagc gaagagttta gtttagtaga ttgttatatc gccccattat tatggcgat 3709

gcaagaactg ggtgtggatt tcagtggggc gggtagcaaa gcaattaaag cttacatggc 3769

acgtgttttt gaacgcgatt cttttatgca atcttttaggc gtgtcggctc cgaaaaactt 3829

aatggatgag aaataatcag tatgctacat aaatcatcac caaagcgctc ttacttggtta 3889

agagcgtatt atgattggtt agtggaataat gatttcaccc cttatttagt ggtggacgcg 3949

acttatgttg gtgtgaaagt ccctgtggaa tatgtcaaag atgggcaaat tgcctcaat 4009

```

ttatctgcga atgcgacagg taatctggta ctaagcaatg aaagtattca gtttagcgcg 4069
 cgttttcgtg gtatttcaca agatattttt attcctatgg gggctgcgtt agccatttat 4129
 gctcgtgaaa atgggtgatgg tgtactgttt gaacctgaag cgatttatga tgagctcgca 4189
 acacaaaata ttggtattga gcagccactg agctttgttg aggctgtcga taaacaaaaa 4249
 accagtgaga atactcaaaa aagcacaaac aaagacaaaa cgacggaaaa aaaagcgact 4309
 tctcatttaa gaattattaa ataaaagagg ttttctttct tcataaaaaa acacgctttt 4369
 acgcgtgttt ttttggtgcg gacagtttat tgtgccattt tttttgcggc ttttaagaag 4429
 ccttgccgac tegtgtagat gtcactttta ttctgtgccg ctaaaatcat atccgacatt 4489
 tcacgaaagg ccccttgctc acctttcagg cttagtacgt gatcagcgtg ctttttgata 4549
 taagcggcgc atcttgtagt gcaaaggcaa caccacagcg gcaaaagcag gcagatcaac 4609
 gctgtcatca ccaatataag ccgtttcttg cgcacagaca ttggcttggt gtatcaattc 4669
 aagacaggcg ctttcttttt ccaatttgcc gaggaaaaag tgttggtatgc ctagatctgc 4729
 aatacgtttg cgtagaatcg gggaatctcg ccccgagagt accgcgactt gaatgccaga 4789
 ttccattaac attctgatcc ccaagccatc acgaacatga aagggtttga aagcttcacc 4849
 atgggcatcg taatgcaaag agccgtcggg cagtacaccg tcgatatctg taatcacaaa 4909
 ttttaattttt ttgagttttt ccgttga 4936

<210> 30

<211> 564

<212> PRT

<213> *Pasteurella multocida*

<400> 30

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

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

Gly Trp Ser Tyr Tyr Leu Gly Leu Lys Tyr Asp Val Asn His Tyr Leu
 465 470 475 480
 Ser Leu Phe Thr Asn Phe Ser Lys Thr Trp Arg Ala Pro Val Ile Asp
 485 490 495
 Glu Gln Tyr Glu Thr Gln Tyr Ser Gln Ala Ser Val Ser Ala Thr Ser
 500 505 510
 Leu Asn Leu Glu Lys Glu Met Ile Asn Gln Thr Arg Val Gly Gly Ile
 515 520 525
 Ile Thr Leu Asn His Leu Phe Gln Glu Asn Asp Ala Phe Gln Phe Arg
 530 535 540
 Thr Thr Tyr Phe Tyr Asn Arg Gly Lys Asn Glu Ile Phe Lys Thr Arg
 545 550 555 560
 Gly Val Asn Arg

<210> 31
 <211> 9814
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (4762)..(7662)

<220>
 <223> iroA

<400> 31
 gtcgacctgc agcagacaat gtccactgtg taatagtcca acgactgtta taaaaatctt 60
 ccgctgcttt ttctaattgtt tgtacacggg gtttttcaaa ttcttccaaa ttcttggttg 120
 gttggactaa aagttgttca gccgcccgtt taaaattggc gacaaaatcc gattgtttga 180
 ttaaaccata ggattttgct tggattttgtg cgccggctgc ttcacccaat ttatcgaaaa 240
 attcaggcgt ataagtcacg tttgggatcg taggcgcat gatctgatta acaccagcct 300
 gttgtaatgc tccccattgc tgtgccatcg tttgtgcat ggttttaata ctggctaaca 360
 cgtaggcttg tttctcttca ggtgttgtct tggttactgc tgttgctaata actgtcgcca 420
 aatcattacc acctgcccac agaatatgta aagcttcttt ttgactggc gcatgtaaat 480
 actcgttgat ctgcttttct agtgctaaat gaggttggtc tgctgttcta gtattatgtg 540
 caccaacaat caccaccacg ctgtacgcgt agttcaaacc accttggtga gaaggtatta 600
 attttttccc aaatgcttga gctaaatatt catcataaag gtgatgatag ttccatcag 660
 cctttaaata agaggctttc ttattccaac ctggttgccc catatcactt aaactatcac 720
 caaacacgac aacatcttgt gccagagcag ccgaacttag tgaacaaaat aatgcgaatg 780
 aaagtgtatt aattttcaca ataatgtcct tcaattattc atcgtcagtc aaaaatttgc 840

gtcacatcac gttgattata ggaagatacc tagccagacc actactggta tgaacagaag 900
 tcaatgttta atcacataaa aaagcctctg tgctttcaca cagaggcttt tatgtccatt 960
 cacctactca aattacatcg cttgagtaaa ggtacgcgta atcacgtctt gttgttgttc 1020
 tttggttaac gagttaaagc gtactgcata acccgaaaca cgaatgggta attgtggata 1080
 tttctccgga ttttccattg catctaaca catttcacgg ttcacgtacgt tcacgtttaa 1140
 gtgttggtcg ccttcaatcg ttgcttcacg gtggaagtaa ccgtccatta gacctgcaag 1200
 gttacgtttt tgtgcttcgt aatctttacc taaggcattt ggtacgattg agaaggata 1260
 agaaatacca tctttcgcac aagcaaatgg caatttcgca acagaagtta acgatgctac 1320
 tgcacctttt tggtcacgac cgtgcattgg gttcgcaccc ggtccaaatg gtgcaccaga 1380
 acgacgacca tctgggggtg tacctgtttt cttaccataa accacgttag atgtaatagt 1440
 aagtacagat tgtgtcgggtg tcgcattacg ataagtaccc aatttttgga ttttcttcat 1500
 aaagcggtca actaaatcac aagcgatttc atcaacacgg ttatcgttgt taccgaattg 1560
 tggatattcg ccttcaattt caaagtcgat tgccacatct tttgcaatac caaccacttc 1620
 acccgcttta tttttgattt cgatatcacc acgaactggg ttcacttttcg catatttaat 1680
 ggcagataaa gagtccgctg cgacagaaaag ccctgcgata ccacaagcca tagtacggaa 1740
 tacatcacga tcatgaagtg ccattagtgc ggcttcatac gcgtatttat cgtgcataaa 1800
 gtgaatgatg ttcaatgcag taacatattg tttcgctaac caatccataa agctgtctaa 1860
 gcgcgtcatg acatcatcat aatctaagta ttcgctggta attggatcgg ttttcgggtc 1920
 tacttgggtca cctgattttt catccacacc gccattgatt gcgtataaca aggttttcgc 1980
 taagtgggca cgtgcaccga agaattgcat ctttttacc acgatcattg gcgatacaca 2040
 gcatgcaatc gcatagtcac cgttttgga gtcaggacgc attaagtcac cgttttcata 2100
 ctgaacagaa gacgtatcga tagacacttt tgccgcataa cgtttgaaac cttctggtaa 2160
 tttttcagac caaagaatcg ttaagtttg ctctgggtgac ggtcccatcg tataaagggt 2220
 gtgtaagata cggaagctgt ttttggttac taaagtacga ccatctaagc ccataccgcg 2280
 taaggtttcc gttgccaca ttgggtcgcc cgagaataat tgatcgctact ctgggggtacg 2340
 taagaaacgc accatacgtg atttcatgac taagtgggtc attaattctt gtgcttcttg 2400
 ttctgtaatt ttgcctgctt ttaaatacag ctcaatataa atatctaaga aagtcgatac 2460
 acgaccaaata gacatggcag caccgttttg tgatttcact gcagcgggtac gactttgcac 2520
 agttatcgga agataattga aatcataacc agcaacaaat gtcagccgtt ctatttcttc 2580
 tgaagaatat cggcgattgc gttctggcgg aatggctggg tttttcacat tcttgagatg 2640
 attttctttc aagtatttcc attctgtgat tgctgtcgta ataagtgcg aaagagtatt 2700
 ccattctcta agcacacttg ccgcactaac ttgtgaaagt cgttcacac gccactgcac 2760

aaagtgatgt tcttgtaa at cgattaatct cacgtagaa atcggcatat ttagcaagcg 2820
aagtaaacgc aactttttcag cacgatagcc ctttttattt atgctcactt ctttgatata 2880
tttatcgaca agttgtgcaa aagtgatgtc gggaatatca gtgaatacac cgtttatgat 2940
tttttgttct atgtctaacg cccacgcttg cgcacagct ttagtccgaa atgttgctga 3000
tttatagaca ctttttttgc gaatttgaac tcgccaacct gatttttggt tgttaaaagt 3060
cgccacgcct aactaccatt aattttgcac aattcggtgt gcaattttgt gcaattttat 3120
ttcttaa atg ttttagcg gatcataaat gaagaaaaa cagaagtaa acactatata 3180
aaaaaacagt atattttttg ttgaagtgt taatgtagt tgaacttat tgatttttaa 3240
atattaaaga taaagaaaaa gccgacaaa gtcggctttc tttttttatg ctgtttatca 3300
atggtgccta gggccggact cgaaccggca caccgaagg cggttgattt tgaatcaact 3360
gcgtctacca atttcgccac ccaggcta attgataaag agcatcaa at taggtctgta 3420
ttatacctt tcatgatag gttacaagca aaaaatgatt ttagatattc aattgtctt 3480
attttcatca gtgtggctgt tctctcttac tttattcagg tgcagtgaag taacctata 3540
aaaataaagg ttttttggtt aaatttttaa taactttttt gtaaaaagat cgcagtttct 3600
tttgaaaaa agaccgatta caaatataat taaaaactat tatcaatatt gataataatg 3660
ggattttaac catgacattt ataaggataa agtcaagatg atgctaaaag cacaaattgc 3720
agattatatt acacaaaatc cactggcaat tactttggat atggcttcgc actttggcaa 3780
acctgaagg gaaattttat gtgctttacc tgatgagttt gttcgagtgt ttcctgcgga 3840
acgtgcggag gaagtgttg ctgagatcag tagttggggg attttcacga ccattattga 3900
aaaagaagga tcgatttttg aaattaaaga ccgttttccg accgggatgg ttggcggtg 3960
ttattataat ttgaatatga aagatgaaga aggcacgctt catggtcacc ttaaattaga 4020
taacatcagc aaaattgcct ttgtgagttt accgtttcgc ggtaaagaaa gttataacat 4080
cgcatttatt gcgaataatg ggcaactat ttttaaagtt tatttggggc gcgatgctga 4140
gcgtcaatta tttccagaac aagttcaaaa atttaaagca tttatttaga aggttaaaaa 4200
agtaatgaca acaaatcgtc aagaagtatt acaaaatcgt ttaggtccag aaattcaaga 4260
gttaaaggca caatgtaaaa cagtcagct cgctactgtc ggtgaagatg gtaatcccaa 4320
tgtgagttat gcgccatttg caattaataa tggggaatac caagtcttta tttctactat 4380
tgcacgtcat gcacgtaatc tacaagaagt accaaaagtt tctttaatgt tgatcgaaga 4440
tgaaagttaa agtcgtcaga tttttgctcg tcgtcgttta tcttttgatg cggttgctcg 4500
tgttgctcag agagaaagtg aagaatggca ttctggtgtt gaggcactca aagcaagaca 4560
tggtgcatta atggatgaat tgtctcggat gaaagatttt catttgttta gttttaagcc 4620
ctcacaaggg ttatttgtaa aaggtttttg tcaagctttc caagtgaagta atgatgattt 4680


```

agtgagcttt gttcacttgg ttgaaggaca ccaagaataa attttgtcaa ctttttaggg 4740

tatttacttg aggttaggaa a atg cgt aca aca aca ata aaa ttt tct gca 4791
                Met Arg Thr Thr Thr Ile Lys Phe Ser Ala
                1                      5                      10

att aca ttg gca tta ttg agt tat tgt ggg acc att ttg gcg gat agt 4839
Ile Thr Leu Ala Leu Leu Ser Tyr Cys Gly Thr Ile Leu Ala Asp Ser
                15                      20                      25

cat caa gag gcg act gaa ctt gat acg att acc gtt tct tct caa caa 4887
His Gln Glu Ala Thr Glu Leu Asp Thr Ile Thr Val Ser Ser Gln Gln
                30                      35                      40

gat gag atg aat att aaa gag aaa aaa atc ggt gaa act gtg aaa acg 4935
Asp Glu Met Asn Ile Lys Glu Lys Lys Ile Gly Glu Thr Val Lys Thr
                45                      50                      55

gcg agt caa ttg aaa cgc cag caa gta cag gat agt cgt gat ctt gtg 4983
Ala Ser Gln Leu Lys Arg Gln Gln Val Gln Asp Ser Arg Asp Leu Val
                60                      65                      70

cgc tat gaa acc ggt gtg act gtg gta gaa gct gga cgt ttt ggt tcg 5031
Arg Tyr Glu Thr Gly Val Thr Val Val Glu Ala Gly Arg Phe Gly Ser
                75                      80                      85                      90

agc ggt tat gcc att cgt ggt gtg gat gag aac cga gta gca att aca 5079
Ser Gly Tyr Ala Ile Arg Gly Val Asp Glu Asn Arg Val Ala Ile Thr
                95                      100                      105

gta gat ggc tta cat caa gca gaa acc ctt tct tct caa ggc ttt aaa 5127
Val Asp Gly Leu His Gln Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys
                110                      115                      120

gaa tta ttc gaa ggt tac ggc aat ttt aac aat acc cga aat agt gtg 5175
Glu Leu Phe Glu Gly Tyr Gly Asn Phe Asn Asn Thr Arg Asn Ser Val
                125                      130                      135

gaa att gag acg ttg aaa gtc gct aaa atc gcg aaa ggt gct gat tct 5223
Glu Ile Glu Thr Leu Lys Val Ala Lys Ile Ala Lys Gly Ala Asp Ser
                140                      145                      150

gta aaa gtg ggt agt ggt tct ttg gga ggc gct gta ctt ttt gaa aca 5271
Val Lys Val Gly Ser Gly Ser Leu Gly Gly Ala Val Leu Phe Glu Thr
                155                      160                      165                      170

aaa gat gcc aga gat ttc ctg act gaa aaa gat tgg cat atc ggc tat 5319
Lys Asp Ala Arg Asp Phe Leu Thr Glu Lys Asp Trp His Ile Gly Tyr
                175                      180                      185

aaa gcg ggc tac tca acg gca gat aat cag gga tta aat gca gtg act 5367
Lys Ala Gly Tyr Ser Thr Ala Asp Asn Gln Gly Leu Asn Ala Val Thr
                190                      195                      200

ctt gca ggt cgc tat caa atg ttt gat gca ttg att atg cat tct aag 5415
Leu Ala Gly Arg Tyr Gln Met Phe Asp Ala Leu Ile Met His Ser Lys
                205                      210                      215

cga cat gga cat gaa tta gaa aat tat gac tat aaa aat ggc aga gat 5463
Arg His Gly His Glu Leu Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp
                220                      225                      230

```

att caa ggg aaa gaa aga gag aaa gcg gat cct tat acg att acg aaa Ile Gln Gly Lys Glu Arg Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys 235 240 245 250	5511
gaa agt aca tta gtg aaa ttc tct ttt tcg cca aca gaa aat cat cgt Glu Ser Thr Leu Val Lys Phe Ser Phe Ser Pro Thr Glu Asn His Arg 255 260 265	5559
ttt aca gtc gct tct gat act tat ctt cag cat tcc cgc gga cat gat Phe Thr Val Ala Ser Asp Thr Tyr Leu Gln His Ser Arg Gly His Asp 270 275 280	5607
ctt tca tat aat ctt gtt gca aca aca cat att cag tta gat gag aaa Leu Ser Tyr Asn Leu Val Ala Thr His Ile Gln Leu Asp Glu Lys 285 290 295	5655
gaa tct cgt cat gca aat gat ttg aca aaa cgt aaa aat gtt tcc ttt Glu Ser Arg His Ala Asn Asp Leu Thr Lys Arg Lys Asn Val Ser Phe 300 305 310	5703
act tat gaa aat tat act gtt acg cca ttt tgg gat acg ctc aag tta Thr Tyr Glu Asn Tyr Thr Val Thr Pro Phe Trp Asp Thr Leu Lys Leu 315 320 325 330	5751
agc tat tca caa caa aga att aca aca aga gca aga aca gaa gat tat Ser Tyr Ser Gln Gln Arg Ile Thr Thr Arg Ala Arg Thr Glu Asp Tyr 335 340 345	5799
tgt gat gga aat gag tta tgt gat tct tat aaa aat cca tta ggt ctc Cys Asp Gly Asn Glu Leu Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu 350 355 360	5847
caa ttt aaa gat ggt cag att ctt gat cct gca ggg aat aaa att aaa Gln Phe Lys Asp Gly Gln Ile Leu Asp Pro Ala Gly Asn Lys Ile Lys 365 370 375	5895
cta cag ggg tct gga ttg agc act cag att gta gat gaa aat gga aaa Leu Gln Gly Ser Gly Leu Ser Thr Gln Ile Val Asp Glu Asn Gly Lys 380 385 390	5943
cca ttt cct aca aca aca ggt act aat aat gct gct ttt agt aat aat Pro Phe Pro Thr Thr Thr Gly Thr Asn Asn Ala Ala Phe Ser Asn Asn 395 400 405 410	5991
tta cga ctc agg cct aca ggt ttt tgg tta gat tgc tcg gtt ttt gac Leu Arg Leu Arg Pro Thr Gly Phe Trp Leu Asp Cys Ser Val Phe Asp 415 420 425	6039
tgt aat aaa cca ttc act gtt tat aat att agt aat gga aca tat caa Cys Asn Lys Pro Phe Thr Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln 430 435 440	6087
gca aga gag gtt cta ctg tct gaa gag ata act gtg gat ggt aaa tta Ala Arg Glu Val Leu Leu Ser Glu Glu Ile Thr Val Asp Gly Lys Leu 445 450 455	6135
tac aaa aca gct aag gaa gaa gga ggg ctt cca aat tat ttg att tta Tyr Lys Thr Ala Lys Glu Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu 460 465 470	6183
cct aat tct aaa ggt tat ctt cct tat gat tat aaa gaa agg gat ctt Pro Asn Ser Lys Gly Tyr Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu 475 480 485 490	6231

aat acg aat aca aaa caa att aat tta gat tta act aaa aca ttt tta	6279
Asn Thr Asn Thr Lys Gln Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu	
495 500 505	
act ttc aac atc gaa aat aat ctg tca tat ggt gga gtt tat tct cgg	6327
Thr Phe Asn Ile Glu Asn Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg	
510 515 520	
ata gag aaa gaa atg att aat aaa gct ggt tat gag ggg aga aat cct	6375
Ile Glu Lys Glu Met Ile Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro	
525 530 535	
act tgg tgg gct gat aga att tta ggg caa agt agt tac tgt ggt tat	6423
Thr Trp Trp Ala Asp Arg Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr	
540 545 550	
aat gca ttg aag tgt ccg aaa cat gag cca tta acg tca ttt tta att	6471
Asn Ala Leu Lys Cys Pro Lys His Glu Pro Leu Thr Ser Phe Leu Ile	
555 560 565 570	
cca gtt gaa gca acg aca cag tca tta tat ttt gca aat att ctt aag	6519
Pro Val Glu Ala Thr Thr Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys	
575 580 585	
gta cat aat atg att agc ata gat tta gga tat cgt tat gat cat att	6567
Val His Asn Met Ile Ser Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile	
590 595 600	
aaa tat aac cct gaa tac act cca gga gta act cca aaa att cca gat	6615
Lys Tyr Asn Pro Glu Tyr Thr Pro Gly Val Thr Pro Lys Ile Pro Asp	
605 610 615	
gat atg gta aaa ggt ttg ttt att cct atg cca aaa gag cca cag cta	6663
Asp Met Val Lys Gly Leu Phe Ile Pro Met Pro Lys Glu Pro Gln Leu	
620 625 630	
aag gat ttt gat tat aac tat gct aaa ttt ggt gag gcc tat aaa aaa	6711
Lys Asp Phe Asp Tyr Asn Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys	
635 640 645 650	
tgg aaa gaa tat ctg cca aaa aat gcg gaa gaa aat att gct tac att	6759
Trp Lys Glu Tyr Leu Pro Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile	
655 660 665	
gct caa gat aag aca ttt aaa aaa cat tct tat tct ctt ggt gca act	6807
Ala Gln Asp Lys Thr Phe Lys Lys His Ser Tyr Ser Leu Gly Ala Thr	
670 675 680	
ttc gat cct ctg aat ttt tta cga gta caa gta aaa tat tca aaa ggg	6855
Phe Asp Pro Leu Asn Phe Leu Arg Val Gln Val Lys Tyr Ser Lys Gly	
685 690 695	
ttt aga gcc ccg act tcg gat gaa ctt tat ttt acc ttt aag cat cca	6903
Phe Arg Ala Pro Thr Ser Asp Glu Leu Tyr Phe Thr Phe Lys His Pro	
700 705 710	
gat ttt acg att tta ccg aac ccc gtg ttg aaa cca gag gaa gca aaa	6951
Asp Phe Thr Ile Leu Pro Asn Pro Val Leu Lys Pro Glu Glu Ala Lys	
715 720 725 730	
aat caa gag att gca tta aca gtg cac gat aat tgg gga ttt gtt agc	6999
Asn Gln Glu Ile Ala Leu Thr Val His Asp Asn Trp Gly Phe Val Ser	
735 740 745	

aca agt gtt ttc caa aca aag tat cgt cat ttt att gat tta gcg tat	7047
Thr Ser Val Phe Gln Thr Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr	
750 755 760	
tta ggt tca aga aat tta tcg aat tcc gtg gga ggg cag gca caa gca	7095
Leu Gly Ser Arg Asn Leu Ser Asn Ser Val Gly Gly Gln Ala Gln Ala	
765 770 775	
aga gat ttc caa gtt tat caa aat gtc aat gtc gat aat gcc aaa gtt	7143
Arg Asp Phe Gln Val Tyr Gln Asn Val Asn Val Asp Asn Ala Lys Val	
780 785 790	
aaa gga ctt gaa att aat gca cgt ttg aat ttg gga tat ttt tgg cat	7191
Lys Gly Leu Glu Ile Asn Ala Arg Leu Asn Leu Gly Tyr Phe Trp His	
795 800 805 810	
gtg ttg gat gga ttt aat acg agc tat aaa ttc act tac caa cgt ggt	7239
Val Leu Asp Gly Phe Asn Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly	
815 820 825	
cgt ttg gat ggc gat cgt cca atg aat gcg att cag cct aaa gct tct	7287
Arg Leu Asp Gly Asp Arg Pro Met Asn Ala Ile Gln Pro Lys Ala Ser	
830 835 840	
gtt ttt ggt ttg ggc tac gat cat aaa gaa aat aaa ttt ggc gct gat	7335
Val Phe Gly Leu Gly Tyr Asp His Lys Glu Asn Lys Phe Gly Ala Asp	
845 850 855	
tta tat att aca cgt gtg agt gag aaa aaa gcg aaa gac act tat aat	7383
Leu Tyr Ile Thr Arg Val Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn	
860 865 870	
atg ttc tat aaa gaa cag gga tat aaa gat agt gct gtt cgt tgg aga	7431
Met Phe Tyr Lys Glu Gln Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg	
875 880 885 890	
agt gat gac tat acg cta gtt gat gcg gtt ggt tat att aaa ccg att	7479
Ser Asp Asp Tyr Thr Leu Val Asp Ala Val Gly Tyr Ile Lys Pro Ile	
895 900 905	
aag aat tta acg tta cag ttt ggc gtt tat aat ttg aca gac cgt aaa	7527
Lys Asn Leu Thr Leu Gln Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys	
910 915 920	
tac ttg aca tgg gaa tct gct cgt tcg att aaa cca ttt ggt aca agt	7575
Tyr Leu Thr Trp Glu Ser Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser	
925 930 935	
aat tta att aat caa aaa aca ggc gca gga att aat cgt ttt tac tca	7623
Asn Leu Ile Asn Gln Lys Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser	
940 945 950	
cca ggt cgt aac ttt aaa ctc agt gcc gaa atc acc ttc taatcctaag	7672
Pro Gly Arg Asn Phe Lys Leu Ser Ala Glu Ile Thr Phe	
955 960 965	
cctgcgtatg caggctttct ttttagggaa agtgcggtgg atttgacaaa gatttattgc	7732
ttttctgtaa atcaatgcta aaattcacac tcctttgtcg tagctggatt agagatcggc	7792
tagcgatgta tttttaactt aacttttagg agttatcaaa tgtctctaag tacagaaaaa	7852
aaagcagcaa ttgttgctga atttggtcgt gatgcaaaag ataccgggttc ttcagaagtg	7912

caaatcgcat tattaactgc acaaatcaac cacttacaat ctacttttgc aacgcacaaa 7972
aaagaccacc acggtcgtcg tggtttattg cgtatggttt ctgctcgtcg taaactttta 8032
gattacttaa aacgtactaa tcttgagctt tacacttcaa ctatcgtcg tttaggttta 8092
cgtcgtcaat ttgtattagg atttattcca aacaaaaaac ccttgataat tttatcaagg 8152
gttttctttt ttctgcatac taggcatgtt taaattatcg caaacacac cgcacatttc 8212
gtggaaaagt gcggtcattt ttttaattta ttttacttct ttaaacaatga tctcacttgg 8272
gattactgaa ccttgccagt aaagctcagt agcgactttt tcagctaatt gcataaacga 8332
ttgggcaatg tcgctttcag gtgcggcgac aacgggtggg atacctttgt ctaaactctc 8392
acgtaagcga atatgtaatg cctgttgctc taaaactttg acattatatt tttgtgcaat 8452
gcgctcagca ccgcctgttc cgaaaatcgt ttcttgatga ccacaattgc taaaaatag 8512
catcgacata ttttcgataa tgcctaaaac gggtagagaa acacgctcaa acatcgccac 8572
acctttaatc gcatccagta aagcaatatc ttgtggtgtt gtcaccacga ccgccccgt 8632
cactggaatt tgttgagaaa gggtagctg gatatcccct gtaccgggtg gcatatcaat 8692
gactaaataa tctaaatcag gccataaggt ttcttgcaaa agctgactta aggactgct 8752
tgccattgga ccgcgcaaaa tcgtagcatt gtccggttcc attaagaaac caatggaatt 8812
ggcaaaaata tgatgtgctt gaattggggg aatgtgctgg ttatctggcg aagtggggcg 8872
ttgatcagca acccctaaca tgtgtggaat agatggacca taaatatcgg catctaaaat 8932
tccaacacga gcacctgtc tttgtaaggc aagagcaaga ttgacggaaa tagtagattt 8992
tcctacacca cctttaccog atgtcacggc aataatattt tttaccctt ttacggctgg 9052
gtggctatta gcgcgtttta atgtcgcgat ttgataattt aattgccatt tgatgtcttt 9112
gcattctgct aatgtgagaa gttctgtgga gagagcgctc ttgagttgtt cgaatgcagt 9172
attccaagca aacggcatgc tgatttcaat acgtaacgtc tcaccgcctt tttcaatttt 9232
ttgatagca tttaggctga cgagatcttt ttgtaagcta ggatgttgaa attgttgaaa 9292
tgtgttttgg atagcttggt tttgactgtc cgttaaactg tcagaaaata aaattcccat 9352
tgattttata ccgttatatt tggtagctaa ttaaagccct agttaatcac tcaactatat 9412
ttaaccacga agctgtagaa ctgttaagca gaaatgtgga aaagcgcggt taaagtagaa 9472
aaaatactgc gaataaggta acataagcgc caattttttg atgaaaaata ggaatgataa 9532
catggcaaat tcggcacgag atatttttgt cacttgcgcc ttaccttatg caaatggtgc 9592
aattcattta gggcatttat tagaacatat tcaagcagat atttgggtgc gttccaacgt 9652
atgcgtgggc ataaagtga ttttatttgt gcagatgatg cccatggcac accaatcatg 9712
ttaaatacga taaattaggt attacaccaa agcattaatt gtcctcgaa agcagaacat 9772
gtggcggatt tgaaggctta atattagcta tgataatata at 9814

<210> 32

<211> 967

<212> PRT

<213> Pasteurella multocida

<400> 32

```

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

Ser Tyr Cys Gly Thr Ile Leu Ala Asp Ser His Gln Glu Ala Thr Glu
          20           25           30

Leu Asp Thr Ile Thr Val Ser Ser Gln Gln Asp Glu Met Asn Ile Lys
          35           40           45

Glu Lys Lys Ile Gly Glu Thr Val Lys Thr Ala Ser Gln Leu Lys Arg
          50           55           60

Gln Gln Val Gln Asp Ser Arg Asp Leu Val Arg Tyr Glu Thr Gly Val
          65           70           75           80

Thr Val Val Glu Ala Gly Arg Phe Gly Ser Ser Gly Tyr Ala Ile Arg
          85           90           95

Gly Val Asp Glu Asn Arg Val Ala Ile Thr Val Asp Gly Leu His Gln
          100          105          110

Ala Glu Thr Leu Ser Ser Gln Gly Phe Lys Glu Leu Phe Glu Gly Tyr
          115          120          125

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

Val Ala Lys Ile Ala Lys Gly Ala Asp Ser Val Lys Val Gly Ser Gly
          145          150          155          160

Ser Leu Gly Gly Ala Val Leu Phe Glu Thr Lys Asp Ala Arg Asp Phe
          165          170          175

Leu Thr Glu Lys Asp Trp His Ile Gly Tyr Lys Ala Gly Tyr Ser Thr
          180          185          190

Ala Asp Asn Gln Gly Leu Asn Ala Val Thr Leu Ala Gly Arg Tyr Gln
          195          200          205

Met Phe Asp Ala Leu Ile Met His Ser Lys Arg His Gly His Glu Leu
          210          215          220

Glu Asn Tyr Asp Tyr Lys Asn Gly Arg Asp Ile Gln Gly Lys Glu Arg
          225          230          235          240

Glu Lys Ala Asp Pro Tyr Thr Ile Thr Lys Glu Ser Thr Leu Val Lys
          245          250          255

Phe Ser Phe Ser Pro Thr Glu Asn His Arg Phe Thr Val Ala Ser Asp
          260          265          270

Thr Tyr Leu Gln His Ser Arg Gly His Asp Leu Ser Tyr Asn Leu Val
          275          280          285

Ala Thr Thr His Ile Gln Leu Asp Glu Lys Glu Ser Arg His Ala Asn
          290          295          300

```

Asp Leu Thr Lys Arg Lys Asn Val Ser Phe Thr Tyr Glu Asn Tyr Thr
 305 310 315 320
 Val Thr Pro Phe Trp Asp Thr Leu Lys Leu Ser Tyr Ser Gln Gln Arg
 325 330 335
 Ile Thr Thr Arg Ala Arg Thr Glu Asp Tyr Cys Asp Gly Asn Glu Leu
 340 345 350
 Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu Gln Phe Lys Asp Gly Gln
 355 360 365
 Ile Leu Asp Pro Ala Gly Asn Lys Ile Lys Leu Gln Gly Ser Gly Leu
 370 375 380
 Ser Thr Gln Ile Val Asp Glu Asn Gly Lys Pro Phe Pro Thr Thr Thr
 385 390 395 400
 Gly Thr Asn Asn Ala Ala Phe Ser Asn Asn Leu Arg Leu Arg Pro Thr
 405 410 415
 Gly Phe Trp Leu Asp Cys Ser Val Phe Asp Cys Asn Lys Pro Phe Thr
 420 425 430
 Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln Ala Arg Glu Val Leu Leu
 435 440 445
 Ser Glu Glu Ile Thr Val Asp Gly Lys Leu Tyr Lys Thr Ala Lys Glu
 450 455 460
 Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr
 465 470 475 480
 Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu Asn Thr Asn Thr Lys Gln
 485 490 495
 Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn
 500 505 510
 Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg Ile Glu Lys Glu Met Ile
 515 520 525
 Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro Thr Trp Trp Ala Asp Arg
 530 535 540
 Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr Asn Ala Leu Lys Cys Pro
 545 550 555 560
 Lys His Glu Pro Leu Thr Ser Phe Leu Ile Pro Val Glu Ala Thr Thr
 565 570 575
 Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser
 580 585 590
 Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr
 595 600 605
 Thr Pro Gly Val Thr Pro Lys Ile Pro Asp Asp Met Val Lys Gly Leu
 610 615 620
 Phe Ile Pro Met Pro Lys Glu Pro Gln Leu Lys Asp Phe Asp Tyr Asn
 625 630 635 640

Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro
 645 650 655
 Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile Ala Gln Asp Lys Thr Phe
 660 665 670
 Lys Lys His Ser Tyr Ser Leu Gly Ala Thr Phe Asp Pro Leu Asn Phe
 675 680 685
 Leu Arg Val Gln Val Lys Tyr Ser Lys Gly Phe Arg Ala Pro Thr Ser
 690 695 700
 Asp Glu Leu Tyr Phe Thr Phe Lys His Pro Asp Phe Thr Ile Leu Pro
 705 710 715 720
 Asn Pro Val Leu Lys Pro Glu Glu Ala Lys Asn Gln Glu Ile Ala Leu
 725 730 735
 Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr
 740 745 750
 Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu
 755 760 765
 Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr
 770 775 780
 Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn
 785 790 795 800
 Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn
 805 810 815
 Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly Arg Leu Asp Gly Asp Arg
 820 825 830
 Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr
 835 840 845
 Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val
 850 855 860
 Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln
 865 870 875 880
 Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu
 885 890 895
 Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln
 900 905 910
 Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser
 915 920 925
 Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys
 930 935 940
 Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser Pro Gly Arg Asn Phe Lys
 945 950 955 960
 Leu Ser Ala Glu Ile Thr Phe
 965

<400>	33																	
gtcaacccct	ttggctttga	gttgtgctaa	taaagcatcg	tcaaaatgca	agccggcagt	60												
tggtgccgca	accgcgccag	ggactttgtt	ataaacggtt	tgataacggt	ctttatccgc	120												
ttcttcgtca	gggcgatcaa	tataaggggg	caatggcata	tgcccaattt	gctgtaacac	180												
gtctaaaagt	gcggtctgtt	tttgcgcat	ttctaattca	aataaggtat	catggcgcgc	240												
aaccatgatc	attttgacac	catgatgttc	acctaactta	tcttcgccta	accacagttc	300												
tgcccttct	ttcggtgctt	ttgaggagcg	cacatgggct	aaaaagcgtg	tgtcggataa	360												
aatccgctcg	accaacactt	ccaccttacc	gccactggct	ttacgtccaa	acatccttgc	420												
aggaatcacg	cgcgtgttat	taaaaattaa	taagtgcct	tcatgaattt	gatcaaggat	480												
atcagcaaaa	gtgcggtggg	taatctcacc	attttcgccg	ttaagttgta	ataagcgact	540												
agcggtgcca	tccggttttg	ggtaacgagc	aatcagctca	tcgggtaaat	caaaataaaa	600												
gtcagaaaaca	cgcataaata	gggttataaa	aagttatcta	aaaaatcgtg	ggcgtaagtc	660												
tagtgtgaat	tccgctcttg	cacaaggaaa	aatccagatt	ttgttgttta	gtatcgaatt	720												
gagatgattt	tggacaaaaa	aaaagccctt	tcaagaaaga	cgaaagggcg	aaaatatatt	780												
tggagtcata	ctttttaggg	tatgtgtcgg	attatacaca	caaaaataac	aatgcaaca	840												
tttttttaac	aatcatatgt	aagcgtattg	tgtgagaacg	agcgtaaaaa	tgaacgcatt	900												
ctaaaggatg	atztatttag	cctattaaaa	aaacacatga	gatgagagtt	tgcgagagcg	960												
gtaataaaaag	tgcggtgggt	tttagaaaag	ttttgaatag	gatcacaaat	taaacaaagt	1020												
ttgtgaaata	ccaagtagta	gtttttaagt	atatgatgaa	tcatatgcta	aagtttaaac	1080												
ccgttaaata	accaagaggt	ggaag	atg	aca	gaa	gaa	aat	aaa	gga	aag	aga	1132						
			Met	Thr	Glu	Glu	Asn	Lys	Gly	Lys	Arg							
			1				5											
tat	ttt	tta	tgg	ttc	ata	ttg	ttt	atc	ctt	tca	atc	tat	tta	ttt	att	1180		
Tyr	Phe	Leu	Trp	Phe	Ile	Leu	Phe	Ile	Leu	Ser	Ile	Tyr	Leu	Phe	Ile			
10					15					20					25			
acc	ata	caa	gaa	aga	cga	ggg	tat	tgt	ttt	gac	aaa	cgt	gca	tat	att	1228		
Thr	Ile	Gln	Glu	Arg	Arg	Gly	Tyr	Cys	Phe	Asp	Lys	Arg	Ala	Tyr	Ile			
					30				35						40			

cat gag ctt tat act gag caa gag tta att gat cgg ggg att gaa tat	1276
His Glu Leu Tyr Thr Glu Gln Glu Leu Ile Asp Arg Gly Ile Glu Tyr	
45 50 55	
gtg gta tcc acc atg ccg tca ggt gtt att aaa cca gat ggc aca ata	1324
Val Val Ser Thr Met Pro Ser Gly Val Ile Lys Pro Asp Gly Thr Ile	
60 65 70	
aaa gaa gta aag cgt tac acg agt gtc gag gag ttt aaa cag atg aac	1372
Lys Glu Val Lys Arg Tyr Thr Ser Val Glu Glu Phe Lys Gln Met Asn	
75 80 85	
cca gct tgt tgt aca tta acc acc ttt att gat gaa gga ggc gat ggc	1420
Pro Ala Cys Cys Thr Leu Thr Thr Phe Ile Asp Glu Gly Gly Asp Gly	
90 95 100 105	
tat cca gat gat gat gga tat ggt tat gtc aga att gaa tat tta aga	1468
Tyr Pro Asp Asp Asp Gly Tyr Gly Tyr Val Arg Ile Glu Tyr Leu Arg	
110 115 120	
cat tat gtt gag aat cta aaa cct tat cat aga gtg att tat ctt gaa	1516
His Tyr Val Glu Asn Leu Lys Pro Tyr His Arg Val Ile Tyr Leu Glu	
125 130 135	
tat acg ccc tgt gga gag tta agg gaa gag gcg gct ttt tca aaa aat	1564
Tyr Thr Pro Cys Gly Glu Leu Arg Glu Glu Ala Ala Phe Ser Lys Asn	
140 145 150	
taagagtgag gtgaagaaat ggcattacca acagcaacaa taatgaggaa tttatcttta 1624	
tctaaaaatc aattcactct gaaagggatg gaatgcgtag attccctatt tcaagcatgc 1684	
agtaatatgg atcatgggta ctgaggtgga agatggcaga agaaaataaa ggaaagagat 1744	
atTTTTtatg gttcatattg tttatccttt caatctattt atttattacc atacaagaaa 1804	
gacgaggtta ttgttttgac aaatgggaat atatccataa cctttatacc gagcaagagt 1864	
tgatcgatag aggggttgaa tatgtggtat ccaccatgcc gtcagggtgtt tttgaaccag 1924	
atggcacaac aaccgaaata aaacgttatg ctagtgttga ggagtttaaa cagatgaacc 1984	
ctgattgttg taaattaaca agatttatta atgaaggaat agatggctat ccagatgatg 2044	
atggatatgg ttatataaga attgaatatt taagacatta tgttgggaaat tttaaacctg 2104	
atcatagagt gctttatctc gaataacgc cttgtggaga attaagggaa gaggtttctt 2164	
tttaaaaaat aaataatagt gaggtgaaga aatggcatta ccaacagcaa cagaaatcac 2224	
aaatgcatat ttatataaaa ataaattaac tcctaaagcg gaggaaagag tagattcaat 2284	
acaaattctt gaaaaaggag atgaacattt cgaagtaaatt ttttaattgat caaagtactc 2344	
tattgattga aggaaaaaca gtggaattaa tggcagggtat ggcagtttct gcggaaatta 2404	
aaacaggtaa acgcagtgtg ttagattact tatttagccc attaaaaacc acaaaataat 2464	
attaaggaga ataatatgtc gtataataaaa tatactgttg ctttgattac gttctcaaca 2524	
gggatctgta ttccggcaat atgctacgct ctaaattcgc tgggatacag atcctgtttg 2584	
agactatgta gaaaagacta aactttgtgt ggttaactgg gcttcggtaa aattctggaa 2644	

acaaatgggc ttaacccgcg tgatcttata ccgtgagctt tcgcttgatg aaattgccga 2704
 aattcgtcag caagtgccag aaatggaaat tgaagtgttc gtgcatgggg cattatgcat 2764
 ggcgtattct ggacgttggt tattatcagg ctatattaat aaacgtgatc caaatcaagg 2824
 cacctgtacc aatgcgtgcc gttgggaata cagtgttaacc gaagccaaag aagatgagat 2884
 cggcaacatt gtgaatgtgg gtgaagaaat tccagtgaat aatgtagcac cgacacttgg 2944
 cgaaggcgac accaccagta aagtattttt attagcagaa agtcga 2990

<210> 34
 <211> 153
 <212> PRT
 <213> *Pasteurella multocida*

<400> 34
 Met Thr Glu Glu Asn Lys Gly Lys Arg Tyr Phe Leu Trp Phe Ile Leu
 1 5 10 15
 Phe Ile Leu Ser Ile Tyr Leu Phe Ile Thr Ile Gln Glu Arg Arg Gly
 20 25 30
 Tyr Cys Phe Asp Lys Arg Ala Tyr Ile His Glu Leu Tyr Thr Glu Gln
 35 40 45
 Glu Leu Ile Asp Arg Gly Ile Glu Tyr Val Val Ser Thr Met Pro Ser
 50 55 60
 Gly Val Ile Lys Pro Asp Gly Thr Ile Lys Glu Val Lys Arg Tyr Thr
 65 70 75 80
 Ser Val Glu Glu Phe Lys Gln Met Asn Pro Ala Cys Cys Thr Leu Thr
 85 90 95
 Thr Phe Ile Asp Glu Gly Gly Asp Gly Tyr Pro Asp Asp Asp Gly Tyr
 100 105 110
 Gly Tyr Val Arg Ile Glu Tyr Leu Arg His Tyr Val Glu Asn Leu Lys
 115 120 125
 Pro Tyr His Arg Val Ile Tyr Leu Glu Tyr Thr Pro Cys Gly Glu Leu
 130 135 140
 Arg Glu Glu Ala Ala Phe Ser Lys Asn
 145 150

<210> 35
 <211> 1683
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <221> CDS
 <222> (325)..(1230)

<220>
 <223> lgtC

```

<220>
<221> misc_feature
<222> 219
<223> Xaa = any or unknown amino acid

<220>
<221> misc_feature
<222> 226
<223> Xaa = any or unknown amino acid

<220>
<221> misc_feature
<222> 269
<223> Xaa = any or unknown amino acid

<220>
<221> misc_feature
<222> 270
<223> Xaa = any or unknown amino acid

<220>
<221> misc_feature
<222> 274
<223> Xaa = any or unknown amino acid

<400> 35
atatcaaagt ctcattggcaa gaaaattaga aaagagcgat caattattat ttgcaagatt 60

tggtgtattat tcataggcta ggtgaaagat atatttttcc atgatattaa aacgattcag 120

gcagaactgg ctagcttatt acttttagat aattgtatta ttaaaagaag ctgtatgatt 180

gttattctat cattagtgga taataaatat tctttatttt ttgagagata aaaacaattc 240

atattttcaat agaaaacaga aaataaagat tatcaaaaga attatccgtc cttataaata 300

tgagtctgta ttgtgagatg atat atg aat att tta ttt gtt tct gat gat      351
                        Met Asn Ile Leu Phe Val Ser Asp Asp
                          1             5

gtt tat gct aaa cat ctg gtg gtt gcg att aaa agc att ata aat cat      399
Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
  10             15             20             25

aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat      447
Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp
                30             35             40

gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa      495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu
                45             50             55

gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt      543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val
                60             65             70

caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca      591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala
                75             80             85

gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat      639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp
  90             95             100             105

```

```

gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat 687
Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn
110 115 120

aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag 735
Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys
125 130 135

tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt 783
Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe
140 145 150

aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat 831
Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp
155 160 165

gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg 879
Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Gln Met
170 175 180 185

att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc 927
Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val
190 195 200

tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga 975
Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg
205 210 215

ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa 1023
Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu
220 225 230

aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa 1071
Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys
235 240 245

gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa 1119
Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys
250 255 260 265

ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct 1167
Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser
270 275 280

ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc 1215
Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe
285 290 295

aaa tat caa gtc tat taactattga atttttgcaa atgagataag agtatagtgc 1270
Lys Tyr Gln Val Tyr
300

tgattttcttc aaagcgaaaa ggaggaaata gcttggttcta atttattaca ataatggttg 1330

tattcatctt gattttgaag gaaagagagt gttttttgta taaaagcatt ttcgtcacct 1390

aaatttacta atcctccaaa ttctcctcct cgnagaattt ctttcggacc ggtagggcag 1450

tccatggata ttacaggtgt accgcaagcc atgctttcta ggataactgt cggtaacccc 1510

tctttcaaag aggtgtgtaa aaatagctta gcatttttta ttaatggata cggattatct 1570

ttattttcta aaagaaaaca atcttcttgt agattgagtg attctatttg tttctcta 1630

```

ttttctcgac actcaccatc ccaaacaata tatantnttt cttggatacc tcc 1683

<210> 36
 <211> 302
 <212> PRT
 <213> Pasteurella multocida

<220>
 <221> misc_feature
 <222> 219
 <223> Xaa = any or unknown amino acid

<220>
 <221> misc_feature
 <222> 226
 <223> Xaa = any or unknown amino acid

<220>
 <221> misc_feature
 <222> 269
 <223> Xaa = any or unknown amino acid

<220>
 <221> misc_feature
 <222> 270
 <223> Xaa = any or unknown amino acid

<220>
 <221> misc_feature
 <222> 274
 <223> Xaa = any or unknown amino acid

<400> 36
 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
 1 5 10 15
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
 20 25 30
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 35 40 45
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
 85 90 95
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
 100 105 110
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
 115 120 125
 Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
 130 135 140

```

Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
145                      150                      155                      160

Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
                      165                      170                      175

Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
                      180                      185                      190

Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
                      195                      200                      205

Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Xaa Gln Tyr His Lys Gly
210                      215                      220

Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
225                      230                      235                      240

Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
                      245                      250                      255

His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
                      260                      265                      270

Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
275                      280                      285

Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
290                      295                      300

```

```

<210> 37
<211> 2029
<212> DNA
<213> Pasteurella multocida

```

```

<220>
<221> CDS
<222> (2)..(499)

```

```

<220>
<223> mglB

```

```

<220>
<221> misc_feature
<222> 33
<223> Xaa = any or unknown amino acid

```

```

<220>
<221> misc_feature
<222> 99
<223> Xaa = any or unknown amino acid

```

```

<220>
<221> misc_feature
<222> 101
<223> Xaa = any or unknown amino acid

```

```

<220>
<221> misc_feature
<222> 928
<223> n = A or T or G or C

```

<220>
 <221> misc_feature
 <222> 1007
 <223> n = A or T or G or C

<220>
 <221> misc_feature
 <222> 1740
 <223> n = A or T or G or C

<220>
 <221> misc_feature
 <222> 1808
 <223> n = A or T or G or C

<220>
 <221> misc_feature
 <222> 1816
 <223> n = A or T or G or C

<220>
 <221> misc_feature
 <222> 1820
 <223> n = A or T or G or C

<400> 37
 c tta aat aaa gcc ggt aaa att caa tac gtt tta tta aaa ggt aac caa 49
 Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
 1 5 10 15
 gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97
 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
 20 25 30
 nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
 35 40 45
 tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193
 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
 50 55 60
 tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
 65 70 75 80
 gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
 85 90 95
 atc ttc ngg gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
 100 105 110
 ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385
 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
 115 120 125
 gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433
 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
 130 135 140

gaa ggc aca aaa tgg cag tta aaa cga tgg tgt cct acg tat ccc tta 481
 Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
 145 150 155 160

tgt tgg tgt gga tgc gga taacttaaag gagttcctaa aataataaac 529
 Cys Trp Cys Gly Cys Gly
 165

tataacaaaa caagamgttg taattctcgg ggaggtatac cctccccctt tttatgtgag 589
 gttggatatg acaactcaaa ttccaaatca agacagtga atactgctca caatgaccaa 649
 cgtctgtaaa tcctttcccg gtgttaaagc gttagacaat gcaaacctaa ctgtgcgctc 709
 gcattctgtc catgccttaa tgggcaaaaa tggggcgggc aaatcgacct tattaataatg 769
 cttatttggt atttacagta aagatgaagg tgacatcctt ttcttaggca agccagtcaa 829
 ctttaaaacg tcgaaagaag ccttagagaa cgggattttc atggtgcacc aagaacttaa 889
 cttgggttaa caatgtactg taatggataa tcctttggnt aggacgttat ccattaaaag 949
 caggctttgt cgatcacggc aaaatgtatc gtgataccaa agcagatttt tgaagaanta 1009
 gatatcgata tcgatccaaa agaaaaagtg gccaaattgt cagtgtcaca aatgcaaatg 1069
 atcgagatcg caaaggcctt ttcatacaat gccaaaatcg taatcatgga cgaaccgact 1129
 tcttcgcttt cagaaaaaga agttgaacac ctatttaaaa ttatcgcgaa gctaaaacaa 1189
 cgtggctgtg gcattattta ttttcgcac aaaatggacg aaatcttcaa aatttgtgac 1249
 gaaattacga ttttacgcga tggtaaatgg atcaatacgg tcgctgttaa aggaccaca 1309
 atggatcaga ttgtatccat gatggttggg cgtgaactca cgcaacgttt cccacaaaaa 1369
 accaataccc caaaagaaac catcttaacg gtggaaaatc tgaccgcact taatcagcca 1429
 tctattcaag atgttagttt tgaattacgc aaaggcgaag tgctcgccat tgcgggactg 1489
 gttggggcaa aacggtaccg atattgtgga aacgatcttc ggggtgcgtg aacgtaaatc 1549
 tgggtgtgatt aaactacacg ataaggaat gaaaaaccgg aatgcgttcg aagccattaa 1609
 caatggtttt gccttggtca cggaagaacg tcgctctaca gggatttatg cgaatctcag 1669
 tattgagttt aactcattaa tttctaacat gaagaaatcc tatatcagca agttaggttt 1729
 attgagtaac ncaaaaatga aaagcgacac gcaatggggg cattgattcc atgaatgtga 1789
 aaacgccatc acaaaaccna tattggntca ntatctgggg ttgtaaccaa caaaaagtgg 1849
 tcattggtcg ttggttatta acccacctg aaatcttgat gttagacgaa ccaacacgtg 1909
 gtatcgacat tgggtgcgaaa tatgaaattt atcagctgat tatggagtta gccaaaaaag 1969
 ataaaggat catcatgatt tcacttaaag gccagagtta ttaggggtac tgaccgaatt 2029

<210> 38

<211> 166

<212> PRT

<213> Pasteurella multocida

```

<220>
<221> misc_feature
<222> 33
<223> Xaa = any or unknown amino acid

<220>
<221> misc_feature
<222> 99
<223> Xaa = any or unknown amino acid

<220>
<221> misc_feature
<222> 101
<223> Xaa = any or unknown amino acid

<400> 38
Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
 1             5             10             15
Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
                20             25             30
Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
      35             40             45
Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
      50             55             60
Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
      65             70             75             80
Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
                85             90             95
Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
      100             105             110
Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
      115             120             125
Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
      130             135             140
Glu Gly Thr Lys Trp Gln Leu Lys Arg Ser Cys Pro Thr Tyr Pro Leu
      145             150             155             160
Cys Trp Cys Gly Cys Gly
                165

```

```

<210> 39
<211> 2628
<212> DNA
<213> Pasteurella multocida

```

```

<220>
<221> CDS
<222> (326)..(766)

```

```

<220>
<223> mioC

```

```

<400> 39

```

```

gtcaactaga gtaaaataga cacacttaat tacattgtag aggaatcctt ttatgtcttt 60
agaaatttta gatcagtttag aagaaaaaat taacaagcg gttgaaacta tccaattact 120
tcaattggaa attgatgaat taaaagaaaa aaataaccaa tctcaacaag caaatgacgc 180
attacgcagt gaaaatgaac aactaaagag tgagcaccaa aactggcaag aacgtttacg 240
ctcattatta ggcaaaattg ataacgtata attcacttct tattaaggct tagtttttct 300
aagccttatt ttttaggaga aatta atg aaa aca aaa att tgt att atc act 352
          Met Lys Thr Lys Ile Cys Ile Ile Thr
                1                5

ggc agt acg ctt ggt ggt gca gaa tat gtt gca gaa cat att gct gaa 400
Gly Ser Thr Leu Gly Gly Ala Glu Tyr Val Ala Glu His Ile Ala Glu
  10                15                20                25

ata tta gaa caa caa gat tat cct gta cgt tta gaa cat gga cca aat 448
Ile Leu Glu Gln Gln Asp Tyr Pro Val Arg Leu Glu His Gly Pro Asn
          30                35                40

ttt gaa gaa gtg atc gat gaa aaa tgt tgg ctt gtt gtc acc tct acc 496
Phe Glu Glu Val Ile Asp Glu Lys Cys Trp Leu Val Val Thr Ser Thr
          45                50                55

cat ggt gca ggt gaa tta ccg gat aat att aaa cct ctg ttt gaa aaa 544
His Gly Ala Gly Glu Leu Pro Asp Asn Ile Lys Pro Leu Phe Glu Lys
          60                65                70

tta gca ttt cac cca aaa cag tta gct gac tta cgc ttt gcg gtg atc 592
Leu Ala Phe His Pro Lys Gln Leu Ala Asp Leu Arg Phe Ala Val Ile
          75                80                85

ggg tta ggt aat tcg gat tat gat acc ttc tgt cac gca gtg gat cat 640
Gly Leu Gly Asn Ser Asp Tyr Asp Thr Phe Cys His Ala Val Asp His
          90                95                100                105

gtg gaa caa tta ctg cta agc aaa gat gct tta caa ctg tgt gaa tcg 688
Val Glu Gln Leu Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser
          110                115                120

cta aga atg gat atg cta acc att act gat cct gaa cac acg gcc gaa 736
Leu Arg Met Asp Met Leu Thr Ile Thr Asp Pro Glu His Thr Ala Glu
          125                130                135

caa tgg ctc cca caa ttt ctc agt caa tta taatatttat tccctataca 786
Gln Trp Leu Pro Gln Phe Leu Ser Gln Leu
          140                145

atggcatatg taaatcaa atgccatttt tcatctcgat caagcataat atttaaccaa 846
tcaaatacaat attttctctg tggataacta agatcaaaac tgtataaaag ctgtttttat 906
tccctgaata agattgaatg ttttttattc tgtggataac taaagaagtt attcacagtt 966
ttttctggtg ccaaattgag atcttaacaa cttaaaaaat gatctaagtt attcatttaa 1026
aaaaagaaaa ggatcttaat cacagcacta taggatccta ataatacataa taataagatc 1086
tctttatata aaaagatcct atctttatta actcacgatc tttttcacga tcatcgta 1146
gtcttgatca aaaaagtgtt tttcatggat ccataaattt cagtagaata gccaccagc 1206

```

```

aaaaaggatc aaaagatcca taaaatccga gataaattaa caaggttact atgttttata 1266
ctgaaaatta tgatgttatt gtgatcggtg gtggacacgc aggtactgaa gctgcacttg 1326
caccggcacg catgggactc aagaccctat tattaacca taatgttgat acactagggc 1386
aaatgtcttg taatcctgcg attggtggga ttggtaaaagg ccatttagtc cgagaaattg 1446
atgcatgagg cggtttaatg gcaactgctg cggaccaagc aggaatccaa tttcgtacct 1506
taaacagcag caaaggaccg gcggtacgtg ctacacgtgc gcaagctgac cgcgttttat 1566
atcgccaagc agtacgtatt gcattagaaa atcaagaaaa tttagatatt tttcaacaag 1626
aagtgaccga tattatttta gatcaggatc gtgtctgcgg tgttgttact aaaatgggtt 1686
taaaatttca cgcaaaagca gtgattttta cagccggtac tttcctttct ggtaagatcc 1746
acattgggtt agaaaattat acaggtggac gcgcgggtga tcctgcttca gtgatgttag 1806
ccgatcggtt aagagaactg aatttacgtg tanatcggtt aaaaacgggt acaccgcccc 1866
gtattgatgc acgtactatt gatcttctca tactggctaa acaacatggc gatgaaaaat 1926
tacctgtctt ttccttcacg ggatctgttg atcaacaccc acgtcaaatt ccatgtttta 1986
ttaccatac aaatgaacaa acgcatgaag tgatccgtaa taacttacat cgcagcccaa 2046
tgtatgctgg gatcattgaa gggatcggtc cacgttattg cccttctatt gaagataaag 2106
taatgcgtt tcttgagcgt aattctcatc aaatctacct tgaacctgaa gggttgacaa 2166
acaaaacaaa gaaattgcgg atttacaaaa acaagtgcaa gcaactgcaag cagatttaag 2226
cgaaatggca aagaaaaacc gcaatcaagc gttgattgca ggtggatttg gcggtggcat 2286
tgttgacgtc ggtattgagc tcattcgctt gcaatttggg ggctaactga tggcatttga 2346
tgaaaaaaca cgtgcgctgg ttcgtcgcta ctatgtattt gagtttttat cgcttgagca 2406
atcagcaagt aaagctaaag tctcatttaa caccgcgcga cgctggaaga aagaggcggc 2466
aagcaagggc gatgactggg ataaagtgcg tgatgtacaa gtaatggcgg gcaatgagct 2526
gactgatatc aaaaaggat tgttatcggg ctttattatt caatatcgcg caaccatgga 2586
tgagattcaa aactcggatt taaaagcaca agataaagtc ga 2628

```

<210> 40

<211> 147

<212> PRT

<213> *Pasteurella multocida*

<400> 40

```

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

```

```

Glu Tyr Val Ala Glu His Ile Ala Glu Ile Leu Glu Gln Gln Asp Tyr
      20             25             30

```

```

Pro Val Arg Leu Glu His Gly Pro Asn Phe Glu Glu Val Ile Asp Glu
    35             40             45

```

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

<210> 41
 <211> 5191
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (3203) .. (4255)

<220>
 <223> mreB

<400> 41
 ctgcagtacc aaccacccaa atgttgtgct tctgctgtaa ttcacgcaaa gtgcgcgcga 60
 ggttggttac acggattaat ggcacgactt cagcggcacc acaagctact ttacgtgcga 120
 tagcgggttaa ttgggcagat ttatcttttg gtactatcac agcacacacg cccgctgcat 180
 ccgcagtagc caaacaagca cctaagttat gtggatcagt cacaccatct aacactaata 240
 gcaacggatt ggactgattt tgtaaaagcg tatctaaatc tgcttcattc aattctttcg 300
 ctggctgaac acgtgccatg atgccttggt gtacttcgcc ctctgctttt ttatcaaggg 360
 tttggcgatt aacaaattgg atagtaatac ccaaccgatg aagttcattg agcaaagggt 420
 gtaaacgttt atcgtcgcgc cctttgagtg cataaacttc aattaaacgc tctggcgcgt 480
 tgtttaaaaa ggcacttact gcatgaatgc cataaatatt ttcactcatc tactttctct 540
 ttttagctga tttcttactg gcttttttcg tggttggtga tggtttaaca acgcttggtt 600
 ttcttaccgc acttttactg gtgcttggtt tacgtttatg gcgttggttt tcgagacttt 660
 cagcgtagcg tgcatttttc ttgagcttgt ctttggtgtt tttgccttct cgtaatgggt 720
 tacgctcact cgacactaaa gaaaaatcca cttggcggtt ttcaaggcta actgcttcca 780
 cacggatttt taccttatcg ccaatgcggt agatcatacc actattttca ccgattaaac 840

gttgtcgagc gagatcaaat tggtagtagt cgttatctaa ggtagaaatg tggactaagc 900
 catcaataaa gaggtcatct aagcggacaa ataagccaaa acctgtcaca gatgaaatca 960
 cacctgtaaa ttcttcgcct acatgatctt gcatatatct gcatttttagc cagtctgcaa 1020
 catcacgagt ggcacatcgc gcccgctcgt ctgtcatgga gcagtggctc cctaatacat 1080
 ccatgtcatc aagtgtatag tgataccctc ccgtatcagt ggttctccgt ttcgagcctt 1140
 ttagtttggc taacaagtat ttaatccac gatgcaaagt caaatcagga taacggcgaa 1200
 ttggcgaagt aaaatgcgca tattcttcga gtgcaagccc aaagtgccca atattgtcag 1260
 gatgataaac ggcttgactt aacgaacgta atacatgggt tgcaataact catgatctgg 1320
 acgttcgcga atttgctcca ataatttagc gtagtctgcg gtacttggtt tactgccacc 1380
 ttcaaggctt aaaccacatt cactgaggaa ttggcggag cccgtcactt tttcttcgct 1440
 tggacccgca tgaatacggg aaagggctgg ctcttgatgt tttccataa agtttgccgc 1500
 cgcaatattg gcgaggatca tacattcttc aatgatttta tgcgcatcat tacgaataac 1560
 aggtcaatc cgttcgattc gcccatttc attaaacaca aacttacttt caatggtttc 1620
 aaagtcaatg gcgccacgtt gatgacgggc ttccactaag gcttgggtaca ttacatggag 1680
 ttcttttaaa tggggaacca gtgcttgata acgagtacaa agttcttcat cgtcctctaa 1740
 aatacgagca actttggtat aggttaagcg agcatgagag ttcattgaccg cttcataaaa 1800
 ttcattagct gtgattttac cttttgctga aacattcagc tcacagacca tacataagcg 1860
 atcgacttgt gggtttaatg aacaaagtcc attggagagg atttccggta gcataggaac 1920
 aacgcgattt gggaaatata ccgagtttcc acgcgcagt gcttcggtat caagggcagt 1980
 acgtaaacga acatagtagc tgacatcggc aatggcaacc cacagtttcc aaccgcctcc 2040
 acgttttttc tggcaaaaaa ccgcacgtc aaaatcgcg gcatcttcac catcaatggt 2100
 gactaacgga agatggcgta aatcaatacg tcttgatttg gcttcttcg gtacttcttc 2160
 actcagttta gaaacttggt tgaggaccgc gtctggaaaa acatggggaa tatcatgatt 2220
 acggatagca atttccacct ccattccctt tgccatattt tcaccgagaa tttcgcta 2280
 cattccaaca ggttggttaa atgttgcggt acgtggtttt aattcaacta caaccacttg 2340
 tcccatacga gcgccttggc ggtgttcatt cggaattaaa atgtcgcgat taattcgact 2400
 atcgtcaggc actacataac caataccatc ttctaagaaa aaacgaccaa caatctgttt 2460
 tttacgctgt tgtaagacgc ggacaatccg cacttcttgg cgaccacgac ggtcaaaacc 2520
 gctaggttgg gcgaggacat agtcaccgtg cattactcgc tgcatttggc tgttgggtat 2580
 aaaccaatcg ctgtctttac cttcgacttg taaaaacca taaccatcac gatgacctaa 2640
 tacggtccct ttttaataat ccagtttttc cggtaaagcg tagcgtttac gtttagtgaa 2700
 aaccaattgt ccgtcatttt ccattcgtct taagcgacgg cgcattggctt cttgttggtc 2760

```

ttcattttga atagcaaatg tggtcagtaa ttcttctttt gagataggtg cattatgttg 2820
acgaattgta tcaagaataa attcgcgact tgggatcggg ttctcatatt ttgcgagttc 2880
ttcttgatag tttggatctt gcaaatgtgg attgtttttg atttttgccca taatgactcc 2940
ctttgagaat ggaaatacgc attcgtttta tgacctcaag tttgacactc tgatttggtg 3000
aaagcaagta aaaaacctgt tcgtgactga aacaatctgt actcgcggga tttgtcgtgc 3060
atgaaagcgt aaagacaaag caaatttcga caatttacag aaaattctct gttataaagg 3120
tacatttttt gatacattta gcacaatttt tcaatactca aatcagagtg tccattattt 3180
aatttagttc agcgggaattc tt atg tta ttt aaa aaa att cga ggc tta ttt 3232
                        Met Leu Phe Lys Lys Ile Arg Gly Leu Phe
                        1                      5                      10

tca aat gat ctg tcc atc gat ctt ggc aca gcg aat acc tta att tat 3280
Ser Asn Asp Leu Ser Ile Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr
                        15                      20                      25

gtc aaa gga caa ggg att gtt tta gat gaa cct tct gtt gtg gcg att 3328
Val Lys Gly Gln Gly Ile Val Leu Asp Glu Pro Ser Val Val Ala Ile
                        30                      35                      40

cgc caa gaa cgt tca ggt gca tta aaa agc att gct gcg gtt ggt cgt 3376
Arg Gln Glu Arg Ser Gly Ala Leu Lys Ser Ile Ala Ala Val Gly Arg
                        45                      50                      55

gat gcc aaa tta atg tta ggc cgt aca ccg aaa agc att gca gcg att 3424
Asp Ala Lys Leu Met Leu Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile
                        60                      65                      70

cgt cct atg aaa gat ggg gtg atc gca gat ttc ttt gtg aca gaa aaa 3472
Arg Pro Met Lys Asp Gly Val Ile Ala Asp Phe Phe Val Thr Glu Lys
                        75                      80                      85                      90

atg ttg caa tat ttt att aaa caa gtg cac agc agc aat ttt atg cgt 3520
Met Leu Gln Tyr Phe Ile Lys Gln Val His Ser Ser Asn Phe Met Arg
                        95                      100                      105

cca agt cca cgt gtc tta gtt tgt gta cct gcg gga gct acg caa gtc 3568
Pro Ser Pro Arg Val Leu Val Cys Val Pro Ala Gly Ala Thr Gln Val
                        110                      115                      120

gaa cga cgt gca atc aaa gaa tct gcc att ggt gct ggg gca cgc gag 3616
Glu Arg Arg Ala Ile Lys Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu
                        125                      130                      135

gtg tac ttg att gag gaa ccg atg gcg gca gcg att ggt gct aaa tta 3664
Val Tyr Leu Ile Glu Glu Pro Met Ala Ala Ala Ile Gly Ala Lys Leu
                        140                      145                      150

cct gtt tcg act gcc aca ggt tcg atg gtg atc gat atc ggt ggt ggt 3712
Pro Val Ser Thr Ala Thr Gly Ser Met Val Ile Asp Ile Gly Gly Gly
                        155                      160                      165                      170

acg acg gaa gtt gcg gtg att tct tta aat ggc att gtg tat tcc tct 3760
Thr Thr Glu Val Ala Val Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser
                        175                      180                      185

tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat 3808

```

Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr
 190 195 200
 gta cgc aag acg ttc ggt tca att att ggg gaa ccg aca gca gag cgt 3856
 Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg
 205 210 215
 atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc 3904
 Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val
 220 225 230
 cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt 3952
 Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg
 235 240 245 250
 tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg 4000
 Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro
 255 260 265
 tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa 4048
 Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln
 270 275 280
 cca gaa cat gct gcg gat att ttt gaa cgt ggc atg gtc tta act ggt 4096
 Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly
 285 290 295
 ggc ggt gcc ctt att cgt aat att gat gtt tta ctg tca aaa gaa acc 4144
 Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Leu Ser Lys Glu Thr
 300 305 310
 ggt gtg ccg gtt atc atc gcc gat gat cct tta acc tgt gtt gcc cgt 4192
 Gly Val Pro Val Ile Ile Ala Asp Asp Pro Leu Thr Cys Val Ala Arg
 315 320 325 330
 ggt ggt ggc gag gca tta gag atg atc gat atg cac ggt ggt gat att 4240
 Gly Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile
 335 340 345
 ttt agt gac gat atc taatatgatt taaaagtgcg gtgatattag accgcacttt 4295
 Phe Ser Asp Asp Ile
 350
 tactttctctt ttattgctga caaggctagc ctaattcgta tatgaaacct atttttggaa 4355
 aagcacctcc tttagggtctt cgcttaattc tggcgatttt agcatccatt gcattgattg 4415
 ttctggacgg tcaatccaat gcgatgatta aagcacgcag tattatggaa accgcagtag 4475
 gcgggctgta ttatcttgcc aatacaccga gaacgggtatt ggatgggggtt tcagataatt 4535
 tggttgatac caataaattg caaattgaaa accgagtttt gcgtgatcaa ctgcgtgaaa 4595
 aaaatgcaga tttattgttg ttagatcaac tcaaagtaga aaatcaacgc ctgcgcttat 4655
 tgcttaattc ccctctacgt acagatgagt ataaaaaat tgctgaagtt ttaacggcag 4715
 aaactgatgt gtatcgtaag caagtcgtga ttaaccaagg acaacgtgac ggtgcttatg 4775
 tcgggcagcc gattattgat gaaaagggtta ttgttgggca acttatctcc gttggtgaaa 4835
 atacgagtcg cgttcttcta ttgacagatg tgactcattc tattccagta caagtactac 4895

gtaatgatgt ccgtttgatt gctagtggaa caggacggaa tgatgaactg agtttagatc 4955
 atgtgccgcg ttcggtcgat attgtcaaag gggatttatt agtcacttct ggattaggtg 5015
 ggcgtttttt agaaggttat cctgttgcca ttgtggaatc cgtatcacgt gatgggcaaa 5075
 attattttgc tactgtaaca gcaaagccat tagcttcgat tgaacgttta cgctatgttt 5135
 tgcttttatg gccgacgaat gaagagatgc gcaaagtcca gtctatttca cctgca 5191

<210> 42
 <211> 351
 <212> PRT
 <213> *Pasteurella multocida*

<400> 42
 Met Leu Phe Lys Lys Ile Arg Gly Leu Phe Ser Asn Asp Leu Ser Ile
 1 5 10 15
 Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr Val Lys Gly Gln Gly Ile
 20 25 30
 Val Leu Asp Glu Pro Ser Val Val Ala Ile Arg Gln Glu Arg Ser Gly
 35 40 45
 Ala Leu Lys Ser Ile Ala Ala Val Gly Arg Asp Ala Lys Leu Met Leu
 50 55 60
 Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly
 65 70 75 80
 Val Ile Ala Asp Phe Phe Val Thr Glu Lys Met Leu Gln Tyr Phe Ile
 85 90 95
 Lys Gln Val His Ser Ser Asn Phe Met Arg Pro Ser Pro Arg Val Leu
 100 105 110
 Val Cys Val Pro Ala Gly Ala Thr Gln Val Glu Arg Arg Ala Ile Lys
 115 120 125
 Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu Val Tyr Leu Ile Glu Glu
 130 135 140
 Pro Met Ala Ala Ala Ile Gly Ala Lys Leu Pro Val Ser Thr Ala Thr
 145 150 155 160
 Gly Ser Met Val Ile Asp Ile Gly Gly Gly Thr Thr Glu Val Ala Val
 165 170 175
 Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser Ser Val Arg Ile Gly Gly
 180 185 190
 Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr Val Arg Lys Thr Phe Gly
 195 200 205
 Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg Ile Lys Gln Glu Ile Gly
 210 215 220
 Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His
 225 230 235 240
 Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser

```

                245                250                255
Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala
                260                265                270
Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp
                275                280                285
Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg
                290                295                300
Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile
305                310                315                320
Ala Asp Asp Pro Leu Thr Cys Val Ala Arg Gly Gly Gly Glu Ala Leu
                325                330                335
Glu Met Ile Asp Met His Gly Gly Asp Ile Phe Ser Asp Asp Ile
                340                345                350

```

<210> 43
 <211> 2172
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(1464)

<220>
 <223> pnp

```

<400> 43
acc cgc gtt ggg att ggg tgg cac ctg aac cca aat acc gcg tta att 48
Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile
  1                5                10                15

gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc gaa gca tac cgt 96
Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
                20                25                30

atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct 144
Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
                35                40                45

gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc 192
Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
                50                55                60

agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc 240
Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
                65                70                75                80

gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca 288
Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
                85                90                95

gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt 336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
                100                105                110

aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct 384

```

Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	Gly	Glu	Thr	Gln	Ala	Leu	Ala		
		115					120					125					
gtc	gcg	aca	tta	ggt	aca	gaa	cgt	gat	gca	caa	att	att	gat	gaa	tta	432	
Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp	Ala	Gln	Ile	Ile	Asp	Glu	Leu		
		130					135				140						
aca	ggt	gag	cgt	tca	gat	cac	ttc	tta	ttc	cac	tac	aac	ttc	ccg	cca	480	
Thr	Gly	Glu	Arg	Ser	Asp	His	Phe	Leu	Phe	His	Tyr	Asn	Phe	Pro	Pro		
		145				150				155					160		
tat	tct	gtg	ggt	gaa	acc	ggt	atg	att	ggt	tca	cca	aaa	cgt	cgt	gaa	528	
Tyr	Ser	Val	Gly	Thr	Gly	Met	Ile	Gly	Ser	Pro	Lys	Arg	Arg	Glu			
			165					170					175				
att	ggt	cat	ggt	cgt	tta	gcg	aaa	cgc	ggt	gta	gct	gca	gtg	atg	cca	576	
Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg	Gly	Val	Ala	Ala	Val	Met	Pro		
			180					185					190				
aca	ctt	gcc	gag	ttc	ccg	tat	gtg	gta	cgt	gtt	gtc	tct	gaa	atc	aca	624	
Thr	Leu	Ala	Glu	Phe	Pro	Tyr	Val	Val	Arg	Val	Val	Ser	Glu	Ile	Thr		
		195					200					205					
gaa	tca	aat	ggt	tct	tct	tct	atg	gca	tcg	gtt	tgt	ggt	gcg	tct	tta	672	
Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys	Gly	Ala	Ser	Leu		
		210					215				220						
gca	tta	atg	gat	gcg	ggt	gta	cca	att	aaa	gcg	gcg	gtt	gca	ggt	att	720	
Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile	Lys	Ala	Ala	Val	Ala	Gly	Ile		
		225			230				235						240		
gca	atg	ggc	tta	gtc	aaa	gaa	gac	gaa	aaa	ttt	gtg	gtg	ctt	tca	gac	768	
Ala	Met	Gly	Leu	Val	Lys	Glu	Asp	Glu	Lys	Phe	Val	Val	Leu	Ser	Asp		
			245						250					255			
atc	tta	ggt	gat	gaa	gat	cac	tta	ggt	gac	atg	gac	ttc	aaa	gtc	gcg	816	
Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	Asp	Met	Asp	Phe	Lys	Val	Ala		
			260					265					270				
ggt	aca	cgt	acg	ggt	gtg	acg	gca	tta	caa	atg	gat	atc	aaa	atc	gaa	864	
Gly	Thr	Arg	Thr	Gly	Val	Thr	Ala	Leu	Gln	Met	Asp	Ile	Lys	Ile	Glu		
		275					280					285					
ggt	atc	aca	gca	gaa	atc	atg	caa	att	gcg	tta	aac	caa	gcg	aaa	agc	912	
Gly	Ile	Thr	Ala	Glu	Ile	Met	Gln	Ile	Ala	Leu	Asn	Gln	Ala	Lys	Ser		
		290				295					300						
gca	cgt	tta	cac	att	tta	ggt	gtg	atg	gag	caa	gcg	atc	cca	gcg	cca	960	
Ala	Arg	Leu	His	Ile	Leu	Gly	Val	Met	Glu	Gln	Ala	Ile	Pro	Ala	Pro		
		305			310				315						320		
cgt	gcg	gat	att	tct	gat	ttt	gca	ccg	cgt	att	tac	act	atg	aaa	att	1008	
Arg	Ala	Asp	Ile	Ser	Asp	Phe	Ala	Pro	Arg	Ile	Tyr	Thr	Met	Lys	Ile		
			325					330						335			
gat	ccg	aag	aaa	atc	aaa	gat	gtg	atc	ggt	aaa	ggt	ggt	gca	acc	att	1056	
Asp	Pro	Lys	Lys	Ile	Lys	Asp	Val	Ile	Gly	Lys	Gly	Gly	Ala	Thr	Ile		
			340				345						350				
cgt	gcc	tta	aca	gaa	gaa	aca	ggt	acc	tca	att	gat	atc	gat	gat	gat	1104	
Arg	Ala	Leu	Thr	Glu	Glu	Thr	Gly	Thr	Ser	Ile	Asp	Ile	Asp	Asp	Asp		
		355					360					365					

```

ggt acg gtg aag att gct gcg gtt gat ggc aat tca gca aaa gag gtg 1152
Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
370 375 380

atg gcg cgt att gaa gat att act gca gaa gtt gaa gcg ggt gca gtg 1200
Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
385 390 395 400

tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct 1248
Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
405 410 415

atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa 1296
Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
420 425 430

gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg 1344
Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

act gtt aaa gtg gtt gag att gat cgt caa ggt cgt att cgt tta acc 1392
Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
450 455 460

atg aaa gaa gtt gca cca aag caa gaa cac gtt gat tct gtt gtc gca 1440
Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465 470 475 480

gac gtt gcc gca gaa gaa aac gca taagcaataa acaccaacgc ccttcgtgat 1494
Asp Val Ala Ala Glu Asn Ala
485

aaagggcggtt ggtgtgcatg ttgataagta caatttgtgc tttaaggcga agcgaaatga 1554
agcaatttca tccgtgggta aagtgcctgc taattttccc attttgggta tggtgtttaa 1614
cagcttgtgt taatcatgaa caagtttttc tttcaaaaga gaaattaatg ttagcagagc 1674
aacatccgaa tgatcatctt gagcatgagg tgatgggtgc gcaaattagc gaattgttac 1734
ttgttaaagg gttaaaaaaa gaagaacgtg cgattttaca ttttgagcga ggcgtgctgt 1794
acgatagctt aggattgtgg gcattggcgc gttatgattt tgaccaaaca ttagcgttgt 1854
atccaaagtt ggcagcagcg tttaattatt taggtttata tttattgtta gaggaagatt 1914
acagcgcata tctagatata tttaatgtgt tgtttgaact tgatcctcaa tatgagtatg 1974
cattcctaaa tagagggcta aatttttatt acgtcggacg ttatgaatta gctcagcggg 2034
attttcttca attttatcaa gccgataaat cagatccata ccgcacttta tggctttatt 2094
taaatgaatt aaagcataat cctcaggatg cttctaaaaa tcttgctcaa cgagcaatgg 2154
ggctttctga tgaatatt 2172

```

```

<210> 44
<211> 488
<212> PRT
<213> Pasteurella multocida

<400> 44

```

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

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
 340 345 350
 Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp
 355 360 365
 Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
 370 375 380
 Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
 385 390 395 400
 Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser
 405 410 415
 Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
 420 425 430
 Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
 435 440 445
 Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
 450 455 460
 Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
 465 470 475 480
 Asp Val Ala Ala Glu Glu Asn Ala
 485

<210> 45
 <211> 633
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (2)..(631)

<220>
 <223> purF

<400> 45
 c gat ggg gtt tct gtt tat gct gcc cgt gtt cat atg gga caa cgt tta 49
 Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
 1 5 10 15
 ggt gaa aaa att gca cgg gaa tgg gcg gat gtg gat gat att gat gtg 97
 Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
 20 25 30
 gtc att cct gtg cct gaa acc tct aac gat att gct tta cgt att gcg 145
 Val Ile Pro Val Pro Glu Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala
 35 40 45
 cgc gtg tta aat aaa ccg tat cgt caa ggt ttt gtg aaa aat cgc tat 193
 Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
 50 55 60
 gta gga cgt acg ttt att atg ccg ggg cag gca ttg cga gtc agt tct 241
 Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
 65 70 75 80

```

gtt aga cgt aaa ctc aat acc att gct tca gaa ttt aaa gat aag aat 289
Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
      85                      90                      95

gtg tta tta gtt gac gac tcg att gta cgt ggt acc acg tct gaa caa 337
Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
      100                      105                      110

att gtc gaa atg gcg aga gcg gca ggt gcg aag aaa att tat ttt gcc 385
Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lvs Lys Ile Tyr Phe Ala
      115                      120                      125

tct gct gca cca gaa att cgt tat cca aat gtg tat ggt att gat atg 433
Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
      130                      135                      140

cca acc aaa aat gaa ttg atc gct tat ggt cgt gat gta gat gaa att 481
Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
      145                      150                      155                      160

gct aac tta att ggt gtg gat aaa ttg att ttc caa gat ttg gat gcg 529
Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
      165                      170                      175

tta act ggt tct gtg caa caa gaa aat cca agt att caa gac ttt gat 577
Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
      180                      185                      190

tgt tcg gtg ttt aca ggg gtt tat gtg acg ggc gat att aca cct gaa 625
Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
      195                      200                      205

tat ctg ga
Tyr Leu
      210

```

```

<210> 46
<211> 210
<212> PRT
<213> Pasteurella multocida

```

```

<400> 46
Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
  1                      5                      10                      15

Gly Glu Lys Ile Ala Arg Glu Trp Ala Asp Val Asp Asp Ile Asp Val
      20                      25                      30

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

Arg Val Leu Asn Lys Pro Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr
      50                      55                      60

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

Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
      85                      90                      95

Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
      100                      105                      110

```

Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
 115 120 125
 Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
 130 135 140
 Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
 145 150 155 160
 Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
 165 170 175
 Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
 180 185 190
 Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
 195 200 205
 Tyr Leu
 210

<210> 47
 <211> 4788
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <221> CDS
 <222> (1)..(876)

<220>
 <223> rci

<220>
 <223> Nucleotide at position 3084 is A, T, G, or C.

<400> 47
 gac gag gag aga aaa tta gct gat ttg gca aaa ggt atc gct cca gat 48
 Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp
 1 5 10 15
 att att ttt aga gat gta ata gaa cgc tat caa aat gaa gtg tct ata 96
 Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
 20 25 30
 act aaa aaa ggc gcg cga aat gaa att ata aga tta aac cgc ttt tta 144
 Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
 35 40 45
 aga tat gat att tct aat ctg tat att cgt gat tta aga aaa gaa gat 192
 Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
 50 55 60
 ttt gag gag tgg atc aga att cgc cta acc gaa gta tcg gat gct agc 240
 Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
 65 70 75 80
 gtt aga cgt gag ctt gtt act ata tcg tca gtg ctg aca aca gca ata 288
 Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
 85 90 95
 aat aag tgg gga tat att tca agg cat cca atg act ggt att gaa aaa 336

Asn	Lys	Trp	Gly	Tyr	Ile	Ser	Arg	His	Pro	Met	Thr	Gly	Ile	Glu	Lys		
			100					105					110				
cca	aaa	aac	tcg	gca	gaa	aga	aaa	gaa	cga	tat	tca	gaa	cag	gac	att	384	
Pro	Lys	Asn	Ser	Ala	Glu	Arg	Lys	Glu	Arg	Tyr	Ser	Glu	Gln	Asp	Ile		
		115					120					125					
aaa	aca	ata	tta	gaa	aca	gct	aga	tat	tgt	gaa	gat	aaa	cta	ccc	ata	432	
Lys	Thr	Ile	Leu	Glu	Thr	Ala	Arg	Tyr	Cys	Glu	Asp	Lys	Leu	Pro	Ile		
		130					135					140					
aca	ctc	aaa	caa	aga	gta	gca	att	gca	atg	tta	ttt	gct	att	gaa	acc	480	
Thr	Leu	Lys	Gln	Arg	Val	Ala	Ile	Ala	Met	Leu	Phe	Ala	Ile	Glu	Thr		
		145				150				155					160		
gct	atg	cgt	gct	ggc	gag	att	gct	agt	ata	aaa	tgg	gat	aat	gtt	ttt	528	
Ala	Met	Arg	Ala	Gly	Glu	Ile	Ala	Ser	Ile	Lys	Trp	Asp	Asn	Val	Phe		
				165					170					175			
ctt	gaa	aag	aga	ata	gta	cat	tta	ccg	aca	act	aaa	aac	ggg	cac	tct	576	
Leu	Glu	Lys	Arg	Ile	Val	His	Leu	Pro	Thr	Thr	Lys	Asn	Gly	His	Ser		
			180					185					190				
aga	gat	gtg	ccg	ctt	tcg	caa	aga	gct	gtt	gcg	cta	att	tta	aaa	atg	624	
Arg	Asp	Val	Pro	Leu	Ser	Gln	Arg	Ala	Val	Ala	Leu	Ile	Leu	Lys	Met		
		195					200					205					
aaa	gag	gta	gaa	aat	gga	gat	ctt	gtg	ttt	cag	acc	acg	cct	gaa	tca	672	
Lys	Glu	Val	Glu	Asn	Gly	Asp	Leu	Val	Phe	Gln	Thr	Thr	Pro	Glu	Ser		
		210				215					220						
tta	agc	acc	acg	ttt	aga	gtg	tta	aag	aaa	gag	tgt	gga	ctt	gaa	cat	720	
Leu	Ser	Thr	Thr	Phe	Arg	Val	Leu	Lys	Lys	Glu	Cys	Gly	Leu	Glu	His		
					230					235					240		
ctc	cat	ttt	cat	gat	acg	aga	agg	gaa	gcg	ttg	acg	aga	tta	tct	aag	768	
Leu	His	Phe	His	Asp	Thr	Arg	Arg	Glu	Ala	Leu	Thr	Arg	Leu	Ser	Lys		
				245					250					255			
aaa	gta	gat	gta	atg	act	cta	gcc	aaa	att	agc	gga	cat	aga	gat	tta	816	
Lys	Val	Asp	Val	Met	Thr	Leu	Ala	Lys	Ile	Ser	Gly	His	Arg	Asp	Leu		
			260					265					270				
aga	att	tta	caa	aac	aca	tat	tac	gca	ccg	aat	atg	agt	gaa	gtg	gca	864	
Arg	Ile	Leu	Gln	Asn	Thr	Tyr	Tyr	Ala	Pro	Asn	Met	Ser	Glu	Val	Ala		
		275					280					285					
aac	ttg	ttg	gat	taattcactc	ttcttaaata	cgctttttgc	cacttgatta									916	
Asn	Leu	Leu	Asp														
		290															
catcgccagc	cttatatctt	ttactttcat	tacttccttt	ttctaata	gaa	actgggggatg										976	
gaaagtcttg	gcgggtaata	atatgacgag	atgtgtaatt	gtaagaacga	ttaatcatga											1036	
tagaaatgtc	ttcaatacta	agaagaactg	gactatcttc	tttaagttga	gctaaggctc											1096	
caaacctcac	agagcgtagc	acttcatctt	gttgtttctt	tgtagagaa	atattttcca											1156	
tttttacctc	acttaaataa	aaaagccgtc	atggacggct	taataaagca	tttcgctata											1216	
cagttctttt	gaggtgtacc	caatatcgaa	cttgatttga	ttgttttggt	ttgcgatttc											1276	

cagtgccttct tttcgatcaa caaatcttcc gaagttggta ataacaccct gtttcttacc 1336
aattagcggg tattgtgtac cgttctcaat agatttaatt tgtttacgca taaacatgtc 1396
atagtgtctc gcgccagtca ctaaatgaag ttcttttggt gtgtaatctt caagctcgca 1456
cgcagcgcag acgattaatt ctggacgac tcccatcttc ctatctccga gcatttttca 1516
tagcctcaaa ccaagcttgt gcgtctcctt cactgtaaaa taatgaaccg ctttctagca 1576
tttttctgtg cttatctcta ttagcatcaa aatagaatct aataattgtt gagttacctc 1636
ttttaagac ctcttgattg tgggtgtgtg ttttgattgg agcgggcaaa gtaagcggtta 1696
ctgttgggcg tggttcttcc cacattccga ctatatcaaa tggattttct aaatgcggat 1756
atgtgttatg ttcaaaaaa gaagatccat caatcgtcca agaatttctc tcaaattgtg 1816
tcttgctctt gccaatgtga aatacacctt gatataagaa agtggtgaac ggaaagaact 1876
ttgaataatc agcagttaca tatcctttac ttccatttct aagcacaact ggctcaccgg 1936
ttaatgcttt ttctaagtca aatgctttca tttttactc tccagcttgc tcatcaataa 1996
gctcatcaat ccattctcga atttcagatt ggaaattttc taacgaatta ttttcattaa 2056
aataatctgc ttcttttaac ttactcaccg ctgttttact aaagcattta taaaaagac 2116
gcttttcttc aaacaaatca tcttttgaga ttgcgcatac ttttctacg ccctctatac 2176
ttttgtcttg aataaaacta ttaaaaagaa cctcttcttg ctgcttgttt tctactaaaa 2236
tagaaatcgt atattttttt ggatattcca tttttaatcc tttcttttag ataacaaaaa 2296
accgcatttc tgcggttatt ctgtgtatct atttaaaata ttacttatag tttcagcatc 2356
ttctaagtgt aatttagaat agcttgaggt catttttctt ttaacggcaa tctcaattc 2416
ttccagcttt aagctataca agtagtcttt tttatcttta taaatacgac cgtacaccat 2476
tccggataat ttaccttctt catacccat agataaattg atctttctat ctgcaccgcg 2536
cactctaatt gttaaatatt ttcttccaat ttttaagact tcagcctcat gttcaatgtt 2596
tgagcgcag agtgtttcta aaaaatatac ggtatcgcca actttaagat ttttaatcca 2656
atctttattc ataaataccc ttatactttc ggtggcagtg gaagtgggtg ccaatgagtt 2716
actgaagata gatggtaagt acgaagagac ataaagaaaa catcatctcg ccacgcgatt 2776
tttatttccc ctctatctgt ataaatcaga atatcctctc tctcactggg caatctatct 2836
tttacactaa tccagccatc atcttgcgaa aattccacaa tttctggctt ttcaagcacc 2896
aatcagagc cgtaatcttc tttttctctc tcgctcaact gcttttctt gcagtcagcc 2956
ttgccaagga cgacaccgta cacggcataa ggtaaatcat tcaacgcaaa atcctcatga 3016
tcacacatat catctgcgaa ctcatgagct tctactgcac catctaaaca actttgctta 3076
gcttgatnta atgtttcgtg taagttaacg atatgtatgt cattagatac atctactgag 3136
aaaaattttt tttctgtttc tatcatagtt aaattcctta ttcttttatt aatgggcgag 3196

gaatcgggtg ccagtgtgta acgttaatag ctagatcata aattggacca ttctgattta 3256
 tagctacca aaaatattca ccatcagcaa tttctcttga tgcaattgcg taatgctcgc 3316
 catattcacc ttcacaaaaa gcaatgactg gtgtttcaac ttctggtaac ttgtcatcaa 3376
 cactaatcca gttgctatat tcccaatgaa aattaagctt ctcatagcca ttgatgactt 3436
 gatctaacgc aggtcttaat tgggtttctc caacaataat atgtgttggt atcttaattct 3496
 ctgggattcc atctattact tcacaccagt ttttttcaat aaagtccaat ctttttttat 3556
 ctgctaaaag actttcatat tctgcttttg tgattgttac tgtttctgtc atagttaaata 3616
 tcctcatgat aaattccatg tttatttacc ttttttctgg cacaaaaaa cacgctattg 3676
 cgtgctgtct tgattgatat aatcaattaa tctaagccca atccatttca taactggaac 3736
 agccatactg tttccaattg ctttgtatcg tggagaatca gggcattcat ctattgattt 3796
 gttgcgatat gggatttttag tgtaatcgtc tggaaatccc tgtaatcttt cactcaccg 3856
 cggcgttagt tttctaacaa ctgattctac tgataaagca acgcaaggaa cattattacc 3916
 accagttccc attcttgctt ttaagggttg tgaaatatca tcgtgaatac gacaagcttc 3976
 ttcaccctta acctcaaata gaatattttc caatcctcca tttcttccaa tgcaatgcgc 4036
 tgtattttta gaaatgattg gatcttgtga accgtgaaca acaaaagttt cactaccgcc 4096
 agcaagaact ccaccgcttg ctcttaatgt tcccgcaaca tcggatttgc gatattgagc 4156
 aaagcttgtc tcaataaagg cggcaatata ttttgcctgc gttccgctct gttcaatatt 4216
 ccctcgcacg cttttggact caatgagtat ttgtgcaaca ctctgttttc tagcacttgc 4276
 cacaagaaac actcttttac gacgttgggc aactccgaag tattgagcat cgagaactcg 4336
 ccagcagatt gttcggattg aatgcacata accagcgttc gtccatcttc tccctgtgtg 4396
 ctgcaatggc tcacactctt gaaccagtcc agccagaagg tgtccgaatg cggtgtccga 4456
 ggtggatagc acaccgggaa cgttttccca cactgagaatg cactggtggtt tgttgtcatt 4516
 gaatctaaca tagtcgatcg cttctaaaaat ttttaattaaa actaacgtga gatttcctcg 4576
 ctcatcgtct aaactttgac gattgccagc aactgaaaaa gattgacaag gaggaccacc 4636
 aactaaaacg tctggtgccg gaatttcacg atctaataat ttctgttgca attcagtcac 4696
 atcaccaaga ttgggaacgt tagggtaatg gtaagctaata actgcgcttg ggaattgctc 4756
 aatttcagaa aaccagagtg gctctgcgaa tt 4788

<210> 48

<211> 292

<212> PRT

<213> Pasteurella multocida

<400> 48

Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys Gly Ile Ala Pro Asp

1

5

10

15

```

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

```

```

<210> 49
<211> 1618
<212> DNA
<213> Pasteurella multocida

```

```

<220>
<221> CDS
<222> (2)..(1195)

```

<220>

<223> sopE

<400> 49

```

g ggc gat cta tgt ctg aaa ata tct aca tgg tgt caa agt cac aga atc 49
  Gly Asp Leu Cys Leu Lys Ile Ser Thr Trp Cys Gln Ser His Arg Ile
    1             5             10             15

aat caa gca att cgc aca att caa agt cta tca acc gca gtc atc ggt 97
Asn Gln Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly
          20             25             30

att gtc tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat 145
Ile Val Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn
          35             40             45

gaa ccc gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga 193
Glu Pro Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly
          50             55             60

aaa caa ggc acg ctt tca cgt gcg ctt gac ggg att tct gat gta gtc 241
Lys Gln Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val
          65             70             75             80

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac 289
Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
          85             90             95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc 337
Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
          100            105            110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa 385
Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
          115            120            125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac 433
Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
          130            135            140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac 481
Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
          145            150            155            160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg 529
Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
          165            170            175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg 577
Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met
          180            185            190

ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac 625
Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp
          195            200            205

tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa 673
Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu
          210            215            220

cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc 721
Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser
          225            230            235            240

```

```

ggt gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat 769
Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
245 250 255

gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat 817
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
260 265 270

ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc 865
Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
275 280 285

aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att 913
Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
290 295 300

gca ggg gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta 961
Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
305 310 315 320

gtg aaa gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc 1009
Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
325 330 335

aca aaa ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt 1057
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
340 345 350

aac agt gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat 1105
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
355 360 365

tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att 1153
Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
370 375 380

tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg 1195
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385 390 395

taaggggtag aaaatggctt taccacgcaa acttaaattg atgaatttaa tcatcgacgg 1255

taacaaatat ctggcggaag tcacggaagt gactcaacca aaattagcaa tgaaaatcga 1315

agaatttcgc gggggcggtg tgattgggtc ggtggatgac aatctcgggc ttgaaaagct 1375

cgaagcgga tttaaagccg gtggctacat ggtcgaatta attaaaaaat tcggcggggtc 1435

aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495

cacatctgtt gagcttgtga tgcaaggctg atttactgaa attgacagcg gaaacagcaa 1555

agtgggcgat gacactgaac aaacattcaa agtgccttta acgtattaca aaatcattgt 1615

tga 1618

```

```

<210> 50
<211> 398
<212> PRT
<213> Pasteurella multocida
<400> 50

```

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

Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
 340 345 350

Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
 355 360 365

Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
 370 375 380

Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

<210> 51
 <211> 353
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(351)

<220>
 <223> unknown C1

<400> 51
 atg aca tta ttt gat gaa tgt aaa tta gct ctt aga gac gat ttt aat 48
 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1 5 10 15

cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96
 Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30

tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144
 Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45

gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192
 Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60

gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240
 Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80

aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288
 Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95

gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110

gtc atc tat aaa aga ta 353
 Val Ile Tyr Lys Arg
 115

<210> 52
 <211> 117
 <212> PRT
 <213> Pasteurella multocida

<400> 52

```

Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1           5           10           15

Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
          20           25           30

Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
          35           40           45

Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50           55           60

Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65           70           75           80

Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
          85           90           95

Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
          100          105          110

Val Ile Tyr Lys Arg
          115

```

<210> 53

<211> 509

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(507)

<220>

<223> unknown C2

<400> 53

```

atg aaa aat ttt agg aat ata aat att tat agt gat tat gga aag gtt 48
Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1           5           10           15

gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96
Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
          20           25           30

cct tct tta tac ata gat tta att acg gcg cat aat gct ccg aag agt 144
Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
          35           40           45

gaa gag aat tgc ttt gaa tat tac aat gag cgt aat gag ccc acg ttt 192
Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
 50           55           60

tct tcc ttt gga ttt gaa ggg ttt gag aca gag cgg tct agc gcc tct 240
Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
 65           70           75           80

ctt gaa aat ata tat gct cag tat att tat gat gat cca atc tat ggt 288
Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
          85           90           95

```

```

tat gaa cat gtg tat tct ttt ggt agt act ggc gag gga cat ttt atc 336
Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
      100                      105                      110

tgt ttt gat tat cgt gat gat cca aaa ggt gat gaa ccc aaa atc tgt 384
Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
      115                      120                      125

atc gtg att cac gat gaa tat gat gaa aaa aca ggg aaa atg cga ctg 432
Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
      130                      135                      140

ttt cct ata gca gag aat ttt gaa gcg ttt tta gat agt ttg aaa tca 480
Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
      145                      150                      155                      160

ttt gat gaa atg ata gag aag tat tcg ta 509
Phe Asp Glu Met Ile Glu Lys Tyr Ser
      165

```

```

<210> 54
<211> 169
<212> PRT
<213> Pasteurella multocida

```

```

<400> 54
Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
  1           5           10           15

Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu
      20           25           30

Pro Ser Leu Tyr Ile Asp Leu Ile Thr Ala His Asn Ala Pro Lys Ser
      35           40           45

Glu Glu Asn Cys Phe Glu Tyr Tyr Asn Glu Arg Asn Glu Pro Thr Phe
      50           55           60

Ser Ser Phe Gly Phe Glu Gly Phe Glu Thr Glu Arg Ser Ser Ala Ser
      65           70           75           80

Leu Glu Asn Ile Tyr Ala Gln Tyr Ile Tyr Asp Asp Pro Ile Tyr Gly
      85           90           95

Tyr Glu His Val Tyr Ser Phe Gly Ser Thr Gly Glu Gly His Phe Ile
      100          105          110

Cys Phe Asp Tyr Arg Asp Asp Pro Lys Gly Asp Glu Pro Lys Ile Cys
      115          120          125

Ile Val Ile His Asp Glu Tyr Asp Glu Lys Thr Gly Lys Met Arg Leu
      130          135          140

Phe Pro Ile Ala Glu Asn Phe Glu Ala Phe Leu Asp Ser Leu Lys Ser
      145          150          155          160

Phe Asp Glu Met Ile Glu Lys Tyr Ser
      165

```

```

<210> 55
<211> 443

```

<212> DNA

<213> *Pasteurella multocida*

<220>

<221> CDS

<222> (1)..(441)

<220>

<223> unknown C3

<400> 55

```

atg ata aaa tat tta gag gga aat att aac tcg ttt ata tcg gca tta 48
Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
  1             5             10             15

ggt aaa aac gaa agt aat aaa gat att tta aaa tta gta gaa ata gtt 96
Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
             20             25             30

tct tca gat ttt gaa gtg gat gaa cta agt cat aaa gat gaa cac gag 144
Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
             35             40             45

ata tat tat ttg ttt tat aag agg ggt gtt gaa ttt tgt ttt aaa aga 192
Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
             50             55             60

ata gat gaa gag tat gtc tta tat tcg gtt ttc ttt ttc ttg gta gag 240
Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
             65             70             75             80

ggt gat aat tat ttt tca tgc cca ttt att cat gaa tta ata tgt gat 288
Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
             85             90             95

ctt aaa cac gga ttc tca ata gag gat att ata agg ttt tta ggg gag 336
Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
             100             105             110

cca aat ttt aaa ggt agt ggc tgg gta aga tat tct tat aat gga aga 384
Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
             115             120             125

aat att cat ttc gaa ttt aat gaa tct aat gaa tta tcc cag att agc 432
Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
             130             135             140

att ttt att ta 443
Ile Phe Ile
145

```

<210> 56

<211> 147

<212> PRT

<213> *Pasteurella multocida*

<400> 56

```

Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
  1             5             10             15

Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
             20             25             30

```

Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
 35 40 45
 Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
 50 55 60
 Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
 65 70 75 80
 Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
 85 90 95
 Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
 100 105 110
 Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
 115 120 125
 Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
 130 135 140
 Ile Phe Ile
 145

<210> 57
 <211> 8498
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <223> unknown C

<400> 57
 gaattcgaat taagcgagaa aattgctgaa acactagaac aaagtcaatt aaatattagt 60
 caattatcaa ttgttgaaat ttatcctttc aatgaagaac aagggatacg ttttcataat 120
 aaaagtgtgg tacaacttaa accagaagag gtggaatggg catcaatcca ttatcttttc 180
 tttgctggcg atattcagca agtcgctcat ctgcgcgaaag ccgcagaaat gggttgcgtg 240
 gtgattgata tgaaagggat ttgtgccagc ttgcaagacg tccctgtggg gataccggga 300
 gtaaatacagg aaaaattggg agatttacgt cagcgtaata ttgtgtcctt agccgatcca 360
 caagtgcacac aacttgcatt agtcacgccc tcgttgatgt caaatcacga aatcaaagac 420
 attgccgtaa cctcggttatt acctgcatct tatactaacg gagaaacggg aggtaaatta 480
 gcgggacaaa cagcgcgatt gttaaattggc attccaattg atgaaggcga acaacgttta 540
 gcttttgatg ttttccttac gcctgcatcg catttaaata tgcaaattca caagatcttt 600
 ccacaattag ataatgtcgt atttcattct atccaagtgc ctgttttcta cgggatgggg 660
 caaatgggtga gcgtattatc ggattatgca ttagatcctc aatcttgctt agcgagctgg 720
 actgacaatc cggttgatgac ttatcatgca gaaaaatatt gcaccccagt gacgaatggc 780
 gaacaggaaa tggcagaaga gcaagcagca aaattacata taagtgggtt aagtgcggtg 840
 gaaaatgggtc tacaattttg gtcgggttgc gatgaacagc gctttaatct tgctttattg 900

agtgttacgc ttgcagagtt aatttactcg caagggttatt aattttaaagtg tgtttttgca 960
cgatatTTTT atcttgaact ttgagagcgc actcgttttt gacgagtgcg tttttgttaa 1020
aacattcgtt tgaaagacag tgaatgaata gcggagttat tgataagaat caatttatac 1080
aaaagcaact gaatgttatt aatcgaggca ataaacctat tgatagtttt agttggcgcc 1140
ataatacata aactgtactt aataatatgc aatcaatacc tagaaatatt catgacgtaa 1200
tccaacatat cggggagggg attttaagtg atggtagaaa aaacatttag aaatctaaaa 1260
atatatgatg attatgggtc tgtctctcag gaaattattt ttaattttga aaaagagttt 1320
gatataaaac tccctttatc ctatatctca cttgtgaaaa agtataatgg cgtttggttt 1380
aaggaaagtg attttgaata tttatctcaa aatgggaaaa gaataataag ctcatagagt 1440
tttgatagtt ttgagacaaa agataatatc gaaccaatga ataatatatt aagacaatat 1500
atztatgatg atgaaattta tggatataag aatgtttatt ctttggtta cactggaaat 1560
ggtgactttg tctgttttga ttatcgtgat gacccaaaag gtgatgagcc caaaatctgt 1620
atcgtgattc atgatgaata tgatgaaaaa acaggcaagc gtttgttatt gcctgtggca 1680
gaaaattttg aggcattttt agatatgctt tacgattttg atgaacgcta tccgaatggt 1740
tatgaatagg tatttgttta aataatgtgt tgtatttttt aagcattatt tacaactaac 1800
attttaagtg cgggtcaattt tgaaaaagt ttgggctttg agaattgggc gcattttttt 1860
tgaaatatcc ttcaatgatg agcactaatt atggattaga taatgggaat tatcgagata 1920
tggatggtaa taaaggatgg aggctagatt ttgatcctga gaaagtgtt catgtaaaata 1980
tttttgactt tactaaaggt aaaggactag gtaaagcagt taaaaagtca ttctttttga 2040
tagtactgaa caagagtttg aaaaatttta aagcaattaa ataaggaaga taaaatgaca 2100
ttatttgatg aatgtaaatt agctcttaga gacgatttta atctaatttg tgatgaagag 2160
aaggattgtg taatggataa gttttatttc tatttcttgg aaaagaaaga ggaatttaat 2220
tttcaagatt attcatttga agaaatgtat atattttcaa aaatggaacc tgtgtatggt 2280
ttatgtgata gctctaatat acctttgttt aggagtaatt gggaattgat tatcaataat 2340
atatatgatg ttgtctgttt atctacaaaa gtattttttc tagatgatga aaagttaatg 2400
atggaattat ttctgaaga taaagtaaga gtcactata aaagataatt accccttgat 2460
cgcgctcgtg tcagcacgag ttcgctttca ttaaagctct cgttaaagac tagcactagc 2520
agtgagggtg atcgtaatca atttactgaa gaacagttaa ttaaaattaa taagaggctt 2580
gataaaatag agggatttac atggcatcat aactcacaaa gtagtcccca aaatatgtag 2640
ttaataccta caccaattca taaggctgtt cagcatatag gtgaaggcgc ttttaagtga 2700
ggaaagtgat aaaatgaaaa attttaggaa tataaatatt tatagtgatt atggaaagg 2760
tgataaggaa atttatattag aattcgaaaa tgaatttaat ataaagcttc cttctttata 2820

catagattta attacggcgc ataatgctcc gaagagtga gagaattgct ttgaatatta 2880
caatgagcgt aatgagccca cgttttcttc ctttgattt gaaggggttg agacagagcg 2940
gtctagcgc tctcttgaaa atatatatgc tcagtattt tatgatgatc caatctatgg 3000
ttatgaacat gtgtattctt ttggtagtac tggcgaggga cattttatct gttttgatta 3060
tcgtgatgat ccaaaagggtg atgaacccaa aatctgtatc gtgattcacg atgaatatga 3120
tgaaaaaaca gggaaaatgc gactgtttcc tatagcagag aattttgaag cgtttttaga 3180
tagtttgaaa tcatttgatg aaatgataga gaagtattcg taatgtctcc gttcatatct 3240
catagcgatg ctctctcccc tgattttatg gaaattttgt ttaaattagg agggcactaa 3300
aatgaaaaaa ttttatttaa tttttttatt attcctaagt ggatgttttt atcatgatgg 3360
atgtatctat actcctcaga tggtaaattg tttgttgat aaaggagata tatttccatc 3420
aatatctcgg tatcaaaagc cttatagtct agggaaaaacc aattcagaac agcgttgga 3480
ggatgttatg tttgtggag gtaaatatgg tgattataaa ttagagaata taaaaacagt 3540
ggaacaatcg gataaattac atcattgtat gacccaaaaa gggatatatcc atttaactcc 3600
cgcagaatgt ggataccaaa atcctaaatg ggataaaggc gtttgtaatt tataagtgtt 3660
ttggatttta ctttacgaat tttttttgaa aaaagttacc gcaggtatgt ttttaatcaa 3720
agcccagggtg gcgcttggtg gatgtgttat tcgcatagta gttattatgc ggaagtgcta 3780
aatgaattca ttattaaanaa tggaaatanaa gagcgtaatt agcaccgttt gcggtgagt 3840
atttaatttc tcctgatgtt atggaaatat tatttaagtt aggaggtgat taggatgaaa 3900
aagttgttat tgttcagttt attattactt taaatggat gcctatattc ttttgaagag 3960
gagtgtttta gaccgttaat tcagggtggg tcactctgct gtcataagaa taaaggagat 4020
atatttccat caatagcacg tttccaaaaa gtagagaaca tcggaaaaac tgatgccaa 4080
caacgttgga aagatgcggt tgatttgga agtaagtatg gcgatgaaga tttaatatat 4140
ataaatgata ataatttata tagcattttt cactcctgta tggttaaaaa aggatataaa 4200
aagtttcac cgcagaatg tggataccaa aatcctaaat gggataaggg tatttgtaat 4260
ttataagtg tttgaatttt actttacaaa cttttttga aaaatgttac cgctggatg 4320
tctgttttta gggataaaga ttcgttcatt ttctttaaat ttaggcacgg tataaaagag 4380
cttgattatc aaataataat atcgtgttcg tgtccacacg agtaggggtt gattaaagta 4440
ctcctcaaaa gcgagtgcta gctgtgggg aaacgggtgg aaagaaagta aagagtatat 4500
aaaccaattg accgcataac gtgcggtcaa tttctaagat ttatgagttc cagaaaaata 4560
gaccgaaaag tgcggtaaag gggtaacgaa acacaaaaaa taaaaatatg acagcaagct 4620
gtgtcattaa accccagaaa aaaacttgac cgattgttgc actgctgaaa atggcaaaaa 4680
gtaagccgat ttcatagggt agcattgcaa taaaccagat taatccactt ggatgatcac 4740

ttttcattac ggactcctta tttatggctg ataacttaac acttgatttg aaaatttaaag 4800
cagattttaa caatgcgttg agcgatttta aagcgcttaa aacggaattg caacgcgcag 4860
gcgtggagtc tatcagtaag taactcgcca gtttttgcaa tcatttatca tattcacaaa 4920
gccgtaatgc atattggaga aggttaagtg taagtgaagg aagataaaat gaaatttaga 4980
cattttggca tttattatga ttatggcgta gtttcccaag agattatttt agattttgag 5040
gaaacgtttg gtattaaatt accaaaattg tatattgagt tgatcacaaa acataattcc 5100
ccaagattga atagagatca tttcaattat tatgatttct ctacgagtga ggaagaagga 5160
acggaattta tattcaaagg atttgaaaca gaaagtaata ggcatgcgcc gccagaaaat 5220
atttatgcac aatatcttta tgatgatgaa atatatggtt atgaacatgt gtattctttt 5280
ggcagtagcg ctagtgggtga ctttgtctgt tttgattacc gagataatcc gaaaggcagt 5340
gaacctaaaa tttgtcttgt gattcatgat gaatatgatg aagaaacagg caagcattta 5400
ttgtttcctg tggcagaaaa ttttgaggta ttttagata tgctttacga ttttgatgaa 5460
cgctatccga atgggttatga ataggtattt aaataatgta ttgtattttt taagcggtat 5520
ttaataacgt ttaaagtgcg gtcaatttca aaaaagtttt gctttgagga attgaccgtt 5580
tttgatcat ggatatgatg tgagcaattg atatcctgtt tgtgttaact ggcatgtggt 5640
aaagcattcg tcaaagacga gctctagtgg tgagggacta atcatgaatg aactattgga 5700
cttttataga aatataactt tttttgaaga atatgatgaa aactcattca taggaagatg 5760
gcttgattac tcggaatgga atgataaaga atattggaaa ttagagaaaag atttactgaa 5820
aattgctcaa atgtatagaa ctactaatga agtttttcca gatattttta taggggttat 5880
gcgtatcatt gaattattaa tgatacctaa ctggaatagt tttataatat ctaattcaga 5940
aagtgttgat atttatgata gatatgaacg atttaaatat ataatttcaa tacttttcaa 6000
taataaagat gttagactag atggcttttc atatacagaa aagaatgatg atgtatttta 6060
taatgaatag aaaaattaaa agtaagctaa tttgtagaaa taataaaagt ctcgcttgta 6120
ttttttcttt gagatcgtgc ttgagtcac acgagtgcta gctgtaggca gagtgtcttg 6180
gtgattataa aaagttaagg atagtattgt tgatatgaaa gaaaagacta aatattcaat 6240
ggggaatcaa agtgataaaa aataaatttt atatttcttg gttaggattt tcaatatcat 6300
tatatgtttt gcttttatgt agagatttgt tttattctct ttatatgttt tttattatga 6360
tgtatttgtc ttaaaatttt cttttaagga ggcgtttttt actatcttta tttttattgt 6420
gctatgtttc attattcatt attcattatt cattattcat tattcattat tcattatttt 6480
atatataaat atggtaaaag gtctgaatgc caaaaaaga aaccattaag tgaaaatgta 6540
acatacaata aaaggtagta ggaataaata aaatattagg aataacagaa tgataaaata 6600
tttagaggga aatattaact cgtttatatt ggcattaggt aaaaacgaaa gtaataaaga 6660

tatttttaaaa ttagtagaaa tagtttcttc agattttgaa gtggatgaac taagtcataa 6720
agatgaacac gagatatatt atttgtttta taagaggggt gttgaatttt gttttaaaag 6780
aatagatgaa gagtatgtct tatattcggg tttctttttc ttggtagagg ttgataatta 6840
tttttcatgc ccattttatt atgaattaat atgtgatctt aaacacggat tctcaataga 6900
ggatattata aggttttttag gggagccaaa ttttaaaggt agtggctggg taagatattc 6960
ttataatgga agaaatattc atttcgaatt taatgaatct aatgaattat cccagattag 7020
cattttttatt taataattta ggattgggaa cgctctcgtg ttcacacaag tgcggtttga 7080
ttaaagcact tgtcaaaggc gagatccagc tgtgggagat ttgatagaga aatggctctc 7140
aggattgacg ttagtagagg gagcataaat caagaaaaaa catttaaaat aggaacatta 7200
ggtggtgagt aatggaaatc actcgtttta aaatcctact tattgccttg attatattag 7260
gtaatgggta tgtgtttctt ggtggaccag ctaaaaaaca attcgctata gaagcagaaa 7320
caaggcggat ttatcgctact ttaacgaaag aaattatttt tatgaatgga gaatataaac 7380
aatttgagg gcgagtattt caaggattta ctttagtcat ttctttttct cattcaagta 7440
cagaaaaccg cattaagatt ttagaaaaaa ttaaagagat gggatttgat tcaaaaaata 7500
aaacatcaaa accgagtctt catctttttt gtcaaggaga aagtggtttt ttgatcgcag 7560
aaaaacctga atttagaata gattatgaga aaaagatgac ttattgtttg gagtagcaaa 7620
ggaaggcaat gataagtgtt ttttctaatac agatttaatt taagtattaa agtgcggtca 7680
attttgaaaa cgttttactt tgaaaaattg accgtttttt tacatgagag agtgaaagta 7740
caccacctta ggcaatgtgg ttgtggataa ggtgattaag gaatacccaa atgggggtta 7800
tgaagcgagg gtgctgatcc ctaacccgaa agcgaataacc gatcctgatg cgccgaaatt 7860
tttgagagaaa aggggaaatg aaggtgtatc cacaatgttt ccaagaacat ggacagagga 7920
taggttgaaa gtggagttag agcatgcgtt taataataga gtaccaatgg aaaagtttga 7980
aaataaatgg gaagggtataa caaaatcagg cgtgaaagta gaatgggttc tggatagaaa 8040
tggtaaagtg ttgactctat tttgttaatt ttctgtgtct ttttgtaaaa aataagttgt 8100
tgaaataaca tttttctcta taatcaaatac ttaatgataa ttaatatcat taaataagaa 8160
tggtacttta gatgaggatt atatgaaaga tttatcaaaa atgacctgcc ttgaagactt 8220
acgccgtgtt gcgcaacgta aagtgcctaaa aatgttttat gactatgtag tttcaggatc 8280
ttggagcgaa agcacattgc atgccaaccg taatgatatt caagcaatta agctacgtcg 8340
acctgtggcg attttgccca tttctgcatt cagctctgca attcgctcgt tgtgctgttc 8400
tgttgcgcgc gcaagctctc ttgtcgactt gccttttcta attgggcttg ttgctcccaa 8460
taacgtgagg tcgccacatc cactttacgt agtgttga 8498

<210> 58
 <211> 5798
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <221> CDS
 <222> (2686) .. (4446)

<220>
 <223> unknown D1

<400> 58
 gtcgacaaga ataaaacgaa acagcaaata gaattagaat tactacttat taacaataat 60
 ccttttttaa agattctagc tgtttttagat aaaaatatac gtgtgaagct tttggtcaca 120
 ttattattat caggcctata ttatttatat gcagtaaaaa acgattcaaa ttttgtcata 180
 ggtttatcta ttatttttagt ttttattatt gtcattccag ggattttgac aaatgctatt 240
 ttgaaagcta aggtgaaaaa aatcatggta gatttaccag gttttattga cttagtgtgca 300
 gtaaagtgtc aaacagggat tagtattgat gcggctttta aacaagtggc aatcgatttt 360
 aagaaactta atccagatct tacttatgtg atgttaagga ttattagaaa atctgaactt 420
 acgggattat cacaagcgtt acaggatcct tcgatctcat tgccaacaac agaaataaga 480
 atgttttgta ctgttttaca acagagttta aattttgggt cttcaattta ttctcactta 540
 attcagttgt ctgcagatat caggagata caattattaa tcattgagga aaagttaggt 600
 acattatcag ctaaaatgag tatcccatgt attttgttta ttatgttccc aataatcatt 660
 ttaattctag caccaggtat aatgagggtta tttccaaatg ttttttaaatt ttaccaagaa 720
 aatcggtttt gttagttagt ctttatctgt cggttggtgt tctaccatt ctcagcaagg 780
 catgacacag aaaagtatgt catctgaaac aataacggca aaagagactt tatatgaaag 840
 tacgcaaaat tattcggcac tcatttcaact gtatcgcat gtgttgaaag ccaaagaaga 900
 tccttcaata cgctataaat tagcgaagac atactatcag cgagggtgaca gcaaatcttc 960
 tttactttat ttaacgcat tactgaatga taatacgaag cttgctacac aagcgaaaat 1020
 attacagata aaaaatctaa ttcaattaaa taatttccaa gaagcaattt ctgtcgcaaa 1080
 tgaactctta ttaaaatcac ctaatgaagg agaagtatat aatttaagag gtatcgctta 1140
 tgcgcaaaat gggaatttg tgaatgccg aaatgatatc aataaagcaa gagagtctt 1200
 tattaatgat aatgttgcta ttaataattt agccatgcta aatattatta atggcgattt 1260
 taataatgct gtttctttac tgttgccaca atatttaaatt ggcgttaaga attctcgatt 1320
 gattcataat cttgtttttg ctttagttaa aaatgggtgat cttgattatg caaaagatat 1380
 cattgttaaa gagcgtttta atacttcacc agatgattta attaatgcat tgaaaaaac 1440
 tacacatgta tcaaaagggtg taactcggta acactaagga tttgatatga aaaagtcttct 1500

```

atcaaatata aaaggaacct cgtcaattga atttgctttg acgatagcgt tctattttatt 1560
tggtgtgatg tttattttttg aattttgtcg attagcgggt gcgacagcct attgggattt 1620
agctataacg gaaagtgtca gaattgCGaa gaatgaacaa gcaattttctg gaaattatga 1680
agaagcattt aggaaagctc ttacaaagca aaaaaaatc catgatgaat cgacaattgg 1740
atatttggcg ttgttagaag ataataaatt tgatgtaaaa gtccaatatg tggattgtga 1800
taaagaaacg gaatgtatta aaaatcttct gcttaataaa tttcgccaac cacaaaaaaa 1860
tcataaagga gagttaatct ctctacggg gagtcgcgCG acttttagcac aatattcttt 1920
aacttataaa tataagttta tggtgccgtt agtattttatt cctgagtctt ggtctcaagt 1980
agtgtgaac cgtgaatttg ttgtgtaca ggaatttgag cgttctcaat ttatgttagg 2040
agcaaaacca agttctcttg ggacgaatcc atagaaaatt tactcattat ttcgagctat 2100
atatgaaaga gtcaggttta gttaaatca agcatttttg gaaaaataaa aaggcgcgag 2160
tgacgataga gttccttttt atgtcaatgt ttctgattgt gctatttgca tttctcttcg 2220
atttagtaat gttacgttct acattaggca agttagataa tgcctcatat acattagtta 2280
gtattctccg tgaacgtaca cagttgtacg atagagttgc acaaattaat attgatgatc 2340
ataagcaatt tgaagagctt gctaagaaac tgatttatgg tgatcagaat agtaataaaa 2400
ggatcgatgt tgttttagaa tattgggcac aagacggttc tggacggagg attccaaata 2460
tcattggcga ttgtacgctt tacaaaaaac tttctgattt atcctattta tctctcgcct 2520
cagaactcaa taatgaaaga aaaataccgc tttatcaaat tactctttgt gttgaaactc 2580
agggcttggt tgaacaata ttactggata agtctgagcg ttcaacgggg ctgattagat 2640
catcgtcaat gtcagtatca cgataaatta tcgttaggga acttt atg aaa aaa ctt 2697
                                     Met Lys Lys Leu
                                     1

tat tta att cgt tct tgc tat gat tca gtc aga aaa ttt tat gag aat 2745
Tyr Leu Ile Arg Ser Cys Tyr Asp Ser Val Arg Lys Phe Tyr Glu Asn
   5              10              15              20

gag cta ggt gtt tat aca gta atg act gca tta cta gca ttt cca tta 2793
Glu Leu Gly Val Tyr Thr Val Met Thr Ala Leu Leu Ala Phe Pro Leu
          25              30              35

tta gtt ttg att gga ttt acg gtt gat gga act ggg gtt gtg ctt gat 2841
Leu Val Leu Ile Gly Phe Thr Val Asp Gly Thr Gly Val Val Leu Asp
          40              45              50

aaa gca cgt tta gct caa gga atg gat caa gct gct tta gct ttg gtt 2889
Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala Leu Ala Leu Val
          55              60              65

gct gaa aac aat gac tac cga gaa aat aaa aaa cat ggt gat gtt aat 2937
Ala Glu Asn Asn Asp Tyr Arg Glu Asn Lys Lys His Gly Asp Val Asn
          70              75              80

cgg caa gta gta tcg cct caa gac aaa gca aaa ttt ggt ggt aat gaa 2985

```

Arg 85	Gln	Val	Val	Ser	Pro 90	Gln	Asp	Lys	Ala	Lys 95	Phe	Gly	Gly	Asn	Glu 100	
ttt	atg	gcg	aaa	caa	gaa	aag	cgt	aat	caa	gag	ctt	atc	cag	ggg	att	3033
Phe	Met	Ala	Lys	Gln	Glu	Lys	Arg	Asn	Gln	Glu	Leu	Ile	Gln	Gly	Ile	
			105						110					115		
gcc	aaa	ctt	tat	tta	cgt	tca	gaa	aat	gcg	aat	gct	tca	tct	gat	gca	3081
Ala	Lys	Leu	Tyr	Leu	Arg	Ser	Glu	Asn	Ala	Asn	Ala	Ser	Ser	Asp	Ala	
			120					125					130			
cca	atc	act	att	gat	aaa	cct	ttt	cat	tat	tca	tgt	gag	gag	tta	gat	3129
Pro	Ile	Thr	Ile	Asp	Lys	Pro	Phe	His	Tyr	Ser	Cys	Glu	Glu	Leu	Asp	
			135				140					145				
tta	cct	aca	gct	aat	gag	tat	gca	cgt	cgt	aaa	cct	att	gtt	tgt	gaa	3177
Leu	Pro	Thr	Ala	Asn	Glu	Tyr	Ala	Arg	Arg	Lys	Pro	Ile	Val	Cys	Glu	
	150					155					160					
gtg	caa	ggg	ggc	gtc	aat	cgt	aaa	ttt	tgg	ctt	cct	gtc	agt	gaa	tcg	3225
Val	Gln	Gly	Gly	Val	Asn	Arg	Lys	Phe	Trp	Leu	Pro	Val	Ser	Glu	Ser	
	165				170					175					180	
tta	gtt	agt	gaa	gat	aaa	ctg	aaa	aaa	gat	cga	gtt	aga	ctg	gaa	tcc	3273
Leu	Val	Ser	Glu	Asp	Lys	Leu	Lys	Lys	Asp	Arg	Val	Arg	Leu	Glu	Ser	
				185					190					195		
gat	acc	agt	tat	gcg	att	aaa	gaa	aaa	ggc	atc	gtg	att	cct	gtg	gag	3321
Asp	Thr	Ser	Tyr	Ala	Ile	Lys	Glu	Lys	Gly	Ile	Val	Ile	Pro	Val	Glu	
			200					205					210			
cta	atg	ctt	gtt	tcg	gat	tat	tct	ggg	tcg	atg	aat	agt	cat	tta	cag	3369
Leu	Met	Leu	Val	Ser	Asp	Tyr	Ser	Gly	Ser	Met	Asn	Ser	His	Leu	Gln	
		215					220					225				
gat	aaa	aac	ggg	aga	tct	cta	gga	aaa	gct	aaa	att	act	att	tta	aga	3417
Asp	Lys	Asn	Gly	Arg	Ser	Leu	Gly	Lys	Ala	Lys	Ile	Thr	Ile	Leu	Arg	
	230					235					240					
gaa	gtg	gtt	agt	gaa	att	tcg	aaa	att	tta	ttg	cca	gaa	gat	gtt	agc	3465
Glu	Val	Val	Ser	Glu	Ile	Ser	Lys	Ile	Leu	Leu	Pro	Glu	Asp	Val	Ser	
	245				250					255					260	
gaa	ggg	gtg	agc	cct	ttc	aac	cgt	att	ggc	ttt	acg	act	ttt	tct	ggc	3513
Glu	Gly	Val	Ser	Pro	Phe	Asn	Arg	Ile	Gly	Phe	Thr	Thr	Phe	Ser	Gly	
			265						270					275		
ggg	gtt	aga	caa	cgg	gat	gtc	act	gaa	ggc	tgt	gtg	ctt	cca	tat	gaa	3561
Gly	Val	Arg	Gln	Arg	Asp	Val	Thr	Glu	Gly	Cys	Val	Leu	Pro	Tyr	Glu	
			280					285					290			
gga	aaa	ata	tca	caa	act	tct	cga	aaa	tta	act	att	cgt	tat	tgg	att	3609
Gly	Lys	Ile	Ser	Gln	Thr	Ser	Arg	Lys	Leu	Thr	Ile	Arg	Tyr	Trp	Ile	
		295					300					305				
acg	ggg	aat	aat	aca	cct	tgg	aaa	ttt	aat	gct	ggg	aga	tgg	gag	aga	3657
Thr	Gly	Asn	Asn	Thr	Pro	Trp	Lys	Phe	Asn	Ala	Gly	Arg	Trp	Glu	Arg	
	310					315					320					
agt	aca	gtg	tct	ttc	cag	gag	cat	tat	aaa	ggc	tat	tat	gac	aaa	ttc	3705
Ser	Thr	Val	Ser	Phe	Gln	Glu	His	Tyr	Lys	Gly	Tyr	Tyr	Asp	Lys	Phe	
					330					335					340	

cat tct tca act tgt aga ggc tca ggg agc tct aga act tgt caa att	3753
His Ser Ser Thr Cys Arg Gly Ser Gly Ser Ser Arg Thr Cys Gln Ile	
345 350 355	
gat gca aat cct aag aaa att atg gat tat gca cta aaa att aat gac	3801
Asp Ala Asn Pro Lys Lys Ile Met Asp Tyr Ala Leu Lys Ile Asn Asp	
360 365 370	
tgg acg aca att aga gaa tta ttt aat act tat ata gat gta agt ggg	3849
Trp Thr Thr Ile Arg Glu Leu Phe Asn Thr Tyr Ile Asp Val Ser Gly	
375 380 385	
acg att gac caa att tcc cag ttt gat ggt tca aac aga cgt tat gat	3897
Thr Ile Asp Gln Ile Ser Gln Phe Asp Gly Ser Asn Arg Arg Tyr Asp	
390 395 400	
atg gtg ttt act gat gaa gaa cgg tgt ctt ggc gga aat att ggt aga	3945
Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly Asn Ile Gly Arg	
405 410 415 420	
aga aca act cga gct tgg ttt gat caa aaa aat aaa gat att aca aga	3993
Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys Asp Ile Thr Arg	
425 430 435	
gag ttg aat att gtt cgt cct tct ggt tgg act tct gca tct tcg ggg	4041
Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser Ala Ser Ser Gly	
440 445 450	
ctt ctt gtt gga gct aat atc atg atg gac gag aat aag aat cct gat	4089
Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn Lys Asn Pro Asp	
455 460 465	
gcg caa cct tcg aaa ctc ggg aca aat att caa cgt gtt atc tta gta	4137
Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg Val Ile Leu Val	
470 475 480	
tta tct gat ggt gaa gat aac tgg cca act tat agt aca tta acg act	4185
Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser Thr Leu Thr Thr	
485 490 495 500	
ctt tta aac aat ggt atg tgt gac aaa att cga gaa caa ttg ggc aag	4233
Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu Gln Leu Gly Lys	
505 510 515	
tta caa gat cca aat tta cga gag tta cca gga aga att gcg ttt gtt	4281
Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg Ile Ala Phe Val	
520 525 530	
gcg ttt ggc tat agt cca cca gca aac caa gtt gcc gct tgg aaa aaa	4329
Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala Ala Trp Lys Lys	
535 540 545	
tgt gta ggt gat caa tat tat acg gct tat tcg aaa gaa gag ttg tta	4377
Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys Glu Glu Leu Leu	
550 555 560	
gat agt ttc aaa caa att att gga ttt gaa gaa gag gtg ggg cgt tct	4425
Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Glu Val Gly Arg Ser	
565 570 575 580	
tca tct cat aaa ccg aaa ttt taagattgtc caaggataaac gctaaaaaat	4476
Ser Ser His Lys Pro Lys Phe	
585	

ctcttagcac aggctaagag atttttttat gtgtttttca aattttatct actggtgatt 4536
 ttaattcatt acataacata acttttttcgt gaataatata gaatagacaa caataagaat 4596
 taaaacgctc aaggcataga ggcttagtcg aacaaactaa gctattttgc gcgattgatt 4656
 gggatataga tggtattttca aataagcaat aaccatggta ctgagaaaga agatgagtgc 4716
 cgtaataaag tagaagcgat ttttcttttg gctgaaaggt ggtgttagcc ttttccggct 4776
 aaagaaaata gtagcaacgg caatataaag ggcgataaag agcattttgt aaatgaacca 4836
 tgttgttaca ttttgctgaa aaagaagaaa tagcccaatt cccgaacaga acaacagcgt 4896
 atcacttaag tgcggttaaga tttttaatac ttttctgtct cgccaatttt tgccgtgtaa 4956
 ttgcatcatg ccacggataa taaatagact gaggctgaga aaggcacagg caatgtgtag 5016
 ataaataaga taatatgcca tcgatttttt tcctaagata aagaaagcag tagcgaggct 5076
 actgctttta aataatatcg tatttagtga atgaatttaa ctttctgcgc tttcgaccgc 5136
 actttcgctc gcatcactct caatgtcttc ttcacgcaca tcacaaacga gttgtaatcc 5196
 aaccagtgtt tcactttcac ttgttcggat gagacgtact ccttgtgtat ttcgaccgat 5256
 aatattgatt tcgtttacgc gagtacgtac tagcgtaccg gcatcagtaa tgagcataat 5316
 ttgatcgctt tcctcaactt gtgttgctgc aacgacttta ccgttacgct cactcacttt 5376
 aatcgagatc acgcctttgg tgttacgtga tttagttggg tattccgcta attcagtacg 5436
 tttaccataa ccgttttgtg tggcggttaa aatggcgctt tcattttttg gaataacaag 5496
 tgacacgact ttatcaatat tgagatccaa ggcacatta gtattctcat cagagatctc 5556
 ttccatatcg accgcacttt catcatccga caaatcattc gttaacgcca gtttaatacc 5616
 gcgtacacct gttgctgcac gccccatggc acgcacagca ttttactaa agcgaactac 5676
 acgtccttgt gcggagaaga gcatgatttc attttgacca tcggtgatat ccacaccgat 5736
 aagttcgtct tcatcacgca agttgagtgc aataatgcct gttgaacgag gacgactgaa 5796
 tt 5798

<210> 59

<211> 587

<212> PRT

<213> Pasteurella multocida

<400> 59

Met Lys Lys Leu Tyr Leu Ile Arg Ser Cys Tyr Asp Ser Val Arg Lys
 1 5 10 15

Phe Tyr Glu Asn Glu Leu Gly Val Tyr Thr Val Met Thr Ala Leu Leu
 20 25 30

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

Val Val Leu Asp Lys Ala Arg Leu Ala Gln Gly Met Asp Gln Ala Ala

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

```

385          390          395          400
Arg Arg Tyr Asp Met Val Phe Thr Asp Glu Glu Arg Cys Leu Gly Gly
          405          410          415
Asn Ile Gly Arg Arg Thr Thr Arg Ala Trp Phe Asp Gln Lys Asn Lys
          420          425          430
Asp Ile Thr Arg Glu Leu Asn Ile Val Arg Pro Ser Gly Trp Thr Ser
          435          440          445
Ala Ser Ser Gly Leu Leu Val Gly Ala Asn Ile Met Met Asp Glu Asn
          450          455          460
Lys Asn Pro Asp Ala Gln Pro Ser Lys Leu Gly Thr Asn Ile Gln Arg
465          470          475          480
Val Ile Leu Val Leu Ser Asp Gly Glu Asp Asn Trp Pro Thr Tyr Ser
          485          490          495
Thr Leu Thr Thr Leu Leu Asn Asn Gly Met Cys Asp Lys Ile Arg Glu
          500          505          510
Gln Leu Gly Lys Leu Gln Asp Pro Asn Leu Arg Glu Leu Pro Gly Arg
          515          520          525
Ile Ala Phe Val Ala Phe Gly Tyr Ser Pro Pro Ala Asn Gln Val Ala
          530          535          540
Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys
545          550          555          560
Glu Glu Leu Leu Asp Ser Phe Lys Gln Ile Ile Gly Phe Glu Glu Glu
          565          570          575
Val Gly Arg Ser Ser Ser His Lys Pro Lys Phe
          580          585

```

```

<210> 60
<211> 5798
<212> DNA
<213> Pasteurella multocida

```

```

<220>
<221> CDS
<222> (698)..(1468)

```

```

<220>
<223> unknown D2

```

```

<400> 60
gtcgacaaga ataaaacgaa acagcaaata gaattagaat tactacttat taacaataat 60
ccttttttaa agattctagc tgttttagat aaaaatatac gtgtgaagct tttggtcaca 120
ttattattat caggcctata ttatttatat gcagtaaaaa acgattcaaa ttttgtcata 180
ggtttatcta ttatttttagt ttttattatt gtcattccag ggattttgac aaatgctatt 240
ttgaaagcta aggtgaaaaa aatcatggta gatttaccag gttttattga cttagttgca 300
gtaaatgttc aaacagggat tagtattgat gcggctttta aacaagtggc aatcgatttt 360

```

```

aagaaaactta atccagatct tacttatgtg atgttaagga ttattagaaa atctgaactt 420
acgggatttat cacaagcgtt acaggatctt tcgatctcat tgccaacaac agaaataaga 480
atgttttgta ctgttttaca acagagttaa aattttgggtt cttcaattta ttctcactta 540
attcagttgt ctgcagatat caggagagata caattattaa tcattgagga aaagttaggt 600
acattatcag ctaaaatgag tatcccattg attttgttta ttatgttccc aataatcatt 660
ttaattctag caccaggtat aatgagggtta tttccaa atg ttt ttt aaa ttt acc 715
                                Met Phe Phe Lys Phe Thr
                                1           5

aag aaa atc gtt ttt gtt agt tta gct tta tct gtc gtt ggt tgt tct 763
Lys Lys Ile Val Phe Val Ser Leu Ala Leu Ser Val Val Gly Cys Ser
                                10           15           20

acc cat tct cag caa ggc atg aca cag aaa agt atg tca tct gaa aca 811
Thr His Ser Gln Gln Gly Met Thr Gln Lys Ser Met Ser Ser Glu Thr
                                25           30           35

ata acg gca aaa gag act tta tat gaa agt acg caa aat tat tcg gca 859
Ile Thr Ala Lys Glu Thr Leu Tyr Glu Ser Thr Gln Asn Tyr Ser Ala
                                40           45           50

ctc att tca ctg tat cgc gat gtg ttg aaa gcc aaa gaa gat cct tca 907
Leu Ile Ser Leu Tyr Arg Asp Val Leu Lys Ala Lys Glu Asp Pro Ser
                                55           60           65           70

ata cgc tat aaa tta gcg aag aca tac tat cag cga ggt gac agc aaa 955
Ile Arg Tyr Lys Leu Ala Lys Thr Tyr Tyr Gln Arg Gly Asp Ser Lys
                                75           80           85

tct tct tta ctt tat tta acg cca tta ctg aat gat aat acg aag ctt 1003
Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu
                                90           95           100

gct aca caa gcg aaa ata tta cag ata aaa aat cta att caa tta aat 1051
Ala Thr Gln Ala Lys Ile Leu Gln Ile Lys Asn Leu Ile Gln Leu Asn
                                105           110           115

aat ttc caa gaa gca att tct gtc gca aat gaa ctc tta tta aaa tca 1099
Asn Phe Gln Glu Ala Ile Ser Val Ala Asn Glu Leu Leu Leu Lys Ser
                                120           125           130

cct aat gaa gga gaa gta tat aat tta aga ggt atc gct tat gcg caa 1147
Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg Gly Ile Ala Tyr Ala Gln
                                135           140           145           150

aat ggg aat ttg gtg aat gcc cga aat gat atc aat aaa gca aga gag 1195
Asn Gly Asn Leu Val Asn Ala Arg Asn Asp Ile Asn Lys Ala Arg Glu
                                155           160           165

ttc ttt att aat gat aat gtt gct att aat aat tta gcc atg cta aat 1243
Phe Phe Ile Asn Asp Asn Val Ala Ile Asn Asn Leu Ala Met Leu Asn
                                170           175           180

att att aat ggc gat ttt aat aat gct gtt tct tta ctg ttg cca caa 1291
Ile Ile Asn Gly Asp Phe Asn Asn Ala Val Ser Leu Leu Leu Pro Gln
                                185           190           195

tat tta aat ggc gtt aag aat tct cga ttg att cat aat ctt gtt ttt 1339

```



```

Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu Ile His Asn Leu Val Phe
  200                               205                               210

gct tta gtt aaa aat ggt gat ctt gat tat gca aaa gat atc att gtt 1387
Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr Ala Lys Asp Ile Ile Val
  215                               220                               225                               230

aaa gag cgt tta aat act tca cca gat gat tta att aat gca ttg aaa 1435
Lys Glu Arg Leu Asn Thr Ser Pro Asp Asp Leu Ile Asn Ala Leu Lys
                               235                               240                               245

aaa act aca cat gta tca aaa ggt gta act cgg taacactaag gatttgatat 1488
Lys Thr Thr His Val Ser Lys Gly Val Thr Arg
                               250                               255

gaaaaagttt ctatcaaata taaaaggaac ctcgtcaatt gaatttgctt tgacgatagc 1548
gttctattta tttgttgtga tgtttatttt tgaattttgt cgatttagcgg ttgcgacagc 1608
ttattgggat ttagctataa cggaaagtgt cagaattgcg aagaatgaac aagcaatttc 1668
tggaattat gaagaagcat ttaggaaagc tcttaciaag caaaaaaat tccatgatga 1728
atcgacaatt ggatatttgg cgttggttaga agataataaa tttgatgtaa aagtccaata 1788
tgtggattgt gataaagaaa cggaatgtat taaaaatctt ctgcttaata aatttcgcca 1848
accacaaaaa aatcataaag gagagttaat ctctcctacg gggagtcgcg cgacttttagc 1908
acaatattct ttaacttata aatataagtt tatgggtgccg ttagtattta ttcttgagtc 1968
ttgggtctcaa gtagtgctga accgtgaatt tgttggtgta caggaatttg agcgttctca 2028
atztatgtta ggagcaaaac caagttctct tgggacgaat ccatagaaaa ttactcatt 2088
atctcgagct atatatgaaa gagtcagggt tagttaaatt caagcatttt tggaaaaata 2148
aaaagggcgc agtgacgata gagttccttt ttatgtcaat gtttctgatt gtgctatttg 2208
catttctctt cgatttagta atgttacgtt ctacattagg caagttagat aatgcctcat 2268
atacattagt tagtattctc cgtgaacgta cacagttgta cgatagagtt gcacaaatta 2328
atattgatga tcataagcaa tttgaaaagc ttgctaagaa actgatttat ggtgatcaga 2388
atagtaataa aaggatcgat gttgttttag aatattgggc acaagacggt tctggacgga 2448
ggattccaaa tatcattggc gattgtacgc cttacaaaaa actttctgat ttatcctatt 2508
tatctcctcg ctacagaactc aataatgaaa gaaaaatacc gctttatcaa attactcttt 2568
gtgttgaaac tcagggcttg tttgaaacaa tattactgga taagtctgag cgttcaacgg 2628
ggctgattag atcatcgta atgtcagtat cacgataaat tatcgttagg gaactttatg 2688
aaaaaacttt atttaattcg ttcttgctat gattcagtca gaaaatttta tgagaatgag 2748
ctaggtgttt atacagtaat gactgcatta ctagcatttc cattattagt tttgattgga 2808
tttacggttg atggaactgg ggttggtgctt gataaagcac gtttagctca aggaatggat 2868
caagctgctt tagctttggt tgctgaaaac aatgactacc gagaaaataa aaaacatggt 2928

```

gatgttaatc ggcaagtagt atcgccctcaa gacaaagcaa aatttggtgg taatgaattt 2988
atggcgaaac aagaaaagcg taatcaagag cttatccagg gtattgccaa actttattta 3048
cgttcagaaa atgcgaatgc ttcattctgat gcaccaatca ctattgataa accttttcat 3108
tattcatgtg aggagttaga ttacctaca gctaattgagt atgcacgtcg taaacctatt 3168
gtttgtgaag tgcaaggtgg cgtcaatcgt aaattttggc ttctgtcag tgaatcgta 3228
gttagtgaag ataaactgaa aaaagatcga gttagactgg aatccgatac cagttatgcg 3288
attaaagaaa aaggcatcgt gattcctgtg gagctaattgc ttgtttcgga ttattctggt 3348
tcgatgaata gtcatttaca ggataaaaac ggtagatctc taggaaaagc taaaattact 3408
attttaagag aagtggtag tgaaatttcg aaaattttat tgccagaaga tgtagcgaa 3468
ggtgtgagcc ctttcaaccg tattggcttt acgacttttt ctggcgggtg tagacaacgg 3528
gatgtcactg aaggctgtgt gcttccatat gaaggaaaaa tatcacaac ttctcgaaaa 3588
ttaactattc gttattggat tacgggtaat aatacacctt ggaaatttaa tgctgggaga 3648
tgggagagaa gtacagtgtc tttccaggag cattataaag gctattatga caaattccat 3708
tcttcaactt gtagaggctc agggagctct agaacttgct aaattgatgc aaatcctaag 3768
aaaattatgg attatgcact aaaaattaat gactggacga caattagaga attatttaat 3828
acttatatag atgtaagtgg gacgattgac caaatttccc agtttgatgg ttcaaacaga 3888
cgttatgata tgggtgttac tgatgaagaa cgggtgtcttg gcggaaatat tggtagaaga 3948
acaactcgag cttggtttga tcaaaaaaat aaagatatta caagagagtt gaatattggt 4008
cgtccttctg gttggacttc tgcattctcg gggcttcttg ttggagctaa tatcatgatg 4068
gacgagaata agaatcctga tgcgcaacct tcgaaactcg ggacaaatat tcaactgtgt 4128
atcttagtat tatctgatgg tgaagataac tggccaactt atagtacatt aacgactctt 4188
ttaacaatg gtatgtgtga caaaattcga gaacaattgg gcaagttaca agatccaaat 4248
ttacgagagt taccaggaag aattgcgttt gttgcgtttg gctatagtcc accagcaaac 4308
caagttgccg cttggaaaaa atgtgtaggt gatcaatatt atacggctta ttcgaaagaa 4368
gagttgttag atagtttcaa acaaattatt ggatttgaag aagaggtggg gcgttcttca 4428
tctcataaac cgaaatttta agattgtcca aggataacgc taaaaaatct cttagcacag 4488
gctaagagat ttttttatgt gtttttcaaa ttttatctac tggtgatttt aattcattac 4548
ataacataac ttttctgtga ataatacaga atagacaaca ataagaatta aaacgctcaa 4608
ggcatagagg cttagtcgaa caaactaagc tattttgctg gattgattgg gatatagatg 4668
ttatttcaaa taagcaataa ccatggtact gagaaagaag atgagtgccg taataaagta 4728
gaagcgattt ttcttttggc tgaaaggtgg tgtagcctt tttcggctaa agaaaatagt 4788
agcaacggca atataaaggg cgataaagag cattttgtaa atgaaccatg ttgttacatt 4848

ttgctgaaaa agaagaaata gcccaattcc cgaacagaac aacagcgtat cacttaagtg 4908
 cggtaagatt tttataactt ttctgtctcg ccaatttttg cctgttaatt gcatcatgcc 4968
 acggataata aatagactga ggctgagaaa ggcacaggca atgtgtagat aaataagata 5028
 atatgccatc gatttttttc ctaagataaa gaaagcagta gcgaggctac tgcttttaaaa 5088
 taatatcgta tttagtgaat gaatttaact ttctgcgctt tcgaccgcac tttcgtctgc 5148
 atcactctca atgtcttctt catcgacatc acaaacgagt tgtaatccaa ccagtgtttc 5208
 actttcactt gttcggatga gacgtactcc ttgtgtatth cgaccgataa tattgatttc 5268
 gtttacgcga gtacgtacta gcgtaccggc atcagtaatg agcataatth gatcgctttc 5328
 ctcaacttgt gttgctgcaa cgactttacc gttacgctca ctacttttaa tcgagatcac 5388
 gcccttggtg ttacgtgatt tagttgggta ttccgctaatt tcagtacgtt taccataacc 5448
 gttttgtgtg gcgggttaaaa tggcgccttc attttttga ataacaagt acacgacttt 5508
 atcaatattg agatccaagg catcattagt attctcatca gagatctctt ccatatcgac 5568
 cgcactttca tcatccgaca aatcattcgt taacgccagt ttaataccgc gtacacctgt 5628
 tgctgcacgc cccatggcac gcacagcatt ttcactaaag cgaactacac gtccttgtgc 5688
 ggagaagagc atgatttcat tttgaccatc ggtgatatcc acaccgataa gttcgtcttc 5748
 atcacgcaag ttgagtgcaa taatgcctgt tgaacgagga cgactgaatt 5798

<210> 61

<211> 257

<212> PRT

<213> Pasteurella multocida

<400> 61

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

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

Arg

<210> 62
 <211> 1788
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1)..(600)

<220>
 <223> unknown K

<400> 62
 gtc aac act ggg cta att cac agt aac ggt aat gcc aag ctc act ttt 48
 Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe
 1 5 10 15
 aaa gat gac acc agt ttt gtg act gaa gga aat aac ttt atc aca gca 96
 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
 20 25 30
 aaa gac aac tta gaa atc acg gca aaa aat gtt caa att gat caa gcg 144
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
 35 40 45
 aaa aat att caa tta aac gcg aat atc acg atc aat acc aag tct ggt 192
 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
 50 55 60
 ttt gtg aat tac ggt acc tta gca agt gct caa aat tta acg att aat 240
 Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
 65 70 75 80
 acc gaa caa ggc agc att tat aac ata ggc ggt atc ttg ggg gcg ggt 288
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly

	85	90	95	
aaa agt ttg aat ctg agc gcg aaa aga gga gaa aac caa gga gga tat				336
Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr				
	100	105	110	
ctt att aat caa ggt aag agt cta ctc cat tct gaa ggc gcc atg aac				384
Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn				
	115	120	125	
ctc aca gcg gat cgc acg gty tac aat tta ggg aat att ttt gct aaa				432
Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys				
	130	135	140	
ggg gac gcg acg atc aat gca aac gcg tta att aat gat gtt act ctc				480
Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu				
	145	150	155	160
aca ggt cgt ctt gag tat caa gat ctg aaa aaa gat tat acg cgt tat				528
Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr				
	165	170	175	
tat cgt atc aat gaa acg gca aaa cat ggt tgg cat aat aac ttc tat				576
Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr				
	180	185	190	
gaa tta aac gtc gac aga gtt tct tgatttgtgc atcaattttg taaccaccgg				630
Glu Leu Asn Val Asp Arg Val Ser				
	195	200		
ttaataaaac accagcaatt tcaacgccat tcatggcaga taatgccgct gcgacgatca				690
catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat				750
tggtcaaatt acgtgcacag aaagtgatgc cacgaatgcg acgttcattg atcgcgcctt				810
catgaataat ggcagcacct aaatgttttg ctaaataaat ggcacgagtc gcaattaatt				870
ctgcgctcca aggaatacat gccaaagattt taattgggct tttctcaaataaatgataaa				930
tctcagatac ttgattttgt gtgtgttgga aagaatcaaaa aatttctgcc aagtcagggc				990
gagtacgacc agattcatca atcggcgcac taaatttatt gatcacaaca ccaagtaaat				1050
taggggttatt tttgctgcca aataatgagg ctgcggcttt gatgcgttct ttgagttctg				1110
ccggtgtttc cgtcgccggt gctgcaacaa gaatgatttc cgcacatcaagt gcttgagcaa				1170
tttcatagtt aatgctattg gcataagaat gcttacgcgt agggattaaa ccttccacca				1230
cgacaatttc attgtttttg gcgagttggt gatgattttc aacaattttt tctagtacca				1290
catcagattg attttgaccg atgagtgatt cagctacact taacataaat ggttcaactg				1350
tttcaatggg ggtactgggt cgaataattg atgttgtgcg atcaatcata tcttcacctg				1410
agttcggctg agaaattggg ttcataaagc cgactttcgc ccctttttgc tccagtgcac				1470
gtgttaaacc taagctgaca ctggttaagc ctacaccagc actaatcggg ataaggataa				1530
ttgtacgtga cataataaac cctaattttg tgataattta tacaataaga aactgccgat				1590
gaatcggcag ttaattgatc tttacgcgat gcaaaggcgc gcggtatctt gtgcaataac				1650

aagttcttca ttcggttgga tcaccatggc aacaggcgta ttgtctgctg taatcacccc 1710
 ttcatgacca aagcgagccg ctttggtttt atctgaatcc acttgataac cgaacagttt 1770
 taaatggttt aaggttga 1788

<210> 63
 <211> 200
 <212> PRT
 <213> Pasteurella multocida

<400> 63
 Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe
 1 5 10 15
 Lys Asp Asp Thr Ser Phe Val Thr Glu Gly Asn Asn Phe Ile Thr Ala
 20 25 30
 Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn Val Gln Ile Asp Gln Ala
 35 40 45
 Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr Ile Asn Thr Lys Ser Gly
 50 55 60
 Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
 65 70 75 80
 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
 85 90 95
 Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
 100 105 110
 Leu Ile Asn Gln Gly Lys Ser Leu Leu His Ser Glu Gly Ala Met Asn
 115 120 125
 Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu Gly Asn Ile Phe Ala Lys
 130 135 140
 Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
 145 150 155 160
 Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
 165 170 175
 Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
 180 185 190
 Glu Leu Asn Val Asp Arg Val Ser
 195 200

<210> 64
 <211> 278
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (108)..(278)
 <220>

<223> unknown O

<400> 64

```

gaattccaac caaatctcac accagagcaa gaacgctaca tagtggaatg gttggcagaa 60

cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116
                                     Met Lys Ile
                                     1

act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164
Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
      5              10              15

gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212
Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu
      20              25              30              35

gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260
Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu
              40              45              50

agc aaa agg gga cat agt 278
Ser Lys Arg Gly His Ser
              55

```

<210> 65

<211> 57

<212> PRT

<213> Pasteurella multocida

<400> 65

```

Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
      1              5              10              15

Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
      20              25              30

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

Glu Glu Glu Ser Lys Arg Gly His Ser
      50              55

```

<210> 66

<211> 1020

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(597)

<220>

<223> unknown P

<400> 66

```

gtc aac aca tca aaa gtt gag att gac tat gcc gtc act cgt gcg gcg 48
Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
      1              5              10              15

gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att 96

```

Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
20 25 30

tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat 144
Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
35 40 45

ttt gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa 192
Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
50 55 60

ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta 240
Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
65 70 75 80

cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc 288
Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
85 90 95

act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca 336
Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
100 105 110

gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca 384
Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
115 120 125

atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc 432
Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
130 135 140

ggc aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa 480
Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
145 150 155 160

gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc 528
Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
165 170 175

gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat 576
Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
180 185 190

ttt tca aat cgt tta gca tcg taaggggtag aaaatggctt taccacgcaa 627
Phe Ser Asn Arg Leu Ala Ser
195

acttaaattg atgaatttaa tcatcgacgg taacaaatat ctcggcgaag tcacggaagt 687

gactcaacca aaattagcaa tgaaaatcga agaatttcgc gcgggcggta tgattggttc 747

ggcggatgtc aatctcgggc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat 807

ggcgaatta attaaaaaat tcggcgggtc aatcaacggc attccattgc gttttcttgg 867

ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttgtga tgcaaggtcg 927

atttactgaa attgacagcg gaaacagcaa agtgggcgat gacactgaac aaacattcaa 987

agtcgcttta acgtattaca aaatcattgt tga 1020

<210> 67

<211> 199
 <212> PRT
 <213> Pasteurella multocida

<400> 67
 Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
 1 5 10 15
 Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
 20 25 30
 Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
 35 40 45
 Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
 50 55 60
 Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
 65 70 75 80
 Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
 85 90 95
 Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
 100 105 110
 Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
 115 120 125
 Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
 130 135 140
 Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
 145 150 155 160
 Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
 165 170 175
 Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
 180 185 190
 Phe Ser Asn Arg Leu Ala Ser
 195

<210> 68
 <211> 2584
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1042)..(2286)

<220>
 <223> xylA

<400> 68
 gtcgaccagc ttagatatttg cgacgggggtt aatttcttct atcgtttcaa tcattgcggtt 60
 taccattatt ttatggaatc tctctggacc gatgaccatt gccaatattg aaattcctca 120
 cgcgatggtc tttttgggtc ttatttacgt gctgttttagc agtattgtgg catttaaaat 180

```

cggtcgcccc ttaattcagc tcaattttgc caatgaacgc ttaaacgcc actaccgtta 240
ttcacttata cgtctgaaag aatatgctga aagcattgct ttttatcgtg gtgaaaaaat 300
ggaaaaacgt ctattgacca cacaatttaa tcaggtgatt gataacgttt ggcaagtaat 360
ctaccgcacc ttgaaattat cgggttttaa cttaatcatt acgcagattt cggtggtttt 420
tccgctgggtg attcaagtga cacgttattt tcgctgacaa taggtgcata tgagggtggt 480
agaatagcga tacttttctgt tggaaaagta aactctttta tataaataga aatcgcttga 540
atgattctcg ggcaaaaaat aatgtactca tttgcgatct catactgata atggcgaagt 600
aaatatcttc ttacaatatt atggtaatta tcaggtaata ccgtatagcc atagattcca 660
gttctatttt gttttgctaa ataattgatg agcatttgag gcgcaggtaa atccatatct 720
gcaacagaca ttgaaatcat atccttgccg tatttacgag taattgccca tttagcacta 780
tgacaatctg atctatcagt aaaaacatca aacaaattat ccgtcataca tgttctccaa 840
tattggattt atataaactt tagaacttga ggtagattgt tggaattggt aaatctggta 900
tttctattac gttttttctt ttttgtgata taagccacaa taaccaataa tcttaattgt 960
taagtgaat aacgtaattg atcctcccat tgttttacta aattatgtct ctgaaactta 1020
tttgttcagg agaaatcatt t atg tcc act tac ttc gac aaa att gaa aaa 1071
                        Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys
                        1           5           10

gta aat tat gaa ggt gta act tca tct aat ccg ttt gca tat aag cat 1119
Val Asn Tyr Glu Gly Val Thr Ser Ser Asn Pro Phe Ala Tyr Lys His
                        15           20           25

tat gat gct aat caa gtt att tta ggt aag acg atg gct gaa cac tta 1167
Tyr Asp Ala Asn Gln Val Ile Leu Gly Lys Thr Met Ala Glu His Leu
                        30           35           40

cgt tta gcc gtc tgt tat tgg cac act ttc tgt tgg aca ggg aat gat 1215
Arg Leu Ala Val Cys Tyr Trp His Thr Phe Cys Trp Thr Gly Asn Asp
                        45           50           55

atg ttc ggt gtc ggt tct ttc gat cgt tgt tgg cag aag gcg agt gat 1263
Met Phe Gly Val Gly Ser Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp
                        60           65           70

tca tta gca ggt gca aaa caa aaa gca gat atc gct ttt gaa ttt ttc 1311
Ser Leu Ala Gly Ala Lys Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe
                        75           80           85           90

agt aaa tta ggc ata cct tat tat tgt ttt cat gat gtt gat gtt gcg 1359
Ser Lys Leu Gly Ile Pro Tyr Tyr Cys Phe His Asp Val Asp Val Ala
                        95           100           105

cca gaa ggt cat tca ttt aaa gaa tat ttg tcg aac ttt aat aca atg 1407
Pro Glu Gly His Ser Phe Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met
                        110           115           120

atc gat gtt tta gcg cag aaa caa gaa gaa aca ggc gtc aaa ttg ttg 1455
Ile Asp Val Leu Ala Gln Lys Gln Glu Glu Thr Gly Val Lys Leu Leu
                        125           130           135

```

tgg ggg act gca aat tgt ttt aca cac cct cgt tat atg tct ggt gct	1503
Trp Gly Thr Ala Asn Cys Phe Thr His Pro Arg Tyr Met Ser Gly Ala	
140 145 150	
gca aca aat ccg aat cca gaa att ttt gct tgg gct gct gca caa gta	1551
Ala Thr Asn Pro Asn Pro Glu Ile Phe Ala Trp Ala Ala Ala Gln Val	
155 160 165 170	
ttt act gcc atg ggg gca act cag cgt tta ggt ggt gaa aat tat gtt	1599
Phe Thr Ala Met Gly Ala Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val	
175 180 185	
ttg tgg gga gga cgt gaa gga tat gaa acg tta tta aat acc aat tta	1647
Leu Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu	
190 195 200	
aaa cag gag cga gag caa att gga cgt ttc atg caa atg gtg gtt gag	1695
Lys Gln Glu Arg Glu Gln Ile Gga Arg Phe Met Gln Met Val Val Glu	
205 210 215	
cat aaa tat aaa atc ggt ttt aac ggg act ttg ctg att gaa cca aag	1743
His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys	
220 225 230	
cca caa gag cca acg aaa cat caa tat gac tat gat gtg gcg acc gtt	1791
Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val	
235 240 245 250	
tat ggc ttt tta aag cag ttt ggt tta gaa aaa gaa att aaa gtg aat	1839
Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn	
255 260 265	
att gaa gct aat cac gca aca tta gct gga cac act ttc cag cat gaa	1887
Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu	
270 275 280	
gtc gcc atg gct aca gcg tta gat att ttt ggt tct att gat gca aat	1935
Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn	
285 290 295	
cgt ggt gat cca caa tta ggt tgg gat acc gat caa ttc cct aat agc	1983
Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser	
300 305 310	
gta gaa gaa aat act ttg gtc ata tat gaa att ctc aaa gca ggg ggc	2031
Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly	
315 320 325 330	
ttt aca acc ggt ggt ttt aat ttt gat gct aaa atc cgt cgg cag agt	2079
Phe Thr Thr Gly Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser	
335 340 345	
acg gat cct tac gat tta ttt cat gga cat att ggc gcg att gat gta	2127
Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val	
350 355 360	
ctt gcc tta tca cta aaa tgt gcg gcg aaa atg ctt gaa gag caa gct	2175
Leu Ala Leu Ser Leu Lys Cys Ala Ala Lys Met Leu Glu Glu Gln Ala	
365 370 375	
tta caa aaa gtc gtc aat caa cgt tat gct ggt tgg aca tca tca ctt	2223
Leu Gln Lys Val Val Asn Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu	
380 385 390	

ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga 2271
 Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg
 395 400 405 410

cta aca aaa gtg ctt taaaacgttc cggcttacgc cagacatcta gacgattgaa 2326
 Leu Thr Lys Val Leu
 415

taatttcaat attgtctccg cacgtaattc aaaggctttg tgtatgtgcg aatgatattc 2386

acaacaaagt tctgcaaaat cttgaattgc gtgaggtaat ttaaagcgct gacataagcg 2446

tcttgtcggc atgacaccag ctttttcatg tccataatga tgtggcaata tttcttttgg 2506

tgttaaggct tttcctaaat catgacaaat tgcagcaaaa cgtaccgcac ttttgtcact 2566

gtccgtgttt tctgtcga 2584

<210> 69

<211> 415

<212> PRT

<213> Pasteurella multocida

<400> 69

Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys Val Asn Tyr Glu Gly Val
 1 5 10 15

Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val
 20 25 30

Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr
 35 40 45

Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
 50 55 60

Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys
 65 70 75 80

Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro
 85 90 95

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

Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
 115 120 125

Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
 130 135 140

Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
 145 150 155 160

Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
 165 170 175

Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
 180 185 190

Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
 195 200 205

Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
 210 215 220
 Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
 225 230 235 240
 His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
 245 250 255
 Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
 260 265 270
 Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala
 275 280 285
 Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu
 290 295 300
 Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu
 305 310 315 320
 Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe
 325 330 335
 Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu
 340 345 350
 Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys
 355 360 365
 Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn
 370 375 380
 Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile
 385 390 395 400
 Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu
 405 410 415

<210> 70
 <211> 3501
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (298)..(1905)

<220>
 <223> yabk

<400> 70
 gaattcgagg aagggggcgt attacaaatt gaaacggctg cacgtgtagc acaacatgat 60
 aatgcctgtg cggatcattt ccttgccttt ttacttcac cagaagcaca agggcattta 120
 gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180
 cttagagcca cccaaatgaa cacgaaagtg ctcgatacct caaaagttaa tgccgaacaa 240
 gtcaaaaaat ggattgctgt ttggcaaacg accctaacc aataattgtt tgtcttg 297

atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt	345
Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu	
1 5 10 15	
ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc	393
Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala	
20 25 30	
tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg	441
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu	
35 40 45	
ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa	489
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln	
50 55 60	
gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt gcc att gta gca	537
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala	
65 70 75 80	
cga gcc ttt ttt tat caa ccg ttt gtg gcc aag aaa ctg atc ctc aaa	585
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys	
85 90 95	
tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggt	633
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly	
100 105 110	
tta tta ggc gtg tat ggc gct tct ggc tgg tta gcg atg tta agc cag	681
Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln	
115 120 125	
ttt ttc gct tgg gat tgg act cct aat att tac ggc tta aca ggt att	729
Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile	
130 135 140	
tta ctg gcg cat ctt ttt ttt aat gtc cca tta gct tgt cgc ctg ttt	777
Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe	
145 150 155 160	
tta caa ggt ttg caa gca att ccg gtg caa caa cgt cag ctc gcg gca	825
Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala	
165 170 175	
caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc	873
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro	
180 185 190	
tat tta cgc cag caa ttg tta cct gca ttt act ttg att ttc atg ctg	921
Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu	
195 200 205	
tgt ttt acc agt ttt gcg att gtg ctc act tta ggt gcc gga ccg aaa	969
Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys	
210 215 220	
tat acc acg ttg gaa gtg gct atc tat caa gcg att tta ttt gag ttt	1017
Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe	
225 230 235 240	
gat gta ccg aaa gcc ggc tta ttt gcg tta tta caa ttt gtt ttt tgt	1065
Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys	
245 250 255	

ttt ctg tta ttc acg ctg agt agc ttt ttt tct cca gcc ccc gcc acg	1113
Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr	
260 265 270	
aca tta cac agt caa cct act tgg ttt gcg ccc caa tcg tat tgg gtt	1161
Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val	
275 280 285	
aaa tta tgg caa cgt atg atc att gtg tgt gcg aca gta ttt atc tta	1209
Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu	
290 295 300	
tta ccg cta ctc aat acg cta gtt tct gct ttg ctt tcg tct cag ttt	1257
Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Ser Ser Gln Phe	
305 310 315 320	
ttt acc ttg tgg tta caa cct caa tta tgg aaa gca tta ggt tac tcg	1305
Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser	
325 330 335	
ctc acc atc gcc ccc act tct gca ttg ctc gct tta gta ctg tct ttt	1353
Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe	
340 345 350	
gcc tta tta ttg ctt gcc aga gaa tta cat tgg cga cat tat cgc agc	1401
Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser	
355 360 365	
tta tcc cat gtg att tta aat atc ggt gcg acc att tta gcc att cca	1449
Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro	
370 375 380	
acg tta gtg tta gct att ggt tta ttc att tta tta cgt gag atc gat	1497
Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp	
385 390 395 400	
ttt tct cca tac cat ctt ttt ggg gtt gtg gta tgc tgt aac gcg tta	1545
Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu	
405 410 415	
gct gct atg cct ttt gtg ttg cgt att ttg gct tta ccg atg cat aac	1593
Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn	
420 425 430	
aat atg att tat tat gaa aaa tta tgc caa tca ctt aac ctg cgt ggt	1641
Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly	
435 440 445	
tgg caa cgt ttt cga ttg att gaa tgg cac aag ctt cgt gcg cca atg	1689
Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met	
450 455 460	
aaa tac gcc ttt gca ctg gct tgt gcg tta tca tta ggc gat ttc acc	1737
Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr	
465 470 475 480	
gca atc gcg tta ttt ggt cag gct gac ttc aca tcg tta ccg cat ttg	1785
Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu	
485 490 495	
ttg tat caa caa ttg ggg cat tat cgt agt cag gaa gcg gca gta aca	1833
Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr	
500 505 510	

```

gcg ttt att tta ttg gtt ttt tgt ttg agt gtt ttt atg att att gaa 1881
Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
      515                      520                      525

cga cat cag gaa ccg cgt gat gat taatttaaac ggtgttcagt tttcctataa 1935
Arg His Gln Glu Pro Arg Asp Asp
      530                      535

tacctttact tttgagctgg atttgcagat tctgtctcaa caaaaagttg ctattattgg 1995

cgccagtggc gcaggaaga gtaccttatt aaatttgatt gcgggttttg cattgccaca 2055

gcaaggggaa atttggttga atggtgaaaa tcatagccaa actcaacctt atgaacgtcc 2115

ggtatctatt ttgtttcaag aaaacaactt gtttacgcat ttgactgtgg cagagaatat 2175

ggcattaggg ctgaaaccaa gcctaaaact gaccgcactt gaacaacaac gcgtacaaca 2235

agtggcaagt gcagtgggtt tgcagggttt tcttaatcaa ttaccacccc agttatcggg 2295

tgggcaaaaa cagcgtgtgg cgttggcgcg ttgtttatta cgcgataagc caattttgtt 2355

attgatgaa cttttttctg ccttagatcc cgatttacgg gcagaaatgt tgcattttatt 2415

gttacagttg tgtgatgaaa aaaaattaac actcctgatc gtgacacatc aagtgaacga 2475

attacagcag aaaatggatc gtatgattcg ttttgaacat ggtaggatga gtgagtccac 2535

cattttgaag gataatttta acgaaaaaca gaccgcactt taggcggcctt attaattaga 2595

taaggaaaga gaaaaatatg acaacggcaa cggcatttga gattcgtaca cttactcctc 2655

acccgacctt agaattattg tctgtgtgta aaattgaagc cctgtttgag accccttttt 2715

tagatttggg ttatcgggct gcgcaagtgc accgagaaaa cttaatacct aaagccattc 2775

aattatccac tttaatgtcg attaaaacgg ggggatgtcc agaggattgt ggctactgtc 2835

cgcagtcagc acgttatcat actggagtag aaaagcagca attactcgat gtggaagaaa 2895

ttgttgaaaa agccaaaatt gccaaagcac gtggtgcagg gcgcttttgt atgggggctg 2955

catggcgtgg accgaaaccg aaagacattg aaaaagttac cgcaatcatt aaagcgggtga 3015

aagaactggg cttagaaacc tgtggtacct ttggtttatt gcaagatggg atggcagaag 3075

atthaaaaga agcgggtttg gattattata accataatct cgatacagcc ccagaacact 3135

acggtaatgt gattggtacc cgtcaatttg atgatcgat taatacgtta ggtaaagtgc 3195

gtaaagctgg cttaaaagtg tgctgtggcg ggattattgg catgaatgaa acccgtaaag 3255

aaagagcagg attaatgtct agcttagcta atttagaccc gcaaccgaa tcggtgccga 3315

ttaatcaatt agtgaaagtg gaaggtaccc ctttagccga tcgggcagaa ttagactgga 3375

cagaatttgt gcgcactatt gcggtggcgc gtattaccat gccgaaaagc tatgtacgtt 3435

tatcagcagg gcgtcaaggc atgtcggaag aaatgcaagc catgtgcttt atggctggcg 3495

cgaatt 3501

```


<210> 71

<211> 536

<212> PRT

<213> Pasteurella multocida

<400> 71

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

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

<210> 72
 <211> 3182
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1544)..(2809)

<220>
 <223> ygiK

<220>
 <221> misc_feature
 <222> 452
 <223> N = A or T or G or C

<400> 72

```

aactactaag gagttatgta tgaatattag aaaatcatta ctattaatat ccctagcaag 60
cttcatgtca ctttcagttt cagctgcaga aattaatttg aaatttgaaa gttcgaattt 120
tgcaggagaa aaagtttatg aaatccaaaa agaatggact gacaatattg aaaaagcttc 180
caatgggaga ataagtatag agttattacc tctcgactca gtcttaaaat ctagtgacat 240
gctttctggg gttcgaaaata aaattattga tggagcgggt gcaacagcgg caatgtatgc 300
aggcactgac cctggattcg gattaattgg tgatactatt tctgcttgga accatgacga 360
agatatttta aatttttact ataatggagg tggttttgaa gttgttgata atattttcca 420
acaatatggg gccaaactca ttgggtgtatc anttacggga gcagaatcat taccatcgaa 480
agtaaaaaata gctaatactg aagattttta aggtataaaa attcgggctc cctctggtcc 540
tatccaaaaa ttgtttgcaa gattaggagc cgctcctgtt ggtcttctcg gttcagaaat 600
ctatactagt ttagaaaaag gtattattga tgctgccgat ttctcaacgt ttgcaataa 660
tcaagcacia ggagtccatg atattgcaaa atatccaatc tatccgggaa ttcattcttc 720
accagccgtt catatgatta tgaatcataa aacttggagt agcttaactc catcggatca 780
agcattctta attgcttact ttaaagggat ggctctcgat actctgactc gtgctcatta 840
tgaagataaa ctagcatata aagaagcact tgagaaagga gtacaaccag tttcttgga 900
tcaacaagaa attacaaaag ttcgttctat cgctaaagaa atttggcaag agatagctca 960
acaatctgaa ataggtaatc aagtattatc aagtattaat gaaattccta gaatctcaag 1020
gaatgctgca ataatcgtca agatggataa gacgatatcg tcttatccat taaggagtaa 1080
aacatgctta tttctaaata tttattatgg ctctgtaata agctagatca aatattcatt 1140
aaagtagggt attacgtttc ttatattttt ctattagttg ttatcattgg ttttacgagg 1200
ttgttgctcg gtatttatcc tctagcccaa cactttgggt tcatgaagta acaacatttt 1260
taataagtct atcattactt tatgggtggag tagcttggtta cgccagtaat aaacatattg 1320
ccatgacatt tattagacia aaattaccta ataagatcaa atgggttacta gaactcttag 1380
ttgaaatact tattttttatc ttctttattt tgcttagtta cggagcatac ttatcagcta 1440
gagaagcatt atttactcca tcaggaaaat tcaaaatgca aacttctgga agtgtattag 1500
acatgccatt tccagcaatt gaaaaaagtt tcttctttat ttc atg cct cat cat 1555
                                     Met Pro His His
                                     1

tgt tgt tct ttc agt act aca tat att ccg tca cat cta tac aaa ata 1603
Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His Leu Tyr Lys Ile
  5              10              15              20

tca gga gga att atc atg ata agt gca ttt ggg ata ggt att gga act 1651
Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile Gly Ile Gly Thr
      25              30              35

```

ctt att atc ttt tta atg atg att tcc ctt tta ttt att gga atg cca	1699
Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe Ile Gly Met Pro	
40 45 50	
tta ggt ttt ctc act ggg tta atc gct tta gtt att tca tat ctt tgg	1747
Leu Gly Phe Leu Thr Gly Leu Met Ile Ala Leu Val Ile Ser Tyr Leu Trp	
55 60 65	
ttt gat act acc gca ata atg caa atg ata gct tca cgt gtc act gat	1795
Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser Arg Val Thr Asp	
70 75 80	
ttc aca tca tct tac act ttt gta gct gtg cct atg ttt gtt ctt atg	1843
Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met Phe Val Leu Met	
85 90 95 100	
gca aca tta ctt gat aag act gga att gct aga gat ctc tac aac gca	1891
Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp Leu Tyr Asn Ala	
105 110 115	
atg cga gtc att ggc ggt cga tta cga ggt gga att gca att caa tcg	1939
Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile Ala Ile Gln Ser	
120 125 130	
atg ttt gtt gca gtt cta ctt gct acg atg tca ggt att atc ggt gga	1987
Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly Ile Ile Gly Gly	
135 140 145	
gaa act gtt tta tta ggc atg ttg gca tta cca caa atg tta cgc tta	2035
Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln Met Leu Arg Leu	
150 155 160	
ggc tat aat aaa aac tta gct ata gga act gtt gta gca gga gga gca	2083
Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val Ala Gly Gly Ala	
165 170 175 180	
ttg ggt aca atg gtt cct cca agt atc gtg ttg att att tac gga atg	2131
Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile Ile Tyr Gly Met	
185 190 195	
acc gca aat gtt tct att gga gaa cta ttt ctt gca gca att cca gcc	2179
Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala Ala Ile Pro Ala	
200 205 210	
tcc tta cta ctt tct aca ttc tat att tta tat att cta gta ctt tgc	2227
Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile Leu Val Leu Cys	
215 220 225	
tac ttc aaa cct agc tat ggc cct gca atg cct agc tca gaa aat cat	2275
Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser Ser Glu Asn His	
230 235 240	
aca tta acg aaa gaa gat att aaa aaa att att cat gat att gca att	2323
Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His Asp Ile Ala Ile	
245 250 255 260	
cca gta gct atc gcc aca tgg att tta gga agt att tat ggc ggg ata	2371
Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile	
265 270 275	
gca tca atc act gaa tct gcc tgt gtt ggt gta gtt ggg gta ata tta	2419
Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val Gly Val Ile Leu	
280 285 290	

```

gca gca ttc tat cga aaa gaa tta aat ttc aaa ata gta caa gaa tca 2467
Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile Val Gln Glu Ser
      295                      300                      305

cta aaa cat aca atc aat act gtt ggt atg ata atc tgg gtc ggc att 2515
Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile Trp Val Gly Ile
      310                      315                      320

ggc gca aca atg att ata ggt att tat aat cta atg ggt ggg gac cga 2563
Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met Gly Gly Asp Arg
      325                      330                      335                      340

ttt ata gct aac tta ttc gct agc tta gat gcc tct cca att tat act 2611
Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser Pro Ile Tyr Thr
      345                      350                      355

atc att att atg atg gtt att tta tta ata ctt ggt atg ttc tta gat 2659
Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly Met Phe Leu Asp
      360                      365                      370

tgg att ggt gtt gcc atg ttg act ttc ctc aag aca agt aaa gcg aca 2707
Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr Ser Lys Ala Thr
      375                      380                      385

atc aat ttg tgt ttt gac ata gtc agg tac agt att tgg cgt ggt ccc 2755
Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile Trp Arg Gly Pro
      390                      395                      400

tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt 2803
Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly
      405                      410                      415                      420

act ttt tagtaaactct tgcgcgatac gaataaacgc attgatggca tttgctccgt 2859
Thr Phe

tttgtggatc gactgccgca tgagcagatt tgccaaaaaa ttcaattaca tacttcccaa 2919

tcccttttct ttcgttaacg tttccactta gattgccag aagccgatct gtctgaatgg 2979

gaacaagtgt tataccaaga agcgaatcca acaggtgaag tggatgatcgg tatggtgggt 3039

aaatacactg aattaccgga tgcctacaaa tcggttaatg aagccttgaa acacgcaggc 3099

ttaaaaaacc gtcttagcgt gcaaatcaaa tatattgatt cacaagatgt ggaaacccaa 3159

ggcacagaag tgtagaagg cgt 3182

```

<210> 73
 <211> 422
 <212> PRT
 <213> Pasteurella multocida

<400> 73
 Met Pro His His Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His
 1 5 10 15
 Leu Tyr Lys Ile Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile
 20 25 30
 Gly Ile Gly Thr Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe
 35 40 45

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

Ser Lys Ala Thr ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile
385 390 395 400

Trp Arg Gly Pro Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe
405 410 415

Val Gly Arg Gly Thr Phe
420

<210> 74

<211> 2787

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (463) .. (936)

<220>

<223> yhcJ

<400> 74

gttaacacac catgattaat gatgccggtt gaagccactg caacgtaatc gaattgtccg 60
gcatacaaag caagaatggt ggccagtgtg tcatgcatcg cattggcagc atcagcttgt 120
ggcggttgcaa tctgttggtg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
tttgttccac caatatctaa tgctaaacag cgcataaggct ctccttctgt gatgacttat 240
tttgccgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgca 300
gatcctacgg tgacagagta agcaccaatc tcaattgcgg ttttcgccaa ttctgggggtg 360
ttatagcgcc cttctgccat cactcggcag ccagcagcat tcaaattcttt gactaactga 420
taatccggtt cagctggaat ttcaccgcca gtataaccag ac atg gtg cta cca 474
Met Val Leu Pro
1

ata att tct acc cct aag ttg tgg caa tac atc cct tct tca aaa tta 522
Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro Ser Ser Lys Leu
5 10 15 20

gaa caa tcc gcc atg gct aaa caa cct aat tct ttg att cgt tta ata 570
Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu Ile Arg Leu Ile
25 30 35

atg gct tca cgt gta gtt gga cgg acg cga tcg gta cca tca aaa gca 618
Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val Pro Ser Lys Ala
40 45 50

ata ata tcg gcg cct gct gcg gct aac tct tca atg tct tgt aaa aat 666
Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met Ser Cys Lys Asn
55 60 65

ggg cta ata cga acg gga ctg tca ggt aaa tcg cgt tta acg ata cca 714
Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg Leu Thr Ile Pro
70 75 80

ata atc ggt aca ttg acg acg tta cgc gtg gct ttt aaa ttt tcg atc 762
Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe Lys Phe Ser Ile

85	90	95	100	
cct tca ata cgt aac ccg gca gca cca ccg ata acg gat gct tgc gcc				810
Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr Asp Ala Cys Ala	105	110	115	
atg gcg gca aca att tct ggc gag tcc att ggc cca tta tct acg ggc				858
Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro Leu Ser Thr Gly	120	125	130	
tgg caa gat gcg att aag cca tat tta att tgt tct aaa act tgc gga				906
Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser Lys Thr Cys Gly	135	140	145	
tgt gat agt ttt gac ata tta act cca gtc taaatttatc aaaagaagat				956
Cys Asp Ser Phe Asp Ile Leu Thr Pro Val	150	155		
tgactccaat ttgcataggt taatcttaga attaaaaaat aacaacccaaa ataataaaaa				1016
tttgagatct ttgtgcata tttattcata gggaatagac agcttaattt tagttatgat				1076
ttgtcaatcc ttgtattttt ttgtgtttgc tggtttgca tacactgttc taatattgct				1136
ttgagcactt gataaccttg ctcatataaa tgtaatccgt cggtacaaag gcgtaaatcc				1196
agttcacctg tagaatcaca aaagtatttt ttgtgtttcaa cgtaagtcac gtctgacgga				1256
caatgttggt ttaaataaggt attgagcctg tgaatttggt cgtagtgac cgtattaatc				1316
tgattgaccg gtgtggcttc taataaaaag tagtgggacg taggagaaat ggtgtgtagg				1376
tgagtcagaa tgtcatttaa ctatcgcatg acttgcgccg gtgaatacgt ttcttcctta				1436
caaatatcat tgacgcctaa aaaaagaaaa acagattgtc caagttgttg aatccgttta				1496
ggtttaacga taacatccaa atattgtgc gtactgacgc cagaaagtcc taaattggcg				1556
acggtttgtc ccgctaattg aggtgtgcct gctacctgtt cgtcccatat gtcaaaaagt				1616
gaatgaccaa ttaagctgat attggcaggt ttggaaaatt ccgccatttt gctctgatag				1676
cgttgataaa tatcctgatc acttagcatg tgtggacctc tattttgaaa taaaacgcta				1736
agtattatat aaaacctgat atgccggtaa acagtaaact tatcttcctg aggggtaaat				1796
attcaatttt gtgacgaacc tatcatatat gaaataaaac ttcattttct atataaaaa				1856
tagttttttc actttagaat gccaaacgtg tgaaatttat ttcatcatca ttttaacgta				1916
atcccaacgt aaccaataga ggagaactca taatgaaatt taaaaaacta ctacttgcat				1976
ctttatgttt aggtgtttca gttctgtgat ttgcagcaga ttacgatctt aaattcggtg				2036
tggttgcggg tccaagctca aacgaatata aagcagtaga attctttgcg aaagaagtga				2096
aagaaaaatc caatggcaaa attgatgtgg ctattttccc tagctcacag ttaggtgatg				2156
accgtgtgat gattaaacaa ttaaagacg gtgcattaga ctttacgtta ggtgaatcag				2216
cacgtttcca aatttacttc ccagaagcag aagtatttgc gttgccttat atgattccta				2276
attttgaaac ctctaaaaaa gcgttgctcg acacaaaatt tggtaaggt ttattgaaaa				2336

aaattgataa agagttaaac gtacaagtgt tatctgtggc gtataacggg acacgtcaaa 2396
 caacttctaa ccgtgcaatc aacagcattg aagacatgaa aggggttaaaa ttacgtgtac 2456
 ctaacgcggc aaccaacctt gcttatgcaa aatacgtggg tgcagcgcca acaccaatgg 2516
 cattctctga agtttacctt gcgcttcaaa caaactctgt ggatgggtcaa gaaaacccat 2576
 taccgacaat ccaagcacia aaattctatg aagtacaaaa atacttagcg ttaactaacc 2636
 acatcttaaa tgaccaactt tacttaatca gtaacgatac gttggcagat ttaccagaag 2696
 atttacaaaa agtgggttaaa gatgcagcag cgaaagccgc tgaatatcac actaaactct 2756
 tcgttgacgg tgagaacagc ttagttgaat t 2787

<210> 75

<211> 158

<212> PRT

<213> *Pasteurella multocida*

<400> 75

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

<210> 76

<211> 2787

<212> DNA

<213> *Pasteurella multocida*

<220>

<221> CDS

<222> (1949)..(2785)

<220>

<223> yia0

<400> 76

gttaacacac catgattaat gatgccggtt gaagccactg caacgtaatc gaattgtccg 60
gcatacaaag caagaatgtt ggccagtgtg tcatgcatcg cattggcagc atcagcttgt 120
ggcgttgcaa tctgttggcg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
tttgttccac caatatctaa tgctaaacag cgcataaggct ctcccttctgt gatgacttat 240
tttgccgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgca 300
gatcctacgg tgacagagta agcaccaatc tcaattgctg ttttcgcaa ttctgggggtg 360
ttatagcgcc cttctgccat cactcggcag ccagcagcat tcaaactctt gactaactga 420
taatccggtt cagctggaat ttcaccgcca gtataaccag acatggtgct accaataatt 480
tctaccoccta agttgtggca atacatccct tcttcaaaat tagaacaatc cgccatggct 540
aaacaaccta attctttgat tcgtttaata atggcttcac gtgtagttgg acggacgcga 600
tcggtaccat caaaagcaat aatatcggcg cctgctgcgg ctaactcttc aatgtcttgt 660
aaaaatgggc taatacgaac gggactgtca ggtaaatcgc gtttaacgat accaataatc 720
ggtacattga cgacgttacg cgtggctttt aaattttcga tcccttcaat acgtaaccgc 780
gcagcaccac cgataacgga tgcttgccg atggcggcaa caatttctgg cgagtccatt 840
ggcccattat ctacgggctg gcaagatgcg attaagccat atttaatttg ttctaaaact 900
tgccgatgtg atagttttga catattaact ccagtctaaa tttatcaaaa gaagattgac 960
tccaatttgc ataggttaat cttagaatta aaaaataaca accaaaataa taaaaatttg 1020
agatctttgt cgcataattta ttcataggga atagacagct taattttagt tatgatttgt 1080
caatccttgc tattttttgt gtttgctggt ttgcgataca ctgttctaatt attgctttga 1140
gcacttgata accttgctca ttaaaatgta atccgtcggg acaaaggcgt aaatccagtt 1200
caccgttaga atcacaaaag tattttttgtg tttcaacgta agtcacgtct gacggacaat 1260
gttgttttta ataggtattg agcctgtgaa tttgtgcgtt agtgaccgta ttaatctgat 1320
tgaccggtgt ggcttctaata aaaaagtagt gggacgtagg agaaatggtg tgtaggtgag 1380
tcagaatgtc atttaactat cgcataactt ggcgcggtga atacgtttct tccttcaaaa 1440
tatcattgac gcctaaaaaa agaaaaacag attgtccaag ttgttgaatc cgtttagggt 1500
taacgataac atccaaatat tgtcgcgtac tgacgccaga aagtcctaaa ttggcgacgg 1560
tttgtcccg taattgaggt gtgcctgcta cctgttcgtc ccacatgtca aaaagtgaat 1620
gaccaattaa gctgatattg gcaggtttgg aaaattccgc cattttgctc tgatagcggt 1680
gataaatatc ctgatcactt agcatgtgtg gacctctatt ttgaaataaa acgctaagta 1740
ttatataaaa cctgatatgc cggtaaacag taaacttatc ttccgtaggg gtaaatattc 1800

```

aattttgtga cgaacctatc atttatgaaa taaaacttca ttttctatat aaaaaatagt 1860
tttttcactt tagaatgcca aacgtgtgaa atttatttca tcatcatttt aacgtaatcc 1920
caacgtaacc aatagaggag aactcata atg aaa ttt aaa aaa cta cta ctt 1972
                               Met Lys Phe Lys Lys Leu Leu Leu
                               1                               5

gca tct tta tgt tta ggt gtt tca gct tct gta ttt gca gca gat tac 2020
Ala Ser Leu Cys Leu Gly Val Ser Ala Ser Val Phe Ala Ala Asp Tyr
    10                               15                               20

gat ctt aaa ttc ggt atg gtt gcg ggt cca agc tca aac gaa tat aaa 2068
Asp Leu Lys Phe Gly Met Val Ala Gly Pro Ser Ser Asn Glu Tyr Lys
    25                               30                               35                               40

gca gta gaa ttc ttt gcg aaa gaa gtg aaa gaa aaa tcc aat ggc aaa 2116
Ala Val Glu Phe Phe Ala Lys Glu Val Lys Glu Lys Ser Asn Gly Lys
    45                               50                               55

att gat gtg gct att ttc cct agc tca cag tta ggt gat gac cgt gtg 2164
Ile Asp Val Ala Ile Phe Pro Ser Ser Gln Leu Gly Asp Asp Arg Val
    60                               65                               70

atg att aaa caa tta aaa gac ggt gca tta gac ttt acg tta ggt gaa 2212
Met Ile Lys Gln Leu Lys Asp Gly Ala Leu Asp Phe Thr Leu Gly Glu
    75                               80                               85

tca gca cgt ttc caa att tac ttc cca gaa gca gaa gta ttt gcg ttg 2260
Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu
    90                               95                               100

cct tat atg att cct aat ttt gaa acc tct aaa aaa gcg ttg ctc gac 2308
Pro Tyr Met Ile Pro Asn Phe Glu Thr Ser Lys Lys Ala Leu Leu Asp
   105                               110                               115                               120

aca aaa ttt ggt caa ggt tta ttg aaa aaa att gat aaa gag tta aac 2356
Thr Lys Phe Gly Gln Gly Leu Leu Lys Lys Ile Asp Lys Glu Leu Asn
   125                               130                               135

gta caa gtg tta tct gtg gcg tat aac ggt aca cgt caa aca act tct 2404
Val Gln Val Leu Ser Val Ala Tyr Asn Gly Thr Arg Gln Thr Thr Ser
   140                               145                               150

aac cgt gca atc aac agc att gaa gac atg aaa ggg tta aaa tta cgt 2452
Asn Arg Ala Ile Asn Ser Ile Glu Asp Met Lys Gly Leu Lys Leu Arg
   155                               160                               165

gta cct aac gcg gca acc aac ctt gct tat gca aaa tac gtg ggt gca 2500
Val Pro Asn Ala Ala Thr Asn Leu Ala Tyr Ala Lys Tyr Val Gly Ala
   170                               175                               180

gcg cca aca cca atg gca ttc tct gaa gtt tac ctt gcg ctt caa aca 2548
Ala Pro Thr Pro Met Ala Phe Ser Glu Val Tyr Leu Ala Leu Gln Thr
   185                               190                               195                               200

aac tct gtg gat ggt caa gaa aac cca tta ccg aca atc caa gca caa 2596
Asn Ser Val Asp Gly Gln Glu Asn Pro Leu Pro Thr Ile Gln Ala Gln
   205                               210                               215

aaa ttc tat gaa gta caa aaa tac tta gcg tta act aac cac atc tta 2644
Lys Phe Tyr Glu Val Gln Lys Tyr Leu Ala Leu Thr Asn His Ile Leu
   220                               225                               230

```

aat gac caa ctt tac tta atc agt aac gat acg ttg gca gat tta cca 2692
 Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro
 235 240 245

gaa gat tta caa aaa gtg gtt aaa gat gca gca gcg aaa gcc gct gaa 2740
 Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Ala Lys Ala Ala Glu
 250 255 260

tat cac act aaa ctc ttc gtt gac ggt gag aac agc tta gtt gaa tt 2787
 Tyr His Thr Lys Leu Phe Val Asp Gly Glu Asn Ser Leu Val Glu
 265 270 275

<210> 77

<211> 279

<212> PRT

<213> Pasteurella multocida

<400> 77

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

Ala Ser Val Phe Ala Ala Asp Tyr Asp Leu Lys Phe Gly Met Val Ala
 20 25 30

Gly Pro Ser Ser Asn Glu Tyr Lys Ala Val Glu Phe Phe Ala Lys Glu
 35 40 45

Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser
 50 55 60

Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly
 65 70 75 80

Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe
 85 90 95

Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu
 100 105 110

Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu
 115 120 125

Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr
 130 135 140

Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu
 145 150 155 160

Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu
 165 170 175

Ala Tyr Ala Lys Tyr Val Gly Ala Ala Pro Thr Pro Met Ala Phe Ser
 180 185 190

Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn
 195 200 205

Pro Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr
 210 215 220

Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser
 225 230 235 240

Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys
 245 250 255
 Asp Ala Ala Ala Lys Ala Ala Glu Tyr His Thr Lys Leu Phe Val Asp
 260 265 270
 Gly Glu Asn Ser Leu Val Glu
 275

<210> 78
 <211> 2590
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (908)..(1294)

<220>
 <223> yjgF

<400> 78
 ctgcaggctc gattagtggg gcaccgaaag aaaaaaccgt gcaaattatt cagccgcgag 60
 aacagcagcc acgcgggttat tacacgggga tttttggtct gttcgatggt gagtcgttac 120
 aaagtgcggg ggcaattcgt tttattgagc aagtggacga gaaattgatt ttccgcagcg 180
 gtggcgggat tacgatctta agcgagctag aagacgagta ccaagaattg atccaaaaag 240
 tgtatgtacc agtaggataa gcgatgacat ttcctttatt tgagacgacg gctattgtga 300
 acggtgaaat tcagcacctt gccctgcac aacaacgtta tgcggcaagt ttggcgacct 360
 ttacggcgga gaaaggagcg aaagtacagg atcttgcgaa aattattcag attccgacct 420
 cacttgaaca cactcaacat gcgccgataa tccgttgctg gattgattac aatcagcaag 480
 actgtgacgt gcattatttt ccctatcaac gcaaaattta ccgcactttt cagcctgtca 540
 tttgcgatga aattaactat gatctgaaat atgctgatcg ggcattatta aatcagttat 600
 ttgctcagcg tagggattgt gatgagatta tgattatcaa acacggcaag gtgacggatt 660
 gcagtatttg taatctggtg tttcgccaag gtgagcaatg gttcacgcca gatagcccg 720
 tattttacgg cacacaacga gcctgggttat tacaacaagg caaaattcaa gcccgttcca 780
 tcttattgca agagatcgca caatttgaag aaattcggtt aattaatgca ctaaaccgc 840
 tgtaaatttt ccttgaacag cgtaaaataa aacaactttt tcagtcagat aaaaggagat 900
 aaacgac atg acg aaa gta att cat act gac aat gca cca gcc gcc att 949
 Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile
 1 5 10
 ggt cct tat gta caa gcg gta gat tta ggt aat atg ctg tta acc tct 997
 Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser
 15 20 25 30
 ggg caa att cca gtg aat cca aaa acc ggt gaa gtg cca gcg gat atc 1045
 Gly Gln Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile

35	40	45	
gta gca caa gca cgt caa tcg tta gaa aac gtg aaa gcg att gtg gaa			1093
Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu			
50	55	60	
caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg			1141
Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val			
65	70	75	
aaa gat tta aat gac ttt gca g g gtc aat gcg gag tat gaa cgt ttc			1189
Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe			
80	85	90	
ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa			1237
Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu			
95	100	105	110
gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct			1285
Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala			
115	120	125	
gta aaa gcc taatgaatag cttgcattta tcttagtcgt agcaaaacaa			1334
Val Lys Ala			
tctcttttca cttgctctct tcaaagcaag ttgataagtg atttttattg ggcgtttttc			1394
tattgatagc caaaaacgcc ctttactgat agagaataaa ctatgcaaaa tcaagtcatac			1454
gagattctac aataccgttt aaaaccacaa tcaggacaaa cgtttcacca aattatgcgt			1514
gagatcagtg ttccactcca taaacaacat gggattgatg tcattgcgta tggaaattca			1574
ttacatgata ttgacagcta ttatttaatc cgtgcatttg agacagaaac caaattgcaa			1634
cagcagctcg atgcttttta tgccagtgat gattggcgtg atggaccaag agaaagtatc			1694
attgcgctga ttgaaagcag tttaaaatcg gtgatcatgc tcccagacaca ggcaatccat			1754
gcactacgca accattatcc tcaataaaat caacaaccgc acccaatcag tgcggtcatt			1814
ttttcttact ttttcagtgc taagggaaaa acaacgatag tggacgttgt ttaatcaatt			1874
tccaaacaca ttgcgcgata tcacaccaac tctcaatttc tgtttctaaa gaacgcagcg			1934
caacccataa cgcgataaag aaactgacaa tcaaattcac cataccaatc aataacacga			1994
aactaaacc ttgtaagaac atctgccaag taaacgcgcc actgatcgcc atatagccca			2054
aattcgcaga agaaaacgcc acatggcgaa tatctaacgg taaattaagc aaatacccgga			2114
ctaaccctgt taaaccaagc aataaaccaa aacacagatl tcccataatc gaaccgtaat			2174
tatcatgccg gtattctgca aattttagtc gcatattacg ggtcaacaga cggcgtaaaa			2234
tagggtgatt tcttagtcgc atttttaagt tcaaataatt actacgatta tcaaaataac			2294
cagaaataat ccagaaaaag aataaccaga aaccgcgaat ggccggcaaac cataaggacc			2354
ctttcatcgg atcaagggat ttttgttggg aggcaatctc cgcgtcactc aataaagggtg			2414
taccaacata atgttgatag cctagcgcaa gcaaacaagc cacagaaatc gctaaagtga			2474

cattacccaa gactgccact gtttgcgagc gaaacacatc gatcagcagt tgagctaatt 2534
gcagattaac ggatttgcct tgtccattat ccaccgtttc tgcaaaacgt gctgca 2590

<210> 79
<211> 129
<212> PRT
<213> Pasteurella multocida

<400> 79
Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile Gly Pro
1 5 10 15
Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser Gly Gln
20 25 30
Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile Val Ala
35 40 45
Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu Gln Ala
50 55 60
Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val Lys Asp
65 70 75 80
Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe Phe Lys
85 90 95
Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu Val Ala
100 105 110
Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Lys
115 120 125
Ala

<210> 80
<211> 6642
<212> DNA
<213> Pasteurella multocida

<220>
<221> CDS
<222> (463)..(1884)

<220>
<223> yleA

<400> 80
aaccagctc agataagttt aattctggct atggaaagtg gaccaaattc ttcgatctcc 60
caggtttcta aggcgcgata cgggcaaata cgagtatttt cgatatactg ccaagcacct 120
agttgtttta agagattaac ggaagcaaca ctgatcgagc aaatgcgaag atcgtaaggc 180
gaattagggtt gaaactgtgg gagtggggcg tgttcgataa gctggacttg atgtccttgt 240
ttacgtaagc caagcgcaca ggctgcacca accatgccac cgccaaccac gatcatgtct 300
ttttgtatga cgtccatagg attttccttt tctttttgtt acgtattcta ccgtcaatga 360

```

gggaatttca aaagaaatct ctttttttagc tagccagcat aggttcaaga ctgtaaaata 420
gtcagtcaca tttttatagg ttaactgaat tttttaaacg at atg acg caa aaa 474
                                     Met Thr Gln Lys
                                     1

tta cat att aaa acg tgg ggt tgt cag atg aat gaa tat gat tca tct 522
Leu His Ile Lys Thr Trp Gly Cys Gln Met Asn Glu Tyr Asp Ser Ser
  5                10                15                20

aaa atg gca gat ctc tta aac agt act cac ggc tta gag tta aca gaa 570
Lys Met Ala Asp Leu Leu Asn Ser Thr His Gly Leu Glu Leu Thr Glu
                25                30                35

att ccg gaa gaa gcg gat gtg tta ttg tta aac act tgc tca att cgt 618
Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr Cys Ser Ile Arg
                40                45                50

gaa aaa gca caa gaa aaa gtt ttc cat caa tta gga cgt tgg aaa gaa 666
Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly Arg Trp Lys Glu
                55                60                65

tta aag aaa cat aag ccg gga ctc gtt atc ggt gtt ggg ggc tgt gtt 714
Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val Gly Gly Cys Val
                70                75                80

gcc tca caa gaa gga gaa cac att cgt act cgt gct cct tat gtc gat 762
Ala Ser Gln Glu Gly Glu His Ile Arg Thr Arg Ala Pro Tyr Val Asp
                85                90                95                100

att att ttt gga cca caa acc tta cat cgt tta cct gaa atg atc aat 810
Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro Glu Met Ile Asn
                105                110                115

cag atc aga ggt ggt aaa agc tca gta gtc gat gtc agt ttt cca gaa 858
Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val Ser Phe Pro Glu
                120                125                130

att gaa aaa ttc gac cgt tta cca gaa ccg cgt gca gaa ggt cca act 906
Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala Glu Gly Pro Thr
                135                140                145

gct ttc gta tcc att atg gaa ggc tgt aat aaa tat tgc tca ttc tgt 954
Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr Cys Ser Phe Cys
                150                155                160

gtc gtg cct tat acg cgt ggt gaa gaa gtc agt cgt cca gtg gat gat 1002
Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg Pro Val Asp Asp
                165                170                175                180

gta tta ttt gaa att gca cag ttg gca gag caa ggc gtg cgt gaa gtg 1050
Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly Val Arg Glu Val
                185                190                195

aat tta tta gga caa aac gtg aac gct tat cgt ggt gca act cat gat 1098
Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly Ala Thr His Asp
                200                205                210

gac ggt att tgt act ttt gcg gaa ttg tta cgt tta gta gcc gct att 1146
Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu Val Ala Ala Ile
                215                220                225

gat ggt att gac cgt tta cgt ttt acc acc agt cac cca att gag ttc 1194

```


Asp	Gly	Ile	Asp	Arg	Leu	Arg	Phe	Thr	Thr	Ser	His	Pro	Ile	Glu	Phe		
230						235					240						
act	gat	gac	att	att	gat	gtg	tac	cgt	gat	acg	cca	gag	ttg	gtg	agt	1242	
Thr	Asp	Asp	Ile	Ile	Asp	Val	Tyr	Arg	Asp	Thr	Pro	Glu	Leu	Val	Ser		
245					250				255						260		
ttc	tta	cac	tta	cct	gta	caa	agt	ggg	tct	gat	cgt	gtg	tta	tct	atg	1290	
Phe	Leu	His	Leu	Pro	Val	Gln	Ser	Gly	Ser	Asp	Arg	Val	Leu	Ser	Met		
				265				270						275			
atg	aaa	cgc	aat	cat	acg	gca	tta	gaa	tat	aaa	tcg	att	att	cgg	aag	1338	
Met	Lys	Arg	Asn	His	Thr	Ala	Leu	Glu	Tyr	Lys	Ser	Ile	Ile	Arg	Lys		
			280					285					290				
tta	aga	gcg	gtg	cgt	cca	gag	att	caa	att	agc	tca	gat	ttt	att	gtc	1386	
Leu	Arg	Ala	Val	Arg	Pro	Glu	Ile	Gln	Ile	Ser	Ser	Asp	Phe	Ile	Val		
			295				300					305					
ggg	ttc	ccg	ggc	gaa	aca	gca	gaa	gat	ttc	gag	caa	acc	atg	aat	tta	1434	
Gly	Phe	Pro	Gly	Glu	Thr	Ala	Glu	Asp	Phe	Glu	Gln	Thr	Met	Asn	Leu		
	310					315					320						
att	gca	caa	gta	aat	ttt	gat	atg	agt	ttc	agc	ttc	att	tat	tca	gca	1482	
Ile	Ala	Gln	Val	Asn	Phe	Asp	Met	Ser	Phe	Ser	Phe	Ile	Tyr	Ser	Ala		
325					330					335					340		
cgt	cca	ggc	acg	cca	gca	gca	gat	atg	cct	gat	gat	gtg	aca	gaa	gaa	1530	
Arg	Pro	Gly	Thr	Pro	Ala	Ala	Asp	Met	Pro	Asp	Asp	Val	Thr	Glu	Glu		
				345					350					355			
gag	aag	aaa	caa	cgt	tta	tat	gtg	ttg	caa	caa	cgc	att	aac	aat	caa	1578	
Glu	Lys	Lys	Gln	Arg	Leu	Tyr	Val	Leu	Gln	Gln	Arg	Ile	Asn	Asn	Gln		
			360					365					370				
gcc	gcg	caa	ttt	agt	cga	gca	atg	tta	ggc	aca	gaa	cag	cgc	gtg	tta	1626	
Ala	Ala	Gln	Phe	Ser	Arg	Ala	Met	Leu	Gly	Thr	Glu	Gln	Arg	Val	Leu		
			375				380					385					
gtg	gaa	gga	ccc	tcg	aaa	aaa	gat	tta	atg	gaa	ctc	aca	ggg	cgt	aca	1674	
Val	Glu	Gly	Pro	Ser	Lys	Lys	Asp	Leu	Met	Glu	Leu	Thr	Gly	Arg	Thr		
	390					395					400						
gaa	act	aat	cgt	atc	gtc	aat	ttt	gtg	ggc	acg	cct	gat	atg	att	ggg	1722	
Glu	Thr	Asn	Arg	Ile	Val	Asn	Phe	Val	Gly	Thr	Pro	Asp	Met	Ile	Gly		
405					410				415					420			
aag	ttt	gtt	gat	atc	aag	atc	acg	gat	gtg	ttt	act	aac	tca	ctg	cgt	1770	
Lys	Phe	Val	Asp	Ile	Lys	Ile	Thr	Asp	Val	Phe	Thr	Asn	Ser	Leu	Arg		
				425					430					435			
ggg	gaa	gtc	gtt	aga	act	gaa	gaa	caa	atg	gga	ctt	cgc	gtt	gtt	caa	1818	
Gly	Glu	Val	Val	Arg	Thr	Glu	Glu	Gln	Met	Gly	Leu	Arg	Val	Val	Gln		
			440					445					450				
tcg	cca	caa	atg	gtg	att	aat	cgt	act	cgt	aaa	gaa	gat	gaa	ctc	ggc	1866	
Ser	Pro	Gln	Met	Val	Ile	Asn	Arg	Thr	Arg	Lys	Glu	Asp	Glu	Leu	Gly		
			455				460					465					
gtg	gga	cgt	tat	cac	gcg	tagtcgtgct	atcccttcaa	atattttaacc								1914	
Val	Gly	Arg	Tyr	His	Ala												
	470																

gctctcgagt ttctcaagag cggttatattt ttatgaaaaa tttttgataa attgaccgct 1974
ctttttattg cttcatttta tgatagacag cgtgttttct gttattcatc gtatttcctt 2034
ttatttcact tcattaataa attattaaat ttcaattgct tatcaaaatt gttgtttttt 2094
gctttttttc tatttatagc atgggtatatt ttatatacaca catggcgctat ttctccatat 2154
ttttacaaaa aactgtgact tcactctaac tattgttctc tcgtgcttta ctccatttta 2214
taaggcggtt agtttagatc atgttggttt tacaacatat tttgagggtg tttgaagggt 2274
gagcttattt tatagttgag gtgatgatga aaaaatttaa tcctagtata ttggcggttg 2334
ccatatcaag tctgtactc acatccacat tgacctttgg tcaaaccag caacaagata 2394
aagcactctt tgggtgtgaa gaacatcaag aaagcctact ctttcatcag agcttagtag 2454
aacaaggtag tgataatgtg ccaatttggc gcattccgtc tttattaaga acaaaagacg 2514
gtgtattaat tgccgccgca gataagcgtt ggcaacaccg tggtgactgg ggcgatattg 2574
ataccgcaat ccgaattagt catgatgatg ggaaaacatg gggaaatatt acaacgattt 2634
tggatttgcc atcaaagaat ggggaaaaat ccccatcagc accagatcct gtaacattca 2694
acgcgtgggg agatagacaa aattgtacaa cttactgtaa ttctgctttt ttgatcgatg 2754
ctcagatggt acaagataaa cgtaatggta gaattttttt agcagttgat atgtttgccg 2814
atggagcagg tttttttggt gtaaaagaca gtggtaatgg gcgcattaat attgatggta 2874
aacagtatcc tatttttaaat gaaaagcaat cgggtcgaca ttgaaccctg tgttcttaac 2934
tctttcactt gctcaacgtt caccggaatc acgcggtcaa taaaagtcgg tttccagttt 2994
aaacccggtt gaacaatagc gtgtaattca ccaaaacgca tcaccacgcc acgttctgct 3054
tctttgacag tataaaaacc gctaacgccc cagacaattg caccaatcac cgctgcaatt 3114
ggcaataatt taccaagatt taacgatcca ccagaatgag agttattgag tttaccgcca 3174
ttccctgaac cgcctaattt tttcagcaga ttattaaaaa tctcttcaat atcaggtggg 3234
gattgctctt gattgttttg cttacgacct gactggttat cattccaatt cggctgaccg 3294
ccttcattat caggacgctg actctcaggt tttttctgtc cgggtttgcc ccaaggatct 3354
tgatctgaac cgttcaatga cattacgttc tccatttgct aaaaaattgt tacttgttta 3414
aacaaattcc cacagtctaa acaaaatggt ggattaagtc taacgaaact cgttactaaa 3474
tggggatatt ttttatgatt taaagtgccg ccaataaaaa cgcacaatgg tctcattttt 3534
acggcttact acctgacttt tgtcctatcg ctttgctggg catgtttttt cattcacctt 3594
ataataaatg gcgtcgtgta aggtggtttc cgctaataat cccctctgcc aagtaaaata 3654
gtgcacatct aagcactgtg tttggttaat aaaaaagcc aagtaaaacg gcaagcgggtg 3714
actaaagagg agttaactaa gtttctgtat gctagcgtac tattgactct tcttgactg 3774
tgtttgggtt ttattgagggt gaatgaaacc ctacgctgta tttctttggt attgttggt 3834

tattttaagcg ttagccgagt attattttgcg ctcgcgttgt tgggcgtgat catgaatttg 3894
agctattact attatctctt gagtatccct ttattacata aatctttctt actcatggga 3954
gtaggcacg ttctggcact agttacgttt gttttatcac gttataacaa ggcaccgcag 4014
gcaacattac aagctgaatc gcacaatacg tttcaaccac aaacaatgtt acgtaaaaaa 4074
ctaggattca ctttggtggc gacatgtttg attgcctttg ccacgaatta tactattcat 4134
aaatatgaag atattttaac gaatggtgag tcaattattt taaaaacggc acccgttgat 4194
ccgcgttcct tgatgcaagg ggattatatg acgttgaaact atgaaatctt ggcagacatt 4254
agtgaggaat ggggaaaaaa tttagaagag gaaaaaacac agtattttgt ttatgcgttg 4314
ttaaaccgag acagcctagg gattgctacc ttgtgctgctc ttgaaaccaa agcacctaca 4374
acatttgacg ggtgtacacc aaatattttac ttaccggtga atgtcgcgat gtggtggccg 4434
cgttttacaa gtcaagacta cttttttgcc gagggaaaag gtgaatatta tgcacaagct 4494
gaatatgccg aatatcgctt taaaggggga aaagcgttgt tgttcgctt actagataaa 4554
aatttaaaag cattataaaa caaaaggcgg tagtgaaccg cctttatgtt gtatgccact 4614
tacttcaccg caatcattga gccaaaatta aagcattgaa accataattc cacttgttga 4674
aaaccgactt cagctaaacg cattttatgg gcttgaatgc tgtctgtacg catcacattt 4734
tcaagtgcg tgcgtttttg gctgacttca agttcactgt atccattcgc gcgtttaaat 4794
tgatgatgta aatcaatcaa caaggcatc atgttttgat cttcaaaatg aaattttctc 4854
gatagtacca agatcccatt cggttgtaag ccttggtaaa tcttacttaa taaggctcga 4914
cgatcttcag gtggcagaaa ttgcaaagtg aaatttaaaa ttaccatgaa ggcattttcg 4974
atctcgatat ggcgtatatc atcacaaata atgtccacag gtattgtact ttgataggca 5034
ctaacatgct ggcgacaacg atcgaccatg gggtgtgagt tatcaacacc aatgatcttg 5094
acgccgggtt gattaatatg acgacgtgca gataatgttg ccgcaccgcg cgagcacccc 5154
agatcataga cgttgctatt cgccgtaaca aagcgtgatg ccaacatccc aatagcggta 5214
atgatgttgg catagccggg aatagagcgt tggatcatgt cgggaaagac ttcagctacg 5274
ctttcatcaa aagtaaaatc cccaattta gcaatgggga gtcgaaaata gagtatcttt 5334
tgtcataatg tattaaagac cgagaaaaag tgcggtcatt ttagaagaag tttcgacctt 5394
tcacaaataa attatgattt cggaataaaa tgcgccatgg cactttcttc ttgtttaata 5454
cgcacgccta ggataagcaa ataaatgggt aatccaatca atgcggtata ttttgcttgg 5514
cagaaaagcg ataaaccaat taactcggga ataatgttta agaaataatt cgggtgacgt 5574
acgtatttaa acaagaaaga gcggttaatg tgatgttccg gtaaaatgta aagttttact 5634
gtccaaatct ctttcagttc ataaatcacg taaaatagca tggcgatcgc aaagactaaa 5694
atcgccagcc ctatttgtga ggtgctatta aatgctgtgt tttggttatt agcttcaatg 5754

atcgcggcga gataaaatac aacatgggca atggataaca gcgtagaatt gcgtttacca 5814
 tattgtattg caccttttgc aatcaatgct ttttcatggc ggattgaaat agacagacta 5874
 taaaaacgga tcgctaaaat acaggcaaaa gtgatattga taaataacat gtgggttatcc 5934
 ttaacataat tttattccaa taaagtggcg taatataaca aaaaatccga tgatatggca 5994
 tggaaatacg cctttatttt gaacgttcat cgcttttctt tttctttatt ggttgatttg 6054
 taagcataaa taaccttttt atctctcttg gttttccgct ataattgagt gaatttttga 6114
 gcataattaa gagtacaaag gattttgaaa tgatgcgtac acattattgc ggtgcattaa 6174
 accgtgacaa tatcggaaca gaagtaacat tgagtgggtg ggtgcatcgt cgccgtgatt 6234
 taggtggggtt aattttttatt gatatgcgtg atcgtgaagg gattgtacaa gtgtgtttcg 6294
 atccaatata tcaagaagca ctaccacag cagcaagttt acgtaatgag ttttgatttc 6354
 aaattaaagg cgaagtgatt gcccgccag ataatcaaat caacaaaaat atggcaacag 6414
 gcgaagtgga agtggttagca aaatccctgt ctatttataa cagcgcagag ccattacctc 6474
 tcgactttta ccaaaataat acggaagaac agcgtttaaa ataccgttat ttagacttac 6534
 gtgcgccaga aatggcgcaa cgtttaaaaa cagagccaa aattaccagc tttgtgcgtc 6594
 gctttatgga cgaacatggt ttcttagata ttgaaacacc gatgttga 6642

<210> 81

<211> 474

<212> PRT

<213> Pasteurella multocida

<400> 81

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

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

```
<210> 82
<211> 4835
<212> DNA
<213> Pasteurella multocida
```

```
<220>
<221> CDS
<222> (407) .. (1156)
```

<220>
<223> yojB

```

<400> 82
gtcaacgacg gggcggggtct tagaacattg gcatacgggt acgatgacac gccgtgtccc 60
agagctccat cgctccttcc caaataactt ggtttggatg caccatttag atgcgaaaaa 120
acgtgggttta cgtcatggcg ataaagtga gatcagctca cgtcgtggcg aaatgatttc 180
tcacttagat acccgtggac gtaataaagt cccacaaggc ttagtttaca ccactttctt 240
tgatgcagggt cagttagcaa actatctcac tttagatgcg acagacccaa tttcaaaaga 300
aacggacttc aaaaaatgtg cgggtcaaagt ggaaaaagcg taacacgtta aatttaatga 360
ggaacgaccg cactttgctt tcagtaaagt gcggttgga agtcga atg aaa aza 415
                               Met Lys Lys
                               1

```

aca gtt gtg aat cct gaa cgt cgt cga ttt ttt aaa gag gct acg cgc 463
Thr Val Val Asn Pro Glu Arg Arg Arg Phe Phe Lys Glu Ala Thr Arg
5 10 15

act gca ggc ggg ttg gca ggg gtg act ttg ctc ctt ggt ttg caa caa 511
Thr Ala Gly Gly Leu Ala Gly Val Thr Leu Leu Leu Gly Leu Gln Gln
20 25 30 35

aag cag agt ctt gcg cgc gaa ggc gtg gcg tta cgc cca cct ttt gcc 559
Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro Pro Phe Ala
40 45 50

ctt gag aat gag aaa gcg ttt tct gct gcg tgc att cgt tgt ggt cag 607
Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg Cys Gly Gln
 55 60 65

tgt gta caa gcc tgt cca cat gag atg ttg cat ctt gcc tca ctg att 655
Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala Ser Leu Ile
70 75 80

tca ccg atg gaa gca ggt aca ccg tat ttc att gcg cgc gat aag ccc 703
Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg Asp Lys Pro
85 90 95

tgt gaa atg tgt gtg gat att cct tgt gca aaa gcc tgc cca acc ggt 751
Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys Pro Thr Gly
100 105 110 115

gca ttg gat aat caa gca aca gaa atc gat gat gcg cgt atg ggg tta 799
Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg Met Gly Leu
120 125 130

gct gtc ctg cta gat cat gaa act tgt ctg aac tgg caa ggt tta cgc 847
Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln Gly Leu Arg

135	140	145	
tgt gat gtg tgt tat cgc gtc	tgt ccg ctg att aat aaa gcg att acg	895	
Cys Asp Val Cys Tyr Arg Val Cys	Pro Leu Ile Asn Lys Ala Ile Thr		
150	155 160		
tta gtg atg cat cgt aat gag cgt acg ggt aag cac gcc gtc ttt atc	943		
Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala Val Phe Ile			
165	170 175		
cca aca gtg cat tcc gaa gcc tgt aca gga tgt ggc aaa tgt gaa gaa	991		
Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys Cys Glu Glu			
180	185 190 195		
gct tgc gtt cta gaa gaa gcg gca atc aaa gtg tta ccg atg gca tta	1039		
Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro Met Ala Leu			
200	205 210		
gcg aaa ggc atg tta ggt aaa cat tac cgt tta ggt tgg gaa gag aaa	1087		
Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp Glu Glu Lys			
215	220 225		
gaa aaa gcc ggg cat tcc ctt gcg cca gaa ggc att att tct ctc ccg	1135		
Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile Ser Leu Pro			
230	235 240		
act cgg tta ccg gag agc ttg taatggcaaaa ttcaccaaaa tatgcgggta	1186		
Thr Arg Leu Pro Glu Ser Leu			
245	250		
aagaagcacg agaaaagtta ggctggtggt acgccaatcg ctttttgttc tggcgacggt	1246		
taaccacgct gaggattcctt gccatgtttt taagcggacc ttattttggg gtgtggatct	1306		
tgaaggcaa ttacagtagt agtcttttgc ttgatttgat cccgatgact gatcctttga	1366		
ttatggcaga aagtctcgcg accggtttta tgccatccat gaccgcgttg ttgggtgccc	1426		
tgattgtggt ggtgctttat gccattttag ggagtcgcgt tttctgtgct tgggtttgtc	1486		
cgtaaacaat cgtgacagat gcgtccgctt ggctcagacg taaattagaa attcgtcaat	1546		
cggcaaaact cccacgaagt ttacgctatg cgatcttagt gatgattttg ttaggcagtg	1606		
cgctaagcgg gttattactt tgggaatggc tcaatccggt tgcagcacta ggtcgtgcgt	1666		
taatttacgg tttcgggtgcg acagtttggc ttgttcttgc ggtgttttta tttgatttat	1726		
ttattgtcga gcatggttgg tgtgggcatt tatgcccaat aggtgcagcc tatggtgtga	1786		
ttggtgcgaa aggacttttt cgtatcaaag ttgagcatcg ccaacaatgt gataattgca	1846		
tggattgcta taacgtctgt ccagaaccac aagtgttacg cgatccatta catgcaaaaa	1906		
agagtgaaag cccacttgtg ctttcaaaaag attgtatcag ctgtggacgt tgtatcgacg	1966		
tttgccctga aaaagtattt atttttacaa cacgatttaa tcattcagtt aatcattcgg	2026		
gggagtgatc aaaatgaaaa aaacaatgct aattttgacc gcactttttg ctttcacggt	2086		
caatgccaat gaagtcaaag tgggcaaaaag tttaacaagat tcacctgaaa atatcgcgcc	2146		
agccttcac aatacaccaa aagaaagtgg cttggcgccg ttaaactatg tgaaccaacc	2206		

accgatggtg ccacacgcga cgaaaaacta tcaggtgacg aaaaatatca accaatgttt 2266
aacttgatcat agcccagaag cctcacgtgt tactggtgca acacgcatca gtccaaccca 2326
ctttatggat cgtgatggtg acattgtcgg aggcacctca cctcgccgtt acttctgttt 2386
acaatgccat gtctctcaat ctgatgttga gccgattatt caaaatgaat ttaaaccgat 2446
ggctgggtttt ggtaaataag ttaaggacgg aactatgttg aacttaatta aacgcttttg 2506
gaaatgggtt cgctcgccca gtcgtattgc cgttgggtacc ttgattacc ttgcttttat 2566
tgcaggtatt gtctcttggg ttgggtttta ttatggctta gagcaaacca atacagagga 2626
attctgtgtt agttgtcaca gtaatgatgt gtatccagaa tatttacata cggcgcat 2686
tttaaactgc agtggagtaa aagccacttg tctgtattgc catgtaccgc acgaatttat 2746
tccaaaaatg atccgtaaag tccaagccag tcgagaagtg tatgcgcac ttatgggtta 2806
tacggatacc attgataaat ttaactcccg tcgtttgcat atggcagaac gtgaatgggc 2866
acgattaaaa gccataaact cgcaggaatg ccgtaactgc cataactttg agaatatgga 2926
ttttagtcag caaaaaacgg tggcggaata aatgcatgca cttgctataa aagaagaaaa 2986
aacctgtatt gactgtcaca aagggtatgc gcaccaatta ccgcatatga gcggtgttga 3046
gtcgggtttt agtacggaac aaaaataaca cttttcttgt tctccacag gaaatctgca 3106
tcgtattcag gtgcagattt tttattttt acgatcatcc tcacaacctt ttcgctgata 3166
aataggatac aacgctagct acacgctatc ttgctgcttt ttgtgttgtt gtgagggtt 3226
atgtcatctt atctgectct tttattacgt ttgttacaaa ttccgcgttt gggttcgtg 3286
gcgatccagc gtttattgga gcacatcagt ccagcggaat taatggaata tgatacaaaa 3346
gcctttcaac agataggctg gacggcacag cagattcagc gttgggtttac gcctgagaac 3406
cgttatattg atcccgcggt agcctgggta aacgaacaac aacatattgt ggattgggtt 3466
gatctcatt atcctcctt gttaaagcaa acagaagagg caccacttgt cttgtttgtg 3526
aaaggggaag tggctacgt atctgcacag caagtggcga tcgtgggcag tcgtcattgt 3586
tcacgttatg ggaatactg ggcaaattat ttcgccactc aactggctta tgccgatatt 3646
gtggtgacca gtggttttagc gttaggtatt gatgggtttc cacatcaagc ggtagtggat 3706
atccacggga agacgattgc agtattaggc agtgggttag aggtcattta tccgaaaaa 3766
caccgaggtt tagccgaaaa aattattgaa catcaagggt cgttagtgtc tgaattttta 3826
cctttccaac cccctgtggc agaaaatttt ccacgtcgta atcgcatat tagtgggtta 3886
tctttgggga cattagtcat tgaagcctca gaaaacagt gttctttaat tactgcccgc 3946
tatgctttag agcaaatcg agatgttttt gcgttaccgg ggcagattca gcatggattt 4006
agccaagggt gtcataaact gattaaacag ggggcaatat tagtcgaaag tattcaggat 4066
attttagaac atctctcgcc ttattcgcat tgtgccatgc cagcggtgcc tcgtacggag 4126

aacgcctttt ctcaacaagt aacagacaca tcaaccatca atactgcgcg gataacgcc 4186
 gaacatccgg aattatatgc caaaattggc tatatgcccg tcagtattga tgtattagcc 4246
 caacaagtca atctacctat tgatacctta ttagtacagc ttttaacctt ggaattgcaa 4306
 gacttgattg ttgctgaaaa tggattatat cagcgcaa at aacggaaaga gtaaccacaa 4366
 atgagaaaagg actgtgttga aacggctatc aacatcagtc cttgcagtat attatctcat 4426
 atgacacgag acggcagttt catgagatta atagagacta aacgcttgta aatacggtag 4486
 tttgcctcgt tgtagcattt tctcaatatt gcctttgtga tcatcacgac ctaagcctcg 4546
 tagctcaata ttgataccaa tacttttgtc ataaaaaatt tgattcgcg tttgggttttc 4606
 tttgctggtc acactacgtc gggcaccaac attaatcgcc caacagcaag tgctgtattc 4666
 tagtcccaaa tattgtcaa caggctttct caacgcaaga tcttgataat gacgtgctac 4726
 caccgccc at tgatccgtga gtgccatgc cacagttaga ccaagctgtt ttatgtcttg 4786
 tccgtagcgg ttcgccgctg aggtgaggtt ttggtcaata tattgttga 4835

<210> 83

<211> 250

<212> PRT

<213> *Pasteurella multocida*

<400> 83

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

Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys
 180 185 190

Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
 195 200 205

Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
 210 215 220

Glu Glu Lys Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile
 225 230 235 240

Ser Leu Pro Thr Arg Leu Pro Glu Ser Leu
 245 250

<210> 84
 <211> 3494
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (2411)..(2719)

<220>
 <223> yyaM

<400> 84
 gtcaacgac cgaatacgac ggaagaaaac tatatgcaag tcatttatgg caagactgcg 60
 cgtctattcg aagctgcgac gcattgcgcc gcgatacttg ctcatgcgac ggaagcccaa 120
 gaaaatgctt tacgcgaata tgggtgttat ctaggcacag cttttcaatt agtcgatgat 180
 attttagatt atagtgcaga tgcaaaagca ctcggaacaa atattggtga tgatttagcg 240
 gaaggtaaac caacattacc gttattacac gccatgcac acggcaatcc agcacaagca 300
 aaattgattc gcgaagcgat tgagcaaggg ggtaagcgtg atattttaga ggatgtactg 360
 acaattatga cagaacataa atccctcgac tatgcatga tgcgcgctaa acaagaagca 420
 caaaaagccg ttgatgcatg tgcattattg cctgaaaatg aatataaaca agcgtaatt 480
 tcattagctt acttatccgt cgatcgcgct tattaaccac ttaataaggc gagacatggt 540
 agcgtaacga ccgcctaaag tgcggtcatt tatttagtaa ttttaaacac gacaatgaca 600
 gaacaaaaca tccctacgaa aaaaacacgc aaaggcaaag atcctcacgc gccttttgta 660
 cgcgaaaaat taccctacc aaatgggcat acaaattgt tattgcattc ttgttggtcg 720
 ccttgctcgg gagaagtaat ggaggcaatt catgcttcag gtattgaatt tactatttac 780
 ttctacaacc caaacattca ccattaaaa gaatatctca ttcgtaaaga agaaaatatt 840
 cgttttgctg aaaaatgggg cattccggtt attgatgccg attatgatcg tcaagaatgg 900
 tttgaccgtg ccaaaggcat ggaagatgag ccagagcgtg gtattcggtg cactatgtgc 960
 tttgatatgc gttttgaaaa agccgcagaa tatgcacaca acaatgggtt ccccgatttt 1020

```

actagctgct taggtatttc acgttggaac gacatgaacc aaatcaacgg ttgtggacac 1080
cgtgccgccg aaaaatatga tgatgtagtg tattgggatt ataactggcg taaagggtgg 1140
ggctcacaac gtatgattga aatcagtaag cgtgaacggt tttaccagca agaattattgc 1200
ggttgtgtgt attctttgcg tgacacgaat aaatggcgtg aagcaaacgg acgcaaaaaa 1260
attgaaattg gcaaattgta ttattccgcc gattaaaaca accaagtaaa ccatcgtgcc 1320
gtcatataac atggcggcac ttttttaggc tttatatatg caacgttttc gccaatcttt 1380
cgaaacctaa tgctaacgcc tcttcactaa tatttaatgc tggggcaaaa cgcaatacat 1440
taggaccgcg cactaaaatc attagccat tatctgctgc ttttttgaca aattcgctcg 1500
ctcttcctg atattgctcg ataagttctg caccaattaa caaaccttcg ccacggattt 1560
ctttaataa gccacattgc tgattaattt cttgcagctt ttgcataaat ttttcagaag 1620
tgcgctgaat tttttgcaag aatgggtggtg ctgaaatgat atcaatcact ttttctgcca 1680
cggcacaagc gagaggattg ccaccaaagg tgggtgccatg caccgaggt gcaaaacttt 1740
tggcgatctc atgcgttgct aacgaatgag aaaattgtga cagattgggc tccaacggga 1800
cgtgcggtg agattgggga tacgcaagta cgttatgaaa ttgagcaggt gagttctagc 1860
aattatagtg cactgtttgt ctccatttta cagatgaaac gtaatgaggt ggattttagt 1920
ccacatttag cggataaaca acgttatagt tctgatcgtg tgaaccaact tgttggtgaa 1980
ttagatgcgt cttatcgtaa acaagtcgtg gatttgaata acagcggatt gatgccatt 2040
cagtctgtat tcggtacgga cagtaatggg cgtactgctc tcgtgttagg cgcacccttt 2100
aatcatgcgt ggacaaaact aggacaagtt ttaccgcagc ttgaatttga tattaagat 2160
gaaattattg gtcgtggggt aaggaggtta aaataccgtc cagctggagc aaaaagttgg 2220
tggtggccat ttggtcgtgc tgaaggcagt agcggactga aaacaggtac ctattttatg 2280
cagttaagcg ccttagggaa gcaaagtgcg gtggtgatga ccgatgatga tggcaatgcg 2340
ttatctgggg agcaagctca ggcgttttat caagcattac aaaatctctt agcgaaataa 2400
tacagtcaag atg act aaa ctc agt atc cag cga gat aac ttg att tgt 2449
          Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys
            1             5             10

ttg agt tat gtc gca tta atg gga ttc ggc ttt ccc att atg cgt tat 2497
Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr
      15             20             25

atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt ctc 2545
Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu
      30             35             40             45

tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct 2593
Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala
            50             55             60

gag tta aca tct tcg ggg gct ggc gtc cag tcc gtt gcg atg ttg ccg 2641

```

Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro
 65 70 75
 agt tca agt tta ggt ttc tta ata ttg aaa act gta cca tct ttt tca 2689
 Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser
 80 85 90
 tac gtt aca atc tca aca ctt aat cgc gtt tgaccttcg atttttgata 2739
 Tyr Val Thr Ile Ser Thr Leu Asn Arg Val
 95 100
 gtcaaagact actgagtaac gctttagtagc gcgtgaatcg actgttacat aagccgatat 2799
 gtcagaataa gtactgccgg tatatcgtct taatctaaga ttaagcttgc cacttttggt 2859
 cgataaagcg tcaaacgaaa gcacgacttt accgtccttg acttccacct gatcttcaat 2919
 gagcacttga cttagtgcga ccaatcgacc gttggcagtc agtgtcgcaa tgccgtgac 2979
 cgtatcaagc gttacaccgc tattttttcc ccagttttta ttgagctttt cactatgttt 3039
 cagtaagttt ctgccaccaa tctgcaactg attaaactta gttcaagcg tttcactctt 3099
 gactgcaagc gacttggttt catttgtaac cgtctgctca agtgctgtga ttttggatgt 3159
 taaatctaac ttagttgcat tgacttcac agtcattct gactttaact cttttctcgc 3219
 aagtgcgcc acttcatctt tgctagcttt cgtttctttt aagtcagaaa tgccactagt 3279
 attttgcgcc actttagaat cgagcgtttc tagttttgta gagaaagatt tgtctttttc 3339
 gctagccgtt ttttgaatta gctgtatttc actttcgctc aatccaactc tagcagttag 3399
 actgtctagc ttgtcagcag tagatttatt cacagtcgct tgtgattgct tgtgttgaat 3459
 aatatccgcg cttacttccg agatagccac gtcga 3494

<210> 85

<211> 103

<212> PRT

<213> Pasteurella multocida

<400> 85

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

100

<210> 86
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 86
aggccggtac cggccgcct

19

<210> 87
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 87
cggccggtac cggcctagg

19

<210> 88
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 88
catggtaccc attctaac

18

<210> 89
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 89
ctaggtacct acaacctc

18

<210> 90
<211> 119
<212> DNA
<213> Artificial Sequence

<220>
<221>
<222>
<223> Description of Artificial Sequence: transposon
insert

<220>

<221> misc_feature
<222> 25
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 27
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 29
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 31
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 33
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 35
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 37
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 39
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 41
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 43
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 45
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 47
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 49
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 51
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 53
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 55
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 57
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 59
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 61
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 63
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 65
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 67
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 69
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 71
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 73
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 75
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 77
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 79
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 81
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 83
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 85
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 87
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 89
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 91
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 93
<223> N = A or T or G or C

<400> 90
ctaggtacct acaacctcaa gcttnknknk nknknknknk nknknknknk nknknknknk 60
nknknknknk nknknknknk nknknknknk nknkaagctt ggtagaatg ggtaccatg 119

<210> 91
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 91
tacctacaac ctcaagct 18

<210> 92
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 92
taccattctt aaccaagc 18

<210> 93
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 93
tacctacaac ctcaagctt 19

<210> 94
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 94
taccattctt aaccaagctt 20

<210> 95
<211> 19
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 95
ggcagagcat tacgctgac 19

<210> 96
<211> 27
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 96
gtaccggcca ggcggccacg cgtattc 27

<210> 97
 <211> 531
 <212> DNA
 <213> *Actinobacillus pleuropneumoniae*

<220>
 <223> atpG

<400> 97
 tgttgagctt ggttttagtag ggtcgaaagg cgtaagcttt taccaaaatc taggcttaaa 60
 cgtgagatct caagtaacgg gattaggcga taatccggaa atggaacgta tcgtgggcgc 120
 agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcgggtt acgtcgctta 180
 caaccgtttt gaaaatacga tgtcacaaaa acctgttatc gcacagttac ttccggttacc 240
 taaactagat gacgatgaat tagatacgaa aggttcatgg gattatattt atgaaccgaa 300
 tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360
 agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420
 agataatgcg ggtacattaa tcgatgaatt acaattagtg tataacaaag ctgcgccaagc 480
 aagcattaca aatgaattaa acgaaattgt tgcgggtgcc gcagcaattt a 531

<210> 98
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 98
 tctccattcc cttgctgcgg caccc 25

<210> 99
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: primer

<400> 99
 ggattacagc cggatccggg 20

<210> 100
 <211> 1034
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <223> cap5E

<220>
 <221> CDS
 <222> (1) .. (1032)

```

<400> 100
atg ttt aaa aat aaa aca ctt tta att aca ggt gga acg ggt tct ttt 48
Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe
1 5 10 15

ggt aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96
Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile
20 25 30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa 144
Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys
35 40 45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192
Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr
50 55 60

gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct 240
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala
65 70 75 80

gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca 288
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala
85 90 95

gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc 336
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile
100 105 110

caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg 384
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val
115 120 125

tac cca att aat gcg atg ggc att tct aaa gca atg atg gaa aaa gtc 432
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val
130 135 140

atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt 480
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys
145 150 155 160

tgt act cgc tat ggc aat gtc atg gca tcg cgt ggt tcg gtt atc cca 528
Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro
165 170 175

tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat 576
Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp
180 185 190

cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta 624
Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu
195 200 205

gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa 672
Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln
210 215 220

aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa 720
Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu
225 230 235 240

tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat 768
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His

```

245										250										255										
gga	gag	aaa	gca	ttc	gaa	gct	tta	tta	agc	cgt	gaa	gaa	atg	gtt	cat	816														
Gly	Glu	Lys	Ala	Phe	Glu	Ala	Leu	Leu	Ser	Arg	Glu	Glu	Met	Val	His															
			260					265					270																	
gca	att	aat	gaa	ggg	aat	tat	tat	cgc	atc	cca	gcc	gat	caa	cgc	agt	864														
Ala	Ile	Asn	Glu	Gly	Asn	Tyr	Tyr	Arg	Ile	Pro	Ala	Asp	Gln	Arg	Ser															
		275					280					285																		
tta	aat	tac	agt	aaa	tat	gtc	gaa	aaa	ggg	gaa	cca	aaa	att	acc	gaa	912														
Leu	Asn	Tyr	Ser	Lys	Tyr	Val	Glu	Lys	Gly	Glu	Pro	Lys	Ile	Thr	Glu															
	290					295					300																			
gtc	acc	gac	tac	aac	tca	cat	aat	act	gag	cgt	ttg	act	gtc	aag	gaa	960														
Val	Thr	Asp	Tyr	Asn	Ser	His	Asn	Thr	Glu	Arg	Leu	Thr	Val	Lys	Glu															
305					310					315					320															
atg	aag	cag	tta	ctg	ctt	aaa	ctt	gaa	ttc	ata	cag	aaa	atg	att	gag	1008														
Met	Lys	Gln	Leu	Leu	Lys	Leu	Glu	Phe	Ile	Gln	Lys	Met	Ile	Glu																
			325					330					335																	
ggg	gaa	tac	atc	tca	ccg	gag	gta	ta								1034														
Gly	Glu	Tyr	Ile	Ser	Pro	Glu	Val																							
			340																											

<210> 101

<211> 344

<212> PRT

<213> Pasteurella multocida

<400> 101

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

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

<210> 102
 <211> 4931
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> fhaB2
 <220>
 <221> CDS
 <222> (1)..(4929)

<220>
 <221> misc_feature
 <222> 1632
 <223> Xaa = any or unknown amino acid

<400> 102
 atg aac aaa aat cgt tac aaa ctc att ttt agt caa gtc aaa ggt tgt 48
 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
 1 5 10 15
 ctc gtt cct gtg gca gaa tgt att aac tca gct att agc aat ggt tca 96
 Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser

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

Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys	
275 280 285	
caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act	912
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	
290 295 300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa	960
Leu Ile Ala Gly Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	
305 310 315 320	
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga	1008
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	
325 330 335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca	1056
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	
340 345 350	
gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat	1104
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	
355 360 365	
gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg	1152
Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr	
370 375 380	
att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa	1200
Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys	
385 390 395 400	
aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg	1248
Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr	
405 410 415	
aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa	1296
Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys	
420 425 430	
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt	1344
Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly	
435 440 445	
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat	1392
Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp	
450 455 460	
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag	1440
Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu	
465 470 475 480	
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct	1488
Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala	
485 490 495	
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att	1536
Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile	
500 505 510	
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc	1584
Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg	
515 520 525	

ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc	1632
Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser	
530 535 540	
ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa	1680
Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu	
545 550 555 560	
agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta	1728
Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu	
565 570 575	
aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac	1776
Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn	
580 585 590	
gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct	1824
Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala	
595 600 605	
aat ata acg ttg aat gtg gaa gaa aac ttt gtt aat cgt gca gga aca	1872
Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr	
610 615 620	
ctg gca act ggt aaa aca ctg aca att aat acc gaa agt ggc agt att	1920
Leu Ala Thr Gly Lys Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile	
625 630 635 640	
tac aat ctt ggt ggg aca tta ggt gct gga aaa tca tta aaa ctg act	1968
Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr	
645 650 655	
gct aaa tca acg gaa gaa ggt atg gga aat att gtt aac caa gaa aac	2016
Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn	
660 665 670	
ggt tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct	2064
Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser	
675 680 685	
gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat	2112
Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His	
690 695 700	
act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg agt tat	2160
Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr	
705 710 715 720	
aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta	2208
Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val	
725 730 735	
cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa	2256
His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu	
740 745 750	
caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc cgt tct	2304
Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser	
755 760 765	
gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca	2352
Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser	
770 775 780	

aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt	2400
Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe	
785 790 795 800	
aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt aac caa	2448
Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln	
805 810 815	
aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac	2496
Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr	
820 825 830	
tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca	2544
Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala	
835 840 845	
tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc	2592
Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly	
850 855 860	
tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt	2640
Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser	
865 870 875 880	
gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa	2688
Ala Tyr Gln Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys	
885 890 895	
gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat	2736
Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp	
900 905 910	
gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc	2784
Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe	
915 920 925	
att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa	2832
Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu	
930 935 940	
ggg aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag	2880
Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys	
945 950 955 960	
ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca	2928
Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser	
965 970 975	
gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac	2976
Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp	
980 985 990	
ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta	3024
Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu	
995 1000 1005	
ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct cct att	3072
Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile	
1010 1015 1020	
gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc	3120
Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser	
1025 1030 1035 1040	

cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat gag tct	3168
His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser	
1045 1050 1055	
gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa gag atg	3216
Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met	
1060 1065 1070	
ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca	3264
Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro	
1075 1080 1085	
cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt	3312
Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe	
1090 1095 1100	
gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag	3360
Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu	
1105 1110 1115 1120	
ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta	3408
Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu	
1125 1130 1135	
gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa	3456
Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys	
1140 1145 1150	
gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag	3504
Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu	
1155 1160 1165	
tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga	3552
Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg	
1170 1175 1180	
ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa cgt gtt	3600
Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val	
1185 1190 1195 1200	
gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa att gct	3648
Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala	
1205 1210 1215	
aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc	3696
Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg	
1220 1225 1230	
cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag aag aaa	3744
Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Lys Lys	
1235 1240 1245	
caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct gaa cag	3792
Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln	
1250 1255 1260	
aaa caa aaa gct gag gag aaa gtt gca caa gaa aga tta gac att gaa	3840
Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu	
1265 1270 1275 1280	
caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag gca tca	3888
Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser	
1285 1290 1295	

aaa aat gtt tta ttg aaa gcg att gat gaa gaa cgt cca aaa gtg gaa	3936
Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu	
1300 1305 1310	
act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac	3984
Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp	
1315 1320 1325	
tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat aca aaa	4032
Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys	
1330 1335 1340	
ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa	4080
Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln	
1345 1350 1355 1360	
gtg att act cgc tcg att gag aaa aaa gta gat aac cac ctt aac caa	4128
Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln	
1365 1370 1375	
aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat	4176
Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn	
1380 1385 1390	
tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta	4224
Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu	
1395 1400 1405	
act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg tat gtc	4272
Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val	
1410 1415 1420	
aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt tat ttc	4320
Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe	
1425 1430 1435 1440	
gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta ggc act	4368
Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr	
1445 1450 1455	
ggg act atc aga gtt ggt gaa gct aag att aaa gcc aaa gat gtg gtg	4416
Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val	
1460 1465 1470	
aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat	4464
Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn	
1475 1480 1485	
aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca cgt tta	4512
Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu	
1490 1495 1500	
gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat	4560
Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp	
1505 1510 1515 1520	
gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat	4608
Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His	
1525 1530 1535	
tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg	4656
Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser	
1540 1545 1550	

```

gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg aat ctc 4704
Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
      1555                      1560                      1565

aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc tcg ccg 4752
Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
      1570                      1575                      1580

agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa gtc cca 4800
Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
      1585                      1590                      1595                      1600

ctt tta ggc gtg tcc gtc tcc atc cag ttt att cag agc ata cta gtg 4848
Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
      1605                      1610                      1615

agg caa ctt caa gag gga tca atc ttc gaa gta ggg cac tta cat ntt 4896
Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
      1620                      1625                      1630

gcg gta gac aga aga tgt gaa cca agc ggg gag ta 4931
Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
      1635                      1640

```

<210> 103

<211> 1643

<212> PRT

<213> Pasteurella multocida

<220>

<221> misc_feature

<222> 1632

<223> Xaa = any or unknown amino acid

<400> 103

```

Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Gln Val Lys Gly Cys
  1             5             10             15

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

Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
      35             40             45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
      50             55             60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
      65             70             75             80

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

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

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
      115            120            125

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

```

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

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
 485 490 495
 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
 500 505 510
 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
 515 520 525
 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
 530 535 540
 Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
 545 550 555 560
 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
 565 570 575
 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
 580 585 590
 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
 595 600 605
 Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
 610 615 620
 Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
 625 630 635 640
 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
 645 650 655
 Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
 660 665 670
 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
 675 680 685
 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
 690 695 700
 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
 705 710 715 720
 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
 725 730 735
 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
 740 745 750
 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
 755 760 765
 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
 770 775 780
 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
 785 790 795 800
 Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
 805 810 815

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

Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
 1155 1160 1165
 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
 1170 1175 1180
 Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Lys Arg Val
 1185 1190 1195 1200
 Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
 1205 1210 1215
 Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
 1220 1225 1230
 Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys
 1235 1240 1245
 Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
 1250 1255 1260
 Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
 1265 1270 1275 1280
 Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
 1285 1290 1295
 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
 1300 1305 1310
 Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp
 1315 1320 1325
 Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
 1330 1335 1340
 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
 1345 1350 1355 1360
 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
 1365 1370 1375
 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
 1380 1385 1390
 Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
 1395 1400 1405
 Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
 1410 1415 1420
 Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
 1425 1430 1435 1440
 Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
 1445 1450 1455
 Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
 1460 1465 1470
 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
 1475 1480 1485

Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
 1490 1495 1500
 Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
 1505 1510 1515 1520
 Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
 1525 1530 1535
 Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
 1540 1545 1550
 Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
 1555 1560 1565
 Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
 1570 1575 1580
 Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
 1585 1590 1595 1600
 Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
 1605 1610 1615
 Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
 1620 1625 1630
 Ala Val Asp Arg Arg Cys Glu Pro Ser Gly Glu
 1635 1640

<210> 104
 <211> 2009
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> hmbR

<220>
 <221> CDS
 <222> (1)..(2007)

<400> 104
 atc cgt ggc gtt gat aaa gat cgt gtc gct gtt att gtt gat gga ata 48
 Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
 1 5 10 15
 ccg cag gct gaa tcg act ata tct act tcc gca cgt tat tcg act gaa 96
 Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
 20 25 30
 cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg 144
 Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45
 ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg 192
 Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60
 tta ggt gga acc gtg gag ttt acc aca aaa gat att gag gac ttt gtc 240
 Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80

gaa cct ggt cgc cat ttg ggc ttt ttg tct aaa acc ggc tat act tca	288
Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser	
85 90 95	
aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa	336
Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu	
100 105 110	
cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca	384
His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr	
115 120 125	
atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa	432
Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys	
130 135 140	
ccc aat ccg ctc aac tac tat act aca tca tgg tta acg aaa gtc ggt	480
Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly	
145 150 155 160	
tac gat att aat aac act cat cgt ttt aca ctg ttt tta gaa gat cgc	528
Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg	
165 170 175	
cgt gaa aag aag ctt acc gaa gaa aaa aca tta ggg ctt agt gat gca	576
Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala	
180 185 190	
gtg cgt ttt gct aat gat caa acc cct tat ctc cgt tat ggt att gaa	624
Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu	
195 200 205	
tat cga tat aac ggc ttg tct tgg ttg gaa acg gta aag ctt ttt ttg	672
Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu	
210 215 220	
gca aag cag aaa atc gaa caa cgt tct gct ctc caa gag ttt gat att	720
Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile	
225 230 235 240	
aat aat agg aat aaa ttg gat tcg act atg tcg ttt gta tat tta caa	768
Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln	
245 250 255	
aga cag aat ata gct cgg gga gaa ttt tca acg agt cct tta tat tgg	816
Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp	
260 265 270	
ggg ccg agt cgc cat cgt tta tct gcg aaa ttc gaa ttt cgt gat aag	864
Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys	
275 280 285	
ttt tta gaa aat atg aat aag cat ttt acg ttt cgg ccg tgg caa atc	912
Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile	
290 295 300	
aat aga ttc aga caa caa ggt cga aat aac tat aca gaa gtg ttt ccc	960
Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro	
305 310 315 320	
gtt aaa tcc cga gag ttt tct ttt tct ctt atg gac gac att aag att	1008
Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile	
325 330 335	

ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg tgg gat cac tat aac	1056
Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn	
340 345 350	
tat aag cca tta tta aat tct cag cat aat atc aac agg aca cag aga	1104
Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg	
355 360 365	
tta cct tat cca aaa aca tca tcc aaa ttt tcg tat caa ttg agt tta	1152
Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu	
370 375 380	
gag tat caa tta cat cca tca cat caa att gca tac cgt tta agt acc	1200
Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr	
385 390 395 400	
ggg ttt agg gtt ccc cgt gtt gaa gat ctt tat ttt gaa gac cga gga	1248
Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly	
405 410 415	
aaa agt tct tca caa ttt ctt cct aac ccc gat cta caa ccg gaa act	1296
Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr	
420 425 430	
gca ctg aat cat gaa ata agt tac cgt ttc caa aat caa tat gcc cat	1344
Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His	
435 440 445	
ttc agc gtc ggg ctt ttc cgt aca cgt tat cat aac ttt att caa gaa	1392
Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu	
450 455 460	
cgt gag atg acc tgt gat aaa att cca tat gag tat aat agg act tat	1440
Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr	
465 470 475 480	
gga tat tgc acg cat aat act tat gta atg ttt gtt aat gaa cct gaa	1488
Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu	
485 490 495	
gcc gtg att aaa ggg gtt gaa gta agc ggt gct tta aat ggg tcg gca	1536
Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala	
500 505 510	
ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc	1584
Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser	
515 520 525	
aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg	1632
Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp	
530 535 540	
aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt	1680
Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser	
545 550 555 560	
ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa	1728
Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu	
565 570 575	
acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta	1776
Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu	
580 585 590	

agt cca tcc tac ttt gtt gtt gat ttt acg ggg caa gtt aac ctc agt 1824
 Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
 595 600 605
 aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat 1872
 Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
 610 615 620
 tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act 1920
 Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
 625 630 635 640
 tcc cgt tct gtc cgt gct aac agc cca ggc att aat cgg ttt acc gca 1968
 Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
 645 650 655
 cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta 2009
 Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
 660 665

<210> 105
 <211> 669
 <212> PRT
 <213> Pasteurella multocida

<400> 105
 Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
 1 5 10 15
 Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
 20 25 30
 Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45
 Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60
 Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80
 Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
 85 90 95
 Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
 100 105 110
 His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
 115 120 125
 Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
 130 135 140
 Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
 145 150 155 160
 Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
 165 170 175
 Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
 180 185 190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
 195 200 205
 Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
 210 215 220
 Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
 225 230 235 240
 Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
 245 250 255
 Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
 260 265 270
 Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
 275 280 285
 Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
 290 295 300
 Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
 305 310 315 320
 Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
 325 330 335
 Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
 340 345 350
 Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
 355 360 365
 Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
 370 375 380
 Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
 385 390 395 400
 Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
 405 410 415
 Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
 420 425 430
 Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
 435 440 445
 Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
 450 455 460
 Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
 465 470 475 480
 Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
 485 490 495
 Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
 500 505 510
 Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
 515 520 525

Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
 530 535 540
 Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
 545 550 555 560
 Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
 565 570 575
 Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
 580 585 590
 Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
 595 600 605
 Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
 610 615 620
 Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
 625 630 635 640
 Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
 645 650 655
 Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
 660 665

<210> 106
 <211> 908
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> lgtC

<220>
 <221> CDS
 <222> (1)..(906)

<400> 106
 atg aat att tta ttt gtt tct gat gat gtt tat gct aaa cat ctg gtg 48
 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
 1 5 10 15
 gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
 20 25 30
 tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 35 40 45
 gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60
 gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80

```

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta 288
Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
      85                      90                      95

aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta 336
Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
      100                      105                      110

gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt 384
Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys
      115                      120                      125

tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att 432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile
      130                      135                      140

tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt 480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe
      145                      150                      155                      160

aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac 528
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp
      165                      170                      175

ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata 576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile
      180                      185                      190

ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt 624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe
      195                      200                      205

aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga 672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly
      210                      215                      220

aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt 720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
      225                      230                      235                      240

att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa 768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
      245                      250                      255

cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga 816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg
      260                      265                      270

ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc 864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
      275                      280                      285

ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta 908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
      290                      295                      300

```

<210> 107

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 107

```

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

```

<210> 108

<211> 2054

<212> DNA

<213> Pasteurella multocida

<220>

<223> pnp

<220>

<221> CDS

<222> (1)..(2052)

<400> 108

atg gca agt atg gat gat act act gtg ttt gtc aca gtg gtt gcc aaa	48
Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys	
1 5 10 15	
aaa gat gtg aaa gaa ggt caa gac ttc ttc cca tta act gtt aac tat	96
Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr	
20 25 30	
caa gag cgt act tat gct gca ggc cgt att cct ggt ggc ttt ttc aaa	144
Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys	
35 40 45	
cgt gaa ggt cgt cct tct gaa ggc gaa act tta att gct cgt tta att	192
Arg Glu Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile	
50 55 60	
gac cgt cca att cgt cct ctt ttc cca gaa ggt ttt tat aac gaa atc	240
Asp Arg Pro Ile Arg Pro Leu Phe Pro Glu Gly Phe Tyr Asn Glu Ile	
65 70 75 80	
caa atc gtg gcg aca gtg gtg tct gtt aat ccg caa att tgt cca gat	288
Gln Ile Val Ala Thr Val Val Ser Val Asn Pro Gln Ile Cys Pro Asp	
85 90 95	
tta gtg gca atg atc ggt gca tct gcg gca ctt tct tta tca ggt gtg	336
Leu Val Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val	
100 105 110	
cca ttt aat ggc cct atc ggt gcg gca cgt gtt ggt ttt att gat gat	384
Pro Phe Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asp Asp	
115 120 125	
caa ttt gtg tta aac cca acc atg aac gag caa aaa caa agc cgt tta	432
Gln Phe Val Leu Asn Pro Thr Met Asn Glu Gln Lys Gln Ser Arg Leu	
130 135 140	
gac ttg gtt gtc gcg gga aca gat aaa gcg gtg tta atg gtg gaa tct	480
Asp Leu Val Val Ala Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser	
145 150 155 160	
gaa gcc gat gta tta acc gaa gaa caa atg tta gct gcg gtg gtg ttt	528
Glu Ala Asp Val Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe	
165 170 175	
ggt cat cag caa caa caa gtg gtg att gac gcg atc aaa gaa ttt acc	576
Gly His Gln Gln Gln Gln Val Val Ile Asp Ala Ile Lys Glu Phe Thr	
180 185 190	
gca gaa gcc ggt aaa ccg cgt tgg gat tgg gtg gca cct gaa cca aat	624
Ala Glu Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn	
195 200 205	
acc gcg tta att gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc	672
Thr Ala Leu Ile Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly	
210 215 220	

gaa gca tac cgt atc act gaa aaa caa gca cgt tat gaa caa att gat	720
Glu Ala Tyr Arg Ile Thr Glu Lys Gln Ala Arg Tyr Glu Gln Ile Asp	
225 230 235 240	
gcg att aaa gct gat gtg att gca caa atc aca gct gaa gta gca gaa	768
Ala Ile Lys Ala Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu	
245 250 255	
ggc gaa gac atc agt gaa ggg aaa att gtc gat att ttc acc gca ctt	816
Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu	
260 265 270	
gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att	864
Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile	
275 280 285	
gat ggt cgt aca gtg gat act gtt cgt gca tta gat att tgt act ggt	912
Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly	
290 295 300	
gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca	960
Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr	
305 310 315 320	
cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att	1008
Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile	
325 330 335	
att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac	1056
Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr	
340 345 350	
aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca	1104
Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro	
355 360 365	
aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct	1152
Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala	
370 375 380	
gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc	1200
Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val	
385 390 395 400	
tct gaa atc aca gaa tca aat ggt tct tct tct atg gca tcg gtt tgt	1248
Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys	
405 410 415	
ggt gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg	1296
Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala	
420 425 430	
gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg	1344
Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val	
435 440 445	
gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac	1392
Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp	
450 455 460	
ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat	1440
Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp	
465 470 475 480	

```

atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac 1488
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn
485 490 495

caa gcg aaa agc gca cgt tta cac att tta ggt gtg atg gag caa gcg 1536
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala
500 505 510

atc cca gcg cca cgt gcg gat att tct gat ttt gca ccg cgt att tac 1584
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr
515 520 525

act atg aaa att gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt 1632
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly
530 535 540

ggg gca acc att cgt gcc tta aca gaa gaa aca ggt acc tca att gat 1680
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp
545 550 555 560

atc gat gat gat ggt acg gtg aag att gct gcg gtt gat ggc aat tca 1728
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser
565 570 575

gca aaa gag gtg atg gcg cgt att gaa gat att act gca gaa gtt gaa 1776
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu
580 585 590

gcg ggt gca gtg tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt 1824
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly
595 600 605

gcc ttc gtt tct atc gta ggt aac aaa gaa ggc tta gtg cat att tct 1872
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser
610 615 620

caa atc gcg gaa gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg 1920
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val
625 630 635 640

ggg caa gaa gtg act gtt aaa gtg gtt gag att gat cgt caa ggt cgt 1968
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg
645 650 655

att cgt tta acc atg aaa gaa gtt gca cca aag caa gaa cac gtt gat 2016
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp
660 665 670

tct gtt gtc gca gac gtt gcc gca gaa gaa aac gca ta 2054
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala
675 680

```

<210> 109

<211> 684

<212> PRT

<213> Pasteurella multocida

<400> 109

```

Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
1 5 10 15

```

```

Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr

```

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

355	360	365
Lys Arg Arg Glu Ile Gly 370	His Gly Arg Leu Ala 375	Lys Arg Gly Val Ala 380
Ala Val Met Pro Thr 385	Leu Ala Glu Phe Pro 390	Tyr Val Val Arg Val Val 395 400
Ser Glu Ile Thr 405	Glu Ser Asn Gly Ser 410	Ser Ser Met Ala Ser Val Cys 415
Gly Ala Ser Leu Ala 420	Leu Met Asp Ala Gly Val Pro 425	Ile Lys Ala Ala 430
Val Ala Gly Ile Ala 435	Met Gly Leu Val Lys Glu Asp 440	Glu Lys Phe Val 445
Val Leu Ser Asp Ile 450	Leu Gly Asp Glu Asp His 455	Leu Gly Asp Met Asp 460
Phe Lys Val Ala Gly 465	Thr Arg Thr Gly Val Thr 470	Ala Leu Gln Met Asp 475 480
Ile Lys Ile Glu Gly 485	Ile Thr Ala Glu Ile Met Gln 490	Ile Ala Leu Asn 495
Gln Ala Lys Ser 500	Ala Arg Leu His Ile Leu Gly 505	Val Met Glu Gln Ala 510
Ile Pro Ala Pro Arg 515	Ala Asp Ile Ser Asp Phe 520	Ala Pro Arg Ile Tyr 525
Thr Met Lys Ile Asp 530	Pro Lys Lys Ile Lys Asp 535	Val Ile Gly Lys Gly 540
Gly Ala Thr Ile Arg 545	Ala Leu Thr Glu Glu Thr 550	Gly Thr Ser Ile Asp 555 560
Ile Asp Asp Asp Gly 565	Thr Val Lys Ile Ala Ala 570	Val Asp Gly Asn Ser 575
Ala Lys Glu Val Met 580	Ala Arg Ile Glu Asp Ile 585	Thr Ala Glu Val Glu 590
Ala Gly Ala Val Tyr 595	Lys Gly Lys Val Thr Arg 600	Leu Ala Asp Phe Gly 605
Ala Phe Val Ser Ile 610	Val Gly Asn Lys Glu Gly 615	Leu Val His Ile Ser 620
Gln Ile Ala Glu Glu 625	Arg Val Glu Lys Val Ser 630	Asp Tyr Leu Ala Val 635 640
Gly Gln Glu Val Thr 645	Val Lys Val Val Glu Ile 650	Asp Arg Gln Gly Arg 655
Ile Arg Leu Thr Met 660	Lys Glu Val Ala Pro Lys 665	Gln Glu His Val Asp 670
Ser Val Val Ala Asp 675	Val Ala Ala Glu Glu Asn 680	Ala

<210> 110
 <211> 1514
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> purF

<220>
 <221> CDS
 <222> (1)..(1512)

<400> 110
 atg tgt ggt att gtt ggt att gtt agc caa agc ccc gtt aac caa tca 48
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
 1 5 10 15
 att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc 96
 Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
 20 25 30
 ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg 144
 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
 35 40 45
 aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta 192
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu
 50 55 60
 caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc 240
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65 70 75 80
 tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc 288
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
 85 90 95
 tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa 336
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
 100 105 110
 gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat 384
 Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
 115 120 125
 tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa 432
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
 130 135 140
 aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg 480
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
 145 150 155 160
 cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt 528
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
 165 170 175
 cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg 576
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
 180 185 190
 tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc 624
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser

195	200	205	
gaa agt atc gca tta gat Glu Ser Ile Ala Leu Asp 210	aca gtg ggt ttt gag ttt Thr Val Gly Phe Glu Phe 215 220	gta cga gat gta Val Arg Asp Val	672
caa ccc ggc gaa gcg att tat gtc acg ttt gaa ggg gaa atg tat gct Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala 225 230 235 240			720
cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt gaa tac Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr 245 250 255			768
gtc tat ttt gca cgt cca gac tct tgc atc gat ggg gtt tct gtt tat Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr 260 265 270			816
gct gcc cgt gtt cat atg gga caa cgt tta ggt gaa aaa att gca cgg Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg 275 280 285			864
gaa tgg gcg gat gtg gat gat att gat gtg gtc att cct gtg cct gaa Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu 290 295 300			912
acc tct aac gat att gct tta cgt att gcg cgc gtg tta aat aaa ccg Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro 305 310 315 320			960
tat cgt caa ggt ttt gtg aaa aat cgc tat gta gga cgt acg ttt att Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile 325 330 335			1008
atg ccg ggg cag gca ttg cga gtc agt tct gtt aga cgt aaa ctc aat Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn 340 345 350			1056
acc att gct tca gaa ttt aaa gat aag aat gtg tta tta gtt gac gac Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp 355 360 365			1104
tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga Ser Ile Val Arg Gly Thr Ser Glu Gln Ile Val Glu Met Ala Arg 370 375 380			1152
gcg gca ggt gcg aag aaa att tat ttt gcc tct gct gca cca gaa att Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile 385 390 395 400			1200
cgt tat cca aat gtg tat ggt att gat atg cca acc aaa aat gaa ttg Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu 405 410 415			1248
atc gct tat ggt cgt gat gta gat gaa att gct aac tta att ggt gtg Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val 420 425 430			1296
gat aaa ttg att ttc caa gat ttg gat gcg tta act ggt tct gtg caa Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln 435 440 445			1344
caa gaa aat cca agt att caa gac ttt gat tgt tcg gtg ttt aca ggg			1392

Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
 450 455 460

gtt tat gtg acg ggc gat att aca cct gaa tat ctg gat aat att gca 1440
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
 465 470 475 480

gaa cag cgt aat gat atc gcc aag aaa aag cgt gaa aaa gat gct acc 1488
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
 485 490 495

aat ctt gaa atg cac aat gaa aaa ta 1514
 Asn Leu Glu Met His Asn Glu Lys
 500

<210> 111
 <211> 504
 <212> PRT
 <213> Pasteurella multocida

<400> 111
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
 1 5 10 15

Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
 20 25 30

Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
 35 40 45

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

Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65 70 75 80

Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
 85 90 95

Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
 100 105 110

Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
 115 120 125

Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
 130 135 140

Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
 145 150 155 160

His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
 165 170 175

His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
 180 185 190

Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser
 195 200 205

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

Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe Glu Gly Glu Met Tyr Ala
 225 230 235 240
 Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr
 245 250 255
 Val Tyr Phe Ala Arg Pro Asp Ser Cys Ile Asp Gly Val Ser Val Tyr
 260 265 270
 Ala Ala Arg Val His Met Gly Gln Arg Leu Gly Glu Lys Ile Ala Arg
 275 280 285
 Glu Trp Ala Asp Val Asp Asp Ile Asp Val Val Ile Pro Val Pro Glu
 290 295 300
 Thr Ser Asn Asp Ile Ala Leu Arg Ile Ala Arg Val Leu Asn Lys Pro
 305 310 315 320
 Tyr Arg Gln Gly Phe Val Lys Asn Arg Tyr Val Gly Arg Thr Phe Ile
 325 330 335
 Met Pro Gly Gln Ala Leu Arg Val Ser Ser Val Arg Arg Lys Leu Asn
 340 345 350
 Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn Val Leu Leu Val Asp Asp
 355 360 365
 Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg
 370 375 380
 Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala Ser Ala Ala Pro Glu Ile
 385 390 395 400
 Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Lys Asn Glu Leu
 405 410 415
 Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile Ala Asn Leu Ile Gly Val
 420 425 430
 Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala Leu Thr Gly Ser Val Gln
 435 440 445
 Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp Cys Ser Val Phe Thr Gly
 450 455 460
 Val Tyr Val Thr Gly Asp Ile Thr Pro Glu Tyr Leu Asp Asn Ile Ala
 465 470 475 480
 Glu Gln Arg Asn Asp Ile Ala Lys Lys Lys Arg Glu Lys Asp Ala Thr
 485 490 495
 Asn Leu Glu Met His Asn Glu Lys
 500

<210> 112
 <211> 989
 <212> DNA
 <213> Pasteurella multocida

 <220>
 <223> rci

<220>

<221> CDS

<222> (1)..(987)

<400> 112

atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc	48
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser	
1 5 10 15	
aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct	96
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala	
20 25 30	
aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa	144
Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys	
35 40 45	
ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa	192
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln	
50 55 60	
aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga	240
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg	
65 70 75 80	
tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat	288
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp	
85 90 95	
tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa	336
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu	
100 105 110	
gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg	384
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val	
115 120 125	
ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg	432
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met	
130 135 140	
act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat	480
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr	
145 150 155 160	
tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa	528
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu	
165 170 175	
gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta	576
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu	
180 185 190	
ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa	624
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys	
195 200 205	
tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act	672
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr	
210 215 220	

```

aaa aac ggg cac tct aga gat gtg ccg ctt tcg caa aga gct gtt gcg 720
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala
225                230                235                240

cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag 768
Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln
                245                250                255

acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag 816
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu
                260                265                270

tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg 864
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu
275                280                285

acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc 912
Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser
290                295                300

gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat 960
Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn
305                310                315                320

atg agt gaa gtg gca aac ttg ttg gat ta 989
Met Ser Glu Val Ala Asn Leu Leu Asp
                325

```

```

<210> 113
<211> 329
<212> PRT
<213> Pasteurella multocida

```

```

<400> 113
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser
 1          5          10          15

Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala
          20          25          30

Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys
          35          40          45

Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln
          50          55          60

Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg
          65          70          75          80

Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp
          85          90          95

Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu
          100          105          110

Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val
          115          120          125

Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met
          130          135          140

Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr

```

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

<210> 114
 <211> 1190
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> sope

<220>
 <221> CDS
 <222> (1)..(1188)

<400> 114	
atg tct gaa gaa tat cta cat ggt gtc aaa gtc aca gaa atc aat caa	48
Met Ser Glu Glu Tyr Leu His Gly Val Lys Val Thr Glu Ile Asn Gln	
1 5 10 15	
gca att cgc aca att caa agt cta tca acc gca gtc atc ggt att gtc	96
Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val	
20 25 30	
tgt act gca aat gac gca gac aat gaa aca ttc cca ctc aat gaa ccc	144
Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro	
35 40 45	
gtt ctc atc aca aac gtg gca gcg gca att ggc aag gct gga aaa caa	192
Val Leu Ile Thr Asn Val Ala Ala Ile Gly Lys Ala Gly Lys Gln	

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

Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys
 305 310 315 320

gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc aca aaa 1008
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys
 325 330 335

ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt aac agt 1056
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser
 340 345 350

gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat tat cac 1104
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His
 355 360 365

cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att tct gat 1152
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp
 370 375 380

gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg ta 1190
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

<210> 115

<211> 396

<212> PRT

<213> Pasteurella multocida

<400> 115

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

Ala Ile Arg Thr Ile Gln Ser Leu Ser Thr Ala Val Ile Gly Ile Val
 20 25 30

Cys Thr Ala Asn Asp Ala Asp Asn Glu Thr Phe Pro Leu Asn Glu Pro
 35 40 45

Val Leu Ile Thr Asn Val Ala Ala Ala Ile Gly Lys Ala Gly Lys Gln
 50 55 60

Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys
 65 70 75 80

Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu
 85 90 95

Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu
 100 105 110

Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys
 115 120 125

Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys
 130 135 140

Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe
 145 150 155 160

Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln
 165 170 175

Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp
 180 185 190
 Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala
 195 200 205
 Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly
 210 215 220
 Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val
 225 230 235 240
 Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn
 245 250 255
 Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe
 260 265 270
 Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe
 275 280 285
 Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly
 290 295 300
 Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys
 305 310 315 320
 Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys
 325 330 335
 Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser
 340 345 350
 Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His
 355 360 365
 Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp
 370 375 380
 Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
 385 390 395

<210> 116
 <211> 2204
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unkK

<220>
 <221> CDS
 <222> (1)..(2202)

<400> 116
 atg aat aaa aat cgc tat aaa ctc att ttt agt aaa act aaa ggc tgt 48
 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
 1 5 10 15
 ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca 96
 Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser
 20 25 30

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

gaa caa aaa caa gcg att aca aaa gaa aga aca gga aat tcc gaa acc	912
Glu Gln Lys Gln Ala Ile Thr Lys Glu Arg Thr Gly Asn Ser Glu Thr	
290 295 300	
gat atc act ttt gtc gca ggt aac agt aaa tat gat tta aag aca cat	960
Asp Ile Thr Phe Val Ala Gly Asn Ser Lys Tyr Asp Leu Lys Thr His	
305 310 315 320	
caa gtg aca gaa aag cat acc gct gag gca caa ggt gaa att gcg att	1008
Gln Val Thr Glu Lys His Thr Ala Glu Ala Gln Gly Glu Ile Ala Ile	
325 330 335	
agc ggt gcg agt acc ggt gca atg tac ggt aaa aat atc aaa tta atc	1056
Ser Gly Ala Ser Thr Gly Ala Met Tyr Gly Lys Asn Ile Lys Leu Ile	
340 345 350	
gta acg gat aaa ggc gct ggg gta aaa cat gat ggc att att tta tct	1104
Val Thr Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser	
355 360 365	
gag gcg gat att caa att gaa acc cat gag ggc gat gtt gaa tta ggc	1152
Glu Ala Asp Ile Gln Ile Glu Thr His Glu Gly Asp Val Glu Leu Gly	
370 375 380	
aat aca aaa aat aat cag aat gag aat tat gcc aaa gct cat gcg gaa	1200
Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu	
385 390 395 400	
ggg aat ttt acg gtt aaa ggc ggt aag cac gtt att att ggt aag gaa	1248
Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu	
405 410 415	
gtt aaa gcc aac aaa gcg gtc gat att caa gca caa gaa aca aca gta	1296
Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val	
420 425 430	
aga caa aat gcg aaa tta act gcc aaa acg agt gcc aaa att aca gca	1344
Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala	
435 440 445	
agt aag agt gtg aat ctt gaa gat aac gcg aaa ctt att gct aat gag	1392
Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu	
450 455 460	
ctg agc aca aca acc aat aaa tta acc aat aaa ggt agc att tac ggc	1440
Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly	
465 470 475 480	
aag aaa gtg acg cta gat gct gat aat tta gtc aat agt aaa gaa atc	1488
Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile	
485 490 495	
tat gcg tct agc gaa ctt gat att caa acc aaa ggt cgt gat ctt tta	1536
Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu	
500 505 510	
ctt gag gat ggg gtt aat caa cca ctg agt ttc tta aaa ggc gct tca	1584
Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser	
515 520 525	
ttg tta gcg ccg ggg ttt gtc aac act ggg cta att cac agt aac ggt	1632
Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly	
530 535 540	

```

aat gcc aag ctc act ttt aaa gat gac acc agt ttt gtg act gaa gga 1680
Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
545          550          555          560

aat aac ttt atc aca gca aaa gac aac tta gaa atc acg gca aaa aat 1728
Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
565          570          575

gtt caa att gat caa gcg aaa aat att caa tta aac gcg aat atc acg 1776
Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
580          585          590

atc aat acc aag tct ggt ttt gtg aat tac ggt acc tta gca agt gct 1824
Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
595          600          605

caa aat tta acg att aat acc gaa caa ggc agc att tat aac ata ggc 1872
Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
610          615          620

ggt atc ttg ggg gcg ggt aaa agt ttg aat ctg agc gcg aaa aga gga 1920
Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly
625          630          635

gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat 1968
Glu Asn Gln Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
645          650          655

tct gaa ggc gcc atg aac ctc aca gcg gat cgc acg gtg tac aat tta 2016
Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
660          665          670

ggg aat att ttt gct aaa ggt gac gcg acg atc aat gca aac gcg tta 2064
Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
675          680          685

att aat gat gtt act ctc aca ggt cgt ctt gag tat caa gat ctg aaa 2112
Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
690          695          700

aaa gat tat acg cgt tat tat cgt atc aat gaa acg gca aaa cat ggt 2160
Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
705          710          715          720

tgg cat aat aac ttc tat gaa tta aac gtc gac aga gtt tct tg 2204
Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
725          730

```

<210> 117

<211> 734

<212> PRT

<213> Pasteurella multocida

<400> 117

```

Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
 1          5          10          15

```

```

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

```

```

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

```

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

Asn Thr Lys Asn Asn Gln Asn Glu Asn Tyr Ala Lys Ala His Ala Glu
 385 390 395 400
 Gly Asn Phe Thr Val Lys Gly Gly Lys His Val Ile Ile Gly Lys Glu
 405 410 415
 Val Lys Ala Asn Lys Ala Val Asp Ile Gln Ala Gln Glu Thr Thr Val
 420 425 430
 Arg Gln Asn Ala Lys Leu Thr Ala Lys Thr Ser Ala Lys Ile Thr Ala
 435 440 445
 Ser Lys Ser Val Asn Leu Glu Asp Asn Ala Lys Leu Ile Ala Asn Glu
 450 455 460
 Leu Ser Thr Thr Thr Asn Lys Leu Thr Asn Lys Gly Ser Ile Tyr Gly
 465 470 475 480
 Lys Lys Val Thr Leu Asp Ala Asp Asn Leu Val Asn Ser Lys Glu Ile
 485 490 495
 Tyr Ala Ser Ser Glu Leu Asp Ile Gln Thr Lys Gly Arg Asp Leu Leu
 500 505 510
 Leu Glu Asp Gly Val Asn Gln Pro Leu Ser Phe Leu Lys Gly Ala Ser
 515 520 525
 Leu Leu Ala Pro Gly Phe Val Asn Thr Gly Leu Ile His Ser Asn Gly
 530 535 540
 Asn Ala Lys Leu Thr Phe Lys Asp Asp Thr Ser Phe Val Thr Glu Gly
 545 550 555 560
 Asn Asn Phe Ile Thr Ala Lys Asp Asn Leu Glu Ile Thr Ala Lys Asn
 565 570 575
 Val Gln Ile Asp Gln Ala Lys Asn Ile Gln Leu Asn Ala Asn Ile Thr
 580 585 590
 Ile Asn Thr Lys Ser Gly Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala
 595 600 605
 Gln Asn Leu Thr Ile Asn Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly
 610 615 620
 Gly Ile Leu Gly Ala Gly Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly
 625 630 635 640
 Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
 645 650 655
 Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
 660 665 670
 Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
 675 680 685
 Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
 690 695 700
 Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
 705 710 715 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
 725 730

<210> 118
 <211> 251
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unkO

<220>
 <221> CDS
 <222> (1) .. (249)

<400> 118
 atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1 5 10 15
 gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
 20 25 30
 tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
 35 40 45
 gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192
 Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
 50 55 60
 agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
 65 70 75 80
 tgt aat cat ta 251
 Cys Asn His

<210> 119
 <211> 83
 <212> PRT
 <213> Pasteurella multocida

<400> 119
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1 5 10 15
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
 20 25 30
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
 35 40 45
 Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
 50 55 60
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
 65 70 75 80

Cys Asn His

<210> 120

<211> 548

<212> DNA

<213> Pasteurella multocida

<220>

<223> unkP

<220>

<221> CDS

<222> (1)..(546)

<400> 120

```

atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att tca 48
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
  1             5             10             15

aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat ttt 96
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
          20             25             30

gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa ggc 144
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
      35             40             45

atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta cgc 192
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
      50             55             60

acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act 240
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
      65             70             75             80

gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca gtg 288
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
          85             90             95

gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc 336
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
      100             105             110

aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc ggt 384
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
      115             120             125

aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat 432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
      130             135             140

gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa 480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
      145             150             155             160

cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt 528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
          165             170             175

tca aat cgt tta gca tcg ta 548

```

Ser Asn Arg Leu Ala Ser
180

<210> 121
<211> 182
<212> PRT
<213> Pasteurella multocida

<400> 121
Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
1 5 10 15
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
20 25 30
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
35 40 45
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
50 55 60
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
65 70 75 80
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
85 90 95
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
100 105 110
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly
115 120 125
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
130 135 140
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
145 150 155 160
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
165 170 175
Ser Asn Arg Leu Ala Ser
180

<210> 122
<211> 69
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> apvA-or1

<220>
<221> CDS
<222> (1) .. (69)

<400> 122
atg ttt tat gtc atg ctt gcc aat agg acg tct ata att tca tca atc 48
Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
1 5 10 15

gat aag ttt aag ata ctt agc
 Asp Lys Phe Lys Ile Leu Ser
 20

69

<210> 123
 <211> 23
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 123
 Met Phe Tyr Val Met Leu Ala Asn Arg Thr Ser Ile Ile Ser Ser Ile
 1 5 10 15

Asp Lys Phe Lys Ile Leu Ser
 20

<210> 124
 <211> 64
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvA-or2

<220>
 <221> CDS
 <222> (3)..(62)

<400> 124
 ag cta agt atc tta aac tta tcg att gat gaa att ata gac gtc cta
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu
 1 5 10 15

47

ttg gca agc atg aca ta
 Leu Ala Ser Met Thr
 20

64

<210> 125
 <211> 20
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 125
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu Leu
 1 5 10 15

Ala Ser Met Thr
 20

<210> 126
 <211> 653
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvB

<220>
 <221> CDS

<222> (1)..(651)

<400> 126

tta att agc ttt cct ttt att act ttt gca agt aat gtt aat gga gcc	48
Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala	
1 5 10 15	
gaa att gga ttg gga gga gcc cgt gag agt agt att tac tat tct aaa	96
Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys	
20 25 30	
cat aaa gta gca aca aat ccc ttt tta gca ctt gat ctt tct tta ggt	144
His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly	
35 40 45	
aat ttt tat atg aga ggg act gca gga att agc gaa ata gga tat gaa	192
Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu	
50 55 60	
caa tct ttc act gac aat ttc agc gta tca ctg ttt gtt aac cca ttt	240
Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe	
65 70 75 80	
gat ggt ttt tca att aaa gga aaa gac ttg tta cct gga tat caa agt	288
Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser	
85 90 95	
att caa act cgc aaa act caa ttt gcc ttt ggt tgg gga tta aat tat	336
Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr	
100 105 110	
aat ttg gga ggt tta ttc ggc tta aat gat act ttt ata tcc ttg gaa	384
Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu	
115 120 125	
gga aaa agc gga aaa cgt ggt gcg agt agt aat gtc agc tta ctt aaa	432
Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys	
130 135 140	
tcg ttt aat atg acg aaa aat tgg aaa gtt tca cca tat att ggc tca	480
Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser	
145 150 155 160	
agt tat tat tca tct aaa tat aca gat tat tac ttt ggt att aaa caa	528
Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln	
165 170 175	
tcc gaa tta ggt aat aaa att aca tcc gta tat aaa cct aaa gca gct	576
Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala	
180 185 190	
tat gca aca cac ata ggt att aat act gat tat gct ttc acg aac aat	624
Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn	
195 200 205	
ctt ggc atg ggt tta tct gtc ggt tgg at	653
Leu Gly Met Gly Leu Ser Val Gly Trp	
210 215	

<210> 127

<211> 217

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 127

```

Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1             5             10             15

Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
      20             25             30

His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
      35             40             45

Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
      50             55             60

Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
      65             70             75             80

Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
      85             90             95

Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
      100            105            110

Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
      115            120            125

Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
      130            135            140

Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
      145            150            155            160

Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
      165            170            175

Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
      180            185            190

Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
      195            200            205

Leu Gly Met Gly Leu Ser Val Gly Trp
      210            215

```

<210> 128

<211> 242

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvC

<220>

<221> CDS

<222> (1)..(240)

<400> 128

```

atg tgg cgg atg gga gat ttt atg tct aaa gag agg ctg aat gat      48
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1             5             10             15

```

```

atg gct cgc cag att tta tca gcg gcg gag ttg ctc att gca aag gaa 96
Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
      20              25              30

ggg ttg caa aat tta tcg atg agg aaa atc gca agt gaa gcc ggt atc 144
Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
      35              40              45

gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg 192
Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
      50              55              60

gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat 240
Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
      65              70              75              80

at 242

```

```

<210> 129
<211> 80
<212> PRT
<213> Actinobacillus pleuropneumoniae

```

```

<400> 129
Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1              5              10              15

Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
      20              25              30

Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
      35              40              45

Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
      50              55              60

Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
      65              70              75              80

```

```

<210> 130
<211> 527
<212> DNA
<213> Actinobacillus pleuropneumoniae

```

```

<220>
<223> apvD

<220>
<221> CDS
<222> (1)..(525)

```

```

<400> 130
aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa 48
Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
 1              5              10              15

caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96
Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
      20              25              30

gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144

```

```

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
      35              40              45

gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192
Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
      50              55              60

gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa 240
Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
      65              70              75              80

ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg 288
Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
      85              90              95

aca agc caa aag gaa aca gaa gaa gca aaa agt aga tta aat acg gcc 336
Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
      100              105              110

aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384
Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
      115              120              125

aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432
Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
      130              135              140

cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480
Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
      145              150              155              160

tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527
Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
      165              170              175

```

<210> 131

<211> 175

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 131

```

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

Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
      20              25              30

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
      35              40              45

Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
      50              55              60

Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
      65              70              75              80

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

Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
      100              105              110

```

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
 115 120 125
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
 130 135 140
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
 145 150 155 160
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
 165 170 175

<210> 132
 <211> 867
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> atpG
 <220>
 <221> CDS
 <222> (1)..(864)

<400> 132
 atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat 48
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
 1 5 10 15
 act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg 96
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
 20 25 30
 cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tcg gaa aca 144
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr
 35 40 45
 atc cgt aag gtg att agc cat att gcg aaa gga agc att ggt tat aag 192
 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys
 50 55 60
 cac ccg ttt tta act gaa cgt gat att aaa aaa gta ggc tat ctt gtc 240
 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val
 65 70 75 80
 gtt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc 288
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
 85 90 95
 aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt 336
 Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser
 100 105 110
 gtt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat 384
 Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn
 115 120 125
 cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg 432
 Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro
 130 135 140
 gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc 480

Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe
 145 150 155 160
 cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa 528
 Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu
 165 170 175
 aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct 576
 Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro
 180 185 190
 aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att 624
 Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile
 195 200 205
 tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat 672
 Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr
 210 215 220
 tta gaa act cag gta tac caa gca gtt gta gat aac cta gct tct gaa 720
 Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
 225 230 235 240
 caa gcc gct cga atg gta gcg atg aaa gcc gca aca gat aat gcg ggt 768
 Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
 245 250 255
 aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca 816
 Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
 260 265 270
 agc att aca aat gaa tta aac gaa att gtt gcg ggt gcc gca gca att 864
 Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
 275 280 285
 taa 867

<210> 133
 <211> 288
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 133
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
 1 5 10 15
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
 20 25 30
 Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ser Glu Thr
 35 40 45
 Ile Arg Lys Val Ile Ser His Ile Ala Lys Gly Ser Ile Gly Tyr Lys
 50 55 60
 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val
 65 70 75 80
 Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
 85 90 95

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

<210> 134

<211> 534

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> atpH

<220>

<221> CDS

<222> (1)..(531)

<400> 134

atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt 48
 Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1 5 10 15

gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta 96
 Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
 20 25 30

cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att 144
 Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
 35 40 45

aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc 192

```

Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
 50                      55                      60

tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg 240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
 65                      70                      75                      80

gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc 288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
      85                      90                      95

gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt 336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
      100                      105                      110

tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg 384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
      115                      120                      125

atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat 432
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
      130                      135                      140

aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att 480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
      145                      150                      155                      160

gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc 528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
      165                      170                      175

ttg taa
Leu
534

```

<210> 135
 <211> 177
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

```

<400> 135
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe
 1                      5                      10                      15

Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu
      20                      25                      30

Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile
      35                      40                      45

Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile
 50                      55                      60

Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met
 65                      70                      75                      80

Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe
      85                      90                      95

Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val
      100                      105                      110

```


Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala
 115 120 125

Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp
 130 135 140

Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile
 145 150 155 160

Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser
 165 170 175

Leu

<210> 136
 <211> 321
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> dksA

<220>
 <221> CDS
 <222> (1)..(318)

<400> 136
 gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa 48
 Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1 5 10 15

atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act 96
 Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
 20 25 30

cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt 144
 Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
 35 40 45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac 192
 Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
 50 55 60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt 240
 Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
 65 70 75 80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt 288
 Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
 85 90 95

gcg gaa atc cgt gaa aag caa atg ggc tta taa 321
 Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
 100 105

<210> 137
 <211> 106
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 137

Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1 5 10 15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
 20 25 30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
 35 40 45

Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
 50 55 60

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

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
 85 90 95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
 100 105

<210> 138

<211> 33

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> dnaK

<220>

<221> CDS

<222> (1) .. (30)

<400> 138

gct gag ttt gaa gaa gtg aaa gat aat aaa taa
 Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
 1 5 10

33

<210> 139

<211> 10

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 139

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
 1 5 10

<210> 140

<211> 453

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> exbB

<220>

<221> CDS

<222> (1) .. (450)

<400> 140
 atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48
 Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
 1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96
 Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
 20 25 30

gaa cgc gta ctt ttc tac aaa caa ttg gat gtg acc aaa tat gac acg 144
 Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
 35 40 45

cta caa gat ttg gaa att gat acc act cgc aat tta acc acc att tcc 192
 Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
 50 55 60

act atc ggt gcc aac gcc cct tat atc ggt tta tta gga acc gta tta 240
 Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
 65 70 75 80

ggg atc tta ctt acc ttc tat cat tta ggg cat tcc ggc ggt gat att 288
 Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
 85 90 95

gac gcc gca tcc att atg gtt cac ctt tgc ctt gca tta aaa gca acc 336
 Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
 100 105 110

gca gcc ggt atc tta gtc gct att ccg gca atg atg ttc tac agc ggt 384
 Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
 115 120 125

ttt aac cgt aaa gtg gat gaa agc aaa ctt aaa tgg caa gcg att caa 432
 Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
 130 135 140

gct cgt aaa gcc aat caa taa 453
 Ala Arg Lys Ala Asn Gln
 145 150

<210> 141
 <211> 150
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 141
 Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
 1 5 10 15

Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
 20 25 30

Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
 35 40 45

Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
 50 55 60

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

Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
 85 90 95

Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
 100 105 110

Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
 115 120 125

Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
 130 135 140

Ala Arg Lys Ala Asn Gln
 145 150

<210> 142

<211> 720

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> fkpA

<220>

<221> CDS

<222> (1) .. (717)

<400> 142

atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc	48
Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe	
1 5 10 15	
ggt tca gct caa act gca ttt gca gcg gat caa aaa ttc att gac gat	96
Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp	
20 25 30	
tca tca tat gca gtc ggc gta ttg atg ggt aaa aat atc gaa ggc gtc	144
Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val	
35 40 45	
ggt gaa tca caa aaa gaa att ttt tct tat aac caa gat aaa atc ttg	192
Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu	
50 55 60	
gcg ggt gtc caa gat acc atc aaa aaa acc ggt aaa tta acc gat gaa	240
Ala Gly Val Gln Asp Thr Ile Lys Lys Thr Gly Lys Leu Thr Asp Glu	
65 70 75 80	
gat cta caa aaa caa tta aaa tcg ctt gat act tat ctt gca agt caa	288
Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln	
85 90 95	
gaa agc aaa att gcg gcg gag aaa agc aaa gca acc gta gaa gcc ggt	336
Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly	
100 105 110	
aat aaa ttt cgt acc gac tac gaa aaa caa agc ggc gtg aaa aaa acc	384
Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr	
115 120 125	
gct tcc ggt tta ctt tat aaa att gaa aaa gcc ggc acg ggc gaa tcg	432

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
 130 135 140

cct aaa gcg gaa gat acc gtt aaa gtt cac tat aaa ggg aca tta acc 480
 Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
 145 150 155 160

gat ggt acg gta ttc gat agc tca tac gat cgc ggt gag ccg att gaa 528
 Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
 165 170 175

ttc caa tta aac caa tta att ccg ggt tgg att gaa gcg att cca atg 576
 Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
 180 185 190

ttg aaa aaa ggc gga aaa atg gaa atc gtc gtt ccg cct gaa ctt ggt 624
 Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
 195 200 205

tac ggc gaa gcg caa gca ggt aag att ccg gca agt tca acc tta aaa 672
 Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
 210 215 220

ttc gag att gaa ttg tta gat ttc aaa gcg gcc gaa gcg aaa aaa taa 720
 Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
 225 230 235

<210> 143
 <211> 239
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 143
 Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
 1 5 10 15

Val Ser Ala Gln Thr Ala Phe Ala Ala Asp Gln Lys Phe Ile Asp Asp
 20 25 30

Ser Ser Tyr Ala Val Gly Val Leu Met Gly Lys Asn Ile Glu Gly Val
 35 40 45

Val Glu Ser Gln Lys Glu Ile Phe Ser Tyr Asn Gln Asp Lys Ile Leu
 50 55 60

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

Asp Leu Gln Lys Gln Leu Lys Ser Leu Asp Thr Tyr Leu Ala Ser Gln
 85 90 95

Glu Ser Lys Ile Ala Ala Glu Lys Ser Lys Ala Thr Val Glu Ala Gly
 100 105 110

Asn Lys Phe Arg Thr Asp Tyr Glu Lys Gln Ser Gly Val Lys Lys Thr
 115 120 125

Ala Ser Gly Leu Leu Tyr Lys Ile Glu Lys Ala Gly Thr Gly Glu Ser
 130 135 140

Pro Lys Ala Glu Asp Thr Val Lys Val His Tyr Lys Gly Thr Leu Thr
 145 150 155 160

Asp Gly Thr Val Phe Asp Ser Ser Tyr Asp Arg Gly Glu Pro Ile Glu
 165 170 175

Phe Gln Leu Asn Gln Leu Ile Pro Gly Trp Ile Glu Ala Ile Pro Met
 180 185 190

Leu Lys Lys Gly Gly Lys Met Glu Ile Val Val Pro Pro Glu Leu Gly
 195 200 205

Tyr Gly Glu Arg Gln Ala Gly Lys Ile Pro Ala Ser Ser Thr Leu Lys
 210 215 220

Phe Glu Ile Glu Leu Leu Asp Phe Lys Ala Ala Glu Ala Lys Lys
 225 230 235

<210> 144
 <211> 290
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> HI0379

<220>
 <221> CDS
 <222> (3)..(287)

<400> 144
 tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa 47
 His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln
 1 5 10 15

cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95
 Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn
 20 25 30

ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct 143
 Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser
 35 40 45

cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt 191
 Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly
 50 55 60

gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg 239
 Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser
 65 70 75

gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat 287
 Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His
 80 85 90 95

taa 290

<210> 145
 <211> 95
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 145
 His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln Pro

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

<210> 146

<211> 273

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> hupA

<220>

<221> CDS

<222> (1) .. (270)

<400> 146

atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta	48
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu	
1 5 10 15	
agc aag aaa gac gcg aaa gcg gca tta gaa gcg act tta aat gcg atc	96
Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile	
20 25 30	
tct gaa agc cta aaa aat ggc gac acc gtt cag tta atc ggc ttc ggt	144
Ser Glu Ser Leu Lys Asn Gly Asp Thr Val Gln Leu Ile Gly Phe Gly	
35 40 45	
act ttt aaa gta aac gag cgt aat gca cgt acg ggt cgt aac ccg cgt	192
Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg	
50 55 60	
acc ggc gaa gaa atc aaa atc gca gca tct aaa gtg ccg gcg ttt gtt	240
Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val	
65 70 75 80	
gca ggt aaa gca tta aaa gat tta gta aaa taa	273
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys	
85 90	

<210> 147

<211> 90

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 147

Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu

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

<210> 148

<211> 551

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> lpdA

<220>

<221> CDS

<222> (1)..(549)

<400> 148

atg agc aaa gaa atc aaa acg caa gtc gtg gta ctt ggt gcg ggt cct	48
Met Ser Lys Glu Ile Lys Thr Gln Val Val Val Leu Gly Ala Gly Pro	
1 5 10 15	
gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca	96
Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr	
20 25 30	
gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta	144
Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val	
35 40 45	
ggt tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa	192
Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu	
50 55 60	
gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac	240
Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn	
65 70 75 80	
att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa	288
Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys	
85 90 95	
tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta	336
Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val	
100 105 110	
gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt	384
Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg	
115 120 125	


```

gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432
Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
130 135 140

gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480
Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
145 150 155 160

ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528
Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
165 170 175

gaa aaa att act cat tat ggg cc 551
Glu Lys Ile Thr His Tyr Gly
180

```

<210> 149

<211> 183

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 149

```

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

Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
20 25 30

Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
35 40 45

Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
50 55 60

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

Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
85 90 95

Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
100 105 110

Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
115 120 125

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

Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
145 150 155 160

Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
165 170 175

Glu Lys Ile Thr His Tyr Gly
180

```

<210> 150

<211> 1095

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> Omp5-2

<220>

<221> CDS

<222> (1)..(1092)

<400> 150

```

atg aaa aaa tca tta gtt gct tta aca gta tta tcg gct gca gcg gta 48
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Val
  1             5             10             15

gct caa gca gcg cca caa caa aat act ttc tac gca ggt gcg aaa gca 96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
             20             25             30

ggt tgg gcg tca ttc cat gat ggt atc gaa caa tta gat tca gct aaa 144
Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys
             35             40             45

aac aca gat cgc ggt aca aaa tac ggt atc aac cgt aat tca gta act 192
Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
             50             55             60

tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt 240
Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
             65             70             75             80

tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct 288
Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser
             85             90             95

gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca 336
Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala
             100            105            110

cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac 384
His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp
             115            120            125

tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat 432
Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr
             130            135            140

aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa 480
Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln
             145            150            155            160

agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa 528
Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu
             165            170            175

tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca 576
Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala
             180            185            190

agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat 624
Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp
             195            200            205

```

```

atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg 672
ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala
    210                215                220

gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc 720
Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser
    225                230                235                240

tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg 768
Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala
    245                250                255

gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta 816
Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu
    260                265                270

tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa 864
Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys
    275                280                285

gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct 912
Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala
    290                295                300

aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta 960
Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
    305                310                315                320

ggt tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt 1008
Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
    325                330                335

aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt 1056
Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val
    340                345                350

gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa 1095
Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
    355                360

```

<210> 151

<211> 364

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 151

```

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

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
    20                25                30

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

Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
    50          55          60

Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
    65          70          75          80

Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser

```

85								90				95			
Glu	Lys	Pro	Asn	Gly	Lys	Ala	Asp	Lys	Lys	Thr	Phe	Arg	His	Ala	Ala
			100					105					110		
His	Gly	Ala	Thr	Ile	Ala	Leu	Lys	Pro	Ser	Tyr	Glu	Val	Leu	Pro	Asp
		115					120					125			
Leu	Asp	Val	Tyr	Gly	Lys	Val	Gly	Ile	Ala	Leu	Val	Asn	Asn	Thr	Tyr
	130					135					140				
Lys	Thr	Phe	Asn	Ala	Ala	Gln	Glu	Lys	Val	Lys	Thr	Arg	Arg	Phe	Gln
145					150					155					160
Ser	Ser	Leu	Ile	Leu	Gly	Ala	Gly	Val	Glu	Tyr	Ala	Ile	Leu	Pro	Glu
				165					170					175	
Leu	Ala	Ala	Arg	Val	Glu	Tyr	Gln	Trp	Leu	Asn	Asn	Ala	Gly	Lys	Ala
			180					185					190		
Ser	Tyr	Ser	Thr	Leu	Asn	Arg	Met	Gly	Ala	Thr	Asp	Tyr	Arg	Ser	Asp
		195					200					205			
Ile	Ser	Ser	Val	Ser	Ala	Gly	Leu	Ser	Tyr	Arg	Phe	Gly	Gln	Gly	Ala
						215					220				
Ala	Pro	Val	Ala	Ala	Pro	Ala	Val	Glu	Thr	Lys	Asn	Phe	Ala	Phe	Ser
225					230					235					240
Ser	Asp	Val	Leu	Phe	Ala	Phe	Gly	Lys	Ser	Asn	Leu	Lys	Pro	Ala	Ala
				245					250					255	
Ala	Thr	Ala	Leu	Asp	Ala	Met	Gln	Thr	Glu	Ile	Asn	Asn	Ala	Gly	Leu
			260						265				270		
Ser	Asn	Ala	Ala	Ile	Gln	Val	Asn	Gly	Tyr	Thr	Asp	Arg	Ile	Gly	Lys
		275					280					285			
Glu	Ala	Ser	Asn	Leu	Lys	Leu	Ser	Gln	Arg	Arg	Ala	Glu	Thr	Val	Ala
	290					295					300				
Asn	Tyr	Ile	Val	Ser	Lys	Gly	Ala	Pro	Ala	Ala	Asn	Val	Thr	Ala	Val
305					310					315					320
Gly	Tyr	Gly	Glu	Ala	Asn	Pro	Val	Thr	Gly	Ala	Thr	Cys	Asp	Lys	Val
				325					330					335	
Lys	Gly	Arg	Lys	Ala	Leu	Ile	Ala	Cys	Leu	Ala	Pro	Asp	Arg	Arg	Val
			340				345						350		
Glu	Val	Gln	Val	Gln	Gly	Thr	Lys	Glu	Val	Thr	Met				
		355					360								

<210> 152

<211> 1110

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> Omp5

<220>

<221> CDS

<222> (1)..(1107)

<400> 152

atg aaa aaa tca tta gtt gct tta gca gta tta tcg gct gca gca gta	48
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val	
1 5 10 15	
gct caa gca gct cca caa caa aat act ttc tac gca ggt gcg aaa gtt	96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val	
20 25 30	
ggt caa tca tca ttt cac cac ggt gtt aac caa tta aaa tct ggt cac	144
Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His	
35 40 45	
gat gat cgt tat aat gat aaa aca cgt aag tat ggt atc aac cgt aac	192
Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn	
50 55 60	
tct gta act tac ggt gta ttc ggc ggt tac caa atc tta aac caa aat	240
Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn	
65 70 75 80	
aac ttc ggt tta gca gct gaa tta ggc tat gac tac tac ggt cgc gta	288
Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val	
85 90 95	
cgt ggt aac gta gat gaa ttc cgt aca gtt aaa cac tct gct cac ggt	336
Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly	
100 105 110	
tta aac tta gcg tta aaa cca agc tac gaa gta tta cct gac tta gac	384
Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp	
115 120 125	
gtt tac ggt aaa gta ggt att gcg gtt gtt cgt aat gac tat aaa aaa	432
Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys	
130 135 140	
tat ggt gcg gaa aac act aac gaa tca aca aca aaa ttc cac aaa tta	480
Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu	
145 150 155 160	
aaa gca tca act att tta ggt gca ggt gtt gag tac gca att ctt cct	528
Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro	
165 170 175	
gaa tta gcg gca cgt gtt gaa tac caa tac tta aac aaa gcg ggt aac	576
Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn	
180 185 190	
tta aat aaa gca tta gtt cgt tca ggc aca caa gat gtg gac ttc caa	624
Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln	
195 200 205	
tat gct cct gat atc cac tct gta aca gca ggt tta tca tac cgt ttc	672
Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe	
210 215 220	
ggt caa ggc gct gta gca cca gtt gtt gag cca gaa gtt gta act aaa	720
Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys	
225 230 235 240	

```

aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc 768
Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
                245                250                255

tta aaa cca gca gca gca aca gct tta gac gca gct aac act gaa atc 816
Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
                260                265                270

gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca 864
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
                275                280                285

gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt 912
Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
                290                295                300

gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca 960
Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
305                310                315                320

aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca 1008
Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
                325                330                335

aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca 1056
Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
                340                345                350

ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct 1104
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
                355                360                365

atg taa
Met
246

```

```

<210> 153
<211> 369
<212> PRT
<213> Actinobacillus pleuropneumoniae

```

```

<400> 153
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
 1                5                10                15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
                20                25                30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
                35                40                45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
 50                55                60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
 65                70                75                80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
                85                90                95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
100                105                110

```

```

Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
    115                                120                                125

Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
    130                                135                                140

Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
    145                                150                                155                                160

Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
    165                                170                                175

Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
    180                                185                                190

Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
    195                                200                                205

Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
    210                                215                                220

Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
    225                                230                                235                                240

Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
    245                                250                                255

Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
    260                                265                                270

Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
    275                                280                                285

Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
    290                                295                                300

Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
    305                                310                                315                                320

Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
    325                                330                                335

Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
    340                                345                                350

Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
    355                                360                                365

```

Met

<210> 154

<211> 1076

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> pnp new

<220>

<221> CDS

<222> (1)..(1074)

```

<400> 154
aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg 48
Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
1 5 10 15

ggt gcg ccg gaa ccg aat acc gca tta atc aac caa gtt aaa gcg tta 96
Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
20 25 30

gcg gaa gcg cgt atc ggc gat ccg tat cgt att aca gaa aaa caa gcg 144
Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
35 40 45

cgt tac gaa caa atc gat gca att aaa gcg gat gtt atc gca caa tta 192
Arg Tyr Glu Gln Ile Asp Ala Ile Lys Ala Asp Val Ile Ala Gln Leu
50 55 60

acc gca caa gac gaa acc gtt tct gaa ggt gcg att att gat att att 240
Thr Ala Gln Asp Glu Thr Val Ser Glu Gly Ala Ile Ile Asp Ile Ile
65 70 75 80

acc gca tta gaa agt tct att gtt cgc ggt cgt att att gcc ggc gaa 288
Thr Ala Leu Glu Ser Ser Ile Val Arg Gly Arg Ile Ile Ala Gly Glu
85 90 95

ccg cgt att gac ggt cgt acg gta gat acg gtt cgt gca tta gac att 336
Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
100 105 110

tgc acc ggc gta tta cct cgt acg cac ggt tct gca atc ttt act cgc 384
Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
115 120 125

ggt gaa aca caa gca tta gcg gtt gca acc tta ggt act gag cgc gat 432
Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp
130 135 140

gca caa att gtt gac gaa tta acc ggc gag aaa tca gac cgt ttc tta 480
Ala Gln Ile Val Asp Glu Leu Thr Gly Glu Lys Ser Asp Arg Phe Leu
145 150 155 160

ttc cac tat aac ttc cct ccg tac tct gtc ggt gaa acc ggt cgt atc 528
Phe His Tyr Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Arg Ile
165 170 175

ggt tcg ccg aaa cgt cgt gaa atc ggc cac ggt cgt tta gcg aaa cgc 576
Gly Ser Pro Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg
180 185 190

ggt gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg 624
Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val
195 200 205

cgc gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct 672
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala
210 215 220

tcc gta tgc ggc gca tct tta gcg tta atg gac gca ggc gta ccg att 720
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile
225 230 235 240

aaa gcg gcg gtt gcg ggt atc gca atg ggc tta gtg aaa gaa gaa gaa 768
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu

```


	245	250	255	
aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc				816
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly				
	260	265	270	
gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt				864
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu				
	275	280	285	
caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc				912
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile				
	290	295	300	
gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg				960
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met				
	305	310	315	320
gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct				1008
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro				
	325	330	335	
cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc				1056
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile				
	340	345	350	
ggt aaa ggc ggt gcg gtt at				1076
Gly Lys Gly Gly Ala Val				
	355			

<210> 155

<211> 358

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 155

Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
1 5 10 15

Val Ala Pro Glu Pro Asn Thr Ala Leu Ile Asn Gln Val Lys Ala Leu
20 25 30

Ala Glu Ala Arg Ile Gly Asp Ala Tyr Arg Ile Thr Glu Lys Gln Ala
35 40 45

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

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

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

Pro Arg Ile Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile
100 105 110

Cys Thr Gly Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg
115 120 125

Gly Glu Thr Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp

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

<210> 156

<211> 1055

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> potD

<220>

<221> CDS

<222> (1)..(1053)

<400> 156

atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca 48
 Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
 1 5 10 15

tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct 96

Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala	
20 25 30	
caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat	144
Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr	
35 40 45	
gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa	192
Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys	
50 55 60	
gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta	240
Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu	
65 70 75 80	
aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac	288
Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn	
85 90 95	
tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat	336
Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp	
100 105 110	
cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac	384
His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn	
115 120 125	
aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt	432
Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly	
130 135 140	
gca ccg ggt atc gca ttt aac tca aat gac tat aag ggc gat gcg ttc	480
Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe	
145 150 155 160	
act tct tgg ggt gat tta tgg aaa cct gag ttt gcg aat aaa gta caa	528
Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln	
165 170 175	
tta tta gat gac gca cgt gaa gta ttt aac att gcg tta tta aaa tta	576
Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu	
180 185 190	
ggt aaa aac cct aat aca acc aat ccg gaa gag att aaa gcg gct tac	624
Gly Lys Asn Pro Asn Thr Thr Asn Pro Glu Glu Ile Lys Ala Ala Tyr	
195 200 205	
gaa gag tta aga aaa tta cgt cca aac gta ctt tct ttc act tca gac	672
Glu Glu Leu Arg Lys Leu Arg Pro Asn Val Leu Ser Phe Thr Ser Asp	
210 215 220	
aac cca gcg aac tca ttt atc gca ggt gaa gta tct gta ggt caa tta	720
Asn Pro Ala Asn Ser Phe Ile Ala Gly Glu Val Ser Val Gly Gln Leu	
225 230 235 240	
tgg aac ggt tct gta cgt att gcg aaa aaa gaa caa gcg ccg gta aac	768
Trp Asn Gly Ser Val Arg Ile Ala Lys Lys Glu Gln Ala Pro Val Asn	
245 250 255	
atg gtg ttc cca aaa gaa ggt cct gta ctt tgg gtt gat acg tta gcc	816
Met Val Phe Pro Lys Glu Gly Pro Val Leu Trp Val Asp Thr Leu Ala	

```

                260                265                270
att ccg gcg aat gcg aaa aac aaa gaa aat gcg cat aag tta atc aac      864
Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn
                275                280                285

tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt      912
Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly
                290                295                300

tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att      960
Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile
305                310                315

acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca      1008
Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala
                325                330                335

caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta      1055
Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys
                340                345                350

```

<210> 157

<211> 351

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 157

```

Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
  1                5                10                15

Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala
                20                25                30

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

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

Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu
                65                70                75                80

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

Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp
                100                105                110

His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn
                115                120                125

Lys Pro Tyr Asp Gln Gly Asn Lys Tyr Ser Leu Pro Gln Leu Leu Gly
                130                135                140

Ala Pro Gly Ile Ala Phe Asn Ser Asn Asp Tyr Lys Gly Asp Ala Phe
145                150                155                160

Thr Ser Trp Gly Asp Leu Trp Lys Pro Glu Phe Ala Asn Lys Val Gln
                165                170                175

Leu Leu Asp Asp Ala Arg Glu Val Phe Asn Ile Ala Leu Leu Lys Leu

```

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

<210> 158

<211> 525

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> rpmF

<220>

<221> CDS

<222> (1)..(522)

<400> 158

atg	caa	aag	gta	aaa	cta	ccc	ctc	acc	att	gac	cca	tat	aaa	gac	gct	48
Met	Gln	Lys	Val	Lys	Leu	Pro	Leu	Thr	Ile	Asp	Pro	Tyr	Lys	Asp	Ala	
1				5					10					15		

cag	cgt	cga	atg	gat	tac	gaa	ggc	tac	atc	tca	cgt	agt	ctg	ctt	aat	96
Gln	Arg	Arg	Met	Asp	Tyr	Glu	Gly	Tyr	Ile	Ser	Arg	Ser	Leu	Leu	Asn	
			20					25					30			

cgt	ttg	ggc	gaa	tct	gtg	agc	aat	gtg	cta	agc	gat	gca	caa	gtt	act	144
Arg	Leu	Gly	Glu	Ser	Val	Ser	Asn	Val	Leu	Ser	Asp	Ala	Gln	Val	Thr	
			35					40					45			

ctc	tcg	tta	tat	atc	gat	ccg	caa	cgc	tta	acc	gtt	att	aaa	ggc	acg	192
Leu	Ser	Leu	Tyr	Ile	Asp	Pro	Gln	Arg	Leu	Thr	Val	Ile	Lys	Gly	Thr	
50						55					60					

gcg	aca	gtg	gaa	gtg	gaa	ttc	gat	tgc	caa	cga	tgc	ggc	aac	ccg	ttt	240

```

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
 65              70              75              80

aca caa acg ctt gac tgt tgc ttt tgt ttc agt ccg gtg tcc aat atg   288
Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
              85              90              95

gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac   336
Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
              100              105              110

gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc   384
Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
              115              120              125

atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg   432
Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
              130              135              140

tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa   480
Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
              145              150              155              160

aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag       525
Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
              165              170

```

<210> 159

<211> 174

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 159

```

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

Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
              20              25              30

Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
              35              40              45

Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
              50              55              60

Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
 65              70              75              80

Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
              85              90              95

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

Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
              115              120              125

Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
              130              135              140

Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
              145              150              155              160

```

Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
 165 170

<210> 160
 <211> 1302
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> tig

<220>
 <221> CDS
 <222> (1)..(1299)

<400> 160
 atg tca att tct att gaa act tta gaa ggc tta caa cgc cgc gta act 48
 Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
 1 5 10 15
 att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta 96
 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
 20 25 30
 aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144
 Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
 35 40 45
 gta ccg cac gca att atc gaa caa cgt ttc ggt tta gcg gct cgc caa 192
 Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
 50 55 60
 gac gta tta tcc gat gaa atg caa cgt gcg ttc ttt gat gcg gta atc 240
 Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
 65 70 75 80
 gct gag aaa att aac ctt gcc ggt cgt cct acc ttc aca ccg aac aac 288
 Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
 85 90 95
 tac caa ccg agt caa gaa ttc agc ttc act gca act ttt gaa gta ttc 336
 Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
 100 105 110
 ccg gaa gtt gaa tta aaa ggc tta gaa aat atc gaa gtt gaa aaa ccg 384
 Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
 115 120 125
 gtt gta gaa atc aca gaa gct gat tta gac aaa atg atc gat gtg tta 432
 Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
 130 135 140
 cgt aaa caa caa gcg act tgg gct gaa tct caa gca gcg gca caa gcg 480
 Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
 145 150 155 160
 gaa gac cgt gtt gta atc gac ttc gta ggt tct gta gac ggt gaa gag 528
 Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
 165 170 175
 ttt gaa ggc ggt aaa gcg aca gac ttc act tta gca atg ggt caa agt 576
 Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser

180										185										190										
cgt atg atc cct ggt ttt gaa gaa ggt atc gtt ggt cac aaa gcc ggc	624																													
Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly																														
195 200 205																														
gaa caa ttc gat atc gat gtt act ttc cct gaa gaa tac cac gct gaa	672																													
Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu																														
210 215 220																														
aac tta aaa ggt aaa gcg gcg aaa ttc gca att aca ctt aag aaa gta	720																													
Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val																														
225 230 235 240																														
gaa aat atc gta tta cct gaa tta acc gaa gaa ttc gtg aaa aaa ttc	768																													
Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe																														
245 250 255																														
ggt tca gca aaa act gta gaa gat tta cgt gcg gaa att aag aaa aat	816																													
Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn																														
260 265 270																														
atg caa cgt gaa ctt aaa aac gca gta acc gca cgc gtt aaa aac caa	864																													
Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln																														
275 280 285																														
gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca	912																													
Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala																														
290 295 300																														
gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt	960																													
Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg																														
305 310 315 320																														
ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc	1008																													
Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe																														
325 330 335																														
gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc	1056																													
Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr																														
340 345 350																														
gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa	1104																													
Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu																														
355 360 365																														
acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt	1152																													
Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val																														
370 375 380																														
gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta	1200																													
Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val																														
385 390 395 400																														
gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta	1248																													
Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val																														
405 410 415																														
act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa	1296																													
Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln																														
420 425 430																														
ggc taa	1302																													

Gly

<210> 161

<211> 433

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 161

```

Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
  1           5           10           15

Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
          20           25           30

Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
          35           40           45

Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
          50           55           60

Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
          65           70           75           80

Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn
          85           90           95

Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
          100          105          110

Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
          115          120          125

Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
          130          135          140

Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
          145          150          155          160

Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
          165          170          175

Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
          180          185          190

Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
          195          200          205

Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
          210          215          220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
          225          230          235          240

Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
          245          250          255

Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
          260          265          270

Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
          275          280          285

```

Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
 290 295 300
 Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
 305 310 315 320
 Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
 325 330 335
 Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
 340 345 350
 Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
 355 360 365
 Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
 370 375 380
 Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
 385 390 395 400
 Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
 405 410 415
 Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
 420 425 430

Gly

<210> 162

<211> 316

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> tRNA-glu

<400> 162

aatattgcgc tcaaatggca aagcggagag catctttaa tgttggtccc atcgtctaga 60
 ggcctaggac atcgcccttt cacggcggtta accgggggttc gaatccccgt ggggacgcc 120
 tttaaagatg acttttggtg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180
 tgagagatgt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
 agctgaacaa aagcagctaa gtgttttagt gaataaagta tcgcgttgaa tgcgttcaaa 300
 taaaatttga aaatat 316

<210> 163

<211> 85

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> tRNA-leu

<400> 163

gctctggtgg tggaattggt agacacgcta tcttgagggg gtagtgtcca taggatgtgc 60

gagttcagagt ctgcgccaga gcacc

85

<210> 164

<211> 623

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> yaeE

<220>

<221> CDS

<222> (1)..(621)

<400> 164

atg caa gaa ctc aca cct caa atg tgg ggc tta gtc ggc act tca acg	48
Met Gln Glu Leu Thr Pro Gln Met Trp Gly Leu Val Gly Thr Ser Thr	
1 5 10 15	
ctt gaa acg ctc tat atg ggc ttt gcg gcg act tta ctt gct gtg gta	96
Leu Glu Thr Leu Tyr Met Gly Phe Ala Ala Thr Leu Leu Ala Val Val	
20 25 30	
gtc ggt ttg ccg atc ggt ttt ctg gca ttt tta acc ggt aaa gga gag	144
Val Gly Leu Pro Ile Gly Phe Leu Ala Phe Leu Thr Gly Lys Gly Glu	
35 40 45	
att tta gag aat ccg cgt tta cat caa gta tta gat gtg att att aat	192
Ile Leu Glu Asn Pro Arg Leu His Gln Val Leu Asp Val Ile Ile Asn	
50 55 60	
atc ggt cgt tcc gta ccg ttt att att ttg tta gtc gtg ttg tta cct	240
Ile Gly Arg Ser Val Pro Phe Ile Ile Leu Leu Val Val Leu Leu Pro	
65 70 75 80	
ttt acg cgt tta ttg gtc ggg aca acg ctc ggt act acg gcg gcg att	288
Phe Thr Arg Leu Val Gly Thr Thr Leu Gly Thr Thr Ala Ala Ile	
85 90 95	
gtg ccg tta agc gtt tcg gca att ccg ttt ttt gcg cgt tta act tca	336
Val Pro Leu Ser Val Ser Ala Ile Pro Phe Phe Ala Arg Leu Thr Ser	
100 105 110	
aat gcg tta tta gaa atc cca gca ggt tta acc gaa gcg gcg aaa tcg	384
Asn Ala Leu Leu Glu Ile Pro Ala Gly Leu Thr Glu Ala Ala Lys Ser	
115 120 125	
atg ggc gca acg aat tgg caa gtg gtc agt aaa ttt tat tta ccg gaa	432
Met Gly Ala Thr Asn Trp Gln Val Val Ser Lys Phe Tyr Leu Pro Glu	
130 135 140	
tca ctg ccg att tta atc aat ggt atc aca tta act tta gtc gct tta	480
Ser Leu Pro Ile Leu Ile Asn Gly Ile Thr Leu Thr Leu Val Ala Leu	
145 150 155 160	
atc ggt tat tcg gca atg gcg ggt gcg gtc ggc ggc ggc ggt ttg ggt	528
Ile Gly Tyr Ser Ala Met Ala Gly Ala Val Gly Gly Gly Gly Leu Gly	
165 170 175	
aac ctt gcc atc agt tac ggt gaa cac cga aat atg gtc tat gta aaa	576
Asn Leu Ala Ile Ser Tyr Gly Glu His Arg Asn Met Val Tyr Val Lys	
180 185 190	

tgg atc tca aca att att atc gta gcg att gtg atg atc agt caa aa 623
 Trp Ile Ser Thr Ile Ile Ile Val Ala Ile Val Met Ile Ser Gln
 195 200 205

<210> 165

<211> 207

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 165

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

<210> 166

<211> 866

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(864)

<220>

<223> atpG

```

<400> 166
atg gca ggt gct aaa gag ata aga acc aaa att gca agt gtt cgt aat   48
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Arg Asn
  1             5             10             15

aca caa aaa att acc aaa gcg atg gaa atg gtt gcc gca tca aaa atg   96
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met
             20             25             30

cgt aaa acc caa gag cgt atg gcg gct tct cgc cct tat gct gaa agt   144
Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Ser
             35             40             45

att cgc aag gca att agc cat att gcc aaa ggt aac att gag tat aaa   192
Ile Arg Lys Ala Ile Ser His Ile Ala Lys Gly Asn Ile Glu Tyr Lys
             50             55             60

cac cca ttt ttg acc cca cgt ccg gta aaa aaa gtt ggc tat tta gta   240
His Pro Phe Leu Thr Pro Arg Pro Val Lys Lys Val Gly Tyr Leu Val
             65             70             75             80

gtt tca acc gat cgc ggt tta tgt ggt ggc tta aat atc aat tta ttt   288
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe
             85             90             95

aaa acc gtt tta cat gaa ttg aaa gaa aaa gat gac caa ggt gtt aag   336
Lys Thr Val Leu His Glu Leu Lys Glu Lys Asp Asp Gln Gly Val Lys
             100            105            110

tct cga ctt gct gtg gtg gga aat aaa ggg atc tcc ttt ttt aac cca   384
Ser Arg Leu Ala Val Val Gly Asn Lys Gly Ile Ser Phe Phe Asn Pro
             115            120            125

atg ggg cta gag att aaa ggt cat atc aat gga ttg ggt gat aca ccg   432
Met Gly Leu Glu Ile Lys Gly His Ile Asn Gly Leu Gly Asp Thr Pro
             130            135            140

gca atg gaa gat tta gtc ggt att gtt aat ggt atg gta aat gcc tac   480
Ala Met Glu Asp Leu Val Gly Ile Val Asn Gly Met Val Asn Ala Tyr
             145            150            155            160

cgt gaa ggc gaa att gat gaa gtg tat gtg gta tat aac cgt ttt ata   528
Arg Glu Gly Glu Ile Asp Glu Val Tyr Val Val Tyr Asn Arg Phe Ile
             165            170            175

aac acg atg tca caa aaa ccg aca gta caa cag ttg ctt cct ttg cct   576
Asn Thr Met Ser Gln Lys Pro Thr Val Gln Gln Leu Leu Pro Leu Pro
             180            185            190

gca ctg gaa aat gac tca tta gag caa act ggt tct tgg gat tat ctc   624
Ala Leu Glu Asn Asp Ser Leu Glu Gln Thr Gly Ser Trp Asp Tyr Leu
             195            200            205

tat gaa cca aat cca caa gcg tta tta gac agc tta ctg gtt cgt tat   672
Tyr Glu Pro Asn Pro Gln Ala Leu Leu Asp Ser Leu Leu Val Arg Tyr
             210            215            220

tta gaa tct caa gtt tat cag gca gtg gta gat aat ctt gcg tct gaa   720
Leu Glu Ser Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu
             225            230            235            240

cag gct gct cga atg gtg gca atg aaa gca gca acc gat aac gca ggt   768
Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly

```

	245	250	255	
aat ctg att aat gag tta cag tta gtg tat aac aaa gct cgt caa gca				816
Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala				
	260	265	270	
agt att acg aat gaa tta aat gaa att gtc gcg ggt gcc gca gca att				864
Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile				
	275	280	285	
ta				866
<210> 167				
<211> 288				
<212> PRT				
<213> Pasteurella (Mannheimia) haemolytica				
<400> 167				
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Arg Asn				
1 5 10 15				
Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys Met				
20 25 30				
Arg Lys Thr Gln Glu Arg Met Ala Ala Ser Arg Pro Tyr Ala Glu Ser				
35 40 45				
Ile Arg Lys Ala Ile Ser His Ile Ala Lys Gly Asn Ile Glu Tyr Lys				
50 55 60				
His Pro Phe Leu Thr Pro Arg Pro Val Lys Lys Val Gly Tyr Leu Val				
65 70 75 80				
Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe				
85 90 95				
Lys Thr Val Leu His Glu Leu Lys Glu Lys Asp Asp Gln Gly Val Lys				
100 105 110				
Ser Arg Leu Ala Val Val Gly Asn Lys Gly Ile Ser Phe Phe Asn Pro				
115 120 125				
Met Gly Leu Glu Ile Lys Gly His Ile Asn Gly Leu Gly Asp Thr Pro				
130 135 140				
Ala Met Glu Asp Leu Val Gly Ile Val Asn Gly Met Val Asn Ala Tyr				
145 150 155 160				
Arg Glu Gly Glu Ile Asp Glu Val Tyr Val Val Tyr Asn Arg Phe Ile				
165 170 175				
Asn Thr Met Ser Gln Lys Pro Thr Val Gln Gln Leu Leu Pro Leu Pro				
180 185 190				
Ala Leu Glu Asn Asp Ser Leu Glu Gln Thr Gly Ser Trp Asp Tyr Leu				
195 200 205				
Tyr Glu Pro Asn Pro Gln Ala Leu Leu Asp Ser Leu Leu Val Arg Tyr				
210 215 220				
Leu Glu Ser Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu				
225 230 235 240				

Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly
 245 250 255

Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala
 260 265 270

Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile
 275 280 285

<210> 168
 <211> 1463
 <212> DNA
 <213> Pasteurella (Mannheimia) haemolytica

<220>
 <221> CDS
 <222> (1)..(1461)

<220>
 <223> guaB

<400> 168
 atg cta cga att aaa caa gaa gcc ctc act ttt gat gat gtt ctt ctc 48
 Met Leu Arg Ile Lys Gln Glu Ala Leu Thr Phe Asp Asp Val Leu Leu
 1 5 10 15

gtc ccg gca cat tct act gtg ctt cct aat act gct gat ctt tct act 96
 Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
 20 25 30

caa tta act aaa acc att cgt tta aac att ccg atg ctt tct gct gca 144
 Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
 35 40 45

atg gat acc gtt aca gaa act aag ctt gcg atc tcc ctt gct caa gaa 192
 Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
 50 55 60

ggc ggc att ggt ttt atc cat aaa aat atg tcg att gaa cgc cag gca 240
 Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
 65 70 75 80

gac cgt gtg cgt aaa gtg aaa aaa ttt gaa agt ggt att gtt tct gag 288
 Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu
 85 90 95

cca gtg acg att tct cct gat atg aca tta gcg gaa ttg gct gaa ttg 336
 Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu
 100 105 110

gtg aaa aag aac ggt ttt gca ggc tat ccg gtg att gat gaa aac caa 384
 Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln
 115 120 125

aat tta gtg gga att att acc gga cgt gat acc cga ttt gtc acg gat 432
 Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
 130 135 140

tta agc aaa aca gtg cgt gaa ttt atg aca cca aaa gac cgt tta gtg 480
 Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val
 145 150 155 160

acg gta aaa gaa aac gca agc cgt gaa gaa att ttc cac tta atg cac	528
Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His	
165 170 175	
gaa cac cga gtg gag aaa gtg ctg gta gtg aat aat gaa ttt cag tta	576
Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu	
180 185 190	
aaa gga atg att acc cta aaa gac tac caa aaa gcg gaa agc aaa ccg	624
Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ala Glu Ser Lys Pro	
195 200 205	
aat gcc tgt aaa gat gag ttt ggg cgt ttg cgt gtg ggg gcg gca gtg	672
Asn Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val	
210 215 220	
gga gcc ggt ccg ggc aat gaa gaa cga att gat gct tta gta aaa gcg	720
Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp Ala Leu Val Lys Ala	
225 230 235 240	
ggg gtc gat gtg cta tta atc gac tct tcg cac ggg cat tct gaa ggt	768
Gly Val Asp Val Leu Leu Ile Asp Ser Ser His Gly His Ser Glu Gly	
245 250 255	
gta tta caa cgt gtg cgt gaa acc cgt gca aaa tac cct gat tta ccg	816
Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys Tyr Pro Asp Leu Pro	
260 265 270	
att gtt gcc ggt aat att gcc act gca gaa gga gcg att gcg tta gct	864
Ile Val Ala Gly Asn Ile Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala	
275 280 285	
gat gca gga gcc agt gct gtg aaa gta gga atc ggc ccg ggt tca att	912
Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile	
290 295 300	
tgt acc acc aga att gta aca ggc gtt ggc gtg cca caa atc acg gca	960
Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala	
305 310 315 320	
atc gca gaa gcg gca gct gcg ctt aaa gaa cga ggc att cct gtg att	1008
Ile Ala Glu Ala Ala Ala Leu Lys Glu Arg Gly Ile Pro Val Ile	
325 330 335	
gct gat ggt gga att cgt tat tca ggc gat att tca aaa gct att gcc	1056
Ala Asp Gly Gly Ile Arg Tyr Ser Gly Asp Ile Ser Lys Ala Ile Ala	
340 345 350	
gcc ggt gca agt tgc gta atg gtc ggt tcg atg ttt gcc ggc aca gaa	1104
Ala Gly Ala Ser Cys Val Met Val Gly Ser Met Phe Ala Gly Thr Glu	
355 360 365	
gaa gcc ccg ggt gaa att gag ctt tat caa ggc aga gca ttc aaa tcc	1152
Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser	
370 375 380	
tac cgt gga atg gga tca tta ggt gca atg agt aaa ggc tcg tca gat	1200
Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp	
385 390 395 400	
cgc tat ttc caa tct gat aat gcc gcc gac aag ctc gta ccg gaa ggg	1248
Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly	
405 410 415	


```

att gaa ggg cgt atc gct tac aaa ggc tac ttg aaa gaa att atc cac 1296
Ile Glu Gly Arg Ile Ala Tyr Lys Gly Tyr Leu Lys Glu Ile Ile His
      420              425              430

caa caa atg ggc ggc tta cgc tcc tgt atg gga tta acc ggc tgt gcc 1344
Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
      435              440              445

act att gaa gaa ctc cgc acc aaa gca gaa ttt gtc cgc att agt ggt 1392
Thr Ile Glu Glu Leu Arg Thr Lys Ala Glu Phe Val Arg Ile Ser Gly
      450              455              460

gct ggt att aaa gaa agc cac gtc cac gat gtg aca att acc aaa gaa 1440
Ala Gly Ile Lys Glu Ser His Val His Asp Val Thr Ile Thr Lys Glu
      465              470              475              480

gca ccg aac tac cga atg ggt ta 1463
Ala Pro Asn Tyr Arg Met Gly
      485

```

<210> 169

<211> 487

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 169

```

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

Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
      20              25              30

Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
      35              40              45

Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
      50              55              60

Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
      65              70              75              80

Asp Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Glu
      85              90              95

Pro Val Thr Ile Ser Pro Asp Met Thr Leu Ala Glu Leu Ala Glu Leu
      100             105             110

Val Lys Lys Asn Gly Phe Ala Gly Tyr Pro Val Ile Asp Glu Asn Gln
      115             120             125

Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
      130             135             140

Leu Ser Lys Thr Val Arg Glu Phe Met Thr Pro Lys Asp Arg Leu Val
      145             150             155             160

Thr Val Lys Glu Asn Ala Ser Arg Glu Glu Ile Phe His Leu Met His
      165             170             175

Glu His Arg Val Glu Lys Val Leu Val Val Asn Asn Glu Phe Gln Leu
      180             185             190

```

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

<210> 170

<211> 2150

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1) .. (2148)

<220>

<223> pnp

<400> 170

atg act cca att gta aaa cag ttt aaa tac ggt cag cac acc gtg acc	48
Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gly Gln His Thr Val Thr	
1 5 10 15	
tta gaa acc ggt gct atc gca cgc caa gca acg gca gca gta atg gca	96
Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Ala Val Met Ala	
20 25 30	
agt atg gac gac aca acc gta ttt gtt acc gta gta gcg aaa aaa gac	144
Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp	
35 40 45	
gta aaa gaa ggg caa gat ttc ttc cca tta acc gta gat tat caa gag	192
Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asp Tyr Gln Glu	
50 55 60	
cgt act tac gca gcc ggt cgt att ccg ggc ggt ttc ttc aaa cgt gaa	240
Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Phe Phe Lys Arg Glu	
65 70 75 80	
gga cgt cct agc gaa ggt gaa acc tta atc gct cgc ttg atc gac cgt	288
Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg	
85 90 95	
cct gtg cgt cca ctt ttc cca gaa ggt ttc ttt aac gaa att caa gtg	336
Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val	
100 105 110	
att gcg acc gta gta tcg gta aac cca caa atc agt cct gat ctg gtt	384
Ile Ala Thr Val Val Ser Val Asn Pro Gln Ile Ser Pro Asp Leu Val	
115 120 125	
gcg atg atc ggt gca tcg gct gcc ctt tca tta tcc ggc gtg ccg ttt	432
Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe	
130 135 140	
aac ggt cca atc ggt gcg gct cgt gtc ggt ttt atc aac gat caa ttc	480
Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe	
145 150 155 160	
gta tta aac cca acc acc agc gag caa aaa atc agc cgc tta gat tta	528
Val Leu Asn Pro Thr Thr Ser Glu Gln Lys Ile Ser Arg Leu Asp Leu	
165 170 175	
gtg gtt tca ggt aca gac aaa gcc gtg ttg atg gtg gaa tct gaa gcg	576
Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala	
180 185 190	
gat atc tta acc gaa gag caa atg tta gcg gcg gtg gtg ttc ggc cac	624
Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His	
195 200 205	
gag caa caa cag gtt gta atc gaa aac atc aaa gaa ttt gtt aaa gaa	672
Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu	
210 215 220	

gcg ggc aaa cca cgt tgg gat tgg gtt gca cca gag cca aat aca gat Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp 225 230 235 240	720
tta atc aac aaa gta aaa gca tta gca gaa aca cgc ctt ggc gat gct Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala 245 250 255	768
tat cgt atc gta gaa aaa caa gtt cgt tac gag caa atc gat gcg att Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile 260 265 270	816
aaa gca gag gtg att gca caa ctt acc gca gaa gat gaa act gtt tct Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser 275 280 285	864
gaa ggg act atc atc gac atc atc acc gca tta gag agc caa atc gtg Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val 290 295 300	912
cgt agc cgt att att gca ggc gaa cca cgc att gac ggc cgt acg gtg Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val 305 310 315 320	960
gat acc gtg cgt gca ttg gat att tgc acc agt gtg tta cca cgc acc Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr 325 330 335	1008
cac ggt tct gct ctt ttc acc cgt ggc gaa acc caa gca tta gca gta His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val 340 345 350	1056
gca aca ttg ggc aca gag cgt gat gcc caa atc att gac gaa ttg acc Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr 355 360 365	1104
ggc gaa aaa tct gac cgt ttc tta ttc cac tac aat ttc cct cca tac Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr 370 375 380	1152
tct gtg ggc gaa acc ggt cgt atc ggc tcg cca aaa cgc cgt gaa atc Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile 385 390 395 400	1200
ggt cac ggt cgt tta gca aaa cgt ggc gta tta gcc gtg atg cca acc Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr 405 410 415	1248
gct gaa gag ttc ccg tat gta gtg cgt gtg gtg tct gaa atc act gaa Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu 420 425 430	1296
tct aac ggt tct tct tca atg gca tct gtg tgt ggt gcg tct ctt gcg Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala 435 440 445	1344
ttg atg gac gca ggt gtg cca atc aaa gca gcg gtt gcc ggt atc gca Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala 450 455 460	1392
atg ggg ctc gtg aaa gaa gac gag aaa ttc gtg gta ctt tct gac atc Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile 465 470 475 480	1440

tta ggt gat gaa gac cac tta ggc gat atg gac ttt aaa gta gcg gga	1488
Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly	
485 490 495	
acc cgt acc ggt gtg act gcg ctg caa atg gac atc aaa atc gaa ggg	1536
Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly	
500 505 510	
atc acc cct gaa att atg cgt att gcc tta aac caa gct aaa ggt gca	1584
Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala	
515 520 525	
aga atg cac att tta ggt gta atg gaa caa gcc att ccg gca cct cgt	1632
Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg	
530 535 540	
gca gat att tct gac tat gcc cca cgc att cac aca atg aag atc gat	1680
Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp	
545 550 555 560	
ccg aag aaa atc aaa gat gtg att ggt aaa ggc ggt gca aca att cgt	1728
Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg	
565 570 575	
gct tta acc gaa gag acc aat act tct atc gac att gat gat gac ggt	1776
Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Asp Gly	
580 585 590	
acg gtg aaa att gcg gca act gac ggc aat gca gcg aaa gca gta atg	1824
Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met	
595 600 605	
gct cgt att gaa gag atc gtt gcc gaa gtg gaa gta aac caa atc tac	1872
Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr	
610 615 620	
aac ggt aaa gta acc cgt gtg gtg gac ttc ggt gca ttc gtt tcc atc	1920
Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile	
625 630 635 640	
tta ggt ggc aaa gaa ggt tta gtc cac att tca caa atc acc aac gaa	1968
Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu	
645 650 655	
cgt gtt gag cgt gta gcg gac tac tta acc gtt ggt caa gaa gta caa	2016
Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln	
660 665 670	
gtg aaa gtg gta gaa att gac cgt caa gga cgc att cgt ctg acg atg	2064
Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met	
675 680 685	
aaa gac atc aat aat acc aac gag gca aat gca gaa gaa act gta gct	2112
Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala	
690 695 700	
gaa aat gtg gta gaa aca gaa caa gaa aat aat ttc ta	2150
Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe	
705 710 715	

<210> 171

<211> 716

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 171

```

Met Thr Pro Ile Val Lys Gln Phe Lys Tyr Gly Gln His Thr Val Thr
 1          5          10          15

Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Ala Val Met Ala
 20          25          30

Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys Lys Asp
 35          40          45

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

Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys Arg Glu
 65          70          75          80

Gly Arg Pro Ser Glu Gly Glu Thr Leu Ile Ala Arg Leu Ile Asp Arg
 85          90          95

Pro Val Arg Pro Leu Phe Pro Glu Gly Phe Phe Asn Glu Ile Gln Val
100          105          110

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

Ala Met Ile Gly Ala Ser Ala Ala Leu Ser Leu Ser Gly Val Pro Phe
130          135          140

Asn Gly Pro Ile Gly Ala Ala Arg Val Gly Phe Ile Asn Asp Gln Phe
145          150          155          160

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

Val Val Ser Gly Thr Asp Lys Ala Val Leu Met Val Glu Ser Glu Ala
180          185          190

Asp Ile Leu Thr Glu Glu Gln Met Leu Ala Ala Val Val Phe Gly His
195          200          205

Glu Gln Gln Gln Val Val Ile Glu Asn Ile Lys Glu Phe Val Lys Glu
210          215          220

Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp
225          230          235          240

Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala
245          250          255

Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile
260          265          270

Lys Ala Glu Val Ile Ala Gln Leu Thr Ala Glu Asp Glu Thr Val Ser
275          280          285

Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val
290          295          300

Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val
305          310          315          320

```

Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr
 325 330 335
 His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val
 340 345 350
 Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr
 355 360 365
 Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr
 370 375 380
 Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile
 385 390 395 400
 Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr
 405 410 415
 Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu
 420 425 430
 Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala
 435 440 445
 Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala
 450 455 460
 Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile
 465 470 475 480
 Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly
 485 490 495
 Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly
 500 505 510
 Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala
 515 520 525
 Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg
 530 535 540
 Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp
 545 550 555 560
 Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg
 565 570 575
 Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Asp Gly
 580 585 590
 Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met
 595 600 605
 Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr
 610 615 620
 Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile
 625 630 635 640
 Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu
 645 650 655

Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln
660 665 670

Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met
675 680 685

Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala
690 695 700

Glu Asn Val Val Glu Thr Glu Gln Glu Asn Asn Phe
705 710 715

<210> 172
<211> 1517
<212> DNA
<213> Pasteurella (Mannheimia) haemolytica

<220>
<221> CDS
<222> (1)..(1515)

<220>
<223> purF

<400> 172
atg tgc ggc att gtc ggt att att ggg aat tcg ccg gtg aat cag gcg 48
Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala
1 5 10 15

att tat gat ggt tta aca tta ctt caa cac cga gga caa gat gcc gca 96
Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
20 25 30

ggt atc gtc acc ata gac gat gaa aat cgt ttc cgc tta cgc aaa gct 144
Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
35 40 45

aac ggc tta gtc agc gat gtt ttc cag caa gag cat atg gtg aga tta 192
Asn Gly Leu Val Ser Asp Val Phe Gln Gln Glu His Met Val Arg Leu
50 55 60

caa ggc aat gtt gga att ggt cac gtt cgc tac cca aca gca ggt agc 240
Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
65 70 75 80

tca agt gtg tct gaa gcc cag cca ttt tat gtc aat tca cct ttc ggt 288
Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly
85 90 95

att acc tta gtt cac aac ggt aat tta act aat aat gcg gaa ctt aaa 336
Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys
100 105 110

gct cgc tta tac aac gaa gcc cgc cgc cat gtg aac act aat tct gat 384
Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp
115 120 125

tct gaa tcc ctt ctt aat att ttt gct tac ttt tta gat ctc tat tcc 432
Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser
130 135 140

act cag cat tta agc cca gac aat atc ttt gaa acg gtt cgt aaa acc 480

Thr	Gln	His	Leu	Ser	Pro	Asp	Asn	Ile	Phe	Glu	Thr	Val	Arg	Lys	Thr	
145					150					155					160	
aat	gat	agc	att	cgt	ggt	gct	tat	gct	tgc	att	gcg	atg	att	atc	gga	528
Asn	Asp	Ser	Ile	Arg	Gly	Ala	Tyr	Ala	Cys	Ile	Ala	Met	Ile	Ile	Gly	
				165				170						175		
cac	ggt	atg	gtt	gct	ttc	cgt	gac	cca	ttc	ggt	att	cgc	ccg	tta	gtg	576
His	Gly	Met	Val	Ala	Phe	Arg	Asp	Pro	Phe	Gly	Ile	Arg	Pro	Leu	Val	
			180					185					190			
ctg	ggt	aaa	cgt	gaa	atc	gag	ggt	aaa	acc	gaa	tat	atg	ttt	gct	tcg	624
Leu	Gly	Lys	Arg	Glu	Ile	Glu	Gly	Lys	Thr	Glu	Tyr	Met	Phe	Ala	Ser	
		195					200					205				
gaa	agt	gtg	gct	ctt	gat	gta	gtg	ggg	ttt	gaa	ttt	gtg	cga	gat	gtg	672
Glu	Ser	Val	Ala	Leu	Asp	Val	Val	Gly	Phe	Glu	Phe	Val	Arg	Asp	Val	
	210					215					220					
ctg	ccg	ggt	gaa	gcg	att	tat	gtt	acc	ttt	gat	ggg	caa	tta	cat	tcg	720
Leu	Pro	Gly	Glu	Ala	Ile	Tyr	Val	Thr	Phe	Asp	Gly	Gln	Leu	His	Ser	
225					230					235					240	
caa	att	tgt	gcc	gat	aat	cca	aaa	ctg	aat	cct	tgt	att	ttt	gaa	tat	768
Gln	Ile	Cys	Ala	Asp	Asn	Pro	Lys	Leu	Asn	Pro	Cys	Ile	Phe	Glu	Tyr	
				245				250						255		
gtt	tat	ttt	gcc	cgt	cct	gat	tcc	gtc	att	gat	ggc	gtt	tct	gta	tat	816
Val	Tyr	Phe	Ala	Arg	Pro	Asp	Ser	Val	Ile	Asp	Gly	Val	Ser	Val	Tyr	
			260					265					270			
tct	gca	cga	gtg	cat	atg	ggc	gaa	tta	tta	ggt	gag	aaa	att	aaa	cgt	864
Ser	Ala	Arg	Val	His	Met	Gly	Glu	Leu	Leu	Gly	Glu	Lys	Ile	Lys	Arg	
		275					280					285				
gaa	tgg	gga	cga	att	atc	gat	gat	att	gat	gtg	gtg	atc	ccg	att	cct	912
Glu	Trp	Gly	Arg	Ile	Ile	Asp	Asp	Ile	Asp	Val	Val	Ile	Pro	Ile	Pro	
	290					295					300					
gaa	acc	tca	aat	gat	att	gcg	gta	cgt	att	gct	aat	atg	ttg	tat	aaa	960
Glu	Thr	Ser	Asn	Asp	Ile	Ala	Val	Arg	Ile	Ala	Asn	Met	Leu	Tyr	Lys	
305					310					315					320	
ccc	tat	cgt	caa	ggg	ttt	gtt	aaa	aac	cgc	tat	gta	gct	cga	act	ttt	1008
Pro	Tyr	Arg	Gln	Gly	Phe	Val	Lys	Asn	Arg	Tyr	Val	Ala	Arg	Thr	Phe	
				325					330					335		
att	atg	ccg	ggg	caa	gca	cag	cgt	aaa	agc	tcg	gtt	cgc	cgt	aaa	tta	1056
Ile	Met	Pro	Gly	Gln	Ala	Gln	Arg	Lys	Ser	Ser	Val	Arg	Arg	Lys	Leu	
			340					345					350			
aat	gcg	att	gcc	tct	gaa	ttt	aaa	ggc	aaa	agc	gtg	tta	ctg	gtt	gat	1104
Asn	Ala	Ile	Ala	Ser	Glu	Phe	Lys	Gly	Lys	Ser	Val	Leu	Leu	Val	Asp	
		355					360					365				
gat	tct	att	gta	cga	ggt	aca	acg	tct	gaa	caa	atc	gtg	gaa	atg	gca	1152
Asp	Ser	Ile	Val	Arg	Gly	Thr	Thr	Ser	Glu	Gln	Ile	Val	Glu	Met	Ala	
		370				375					380					
cga	gca	gct	ggt	gca	aaa	cgg	gtt	tat	ttt	gcc	tct	gcc	gca	ccg	gaa	1200
Arg	Ala	Ala	Gly	Ala	Lys	Arg	Val	Tyr	Phe	Ala	Ser	Ala	Ala	Pro	Glu	
385					390					395					400	

```

att cgc tac ccg aat gtg tat ggc att gat atg ccg act tgt gaa gaa 1248
Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met Pro Thr Cys Glu Glu
                                405                                410                                415

tta gtg gct tat gat cgc tca gtg gaa gag gtt gca cag atg ata ggg 1296
Leu Val Ala Tyr Asp Arg Ser Val Glu Glu Val Ala Gln Met Ile Gly
                                420                                425                                430

gtg gat aaa ttg att ttc caa gac ctt gaa gca ctt tat aag tct att 1344
Val Asp Lys Leu Ile Phe Gln Asp Leu Glu Ala Leu Tyr Lys Ser Ile
                                435                                440                                445

caa ctg gaa aat ccg act att cat cgc ttt gat gac tct gta ttt aca 1392
Gln Leu Glu Asn Pro Thr Ile His Arg Phe Asp Asp Ser Val Phe Thr
                                450                                455                                460

gga gaa tat att aca ggt gat gta gat aaa tgc tat tta gac agt ata 1440
Gly Glu Tyr Ile Thr Gly Asp Val Asp Lys Cys Tyr Leu Asp Ser Ile
465                                470                                475                                480

gca aga tct cga aac gat aaa gca aaa gca gag gcg gca aaa caa gcc 1488
Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala
                                485                                490                                495

acc aat tta gaa att cat aac gaa aga ta 1517
Thr Asn Leu Glu Ile His Asn Glu Arg
                                500                                505

```

<210> 173

<211> 505

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 173

```

Met Cys Gly Ile Val Gly Ile Ile Gly Asn Ser Pro Val Asn Gln Ala
 1                                5                                10                                15

Ile Tyr Asp Gly Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
                                20                                25                                30

Gly Ile Val Thr Ile Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
                                35                                40                                45

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

Gln Gly Asn Val Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65                                70                                75                                80

Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Phe Gly
                                85                                90                                95

Ile Thr Leu Val His Asn Gly Asn Leu Thr Asn Asn Ala Glu Leu Lys
 100                                105                                110

Ala Arg Leu Tyr Asn Glu Ala Arg Arg His Val Asn Thr Asn Ser Asp
 115                                120                                125

Ser Glu Ser Leu Leu Asn Ile Phe Ala Tyr Phe Leu Asp Leu Tyr Ser
 130                                135                                140

```

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

Ala Arg Ser Arg Asn Asp Lys Ala Lys Ala Glu Ala Ala Lys Gln Ala
 485 490 495

Thr Asn Leu Glu Ile His Asn Glu Arg
 500 505

<210> 174

<211> 386

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

<220>

<221> CDS

<222> (1)..(384)

<220>

<223> yjgF

<400> 174

atg aca gtt atc cac aca gaa aat gca ccg gca gcg att ggg cct tat 48
 Met Thr Val Ile His Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr
 1 5 10 15

gtg caa gca gtt gat tta ggc aat atg gtt tta act tct ggg caa att 96
 Val Gln Ala Val Asp Leu Gly Asn Met Val Leu Thr Ser Gly Gln Ile
 20 25 30

ccc gtg aat cct gaa acc ggc gaa atc ccg agt gat att gtg caa caa 144
 Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln
 35 40 45

acc cgc caa tct ctg aac aac gtg aaa gcc att atc gaa caa gcc ggc 192
 Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly
 50 55 60

tta acc gtt gcc gat att gta aag acc acc gta ttt gtc aaa gat ctt 240
 Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu
 65 70 75 80

aac gac ttc gca aag gta aat gcg gaa tac caa gcc ttc ttc caa gaa 288
 Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu
 85 90 95

aac gaa cac cct aat ttt ccg gct cgt tct tgc gta gaa gtg gct cgt 336
 Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg
 100 105 110

tta cca aaa gat gtt ggc att gag atc gaa gcg att gca gta cgc cga 384
 Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
 115 120 125

ta 386

<210> 175

<211> 128

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 175

Met Thr Val Ile His Thr Glu Asn Ala Pro Ala Ala Ile Gly Pro Tyr
 1 5 10 15

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

Pro Val Asn Pro Glu Thr Gly Glu Ile Pro Ser Asp Ile Val Gln Gln
 35 40 45

Thr Arg Gln Ser Leu Asn Asn Val Lys Ala Ile Ile Glu Gln Ala Gly
 50 55 60

Leu Thr Val Ala Asp Ile Val Lys Thr Thr Val Phe Val Lys Asp Leu
 65 70 75 80

Asn Asp Phe Ala Lys Val Asn Ala Glu Tyr Gln Ala Phe Phe Gln Glu
 85 90 95

Asn Glu His Pro Asn Phe Pro Ala Arg Ser Cys Val Glu Val Ala Arg
 100 105 110

Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Arg Arg
 115 120 125

<210> 176
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <221>
 <222>
 <223> Description of Artificial Sequence: PRIMER

<400> 176
 atggcnggng cnaargarat

20

<210> 177
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <221>
 <222>
 <223> Description of Artificial Sequence: PRIMER

<220>
 <221> misc_feature
 <222> 3
 <223> n = A or T or G or C

<220>
 <221> misc_feature
 <222> 12
 <223> n = A or T or G or C

<220>
 <221> misc_feature
 <222> 15
 <223> n = A or T or G or C

<400> 177
 gcngcyttca tngcnaccat

20

<210> 178

<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 3
<223> N = A or T or G or C

<400> 178
ggnttyatyc ayaaaaayat g 21

<210> 179
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 6
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 12
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 15
<223> N = A or T or G or C

<400> 179
tctttngtra tngtnacatc rtg 23

<210> 180
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 180
gcsggyaaac crcgttgga ttgg 24

<210> 181
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 181
croctaarat rtctgaaagc accac 25

<210> 182
 <211> 20
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PRIMER

<220>
 <221> misc_feature
 <222> 9
 <223> N = A or T or G or C

<220>
 <221> misc_feature
 <222> 15
 <223> N = A or T or G or C

<220>
 <221> misc_feature
 <222> 18
 <223> N = A or T or G or C

<400> 182

atgtgyggna tygtnggnat

20

<210> 183
 <211> 21
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PRIMER

<400> 183
 catatcaata ccatacacat t

21

<210> 184
 <211> 16
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: PRIMER

<220>
 <221> misc_feature
 <222> 3
 <223> N = A or T or G or C

<220>
 <221> misc_feature
 <222> 6
 <223> N = A or T or G or C

<220>
 <221> misc_feature
 <222> 12
 <223> N = A or T or G or C

<400> 184
 ggncctayg tncarg

16

<210> 185
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<220>
<221> misc_feature
<222> 1
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 4
<223> N = A or T or G or C

<220>
<221> misc_feature
<222> 10
<223> N = A or T or G or C

<400> 185
ngcnacytcn acrca 15

<210> 186
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 186
gaagccgccca tacgctcttg gg 22

<210> 187
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 187
gttgcttctt ttgcctgcac tgg 23

<210> 188
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 188
ggctcagaaa caataccact ttca 24

<210> 189
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 189
gcaccaaagc agaattgtc c 21

<210> 190
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 190
ggtgatgatg tcgatgatag tccc 24

<210> 191
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 191
ggcgtattag ccgtgatgcc aacc 24

<210> 192
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 192
gaccacttag gcgatatgga ctt 23

<210> 193
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 193
accatcataa atcgctgat tc 22

<210> 194
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

<400> 194
acctgcggca tcttgcctc 20

<210> 195
<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PRIMER

<400> 195

acgggtttat tttgcctctg

20

<210> 196

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PRIMER

<400> 196

cgccggtttc aggattcacg gg

22

<210> 197

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: PRIMER

<400> 197

ctgaacaacg tgaaagccat

20