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(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.



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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
5 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
10 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
15 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
20 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
25 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
5 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,
10 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
15 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
20 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
25 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,
30 *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.

The discussion of the background to the invention herein is included to explain the context of the invention. This is not to be taken as an admission that any of the material referred to was published, known or part of the common general knowledge as at the priority date of any of the claims.

Throughout the description and claims of the specification the word "comprise" and variations of the word, such as "comprising" and "comprises", is not intended to exclude other additives, components, integers or steps.

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.*

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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.

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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 gallanum*, *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
5 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
10 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
15 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
20 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
25 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-
30 438 (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 Ribi 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

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

20

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).

30

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).

20

25

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 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 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 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 *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 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 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
20 selected by quantitative analysis as being 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.

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	mucB	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 (HI1207)	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	hxcC	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 atpG 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).

5 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:λpir 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 µg/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:λpir (λpir, *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 µg/ml ampicillin (Sigma), 50 µg/ml nalidixic acid (N⁵⁰)(Sigma), and 50 (K⁵⁰) or 100 (K¹⁰⁰) µg/ml of kanamycin (Sigma).

25 Matings were set up by growing each *E. coli* S17-1:λpir/pTEF1:[NK]₃₅ clone and the AP225 strain to late log phase. A 50 µl aliquot of culture for each tagged-pTEF-1 clone was mixed with 150 µl of the APP225 culture, and then 50 µl of each mating mixture was spotted onto 0.22 µm filters previously placed onto BHIV¹⁰ plates containing 100 µM IPTG and 10 mM MgSO₄. Following overnight incubation at 37°C with 5% CO₂, mating mixtures were washed off of each filter into 2 ml of PBS and 200 µl 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 *HindIII* 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
	<u>Start Codon - NO Stop Codon</u>			
20	lpdA	SEQ ID NO: 148	<u>RNA or Noncoding Sequences</u>	
	potD	SEQ ID NO: 156	tRNA-leu	SEQ ID NO: 162
	yaeE	SEQ ID NO: 164	tRNA-glu	SEQ ID NO: 163
	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 insertions were detected in the 110 mutants screened as determined by production of multiple PCR bands and generation of multiple sequence electropherograms.

30

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

A representative clone from each of the unique attenuated mutant 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 x 10⁶ CFU each of the wild type and mutant 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 mutant in both the input cultures and in the lung lavage samples. A Competitive Index (CI) was calculated as the [mutant CFU / wild type CFU]_{input} / [mutant CFU / wild type CFU]_{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 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.

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.
5	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
10	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
15				
	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
20				
	AP17C9	<i>tRNA-leu</i>	Protein Synthesis	.059
	AP5D6	<i>tRNA-glu</i>	Protein Synthesis	.055
	AP18B2	<i>rpmF</i>	Protein Synthesis	.112
25	AP10E7	<i>yaeA</i>	Unknown	.001
	AP19A5	H10379	Unknown	.061
	AP10C10	<i>apvA</i>	Unknown	.157
	AP18F5	<i>apvB</i>	Unknown	.103
	AP2A6	<i>apvC</i>	Unknown	.091
30	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
5 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
10 *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
15 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
20 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
25 *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
30 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 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 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, *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 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 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 [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 1.5×10^5 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>	<u>% Mortality following intranasal challenge</u>	
		<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 LD_{50} 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 µl reaction was set up using 3.3X XL buffer II (PE Applied Biosystems), 200 µM 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 µl 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 GGCTCAGAAACAATACCACITTTCA SEQ ID NO: 188
	HindIII, TaqI	TEF268 GCACCAAAGCAGAATTTGTCC SEQ ID NO: 189
pnf	ClaI, HincII	TEF219 GGTGATGATGTGCGATGATAGTCCC SEQ ID NO: 190
	TaqI,	TEF220 GGC GTATTAGCCGTGATGCCAACC 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, pnf, 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.

THE CLAIMS DEFINING THE INVENTION ARE AS FOLLOWS:

1. An attenuated *Pasteurellaceae* bacterium selected from the group consisting of *Pasteurella (Mannheimia) haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae*, and *Haemophilus somnus* comprising a mutation in a polynucleotide sequence that encodes an atpG polypeptide comprising an amino acid sequence at least 70% identical to the atpG amino acid sequence of SEQ ID NO: 167, wherein the mutation results in decreased virulence and attenuation of the bacterium.
2. The bacterium of claim 1, wherein the mutation results in deletion of all or part of the polynucleotide sequence that encodes the atpG polypeptide.
3. The bacterium of claim 1, wherein the mutation results in an insertion in the polynucleotide sequence that encodes the atpG polypeptide.
4. The bacterium of claim 1 that is a *Pasteurella (Mannheimia) haemolytica* bacterium.
5. An immunogenic composition comprising the bacterium according to any one of claims 1 to 4.
6. A vaccine composition comprising the immunogenic composition according to claim 5 and a pharmaceutically acceptable carrier.
7. The vaccine composition according to claim 6, further comprising an adjuvant.
8. An attenuated *Pasteurellaceae* bacterium selected from the group consisting of *Pasteurella (Mannheimia) haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae*, and *Haemophilus somnus* comprising a mutation in a polynucleotide sequence that encodes an atpG polypeptide, wherein the polynucleotide sequence hybridizes to the complement of a polynucleotide sequence set forth in SEQ ID NO: 166 under stringent conditions, such conditions comprising a final wash in buffer comprising 2X SSC/0.1% SDS, at 35°C to 45°C.
9. The bacterium of claim 8, wherein the mutation is in the polynucleotide sequence set forth in SEQ ID NO: 166.

10. An immunogenic composition comprising the bacterium according to claim 8 or 9.
11. A vaccine composition comprising the immunogenic composition according to claim 10 and a pharmaceutically acceptable carrier.
- 5 12. The vaccine composition of claim 11 further comprising an adjuvant.
13. The bacterium of claim 8 that is a *Pasteurella (Mannheimia) haemolytica* bacteria.
- 10 14. An immunogenic composition comprising the bacterium according to claim 13.
15. A vaccine composition comprising the immunogenic composition according to claim 14 and a pharmaceutically acceptable carrier.
- 15 16. The vaccine composition of claim 15 further comprising an adjuvant.
17. The bacterium of claim 1 or claim 8, substantially as hereinbefore described.

SEQUENCE LISTING

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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 aggatcggtat atggcaactg gaaaaattgt acaaatcatc 1280
Ala Ile

gggtcggtta ttgacgttga attcccacaa gatgcagtac caaaagtata tgatgcctta 1340

aatgttgaaa caggtttagt acttgaagtt caacaacaat taggtggtgg tgtagtccgc 1400

tgtatcgcaa tgggatcatc tgatggatta aaacgcgggt taagcgtaac aaatacgaat 1460

aacccaatct ctgttccagt gggaacgaaa acattgggtc gtatcatgaa cgtattgggt 1520

gaaccaatcg atgagcaagg tgaaatcggg gcagaagaga attggtctat tcaccgtgcg 1580

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<212> PRT

<213> Pasteurella multocida

<400> 4

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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
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Ala Ser Ile	Thr Asn Glu Leu	Asn Glu Ile Val Ala	Gly Ala Ala Ala
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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 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	
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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	

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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

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 <213> Pasteurella multocida

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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

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

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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

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Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala
130 135 140

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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 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

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Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu
225 230

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 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
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 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
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          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 Leu Asn Ser Leu Arg Lys Asn Phe Thr
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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

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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
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 Lys Leu

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 <213> Pasteurella multocida

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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
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<210> 11
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 <213> Pasteurella multocida

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 <222> (856) .. (1389)

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 Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg
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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
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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 tcc 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
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att ggt tta agc agt gca atc aaa ggc tta atg att agc atc acc cat 1131
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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 ttctcggtcg gtatagatta aatttcttgc acgacaaaact gcagggaatg 1479

tcttgctaata aatcttgctt tacgctgctt taagcgtttt aaacgtaatg cgcgtccttg 1539

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<213> Pasteurella multocida

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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
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Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys Gln Arg Arg Leu
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Phe His

<210> 13

<211> 4426

<212> DNA

<213> Pasteurella multocida

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<222> (2756) .. (3211)

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<223> exbB

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Gly Leu Leu Ala Phe Met Ser Phe Ile Met Val Trp Leu Val Ile Glu
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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
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Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile Gly
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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
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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

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Lys Lys Ala Lys Gln Gln Ala
150

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<211> 152

<212> PRT

<213> Pasteurella multocida

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		20						25					30		
Glu	Arg	Phe	Leu	Phe	Leu	Ser	Arg	Val	Asn	Val	Ala	Ser	Tyr	Glu	Ser
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Ile	His	Glu	Leu	Asp	Ile	Asp	Leu	Gln	Arg	His	Leu	Thr	Ala	Ile	Ser
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Asp	Ala	Ala	Ala	Ile	Met	Val	His	Leu	Ser	Leu	Ala	Leu	Lys	Ala	Thr
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Tyr Thr Ser Cys Pro Leu Ile Thr Gln Leu Gly Lys Gly Met Leu Val	
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425 430 435

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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

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Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu Val Lys Leu Asp Thr Asn
475 480 485

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Pro Leu Met Arg Val Lys Ser Ser Val Arg Phe Leu Gly Ser Pro Phe
520 525 530

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Phe Ser Ile Ser Pro Ser Met Leu Ala Ser Leu Ser Ala Gln Phe Lys
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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

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Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu Thr Glu Gly Asn Asn Phe
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<212> PRT

<213> Pasteurella multocida

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 Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
 35 40 45
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 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
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 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
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 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
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 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
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 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
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 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
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 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
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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
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<213> Pasteurella multocida

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His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu	
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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	
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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	
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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	
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ccg caa gtg agt gtc gga ttc aat aat tca ggt gct ggc aat aat gcc	480
Pro Gln Val Ser Val Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala	
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Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu	
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Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys	
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Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr	
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Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr	
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Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu	
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Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser	
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Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser	
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Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser	
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Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser	
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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	
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 <213> Pasteurella multocida

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 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
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 115 120 125
 Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe
 130 135 140
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 145 150 155 160
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 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
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 Ser Phe

<210> 21
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 <222> (639)..(1022)

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 cgagcagttg ctattttttt attgtcgaac aataatagta tttgaaccct cgagagtaaa 540
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<213> Pasteurella multocida
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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

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Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
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 Ile Asp Thr Glu Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
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<210> 23
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 <213> Pasteurella multocida

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 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	
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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	
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ggt 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	
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Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val	
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Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr	
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Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro	
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Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile	
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Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser	
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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	
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220 225 230 235	
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Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys	
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Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly	
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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
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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
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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
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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
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Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala
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Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile Ser Leu Ala Gln Glu
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Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser Ile Glu Arg Gln Ala
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Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser Gly Ile Val Ser Asp
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Pro Val Thr Val Ser Pro Thr Leu Ser Leu Ala Glu Leu Ser Glu Leu
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Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val Val Asp Asp Glu Lys
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Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr Arg Phe Val Thr Asp
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Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro Lys Ala Arg Leu Val
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Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile Phe Gly Leu Met His
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Thr His Arg Val Glu Lys Val Leu Val Val Ser Asp Asp Phe Lys Leu
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Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys Ser Glu Gln Lys Pro
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Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg Val Gly Ala Ala Val
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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
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Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly Ala Ile Ala Leu Ala
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Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile Gly Pro Gly Ser Ile
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Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val Pro Gln Ile Thr Ala
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 Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile Ser Lys Ala Ile Ala
 340 345 350
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 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
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 435 440 445
 Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
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 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
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 gta caa gtt gcc 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
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Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala	
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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	
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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 Glu Lys Leu Gln Val	
95 100 105	
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Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met	
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Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile	
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Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala	
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Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu	
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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	
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Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly	
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Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val	
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His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile	
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Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu	
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Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu	
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Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu	
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Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg	
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Ile Pro Glu Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln	
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Ser Ala Asn Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly	
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Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro	
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Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp	
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Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His	
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Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu	
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 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
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 Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val Glu Ile Asp
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 115 120 125
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 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
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 305 310 315 320
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 325 330 335
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 Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val
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 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp
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 Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val
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 Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn
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 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
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Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu
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Asn Val
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Phe Leu Glu Asp Arg Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu
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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

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Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser	
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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
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115 120 125	
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210 215 220	
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Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala	
225 230 235 240	
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Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp	
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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	

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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 1353
Gln Val
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<210> 28
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<212> PRT
<213> Pasteurella multocida

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

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 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
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 Gln Val
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 <213> Pasteurella multocida

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 catggctagc attctagcaa aaattagttg aggaaaatag cggtcttggt ttgcttaaaa 180
 aacaaccac cccgtagggc acggctgttt ctttttgaga aattacgctt cttcatcttg 240
 atcttttttc aagatctcat cttcattgag ttttaaaaga cgggcaatcg cattgcggta 300
 ggagatttca aggctttctc gactagtagc aatgacacct tgatcgatta agaaaccgtc 360
 attgacatca taaaccaaac catgtaatga gagttttttc ccattttttc acgcggattt 420
 aatgattgac gagcgacctt agttataaac ttgctctgcg acgttaattt tcgtcagcat 480
 atcagcccgt ttttcaggcg gtaaattgcc aagtaaatga ctatgcttat accaaatatt 540
 gcgtaagtgg agtaaccagt tattaattaa acctaaatct tgatccgcca ttgcggcttt 600
 aattccacca cagtttgat gtccacaaat aataatgtgt tcaatattta agacctcaac 660
 ggcattattgc acaacagata aacagtttaa atcgggtgtga atgacttgat ttgcaacatt 720
 acgatgcaca aacagctcac ccggtcctaa atttgtaaat ttttctgcag gaacacggct 780
 atccgagcaa ccaatccaaa gatagctcgg ggtttgatga tcagccaatt ctttaaagta 840

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aatagacagt gggtaaagaa aggcataaaa ttgtatagga taacttgttt 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

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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	
ggg 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	
ggg 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	


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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 tagagttggt tgaaatgact gaaaaattag acctatacgt 2809
Gly Val Asn Arg

tactgttaaa ggtggcggtta tttctggtca agcgggtgca atccgtcacg gtatcactcg 2869

tgcattaatc gaatatgatg agagtttacg ctctgtatta cgcgcagctg gtttcgttac 2929

tcgcgatgca 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 caaagtttaa 3169

taaattttta ttcatthttag agctgtcggg ggaatagatg acaagcgtcg caaataaacg 3229

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agagcgtatt atgattgggt agtggataat gatttcaccc cttatttagt ggtggacgcg 3949

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<211> 564

<212> PRT

<213> *Pasteurella multocida*

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      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

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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
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Pro Asn Ser Lys Gly Tyr Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu	
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 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

[illegible]

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 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
taagagtggag gtgaagaaat ggcattacca acagcaacaa taatgaggaa tttatcttta 1624
tctaaaaatc aattcactct gaaagggatg gaatgcgtag attccctatt tcaagcatgc 1684
agtaatatgg atcatgggta ctgaggtgga agatggcaga agaaaataaa ggaagagat 1744
atTTTTtatg gttcatattg tttatccttt caatctattt atttattacc atacaagaaa 1804
gacgaggtta ttgttttgac aaatgggaat atatccataa cctttataacc gagcaagagt 1864
tgatcgatag aggggttgaa tatgtggtat ccaccatgcc gtcaggtggt tttgaaccag 1924
atggcacaac aaccgaaata aaacgttatg ctagtgttga ggagtttaaa cagatgaacc 1984
ctgattgttg taaattaaca agatttatta atgaaggaaat agatggctat ccagatgatg 2044
atggatatgg ttatataaga attgaatatt taagacatta tgttggaat tttaaactg 2104
atcatagagt gctttatctc gaataacgc cttgtggaga attaaggga gaggtttctt 2164
tttaaaaaat aaataatagt gaggtgaaga aatggcatta ccaacagcaa cagaaatcac 2224
aaatgcatat ttatataaaa ataaattaac toctaaagcg gaggaagag tagattcaat 2284
acaaattctt gaaaaaggag atgaacattt cgaagtaaatt tttaattgat caaagtactc 2344
tattgattga aggaaaaaca gtggaattaa tggcaggtat ggcagtttct gcggaatta 2404
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attaaggaga ataatatgtc gtataataaa tatactgttg ctttgattac gttctcaaca 2524
gggatctgta ttccggcaat atgctacgct cttaaattcgc tgggatacag atcctgtttg 2584
agactatgta gaaaagacta aactttgtgt ggttaactgg gcttcggtaa aattctggaa 2644

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

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

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 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
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 <212> DNA
 <213> *Pasteurella multocida*

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gcagaactgg ctagcttata acttttagat aattgtatta ttaaaagaag ctgtatgatt 180
gttattctat cattagtgga taataaatat tctttatttt ttgagagata aaaacaattc 240
atatttcaat 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

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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 gcc 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 gcttgttcta atttattaca ataatggttg 1330

tattcatctt gattttgaag gaaagagagt gttttttgta taaaagcatt ttcgtcacct 1390

aaatttacta atcctccaaa ttctctcct cgnagaatct ctttcggacc ggtagggcag 1450

tccatggata ttacaggtgt accgcaagcc atgctttcta ggataactgt cggtaacccc 1510

tctttcaaag aggtgtgtaa aaatagctta gcatttttta ttaatggata cggattatct 1570

ttatttccta aaagaaaaca atcttcttgt agattgagtg attctatttg tttctcta 1630

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ttttctcgac actcaccatc ccaaacaata tatancnttt cttggatacc tcc 1683

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

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<220>
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 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

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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

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

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

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<220>
<223> mglB

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

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<220>
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 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

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gaa ggc aca aaa tgg cag tta aaa cga tgc 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 taacttaaac gagttcctaa aataataaac 529
Cys Trp Cys Gly Cys Gly
165

tataacaaaa caagamgttg taattctcgg ggagggtatac cctccccctt tttatgtgag 589
gttggtatag acaactcaaa ttccaaatca agacagtga atactgtc caatgaccaa 649
cgtctgtaaa tcctttcccg gtgttaaagc gttagacaat gcaaacctaa ctgtgcgctc 709
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cttgggtaaa caatgtactg taatggataa tcctttggnt aggacgttat ccattaaaag 949
caggctttgt cgatcacggc aaaatgtatc gtgataccaa agcagatttt tgaagaanta 1009
gatatcgata tcgatccaaa agaaaaagtg gccaaattgt cagtgtcaca aatgcaaagt 1069
atcgagatcg caaaggcctt ttcatacaat gccaaaatcg taatcatgga cgaaccgact 1129
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cgtggctgtg gcattattta ttttcgcac aaaatggacg aaatcttcaa aatttgtgac 1249
gaaattacga ttttacgca tggtaaattg atcaatacgg tcgctgttaa aggcaccaca 1309
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accaataccc caaaagaaac catcttaacg gtggaaaatc tgaccgcact taatcagcca 1429
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gtatcgacat tgggtcgaaa tatgaaattt atcagctgat tatggagtta gccaaaaaag 1969
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<210> 38

<211> 166

<212> PRT

<213> Pasteurella multocida

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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

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

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<222> (326)..(766)

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<220>
<223> mioC

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<400> 39

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tcaattggaa attgatgaat taaaagaaaa aaataaccaa tctcaacaag caaatgacgc 180
attacgcagt gaaaaatgaac 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 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
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<213> Pasteurella multocida

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 Asp Asn Ile Lys Pro Leu Phe Glu Lys Leu Ala Phe His Pro Lys Gln
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 Ser Gln Leu
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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
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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
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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
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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
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Pro Ser Pro Arg Val Leu Val Cys Val Pro Ala Gly Ala Thr Gln Val
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Glu Arg Arg Ala Ile Lys Glu Ser Ala Ile Gly Ala Gly Ala Arg Glu
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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
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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
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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
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tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat 3808

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Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr
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 Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg
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 Gly Val Pro Val Ile Ile Ala Asp Asp Pro Leu Thr Cys Val Ala Arg
 315 320 325 330
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 Gly Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile
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<211> 351

<212> PRT

<213> Pasteurella multocida

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 Gly Arg Thr Pro Lys Ser Ile Ala Ala Ile Arg Pro Met Lys Asp Gly
 65 70 75 80
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 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
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 Gly Ser Met Val Ile Asp Ile Gly Gly Gly Thr Thr Glu Val Ala Val
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 Ile Ser Leu Asn Gly Ile Val Tyr Ser Ser Ser Val Arg Ile Gly Gly
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 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
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 Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His
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 Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser

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Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg
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Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile
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Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
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Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
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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
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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
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Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
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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
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aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct   384

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Arg	Ala	Leu	Thr	Glu	Glu	Thr	Gly	Thr	Ser	Ile	Asp	Ile	Asp	Asp	Asp		
		355				360						365					

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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 Glu Asn Ala
485

aaagggcggtt ggtgtgcatg ttgataagta caatttgtgc ttttaaggcga agcgaaatga 1554
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<210> 44

<211> 488

<212> PRT

<213> Pasteurella multocida

<400> 44

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 20 25 30
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 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
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<210> 45
 <211> 633
 <212> DNA
 <213> Pasteurella multocida

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

<220>
 <223> purF

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 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

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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 Lys 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 633
Tyr Leu
      210

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

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<400> 46
Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
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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

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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>
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 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	
	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	ggt	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	
	225				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	ttctaatagaa	actgggggatg											976
gaaagtcttg	gcgggtaata	atatgacgag	atgtgtaatt	gtaagaacga	ttaatcatga											1036
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cagttctttt	gaggtgtacc	caatatcgaa	cttgatttga	ttgttttggt	ttgcgatttc											1276

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gaatcgggtg ccagtgtgta acgttaatag ctagatcata aattggacca ttctgattta 3256
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<210> 48

<211> 292

<212> PRT

<213> Pasteurella multocida

<400> 48

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 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
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 275 280 285
 Asn Leu Leu Asp
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<210> 49
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 <212> DNA
 <213> Pasteurella multocida

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 <222> (2)..(1195)

<220>

<223> sopE

<400> 49

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    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 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

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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

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 gcgggcggta tgattggttc ggtggatgtc aatctcgggc ttgaaaagct 1375

cgaagcggaa tttaaagccg gtggctacat ggtcgaatta attaaaaaat tcggcggggtc 1435

aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495

cacatctggt gagcttgtga tgcaaggctc atttactgaa attgacagcg gaaacagcaa 1555

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<210> 50

<211> 398

<212> PRT

<213> Pasteurella multocida

<400> 50

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 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

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 <213> Pasteurella multocida

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 <222> (1)..(351)

<220>
 <223> unknown C1

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 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

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 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
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 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
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 <211> 509
 <212> DNA
 <213> Pasteurella multocida

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 <222> (1)..(507)

<220>
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 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

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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

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<210> 54
<211> 169
<212> PRT
<213> Pasteurella multocida

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<400> 54
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  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
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<210> 55
<211> 443

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<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(441)

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<223> unknown C3

<400> 55

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  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

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Ile Phe Ile
145

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<210> 56

<211> 147

<212> PRT

<213> Pasteurella multocida

<400> 56

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  1           5           10          15

Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
          20           25           30

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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
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<210> 57
 <211> 8498
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 <213> *Pasteurella multocida*

<220>
 <223> unknown C

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 aaaagtgtgg tacaacttaa accagaagag gtggaatggt catcaatcca ttatcctttc 180
 tttgctggcg atattcagca agtcgctcat ctgcgaaaag ccgcagaaat gggttgcgtg 240
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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		

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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
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Val Gly Arg Ser Ser Ser His Lys Pro Lys Phe
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<210> 60
<211> 5798
<212> DNA
<213> Pasteurella multocida

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<220>
<221> CDS
<222> (698)..(1468)

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<220>
<223> unknown D2

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ttattattat caggcctata ttatttatat gcagtaaaaa acgattcaaa ttttgtcata 180
ggtttatcta ttatttttagt ttttattatt gtcattccag ggattttgac aaatgctatt 240
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gtaaatgttc aaacagggat tagtattgat gcggctttta aacaagtggc aatcgatttt 360

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aagaaactta atccagatct tacttatgtg atgttaagga ttattagaaa atctgaactt 420
acgggattat cacaagcggt acaggatctt tcgatctcat tgccaacaac agaaataaga 480
atgttttgta ctgttttaca acagagttta aattttgggt cttcaattta ttctcactta 540
attcagttgt ctgcagatat cagggagata caattattaa tcattgagga aaaggttaggt 600
acattatcag ctaaaatgag tatccatttg attttggtta ttatgttccc aataatcatt 660
ttaattctag caccaggtat aatgagggta 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
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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
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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
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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
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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
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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

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 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
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<210> 61

<211> 257

<212> PRT

<213> Pasteurella multocida

<400> 61

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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
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 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		
ttaataaaaac accagcaatt tcaacgccat tcatggcaga taatgccgct gcgacgatca				690
catcaggacg atccgcggaa gtgacaagta aacttccaac gcggaaatgt tccaccatat				750
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catgaataat ggcagcacct aaatgtttgg ctaaatcaat ggcacgagtc gcaattaatt				870
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gagtacgacc agattcatca atcggcgcat taaatttatt gatcacaaca ccaagtaaat				1050
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<210> 63
 <211> 200
 <212> PRT
 <213> Pasteurella multocida

<400> 63
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 20 25 30
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 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
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 180 185 190
 Glu Leu Asn Val Asp Arg Val Ser
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<210> 64
 <211> 278
 <212> DNA
 <213> Pasteurella multocida

<220>
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 <222> (108)..(278)
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<223> unknown O

<400> 64

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                                     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
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<210> 65

<211> 57

<212> PRT

<213> Pasteurella multocida

<400> 65

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      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
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<210> 66

<211> 1020

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (1)..(597)

<220>

<223> unknown P

<400> 66

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  1              5              10              15
gca atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att 96

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Ala	Met	Arg	Ala	Tyr	Leu	Asp	Lys	Glu	Gln	Gly	Trp	His	Thr	Ser	Ile		
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Arg	Thr	Thr	Ala	Glu	Asp	Pro	Leu	Phe	Lys	Phe	Glu	Val	Tyr	Thr	Arg		
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Val	Asp	Lys	Asp	Ile	Ser	Val	Thr	Leu	Val	Lys	Asp	Ile	Ile	Glu	Ala		
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Glu	Gln	Leu	Gly	Phe	Asn	Gln	Tyr	Ile	Ser	Asp	Glu	Tyr	Leu	Val	Asp		
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Val Asn Tyr Glu Gly Val Thr Ser Ser Asn Pro Phe Ala Tyr Lys His
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Tyr Asp Ala Asn Gln Val Ile Leu Gly Lys Thr Met Ala Glu His Leu
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cgt tta gcc gtc tgt tat tgg cac act ttc tgt tgg aca ggg aat gat 1215
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Ser Lys Leu Gly Ile Pro Tyr Tyr Cys Phe His Asp Val Asp Val Ala
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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
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Phe Thr Ala Met Gly Ala Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val	
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Lys Gln Glu Arg Glu Gln Ile Gly Arg Phe Met Gln Met Val Val Glu	
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His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys	
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Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val	
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Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn	
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Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu	
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Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn	
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Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser	
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Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly	
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Phe Thr Thr Gly Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser	
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Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val	
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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	
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 Leu Thr Lys Val Leu
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<213> Pasteurella multocida

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 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
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Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
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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
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Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
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Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
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Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
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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
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 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
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 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
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Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu	
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Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala	
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Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu	
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Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln	
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Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala	
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Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys	
85 90 95	
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Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly	
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Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys	
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Arg His Gln Glu Pro Arg Asp Asp
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3501

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<400> 71

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Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala
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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
  
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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
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 Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
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 Arg His Gln Glu Pro Arg Asp Asp
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<210> 72
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 <212> DNA
 <213> Pasteurella multocida

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 <223> ygiK

<220>
 <221> misc_feature
 <222> 452
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tgcaggagaa aaagtttatg aaatccaaaa agaattggact gacaatattg aaaaagcttc 180
caatgggaga ataagtatag agttattacc tctcgactca gtcttaaaat ctagtgcacat 240
gctttctggg gttcgaataa aaattattga tggagcgggt gcaacagcgg caatgtatgc 300
aggcactgac cctggattcg gattaattgg tgatactatt tctgcttggg accatgacga 360
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acaatatggg gccaaactca ttgggtgtatc anttacggga gcagaatcat taccatcgaa 480
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tatccaaaaa ttgtttgcaa gattaggagc cgctcctgtt ggtcttccctg gttcagaaat 600
ctatactagt ttagaaaaag gtattattga tgctgccgat ttctcaacgt ttgcaaataa 660
tcaagcaciaa ggagtccatg atattgcaaa atatccaatc tatccgggaa ttcattcttc 720
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acatgccatt tccagcaatt gaaaaaggt tcttctttat ttc atg cct cat cat 1555
Met Pro His His
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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 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	
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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	
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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 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 tagtaaatct tgcgcgatac gaataaacgc attgatggca tttgctccgt 2859
 Thr Phe
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 aaatacactg aattaccgga tgcctacaaa tcggttaatg aagccttgaa acacgcaggc 3099
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<210> 73

<211> 422

<212> PRT

<213> Pasteurella multocida

<400> 73

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 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

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ggcggttgcaa tctgttggcg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
tttgttccac caatatctaa tgctaaacag cgcataggct ctcttctgt gatgacttat 240
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gatcctacgg tgacagagta agcaccaatc tcaattgcgg ttttcgcaa ttctgggggtg 360
ttatagcgcc cttctgccat cactcggcag ccagcagcat tcaaattctt 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 tgg 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 tgg gcg cct gct gcg gct aac tct tca atg tct tgt aaa aat 666
Ile Ile Ser Ala Pro Ala Ala Asn Ser Ser Met Ser Cys Lys Asn
55 60 65

ggg cta ata cga acg gga ctg tca ggt aaa tgg 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 tgg 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 taaattttatc aaaagaagat	956			
Cys Asp Ser Phe Asp Ile Leu Thr Pro Val				
	150	155		
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tttgagatct ttgtcgcata ttattcata gggaatagac agcttaattt tagttatgat	1076			
ttgtcaatcc ttgtattttt ttgtgtttgc tggtttgca tacactgttc taatattgct	1136			
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aagaaaaatc caatggcaaa attgatgtgg ctattttccc tagctcacag ttaggtgatg	2156			
accgtgtgat gattaaacaa ttaaaagacg gtgcattaga ctttacgtta ggtgaatcag	2216			
cacgtttcca aatttacttc ccagaagcag aagtatttgc gttgccttat atgattccta	2276			
attttgaaac ctctaaaaaa gcgttgctcg acacaaaatt tggtaaggt ttattgaaaa	2336			

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 atttacaaaa agtgggttaaa gatgcagcag cgaaagccgc tgaatatcac actaaactct 2756
 tcgttgacgg tgagaacagc ttagttgaat t 2787

<210> 75
 <211> 158
 <212> PRT
 <213> *Pasteurella multocida*

<400> 75
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 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> yiaO

<400> 76

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ggcggttgcaa tctgttggtg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
tttgttccac caatatctaa tgctaaacag cgcataggct ctcttctgt gatgacttat 240
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ggtacattga cgacgttacg cgtggctttt aaattttcga tcccttcaat acgtaaccgg 780
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ggcccattat ctacgggctg gcaagatgcg attaagccat atttaatttg ttctaaaact 900
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tccaatttgc ataggttaat cttagaatta aaaaataaca accaaaataa taaaaatttg 1020
agatctttgt cgcataattt ttcataggga atagacagct taattttagt tatgatttgt 1080
caatccttgc tattttttgt gtttgcgtgt ttgcgataca ctgttcta attgctttga 1140
gcacttgata acctgtctca ttaaaatgta atccgtcggg acaaaggcgt aaatccagtt 1200
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Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu
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<213> Pasteurella multocida

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Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser
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Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly
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Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe
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Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu
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Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu
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Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr
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Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu
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Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu
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Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val				
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Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr Cys Ser Ile Arg
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<212> PRT

<213> Pasteurella multocida

<400> 81

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<212> PRT

<213> *Pasteurella multocida*

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 tac gtt aca atc tca aca ctt aat cgc gtt tgaccttccg 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
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 gagcacttga cttagtgcga ccaatcgacc gttggcagtc agtgtcgcaa tgccgtgac 2979
 cgtatcaagc gttacaccgc ttttttttcc ccagttttta ttgagctttt cactatgttt 3039
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 gactgcaagc gacttgtttt cattgctaac cgtctgctca agtgctgtga ttttgatgt 3159
 taaatctaac ttagttgcat tgacttcac agtcattctt gactttaact cttttctcgc 3219
 aagtgacgcc acttcatctt tgctagcttt cgtttctttt aagtcagaaa tgccactagt 3279
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 gctagccgtt ttttgaatta gctgtatttc actttcgctc aatccaactc tagcagttag 3399
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 aatatccgcg cttacttccg agatagccac gtcca 3494

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 <213> Pasteurella multocida

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 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
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<223> Description of Artificial Sequence: PRIMER

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<210> 88
<211> 18
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<220>
<223> Description of Artificial Sequence: primer

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<210> 89
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<220>
<223> Description of Artificial Sequence: primer

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<210> 90
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<220>
<223> Description of Artificial Sequence: primer

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<210> 92
<211> 18
<212> DNA
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<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
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<220>
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<400> 95
ggcagagcat tacgctgac 19

<210> 96
<211> 27
<212> DNA
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<220>
<223> Description of Artificial Sequence: primer

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 <211> 531
 <212> DNA
 <213> *Actinobacillus pleuropneumoniae*

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 agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcggttt acgtcgctta 180
 caaccgtttt gaaaatacga tgtcacaaaa acctgttatc gcacagttac ttccggttacc 240
 taaactagat gacgatgaat tagatacga aggttcattg gattatattt atgaaccgaa 300
 tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360
 agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420
 agataatgcg ggtacattaa tcgatgaatt acaattagtg tataacaaag ctcgccaagc 480
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<220>
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<220>
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<220>
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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

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	245	250	255	
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Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His	260	265	270	
gca att aat gaa ggt 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 Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu	325	330	335	
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<211> 344

<212> PRT

<213> Pasteurella multocida

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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
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 Gly Glu Tyr Ile Ser Pro Glu Val
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<210> 102
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 <222> (1)..(4929)

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 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

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tct gat tca aca tcc aca tca gaa caa gtt gaa gag gaa cct ttc ctt			144
Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu			
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Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr			
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ttc aat cct gtt tcg tat gca atg caa ttg act tgg aaa cag ctt tct			240
Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser			
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att tta ttt tta act gtg att tct gtt cct gtt ttg gct gag gga aaa			288
Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys			
85	90	95	
ggg gat gaa aga aat caa tta aca gtg att gat aat agc gat cat att			336
Gly Asp Glu Arg Asn Gln Leu Thr Val Ile Asp Asn Ser Asp His Ile			
100	105	110	
aaa tta gat gca tct aat ctt gct ggt aat gat aaa aca aaa atc tat			384
Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr			
115	120	125	
caa gca gaa aat aaa gtt ctg gtt att gat att gct aaa cca aat ggg			432
Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly			
130	135	140	
aaa ggg att tca gat aac cgt ttt gaa aaa ttt aat att cca aat agc			480
Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser			
145	150	155	160
gcg gtg ttt aat aat aat ggg act gaa gcg cag gca aga tca aca tta			528
Ala Val Phe Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu			
165	170	175	
att ggt tac att ccg caa aat caa aat tta agg gga ggg aaa gaa gct			576
Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala			
180	185	190	
gat gtt ata tta aat caa gtg aca ggt cct caa gaa agt aaa att gtt			624
Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val			
195	200	205	
ggc gcg ctt gaa gta tta ggt aaa aaa gct gat atc gtc att gca aac			672
Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn			
210	215	220	
caa aat ggt att acc tta aat ggt gta aga aca ata aat tca gat cgt			720
Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg			
225	230	235	240
ttt gtt gcc act acg agt gag ctt ata gat ccg aat cag atg atg tta			768
Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu			
245	250	255	
aag gtt aca aaa gga aat gtg atc att gat att gat ggt ttt tcg aca			816
Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr			
260	265	270	
gat gga tta aag tat tta gat att att gct aaa aaa att gaa caa aag			864

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Gln	Ser	Ile	Thr	Ser	Gly	Asp	Asn	Ser	Glu	Ala	Lys	Thr	Asp	Val	Thr	
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Lys	Thr	Ser	Gly	Glu	Asn	Val	Ser	Asn	Asp	Val	Ile	Ala	Ile	Thr	Gly	
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Ser	Ser	Thr	Gly	Ala	Met	His	Gly	Lys	Asn	Ile	Lys	Leu	Ile	Val	Thr	
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Asp	Lys	Gly	Ala	Gly	Val	Lys	His	Asp	Gly	Ile	Ile	Leu	Ser	Glu	Asn	
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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	ggt	ttt	ggt	ggc	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	ggt	aaa	atc	aga	aaa	1296
Lys	Ser	Asp	Glu	Ile	Ser	Leu	Glu	Ala	Lys	Gln	Val	Lys	Ile	Arg	Lys	
			420					425					430			
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Asn	Ala	Glu	Ile	Arg	Ser	Thr	Thr	Gln	Ala	Lys	Ile	Val	Ala	Lys	Gly	
		435					440					445				
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Ala	Leu	Ser	Ile	Glu	Gln	Asn	Ala	Lys	Leu	Val	Ala	Lys	Lys	Ile	Asp	
	450					455					460					
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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	
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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	
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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	
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Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser	
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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 Thr 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	
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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 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	

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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 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	
ggt 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	
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Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu	
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Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile	
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Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser	
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His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser	
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Asp Thr Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met	
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ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca	3264
Pro Asp Lys Leu Gly Ile Ser Arg Asp Arg Gly Asn Lys Pro	
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Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe	
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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	
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Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg	
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Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys	
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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	
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1265 1270 1275 1280	
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Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp	
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ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa	4080
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Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe	
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Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr	
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Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val	
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Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn	
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1490 1495 1500	
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Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp	
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Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser	
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Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
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Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
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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
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Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
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Ile Leu Phe Leu Thr Val Ile Ser Val Pro Val Leu Ala Glu Gly Lys
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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
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Gln Ala Glu Asn Lys Val Leu Val Ile Asp Ile Ala Lys Pro Asn Gly
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Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
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 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
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 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
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 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
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 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
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 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
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 305 310 315 320
 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
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 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
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 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
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 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
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 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 ccg 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	
ggt 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	

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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

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<210> 105
<211> 669
<212> PRT
<213> Pasteurella multocida

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<400> 105
Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
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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

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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
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 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

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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

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<210> 107

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 107

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Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
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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

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<210> 108

<211> 2054

<212> DNA

<213> Pasteurella multocida

<220>

<223> pnp

<220>

<221> CDS

<222> (1)..(2052)

<400> 108

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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 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 tgc 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
 ggt 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	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 His Gly Arg Leu Ala Lys Arg Gly Val Ala 370 375 380		
Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val 385 390 395 400		
Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys 405 410 415		
Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala 420 425 430		
Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val 435 440 445		
Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp 450 455 460		
Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp 465 470 475 480		
Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn 485 490 495		
Gln Ala Lys Ser Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala 500 505 510		
Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr 515 520 525		
Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly 530 535 540		
Gly Ala Thr Ile Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp 545 550 555 560		
Ile Asp Asp Asp Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser 565 570 575		
Ala Lys Glu Val Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu 580 585 590		
Ala Gly Ala Val Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly 595 600 605		
Ala Phe Val Ser Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser 610 615 620		
Gln Ile Ala Glu Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val 625 630 635 640		
Gly Gln Glu Val Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg 645 650 655		
Ile Arg Leu Thr Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp 660 665 670		
Ser Val Val Ala Asp Val Ala Ala Glu Glu Asn Ala 675 680		

<210> 110
 <211> 1514
 <212> DNA
 <213> *Pasteurella multocida*

<220>
 <223> purF

<220>
 <221> CDS
 <222> (1)..(1512)

<400> 110
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 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	gta cga gat gta Val Arg Asp Val 220	672
caa ccc ggc gaa gcg att tat gtc acg ttt Gln Pro Gly Glu Ala Ile Tyr Val Thr Phe 225	gaa ggg gaa atg tat gct Glu Gly Glu Met Tyr Ala 235		720
cag caa tgc gca gac aaa cca aca tta aca cct tgt att ttt Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe 245	gaa tac Glu Tyr 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			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			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			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			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			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			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			1104
tcg att gta cgt ggt acc acg tct gaa caa att gtc gaa atg gcg aga Ser Ile Val Arg Gly Thr Thr Ser Glu Gln Ile Val Glu Met Ala Arg 370			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			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			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			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			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	


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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 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

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<210> 113
<211> 329
<212> PRT
<213> Pasteurella multocida

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<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

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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
 225 230 235 240
 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
 305 310 315 320
 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 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			240
Gly Thr Leu Ser Arg Ala Leu Asp Gly Ile Ser Asp Val Val Asn Cys			
65	70	75	80
aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac gaa gaa			288
Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp Glu Glu			
	85	90	95
aca aaa gca agt gaa atg aac acg gca att att gcc aca atc aca gaa			336
Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile Thr Glu			
	100	105	110
gaa ggg cag tac aca gcc ttg aag gcg tta ttg att gcg aaa aac aaa			384
Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys Asn Lys			
	115	120	125
ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac aca aaa			432
Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp Thr Lys			
	130	135	140
gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac gca ttt			480
Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn Ala Phe			
	145	150	155
gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg gtg caa			528
Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala Val Gln			
	165	170	175
tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg gcc gat			576
Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met Gly Asp			
	180	185	190
ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac tat gcc			624
Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala			
	195	200	205
gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa cag gcc			672
Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly			
	210	215	220
tgg cat acg tct att tca aat aaa ggc att aat gcc gtg agc ggt gtc			720
Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val			
	225	230	235
aca caa cca ctc tat ttt gac att aac gac agc tcg act gat gtg aac			768
Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn			
	245	250	255
tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat gcc ttt			816
Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe			
	260	265	270
cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc aag ttt			864
Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe			
	275	280	285
gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg			912
Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly			
	290	295	300
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 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 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
 625 630 635 640

gaa aac caa gga gga tat ctt att aat caa ggt aag agt cta ctc cat 1968
 Glu Asn Gln Gly 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	ggg	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	ggg	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 47
 Leu Ser Ile Leu Asn Leu Ser Ile Asp Glu Ile Ile Asp Val Leu
 1 5 10 15

ttg gca agc atg aca ta 64
 Leu Ala Ser Met Thr
 20

<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

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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

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<210> 128

<211> 242

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> apvC

<220>

<221> CDS

<222> (1)..(240)

<400> 128

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atg tgg cgg atg gga gat ttt atg tct aaa 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

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<210> 130
 <211> 527
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvD

<220>
 <221> CDS
 <222> (1)..(525)

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<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 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 tgc 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 gcg 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

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<210> 135
<211> 177
<212> PRT
<213> Actinobacillus pleuropneumoniae

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<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

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<220>
<223> dnaK

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<220>
<221> CDS
<222> (1)..(30)

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```

<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

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<220>
<223> exbB

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<220>
<221> CDS
<222> (1)..(450)

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<400> 140

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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 tcg 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

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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 cgc 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
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 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 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 80
 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

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      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             80
Ala Gly Lys Ala Leu Lys Asp Leu Val Lys
      85             90

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<210> 148
 <211> 551
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> lpdA

<220>
 <221> CDS
 <222> (1)..(549)

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<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

ggg 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

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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 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				
	210					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

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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	

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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 1110
Met

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<210> 153
<211> 369
<212> PRT
<213> Actinobacillus pleuropneumoniae

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<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

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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)

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<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

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	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

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      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

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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 Ile Pro Ala Asn Ala Lys Asn Lys Glu Asn Ala His Lys Leu Ile Asn 275 280 285			864
tac tta tta agc gca ccg gtt gcg gaa aaa tta acg tta gaa atc ggt Tyr Leu Leu Ser Ala Pro Val Ala Glu Lys Leu Thr Leu Glu Ile Gly 290 295 300			912
tat ccg act tca aac gta gaa gcg tta aaa aca tta cca aaa gag att Tyr Pro Thr Ser Asn Val Glu Ala Leu Lys Thr Leu Pro Lys Glu Ile 305 310 315 320			960
acc gaa gat ccg gca atc tat ccg aca gct gat gtg tta aaa gcg gca Thr Glu Asp Pro Ala Ile Tyr Pro Thr Ala Asp Val Leu Lys Ala Ala 325 330 335			1008
caa tgg caa gac gat gta ggt aat gca atc gaa ctt tac gaa aaa ta Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys 340 345 350			1055

<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

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<210> 158
<211> 525
<212> DNA
<213> Actinobacillus pleuropneumoniae

<220>
<223> rpmF

<220>
<221> CDS
<222> (1)..(522)
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<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	ggt	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	ggg	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	qgt	aac	ccg	ttt	240	

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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

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<210> 159

<211> 174

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 159

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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

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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	ggg	ttt	gaa	gaa	ggg	atc	gtt	ggg	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	ggg	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		
ggg	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	ggg	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	ggg	ggg	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	ggg	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	ggg	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

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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

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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 catctttaaa tgttggtcccc atcgtctaga 60
 ggcctaggac atcgcccttt cacggcggtta accgggggttc gaatccccgt ggggacgccca 120
 tttaaagatg acttttggtg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180
 tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
 agctgaacaa aagcagctaa gtgttttagtt 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

gagttcgagt ctcgccccaga 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 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

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<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

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                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

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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 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	720
Ala Gly Lys Pro Arg Trp Asp Trp Val Ala Pro Glu Pro Asn Thr Asp	
225 230 235 240	
tta atc aac aaa gta aaa gca tta gca gaa aca cgc ctt ggc gat gct	768
Leu Ile Asn Lys Val Lys Ala Leu Ala Glu Thr Arg Leu Gly Asp Ala	
245 250 255	
tat cgt atc gta gaa aaa caa gtt cgt tac gag caa atc gat gcg att	816
Tyr Arg Ile Val Glu Lys Gln Val Arg Tyr Glu Gln Ile Asp Ala Ile	
260 265 270	
aaa gca gag gtg att gca caa ctt acc gca gaa gat gaa act gtt tct	864
Lys Ala Glu Val Ile Ala Gln Thr Ala Glu Asp Glu Thr Val Ser	
275 280 285	
gaa ggg act atc atc gac atc atc acc gca tta gag agc caa atc gtg	912
Glu Gly Thr Ile Ile Asp Ile Ile Thr Ala Leu Glu Ser Gln Ile Val	
290 295 300	
cgt agc cgt att att gca ggc gaa cca cgc att gac ggc cgt acg gtg	960
Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr Val	
305 310 315 320	
gat acc gtg cgt gca ttg gat att tgc acc agt gtg tta cca cgc acc	1008
Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Ser Val Leu Pro Arg Thr	
325 330 335	
cac ggt tct gct ctt ttc acc cgt ggc gaa acc caa gca tta gca gta	1056
His Gly Ser Ala Leu Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala Val	
340 345 350	
gca aca ttg ggc aca gag cgt gat gcc caa atc att gac gaa ttg acc	1104
Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu Thr	
355 360 365	
ggc gaa aaa tct gac cgt ttc tta ttc cac tac aat ttc cct cca tac	1152
Gly Glu Lys Ser Asp Arg Phe Leu Phe His Tyr Asn Phe Pro Pro Tyr	
370 375 380	
tct gtg ggc gaa acc ggt cgt atc ggc tcg cca aaa cgc cgt gaa atc	1200
Ser Val Gly Glu Thr Gly Arg Ile Gly Ser Pro Lys Arg Arg Glu Ile	
385 390 395 400	
ggt cac ggt cgt tta gca aaa cgt ggc gta tta gcc gtg atg cca acc	1248
Gly His Gly Arg Leu Ala Lys Arg Gly Val Leu Ala Val Met Pro Thr	
405 410 415	
gct gaa gag ttc ccg tat gta gtg cgt gtg gtg tct gaa atc act gaa	1296
Ala Glu Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr Glu	
420 425 430	
tct aac ggt tct tct tca atg gca tct gtg tgt ggt gcg tct ctt gcg	1344
Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu Ala	
435 440 445	
ttg atg gac gca ggt gtg cca atc aaa gca gcg gtt gcc ggt atc gca	1392
Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile Ala	
450 455 460	
atg ggg ctc gtg aaa gaa gac gag aaa ttc gtg gta ctt tct gac atc	1440
Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp Ile	
465 470 475 480	

tta ggt gat gaa gac cac tta ggc gat atg gac ttt aaa gta gcg gga Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala Gly	1488
485 490 495	
acc cgt acc ggt gtg act gcg ctg caa atg gac atc aaa atc gaa ggg Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu Gly	1536
500 505 510	
atc acc cct gaa att atg cgt att gcc tta aac caa gct aaa ggt gca Ile Thr Pro Glu Ile Met Arg Ile Ala Leu Asn Gln Ala Lys Gly Ala	1584
515 520 525	
aga atg cac att tta ggt gta atg gaa caa gcc att ccg gca cct cgt Arg Met His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro Arg	1632
530 535 540	
gca gat att tct gac tat gcc cca cgc att cac aca atg aag atc gat Ala Asp Ile Ser Asp Tyr Ala Pro Arg Ile His Thr Met Lys Ile Asp	1680
545 550 555 560	
ccg aag aaa atc aaa gat gtg att ggt aaa ggc ggt gca aca att cgt Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile Arg	1728
565 570 575	
gct tta acc gaa gag acc aat act tct atc gac att gat gat gac ggt Ala Leu Thr Glu Glu Thr Asn Thr Ser Ile Asp Ile Asp Asp Asp Gly	1776
580 585 590	
acg gtg aaa att gcg gca act gac ggc aat gca gcg aaa gca gta atg Thr Val Lys Ile Ala Ala Thr Asp Gly Asn Ala Ala Lys Ala Val Met	1824
595 600 605	
gct cgt att gaa gag atc gtt gcc gaa gtg gaa gta aac caa atc tac Ala Arg Ile Glu Glu Ile Val Ala Glu Val Glu Val Asn Gln Ile Tyr	1872
610 615 620	
aac ggt aaa gta acc cgt gtg gtg gac ttc ggt gca ttc gtt tcc atc Asn Gly Lys Val Thr Arg Val Val Asp Phe Gly Ala Phe Val Ser Ile	1920
625 630 635 640	
tta ggt ggc aaa gaa ggt tta gtc cac att tca caa atc acc aac gaa Leu Gly Gly Lys Glu Gly Leu Val His Ile Ser Gln Ile Thr Asn Glu	1968
645 650 655	
cgt gtt gag cgt gta gcg gac tac tta acc gtt ggt caa gaa gta caa Arg Val Glu Arg Val Ala Asp Tyr Leu Thr Val Gly Gln Glu Val Gln	2016
660 665 670	
gtg aaa gtg gta gaa att gac cgt caa gga cgc att cgt ctg acg atg Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr Met	2064
675 680 685	
aaa gac atc aat aat acc aac gag gca aat gca gaa gaa act gta gct Lys Asp Ile Asn Asn Thr Asn Glu Ala Asn Ala Glu Glu Thr Val Ala	2112
690 695 700	
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705 710 715	

<210> 171

<211> 716

<212> PRT

<213> Pasteurella (Mannheimia) haemolytica

<400> 171

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Leu Glu Thr Gly Ala Ile Ala Arg Gln Ala Thr Ala Ala Val Met Ala
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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

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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

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<222> (1)..(1515)

<220>
<223> purF

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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 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	ggg	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	ggg	atg	gtt	gct	ttc	cgt	gac	cca	ttc	ggg	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	ggg	aaa	cgt	gaa	atc	gag	ggg	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	ggg	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	ggg	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	ggg	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	ggg	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
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<210> 173
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 <212> PRT
 <213> Pasteurella (Mannheimia) haemolytica

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 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
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<210> 174

<211> 386

<212> DNA

<213> Pasteurella (Mannheimia) haemolytica

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<222> (1)..(384)

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<223> yjgF

<400> 174

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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
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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
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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

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20

<210> 177

<211> 20

<212> DNA

<213> Artificial Sequence

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<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

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<222> 3
<223> N = A or T or G or C

<400> 178
ggnttyatyc ayaaaaayat g 21

<210> 179
<211> 23
<212> DNA
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<220>
<223> Description of Artificial Sequence: PRIMER

<220>
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<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
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<210> 181
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: PRIMER

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22

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