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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

FIELD OF THE INVENTION

5 The present invention relates generally to the identification of genes responsible for virulence of *Pasteurella multocida* and *Actinobacillus pleuropneumoniae* 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

10 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 haemolytica*, *Actinobacillus pleuropneumoniae* and
15 *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
20 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].

25 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
30 fever and depression, generally followed by quick death. Transmission is most likely through aerosol contact, but infection can also arise during periods of significant climatic change. In rabbits, infection gives rise to recurring purulent rhinitis, generally followed by conjunctivitis, otitis media, sinusitis, subcutaneous abscesses, and chronic

bronchopneumonia. In severe infections, rabbit mortality arises from acute fibrinous bronchopneumonia, septicemia, or endotoxemia. Disease states normally arise during periods of stress. In pigs, common *P. multocida* disease states include atrophic rhinitis and bacterial pneumonia. Similar pneumonia conditions are also detected in dogs, cats, goats, and sheep. *P. multocida* is commonly detected in oral flora of many animals and is therefore a common contaminant in bite and scratch wounds.

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

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

extracellular cytolytic toxins. Despite purification and, in some instances cloning, of these virulence factors, the exact role of these virulence factors in *A. pleuropneumoniae* infection is poorly understood.

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

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

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

In attempts to produce vaccine compositions, traditional killed whole cell bacteria have provided only serotype-specific protection [MacInnes and Smart, *supra*], however, it has been demonstrated that natural infection with a highly virulent serotype can stimulate strong protective immunity against multiple serotypes [Nielsen, *Nord Vet Med.* 31:407-13 (1979), Nielsen, *Nord Vet Med.* 36:221-234 (1984), Nielsen, *Can J Vet*

Res. 29:580-582 (1988), Nielsen, *ACTA Vet Scand.* 15:80-89 (1994)]. One defined live-attenuated vaccine strain producing an inactive form of the ApxII toxin has shown promise for cross protection in swine [Prideaux, *et al.*, *Infection & Immunity* 67:1962-1966 (1999)], while other undefined live-attenuated mutants have also shown promise
5 [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
10 rational construction of live attenuated bacterial strains for use in vaccines that will safely stimulate protective immunity against homologous and heterologous *P. multocida* and *A. pleuropneumoniae* serotypes. There further exists a need to identify attenuated bacterial strains and genes required for bacterial virulence, thereby facilitating development of methods to identify anti-bacterial agents.

SUMMARY OF THE INVENTION

In general, the present invention provides materials and methods for production and use of vaccine compositions comprising attenuated gram negative bacteria. In one aspect, vaccine compositions of the invention comprise attenuated
20 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*,
25 Bisgaard taxon 11, *H. aegyptius*, *H. aphrophilus*, *H. aphrophilus* (*H. parainfluenzae*), *H. ducreyi*, *H. haemoglobinophilus*, *H. haemolyticus*, *H. influenzae*, *H. paracuniculus*, *H. paragallinarum*, *H. parahaemolyticus*, *H. parainfluenzae*, (*H. paraphrophilus*), *H. paraphrohaemolyticus*, *H. paraphrophilus*, *H. parasuis*, *H. parasuis* type 5, *H. segnis*, *H. somnus*, *Haemophilus* minor group, *Haemophilus* taxon C, *P. aerogenes*, *P. anatis*,
30 *P. avium* (*H. avium*), *P. canis*, *P. dagmatis*, *P. gallinarum*, *P. haemolytica*, *P. trehalosi* (*P. haemolytica* biotype T), *P. langaa*, *P. multocida*, *P. pneumotropica*, *P. stomatis*, *P.*

volantium (*H. parainfluenzae*), *P. volantium*, *Pasteurella* species A, *Pasteurella* species B, and *Haemophilus paraphrohaemolyticus*. Preferably, vaccine compositions comprise attenuated *Pasteurella haemolytica*, *Actinobacillus pleuropneumoniae*, *Haemophilus somnus*, or *Pasteurella multocida* bacteria. In a most preferred 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, 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, and 164, or species homologs thereof, wherein the mutation inhibits or abolishes expression and/or biological activity of an encoded gene product (*i.e.*, the polypeptide encoded by a gene); said functional mutation resulting in attenuated virulence of the bacterial strain. As understood in the art, species homologs include genes found in two or more different species which possess substantial polynucleotide sequence homology and possess the same, or similar, biological functions and/or properties. Preferably polynucleotide sequences which represent species homologs will hybridize under moderately stringent conditions, as described herein by example, and possess the same or similar biological activities and or properties. In another aspect, polynucleotides representing species homologs will share greater than about 60% sequence homology, greater than about 70% sequence homology, greater than about 80% sequence homology, greater than about 90% sequence homology or greater than about 95% sequence homology. 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 part of a specific gene sequence is deleted. In one aspect, the mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene. In another

aspect, the mutation results in an insertion in the gene, wherein the insertion causes decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene. 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 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, 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, and 164, or species homologs thereof, polynucleotides encoding a virulence gene product encoded by a polynucleotide 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, and 164, or a species homolog thereof, and polynucleotide that hybridize, under moderately to highly stringent 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, and 164, 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, 163, and 164, 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, and 164, 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, and 164, 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, and 164, 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.

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"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

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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.

The identification of bacterial, and more particularly *P. multocida* and *A. pleuropneumoniae* 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, and 164. 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* and *A. pleuropneumoniae* 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* and *A. pleuropneumoniae* can provide information regarding similar genes, *i.e.*, species homologs, 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 *P. haemolytica*,

Aeromonas hydrophila, *Aeromonas salmonicida*, *Salmonella typhimurium*, *Salmonella enteritidis*, *Salmonella dublin*, *Salmonella gallinarum*, *Bordetella pertussis*, *Yersinia enterocolitica*, *Neisseria gonorrhoeae*, and *Bacillus anthracis*. In many of these species, attenuated bacterial strains bearing mutations in the *aroA* gene have proven to be effective in vaccine formulations. Using the virulence genes sequences identified in *P. multocida*, similar or homologous genes can be identified in other organisms, particularly within the *Pasteurella* family, as well as *A. pleuropneumoniae* 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* and *A. pleuropneumoniae* 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. haemolytica*, *A. pleuropneumoniae* and *H. somnus*) include genes *exbB*, *atpG*, and *pnp*.

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. In one aspect, therefore, the attenuated *P. multocida* strains, as well as other gram-negative mutant bacterial strains of the invention can bear one or more mutations which result in an insertion in the gene, with the insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene. 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 attenuated *P. multocida* strains, as well as other gram-negative mutant bacterial strains of the invention therefore include those bearing one or more mutation which results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of the virulence gene.

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* or *A. pleuropneumoniae* 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* or *A. pleuropneumoniae*) 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* or *A. pleuropneumoniae* 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* or *A. pleuropneumoniae*. An expression cassette, containing a promoter active in *P. multocida* or *A. pleuropneumoniae* and the appropriate marker gene, is cloned between the flanking sequences. The plasmid is introduced into wild-type *P. multocida* or *A. pleuropneumoniae*. 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*, 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* or *A. pleuropneumoniae* 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* or *A. pleuropneumoniae* 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, and 164, and species homologs thereof, and polypeptides having amino acids sequences encoded by the polynucleotides.

The present invention provides novel purified and isolated *P. multocida* and *A. pleuropneumoniae* 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, 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 *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. 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, 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, and 164, 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, 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, and 164, according to Watson-Crick base pairing rules for DNA. Also preferred are 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, 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, and 164, and species homologs thereof. The invention further embraces species, preferably bacterial, homologs of the *P. multocida* and *A. pleuropneumoniae* DNA.

The polynucleotide sequence information provided by the invention makes possible the identification and isolation of polynucleotides encoding related 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, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 5 152, 154, 156, 158, 160, 162, 163, and 164, 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.

The invention also embraces DNA sequences encoding bacterial gene products which hybridize under moderately to highly stringent conditions to the 10 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, 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, and 164, and species homologs thereof. DNA 15 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 20 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 25 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. 30 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.

5 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)],
10 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* and *A. pleuropneumoniae* virulence polypeptides encoded by a polynucleotide of the invention.
15 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, and 120, 122, 124, 126, 128, 130, 132,
20 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, 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,
25 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, and species homologs thereof; b) DNA molecules encoding *P. multocida* or *A. pleuropneumoniae* 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,
30 112, 114, 116, 118, and 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, and 164, 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, *i.e.*, species homologs and orthologs, 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	G A P
Non-polar	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.*,
5 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
10 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
15 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.
20 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>
5	Non-polar (hydrophobic)	
	A. Aliphatic:	A L I V P
	B. Aromatic:	F W
10	C. Sulfur-containing:	M
	D. Borderline:	G
	Uncharged-polar	
	A. Hydroxyl:	S T Y
	B. Amides:	N Q
15	C. Sulfhydryl:	C
	D. Borderline:	G
	Positively Charged (Basic):	K R H
	Negatively Charged (Acidic):	
	DE	

20

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.

30

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.

35

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
5 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
10 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
15 of the virulence polypeptides of the invention are also contemplated, provided that the antibodies are first and foremost specific for, as defined above, a virulence polypeptide of the invention from which the fragment was derived.

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

The invention further contemplates methods to modulate gene expression through use of ribozymes. For a review, see Gibson and Shillito, *Mol. Biotech.* 7:125-137 (1997). Ribozyme technology can be utilized to inhibit translation of mRNA in a sequence specific manner through (i) the hybridization of a complementary RNA to a target mRNA and (ii) cleavage of the hybridized mRNA through nuclease activity inherent to the complementary strand. Ribozymes can be identified by empirical methods but more preferably are specifically designed based on accessible sites on the target mRNA [Bramlage, *et al.*, *Trends in Biotech* 16:434-438 (1998)]. Delivery of ribozymes to target cells can be accomplished using either exogenous or endogenous delivery techniques well known and routinely practiced in the art. Exogenous delivery methods can include use of targeting liposomes or direct local injection. Endogenous methods include use of viral vectors and non-viral plasmids.

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 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). 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 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*].

The identification of *P. multocida* and *A. pleuropneumoniae* 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, 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, 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 (*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, 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, and 164, 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, 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, and 164, 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, 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, and 164, 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.

5 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.

10 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 the virulence gene product is
15 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 with a binding partner is assessed in the presence
20 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 partner. Other assays are also contemplated in those instances wherein
25 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.

30 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 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.

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 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 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.

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 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 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 theobroma.

5 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 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.

10 The vaccine compositions may be introduced into the subject to be immunized by any conventional method including, *e.g.*, by intravenous, intradermal, 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.

15 The invention also comprehends use of an attenuated bacterial strain of the invention for manufacture of a vaccine medicament to prevent or alleviate 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.

20 The present invention is illustrated by the following examples. Example 1 describes constructions of *P. multocida* mutants. Example 2 relates to 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. 25 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.

30

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 *KpnI* restriction site in the multiple cloning region and then to introduce a new *KpnI* site in the mini-Tn10 region. The plasmid was digested with *KpnI* 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 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 adaptor was ligated into the *SfiI* site to create plasmid pTEF-1. Oligonucleotides TEF1 and TEF3 (as well as all other oligonucleotides described herein) were synthesized by Genosys Biotechnologies (The Woodlands, TX).

TEF1 5'-AGGCCGGTACCGGCCGCCT SEQ ID NO: 86

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 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.

TEF14 5'-CATGGTACCCATTCTAAC SEQ ID NO: 88

10 TEF15 5'-CTAGGTACCTACAACCTC SEQ ID NO: 89

TEF26 SEQ ID NO: 90

5'-CTAGGTACCTACAACCTCAAGCTT-[NK]₃₅-

AAGCTTGGTTAGAATGGGTACCATG

15

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.

20

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),

30

200 μ M dNTPs, 140 pmol each of primers TEF5 (SEQ ID NO: 91) and TEF6 (SEQ ID NO: 92), 2 mM $MgCl_2$, 2.5 units Amplitaq (PE Applied Biosystems) and 1 ng of plasmid DNA.

5 TEF5 5'-TACCTACAACCTCAAGCT SEQ ID NO: 91

 TEF6 5'-TACCCATTCTAACCAAGC SEQ ID NO: 92

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

 TEF24 5'-TACCTACAACCTCAAGCTT SEQ ID NO: 93

20

 TEF25 5'-TACCCATTCTAACCAAGCTT SEQ ID NO: 94

25 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 *HindIII* in a total reaction volume of 90 μ l 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.

30 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 TM Dot-Blot Apparatus from Schleicher and Schuell (Keene, NH, USA). Each well was washed with 150 μ l of Neutralization Solution (0.5 M Tris /3 M NaCl, pH 7.5) and 150 μ l of 2X SSC. Membranes were UV-crosslinked in a Stratalinker (Stratagene, La Jolla, CA, USA) and prehybridized for one hour in 20 mls DIG EasyHyb Buffer at 42°C. The denatured probe was added and hybridization carried out overnight at 42°C. The membrane was washed two times in 2X SSC containing 0.1% SDS for five minutes each wash. Two high stringency washes were performed in 50 ml of pre-warmed 0.1X SSC buffer containing 0.1% SDS at 68°C for 15 minutes before proceeding with standard Genius Detection protocols (Genius Manual).

It is desirable to use a non-radioactive detection system for safety, lower cost, ease of use, and reduction of hazardous materials. In initial experiments using similar procedures previously described [Mei, *et al.*, *Mol Microbiol.* 26:399-407 (1997)], unacceptable background levels of hybridization were obtained in 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: λ pir (pir, *recA*, *thi*, *pro*, *hsd*, (r-m⁺), RP4-2, (Tc::Mu), (Km::Tn7), [TmpR], [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 μ l 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 μ l 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 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 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 μ g of genomic DNA from input and recovered pools was used as template. Semi-quantitative analysis indicates whether a significant reduction in a single clone has occurred. If a mutant is unable to survive within the host, then the recovered signal should be very low compared to the input signal yielding a high input/recovered ratio. Most mutants will grow as well *in vivo* as *in vitro* and therefore a ratio of their signals should be approximately equal to 1. Clones selected by quantitative analysis as being highly reduced in the recovered pool were 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

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 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 10², 10³, 10⁴ and 10⁵ 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 LD₅₀ 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 LD₅₀ of at least 10 fold higher than the wild type strain. The clones and their approximate LD₅₀ 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 LD₅₀ 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 LD₅₀ 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 x 10 ⁶
11	PM1D1	dsbB	10/10, 5/10	10/10, 5/5	8.4 x 10 ⁴
3	PM1BD7	atpG	5/5, 10/10	10/10	>3 x 10 ⁵
74	PM1BE11	yhcJ (H10145)	10/10	5/10	>2 x 10 ⁵
70	PM1BF6	yabK (H11020)	3/5, 8/10	9/9	>2 x 10 ⁵
19	PM2G8	thaC	4/5, 9/10	9/9	>4 x 10 ⁵

Nucleotide SEQ ID NO:	Representative Isolate	PossibleGene Function	Vaccination # survivors/total	Challenge # survivors/total	LD ₅₀
76	PM3C9	viaO (HI0146)	3/5		>6 x 10 ⁵
118	PM3G41	UnkO	4/5, 10/10	10/10	>3 x 10 ⁵
31	PM7B4	iroA (UnkB)	0/5		
17	PM4C6	fhaB (fhaB2)	2/5, 10/10, 9/10	10/10, 9/9	>3 x 10 ⁶
9	PM4G10-T9	dnaA	4/5		>5 x 10 ⁵
1	PM4D5-T5	atpB	5/5		>4 x 10 ⁵
53	PM4D5-T1	UnkC2	5/5		>4 x 10 ⁵
15	PM4F2	fhaB (fhaB1)	3/5, 6/10, 10/10	6/6, 10/10	>3 x 10 ⁵
41	PM5F7	mreB	4/5		1 x 10 ³
7	PM5E2	devB	0/5, 3/10	2/3	?
68	PM6H5-T1	xylA	5/5		>3 x 10 ⁵
78	PM6H8	yigF (HI0719)	5/5, 9/10	9/9	>3 x 10 ⁵
108	PM7D12	pnp	5/5, 9/10	9/9	
51	PM8C1R1-T2	UnkC1	5/5		-6 x 10 ⁵
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
15	PM19A1	exbB	5/5, 10/10	10/10	>1.2 x 10 ⁵
112	PM19D4	rcl	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.

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

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 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 Group, Inc., Madison] were used to search for homologous sequences in currently available databases.

15 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 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 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.

Example 5 Identification of Related Genes in Other Species

30 In separate experiments, STM was also performed using *Actinobacillus pleuropneumoniae* (App). One of the App strains contained an insertion in a gene that 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).

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

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).

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 μl 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 μ l from each well to a new flat bottomed 96 well plate (Corning Costar) containing 100 μ l 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 μ l from each of the wells of the microtiter

plate. The culture was diluted appropriately in BHI to approximately 2×10^6 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.

5 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 $450 \times g$ for 10 minutes to separate out large debris. Supernatants were then centrifuged at $2,800 \times g$ to pellet the bacteria. Pellets were resuspended in 5 mls BHI and plated in

10 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)].

15 Recovery from the animals routinely was in the 10^8 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

20 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.

25

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

30 The labeled PCR product was then digested with *Hind*III to separate the constant primer arms from the unique tag region. The region containing the labeled variable tag was excised and the entire gel slice was then dissolved and denatured in DIG

EasyHyb. Dot blots were prepared and detected using the standard CSPD detection protocol. Film exposures were made for visual evaluation, and luminescent counts per second (LCPS) were determined for each dot blot sample. The $LCPS_{input} / LCPS_{recovered}$ ratio for each mutant was used to determine mutants likely to be attenuated.

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

Example 8

Identification of *A. pleuropneumoniae* Virulence Genes

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

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

Table 2
A. pleuropneumoniae Open Reading Frames

	<u>Complete Open Reading Frame</u>		<u>NO Start Codon - Stop Codon</u>	
5	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>	
10	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
15	<u>Start Codon - NO Stop Codon</u>		<u>RNA or Noncoding Sequences</u>	
	lpdA	SEQ ID NO: 148	tRNA-leu	SEQ ID NO: 162
	potD	SEQ ID NO: 156	tRNA-glu	SEQ ID NO: 163
	yaeE	SEQ ID NO: 164		
	apvC	SEQ ID NO: 128		
20				

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.

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.
AP20A6	<i>atpH</i>	ATP synthase	.009
AP7F10	<i>atpG</i>	ATP synthase	.013
AP17C6	<i>lpdA</i>	dihydroipoamide dehydrogenase	.039
AP11E7	<i>exbB</i>	transport of iron compounds	.003,.003,.006
AP3H7	<i>potD</i>	Spermidine/putrescine transport	.308
AP8H6	<i>OmpP5</i>	Adhesin / OmpA homolog	.184
AP18H8	<i>OmpP5-2</i>	Adhesin / OmpA homolog	.552
AP13E9	<i>tig</i>	Peptidyl-prolyl isomerase	.050
AP13C2	<i>fkpA</i>	Peptidyl-prolyl isomerase	<.001
AP15C11	<i>pnp</i>	Polynucleotide phosphorylase	.032
AP18F12	<i>hupA</i>	Histone - like protein	.001
AP20F8	<i>dksA</i>	Dosage dependent suppressor of dnaK mutations	.075
AP5G4	<i>dnaK</i>	Heat shock protein - molecular chaperone	.376

AP17C9	<i>tRNA-leu</i>	Protein Synthesis (gene regulation?)	.059
AP5D6	<i>tRNA-glu</i>	Protein Synthesis	.055
AP18B2	<i>rpmF</i>	Protein Synthesis	.112
AP10E7	<i>vaeA</i>	Unknown	.001
AP19A5	HI0379	Unknown	.061
AP10C10	<i>apvA</i>	Unknown	.157
AP18F5	<i>apvB</i>	Unknown	.103
AP2A6	<i>apvC</i>	Unknown	.091
AP2C11	<i>apvD</i>	Unknown	.014

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

Example 10 Characterization of Attenuated *A. pleuropneumoniae* Virulence Genes

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

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

LpdA is a dihydrolipoamide dehydrogenase that is a component of two enzymatic complexes: pyruvate dehydrogenase and 2-oxoglutarate dehydrogenase.

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

5 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
10 *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.*
15 *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
20 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
25 (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)].
30 OMP P5 in nontypeable *Haemophilus influenzae* has been shown to encode a fimbrial subunit protein expressed as a filamentous structure [Sirakova, *et al.*, *Infect Immun.*

62:2002-20 (1994)] that contributes to virulence and binding of both mucin and epithelial cells [Miyamoto and Bakaletz, *Microb Pathog.* 21:343-56 (1996), Reddy, *et al.*, *Infect Immun.* 64:1477-9 (1996), Sirakova, *et al.*, *Infect Immun.* 62:2002-20 (1994)]. A significant finding was identification of two distinct ORF's that appear to encode OMP P5 homologues. This is also the case with two very similar proteins, MOMP and OmpA2 from *Haemophilus ducreyi*. It remains to be determined whether both are functionally involved in the production of fimbriae and whether the presence of two such ORFs represents a divergent duplication with redundant or complementing functions. Interestingly, the two OMP P5 mutants seem to have disparate CI values, suggesting a difference in essentiality or functionality for only one copy. OMP P5 has been shown to undergo molecular variation during chronic infections [Duim, *et al.*, *Infect Immun.* 65:1351-1356 (1997)], however, this appears to be restricted to a single gene undergoing point mutations resulting in amino acid changes rather than "type switching" due to differential expression of multiple genes.

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

include an unknown influence on cell division [Guthrie, and Wickner, *J Bacteriol.* 172:5555-62 (1990)] in *E. coli*, a role in the secretion and activation of the *Streptococcus pyogenes* cysteine proteinase [Lyon, *et al.*, *EMBO J.* 17:6263-75 (1998)] and survival under starvation conditions in *Bacillus subtilis* [Gothel, *et al.*, *Biochemistry* 37:13392-9 (1998)].

Bacterial pathogens employ many mechanisms to coordinately regulate gene expression in order to survive a wide variety of environmental conditions within the host. Differences in mRNA stability can modulate gene expression in prokaryotes [Belasco and Higgins, *Gene* 72:15-23 (1988)]. For example, *rnr* (*vacB*) is required for expression of plasmid borne virulence genes in *Shigella flexneri* [Tobe, *et al.*, *J Bacteriol.* 174:6359-67 (1992)] and encodes the RnaseR ribonuclease [Cheng, *et al.*, *J Biol. Chem.* 273:14077-14080 (1998)]. PNP is a polynucleotide phosphorylase that is involved in the degradation of mRNA. Null *pnp* / *rnr* mutants are lethal, suggesting a probable overlap of function. It therefore is possible that both *rnr* and *pnp* are 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 *vaeA* 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 Bm5R1 [Paimier, *J Biol Chem.* 273:18109-16 (1998)] is doubtful. The *apvD* gene is also most similar to a putative membrane protein (b0878) with unknown function from *E. coli* [Blattner, *et al.*, *Science* 277:1453-1474 (1997)]. Two other unknowns, *apvA* and *apvB* had no significant matches in the public databases.

Example 11

Safety and Efficacy of *A. pleuropneumoniae* Mutants

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

pig of wild type APP225. All surviving animals were euthanized and necropsied on day 42 of the study. Results are shown in Table 4.

Table 4
Efficacy of *A. pleuropneumoniae* Mutants

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

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 April 6, 2000CI of the 7 mutants tested shown in Example 9) had four deaths. Wildtype LD₅₀ using this model was generally 1×10^7 CFU, indicating that each of these mutants is at least 100 fold attenuated and that there is a reasonable correlation between CI and attenuation.

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

WHAT IS CLAIMED IS:

1. A gram-negative bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128, and 130, or species homologs thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.
2. The gram-negative bacteria of claim 1 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.
3. The gram-negative bacteria of claim 1 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.
4. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of all or part of said gene.
5. The gram-negative bacteria of claim 1 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.
6. The gram-negative bacteria of claim 1 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.
7. An attenuated *Pasteurellaceae* bacteria comprising a mutation in a gene represented by a nucleotide sequence set forth in any one of SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124,

126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164, or a species homolog thereof, said mutation resulting in decreased activity of a gene product encoded by the mutated gene.

8. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

9. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

10. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in deletion of all or part of said gene.

11. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

12. The *Pasteurellaceae* bacteria of claim 7 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

13. The *Pasteurellaceae* bacteria of claim 7 selected from the group consisting of *Pasteurella haemolytica*, *Pasteurella multocida*, *Actinobacillus pleuropneumoniae* and *Haemophilus somnus*.

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

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

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

17. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40%, at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

18. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

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

20. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

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

22. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in deletion of all or part of said gene.

23. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least

about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

24. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

25. The attenuated *Pasteurellaceae* bacteria of claim 13 that is a *A. pleuropneumoniae* bacteria.

26. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

27. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in expression of an inactive gene product encoded by the mutated gene.

28. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in deletion of all or part of said gene.

29. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

30. The *Pasteurellaceae* bacteria of claim 25 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

31. An immunogenic composition comprising the bacteria according to any one of claims 1 through 30.

32. A vaccine composition comprising the immunogenic composition according to claim 31 and a pharmaceutically acceptable carrier.

33. The vaccine composition according to claim 32 further comprising an adjuvant.

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

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

36. A purified and isolated *Pasteurellaceae* polynucleotide comprising a nucleotide sequence selected from the group consisting of nucleotide sequences set forth in SEQ ID NOs: 1, 3, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 29, 31, 33, 37, 39, 41, 51, 53, 55, 57, 58, 60, 68, 70, 72, 74, 76, 78, 80, 82, 84, 100, 102, 104, 106, 108, 110, 112,

114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163, and 164. .

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

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

- a) the polynucleotide according to claim 37,
- b) polynucleotides encoding a polypeptide encoded by the polynucleotide of (a), and
- c) polynucleotides that hybridize to the complement of the polynucleotides of (a) or (b) under moderate stringency conditions.

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

40. The polynucleotide of claim 39 which is a DNA.

41. A vector comprising the DNA of claim 40.

42. The vector of claim 41 that is an expression vector, wherein the DNA is operatively linked to an expression control DNA sequence.

43. A host cell stably transformed or transfected with the DNA of claim 40 in a manner allowing the expression of the encoded polypeptide in said host cell.

44. A method for producing a recombinant polypeptide comprising culturing the host cell of claim 43 in a nutrient medium and isolating the encoded polypeptide from said host cell or said nutrient medium.

45. A purified polypeptide produced by the method of claim 44.

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

47. An antibody that is specifically reactive with the polypeptide of claim 46.

48. The antibody of claim 47 that is a monoclonal antibody.

49. A method of using the monoclonal antibody of claim 39 for identifying a bacteria of claim 1, 7, 13, or 19 comprising the step of contacting an extract of bacteria with said monoclonal antibody and detecting the absence of binding of said monoclonal antibody.

50. A method of identifying an anti-bacterial agent comprising the steps of assaying potential agents for the ability to interfere with expression or activity of gene products represented by the amino acid sequences set forth in any one of SEQ ID NOS: 2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123,

125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, and 165 and identifying an agent that interferes with expression or activity of said gene products.

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

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

SEQUENCE LISTING

<110> Lowery E., David
Fuller E., Troy
Kennedy J., Michael

序列表

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aacaatagtt ttaacaata ttcttcatt ttttataagt aagtacttaa atataaagca 180

ttttcataaa tatcaataaa ggattagtt atg gca gca gag ctt aca aca gcg 233

Met Ala Ala Glu Leu Thr Thr Ala
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tgg cat gtt cat tta gat acc ctt cta ttt tca att att tca ggt gca 329

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Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile
      90                      95                      100

gat ttg atc cca gta gat ttc cta cct caa tta gcc cat tta ttt ggt 569
Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly
105                      110                      115                      120

att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta 617
Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu
      125                      130                      135

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Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys
      140                      145                      150

tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt 713
Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe
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aat cat cct ttg tta att ccg gtt aac tta gcg ctt gaa tca gtc aca 761
Asn His Pro Leu Leu Ile Pro Val Asn Leu Ala Leu Glu Ser Val Thr
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Leu Leu Ala Lys Pro Val Ser Leu Ala Phe Arg Leu Phe Gly Asn Met
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      205                      210                      215

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Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp
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atg ctt aca gtg gtt tat ttg agt atg ggt tat aac aaa gca gaa cac 1001
Met Leu Thr Val Val Tyr Leu Ser Met Gly Tyr Asn Lys Ala Glu His
      250                      255                      260

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taatttttta taaacaaaac cagaccttgg gtctaaattt caatcttatg gagaacatta 1061
tggaacactg taattactac aacaatcatc gcactctgnaa ttnttcttgc t 1112

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<210> 2

<211> 264

<212> PRT

<213> Pasteurella multocida

<400> 2

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Met Ala Ala Glu Leu Thr Thr Ala Gly Tyr Ile Gly His His Leu Ala
  1                      5                      10                      15

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

<210> 3

<211> 1972

<212> DNA

<213> Pasteurella multocida

<220>

<221> CDS

<222> (364) .. (1230)

<220>

<223> atpG

<400> 3

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acaacaagca ttagtggttat ttgcagtaga gtttgggttac ttagaagaag tggacttaga 180
tcgtattggg tcatattgaat cagcactttt agagtatgct aaccataact atgctgattt 240
tatgcgtgag ttaacccaat ctggcaatta caatgatgaa attaaagagt cattaaaagg 300
cattttggat agcttcaaag caaacagtgc gtggtaagtt aacactttta atggagagac 360

aaa atg gca ggt gct aaa gag ata aga acc aaa atc gcg agt gta aaa 408
Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys
1 5 10 15

agt aca caa aaa att act aaa gcg atg gaa atg gtt gct gcc tcg aaa 456
Ser Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Ala Ser Lys
20 25 30

atg cgt aaa acg caa gaa cgc atg tct tct tca cgc cct tat tca gaa 504
Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
35 40 45

aca ata cgt aac gtg att agc cac gtt tcc aaa gca acg att ggt tac 552
Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr
50 55 60

aag cat cca ttt tta gtg gat cgc gaa gta aaa aaa gtg ggc atg att 600
Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
65 70 75

gtt gtg tcc aca gat cgt ggt ctt tgt ggt ggc tta aac gtg aac ttg 648
Val Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Val Asn Leu
80 85 90 95

ttt aaa act gta tta aat gaa atg aaa gaa tgg aaa gaa aaa gat gtt 696
Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
100 105 110

tcc gtt caa ttg agt tta atc ggt tct aaa tct atc aac ttt ttc caa 744
Ser Val Gln Leu Ser Leu Ile Gly Ser Lys Ser Ile Asn Phe Phe Gln
115 120 125

tct ttg gga att aaa att tta acc caa gat tca ggt att ggt gat act 792
Ser Leu Gly Ile Lys Ile Leu Thr Gln Asp Ser Gly Ile Gly Asp Thr
130 135 140

ccc tct gtt gag cag tta att ggt tca gtc aat tct atg att gat gct 840
Pro Ser Val Glu Gln Leu Ile Gly Ser Val Asn Ser Met Ile Asp Ala
145 150 155

tat aaa aaa ggg gaa gta gat gtt gtg tat tta gtt tat aac aaa ttt 888
Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
160 165 170 175

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

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

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195	200	205	
tat att tac gaa cct gat gcg aaa gta tta tta gat aat tta ttg gtt			1032
Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val			
210	215	220	
cgt tat tta gaa tct cag gtt tat caa gca gca gtt gaa aac ctt gct			1080
Arg Tyr Leu Glu Ser Gln Val Tyr Gln Ala Ala Val Glu Asn Leu Ala			
225	230	235	
tct gag caa gcc gct cga atg gtc gcc atg aaa gca gca aca gat aac			1128
Ser Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn			
240	245	250	255
gca ggt aac tta att aat gag tta cag tta gtc tat aac aaa gct cgt			1176
Ala Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg			
260	265	270	
caa gca agt att aca aat gaa tta aat gaa att gtt gcc ggt gca gca			1224
Gln Ala Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala			
275	280	285	
gca att taacaaatag aggatcggtat atggcaactg gaaaaattgt acaaatcatc			1280
Ala Ile			
gggtgcgggtta ttgacgttga attcccacaa gatgcagtac caaaagtata tgatgcctta			1340
aatggtgaaa cagggttagt acttgaagtt caacaacaat taggtggtgg ttaggttcgc			1400
tgtatcgcaa tgggatcatc tgatggatta aaacgcggtt taagcgtaac aaatacgaat			1460
aaccaatatt ctgttcaggt gggaacgaaa acattgggtc gtatcatgaa cgtattgggt			1520
gaaccaatcg atgagcaagg tgaaatcggt gcagaagaga attggtctat tcaccgtgcg			1580
ccaccaagtt atgaagaaca atctaacagt actgaacttt tagaaacggg aattaaagtt			1640
atcgacttag tttgtccgtt tgcgaaaggg ggtaaagtag gtttattcgg tgggtgcgggt			1700
gtcggtaaaa ccgtcaatat gatggaatta atccgtaaca tcgcaattga gcactcaggt			1760
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atgaaagact ctaacgtatt agataaagtg tctcttgttt atggtcaaat gaacgagcca			1880
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<210> 4

<211> 289

<212> PRT

<213> Pasteurella multocida

<400> 4

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1				5					10					15	

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


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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                      80

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                      160

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                      240

Glu Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala
      245                      250                      255

Gly Asn Leu Ile Asn Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln
      260                      265                      270

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

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

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<220>
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<222> (1) .. (813)

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<220>

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<223> cap5E

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

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

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

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<210> 6

<211> 271

<212> PRT

<213> Pasteurella multocida

<400> 6

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 35 40 45

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

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

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

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

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

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

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

<210> 7
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 <213> Pasteurella multocida

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<220>
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 aaggaaagat c atg aat aca atc att ttt gac agt gca cag cat gcc gta 4070
 Met Asn Thr Ile Ile Phe Asp Ser Ala Gln His Ala Val
 1 5 10
 gag aaa att gca caa gaa ttg tta gcg tat agc tta gaa ggt cgc cct 4118
 Glu Lys Ile Ala Gln Glu Leu Leu Ala Tyr Ser Leu Glu Gly Arg Pro
 15 20 25
 gtg cat att tcc tta tcc gga ggc tca acg ccg aaa ttg tta ttt aaa 4166
 Val His Ile Ser Leu Ser Gly Gly Ser Thr Pro Lys Leu Leu Phe Lys
 30 35 40 45
 act tta gct caa gca ccg tat aac acc gag att caa tgg aaa aat ttg 4214
 Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu

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cat ttt tgg tgg ggc gat gat cgt atg gtg cca cca acc gat cca gaa				4262
His Phe Trp Trp Gly Asp Asp Arg Met Val Pro Pro Thr Asp Pro Glu				
	65	70	75	
agt aat tac ggc gag gtg caa aaa ttg tta ttc gat cat att cag atc				4310
Ser Asn Tyr Gly Glu Val Gln Lys Leu Leu Phe Asp His Ile Gln Ile				
	80	85	90	
cct gca gaa aat att cac cgc att cgt ggt gaa gcc ccc gtt gag agt				4358
Pro Ala Glu Asn Ile His Arg Ile Arg Gly Glu Ala Pro Val Glu Ser				
	95	100	105	
gaa ctt cac cgt ttt gaa caa gcg cta agt gcg gtc att cct ggg caa				4406
Glu Leu His Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln				
	110	115	120	125
gtt ttt gat tgg att att ttg ggc atg gga acg gac ggg cac acg gcc				4454
Val Phe Asp Trp Ile Ile Leu Gly Met Gly Thr Asp Gly His Thr Ala				
	130	135	140	
tca tta ttc ccg cat caa acc gat ttt gac gat cct cat ttc gcc gtg				4502
Ser Leu Phe Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val				
	145	150	155	
atc gcg aaa cac cct gaa aca ggg caa att cgt att tca aaa aca gcg				4550
Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala				
	160	165	170	
aaa ttg att gaa caa gca aag cgg gtg acc tat ttg gtg aca ggt agc				4598
Lys Leu Ile Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser				
	175	180	185	
agt aaa gcc gag atc tta aaa gaa att caa act act ccg gca gaa caa				4646
Ser Lys Ala Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln				
	190	195	200	205
ctg cct tat cct gct gcg aaa atc aaa gcg aag cat ggg gtg acg gaa				4694
Leu Pro Tyr Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu				
	210	215	220	
tggtat ttg gat aag gat gcg gca aaa tta ctg taatgcgtcg tgagattttt				4747
Trp Tyr Leu Asp Lys Asp Ala Ala Lys Leu Leu				
	225	230		
caacattttt gcaaagagac ttgaaacaaa atagaccata gcgttcgttt tcaacgagtg				4807
ctgaaaatga aggctctcgt tgaaaatggc gccatttagt gggtaagctt aaggttcgc				4867
cagacagcgc tatcaaaagg gtaaaagaat gtatcaactc tattttaatc caccaaaatc				4927
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<211> 232

<212> PRT

<213> Pasteurella multocida

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

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

Pro His Gln Thr Asp Phe Asp Asp Pro His Phe Ala Val Ile Ala Lys
 145 150 155 160

His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala Lys Leu Ile
 165 170 175

Glu Gln Ala Lys Arg Val Thr Tyr Leu Val Thr Gly Ser Ser Lys Ala
 180 185 190

Glu Ile Leu Lys Glu Ile Gln Thr Thr Pro Ala Glu Gln Leu Pro Tyr
 195 200 205

Pro Ala Ala Lys Ile Lys Ala Lys His Gly Val Thr Glu Trp Tyr Leu
 210 215 220

Asp Lys Asp Ala Ala Lys Leu Leu
 225 230

<210> 9
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 gaagctgcgc accctgatat cgaattatat accgcacacg ttgatagtca cttaaataa 180
 caaggttata ttattccagg tcttggtgat gccggtgata aaatttttgg cactaaataa 240
 tcccaacaca agcggcatct tatgccgctt tttccgttc aatttatagc gcttacaatc 300
 ttaacagctt gaacactata aaatgaaaag ttaattcaga cagagagttg aaacttaaca 360
 tgacaaatca aaatccocct gttcttctag aacaaaatca cgcaaaacaa gccttcggtg 420
 ggctacaaat gctttttgtt gccttcggtg ctttagtctt tgttcccttg attacgggtt 480
 taaatgccaa tactgcctta ttgaccgcag ggattgggac actcttattc caactttgta 540
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 atggcgtggc aacatggggc attgctacta ctatgggggg gctggtgttt actggactgg 660
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 ttaagggtta agtc ttg ctt aac cct tca ttt ttc gtt tat cct tat tct 1670
 Leu Leu Asn Pro Ser Phe Phe Val Tyr Pro Tyr Ser
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 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
 45 50 55 60
 tgt cta aca caa caa ttt ttt tat att tgg ggc gag caa agc agt ggt 1862
 Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
 65 70 75
 aaa agt cac ctc tta aaa ggc att act cat cat ttt ttc ctt tta cag 1910
 Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
 80 85 90
 cgc ccc gct atc tat gtg ccc tta gaa aaa tcc caa tat ttc tca ccg 1958
 Arg Pro Ala Ile Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro
 95 100 105
 gcg gta ctc gaa aac tta gaa caa caa caa ttg gtt tgt tta gat aat 2006
 Ala Val Leu Glu Asn Leu Glu Gln Gln Gln Leu Val Cys Leu Asp Asn
 110 115 120
 tta cag gca att ata ggc aat act gaa tgg gaa tta gcg att ttt gat 2054
 Leu Gln Ala Ile Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp
 125 130 135 140

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

 gca aat caa tcc cca act gca tta cct gta agt tta cct gac tta gct 2150
 Ala Asn Gln Ser Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala
 160 165 170

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

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

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

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

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

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 Lys Leu

<210> 10

<211> 254

<212> PRT

<213> Pasteurella multocida

<400> 10

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

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

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

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

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

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

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

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

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

Pro Thr Ala Leu Pro Val Ser Leu Pro Asp Leu Ala Ser Arg Leu Arg
 165 170 175

Trp Gly Glu Ser Tyr Gln Leu Val Pro Leu Asn Asp Gln Gln Lys Ile
 180 185 190

His Val Leu Gln Lys Asn Ala His Gln Arg Gly Ile Glu Leu Pro Asp
 195 200 205

Glu Val Ala Asn Phe Leu Leu Lys Arg Leu Glu Arg Asp Met Lys Thr
 210 215 220

Leu Phe Glu Ala Leu Ser Lys Leu Asp Lys Ala Ser Leu Gln Ala Gln
 225 230 235 240

Arg Lys Leu Thr Ile Pro Phe Val Lys Glu Ile Leu Lys Leu
 245 250

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

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<220>
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atggcattgc cttataccat cgtattatcc tgtattgggt tattgactgt ggaatatatt 780
 ttgcctggcg caaccaatgt gctcattcaa attgggtttat taaaaccaat gtaatgacaa 840
 gtaaaaggag gaaac atg cta agc ttt ttt aag aca ctc tca aca aaa cga 891
 Met Leu Ser Phe Phe Lys Thr Leu Ser Thr Lys Arg
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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
 15 20 25
 gct ctt tat ttt caa cat ggc atg ggg ctc gcc cct tgt gtc atg tgt 987
 Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys
 30 35 40
 att tac gag agg gta gct att ctt ggc att gct ttc tcc ggt tta ttg 1035
 Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu
 45 50 55 60
 ggg tta ctc tac ccg agt tcg atg ctt ttg cgc ctt gtg gcg tta tta 1083
 Gly Leu Leu Tyr Pro Ser Ser Met Leu Leu Arg Leu Val Ala Leu Leu
 65 70 75
 att ggt tta agc agt gca atc aaa ggc tta atg att agc atc acc cat 1131
 Ile Gly Leu Ser Ser Ala Ile Lys Gly Leu Met Ile Ser Ile Thr His
 80 85 90
 tta gat cta caa ctt tac cct gca cct tgg aaa caa tgt tca gcg gtg 1179
 Leu Asp Leu Gln Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val
 95 100 105
 gca gaa ttt ccc gag act tta ccc tta gat cag tgg ttt cct gca ctc 1227
 Ala Glu Phe Pro Glu Thr Leu Pro Leu Asp Gln Trp Phe Pro Ala Leu
 110 115 120
 ttc ctc cct tca ggc tca tgc agt gaa gta aca tgg caa ttt ctc ggc 1275
 Phe Leu Pro Ser Gly Ser Cys Ser Glu Val Thr Trp Gln Phe Leu Gly
 125 130 135 140
 ttt tct atg gtg caa tgg atc gtc gtc att ttt gca ctc tat acc tta 1323
 Phe Ser Met Val Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu
 145 150 155
 tta ctt gct ctc att ttc atc agc caa gtc aaa cgt cta aaa ccc aag 1371
 Leu Leu Ala Leu Ile Phe Ile Ser Gln Val Lys Arg Leu Lys Pro Lys
 160 165 170
 cag cgc aga ctc ttt cat taagtcataa aaaatgggtgc gataaagcac 1419
 Gln Arg Arg Leu Phe His
 175
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<210> 12

<211> 178

<212> PRT

<213> Pasteurella multocida

<400> 12

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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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 165 170 175
 Phe His

<210> 13

<211> 4426

<212> DNA

<213> Pasteurella multocida

<220>

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<222> (2756) .. (3211)

<220>

<223> exbB

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 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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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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Thr Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile
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Gly Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile
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Asp Ala Ala Ala Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
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Ala Val Gly Ile Leu Val Ala Ile Pro Ala Met Val Cys Tyr Asn Gly
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Met
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Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val	
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tat gaa agt gca gat gct gtt gta cca aca cca cgt agt aga aat gtg Tyr Glu Ser Ala Asp Ala Val Val Pro Thr Pro Arg Ser Arg Asn Val 1670 1675 1680	5576
gac agt acc gat ctt gtg gac aat cca ctg tat gct agt gcc act aca Asp Ser Thr Asp Leu Val Asp Asn Pro Leu Tyr Ala Ser Ala Thr Thr 1685 1690 1695	5624
aaa gca aac atc cat gat tat gaa gaa att cca gcc gtt tat agc aaa Lys Ala Asn Ile His Asp Tyr Glu Glu Ile Pro Ala Val Tyr Ser Lys 1700 1705 1710	5672
gtc ggt gat aac aat gct gat ctt gtt cgt cat aaa acg gca act agt Val Gly Asp Asn Asn Ala Asp Leu Val Arg His Lys Thr Ala Thr Ser 1715 1720 1725	5720

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Asp Glu His Leu Tyr Ala Glu Ile Asn Glu Pro Thr Tyr Ser Arg Val			
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gac tat gcc gat gtc gtg caa gca cat aca aga aag gca gat gat cca			5864
Asp Tyr Ala Asp Val Val Gln Ala His Thr Arg Lys Ala Asp Asp Pro			
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Leu Pro Ala Leu Pro Asn Gln Gly Lys Ala Arg Thr Val Asn Asp Gly			
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Ser Glu His Ile Tyr Thr Asp Ile Ser Asp Val Gly Thr Gln Thr Lys			
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gct att gat agt act tat gca aca gta ggc atg ccg aaa gcg aat gcc			6008
Ala Ile Asp Ser Thr Tyr Ala Thr Val Gly Met Pro Lys Ala Asn Ala			
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Val Asn Leu Ile Gly Gln Asn Gly Leu Gly Ser Ile Tyr His Ser Pro			
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gac agt gct tat aaa aca tgg caa ttg ctt gat caa ttt gcc aac aaa			6104
Asp Ser Ala Tyr Lys Thr Trp Gln Leu Leu Asp Gln Phe Ala Asn Lys			
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ggc gga gat gcg gtc ttc tta cgc cct gca aca gaa atg aaa tgt gca			6152
Gly Gly Asp Ala Val Phe Leu Arg Pro Ala Thr Glu Met Lys Cys Ala			
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Gly Ala Pro Leu Lys Tyr Thr Phe Ile Val Arg Asp Tyr Leu Leu Arg			
1875	1880		1885
cgc cat acc tta gat aaa tca aga tta ttt tat aac gca cat aat aaa			6248
Arg His Thr Leu Asp Lys Ser Arg Leu Phe Tyr Asn Ala His Asn Lys			
1890	1895		1900
acc tta ttt agc gtg cct atc gtt gat gca aaa gtc aaa atg ctg ttt			6296
Thr Leu Phe Ser Val Pro Ile Val Asp Ala Lys Val Lys Met Leu Phe			
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Ala Glu Lys Asn Ile Gln Val Asn Tyr Asp Arg Ser Leu Thr Ala Ile			
1925	1930		1935
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Asp Leu Ser Lys Arg Ile Ala Thr Phe Asn Ser Pro Glu Gly Val Val			
1940	1945		1950
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Glu Val Pro Tyr Asp Phe Ile Asn Val Val Pro Pro Met Arg Ala Pro			
1955	1960		1965

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1990 1995 2000

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

Val Ala Val His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn
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 Gly Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala
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 Tyr Gln Lys Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys
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Val Ser Asn Asp Val Ile Ala Ile Thr Gly Ser Ser Thr Gly Ala Met	
330 335 340	
cat ggt aaa aat att aag ttg att gtg aca gat aaa ggt gca ggc gta	2552
His Gly Lys Asn Ile Lys Leu Ile Val Thr Asp Lys Gly Ala Gly Val	
345 350 355	
aaa cat gat gga att att ttg tct gaa aat gat att cag att gaa atg	2600
Lys His Asp Gly Ile Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met	
360 365 370	
aat gaa ggt gac tta gaa ctt ggc aat acg att cag caa aca gtg gta	2648
Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr Ile Gln Gln Thr Val Val	
375 380 385 390	
aaa aaa gac cga aat att cga gcc aag aaa aaa att gaa gtg aaa aac	2696
Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys Lys Ile Glu Val Lys Asn	
395 400 405	
gct aat cgt gtt ttt gtt ggt agt caa acg aaa tca gat gaa att tcg	2744
Ala Asn Arg Val Phe Val Gly Ser Gln Thr Lys Ser Asp Glu Ile Ser	
410 415 420	
tta gag gcg aaa caa gtt aaa atc aga aaa aac gca gag att agg agt	2792
Leu Glu Ala Lys Gln Val Lys Ile Arg Lys Asn Ala Glu Ile Arg Ser	
425 430 435	
acg aca caa gcc aaa atc gta gca aag ggt gcc ctg tct att gag caa	2840
Thr Thr Gln Ala Lys Ile Val Ala Lys Gly Ala Leu Ser Ile Glu Gln	
440 445 450	
aat gcg aag ctc gtc gct aaa aag ata gat gtg gca aca gaa act cta	2888
Asn Ala Lys Leu Val Ala Lys Lys Ile Asp Val Ala Thr Glu Thr Leu	
455 460 465 470	
act aat gct ggg cgt att tat ggt cga gag gtt aag ctt gac act aat	2936
Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu Val Lys Leu Asp Thr Asn	
475 480 485	

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

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

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

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

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

 tta act ttt aaa gaa aaa acc agt ttt tta aca gag ggc aat aat ttt 3224
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 Ile Arg Ala Lys Asp Ala Leu
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<212> PRT

<213> Pasteurella multocida

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 35 40 45

 Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
 50 55 60

 Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
 65 70 75 80

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

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

 Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
 115 120 125

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

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
 145 150 155 160
 Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
 165 170 175
 Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
 180 185 190
 Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
 195 200 205
 Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
 210 215 220
 Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg
 225 230 235 240
 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
 245 250 255
 Lys Val Thr Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr
 260 265 270
 Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys
 275 280 285
 Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr
 290 295 300
 Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys
 305 310 315 320
 Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly
 325 330 335
 Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr
 340 345 350
 Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn
 355 360 365
 Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr
 370 375 380
 Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys
 385 390 395 400
 Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr
 405 410 415
 Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys
 420 425 430
 Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly
 435 440 445
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Val	Asp	Leu	Ala	Gly	Glu	Lys	Val	Ser	Leu	Asn	Phe	Gly	Asp	Ile	Ile	
1				5				10				15				
cat	gct	tac	caa	aac	cag	ccc	cta	tca	aca	aaa	ggt	ggt	ttt	caa	tta	96
His	Ala	Tyr	Gln	Asn	Gln	Pro	Leu	Ser	Thr	Lys	Val	Val	Phe	Gln	Leu	
20				25				30								
gtg	aaa	gat	ttg	acg	gaa	ggt	tta	tac	cgt	tct	ggc	tac	gtg	aca	agt	144
Val	Lys	Asp	Leu	Thr	Glu	Val	Leu	Tyr	Arg	Ser	Gly	Tyr	Val	Thr	Ser	
35				40				45								
gca	att	ggt	tta	aaa	aat	tca	aaa	atc	agc	aat	ggc	gat	ctt	gaa	ttt	192
Ala	Ile	Gly	Leu	Lys	Asn	Ser	Lys	Ile	Ser	Asn	Gly	Asp	Leu	Glu	Phe	
50				55				60								
att	gta	ctg	tgg	gga	aga	act	cgc	gat	ctg	ttt	gtg	aat	ggg	gag	aaa	240
Ile	Val	Leu	Trp	Gly	Arg	Thr	Arg	Asp	Leu	Phe	Val	Asn	Gly	Glu	Lys	
65				70				75				80				
cca	acc	cgt	ttt	aga	gat	aaa	aca	atg	tta	tca	gtc	cta	ccc	aat	tta	288
Pro	Thr	Arg	Phe	Arg	Asp	Lys	Thr	Met	Leu	Ser	Val	Leu	Pro	Asn	Leu	
85				90				95								
atc	gga	aat	cgc	tta	agt	att	cac	gac	att	gac	cag	ttg	atc	gaa	atc	336
Ile	Gly	Asn	Arg	Leu	Ser	Ile	His	Asp	Ile	Asp	Gln	Leu	Ile	Glu	Ile	
100				105				110								

tta aat act acg aat aaa aaa gcc aca gtg aat gtg gtt gca agt gaa	384
Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu	
115 120 125	
gaa aaa ggc agc tca aat cta aat att gaa aga caa tat gat gtt ttt	432
Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe	
130 135 140	
ccg caa gtg agt gtc gga ttc aat aat tca ggt gct ggc aat aat gcc	480
Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala	
145 150 155 160	
aat ggg cgt aat caa gct aca ttg aat att gct tgg agt gat cta tta	528
Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu	
165 170 175	
ggc acg aat gat cgt tgg agt ttc tcg agt agt tac cgt tta tat aaa	576
Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys	
180 185 190	
aat cat cat gct aac cag caa cgc aat tat act ttg tct tac agt cag	624
Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln	
195 200 205	
cct ata ggc ttt tct aca gta gaa att aaa gca tcg gaa tct acg tat	672
Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr	
210 215 220	
gaa aaa gaa ctt cgc ggt ata aat act cat tct tct cat ggg aaa acc	720
Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr	
225 230 235 240	
caa agc tta gct gtc aag ctg atg cat gtg tta ttg cgt aat aag gag	768
Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu	
245 250 255	
agt att tta tct aca tat acc gag ttc gag ttt aaa aaa cgg att agt	816
Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser	
260 265 270	
tat ttt tct gat att ttg att ggg aaa tat cac aat aat aaa gtg agc	864
Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser	
275 280 285	
gta ggg tta tct tac atg act aat ttt gct tac ggg aag ctt tac agc	912
Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser	
290 295 300	
gac att gct tac gcg aat ggg ttg aga tgg ttt ggg gcg aat tat tca	960
Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser	
305 310 315 320	
gca tat gat gca aat cgt gaa aaa acc tta aaa tta ttg tca gga agt	1008
Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser	
325 330 335	
att aat tgg cag cgt cca ata tcc ctg ttt gaa cgt gcg atg aat tat	1056
Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr	
340 345 350	
caa tta cgt att ggt gcc caa tat ggt ttt gat agt ttg tat tct gaa	1104
Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu	

355	360	365	
aat caa ttt tca att ggt gat gaa tat aca gta aga gga ttt aaa ggt			1152
Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly			
370	375	380	
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Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr			
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gtt cct ttt tat cca caa aaa gca tat tta tct cag gta tcc cct ttt			1248
Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe			
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att gga ttt gat atg ggt aaa gta cat att aaa tca aag cat aaa aca			1296
Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr			
420	425		430
acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta			1344
Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu			
435	440		445
ttt tca tta tca tta acc tat gca caa cca atg aat ggt gtg agt ggt			1392
Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly			
450	455		460
gtt acg caa cat cgt caa aaa ccg att tat tat ttc tca gga tca ctt			1440
Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu			
465	470		475
tct ttt taatctcttt taagttaaag gattaactta atatgaacaa aaatcggtac			1496
Ser Phe			
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gctattagca atgggttcac tgattcaaca tccacatcag aacaagttga agaggaacct			1616
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<212> PRT

<213> Pasteurella multocida

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Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
 35 40 45

Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe
 50 55 60

Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys
 65 70 75 80

Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
 85 90 95

Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
 100 105 110

Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu
 115 120 125

Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe
 130 135 140
 Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala
 145 150 155 160
 Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu
 165 170 175
 Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys
 180 185 190
 Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln
 195 200 205
 Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr
 210 215 220
 Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr
 225 230 235 240
 Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu
 245 250 255
 Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser
 260 265 270
 Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser
 275 280 285
 Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser
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 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
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 Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu
 355 360 365
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 385 390 395 400
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 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

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 <212> DNA
 <213> Pasteurella multocida

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tggttttggt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656
 Met Lys Gln Ile Pro Met
 1 5

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 10 15 20

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 Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu
 25 30 35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag 800
 His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln
 40 45 50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg 848
 Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu Ile Glu Gly Lys Leu Ala
 55 60 65 70

aat agt caa att att gat gtc aca aag atc cca aat aat ggc aaa gtg 896
 Asn Ser Gln Ile Ile Asp Val Thr Lys Ile Pro Asn Asn Gly Lys Val
 75 80 85

 att ttt ggt gcc aca att ttg tta ctg aat att gac acg gaa gaa gaa 944
 Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn Ile Asp Thr Glu Glu Glu
 90 95 100

 gtc tcg tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg 992
 Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly
 105 110 115

 cta att tca gtt aac gcc acg cga ttg aat tagagaaagc taaatggatt 1042
 Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
 120 125

 gcccaagatc ttggcgtcaa acaaacgtta attgacactt ccgtcattaa agcgattacg 1102
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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

 Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
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 115 120 125

<210> 23
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 <213> Pasteurella multocida

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 <222> (980) .. (2440)

<220>

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<400> 23

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agcaacgaaa tctgtataat gcgaccgcaa tattttttac ccttttattt tccatatcaa 960
cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
          Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
              1              5              10

gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
              15              20              25

gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca 1108
Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro
              30              35              40

atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc 1156
Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile
              45              50              55

tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct 1204
Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser
              60              65              70              75

att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc 1252
Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser
              80              85              90

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

```

95						100						105						
gaa tta agt gaa tta gtg aag aaa aat ggt ttt gcg agt ttc cct gtt																1348		
Glu Leu Ser Glu Leu Val Lys Lys Asn Gly Phe Ala Ser Phe Pro Val																		
110	115						120											
gtt gat gat gaa aaa aat ctt gtc ggt atc att act ggt cgt gat aca																1396		
Val Asp Asp Glu Lys Asn Leu Val Gly Ile Ile Thr Gly Arg Asp Thr																		
125	130						135											
cgc ttt gtc acg gat tta aat aaa aca gtg gcg gac ttt atg acc cct																1444		
Arg Phe Val Thr Asp Leu Asn Lys Thr Val Ala Asp Phe Met Thr Pro																		
140	145						150						155					
aaa gct cgt ctt gtc acg gtg aaa cgc aat gca agt cgc gat gaa att																1492		
Lys Ala Arg Leu Val Thr Val Lys Arg Asn Ala Ser Arg Asp Glu Ile																		
160	165						170											
ttt ggt cta atg cat aca cac cgt gta gaa aaa gtc ctt gtt gtc agc																1540		
Phe Gly Leu Met His Thr His Arg Val Glu Lys Val Leu Val Val Ser																		
175	180						185											
gac gat ttc aaa tta aaa ggc atg atc acc tta aaa gac tac caa aaa																1588		
Asp Asp Phe Lys Leu Lys Gly Met Ile Thr Leu Lys Asp Tyr Gln Lys																		
190	195						200											
tcc gag caa aaa cca caa gcc tgt aaa gat gaa ttt ggt cgt tta cgt																1636		
Ser Glu Gln Lys Pro Gln Ala Cys Lys Asp Glu Phe Gly Arg Leu Arg																		
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gtc ggt gct gca gta gga gca gga cct ggt aat gaa gaa cgt att gat																1684		
Val Gly Ala Ala Val Gly Ala Gly Pro Gly Asn Glu Glu Arg Ile Asp																		
220	225						230						235					
gca tta gtg aaa gca ggg gtc gat gtg tta ttg att gac tca tca cac																1732		
Ala Leu Val Lys Ala Gly Val Asp Val Leu Leu Ile Asp Ser Ser His																		
240	245						250											
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Gly His Ser Glu Gly Val Leu Gln Arg Val Arg Glu Thr Arg Ala Lys																		
255	260						265											
tac cca gat ttg cca att gtt gca ggt aat gtg gca acc gct gaa ggc																1828		
Tyr Pro Asp Leu Pro Ile Val Ala Gly Asn Val Ala Thr Ala Glu Gly																		
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Ala Ile Ala Leu Ala Asp Ala Gly Ala Ser Ala Val Lys Val Gly Ile																		
285	290						295											
ggg cct ggt tca att tgt aca aca cgt att gtc aca ggc gtg ggc gtt																1924		
Gly Pro Gly Ser Ile Cys Thr Thr Arg Ile Val Thr Gly Val Gly Val																		
300	305						310						315					
cca caa att aca gcg att gcc gat gcg gca gaa gca cta aaa gat cgg																1972		
Pro Gln Ile Thr Ala Ile Ala Asp Ala Ala Glu Ala Leu Lys Asp Arg																		
320	325						330											
ggg att cct gtg att gca gat ggc ggt atc cgt ttc tct ggt gat att																2020		
Gly Ile Pro Val Ile Ala Asp Gly Gly Ile Arg Phe Ser Gly Asp Ile																		
335	340						345											

tgc 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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Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly	
365 370 375	
cgt gcc ttt aaa tct tat cga ggt atg gga tgc tta ggt gcg atg agc	2164
Arg Ala Phe Lys Ser Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser	
380 385 390 395	
aaa ggc tca agc gac cgc tat ttc cag tcc gat aat gca gct gac aaa	2212
Lys Gly Ser Ser Asp Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys	
400 405 410	
tta gta cca gaa ggt att gaa gga cgt att cca tat aaa gga ttc tta	2260
Leu Val Pro Glu Gly Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu	
415 420 425	
aaa gaa att atc cat caa caa atg ggt gga ttg cgt tct tgt atg ggc	2308
Lys Glu Ile Ile His Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly	
430 435 440	
tta acg ggt tgt gca acc att gat gaa ctc cgt acc aaa gcg cag ttt	2356
Leu Thr Gly Cys Ala Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe	
445 450 455	
gtg cgc att agt ggt gca ggg atc caa gaa agc cat gtg cat gat gtg	2404
Val Arg Ile Ser Gly Ala Gly Ile Gln Glu Ser His Val His Asp Val	
460 465 470 475	
act atc aca aaa gaa gcc cct aat tat cgt atg ggt taaacattgc	2450
Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly	
480 485	
ttaggtgggg attatcccca cctaagttta ttttaaataa caacgttaat agagaagctt	2510
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 ccaaaaataa aagaaaagtt tcgtgatgca caaagcctga tttggacaga tgatctcaat 3530
 cataaaatcg gttttaccag tgatgaccgc gctatcgtct ttgataaagc ggacattgaa 3590
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 cttaaagcac aagtgggcga tgatgaagtg atttttaggt tatctggtgg cgttaactgc 4610
 cgtataggca gcttagaaaa agtgtccgcg ctcacgttaa tccccgtaag cgttga 4666

<210> 24

<211> 487

<212> PRT

<213> *Pasteurella multocida*

<400> 24

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

Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala

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

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

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

17. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least about 40% at least about 50%, at least about 60%, at least about 70%, at least about 80%, at least about 90%, at least about 95%, at least about 98%, or at least about 99% of said gene.

18. The *Pasteurellaceae* bacteria of claim 13 wherein said mutation results in an insertion in the gene, said insertion causing decreased expression of a gene product encoded by the mutated gene and/or expression of an inactive gene product encoded by the mutated gene.

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

20. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in decreased expression of a gene product encoded by the mutated gene.

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

22. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in deletion of all or part of said gene.

23. The *Pasteurellaceae* bacteria of claim 19 wherein said mutation results in deletion of at least about 10%, at least about 20%, at least about 30%, at least

65	70	75	
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg 80 85 90			469
att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val 95 100 105			517
gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met 110 115 120 125			565
gtg gat atg atg gat gcg gta gga cat ggt ttt tcg gcg tta gaa att Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile 130 135 140			613
gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala 145 150 155			661
cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu 160 165 170			709
aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp 175 180 185			757
gta gtg cat acc cac aaa tca aga aca gta cag ctt gct cgt atg ggt Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly 190 195 200 205			805
tta ttt aga acg ctc gca tgg ctt tat atg ttt aaa cac tac tcg gtg Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val 210 215 220			853
cat gat ttt gcc gaa ttt cta gag ctt tat ggt atg ccg att cgt att His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile 225 230 235			901
ggt aaa tac cca ttt ggg gca acg aat gac gaa aag cgc aca tta ttg Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu 240 245 250			949
cgt gca ctt gct caa atc gga cat aac gca gca ggg att atg cca gaa Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu 255 260 265			997
gga atg aat gtt gag ttg cat aat gtg aca aac act act ggc tcg gct Gly Met Asn Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala 270 275 280 285			1045
gga agc aac ccg ttt ttg caa atg gtg gac tgg tgt gaa aag tcc gcc Gly Ser Asn Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala 290 295 300			1093
gca cgt ttg att cta ggg caa aca tta aca agc ggt gca gat ggt aaa Ala Arg Leu Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys 305 310 315			1141

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 Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp
 320 325 330

ttg ctt gtg tct gat gct aaa cag att gca caa act att aca caa cag 1237
 Leu Leu Val Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln
 335 340 345

att att ctg cca tat ctt caa att aac att gat ccg aat att ttg cct 1285
 Ile Ile Leu Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro
 350 355 360 365

tct cgt gtg ccg tat ttc gag ttt gac acg aaa gaa tat gct gat tta 1333
 Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu
 370 375 380

agt gtc cta gcg gat gct att cct aag ctt gtg agc gta gga gtg cgc 1381
 Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg
 385 390 395

att cct gaa aat tgg gtg cgt gat aaa gcg ggc att cca gaa ccg cag 1429
 Ile Pro Glu Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln
 400 405 410

gaa aat gaa acg att tta agt gcg gtt caa cat gat ttt aaa aca gat 1477
 Glu Asn Glu Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp
 415 420 425

tta aac gat gtt gaa aat ccg aaa aaa cag acc gca ctt tct gta caa 1525
 Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln
 430 435 440 445

aat cac gtg aca ggt tgt cag tgt gat ggc tgt cgt ggt gtt gca tta 1573
 Asn His Val Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu
 450 455 460

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 Ser Ala Asn Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly
 465 470 475

ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca 1669
 Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro
 480 485 490

atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat 1717
 Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp
 495 500 505

gag gcg gca ~~gaa~~ aaa ctc gct gaa gca tac cca gaa att tca agt cac 1765
 Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His
 510 515 520 525

gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt 1813
 Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu
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 Gly Gly Thr Asn Val
 545

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<211> 546

<212> PRT

<213> Pasteurella multocida

<400> 26

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

Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe
 210 215 220
 Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile Gly Lys Tyr
 225 230 235 240
 Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu Arg Ala Leu
 245 250 255
 Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu Gly Met Asn
 260 265 270
 Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala Gly Ser Asn
 275 280 285
 Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala Ala Arg Leu
 290 295 300
 Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys Thr Ser Thr
 305 310 315 320
 Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp Leu Leu Val
 325 330 335
 Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu
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 Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val
 355 360 365
 Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu Ser Val Leu
 370 375 380
 Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg Ile Pro Glu
 385 390 395 400
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 405 410 415
 Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp Leu Asn Asp
 420 425 430
 Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln Asn His Val
 435 440 445
 Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu Ser Ala Asn
 450 455 460
 Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly Leu Ala Gln
 465 470 475 480
 Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro Met Val Lys
 485 490 495
 Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp Glu Ala Ala
 500 505 510
 Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His Glu His Glu
 515 520 525
 Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu Gly Gly Thr
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Asn Val
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<400> 27

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

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

cgt tat ggt att gaa tat cga tat aac ggc ttg tct tgg ttg gaa acg 193
Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
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gta aag ctt ttt ttg gca aag cag aaa atc gaa caa cgt tct gct ctc 241
Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
      65             70             75             80

caa gag ttt gat att aat aat agg aat aaa ttg gat tcg act atg tcg 289
Gln Glu Phe Asp Ile Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser
      85             90             95

ttt gta tat tta caa aga cag aat ata gct cgg gga gaa ttt tca acg 337
Phe Val Tyr Leu Gln Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr
      100             105             110

agt cct tta tat tgg ggg ccg agt cgc cat cgt tta tnt gcg aaa ttc 385
Ser Pro Leu Tyr Trp Gly Pro Ser Arg His Arg Leu Xaa Ala Lys Phe
      115             120             125

gaa ttt cgt gat ang ttt tta gaa aat atg aat aag cnt ttt acg ttt 433
Glu Phe Arg Asp Xaa Phe Leu Glu Asn Met Asn Lys Xaa Phe Thr Phe
      130             135             140

cgg ccg tgg caa atc aat ana ttc aga caa caa ggt cga aat aac tat 481
Arg Pro Trp Gln Ile Asn Xaa Phe Arg Gln Gln Gly Arg Asn Asn Tyr
      145             150             155             160

aca gaa gtg ttt ccc gtt aaa tcc cga gag ttt tct ttt tct ctt atg 529
Thr Glu Val Phe Pro Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met
      165             170             175

gac gac att aag att ggc gaa ttg cta cat ctc gga ttg ggc ggt cgg 577

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Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile		
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aac agg aca cag aga tta cct tat cca aaa aca tca tcc aaa ttt tcg	673	
Asn Arg Thr Gln Arg Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser		
210	215	220
tar caa ttg agt tta gag tat caa tta cat cca tca cat caa att gca	721	
Tyr Gln Leu Ser Leu Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala		
225	230	235
tac cgt tta agt acc ggt ttt agg gtt ccc cgt gtt gaa gat ctt tat	769	
Tyr Arg Leu Ser Thr Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr		
245	250	255
ttt gaa gac cga gga aaa agt tct tca caa ttt ctt cct aac ccc gat	817	
Phe Glu Asp Arg Gly Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp		
260	265	270
cta caa ccg gaa act gca ctg aat cat gaa ata agt tac cgt ttc caa	865	
Leu Gln Pro Glu Thr Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln		
275	280	285
aat caa tat gcc cat ttc agc gtc ggg ctt ttc cgt aca cgt tat cat	913	
Asn Gln Tyr Ala His Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His		
290	295	300
aac ttt att caa gaa cgt gag atg acc tgt gat aaa att cca tat gag	961	
Asn Phe Ile Gln Glu Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu		
305	310	315
tat aat agg act tat gga tat tgc acg cat aat act tat gta atg ttt	1009	
Tyr Asn Arg Thr Tyr Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe		
325	330	335
gtt aat gaa cct gaa gcc gtg att aaa ggg gtt gaa gta agc ggt gct	1057	
Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala		
340	345	350
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Leu Asn Gly Ser Ala Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu		
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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
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

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Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
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Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
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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
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 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
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 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
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 Val Asn Glu Pro Glu Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala
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 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
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 Cys Gly Ile Gln Ile Gly Leu Ala Ser Asn Pro Asn Pro Pro Asp Val
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 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	
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gaa caa aaa aat att gat ttg tta tta ttt ggt tct gta aga aat gca	1701
Glu Gln Lys Asn Ile Asp Leu Leu Leu Phe Gly Ser Val Arg Asn Ala	
195 200 205	
agc aat tat aca aga cct gat aaa agt aaa att ctt ttt tca aaa aac	1749
Ser Asn Tyr Thr Arg Pro Asp Lys Ser Lys Ile Leu Phe Ser Lys Asn	
210 215 220	
aat caa aaa agt gga tta ata aaa gta aat tgg caa att act cct gaa	1797
Asn Gln Lys Ser Gly Leu Ile Lys Val Asn Trp Gln Ile Thr Pro Glu	
225 230 235 240	
cat tta tta act tta tcc agt gtt tat ggc att cat aaa ggg tgg gaa	1845
His Leu Leu Thr Leu Ser Ser Val Tyr Gly Ile His Lys Gly Trp Glu	
245 250 255	
cct tgg gca gca aaa aga gat gtg atg tgc aga cca aca gaa aca gaa	1893
Pro Trp Ala Ala Lys Arg Asp Val Met Ser Arg Pro Thr Glu Thr Glu	
260 265 270	
ata aaa cac tat ggg att gat gtt gcg tgg aaa cgt aaa ctt gtt tat	1941
Ile Lys His Tyr Gly Ile Asp Val Ala Trp Lys Arg Lys Leu Val Tyr	
275 280 285	
cga gat caa aaa gat gaa agt tat tca ttg aaa tat cgc tat tta cct	1989
Arg Asp Gln Lys Asp Glu Ser Tyr Ser Leu Lys Tyr Arg Tyr Leu Pro	
290 295 300	
gaa aat aat aag tgg att aat ttg tct gtt cag ctg agt tat agt aaa	2037
Glu Asn Asn Lys Trp Ile Asn Leu Ser Val Gln Leu Ser Tyr Ser Lys	
305 310 315 320	
aca gag cag aat gat act cgc cat gag aaa gtc act tct tca ttc cta	2085
Thr Glu Gln Asn Asp Thr Arg His Glu Lys Val Thr Ser Ser Phe Leu	
325 330 335	
ggc 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	
ggc tgg tct tat tat tta ggc 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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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	
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Thr Thr Tyr Phe Tyr Asn Arg Gly Lys Asn Glu Ile Phe Lys Thr Arg	545	550	555	560
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<211> 564

<212> PRT

<213> Pasteurella multocida

<400> 30

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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
Gly Gly Phe Arg Pro Gly Gly Gln Thr Leu Asn Ile Asn Gly Met Gly	85	90	95
Asp Ala Glu Asp Val Arg Val Gln Leu Asp Gly Ala Thr Lys Ser Phe	100	105	110
Glu Lys Tyr Gln Gln Gly Ser Ile Phe Ile Glu Pro Glu Leu Leu Arg	115	120	125
Lys Val Thr Val Asp Lys Gly Asn Tyr Ser Pro Gln Tyr Gly Asn Gly	130	135	140
Gly Phe Ala Gly Thr Val Lys Phe Glu Thr Lys Asp Ala Thr Asp Phe	145	150	155
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
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
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
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 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
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 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
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 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
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 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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 ttgatcagca acccctaaca tgtgtggaat agatggacca taaatatcgg catctaaaat 8932
 tccaacacga gcacctgtgc tttgtaaggc aagagcaaga ttgacggaaa tagtagattt 8992
 tcttacacca cctttaccgg atgtcacggc aataatattt ttaccacctt ttacggctgg 9052
 gtggctatta gcgcgtttta atgtcgcgat ttgataattt aattgccatt tgatgtcttt 9112
 gcattctgct aatgtgagaa gttctgtgga gagagcgtc ttgagttgtt cgaatgcagt 9172
 attccaagca aacggcatgc tgatttcaat acgtaacgtc tcaccgcctt tttcaatttt 9232
 tttgatagca tttaggctga cgagatcttt ttgtaagcta ggatgttgaa attgttgaaa 9292
 tgtgttttgg atagcttggt tttgactgtc cgttaaactg tcagaaaata aaattcccat 9352
 tgattttatc ccgttatttt tgggtggctaa ttaaagccct agttaatcac tcaactatat 9412
 ttaaccacga agctgtagaa ctgttaagca gaaatgtgga aaagcgcggt taaagtagaa 9472
 aaaatactgc gaataaggta acataagcgc caattttttg atgaaaaata ggaatgataa 9532
 catggcaaat tcggcacgcg atattttggg cacttgcgcc ttaccttatg caaatgggtgc 9592
 aattcattta gggcatttat tagaacatat tcaagcagat atttgggtgc gttccaacgt 9652
 atgctgtggg ataaagtgc ttttatttgt gcagatgatg cccatggcac accaatcatg 9712
 ttaaattgca taaattagggt attacaccaa agcattaatt gctcctcgaa agcagaacat 9772
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<210> 32

<211> 967

<212> PRT

<213> Pasteurella multocida

<400> 32

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

100					105					110						
Ala	Glu	Thr	Leu	Ser	Ser	Gln	Gly	Phe	Lys	Glu	Leu	Phe	Glu	Gly	Tyr	
115					120					125						
Gly	Asn	Phe	Asn	Asn	Thr	Arg	Asn	Ser	Val	Glu	Ile	Glu	Thr	Leu	Lys	
130					135					140						
Val	Ala	Lys	Ile	Ala	Lys	Gly	Ala	Asp	Ser	Val	Lys	Val	Gly	Ser	Gly	
145					150					155					160	
Ser	Leu	Gly	Gly	Ala	Val	Leu	Phe	Glu	Thr	Lys	Asp	Ala	Arg	Asp	Phe	
165					170					175						
Leu	Thr	Glu	Lys	Asp	Trp	His	Ile	Gly	Tyr	Lys	Ala	Gly	Tyr	Ser	Thr	
180					185					190						
Ala	Asp	Asn	Gln	Gly	Leu	Asn	Ala	Val	Thr	Leu	Ala	Gly	Arg	Tyr	Gln	
195					200					205						
Met	Phe	Asp	Ala	Leu	Ile	Met	His	Ser	Lys	Arg	His	Gly	His	Glu	Leu	
210					215					220						
Glu	Asn	Tyr	Asp	Tyr	Lys	Asn	Gly	Arg	Asp	Ile	Gln	Gly	Lys	Glu	Arg	
225					230					235					240	
Glu	Lys	Ala	Asp	Pro	Tyr	Thr	Ile	Thr	Lys	Glu	Ser	Thr	Leu	Val	Lys	
245					250					255						
Phe	Ser	Phe	Ser	Pro	Thr	Glu	Asn	His	Arg	Phe	Thr	Val	Ala	Ser	Asp	
260					265					270						
Thr	Tyr	Leu	Gln	His	Ser	Arg	Gly	His	Asp	Leu	Ser	Tyr	Asn	Leu	Val	
275					280					285						
Ala	Thr	Thr	His	Ile	Gln	Leu	Asp	Glu	Lys	Glu	Ser	Arg	His	Ala	Asn	
290					295					300						
Asp	Leu	Thr	Lys	Arg	Lys	Asn	Val	Ser	Phe	Thr	Tyr	Glu	Asn	Tyr	Thr	
305					310					315					320	
Val	Thr	Pro	Phe	Trp	Asp	Thr	Leu	Lys	Leu	Ser	Tyr	Ser	Gln	Gln	Arg	
325					330					335						
Ile	Thr	Thr	Arg	Ala	Arg	Thr	Glu	Asp	Tyr	Cys	Asp	Gly	Asn	Glu	Leu	
340					345					350						
Cys	Asp	Ser	Tyr	Lys	Asn	Pro	Leu	Gly	Leu	Gln	Phe	Lys	Asp	Gly	Gln	
355					360					365						
Ile	Leu	Asp	Pro	Ala	Gly	Asn	Lys	Ile	Lys	Leu	Gln	Gly	Ser	Gly	Leu	
370					375					380						
Ser	Thr	Gln	Ile	Val	Asp	Glu	Asn	Gly	Lys	Pro	Phe	Pro	Thr	Thr	Thr	
385					390					395					400	
Gly	Thr	Asn	Asn	Ala	Ala	Phe	Ser	Asn	Asn	Leu	Arg	Leu	Arg	Pro	Thr	
405					410					415						
Gly	Phe	Trp	Leu	Asp	Cys	Ser	Val	Phe	Asp	Cys	Asn	Lys	Pro	Phe	Thr	
420					425					430						

Val Tyr Asn Ile Ser Asn Gly Thr Tyr Gln Ala Arg Glu Val Leu Leu
 435 440 445
 Ser Glu Glu Ile Thr Val Asp Gly Lys Leu Tyr Lys Thr Ala Lys Glu
 450 455 460
 Glu Gly Gly Leu Pro Asn Tyr Leu Ile Leu Pro Asn Ser Lys Gly Tyr
 465 470 475 480
 Leu Pro Tyr Asp Tyr Lys Glu Arg Asp Leu Asn Thr Asn Thr Lys Gln
 485 490 495
 Ile Asn Leu Asp Leu Thr Lys Thr Phe Leu Thr Phe Asn Ile Glu Asn
 500 505 510
 Asn Leu Ser Tyr Gly Gly Val Tyr Ser Arg Ile Glu Lys Glu Met Ile
 515 520 525
 Asn Lys Ala Gly Tyr Glu Gly Arg Asn Pro Thr Trp Trp Ala Asp Arg
 530 535 540
 Ile Leu Gly Gln Ser Ser Tyr Cys Gly Tyr Asn Ala Leu Lys Cys Pro
 545 550 555 560
 Lys His Glu Pro Leu Thr Ser Phe Leu Ile Pro Val Glu Ala Thr Thr
 565 570 575
 Gln Ser Leu Tyr Phe Ala Asn Ile Leu Lys Val His Asn Met Ile Ser
 580 585 590
 Ile Asp Leu Gly Tyr Arg Tyr Asp His Ile Lys Tyr Asn Pro Glu Tyr
 595 600 605
 Thr Pro Gly Val Thr Pro Lys Ile Pro Asp Asp Met Val Lys Gly Leu
 610 615 620
 Phe Ile Pro Met Pro Lys Glu Pro Gln Leu Lys Asp Phe Asp Tyr Asn
 625 630 635 640
 Tyr Ala Lys Phe Gly Glu Ala Tyr Lys Lys Trp Lys Glu Tyr Leu Pro
 645 650 655
 Lys Asn Ala Glu Glu Asn Ile Ala Tyr Ile Ala Gln Asp Lys Thr Phe
 660 665 670
 Lys Lys His Ser Tyr Ser Leu Gly Ala Thr Phe Asp Pro Leu Asn Phe
 675 680 685
 Leu Arg Val Gln Val Lys Tyr Ser Lys Gly Phe Arg Ala Pro Thr Ser
 690 695 700
 Asp Glu Leu Tyr Phe Thr Phe Lys His Pro Asp Phe Thr Ile Leu Pro
 705 710 715 720
 Asn Pro Val Leu Lys Pro Glu Glu Ala Lys Asn Gln Glu Ile Ala Leu
 725 730 735
 Thr Val His Asp Asn Trp Gly Phe Val Ser Thr Ser Val Phe Gln Thr
 740 745 750
 Lys Tyr Arg His Phe Ile Asp Leu Ala Tyr Leu Gly Ser Arg Asn Leu
 755 760 765

Ser Asn Ser Val Gly Gly Gln Ala Gln Ala Arg Asp Phe Gln Val Tyr
 770 775 780
 Gln Asn Val Asn Val Asp Asn Ala Lys Val Lys Gly Leu Glu Ile Asn
 785 790 795 800
 Ala Arg Leu Asn Leu Gly Tyr Phe Trp His Val Leu Asp Gly Phe Asn
 805 810 815
 Thr Ser Tyr Lys Phe Thr Tyr Gln Arg Gly Arg Leu Asp Gly Asp Arg
 820 825 830
 Pro Met Asn Ala Ile Gln Pro Lys Ala Ser Val Phe Gly Leu Gly Tyr
 835 840 845
 Asp His Lys Glu Asn Lys Phe Gly Ala Asp Leu Tyr Ile Thr Arg Val
 850 855 860
 Ser Glu Lys Lys Ala Lys Asp Thr Tyr Asn Met Phe Tyr Lys Glu Gln
 865 870 875 880
 Gly Tyr Lys Asp Ser Ala Val Arg Trp Arg Ser Asp Asp Tyr Thr Leu
 885 890 895
 Val Asp Ala Val Gly Tyr Ile Lys Pro Ile Lys Asn Leu Thr Leu Gln
 900 905 910
 Phe Gly Val Tyr Asn Leu Thr Asp Arg Lys Tyr Leu Thr Trp Glu Ser
 915 920 925
 Ala Arg Ser Ile Lys Pro Phe Gly Thr Ser Asn Leu Ile Asn Gln Lys
 930 935 940
 Thr Gly Ala Gly Ile Asn Arg Phe Tyr Ser Pro Gly Arg Asn Phe Lys
 945 950 955 960
 Leu Ser Ala Glu Ile Thr Phe
 965

<210> 33
 <211> 2990
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (1106)..(1564)

<220>
 <223> kdtB

<400> 33
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 tggtgcccga accgcgccag ggactttgtt ataaacgggt tgataacgtt ctttatccgc 120
 ttcttctgtca gggcgatcaa tataaggggg caatggcata tgcccaattt gctgtaacac 180
 gtctaaaagt gcggtctgtt tttgcgcgat ttctaattca aataaggtat catggcgcgc 240
 aaccatgatc attttgacac catgatgttc acctaaccta tcttcgccta accacagttc 300

82

tat acg ccc tgt gga gag tta agg gaa gag gcg gct ttt tca aaa aat 1564
 Tyr Thr Pro Cys Gly Glu Leu Arg Glu Glu Ala Ala Phe Ser Lys Asn
 140 145 150

taagagtgag gtgaagaaat ggcattacca acagcaacaa taatgaggaa tttatcttta 1624
 tctaaaaatc aattcactct gaaagggatg gaatgcgtag attccctatt tcaagcatgc 1684
 agtaatatgg atcatgggta ctgaggtgga agatggcaga agaaaaataa ggaaagagat 1744
 attttttatg gttcataattg tttatccttt caatctatatt atttattacc atacaagaaa 1804
 gacgaggtta ttgttttgac aaatgggaat atatccataa cttttatacc gagcaagagt 1864
 tgatcgatag aggggttgaa tatgtggtat ccaccatgcc gtcaggtgtt tttgaaccag 1924
 atggcacaac aaccgaaata aaacggtatg ctagtgttga ggagttaaa cagatgaacc 1984
 ctgattgttg taaattaaca agatttatta atgaaggaat agatggctat ccagatgatg 2044
 atggatatgg ttatataaga attgaatatt taagacatta tgttggaat tttaaacctg 2104
 atcatagagt gctttatctc gaataacgc cttgtggaga attaaggga gaggtttctt 2164
 tttaaaaaat aaataatagt gaggtgaaga aatggcatta ccaacagcaa cagaaatcac 2224
 aatgcataat ttatataaaa ataaattaac tcctaaagcg gaggaagag tagattcaat 2284
 acaaattctt gaaaaaggag atgaacattt cgaagtaaatt ttaattgat caaagtactc 2344
 tattgattga aggaaaaaca gtggaattaa tggcaggtat ggcagtttct gcggaaatta 2404
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 attaaggaga ataatatgtc gtataataaaa tatactgttg ctttgattac gttctcaaca 2524
 gggatctgta ttccggcaat atgctacgct ctaaattcgc tgggatacag atcctgtttg 2584
 agactatgta gaaaagacta aactttgtgt ggttaactgg gcttcggtaa aattctggaa 2644
 acaaatgggc ttaaccgcg tgatcttacc ccgtgagctt tcgcttgatg aaattgccga 2704
 aattcgtcag caagtgccag aaatggaaat tgaagtgttc gtgcatgggg cattatgcat 2764
 ggcgtrattct ggacgttggt tattatcagg ctatattaat aaacgtgac caaatcaagg 2824
 cacctgtacc aatgcgtgcc gttgggaata cagtgtaac gaagccaaag aagatgagat 2884
 cggcaacatt gtgaatgtgg gtgaagaaat tccagtgaat aatgtagcac cgacacttgg 2944
 cgaaggcgac accaccagta aagtattttt attagcagaa agtcga 2990

<210> 34

<211> 153

<212> PRT

<213> Pasteurella multocida

<400> 34

Met Thr Glu Glu Asn Lys Gly Lys Arg Tyr Phe Leu Trp Phe Ile Leu
 1 5 10 15

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

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

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

<220>
 <223> lgtC

<400> 35
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 tgggtattat tcataggcta ggtgaaagat atatttttcc atgatattaa aacgattcag 120
 gcagaactgg ctagcttatt acttttagat aattgtatta ttaaaagaag ctgtatgatt 180
 gttattctat cattagtggg taataaatat tctttatttt ttgagagata aaaacaattc 240
 atatttcaat agaaaacaga aaataaagat tatcaaaaga attatccggtc cttataaata 300
 tgagtctgta ttgtgagatg atat atg aat att tta ttt gtt tct gat gat 351
 Met Asn Ile Leu Phe Val Ser Asp Asp
 1 5
 gtt tat gct aaa cat ctg gtg gtt gcg att aaa agc att ata aat cat 399
 Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
 10 15 20 25
 aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat 447
 Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp
 30 35 40

gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa	495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu	
45 50 55	
gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt	543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val	
60 65 70	
caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca	591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala	
75 80 85	
gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat	639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp	
90 95 100 105	
gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat	687
Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn	
110 115 120	
aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag	735
Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys	
125 130 135	
tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt	783
Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe	
140 145 150	
aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat	831
Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp	
155 160 165	
gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg	879
Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Gln Met	
170 175 180 185	
att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc	927
Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val	
190 195 200	
tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga	975
Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg	
205 210 215	
ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa	1023
Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu	
220 225 230	
aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa	1071
Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys	
235 240 245	
gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa	1119
Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys	
250 255 260 265	
ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct	1167
Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser	
270 275 280	
ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc	1215
Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe	

285

290

295

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

tgattttcttc aaagcgaaaa ggaggaaata gcttggttcta atttattaca ataatgggtg 1330
 tattcatctt gatttttgaag gaaagagagt gttttttgta taaaagcatt ttcgtcacct 1390
 aaatttacta atcctccaaa ttctctctct cgnagaattt ctttcggacc ggtagggcag 1450
 tccatggata ttacaggtgt accgcaagcc atgcttttcta ggataactgt cggtaacccc 1510
 tctttcaaag aggtgtgtaa aaatagctta gcatttttta ttaatggata cggattatct 1570
 ttattttcta aaagaaaaca atcttcttgt agattgagtg attctatttg tttctcta 1630
 ttttctcgac actcaccatc ccaaacaata tatancnttt cttggatacc tcc 1683

<210> 36

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 36

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 Xaa Gln Tyr His Lys Gly
 210 215 220

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

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

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

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

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

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

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

<220>
 <223> mglB

<400> 37
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 Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
 1 5 10 15

gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97
 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
 20 25 30

nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
 35 40 45

tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193
 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
 50 55 60

tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
 65 70 75 80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
 85 90 95

atc ttc ngc gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
 100 105 110

ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385
 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
 115 120 125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433
 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
 130 135 140

gaa ggc aca aaa tgg cag tta aaa cga tcg 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 ggaggtatac cctccccctt tttatgtgag 589
 gttggatatg acaactcaaa ttccaaatca agacagtga atactgctca caatgaccaa 649
 cgtctgtaaa tcctttcccg gtgttaaagc gttagacaat gcaaacctaa ctgtgcgctc 709
 gcattctgtc catgccttaa tgggcgaaaa tggggcgggc aaatcgacct tattaatatg 769
 cttatttggt atttacagta aagatgaagg tgacatcctt ttcttaggca agccagtcaa 829
 ctttaaaacg tcgaaagaag ccttagagaa cgggattttc atgggtgcacc aagaacttaa 889
 cttgggttaa caatgtactg taatggataa tcctttggnt aggacgttat ccattaaaag 949
 caggcctttgt cgatcacggc aaaatgtatc gtgataccaa agcagatttt tgaagaanta 1009
 gatatcgata tcgatccaaa agaaaaagtg gccaaattgt cagtgtcaca aatgcaaagt 1069
 atcgagatcg caaaggcctt ttcatacaat gccaaaatcg taatcatgga cgaaccgact 1129
 tcttcgcttt cagaaaaaga agttgaacac ctatttaaaa ttatcgcgaa gctaaaacaa 1189
 cgtggctgtg gcattattta tatttcgcac aaaatggacg aaatcttcaa aatttgtgac 1249
 gaaattacga ttttacgca tggtaaatgg atcaatacgg tcgctgttaa aggcaccaca 1309
 atggatcaga ttgtatccat gatggttggg cgtgaactca cgcaacgttt ccacacaaaa 1369
 accaataccc caaaagaaac catcttaacg gtggaaaatc tgaccgcact taatcagcca 1429
 tctattcaag atgttagttt tgaattacgc aaaggcgaag tgctcgcat tgcgggactg 1489
 gttggggcaa aacggtaccg atattgtgga aacgatcttc ggggtgcgtg aacgtaaatc 1549
 tgggtgtgatt aaactacacg ataaggaaat gaaaaaccgg aatgcgttcg aagccattaa 1609
 caatggtttt gccttgggtc cggagaacg tcgctctaca gggatttatg cgaatctcag 1669
 tattgagttt aactcattaa tttctaacat gaagaaatcc tatatcagca agtttagttt 1729
 attgagtaac ncaaaaatga aaagcgacac gcaatggggg cattgattcc atgaatgtga 1789
 aaacgccatc acaaaaccna tattggntca ntatctgggg tggtaaccaa caaaaagtgg 1849
 tcattggctg ttggttatta acccaccctg aaatcttgat gttagacgaa ccaacacgtg 1909

gtatcgacat tgggtgcgaaa tatgaaattt atcagctgat tatggagtta gccaaaaaag 1969
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 <212> PRT
 <213> Pasteurella multocida

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 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
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 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
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<210> 39
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 <212> DNA
 <213> Pasteurella multocida

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<400> 39
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90

ctgaaaatta tgatgttatt gtgatcggtg gtggacacgc aggtactgaa gctgcacttg 1326
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 aaatgtcttg taatcctgcg attggtggga ttggtaaagg ccatttagtc cgagaaattg 1446
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<211> 147

<212> PRT

<213> Pasteurella multocida

<400> 40

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

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

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

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

<220>
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<220>
 <223> mreB

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 tagcgggttaa ttgggcagat ttatcttttg gtactatcac agcacacacg cccgctgcat 180
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tca aat gat ctg tcc atc gat ctt ggc aca gcg aat acc tta att tat 3280
Ser Asn Asp Leu Ser Ile Asp Leu Gly Thr Ala Asn Thr Leu Ile Tyr
                        15             20             25

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

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

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

cgt cct atg aaa gat ggg gtg atc gca gat ttc ttt gtg aca gaa aaa 3472
Arg Pro Met Lys Asp Gly Val Ile Ala Asp Phe Phe Val Thr Glu Lys
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atg ttg caa tat ttt att aaa caa gtg cac agc agc aat ttt atg cgt 3520
Met Leu Gln Tyr Phe Ile Lys Gln Val His Ser Ser Asn Phe Met Arg
                        95             100             105

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

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

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

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

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

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175										180					185					
tca gtc cgc att ggt ggt gat cgt ttt gat gag gcg att att tct tat	3808																			
Ser Val Arg Ile Gly Gly Asp Arg Phe Asp Glu Ala Ile Ile Ser Tyr																				
190	195	200																		
gta cgc aag acg ttc ggt tca att att ggg gaa ccg aca gca gag cgt	3856																			
Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg																				
205	210	215																		
atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc	3904																			
Ile Lys Gln Glu Ile Gly Ser Ala Phe Ile Gln Glu Gly Asp Glu Val																				
220	225	230																		
cgt gaa att gaa gtg cat ggt cat aac tta gca gaa ggt gcg ccg cgt	3952																			
Arg Glu Ile Glu Val His Gly His Asn Leu Ala Glu Gly Ala Pro Arg																				
235	240	245	250																	
tct ttc aaa ctc acc tca cgt gat gtg tta gaa gct att caa gcc ccg	4000																			
Ser Phe Lys Leu Thr Ser Arg Asp Val Leu Glu Ala Ile Gln Ala Pro																				
255	260	265																		
tta aat ggc att gtt gcg gca gtg cgc acg gcc ttg gaa gag tgt caa	4048																			
Leu Asn Gly Ile Val Ala Ala Val Arg Thr Ala Leu Glu Glu Cys Gln																				
270	275	280																		
cca gaa cat gct gcg gat att ttt gaa cgt ggc atg gtc tta act ggt	4096																			
Pro Glu His Ala Ala Asp Ile Phe Glu Arg Gly Met Val Leu Thr Gly																				
285	290	295																		
ggc ggt gcc ctt att cgt aat att gat gtt tta ctg tca aaa gaa acc	4144																			
Gly Gly Ala Leu Ile Arg Asn Ile Asp Val Leu Leu Ser Lys Glu Thr																				
300	305	310																		
ggg ggt gcc gtt atc atc gcc gat gat cct tta acc tgt gtt gcc cgt	4192																			
Gly Val Pro Val Ile Ile Ala Asp Asp Pro Leu Thr Cys Val Ala Arg																				
315	320	325	330																	
ggg ggt ggc gag gca tta gag atg atc gat atg cac ggt ggt gat att	4240																			
Gly Gly Gly Glu Ala Leu Glu Met Ile Asp Met His Gly Gly Asp Ile																				
335	340	345																		
ttt agt gac gat atc taatatgatt taaaagtgcg gtgatattag accgcacttt	4295																			
Phe Ser Asp Asp Ile																				
350																				
tacttctctt ttattgctga caaggctagc ctaattcgta tatgaaacct atttttggaa	4355																			
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<210> 42

<211> 351

<212> PRT

<213> Pasteurella multocida

<400> 42

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

Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His
225 230 235 240

Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser
245 250 255

Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala
260 265 270

Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp
275 280 285

Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg
290 295 300

Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile
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Ala Asp Asp Pro Leu Thr Cys Val Ala Arg Gly Gly Gly Glu Ala Leu
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<210> 43

<211> 2172

<212> DNA

<213> Pasteurella multocida

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<222> (1) .. (1464)

<220>

<223> pnp

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

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

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

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

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

gtg gat act gtt cgt gca tta gat att tgt act ggt gtt tta cca cgt	336
Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg	
100 105 110	
aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct	384
Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala	
115 120 125	
gtc gcg aca tta ggt aca gaa cgt gat gca caa att att gat gaa tta	432
Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu	
130 135 140	
aca ggt gag cgt tca gat cac ttc tta ttc cac tac aac ttc ccg cca	480
Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro	
145 150 155 160	
tat tct gtg ggt gaa acc ggt atg att ggt tca cca aaa cgt cgt gaa	528
Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu	
165 170 175	
att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct gca gtg atg cca	576
Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro	
180 185 190	
aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc tct gaa atc aca	624
Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr	
195 200 205	
gaa tca aat ggt tct tct tct atg gca tcg gtt tgt ggt gcg tct tta	672
Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu	
210 215 220	
gca tta atg gat gcg ggt gta cca att aaa gcg gcg gtt gca ggt att	720
Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile	
225 230 235 240	
gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg gtg ctt tca gac	768
Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp	
245 250 255	
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Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala	
260 265 270	
ggt aca cgt acg ggt gtg acg gca tta caa atg gat atc aaa atc gaa	864
Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu	
275 280 285	
ggt atc aca gca gaa atc atg caa att gcg tta aac caa gcg aaa agc	912
Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser	
290 295 300	
gca cgt tta cac att tta ggt gtg atg gag caa gcg atc cca gcg cca	960
Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro	
305 310 315 320	
cgt gcg gat att tct gat ttt gca ccg cgt att tac act atg aaa att	1008
Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile	
325 330 335	
gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt ggt gca acc att	1056
Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile	

340	345	350	
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Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp			
355	360	365	
ggt acg gtg aag att gct gcg gtt gat ggc aat tca gca aaa gag gtg			1152
Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val			
370	375	380	
atg gcg cgt att gaa gat att act gca gaa gtt gaa gcg ggt gca gtg			1200
Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val			
385	390	395	400
tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct			1248
Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser			
405	410	415	
atc gta ggt aac aaa gaa ggc tta gtg cat att tct caa atc gcg gaa			1296
Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu			
420	425	430	
gag cgt gtt gag aaa gtg agt gat tat ctt gca gtg ggg caa gaa gtg			1344
Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val			
435	440	445	
act gtt aaa gtg gtt gag att gat cgt caa ggt cgt att cgt tta acc			1392
Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr			
450	455	460	
atg aaa gaa gtt gca cca aag caa gaa cac gtt gat tct gtt gtc gca			1440
Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala			
465	470	475	480
gac gtt gcc gca gaa gaa aac gca taagcaataa acaccaacgc ccttcgtgat			1494
Asp Val Ala Ala Glu Glu Asn Ala			
485			
aaagggcggtt ggtgtgcatg ttgataagta caatttgtgc tttaaggcga agcgaaatga 1554			
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 <212> PRT
 <213> Pasteurella multocida

<400> 44
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 20 25 30
 Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
 35 40 45
 Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
 50 55 60
 Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
 65 70 75 80
 Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
 85 90 95
 Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
 100 105 110
 Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
 115 120 125
 Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
 130 135 140
 Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
 145 150 155 160
 Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
 165 170 175
 Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro
 180 185 190
 Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr
 195 200 205
 Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu
 210 215 220
 Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile
 225 230 235 240
 Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp
 245 250 255
 Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala
 260 265 270
 Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu
 275 280 285
 Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser
 290 295 300

Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
 305 310 315 320

Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
 325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
 340 345 350

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

Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
 370 375 380

Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
 385 390 395 400

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

Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
 420 425 430

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
 435 440 445

Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
 450 455 460

Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
 465 470 475 480

Asp Val Ala Ala Glu Glu Asn Ala
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<211> 633

<212> DNA

<213> Pasteurella multocida

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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

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

<210> 46

<211> 210

<212> PRT

<213> *Pasteurella multocida*

<400> 46

Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
 1 5 10 15

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

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

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

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

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

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

Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
115 120 125

Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
130 135 140

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

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

Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
180 185 190

Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
195 200 205

Tyr Leu
210

<210> 47

<211> 4788

<212> DNA

<213> Pasteurella multocida

<220>

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<222> (1) .. (876)

<220>

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<400> 47

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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 Ile				
130	135	140		
aca ctc aaa caa aga gta gca att gca atg tta ttt gct att gaa acc	480			
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr				
145	150	155	160	
gct atg cgt gct ggt gag att gct agt ata aaa tgg gat aat gtt ttt	528			
Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe				
165	170	175		
ctt gaa aag aga ata gta cat tta ccg aca act aaa aac ggg cac tct	576			
Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser				
180	185	190		
aga gat gtg ccg ctt tcg caa aga gct gtt gcg cta att tta aaa atg	624			
Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met				
195	200	205		
aaa gag gta gaa aat gga gat ctt gtg ttt cag acc acg cct gaa tca	672			
Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser				
210	215	220		
tta agc acc acg ttt aga gtg tta aag aaa gag tgt gga ctt gaa cat	720			
Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His				
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 cgccttttgc cacttgatta	916			
Asn Leu Leu Asp				
290				
catcgccagc cttatatctt ttactttcat tacttctttt ttctaatgaa actgggggatg	976			
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4788

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<211> 292

<212> PRT

<213> Pasteurella multocida

<400> 48

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

Asn Leu Leu Asp
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<210> 49

<211> 1618

<212> DNA

<213> Pasteurella multocida

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<221> CDS

<222> (2) .. (1195)

<220>

<223> sopE

<400> 49

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

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

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

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

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac 289
Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
    85             90             95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc 337
Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
    100            105            110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa 385
Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
    115            120            125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac 433
Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
    130            135            140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac 481
Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
    145            150            155            160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg 529
Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
    165            170            175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg 577

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Gly	Asp	Phe	Leu	Ser	Phe	Asn	Val	Asn	Thr	Ser	Lys	Val	Glu	Ile	Asp	
		195					200				205					
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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	
ggc	gtc	aca	caa	cca	ctc	tat	ttt	gac	att	aac	gac	agc	tcg	act	gat	769
Gly	Val	Thr	Gln	Pro	Leu	Tyr	Phe	Asp	Ile	Asn	Asp	Ser	Ser	Thr	Asp	
			245					250						255		
gtg	aac	tat	ctc	aat	gaa	caa	ggc	atc	acg	tgt	tgc	gtg	aat	cat	aat	817
Val	Asn	Tyr	Leu	Asn	Glu	Gln	Gly	Ile	Thr	Cys	Cys	Val	Asn	His	Asn	
		260					265					270				
ggc	ttt	cgt	ttt	tgg	ggc	tta	cgc	acg	act	gca	gaa	gat	cca	tta	ttc	865
Gly	Phe	Arg	Phe	Trp	Gly	Leu	Arg	Thr	Thr	Ala	Glu	Asp	Pro	Leu	Phe	
	275					280						285				
aag	ttt	gaa	gtg	tac	acc	cgc	act	gca	caa	atc	tta	aaa	gat	acg	att	913
Lys	Phe	Glu	Val	Tyr	Thr	Arg	Thr	Ala	Gln	Ile	Leu	Lys	Asp	Thr	Ile	
	290					295					300					
gca	ggg	gcg	ttt	gat	tgg	gca	gtg	gat	aaa	gat	att	tct	gtc	acg	cta	961
Ala	Gly	Ala	Phe	Asp	Trp	Ala	Val	Asp	Lys	Asp	Ile	Ser	Val	Thr	Leu	
305					310				315						320	
gtg	aaa	gat	att	att	gaa	gca	atc	aat	gcg	aag	tgg	cgt	gat	tac	acc	1009
Val	Lys	Asp	Ile	Ile	Glu	Ala	Ile	Asn	Ala	Lys	Trp	Arg	Asp	Tyr	Thr	
			325					330						335		
aca	aaa	ggc	tac	tta	att	ggc	ggt	aaa	gcg	tgg	ctt	aat	aaa	gag	ctt	1057
Thr	Lys	Gly	Tyr	Leu	Ile	Gly	Gly	Lys	Ala	Trp	Leu	Asn	Lys	Glu	Leu	
		340						345					350			
aac	agt	gca	acg	aat	tta	aaa	gat	gcg	aag	ttg	ttg	atc	tct	tat	gat	1105
Asn	Ser	Ala	Thr	Asn	Leu	Lys	Asp	Ala	Lys	Leu	Leu	Ile	Ser	Tyr	Asp	
	355						360					365				
tat	cac	cca	gta	cca	ccg	ctc	gaa	cag	cta	ggc	ttt	aat	cag	tac	att	1153
Tyr	His	Pro	Val	Pro	Pro	Leu	Glu	Gln	Leu	Gly	Phe	Asn	Gln	Tyr	Ile	
	370					375					380					
tct	gat	gaa	tac	ctt	gtt	gat	ttt	tca	aat	cgt	tta	gca	tcg			1195
Ser	Asp	Glu	Tyr	Leu	Val	Asp	Phe	Ser	Asn	Arg	Leu	Ala	Ser			
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 <213> Pasteurella multocida

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 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
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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
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 100 105 110

gtc atc tat aaa aga ta 353
 Val Ile Tyr Lys Arg
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 20 25 30

Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45

Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60

Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80

Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95

Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110

Val Ile Tyr Lys Arg
 115

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 Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1 5 10 15

gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96
 Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu

[illegible]

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<212> PRT
<213> Pasteurella multocida
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      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

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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
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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

gtt 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
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 Ile Phe Ile
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443

<210> 56
 <211> 147
 <212> PRT
 <213> Pasteurella multocida

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

Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
 35 40 45

Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
 50 55 60

Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
 65 70 75 80

Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
 85 90 95

Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
 100 105 110

Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
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Val Gly Arg Ser Ser Ser His Lys Pro Lys Phe
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ggtttatcta ttattttagt ttttattatt gtcattccag ggattttgac aaatgctatt 240
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aagaaactta atccagatct tacttatgtg atgttaagga ttattagaaa atctgaactt 420
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acattatcag ctaaaatgag tatccatttg attttgttta ttatgttccc aataatcatt 660
ttaattctag cactaggtat 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

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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			
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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			
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Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu			
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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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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
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Phe Phe Ile Asn Asp Asn Val Ala Ile Asn Asn Leu Ala Met Leu Asn			
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Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu Ile His Asn Leu Val Phe			
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gct tta gtt aaa aat ggt gat ctt gat tat gca aaa gat atc att gtt			1387
Ala Leu Val Lys Asn Gly Asp Leu Asp Tyr Ala Lys Asp Ile Ile Val			
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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			
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 <213> Pasteurella multocida

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 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

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Arg

<210> 62

<211> 1788

<212> DNA

<213> Pasteurella multocida

<220>

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<222> (1)..(600)

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<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 gtg 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

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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
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 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
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<211> 200

<212> PRT

<213> *Pasteurella multocida*

<400> 63

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 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

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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
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 Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
 20 25 30

tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat 144
 Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
 35 40 45

ttt gac att aac gac agc tgc act gat gtg aac tat ctc aat gaa caa 192
 Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
 50 55 60

ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta 240
 Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
 65 70 75 80

cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc 288
 Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
 85 90 95

act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca 336
 Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
 100 105 110

gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca 384
 Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
 115 120 125

atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc 432
 Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
 130 135 140

ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa 480
 Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
 145 150 155 160

gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc 528
 Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
 165 170 175

gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat 576
 Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
 180 185 190

ttt tca aat cgt tta gca tcg taaggggtag aaaatggcctt taccacgcaa 627
 Phe Ser Asn Arg Leu Ala Ser
 195

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<210> 67

<211> 199

<212> PRT

<213> Pasteurella multocida

<400> 67

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 35 40 45

Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
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 Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
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 Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
 85 90 95
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 100 105 110
 Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
 115 120 125
 Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
 130 135 140
 Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
 145 150 155 160
 Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
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 180 185 190
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 cggtcgcccg ttaattcagc tcaattttgc caatgaacgc ttaaacgcca actaccgtta 240
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 tccgctgggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgagggtggt 480
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138

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gta	gaa	gaa	aat	act	ttg	gtc	ata	tat	gaa	att	ctc	aaa	gca	ggg	ggc	2031				
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Phe	Thr	Thr	Gly	Gly	Phe	Asn	Phe	Asp	Ala	Lys	Ile	Arg	Arg	Gln	Ser					
			335					340						345						
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Thr	Asp	Pro	Tyr	Asp	Leu	Phe	His	Gly	His	Ile	Gly	Ala	Ile	Asp	Val					
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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																
				415																

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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
 85 90 95
 Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
 100 105 110
 Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
 115 120 125
 Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
 130 135 140
 Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
 145 150 155 160
 Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
 165 170 175
 Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
 180 185 190
 Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
 195 200 205
 Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
 210 215 220
 Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
 225 230 235 240

His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
 245 250 255

Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
 260 265 270

Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala
 275 280 285

Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu
 290 295 300

Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu
 305 310 315 320

Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe
 325 330 335

Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu
 340 345 350

Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys
 355 360 365

Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn
 370 375 380

Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile
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Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu
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 gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180
 cttagagcca cccaaatgaa cacgaaagtg ctcgatacct caaaagtgaa tgccgaacaa 240
 gtcaaaaaat ggattgctgt ttggcaaacg accctaaccc aataattggt tgtcttg 297
 atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt 345
 Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
 1 5 10 15
 ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc 393

Gly Gly Met	Leu Val	Ile Val	Phe Leu	Ser Ala	Phe Tyr	Ala Phe	Ala												
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Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu		35		40		45													
ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa	489																		
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln		50		55		60													
gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt ggc att gta gca	537																		
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala		65		70		75													80
cga gcc ttt ttt tat caa ccg ttt gtg ggc aag aaa ctg atc ctc aaa	585																		
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys			85			90													95
tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggc	633																		
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly			100			105													110
tta tta ggc gtg tat ggc gct tct ggc tgg tta gcg atg tta agc cag	681																		
Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln		115				120													125
ttt ttc gct tgg gat tgg act cct aat att tac ggc tta aca ggt att	729																		
Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile		130				135													140
tta ctg gcg cat ctt ttt ttt aat gtc cca tta gct tgt cgc ctg ttt	777																		
Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe		145				150													160
tta caa ggt ttg caa gca att ccg gtg caa caa cgt cag ctc gcg gca	825																		
Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala			165			170													175
caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc	873																		
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro			180			185													190
tat tta cgc cag caa ttg tta cct gca ttt act ttg att ttc atg ctg	921																		
Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu			195			200													205
tgt ttt acc agt ttt gcg att gtg ctc act tta ggt ggc gga ccg aaa	969																		
Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys		210				215													220
tat acc acg ttg gaa gtg gct atc tat caa gcg att tta ttt gag ttt	1017																		
Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe		225				230													240
gat gta ccg aaa gcc ggc tta ttt gcg tta tta caa ttt gtt ttt tgt	1065																		
Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys			245			250													255
ttt ctg tta ttc acg ctg agt agc ttt ttt tct cca gcc ccc gcc acg	1113																		
Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr			260			265													270

aca tta cac agt caa cct act tgg ttt gcg ccc caa tcg tat tgg gtt	1161
Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val	
275 280 285	
aaa tta tgg caa cgt atg atc att gtg tgt gcg aca gta ttt atc tta	1209
Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu	
290 295 300	
tta ccg cta ctg aat acg cta gtt tct gct ttg ctt tcg tct cag ttt	1257
Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe	
305 310 315 320	
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Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser	
325 330 335	
ctc acc atc gcc ccc act tct gca ttg ctc gct tta gta ctg tct ttt	1353
Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe	
340 345 350	
gcc tta tta ttg ctt gcc aga gaa tta cat tgg cga cat tat cgc agc	1401
Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser	
355 360 365	
tta tcc cat gtg att tta aat atc ggt gcg acc att tta gcc att cca	1449
Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro	
370 375 380	
acg tta gtg tta gct att ggt tta ttc att tta tta cgt gag atc gat	1497
Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp	
385 390 395 400	
ttt tct cca tac cat ctt ttt ggg gtt gtg gta tgc tgt aac gcg tta	1545
Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu	
405 410 415	
gct gct atg cct ttt gtg ttg cgt att ttg gct tta ccg atg cat aac	1593
Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn	
420 425 430	
aat atg att tat tat gaa aaa tta tgc caa tca ctt aac ctg cgt ggt	1641
Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly	
435 440 445	
tgg caa cgt ttt cga ttg att gaa tgg cac aag ctt cgt gcg cca atg	1689
Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met	
450 455 460	
aaa tac gcc ttt gca ctg gct tgt gcg tta tca tta ggc gat ttc acc	1737
Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr	
465 470 475 480	
gca atc gcg tta ttt ggt cag gct gac ttc aca tcg tta ccg cat ttg	1785
Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu	
485 490 495	
ttg tat caa caa ttg ggg cat tat cgt agt cag gaa gcg gca gta aca	1833
Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr	
500 505 510	
gcg ttt att tta ttg gtt ttt tgt ttg agt gtt ttt atg att att gaa	1881
Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu	

515

520

525

cga cat cag gaa ccg cgt gat gat taatttaaac ggtgttcagt tttcctataa 1935
 Arg His Gln Glu Pro Arg Asp Asp
 530 535

tacctttact tttgagctgg atttgacagat tcttgctcaa caaaaagttg ctattattgg 1995
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<211> 536

<212> PRT

<213> Pasteurella multocida

<400> 71

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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
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Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln
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Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile
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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
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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
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 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
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 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
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 435 440 445
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 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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 Arg His Gln Glu Pro Arg Asp Asp
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Met Pro His His

3

5

10

15

20

25

30

35

40

45

50

tta ggt ttt ctc act ggg tta atc gct tta gtt att tca tat ctt tgg	1747
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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	
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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	
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ggc tat aat aaa aac tta gct ata gga act gtt gta gca gga gga gca	2083
Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val Ala Gly Gly Ala	
165 170 175 180	
ttg ggt aca atg gtt cct cca agt atc gtg ttg att att tac gga atg	2131
Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile Ile Tyr Gly Met	
185 190 195	
acc gca aat gtt tct att gga gaa cta ttt ctt gca gca att cca gcc	2179
Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala Ala Ile Pro Ala	
200 205 210	
tcc tta cta ctt tct aca ttc tat att tta tat att cta gta ctt tgc	2227
Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile Leu Val Leu Cys	
215 220 225	
tac ttc aaa cct agc tat ggc cct gca atg cct agc tca gaa aat cat	2275
Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser Ser Glu Asn His	
230 235 240	
aca tta acg aaa gaa gat att aaa aaa att att cat gat att gca att	2323
Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His Asp Ile Ala Ile	
245 250 255 260	
cca gta gct atc gcc aca tgg att tta gga agt att tat ggc ggg ata	2371
Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile	
265 270 275	
gca tca atc act gaa tct gcc tgt gtt ggt gta gtt ggg gta ata tta	2419
Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val Gly Val Ile Leu	
280 285 290	
gca gca ttc tat cga aaa gaa tta aat ttc aaa ata gta caa gaa tca	2467
Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile Val Gln Glu Ser	

295	300	305	
cta aaa cat aca atc aat act gtt ggt atg ata atc tgg gtc ggc att			2515
Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile Trp Val Gly Ile			
310	315	320	
ggc gca aca atg att ata ggt att tat aat cta atg ggt ggg gac cga			2563
Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met Gly Gly Asp Arg			
325	330	335	340
ttt ata gct aac tta ttc gct agc tta gat gcc tct cca att tat act			2611
Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser Pro Ile Tyr Thr			
	345	350	355
atc att att atg atg gtt att tta tta ata ctt ggt atg ttc tta gat			2659
Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly Met Phe Leu Asp			
	360	365	370
tgg att ggt gtt gcc atg ttg act ttc ctc aag aca agt aaa gcg aca			2707
Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr Ser Lys Ala Thr			
	375	380	385
atc aat ttg tgt ttt gac ata gtc agg tac agt att tgg cgt ggt ccc			2755
Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile Trp Arg Gly Pro			
	390	395	400
tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt			2803
Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly			
405	410	415	420
act ttt tagtaaatct tgcgcgatac gaataaacgc attgatggca tttgctccgt			2859
Thr Phe			
tttgtggatc gactgccgca tgagcagatt tgccaaaaaa ttcaattaca tacttcccaa			2919
tccctttttct ttcggttaacg ttccactta gattgcccgag aagccgatct gtctgaatgg			2979
gaacaagtgt tataccaaga agcgaatcca acaggtgaag tggatgatcgg tatggtgggt			3039
aaatacactg aattaccgga tgctacaaa tcggttaatg aagccttgaa acacgcaggc			3099
ttaaaaaacc gtcttagcgt gcaaatcaaa tatattgatt cacaagatgt ggaaacaaaa			3159
ggcacagaag tgttagaagg cgt			3182

<210> 73

<211> 422

<212> PRT

<213> Pasteurella multocida

<400> 73

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Leu	Tyr	Lys	Ile	Ser	Gly	Gly	Ile	Ile	Met	Ile	Ser	Ala	Phe	Gly	Ile
			20					25					30		

Gly	Ile	Gly	Thr	Leu	Ile	Ile	Phe	Leu	Met	Met	Ile	Ser	Leu	Leu	Phe
		35					40					45			

Ile	Gly	Met	Pro	Leu	Gly	Phe	Leu	Thr	Gly	Leu	Ile	Ala	Leu	Val	Ile

50					55					60					
Ser	Tyr	Leu	Trp	Phe	Asp	Thr	Thr	Ala	Ile	Met	Gln	Met	Ile	Ala	Ser
65					70					75					80
Arg	Val	Thr	Asp	Phe	Thr	Ser	Ser	Tyr	Thr	Phe	Val	Ala	Val	Pro	Met
				85					90					95	
Phe	Val	Leu	Met	Ala	Thr	Leu	Leu	Asp	Lys	Thr	Gly	Ile	Ala	Arg	Asp
			100					105					110		
Leu	Tyr	Asn	Ala	Met	Arg	Val	Ile	Gly	Gly	Arg	Leu	Arg	Gly	Gly	Ile
		115					120					125			
Ala	Ile	Gln	Ser	Met	Phe	Val	Ala	Val	Leu	Leu	Ala	Thr	Met	Ser	Gly
		130					135					140			
Ile	Ile	Gly	Gly	Glu	Thr	Val	Leu	Leu	Gly	Met	Leu	Ala	Leu	Pro	Gln
145					150					155					160
Met	Leu	Arg	Leu	Gly	Tyr	Asn	Lys	Asn	Leu	Ala	Ile	Gly	Thr	Val	Val
				165					170					175	
Ala	Gly	Gly	Ala	Leu	Gly	Thr	Met	Val	Pro	Pro	Ser	Ile	Val	Leu	Ile
			180					185					190		
Ile	Tyr	Gly	Met	Thr	Ala	Asn	Val	Ser	Ile	Gly	Glu	Leu	Phe	Leu	Ala
		195					200					205			
Ala	Ile	Pro	Ala	Ser	Leu	Leu	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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ggcgttgcaa tctgttggcg ttgtttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
tttgttccac caatatctaa tgctaaacag cgcataaggt ctccttctgt gatgacttat 240
tttgccgatt tgacggcatc ggcaaaccag cttacgatat gttcgaggcg agtcagcgca 300
gatectacgg tgacagagta agcaccaate tcaattgcgg ttttcgcaa ttctggggtg 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 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 taaatttatc aaaagaagat 956
 Cys Asp Ser Phe Asp Ile Leu Thr Pro Val
 150 155
 tgactccaat ttgcataggt taatcttaga attaaaaaat aacaacccaaa ataataaaaa 1016
 ttgagatct ttgtcgcata ttatttcata gggaatagac agcttaattt tagttatgat 1076
 ttgtcaatcc ttgtatattt ttgtgtttgc tggtttgoga tacactgttc taatattgct 1136
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 aagaaaaatc caatggcaaa attgatgtgg ctattttccc tagctcacag ttaggtgatg 2156
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 aaattgataa agagttaaac gtacaagtgt tatctgtggc gtataacggt acacgtcaaa 2396
 caacttctaa ccgtgcaatc aacagcattg aagacatgaa aggggttaaaa ttacgtgtac 2456
 ctaacgcggc aaccaacott gcttatgcaa aatacgtggg tgcagcgcca acaccaatgg 2516
 cattctctga agtttacott gcgcttcaaa caaactctgt ggatgggtcaa gaaaacccat 2576
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 acatcttaaa tgaccaactt tacttaatca gtaacgatac gttggcagat ttaccagaag 2696
 atttacaaaa agtggttaaa gatgcagcag cgaaagccgc tgaatatcac actaaactct 2756
 tcgttgacgg tgagaacagc ttagttgaat t 2787

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

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

<210> 76
 <211> 2787
 <212> DNA
 <213> Pasteurella multocida
 <220>

<221> CDS

<222> (1949) .. (2785)

<220>

<223> yiaO

<400> 76

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 ggcgttgcaa tctgttggcg ttgttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
 tttgttccac caatatctaa tgctaaacag cgcataaggct ctcttctgt gatgacttat 240
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 gatcctacgg tgacagagta agcaccaatc tcaattgcgg ttttcgcaa ttctggggtg 360
 ttatagcgcc cttctgccat cactcggcag ccagcagcat tcaaattctt gactaactga 420
 taatccggtt cagctggaat ttcaccgcca gtataaccag acatggtgct accaataatt 480
 tctaccccta agttgtggca atacatccct tcttcaaaat tagaacaatc cgccatggct 540
 aaacaacctt attctttgat tcgtttaata atggcttcac gtgtagttgg acggacgca 600
 tcggtaccat caaaagcaat aatatcggcg cctgctcggg ctaactcttc aatgtcttgt 660
 aaaaatgggc taatacgaac gggactgtca ggtaaatcgc gtttaacgat accaataatc 720
 ggtacattga cgacgttacg cgtggctttt aaattttcga tcccttcaat acgtaaccgc 780
 gcagcaccac cgataacgga tgcttgccgc atggcggcaa caatttctgg cgagtccatt 840
 ggcccattat ctacgggctg gcaagatgcg attaagccat atttaatttg ttctaaaact 900
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 caatccttgc tattttttgt gtttgcgtgt ttgcgataca ctgttcta attgctttga 1140
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 caccgttaga atcacaaaag tatttttgtg tttcaacgta agtcacgtct gacggacaat 1260
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 tttgtccgc taattgaggt gtgcctgcta cctgttcgtc ccacatgtca aaaagtgaat 1620
 gaccaattaa gctgatattg gcaggttcgg aaaattccgc cattttgctc tgatagcgtt 1680

155

205					210					215					
aaa ttc tat	gaa gta caa	aaa tac tta	gcg tta act	aac cac atc	tta	2644									
Lys Phe Tyr	Glu Val Gln	Lys Tyr Leu	Ala Leu Thr	Asn His Ile	Leu										
	220		225		230										
aat gac caa	ctt tac tta	atc agt aac	gat acg ttg	gca gat rta	cca	2692									
Asn Asp Gln	Leu Tyr Leu	Ile Ser Asn	Asp Thr Leu	Ala Asp Leu	Pro										
	235		240		245										
gaa gat tta	caa aaa gtg	gtt aaa gat	gca gca gcg	aaa gcc gct	gaa	2740									
Glu Asp Leu	Gln Lys Val	Val Lys Asp	Ala Ala Ala	Lys Ala Ala	Glu										
	250		255		260										
tat cac act	aaa ctc ttc	gtt gac ggt	gag aac agc	tta gtt gaa	tt	2787									
Tyr His Thr	Lys Leu Phe	Val Asp Gly	Glu Asn Ser	Leu Val Glu											
265		270		275											

<210> 77

<211> 279

<212> PRT

<213> Pasteurella multocida

<400> 77

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

195	200	205
Pro Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr		
210	215	220
Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser		
225	230	235 240
Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys		
245	250	255
Asp Ala Ala Ala Lys Ala Ala Glu Tyr His Thr Lys Leu Phe Val Asp		
260	265	270
Gly Glu Asn Ser Leu Val Glu		
275		

<210> 78
 <211> 2590
 <212> DNA
 <213> Pasteurella multocida

<220>
 <221> CDS
 <222> (908)..(1294)

<220>
 <223> yigF

<400> 78
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 aaagtgcggg ggcaattcgt ttattgagc aagtggacga gaaattgatt ttccgcagcg 180
 gtggcgggat tacgatctta agcgagctag aagacgagta ccaagaattg atccaaaaag 240
 tgtatgtacc agtaggataa gcgatgacat ttcctttatt tgagacgatc gctattgtga 300
 acggtgaaat tcagcacctt gccctgcac aacaacgtta tgccggcaagt ttggcgacct 360
 tttacggcga gaaaggagcg aaagtacagg atcttgcgaa aattattcag attccgacct 420
 cacttgaaca cactcaacat gcgccgataa tccgttgctg gattgattac aatcagcaag 480
 actgtgacgt gcattatatt ccctatcaac gcaaaattta ccgcactttt cagcctgtca 540
 tttgcgatga aattaactat gatctgaaat atgctgacgc ggcattatta aatcagttat 600
 rtgctcagcg tagggattgt gatgagatta tgattatcaa acacggcaag gtgacggatt 660
 gcagtattgg taatctgggtg ttccgccaaag gtgagcaatg gttcacgcca gatagcccgt 720
 tattttacgg cacacaacga gcctgggttat tacaacaagg caaaattcaa gcccgttcca 780
 tcttattgca agagatcgca caatttgaag aaattcggtt aattaatgca ctaaattccgc 840
 tgtaaatttt ccttgaacag cgtaaaataa aacaactttt tcagtcagat aaaaggagat 900
 aaacgac atg acg aaa gta att cat act gac aat gca cca gcc gcc att 949

Met	Thr	Lys	Val	Ile	His	Thr	Asp	Asn	Ala	Pro	Ala	Ala	Ile	
1				5					10					
ggt cct tat gta caa gcg gta gat tta ggt aat atg ctg tta acc tct	997													
Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser														
15 20 25 30														
ggg caa att cca gtg aat cca aaa acc ggt gaa gtg cca gcg gat atc	1045													
Gly Gln Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile														
35 40 45														
gta gca caa gca cgt caa tct tta gaa aac gtg aaa gcg att gtg gaa	1093													
Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu														
50 55 60														
caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg	1141													
Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val														
65 70 75														
aaa gat tta aat gac ttt gca gcg gtc aat gcg gag tat gaa cgt ttc	1189													
Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe														
80 85 90														
ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa	1237													
Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu														
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Val Lys Ala														
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<211> 129

<212> PRT

<213> Pasteurella multocida

<400> 79

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 20 25 30

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 35 40 45

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

Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe Phe Lys
 85 90 95

Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu Val Ala
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Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala Val Lys
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<222> (463) .. (1884)

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Met Thr Gln Lys
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Leu His Ile Lys Thr Trp Gly Cys Gln Met Asn Glu Tyr Asp Ser Ser
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Lys Met Ala Asp Leu Asn Ser Thr His Gly Leu Glu Leu Thr Glu
25 30 35
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Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr Cys Ser Ile Arg
40 45 50
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Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly Arg Trp Lys Glu
55 60 65
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Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val Gly Gly Cys Val
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gcc tca caa gaa gga gaa cac att cgt act cgt gct cct tat gtc gat 762
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85 90 95 100
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Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro Glu Met Ile Asn
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Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val Ser Phe Pro Glu
120 125 130
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Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala Glu Gly Pro Thr
135 140 145
gct ttc gta tcc att atg gaa ggc tgt aat aaa tat tgc tca ttc tgt 954
Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr Cys Ser Phe Cys
150 155 160
gtc gtg cct tat acg cgt ggt gaa gaa gtc agt cgt cca gtg gat gat 1002
Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg Pro Val Asp Asp
165 170 175 180

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Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly Ala Thr His Asp	
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gac ggt att tgt act ttt gcg gaa ttg tta cgt tta gta gcc gct att	1146
Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu Val Ala Ala Ile	
215 220 225	
gat ggt att gac cgt tta cgt ttt acc acc agt cac cca att gag ttc	1194
Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His Pro Ile Glu Phe	
230 235 240	
act gat gac att att gat gtg tac cgt gat acg cca gag ttg gtg agt	1242
Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro Glu Leu Val Ser	
245 250 255 260	
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Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg Val Leu Ser Met	
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Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser Ile Ile Arg Lys	
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375 380 385	
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Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu Thr Gly Arg Thr	
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gaa act aat cgt atc gtc aat ttt gtg ggc acg cct gat atg att ggg	1722
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Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr Asn Ser Leu Arg	

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Val Gly Arg Tyr His Ala				
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<211> 474

<212> PRT

<213> Pasteurella multocida

<400> 81

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Pro	Tyr	Val	Asp	Ile	Ile	Phe	Gly	Pro	Gln	Thr	Leu	His	Arg	Leu	Pro
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Glu	Met	Ile	Asn	Gln	Ile	Arg	Gly	Gly	Lys	Ser	Ser	Val	Val	Asp	Val
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Ser	Phe	Pro	Glu	Ile	Glu	Lys	Phe	Asp	Arg	Leu	Pro	Glu	Pro	Arg	Ala
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Cys	Ser	Phe	Cys	Val	Val	Pro	Tyr	Thr	Arg	Gly	Glu	Glu	Val	Ser	Arg
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Pro	Val	Asp	Asp	Val	Leu	Phe	Glu	Ile	Ala	Gln	Leu	Ala	Glu	Gln	Gly
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Val	Arg	Glu	Val	Asn	Leu	Leu	Gly	Gln	Asn	Val	Asn	Ala	Tyr	Arg	Gly
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Pro	Ile	Glu	Phe	Thr	Asp	Asp	Ile	Ile	Asp	Val	Tyr	Arg	Asp	Thr	Pro
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Glu	Leu	Val	Ser	Phe	Leu	His	Leu	Pro	Val	Gln	Ser	Gly	Ser	Asp	Arg
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Val	Leu	Ser	Met	Met	Lys	Arg	Asn	His	Thr	Ala	Leu	Glu	Tyr	Lys	Ser
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Ile	Ile	Arg	Lys	Leu	Arg	Ala	Val	Arg	Pro	Glu	Ile	Gln	Ile	Ser	Ser
		290				295					300				
Asp	Phe	Ile	Val	Gly	Phe	Pro	Gly	Glu	Thr	Ala	Glu	Asp	Phe	Glu	Gln
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Thr	Met	Asn	Leu	Ile	Ala	Gln	Val	Asn	Phe	Asp	Met	Ser	Phe	Ser	Phe
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Ile	Tyr	Ser	Ala	Arg	Pro	Gly	Thr	Pro	Ala	Ala	Asp	Met	Pro	Asp	Asp
			340					345					350		
Val	Thr	Glu	Glu	Glu	Lys	Lys	Gln	Arg	Leu	Tyr	Val	Leu	Gln	Gln	Arg
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Gln Arg Val Leu Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu
 385 390 395 400

Thr Gly Arg Thr Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro
 405 410 415

Asp Met Ile Gly Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr
 420 425 430

Asn Ser Leu Arg Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu
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aag cag agt ctt gcg cgc gaa ggc gtg gcg tta cgc cca cct ttt gcc 559
 Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro Pro Phe Ala
 40 45 50

ctt gag aat gag aaa gcg ttt tct gct gcg tgc att cgt tgt ggt cag 607
 Leu Glu Asn Glu Lys Ala Phe Ser Ala Ala Cys Ile Arg Cys Gly Gln
 55 60 65

tgt gta caa gcc tgt cca cat gag atg ttg cat ctt gcc tca ctg att 655
 Cys Val Gln Ala Cys Pro His Glu Met Leu His Leu Ala Ser Leu Ile
 70 75 80

tca ccg atg gaa gca ggt aca ccg tat ttc att gcg cgc gat aag ccc 703
 Ser Pro Met Glu Ala Gly Thr Pro Tyr Phe Ile Ala Arg Asp Lys Pro
 85 90 95

tgt gaa atg tgt gtg gat att cct tgt gca aaa gcc tgc cca acc ggt 751
 Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys Pro Thr Gly
 100 105 110 115

gca ttg gat aat caa gca aca gaa atc gat gat gcg cgt atg ggg tta 799
 Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg Met Gly Leu
 120 125 130

gct gtc ctg cta gat cat gaa act tgt ctg aac tgg caa ggt tta cgc 847
 Ala Val Leu Leu Asp His Glu Thr Cys Leu Asn Trp Gln Gly Leu Arg
 135 140 145

tgt gat gtg tgt tat cgc gtc tgt ccg ctg att aat aaa gcg att acg 895
 Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys Ala Ile Thr
 150 155 160

tta gtg atg cat cgt aat gag cgt acg ggt aag cac gcc gtc ttt atc 943
 Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala Val Phe Ile
 165 170 175

cca aca gtg cat tcc gaa gcc tgt aca gga tgt ggc aaa tgt gaa gaa 991
 Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys Cys Glu Glu
 180 185 190 195

gct tgc gtt cta gaa gaa gcg gca atc aaa gtg tta ccg atg gca tta 1039
 Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro Met Ala Leu
 200 205 210

gcg aaa ggc atg tta ggt aaa cat tac cgt tta ggt tgg gaa gag aaa 1087
 Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp Glu Glu Lys
 215 220 225

gaa aaa gcc ggg cat tcc ctt gcg cca gaa ggc att att tct ctc ccg 1135
 Glu Lys Ala Gly His Ser Leu Ala Pro Glu Gly Ile Ile Ser Leu Pro
 230 235 240

act cgg tta ~~ccg~~ gag agc ttg taatggcaaaa ttcaccaaaa tatgcgggta 1186
 Thr Arg Leu Pro Glu Ser Leu
 245 250

aagaagcacg agaaaagtta ggctggtggt acgccaatcg ctttttgttc tggcgacggt 1246

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<210> 83

<211> 250

<212> PRT

<213> Pasteurella multocida

<400> 83

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Ala Thr Arg Thr Ala Gly Gly Leu Ala Gly Val Thr Leu Leu Leu Gly
 20 25 30

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

<210> 84
 <211> 3494
 <212> DNA
 <213> Pasteurella multocida

<220>
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 <222> (2411)..(2719)

<220>
 <223> yyaM

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acaattatga cagaacataa atccctcgac tatgcgatga tgcgcgctaa acaagaagca 420
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 tacagtcaag atg act aaa ctc agt atc cag cga gat aac ttg att tgt 2449
 Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys
 1 5 10
 ttg agt tat gtc gca tta atg gga ttc ggc ttt ccc att atg cgt tat 2497
 Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr
 15 20 25
 atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt ctc 2545
 Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu
 30 35 40 45
 tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct 2593
 Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala
 50 55 60
 gag tta aca tct tcg ggg gct ggc gtc cag tcc gtt gcg atg ttg ccg 2641
 Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro
 65 70 75
 agt tca agt tta ggt ttc tta ata ttg aaa act gta cca tct ttt tca 2689
 Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser
 80 85 90
 tac gtt aca atc tca aca ctt aat cgc gtt tgaccttcg atttttgata 2739
 Tyr Val Thr Ile Ser Thr Leu Asn Arg Val
 95 100
 gtcaaagact actgagtaac gcttgtagtc gcgtgaatcg actgttacat aagccgarat 2799
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aatatccgcg cttacttccg agatagccac gtcca 3494

<210> 85
 <211> 103
 <212> PRT
 <213> Pasteurella multocida

<400> 85
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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
 Ile Ser Thr Leu Asn Arg Val
 100

<210> 86
 <211> 19
 <212> DNA
 <213> Artificial Sequence

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

<400> 86
 aggccggtac cggccgcct

19

<210> 87
 <211> 19
 <212> DNA
 <213> Artificial Sequence

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

<400> 87
 cggccggtac cggcctagg

19

<210> 88
 <211> 18
 <212> DNA
 <213> Artificial Sequence

金替力

人I₂序列

人I₂序列描述

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<220>

<223> Description of Artificial Sequence: primer

<400> 93

tacctacaac ctcaagctt

19

<210> 94

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 94

taccattctt aaccaagctt

20

<210> 95

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 95

ggcagagcat tacgctgac

19

<210> 96

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 96

gtaccggcca ggcggccacg cgtattc

27

<210> 97

<211> 531

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> atpG

<400> 97

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agttaatgaa atgattaatg cgttcgaaa cggagaagtg gatgcgggtt acgtcgctta 180

caaccgtttt gaaaatacga tgtcacaaaa acctgttata gcacagttac ttccgttacc 240

taaactagat gacgatgaat tagatacga aggttcattg gattatattt atgaaccgaa 300

tccacaagtt ttattggata gtttacttgt tcggtatttta gaaactcagg tataccaagc 360
 agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420
 agataatgcg ggtacattaa tcgatgaatt acaattagtg tataacaaag ctgcgcaagc 480
 aagcattaca aatgaattaa acgaaattgt tgcgggtgcc gcagcaattt a 531

<210> 98

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

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25

<210> 99

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 99

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20

<210> 100

<211> 1034

<212> DNA

<213> Pasteurella multocida

<220>

<223> cap5E

<220>

<221> CDS

<222> (1)..(1032)

<400> 100

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Met Phe Lys Asn Lys Thr Leu Leu Ile Thr Gly Gly Thr Gly Ser Phe

1

5

10

15

ggg aat gct gta ctc aaa cgt ttc tta gaa aca gat att cga gaa att 96

Gly Asn Ala Val Leu Lys Arg Phe Leu Glu Thr Asp Ile Arg Glu Ile

20

25

30

cgt gtt ttt tcg cgt gat gag aag aaa caa gat gac atg cgg aaa aaa 144

Arg Val Phe Ser Arg Asp Glu Lys Lys Gln Asp Asp Met Arg Lys Lys

35

40

45

tat aat gat gca aaa tta aaa ttt tat att ggc gat gtt cgt gac tac 192

Tyr Asn Asp Ala Lys Leu Lys Phe Tyr Ile Gly Asp Val Arg Asp Tyr

50

55

60

gat agt att tta aat gcc tcg cga ggt gtt gac tat att tat cat gct	240
Asp Ser Ile Leu Asn Ala Ser Arg Gly Val Asp Tyr Ile Tyr His Ala	
65 70 75 80	
gcc gca tta aag caa gtg cct tca tgc gag ttt tat ccg tta gag gca	288
Ala Ala Leu Lys Gln Val Pro Ser Cys Glu Phe Tyr Pro Leu Glu Ala	
85 90 95	
gtg aaa acc aat att tta ggt acg gca aat gtc tta gaa gcc gcc atc	336
Val Lys Thr Asn Ile Leu Gly Thr Ala Asn Val Leu Glu Ala Ala Ile	
100 105 110	
caa aac cag ata aaa cgc gtc gtc tgt ctt agc aca gat aaa gcg gtg	384
Gln Asn Gln Ile Lys Arg Val Val Cys Leu Ser Thr Asp Lys Ala Val	
115 120 125	
tac cca att aat gcg atg ggc att tct aaa gca atg atg gaa aaa gtc	432
Tyr Pro Ile Asn Ala Met Gly Ile Ser Lys Ala Met Met Glu Lys Val	
130 135 140	
atc atc gca aaa tcg cgt aac cta gaa ggc aca cca acg aca atc tgt	480
Ile Ile Ala Lys Ser Arg Asn Leu Glu Gly Thr Pro Thr Thr Ile Cys	
145 150 155 160	
tgt act cgc tat ggc aat gtc atg gca tcg cgt ggt tcg gtt atc cca	528
Cys Thr Arg Tyr Gly Asn Val Met Ala Ser Arg Gly Ser Val Ile Pro	
165 170 175	
tta ttt gtc gat caa ata cgt caa ggc aag cct ttt act att act gat	576
Leu Phe Val Asp Gln Ile Arg Gln Gly Lys Pro Phe Thr Ile Thr Asp	
180 185 190	
cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta	624
Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu	
195 200 205	
gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa	672
Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln	
210 215 220	
aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa	720
Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu	
225 230 235 240	
tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat	768
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His	
245 250 255	
gga gag aaa gca ttc gaa gct tta tta agc cgt gaa gaa atg gtt cat	816
Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His	
260 265 270	
gca att aat gaa 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	Lys	Leu	Glu	Phe	Ile	Gln	Lys	Met	Ile	Glu		
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<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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 Met Lys Gln Leu Leu Leu Lys Leu Glu Phe Ile Gln Lys Met Ile Glu
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 Gly Glu Tyr Ile Ser Pro Glu Val
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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
 20 25 30
 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
 35 40 45
 cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg 192
 Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
 50 55 60
 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
 65 70 75 80
 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 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
Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys	
275 280 285	
caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act	912
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	
290 295 300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa	960
Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	
305 310 315 320	
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga	1008
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	
325 330 335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca	1056
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	
340 345 350	
gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat	1104
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	

355	360	365	
gat att cag att gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr 370 375 380			1152
att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys 385 390 395 400			1200
aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr 405 410 415			1248
aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys 420 425 430			1296
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly 435 440 445			1344
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp 450 455 460			1392
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu 465 470 475 480			1440
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala 485 490 495			1488
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile 500 505 510			1536
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg 515 520 525			1584
ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser 530 535 540			1632
ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu 545 550 555 560			1680
agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu 565 570 575			1728
aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn 580 585 590			1776
gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala 595 600 605			1824

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	
ggg tta ttc cat aca ctc ggt aat atg atg tta gaa gca gag cgt tct	2064
Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser	
675 680 685	
gtt tat aat att ggc gat att tat gcg agt aaa aaa tta aca gtt cat	2112
Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His	
690 695 700	
act cat aat ttg att aat gat gtg cgt tta tct ggc aat gtg agt tat	2160
Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr	
705 710 715 720	
aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta	2208
Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val	
725 730 735	
cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa	2256
His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu	
740 745 750	
caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc cgt tct	2304
Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser	
755 760 765	
gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca	2352
Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser	
770 775 780	
aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt	2400
Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe	
785 790 795 800	
aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt aac caa	2448
Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln	
805 810 815	
aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac	2496
Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr	
820 825 830	
tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca	2544
Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala	
835 840 845	
tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc	2592
Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly	

850	855	860	
tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt			2640
Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser			
865	870	875	880
gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa			2688
Ala Tyr Gln Leu 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
ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca			2928
Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser			
	965	970	975
gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac			2976
Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp			
	980	985	990
ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta			3024
Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu			
	995	1000	1005
ttt att gat aat agt atc caa tta gaa aag aaa aag ttg tct cct att			3072
Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile			
	1010	1015	1020
gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc			3120
Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser			
	1025	1030	1035
cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat gag tct			3168
His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser			
	1045	1050	1055
gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa gag atg			3216
Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met			
	1060	1065	1070
ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca			3264
Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro			
	1075	1080	1085
cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt			3312
Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe			
	1090	1095	1100

gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu 1105 1110 1115 1120	3360
ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu 1125 1130 1135	3408
gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys 1140 1145 1150	3456
gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu 1155 1160 1165	3504
tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg 1170 1175 1180	3552
ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa cgt gtt Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val 1185 1190 1195 1200	3600
gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa att gct Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala 1205 1210 1215	3648
aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg 1220 1225 1230	3696
cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag aag aaa Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys 1235 1240 1245	3744
caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct gaa cag Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln 1250 1255 1260	3792
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act gat cca ctt ttc cgt aca aaa ttg aaa tat atc aat caa gat gac Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp 1315 1320 1325	3984
tat gct ggt gca aat tat ttc ttc aat aaa gtt ggt tta aat aca aaa Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys 1330 1335 1340	4032
ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln 1345 1350 1355 1360	4080

1345	1350	1355	1360	
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Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln				
	1365	1370	1375	
aaa tac aat ctc agc gat gtg gaa tta gtt aaa cag ctg atg gac aat				4176
Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn				
	1380	1385	1390	
tcc aca aca caa gcg cag gag ttg gat ttg aaa cta ggt gcg gca tta				4224
Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu				
	1395	1400	1405	
act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg tat gtc				4272
Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val				
	1410	1415	1420	
aaa acg aag gta aag ggc aaa gat gtg ttt gtt cca aag gtt tat ttc				4320
Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe				
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gct tct gaa acg ctc gta gaa gcc caa aaa tta caa ggt tta ggc act				4368
Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr				
	1445	1450	1455	
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Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val				
	1460	1465	1470	
aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat				4464
Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn				
	1475	1480	1485	
aaa atc aaa aat caa ggg agt atc tta agt act caa gaa aca cgt tta				4512
Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu				
	1490	1495	1500	
gtc ggg cgt aaa ggt att gaa aac gta tct cgt tca ttt gca aat gat				4560
Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp				
	1505	1510	1515	1520
gaa tta gga gtc act gca caa cgc tca gaa atc aaa acg gaa ggt cat				4608
Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His				
	1525	1530	1535	
tta cat ctt gaa aca gat aag gat tca act att gat gta caa gca tcg				4656
Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser				
	1540	1545	1550	
gat att aaa gca aaa aca agc ttt gtg aag act ggt gat gtg aat ctc				4704
Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu				
	1555	1560	1565	
aaa aat aca tac aat act aaa cat gcc tac cgt gag aaa ttc tcg ccg				4752
Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro				
	1570	1575	1580	
agt gca cta caa gtt gca gaa ctt gat gtg gca ggg ctt aaa gtc cca				4800
Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro				
	1585	1590	1595	1600

ctt tta ggc gtg tcc gtc tcc atc cag ttt att cag agc ata cta gtg 4848
 Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
 1605 1610 1615

agg caa ctt caa gag gga tca atc ttc gaa gta ggg cac tta cat ntt 4896
 Arg Gln Leu Gln Glu Gly Ser Ile Phe Glu Val Gly His Leu His Xaa
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gcg gta gac aga aga tgt gaa cca agc ggg gag ta 4931
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 1635 1640

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<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

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
 50 55 60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
 65 70 75 80

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

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

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
 115 120 125

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

Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
 145 150 155 160

Ala Val Phe Asn Asn Asn Gly Thr Glu Ala Gln Ala Arg Ser Thr Leu
 165 170 175

Ile Gly Tyr Ile Pro Gln Asn Gln Asn Leu Arg Gly Gly Lys Glu Ala
 180 185 190

Asp Val Ile Leu Asn Gln Val Thr Gly Pro Gln Glu Ser Lys Ile Val
 195 200 205

Gly Ala Leu Glu Val Leu Gly Lys Lys Ala Asp Ile Val Ile Ala Asn
 210 215 220

Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg

225		230		235		240
Phe Val Ala Thr	Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu					
	245		250		255	
Lys Val Thr	Lys Gly Asn Val Ile Ile Asp Ile Asp Gly Phe Ser Thr					
	260		265		270	
Asp Gly Leu	Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys					
	275		280		285	
Gln Ser Ile	Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr					
	290		295		300	
Leu Ile Ala	Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys					
305		310		315		320
Lys Thr Ser	Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly					
	325		330		335	
Ser Ser Thr	Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr					
	340		345		350	
Asp Lys Gly	Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn					
	355		360		365	
Asp Ile Gln	Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr					
	370		375		380	
Ile Gln Gln	Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys					
385		390		395		400
Lys Ile Glu	Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr					
	405		410		415	
Lys Ser Asp	Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys					
	420		425		430	
Asn Ala Glu	Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly					
	435		440		445	
Ala Leu Ser	Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp					
	450		455		460	
Val Ala Thr	Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu					
465		470		475		480
Val Lys Leu	Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala					
	485		490		495	
Glu Arg Lys	Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile					
	500		505		510	
Gln Asp Arg	Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg					
	515		520		525	
Phe Leu Gly	Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser					
	530		535		540	
Leu Ser Ala	Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu					
545		550		555		560

Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
 565 570 575
 Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn
 580 585 590
 Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala
 595 600 605
 Asn Ile Thr Leu Asn Val Glu Glu Asn Phe Val Asn Arg Ala Gly Thr
 610 615 620
 Leu Ala Thr Gly Lys Thr Leu Thr Ile Asn Thr Glu Ser Gly Ser Ile
 625 630 635 640
 Tyr Asn Leu Gly Gly Thr Leu Gly Ala Gly Lys Ser Leu Lys Leu Thr
 645 650 655
 Ala Lys Ser Thr Glu Glu Gly Met Gly Asn Ile Val Asn Gln Glu Asn
 660 665 670
 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
 675 680 685
 Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr Val His
 690 695 700
 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
 705 710 715 720
 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
 725 730 735
 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
 740 745 750
 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
 755 760 765
 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
 770 775 780
 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
 785 790 795 800
 Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
 805 810 815
 Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
 820 825 830
 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
 835 840 845
 Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly
 850 855 860
 Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser
 865 870 875 880
 Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys
 885 890 895

Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
900 905 910

Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe
915 920 925

Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu
930 935 940

Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
945 950 955 960

Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser
965 970 975

Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp
980 985 990

Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu
995 1000 1005

Phe Ile Asp Asn Ser Ile Gln Leu Glu Lys Lys Lys Leu Ser Pro Ile
1010 1015 1020

Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser
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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 Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met
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Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro
1075 1080 1085

Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe
1090 1095 1100

Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
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Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
1125 1130 1135

Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
1140 1145 1150

Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
1155 1160 1165

Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
1170 1175 1180

Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
1185 1190 1195 1200

Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
1205 1210 1215

Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
1220 1225 1230

Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Glu Lys Lys
 1235 1240 1245
 Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala Glu Gln
 1250 1255 1260
 Lys Gln Lys Ala Glu Glu Lys Val Ala Gln Glu Arg Leu Asp Ile Glu
 1265 1270 1275 1280
 Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu Ala Ser
 1285 1290 1295
 Lys Asn Val Leu Leu Lys Ala Ile Asp Glu Glu Arg Pro Lys Val Glu
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 Thr Asp Pro Leu Phe Arg Thr Lys Leu Lys Tyr Ile Asn Gln Asp Asp
 1315 1320 1325
 Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
 1330 1335 1340
 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln
 1345 1350 1355 1360
 Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln
 1365 1370 1375
 Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn
 1380 1385 1390
 Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu
 1395 1400 1405
 Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val
 1410 1415 1420
 Lys Thr Lys Val Lys Gly Lys Asp Val Phe Val Pro Lys Val Tyr Phe
 1425 1430 1435 1440
 Ala Ser Glu Thr Leu Val Glu Ala Gln Lys Leu Gln Gly Leu Gly Thr
 1445 1450 1455
 Gly Thr Ile Arg Val Gly Glu Ala Lys Ile Lys Ala Lys Asp Val Val
 1460 1465 1470
 Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn
 1475 1480 1485
 Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Gln Glu Thr Arg Leu
 1490 1495 1500
 Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp
 1505 1510 1515 1520
 Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His
 1525 1530 1535
 Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser
 1540 1545 1550
 Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu
 1555 1560 1565

Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro
 1570 1575 1580

Ser Ala Leu Gln Val Ala Glu Leu Asp Val Ala Gly Leu Lys Val Pro
 1585 1590 1595 1600

Leu Leu Gly Val Ser Val Ser Ile Gln Phe Ile Gln Ser Ile Leu Val
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<213> Pasteurella multocida

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cgc cag gct gaa tcg act ata tct act tcc gca cgt tat tcg act gaa 96
 Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
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cgt cat aat ggt aat att aat aat att gaa tac gaa aat gtt agt tcg 144
 Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45

ttg aaa gtt caa aaa ggg gca gct tct gta atg tat ggt agc ggt gcg 192
 Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60

tta ggt gga acc gtg gag ttt acc aca aaa gat att gag gac ttt gtc 240
 Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80

gaa cct ggt cgc cat ttg ggc ttt ttg tct aaa acc ggc tat act tca 288
 Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
 85 90 95

aaa aac aga gaa tat cgt caa gtc atc gga gtt gga ggg aaa ggg gaa 336
 Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
 100 105 110

cac ttt ttt ggt ttt gta caa tta acc aaa cgt tgg ggg cat gaa aca 384
 His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
 115 120 125

atc aac aac ggc aaa ggt aca gac att ctc ggc gaa cat cga ggt aaa 432

Ile	Asn	Asn	Gly	Lys	Gly	Thr	Asp	Ile	Leu	Gly	Glu	His	Arg	Gly	Lys		
130						135					140						
ccc	aat	ccg	ctc	aac	tac	tat	act	aca	tca	tgg	tta	acg	aaa	gtc	ggc	480	
Pro	Asn	Pro	Leu	Asn	Tyr	Tyr	Thr	Thr	Ser	Trp	Leu	Thr	Lys	Val	Gly		
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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	ggc	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		
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aat	aat	agg	aat	aaa	ttg	gat	tcg	act	atg	tcg	ttt	gta	tat	tta	caa	768	
Asn	Asn	Arg	Asn	Lys	Leu	Asp	Ser	Thr	Met	Ser	Phe	Val	Tyr	Leu	Gln		
				245					250						255		
aga	cag	aat	ata	gct	cgg	gga	gaa	ttt	tca	acg	agt	cct	tta	tat	tgg	816	
Arg	Gln	Asn	Ile	Ala	Arg	Gly	Glu	Phe	Ser	Thr	Ser	Pro	Leu	Tyr	Trp		
			260					265							270		
ggg	ccg	agt	cgc	cat	cgt	tta	tct	gcg	aaa	ttc	gaa	ttt	cgt	gat	aag	864	
Gly	Pro	Ser	Arg	His	Arg	Leu	Ser	Ala	Lys	Phe	Glu	Phe	Arg	Asp	Lys		
		275				280							285				
ttt	tta	gaa	aat	atg	aat	aag	cat	ttt	acg	ttt	cgg	ccg	tgg	caa	atc	912	
Phe	Leu	Glu	Asn	Met	Asn	Lys	His	Phe	Thr	Phe	Arg	Pro	Trp	Gln	Ile		
	290					295					300						
aat	aga	ttc	aga	caa	caa	ggc	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	ggc	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	
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
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cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta 2009
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<213> Pasteurella multocida

<400> 105

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Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45

Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
 85 90 95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
 100 105 110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
 115 120 125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
 130 135 140

Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
 145 150 155 160

Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
 165 170 175

Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
 180 185 190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
 195 200 205

Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
 210 215 220

Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
 225 230 235 240

Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
 245 250 255
 Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
 260 265 270
 Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
 275 280 285
 Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
 290 295 300
 Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
 305 310 315 320
 Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
 325 330 335
 Gly Glu Leu Leu His Leu Gly Leu Gly Gly Arg Trp Asp His Tyr Asn
 340 345 350
 Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile Asn Arg Thr Gln Arg
 355 360 365
 Leu Pro Tyr Pro Lys Thr Ser Ser Lys Phe Ser Tyr Gln Leu Ser Leu
 370 375 380
 Glu Tyr Gln Leu His Pro Ser His Gln Ile Ala Tyr Arg Leu Ser Thr
 385 390 395 400
 Gly Phe Arg Val Pro Arg Val Glu Asp Leu Tyr Phe Glu Asp Arg Gly
 405 410 415
 Lys Ser Ser Ser Gln Phe Leu Pro Asn Pro Asp Leu Gln Pro Glu Thr
 420 425 430
 Ala Leu Asn His Glu Ile Ser Tyr Arg Phe Gln Asn Gln Tyr Ala His
 435 440 445
 Phe Ser Val Gly Leu Phe Arg Thr Arg Tyr His Asn Phe Ile Gln Glu
 450 455 460
 Arg Glu Met Thr Cys Asp Lys Ile Pro Tyr Glu Tyr Asn Arg Thr Tyr
 465 470 475 480
 Gly Tyr Cys Thr His Asn Thr Tyr Val Met Phe Val Asn Glu Pro Glu
 485 490 495
 Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
 500 505 510
 Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
 515 520 525
 Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
 530 535 540
 Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
 545 550 555 560
 Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
 565 570 575

Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
 580 585 590

Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
 595 600 605

Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
 610 615 620

Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr
 625 630 635 640

Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
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Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
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gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
 20 25 30

tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 35 40 45

gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60

gag aaa gaa ~~ttt~~ gag agt ttt cct gtt caa att agt tat att tct tta 240
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80

gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta 288
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
 85 90 95

aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta 336
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
 100 105 110

gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgt 384
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys

115	120	125	
tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tcg att			432
Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile			
130	135	140	
tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt			480
Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe			
145	150	155	160
aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac			528
Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp			
	165	170	175
ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata			576
Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile			
	180	185	190
ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt			624
Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe			
	195	200	205
aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga			672
Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly			
	210	215	220
aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt			720
Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val			
	225	230	235
att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa			768
Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys			
	245	250	255
cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga			816
His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg			
	260	265	270
ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc			864
Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala			
	275	280	285
ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta			908
Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr			
	290	295	300

<210> 107

<211> 302

<212> PRT

<213> Pasteurella multocida

<400> 107

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

<210> 108

<211> 2054

<212> DNA

<213> Pasteurella multocida

<220>

<223> pnp

<220>

<221> CDS

<222> (1) .. (2052)

<400> 108

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

245										250										255									
ggc	gaa	gac	atc	agt	gaa	ggg	aaa	att	gtc	gat	att	ttc	acc	gca	ctt					816									
Gly	Glu	Asp	Ile	Ser	Glu	Gly	Lys	Ile	Val	Asp	Ile	Phe	Thr	Ala	Leu														
			260					265						270															
gaa	agc	caa	atc	gta	cgt	agc	cgt	atc	att	gct	ggc	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	ggc	cgt	aca	gtg	gat	act	gtt	cgt	gca	tta	gat	att	tgt	act	ggc					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	ggc	tct	gcg	att	ttc	acc	cgt	ggc	gaa	aca					960									
Val	Leu	Pro	Arg	Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg	Gly	Glu	Thr														
			305					310						315															
cag	gcg	tta	gct	gtc	gcg	aca	tta	ggc	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															
att	gat	gaa	tta	aca	ggc	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														
								345						350															
aac	ttc	ccg	cca	tat	tct	gtg	ggc	gaa	acc	ggc	atg	att	ggc	tca	cca					1104									
Asn	Phe	Pro	Pro	Tyr	Ser	Val	Gly	Glu	Thr	Gly	Met	Ile	Gly	Ser	Pro														
								360						365															
aaa	cgt	cgt	gaa	att	ggc	cat	ggc	cgt	tta	gcg	aaa	cgc	ggc	gta	gct					1152									
Lys	Arg	Arg	Glu	Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg	Gly	Val	Ala														
								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														
								390						395															
tct	gaa	atc	aca	gaa	tca	aat	ggc	tct	tct	tct	atg	gca	tcg	gtt	tgt					1248									
Ser	Glu	Ile	Thr	Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala	Ser	Val	Cys														
								405						410															
ggc	gcg	tct	tta	gca	tta	atg	gat	gcg	ggc	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															
gtt	gca	ggc	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															
gtg	ctt	tca	gac	atc	tta	ggc	gat	gaa	gat	cac	tta	ggc	gac	atg	gac					1392									
Val	Leu	Ser	Asp	Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly	Asp	Met	Asp														
								450						455															
ttc	aaa	gtc	gcg	ggc	aca	cgt	acg	ggc	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															
atc	aaa	atc	gaa	ggc	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															

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
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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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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 trt 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 Thr Val Gly Phe Glu 215	ttt gta cga gat gta Phe Val Arg Asp Val 220	672
caa ccc ggc gaa gcg att Gln Pro Gly Glu Ala Ile 225	tat gtc acg ttt gaa Tyr Val Thr Phe Glu 230	ggg gaa atg tat gct Gly Glu Met Tyr Ala 235	720
cag caa tgc gca gac aaa Gln Gln Cys Ala Asp 245	cca aca tta aca cct Pro Thr Leu Thr Pro 250	tgt att ttt gaa tac Cys Ile Phe Glu Tyr 255	768
gtc tat ttt gca cgt cca Val Tyr Phe Ala Arg 260	gac tct tgc atc gat Asp Ser Cys Ile Asp 265	ggg gtt tct gtt tat Gly Val Ser Val Tyr 270	816
gct gcc cgt gtt cat atg Ala Ala Arg Val His 275	gga caa cgt tta ggt Gly Gln Arg Leu Gly 280	gaa aaa att gca cgg Glu Lys Ile Ala Arg 285	864
gaa tgg gcg gat gtg gat Glu Trp Ala Asp Val 290	gat att gat gtg gtc Asp Ile Asp Val Val 295	att cct gtg cct gaa Ile Pro Val Pro Glu 300	912
acc tct aac gat att gct Thr Ser Asn Asp Ile 305	tta cgt att gcg cgc Leu Arg Ile Ala Arg 310	gtg tta aat aaa ccg Val Leu Asn Lys Pro 315	960
tat cgt caa ggt ttt gtg Tyr Arg Gln Gly Phe 325	aaa aat cgc tat gta Lys Asn Arg Tyr Val 330	gga cgt acg ttt att Arg Thr Phe Ile 335	1008
atg ccg ggg cag gca ttg Met Pro Gly Gln Ala 340	cga gtc agt tct gtt Arg Val Ser Ser Val 345	aga cgt aaa ctc aat Arg Arg Lys Leu Asn 350	1056
acc att gct tca gaa ttt Thr Ile Ala Ser Glu 355	aaa gat aag aat gtg Lys Asp Lys Asn Val 360	tta tta gtt gac gac Leu Leu Val Asp Asp 365	1104
tcg att gta cgt ggt acc Ser Ile Val Arg Gly 370	acg tct gaa caa att Thr Ser Glu Gln Ile 375	gtc gaa atg gcg aga Val Glu Met Ala Arg 380	1152
gcg gca ggt gcg aag aaa Ala Ala Gly Ala Lys 385	att tat ttt gcc tct Ile Tyr Phe Ala Ser 390	gct gca cca gaa att Ala Ala Pro Glu Ile 395	1200
cgt tat cca aat gtg tat Arg Tyr Pro Asn Val 405	ggt att gat atg cca Gly Ile Asp Met Pro 410	acc aaa aat gaa ttg Thr Lys Asn Glu Leu 415	1248
atc gct tat ggt cgt gat Ile Ala Tyr Gly Arg 420	gta gat gaa att gct Val Asp Glu Ile Ala 425	aac tta att ggt gtg Asn Leu Ile Gly Val 430	1296
gat aaa ttg att ttc caa Asp Lys Leu Ile Phe 435	gat ttg gat gcg tta Leu Asp Ala Leu Thr 440	act ggt tct gtg caa Thr Gly Ser Val Gln 445	1344

caa gaa aat cca agt att caa gac ttt gat tgt tct 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
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<210> 111

<211> 504

<212> PRT

<213> Pasteurella multocida

<400> 111

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

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

<210> 112

<211> 989

<212> DNA

<213> Pasteurella multocida

<220>

<223> rci

<220>

<221> CDS

<222> (1)..(987)

<400> 112

atg gca aca ata aga aaa cgt ggt aac tca tat cgt gct gag ata agc	48
Met Ala Thr Ile Arg Lys Arg Gly Asn Ser Tyr Arg Ala Glu Ile Ser	
1 5 10 15	
aaa aac gga gta agg aaa tca gca aca ttt aag act aaa tca gaa gct	96
Lys Asn Gly Val Arg Lys Ser Ala Thr Phe Lys Thr Lys Ser Glu Ala	
20 25 30	
aat gcg tgg gct gtt gac gag gag aga aaa tta gct gat ttg gca aaa	144
Asn Ala Trp Ala Val Asp Glu Glu Arg Lys Leu Ala Asp Leu Ala Lys	
35 40 45	
ggt atc gct cca gat att att ttt aga gat gta ata gaa cgc tat caa	192
Gly Ile Ala Pro Asp Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln	
50 55 60	
aat gaa gtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga	240
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg	
65 70 75 80	
tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat	288
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp	
85 90 95	
tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa	336
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu	
100 105 110	
gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg	384
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val	
115 120 125	
ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg	432
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met	
130 135 140	
act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat	480
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr	
145 150 155 160	
tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa	528
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu	
165 170 175	
gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta	576
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu	
180 185 190	
ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa	624
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys	
195 200 205	
tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act	672
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr	

210	215	220	
aaa aac ggg cac tct aga gat gtg ccg ctt tcg caa aga gct gtt gcg			720
Lys Asn Gly His Ser Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala			
225	230	235	240
cta att tta aaa atg aaa gag gta gaa aat gga gat ctt gtg ttt cag			768
Leu Ile Leu Lys Met Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln			
	245	250	255
acc acg cct gaa tca tta agc acc acg ttt aga gtg tta aag aaa gag			816
Thr Thr Pro Glu Ser Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu			
	260	265	270
tgt gga ctt gaa cat ctc cat ttt cat gat acg aga agg gaa gcg ttg			864
Cys Gly Leu Glu His Leu His Phe His Asp Thr Arg Arg Glu Ala Leu			
	275	280	285
acg aga tta tct aag aaa gta gat gta atg act cta gcc aaa att agc			912
Thr Arg Leu Ser Lys Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser			
	290	295	300
gga cat aga gat tta aga att tta caa aac aca tat tac gca ccg aat			960
Gly His Arg Asp Leu Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn			
305	310	315	320
atg agt gaa gtg gca aac ttg ttg gat ta			989
Met Ser Glu Val Ala Asn Leu Leu Asp			
	325		

<210> 113

<211> 329

<212> PRT

<213> Pasteurella multocida

<400> 113

Met	Ala	Thr	Ile	Arg	Lys	Arg	Gly	Asn	Ser	Tyr	Arg	Ala	Glu	Ile	Ser
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Lys	Asn	Gly	Val	Arg	Lys	Ser	Ala	Thr	Phe	Lys	Thr	Lys	Ser	Glu	Ala
			20					25					30		

Asn	Ala	Trp	Ala	Val	Asp	Glu	Glu	Arg	Lys	Leu	Ala	Asp	Leu	Ala	Lys
		35					40					45			

Gly	Ile	Ala	Pro	Asp	Ile	Ile	Phe	Arg	Asp	Val	Ile	Glu	Arg	Tyr	Gln
	50					55					60				

Asn	Glu	Val	Ser	Ile	Thr	Lys	Lys	Gly	Ala	Arg	Asn	Glu	Ile	Ile	Arg
65					70					75					80

Leu	Asn	Arg	Phe	Leu	Arg	Tyr	Asp	Ile	Ser	Asn	Leu	Tyr	Ile	Arg	Asp
			85						90					95	

Leu	Arg	Lys	Glu	Asp	Phe	Glu	Glu	Trp	Ile	Arg	Ile	Arg	Leu	Thr	Glu
			100					105					110		

Val	Ser	Asp	Ala	Ser	Val	Arg	Arg	Glu	Leu	Val	Thr	Ile	Ser	Ser	Val
		115					120					125			

Leu	Thr	Thr	Ala	Ile	Asn	Lys	Trp	Gly	Tyr	Ile	Ser	Arg	His	Pro	Met

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

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

gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att gca ggg 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

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

245										250										255									
atg	cag	tta	aat	gtc	acg	caa	ggt	aca	gtg	aca	att	ggg	gtg	gat	gga														
Met	Gln	Leu	Asn	Val	Thr	Gln	Gly	Thr	Val	Thr	Ile	Gly	Val	Asp	Gly														816
			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														
					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														
					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														
					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	
ggg 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

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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

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

Glu Asn Gln Gly Gly Tyr Leu Ile Asn Gln Gly Lys Ser Leu Leu His
 645 650 655

Ser Glu Gly Ala Met Asn Leu Thr Ala Asp Arg Thr Val Tyr Asn Leu
 660 665 670

Gly Asn Ile Phe Ala Lys Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu
 675 680 685

Ile Asn Asp Val Thr Leu Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys
 690 695 700

Lys Asp Tyr Thr Arg Tyr Tyr Arg Ile Asn Glu Thr Ala Lys His Gly
 705 710 715 720

Trp His Asn Asn Phe Tyr Glu Leu Asn Val Asp Arg Val Ser
 725 730

<210> 118
 <211> 251
 <212> DNA
 <213> Pasteurella multocida

<220>
 <223> unkO

<220>
 <221> CDS
 <222> (1)..(249)

<400> 118
 atg aaa att act att aca cga aat cat cca gaa gta ttt caa gaa tcc 48
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1 5 10 15

gct cgt tta gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca 96
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
 20 25 30

tta aca ttg gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt 144
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
 35 40 45

gag gag gaa agc aaa agg gga cat agt att aag gtt gta tta aaa gga 192
 Glu Glu Glu Ser Lys Arg Gly His Ser Ile Lys Val Val Leu Lys Gly
 50 55 60

agt cac gaa gtt att aag tca gag gtg aat aca aat gaa aaa aat cat 240
 Ser His Glu Val Ile Lys Ser Glu Val Asn Thr Asn Glu Lys Asn His
 65 70 75 80

tgt aat cat ta 251
 Cys Asn His

<210> 119
 <211> 83
 <212> PRT
 <213> Pasteurella multocida

<400> 119

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

<210> 120

<211> 548

<212> DNA

<213> Pasteurella multocida

<220>

<223> unkP

<220>

<221> CDS

<222> (1) .. (546)

<400> 120

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

115	120	125	
aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat			432
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp			
130	135	140	
gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa			480
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu			
145	150	155	160
cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt			528
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe			
	165	170	175
tca aat cgt tta gca tcg ta			548
Ser Asn Arg Leu Ala Ser			
180			

<210> 121

<211> 182

<212> PRT

<213> Pasteurella multocida

<400> 121

Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser	
1	15
Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe	
20	30
Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly	
35	45
Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg	
50	60
Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr	
65	80
Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val	
85	95
Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile	
100	110
Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly	
115	125
Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp	
130	140
Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu	
145	160
Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe	
165	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 69
 Asp Lys Phe Lys Ile Leu Ser
 20

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

210

215

<210> 128
 <211> 242
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> apvC

<220>
 <221> CDS
 <222> (1)..(240)

<400> 128
 atg tgg cgg atg gga gat ttt atg tct aaa 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
 ggt ttg caa aat tta tcg atg agg aaa atc gca agt gaa gcc ggt atc 144
 Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
 35 40 45
 gca aca ggc acg ctt tat ctc tat ttc aaa acg aaa gac gag tta ctg 192
 Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
 50 55 60
 gat tgt ttg gcg gaa caa tta cat gaa cga tat tat cgt tat ctg aat 240
 Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
 65 70 75 80
 at 242

<210> 129
 <211> 80
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 129
 Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1 5 10 15
 Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
 20 25 30
 Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
 35 40 45
 Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
 50 55 60
 Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
 65 70 75 80

<210> 130

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

<220>
 <223> apvD

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

<400> 130
 aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa 48
 Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
 1 5 10 15
 caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96
 Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
 20 25 30
 gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144
 Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
 35 40 45
 gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192
 Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
 50 55 60
 gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa 240
 Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
 65 70 75 80
 ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg 288
 Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
 85 90 95
 aca agc caa aag gaa aca gaa gaa gca aaa agt aga tta aat acg gcc 336
 Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
 100 105 110
 aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384
 Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
 115 120 125
 aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
 130 135 140
 cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
 145 150 155 160
 tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
 165 170 175

<210> 131
 <211> 175
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 131

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

Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
 20 25 30

Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
 35 40 45

Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
 50 55 60

Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
 65 70 75 80

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

Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
 100 105 110

Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
 115 120 125

Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
 130 135 140

Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
 145 150 155 160

Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
 165 170 175

<210> 132

<211> 867

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> atpG

<220>

<221> CDS

<222> (1)..(864)

<400> 132

atg gca ggt gcg aaa gag ata aga acc aaa att gca agt gtg aaa aat 48
 Met Ala Gly Ala Lys Glu Ile Arg Thr Lys Ile Ala Ser Val Lys Asn
 1 5 10 15

act caa aaa atc acc aaa gca atg gaa atg gtt gct acc tct aaa atg 96
 Thr Gln Lys Ile Thr Lys Ala Met Glu Met Val Ala Thr Ser Lys Met
 20 25 30

cgt aaa acg caa gag cgt atg gct gcc agt cgt cct tat tct 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 His Pro Phe Leu Thr Glu Arg Asp Ile Lys Lys Val Gly Tyr Leu Val 65 70 75 80			240
ggt tcg acc gat cgc ggt tta tgc ggt ggc ctt aat atc aat tta ttc Val Ser Thr Asp Arg Gly Leu Cys Gly Gly Leu Asn Ile Asn Leu Phe 85 90 95			288
aaa gcg act ttg aat gaa ttt aaa acg tgg aaa gat aaa gac gtt agt Lys Ala Thr Leu Asn Glu Phe Lys Thr Trp Lys Asp Lys Asp Val Ser 100 105 110			336
ggt gag ctt ggt tta gta ggg tcg aaa ggc gta agc ttt tac caa aat Val Glu Leu Gly Leu Val Gly Ser Lys Gly Val Ser Phe Tyr Gln Asn 115 120 125			384
cta ggc tta aac gtg aga tct caa gta acg gga tta ggc gat aat ccg Leu Gly Leu Asn Val Arg Ser Gln Val Thr Gly Leu Gly Asp Asn Pro 130 135 140			432
gaa atg gaa cgt atc gtg ggc gca gtt aat gaa atg att aat gcg ttc Glu Met Glu Arg Ile Val Gly Ala Val Asn Glu Met Ile Asn Ala Phe 145 150 155 160			480
cga aac gga gaa gtg gat gcg gtt tac gtc gct tac aac cgt ttt gaa Arg Asn Gly Glu Val Asp Ala Val Tyr Val Ala Tyr Asn Arg Phe Glu 165 170 175			528
aat acg atg tca caa aaa cct gtt atc gca cag tta ctt ccg tta cct Asn Thr Met Ser Gln Lys Pro Val Ile Ala Gln Leu Leu Pro Leu Pro 180 185 190			576
aaa cta gat gac gat gaa tta gat acg aaa ggt tca tgg gat tat att Lys Leu Asp Asp Asp Glu Leu Asp Thr Lys Gly Ser Trp Asp Tyr Ile 195 200 205			624
tat gaa ccg aat cca caa gtt tta ttg gat agt tta ctt gtt cgt tat Tyr Glu Pro Asn Pro Gln Val Leu Leu Asp Ser Leu Leu Val Arg Tyr 210 215 220			672
tta gaa act cag gta tac caa gca gtt gta gat aac cta gct tct gaa Leu Glu Thr Gln Val Tyr Gln Ala Val Val Asp Asn Leu Ala Ser Glu 225 230 235 240			720
caa gcc gct cga atg gta gcg atg aaa gcc gca aca gat aat gcg ggt Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly 245 250 255			768
aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala 260 265 270			816
agc att aca aat gaa tta aac gaa att gtt gcg ggt gcc gca gca att Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile 275 280 285			864
taa			867

<210> 133

<211> 288

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 133

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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

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<210> 134

<211> 534

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> atpH

<220>

<221> CDS

<222> (1)..(531)

<400> 134

atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt	48
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe	
1 5 10 15	
gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta	96
Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu	
20 25 30	
cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att	144
Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile	
35 40 45	
aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc	192
Asn Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile	
50 55 60	
tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg	240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met	
65 70 75 80	
gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc	288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe	
85 90 95	
gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt	336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val	
100 105 110	
tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg	384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala	
115 120 125	
atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat	432
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp	
130 135 140	
aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att	480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile	
145 150 155 160	
gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc	528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser	
165 170 175	
ttg taa	534
Leu	

<210> 135

<211> 177

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 135

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

<210> 136

<211> 321

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> dksA

<220>

<221> CDS

<222> (1)..(318)

<400> 136

gca tgg cat gtg caa att atg gac gaa gct gag cgt aca aaa aac caa 48
 Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1 5 10 15
 atg cag gaa gaa gtc gct aat ttc gcc gat cct gcg gac cgc gcc act 96
 Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
 20 25 30
 cag gaa gaa gaa ttc agt ctt gaa tta aga aac cgt gac cgt gag cgt 144

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
 35 40 45

aaa ttg ctt aag aag att gag caa acg tta aat agc att gcc gaa gac 192
 Lys Leu Leu Lys Lys Ile Glu Gln Thr Leu Asn Ser Ile Ala Glu Asp
 50 55 60

gaa tac ggc tat tgc gaa act tgc ggt gtt gaa atc ggt tta cgt cgt 240
 Glu Tyr Gly Tyr Cys Glu Thr Cys Gly Val Glu Ile Gly Leu Arg Arg
 65 70 75 80

tta gaa gcg cgc ccg acc gcg gat atg tgt atc gat tgc aaa aca ctt 288
 Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
 85 90 95

gcg gaa atc cgt gaa aag caa atg ggc tta taa 321
 Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
 100 105

<210> 137
 <211> 106
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 137
 Ala Trp His Val Gln Ile Met Asp Glu Ala Glu Arg Thr Lys Asn Gln
 1 5 10 15

Met Gln Glu Glu Val Ala Asn Phe Ala Asp Pro Ala Asp Arg Ala Thr
 20 25 30

Gln Glu Glu Glu Phe Ser Leu Glu Leu Arg Asn Arg Asp Arg Glu Arg
 35 40 45

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

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

Leu Glu Ala Arg Pro Thr Ala Asp Met Cys Ile Asp Cys Lys Thr Leu
 85 90 95

Ala Glu Ile Arg Glu Lys Gln Met Gly Leu
 100 105

<210> 138
 <211> 33
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> dnaK

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

<400> 138
 gct gag ttt gaa gaa gtg aaa gat aat aaa taa 33

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
 1 5 10

<210> 139

<211> 10

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 139

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
 1 5 10

<210> 140

<211> 453

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> exbB

<220>

<221> CDS

<222> (1)..(450)

<400> 140

atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48
 Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
 1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96
 Leu Gly Leu Leu Leu 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
 Ala Arg Lys Ala Asn Gln
 145 150

453

<210> 141
 <211> 150
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 141
 Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
 1 5 10 15
 Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
 20 25 30
 Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
 35 40 45
 Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
 50 55 60
 Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
 65 70 75 80
 Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
 85 90 95
 Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
 100 105 110
 Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
 115 120 125
 Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
 130 135 140
 Ala Arg Lys Ala Asn Gln
 145 150

<210> 142
 <211> 720
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> fkpA

<220>
 <221> CDS
 <222> (1) .. (717)

<400> 142
 atg tta aaa aat aaa ctt tct gtt ctt gca atc gta gcc ggt acg ttc 48
 Met Leu Lys Asn Lys Leu Ser Val Leu Ala Ile Val Ala Gly Thr Phe
 1 5 10 15
 gtt 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

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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

gtt 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

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<210> 143

<211> 239

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 143

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

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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 Gly Tyr Gln Leu Gly Lys Gln
 1 5 10 15

cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95
 Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn

	20	25	30	
ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct				143
Leu Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser				
	35	40	45	
cag tgc tta acc cat cat tta tgg gaa cgt tta gaa gaa caa atc ggt				191
Gln Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly				
	50	55	60	
gtg ttt tta aat acg att act tta gcg gaa ctt gtt gaa gaa cat tcg				239
Val Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser				
	65	70	75	
gat cac gat tgt gaa aaa gaa cat tgc cac gat cat tca cac aaa cat				287
Asp His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His				
	80	85	90	95
taa				290

<210> 145

<211> 95

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 145

His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln Pro			
1	5	10	15

Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn Leu			
	20	25	30

Asp Val Thr Lys Cys Lys Gly Ser Gly Asn Cys Ser Lys Asn Ser Gln			
	35	40	45

Cys Leu Thr His His Leu Trp Glu Arg Leu Glu Glu Gln Ile Gly Val			
	50	55	60

Phe Leu Asn Thr Ile Thr Leu Ala Glu Leu Val Glu Glu His Ser Asp			
	65	70	75

His Asp Cys Glu Lys Glu His Cys His Asp His Ser His Lys His			
	85	90	95

<210> 146

<211> 273

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> hupA

<220>

<221> CDS

<222> (1) .. (270)

<400> 146

atg aac aaa act gag tta atc gat gca atc gca gct ggt gca gag tta			
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu			
1	5	10	15


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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

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<210> 147
 <211> 90
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

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<400> 147
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu
  1                      5                      10                      15

Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile
      20                      25                      30

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

Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg
      50                      55                      60

Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val
      65                      70                      75                      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

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gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca 96
 Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
 20 25 30

gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta 144
 Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
 35 40 45

ggt tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa 192
 Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
 50 55 60

gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac 240
 Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
 65 70 75 80

att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa 288
 Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
 85 90 95

tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta 336
 Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
 100 105 110

gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt 384
 Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
 115 120 125

gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432
 Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
 130 135 140

gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480
 Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
 145 150 155 160

ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
 165 170 175

gaa aaa att act cat tat ggg cc 551
 Glu Lys Ile Thr His Tyr Gly
 180

<210> 149

<211> 183

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 149

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

Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
 20 25 30

Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
 35 40 45

Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
 50 55 60

Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
65 70 75 80

Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
85 90 95

Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
100 105 110

Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
115 120 125

Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
130 135 140

Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
145 150 155 160

Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
165 170 175

Glu Lys Ile Thr His Tyr Gly
180

<210> 150

<211> 1095

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> Omp5-2

<220>

<221> CDS

<222> (1) .. (1092)

<400> 150

atg aaa aaa tca tta gtt gct tta aca gta tta tcg gct gca gcg gta	48
Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala 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	
ggg 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
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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Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val	
1 5 10 15	
gct caa gca gct cca caa caa aat act ttc tac gca ggt gcg aaa gtt	96
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val	
20 25 30	
ggt caa tca tca ttt cac cac ggt gtt aac caa tta aaa tct ggt cac	144
Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His	
35 40 45	
gat gat cgt tat aat gat aaa aca cgt aag tat ggt atc aac cgt aac	192
Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn	
50 55 60	
tct gta act tac ggt gta ttc ggc ggt tac caa atc tta aac caa aat	240
Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn	
65 70 75 80	
aac ttc ggt tta gca gct gaa tta ggc tat gac tac tac ggt cgc gta	288
Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val	
85 90 95	
cgt ggt aac gta gat gaa ttc cgt aca gtt aaa cac tct gct cac ggt	336
Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly	
100 105 110	

tta aac tta gcg tta aaa cca agc tac gaa gta tta cct gac tta gac	384
Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp	
115 120 125	
ggt tac ggt aaa gta ggt att gcg gtt gtt cgt aat gac tat aaa aaa	432
Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys	
130 135 140	
tat ggt gcg gaa aac act aac gaa tca aca aca aaa ttc cac aaa tta	480
Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu	
145 150 155 160	
aaa gca tca act att tta ggt gca ggt gtt gag tac gca att ctt cct	528
Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro	
165 170 175	
gaa tta gcg gca cgt gtt gaa tac caa tac tta aac aaa gcg ggt aac	576
Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn	
180 185 190	
tta aat aaa gca tta gtt cgt tca ggc aca caa gat gtg gac ttc caa	624
Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln	
195 200 205	
tat gct cct gat atc cac tct gta aca gca ggt tta tca tac cgt ttc	672
Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe	
210 215 220	
ggt caa ggc gct gta gca cca gtt gtt gag cca gaa gtt gta act aaa	720
Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys	
225 230 235 240	
aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc	768
Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser	
245 250 255	
tta aaa cca gca gca gca aca gct tta gac gca gct aac act gaa atc	816
Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile	
260 265 270	
gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca	864
Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr	
275 280 285	
gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt	912
Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg	
290 295 300	
gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca	960
Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala	
305 310 315 320	
aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca	1008
Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala	
325 330 335	
aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca	1056
Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala	
340 345 350	
ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct	1104
Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala	

355 360 365 1110

atg taa
Met

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

<400> 153
Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
1 5 10 15
Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
20 25 30
Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
35 40 45
Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
50 55 60
Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
65 70 75 80
Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
85 90 95
Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
100 105 110
Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
115 120 125
Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
130 135 140
Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
145 150 155 160
Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
165 170 175
Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
180 185 190
Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
195 200 205
Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
210 215 220
Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
225 230 235 240
Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
245 250 255
Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
260 265 270

Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
 275 280 285

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

Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
 305 310 315 320

Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
 325 330 335

Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
 340 345 350

Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
 355 360 365

Met

<210> 154
 <211> 1076
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> pnp new

<220>
 <221> CDS
 <222> (1)..(1074)

<400> 154
 aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg 48
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 1 5 10 15

gtt 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 gcg 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	
ggg 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	
ggg tgc 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	
ggg gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg	624
Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val	
195 200 205	
cgc gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct	672
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala	
210 215 220	
tcc gta tgc ggc gca tct tta gcg tta atg gac gca ggc gta ccg att	720
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile	
225 230 235 240	
aaa gcg gcg gtt gcg ggt atc gca atg ggc tta gtg aaa gaa gaa gaa	768
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu	
245 250 255	
aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc	816
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly	
260 265 270	
gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt	864
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu	
275 280 285	
caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc	912
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile	
290 295 300	
gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg	960
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met	
305 310 315 320	
gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct	1008
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro	
325 330 335	
cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc	1056
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile	
340 345 350	
ggg aaa ggc ggt gcg gtt at	1076
Gly Lys Gly Gly Ala Val	

355

<210> 155

<211> 358

<212> PRT

<213> *Actinobacillus pleuropneumoniae*

<400> 155

Asn	Ile	Lys	Glu	Phe	Val	Lys	Glu	Ala	Gly	Lys	Pro	Arg	Trp	Asp	Trp
1				5					10					15	

Val	Ala	Pro	Glu	Pro	Asn	Thr	Ala	Leu	Ile	Asn	Gln	Val	Lys	Ala	Leu
			20					25					30		

Ala	Glu	Ala	Arg	Ile	Gly	Asp	Ala	Tyr	Arg	Ile	Thr	Glu	Lys	Gln	Ala
		35					40					45			

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

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

Thr	Ala	Leu	Glu	Ser	Ser	Ile	Val	Arg	Gly	Arg	Ile	Ile	Ala	Gly	Glu
				85					90					95	

Pro	Arg	Ile	Asp	Gly	Arg	Thr	Val	Asp	Thr	Val	Arg	Ala	Leu	Asp	Ile
			100					105					110		

Cys	Thr	Gly	Val	Leu	Pro	Arg	Thr	His	Gly	Ser	Ala	Ile	Phe	Thr	Arg
		115					120					125			

Gly	Glu	Thr	Gln	Ala	Leu	Ala	Val	Ala	Thr	Leu	Gly	Thr	Glu	Arg	Asp
	130				135						140				

Ala	Gln	Ile	Val	Asp	Glu	Leu	Thr	Gly	Glu	Lys	Ser	Asp	Arg	Phe	Leu
145					150					155					160

Phe	His	Tyr	Asn	Phe	Pro	Pro	Tyr	Ser	Val	Gly	Glu	Thr	Gly	Arg	Ile
			165						170					175	

Gly	Ser	Pro	Lys	Arg	Arg	Glu	Ile	Gly	His	Gly	Arg	Leu	Ala	Lys	Arg
			180					185					190		

Gly	Val	Leu	Ala	Val	Met	Pro	Thr	Ala	Glu	Glu	Phe	Pro	Tyr	Val	Val
	195						200					205			

Arg	Val	Val	Ser	Glu	Ile	Thr	Glu	Ser	Asn	Gly	Ser	Ser	Ser	Met	Ala
	210					215					220				

Ser	Val	Cys	Gly	Ala	Ser	Leu	Ala	Leu	Met	Asp	Ala	Gly	Val	Pro	Ile
225					230					235					240

Lys	Ala	Ala	Val	Ala	Gly	Ile	Ala	Met	Gly	Leu	Val	Lys	Glu	Glu	Glu
			245						250					255	

Lys	Phe	Val	Val	Leu	Ser	Asp	Ile	Leu	Gly	Asp	Glu	Asp	His	Leu	Gly
		260						265					270		

Asp	Met	Asp	Phe	Lys	Val	Ala	Gly	Thr	Arg	Glu	Gly	Val	Thr	Ala	Leu
	275						280						285		

Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile
 290 295 300

Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met
 305 310 315 320

Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro
 325 330 335

Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile
 340 345 350

Gly Lys Gly Gly Ala Val
 355

<210> 156
 <211> 1055
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> potD

<220>
 <221> CDS
 <222> (1) .. (1053)

<400> 156
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 Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
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tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct 96
 Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala
 20 25 30

caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat 144
 Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr
 35 40 45

gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa 192
 Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys
 50 55 60

gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta 240
 Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu
 65 70 75 80

aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac 288
 Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn
 85 90 95

tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat 336
 Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp
 100 105 110

cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac 384
 His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn
 115 120 125

aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt 432

Lys	Pro	Tyr	Asp	Gln	Gly	Asn	Lys	Tyr	Ser	Leu	Pro	Gln	Leu	Leu	Gly		
130						135					140						
gca	ccg	ggt	atc	gca	ttt	aac	tca	aat	gac	tat	aag	ggc	gat	gcg	ttc	480	
Ala	Pro	Gly	Ile	Ala	Phe	Asn	Ser	Asn	Asp	Tyr	Lys	Gly	Asp	Ala	Phe		
145					150					155					160		
act	tct	tgg	ggt	gat	tta	tgg	aaa	cct	gag	ttt	gcg	aat	aaa	gta	caa	528	
Thr	Ser	Trp	Gly	Asp	Leu	Trp	Lys	Pro	Glu	Phe	Ala	Asn	Lys	Val	Gln		
				165					170					175			
tta	tta	gat	gac	gca	cgt	gaa	gta	ttt	aac	att	gcg	tta	tta	aaa	tta	576	
Leu	Leu	Asp	Asp	Ala	Arg	Glu	Val	Phe	Asn	Ile	Ala	Leu	Leu	Lys	Leu		
				180				185						190			
ggt	aaa	aac	cct	aat	aca	acc	aat	ccg	gaa	gag	att	aaa	gcg	gct	tac	624	
Gly	Lys	Asn	Pro	Asn	Thr	Thr	Asn	Pro	Glu	Glu	Ile	Lys	Ala	Ala	Tyr		
		195					200					205					
gaa	gag	tta	aga	aaa	tta	cgt	cca	aac	gta	ctt	tct	ttc	act	tca	gac	672	
Glu	Glu	Leu	Arg	Lys	Leu	Arg	Pro	Asn	Val	Leu	Ser	Phe	Thr	Ser	Asp		
	210					215					220						
aac	cca	gcg	aac	tca	ttt	atc	gca	ggt	gaa	gta	tct	gta	ggt	caa	tta	720	
Asn	Pro	Ala	Asn	Ser	Phe	Ile	Ala	Gly	Glu	Val	Ser	Val	Gly	Gln	Leu		
225					230					235					240		
tgg	aac	ggt	tct	gta	cgt	att	gcg	aaa	aaa	gaa	caa	gcg	ccg	gta	aac	768	
Trp	Asn	Gly	Ser	Val	Arg	Ile	Ala	Lys	Lys	Glu	Gln	Ala	Pro	Val	Asn		
				245					250					255			
atg	gtg	ttc	cca	aaa	gaa	ggt	cct	gta	ctt	tgg	gtt	gat	acg	tta	gcc	816	
Met	Val	Phe	Pro	Lys	Glu	Gly	Pro	Val	Leu	Trp	Val	Asp	Thr	Leu	Ala		
			260					265					270				
att	ccg	gcg	aat	gcg	aaa	aac	aaa	gaa	aat	gcg	cat	aag	tta	atc	aac	864	
Ile	Pro	Ala	Asn	Ala	Lys	Asn	Lys	Glu	Asn	Ala	His	Lys	Leu	Ile	Asn		
		275					280					285					
tac	tta	tta	agc	gca	ccg	gtt	gcg	gaa	aaa	tta	acg	tta	gaa	atc	ggt	912	
Tyr	Leu	Leu	Ser	Ala	Pro	Val	Ala	Glu	Lys	Leu	Thr	Leu	Glu	Ile	Gly		
	290					295					300						
tat	ccg	act	tca	aac	gta	gaa	gcg	tta	aaa	aca	tta	cca	aaa	gag	att	960	
Tyr	Pro	Thr	Ser	Asn	Val	Glu	Ala	Leu	Lys	Thr	Leu	Pro	Lys	Glu	Ile		
305					310					315					320		
acc	gaa	gat	ccg	gca	atc	tat	ccg	aca	gct	gat	gtg	tta	aaa	gcg	gca	1008	
Thr	Glu	Asp	Pro	Ala	Ile	Tyr	Pro	Thr	Ala	Asp	Val	Leu	Lys	Ala	Ala		
				325					330					335			
caa	tgg	caa	gac	gat	gta	ggt	aat	gca	atc	gaa	ctt	tac	gaa	aaa	ta	1055	
Gln	Trp	Gln	Asp	Asp	Val	Gly	Asn	Ala	Ile	Glu	Leu	Tyr	Glu	Lys			
			340					345					350				

<210> 157

<211> 351

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 157

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

Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys
 340 345 350

<210> 158

<211> 525

<212> DNA

<213> Actinobacillus pleuropneumoniae

<220>

<223> rpmF

<220>

<221> CDS

<222> (1) .. (522)

<400> 158

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Met	Gln	Lys	Val	Lys	Leu	Pro	Leu	Thr	Ile	Asp	Pro	Tyr	Lys	Asp	Ala	
1				5					10					15		
cag	cgt	cga	atg	gat	tac	gaa	ggc	tac	atc	tca	cgt	agt	ctg	ctt	aat	96
Gln	Arg	Arg	Met	Asp	Tyr	Glu	Gly	Tyr	Ile	Ser	Arg	Ser	Leu	Leu	Asn	
			20					25					30			
cgt	ttg	ggc	gaa	tct	gtg	agc	aat	gtg	cta	agc	gat	gca	caa	gtt	act	144
Arg	Leu	Gly	Glu	Ser	Val	Ser	Asn	Val	Leu	Ser	Asp	Ala	Gln	Val	Thr	
		35					40					45				
ctc	tcg	tta	tat	atc	gat	cgc	caa	cgc	tta	acc	gtt	att	aaa	ggc	acg	192
Leu	Ser	Leu	Tyr	Ile	Asp	Pro	Gln	Arg	Leu	Thr	Val	Ile	Lys	Gly	Thr	
	50					55					60					
gcg	aca	gtg	gaa	gtg	gaa	ttc	gat	tgc	caa	cga	tgc	ggc	aac	ccg	ttt	240
Ala	Thr	Val	Glu	Val	Glu	Phe	Asp	Cys	Gln	Arg	Cys	Gly	Asn	Pro	Phe	
65					70				75						80	
aca	caa	acg	ctt	gac	tgt	tcg	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	ggc	gaa	gta	aat	tta	cta	gat	atg	atc	gaa	gat	gga	ttt	atc	384
Glu	Phe	Gly	Glu	Val	Asn	Leu	Leu	Asp	Met	Ile	Glu	Asp	Gly	Phe	Ile	
		115					120					125				
atc	gaa	ttg	cct	cta	gtc	ccg	atg	cat	agt	gaa	gaa	cac	tgt	gaa	gtg	432
Ile	Glu	Leu	Pro	Leu	Val	Pro	Met	His	Ser	Glu	Glu	His	Cys	Glu	Val	
		130				135						140				
tcc	gtg	agt	gaa	cag	gtg	ttt	ggc	gaa	ttg	cct	gaa	gaa	ttg	gcg	aaa	480
Ser	Val	Ser	Glu	Gln	Val	Phe	Gly	Glu	Leu	Pro	Glu	Glu	Leu	Ala	Lys	
145					150					155					160	
aaa	cct	aac	ccg	ttc	gct	gta	tta	gct	aat	tta	aag	aaa	aac	tag		525
Lys	Pro	Asn	Pro	Phe	Ala	Val	Leu	Ala	Asn	Leu	Lys	Lys	Asn			
				165					170							

<210> 159
 <211> 174
 <212> PRT
 <213> Actinobacillus pleuropneumoniae

<400> 159
 Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala
 1 5 10 15
 Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
 20 25 30
 Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
 35 40 45
 Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
 50 55 60
 Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
 65 70 75 80
 Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
 85 90 95
 Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
 100 105 110
 Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
 115 120 125
 Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
 130 135 140
 Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
 145 150 155 160
 Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
 165 170

<210> 160
 <211> 1302
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> tig

<220>
 <221> CDS
 <222> (1) .. (1299)

<400> 160
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 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	ggc	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	ggc	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	ggt	gaa	tta	aaa	ggc	tta	gaa	aat	atc	gaa	ggt	gaa	aaa	ccg	384
Pro	Glu	Val	Glu	Leu	Lys	Gly	Leu	Glu	Asn	Ile	Glu	Val	Glu	Lys	Pro	
	115					120					125					
ggt	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	ggt	gta	atc	gac	ttc	gta	ggc	tct	gta	gac	ggc	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	ggc	aaa	gcg	aca	gac	ttc	act	tta	gca	atg	ggc	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	ggc	ttt	gaa	gaa	ggc	atc	ggt	ggc	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	ggt	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	ggc	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		
ggc	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	ggt	aaa	aac	caa	864
Met	Gln	Arg	Glu	Leu	Lys	Asn	Ala	Val	Thr	Ala	Arg	Val	Lys	Asn	Gln	
		275					280					285				

gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca 912
 Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
 290 295 300

gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt 960
 Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
 305 310 315 320

ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc 1008
 Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
 325 330 335

gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc 1056
 Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
 340 345 350

gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa 1104
 Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
 355 360 365

acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt 1152
 Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
 370 375 380

gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta 1200
 Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
 385 390 395 400

gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta 1248
 Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
 405 410 415

act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa 1296
 Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
 420 425 430

ggc taa 1302
 Gly

<210> 161

<211> 433

<212> PRT

<213> Actinobacillus pleuropneumoniae

<400> 161

Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
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Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
 20 25 30

Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
 35 40 45

Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
 50 55 60

Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
 65 70 75 80

Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn

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

Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
 420 425 430

Gly

<210> 162
 <211> 316
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> tRNA-glu

<400> 162
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 ggcctaggac atcgcccttt cacggcggtt accgggggttc gaatccccgt ggggacgcca 120
 tttaaagatg acttttggtg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180
 tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
 agctgaacaa aagcagctaa gtgttttagt gaataaagta tcgcgttgaa tgcgttcaaa 300
 taaaatttga aaatat 316

<210> 163
 <211> 85
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> tRNA-leu

<400> 163
 gctctggtgg tggaattggt agacacgcta tcttgagggg gtagtgtcca taggatgtgc 60
 gagttcgagt ctgcccaga gcacc 85

<210> 164
 <211> 623
 <212> DNA
 <213> Actinobacillus pleuropneumoniae

<220>
 <223> yaeE

<220>
 <221> CDS
 <222> (1)..(621)

<400> 164
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 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

PATENT COOPERATION TREATY

PCT

INTERNATIONAL SEARCH REPORT

(PCT Article 18 and Rules 43 and 44)

Applicant's or agent's file reference 28341/6227.1	FOR FURTHER ACTION see Notification of Transmittal of International Search Report (Form PCT/ISA/220) as well as, where applicable, item 5 below.	
International application No. PCT/US 00/ 09218	International filing date (day/month/year) 06/04/2000	(Earliest) Priority Date (day/month/year) 09/04/1999
Applicant PHARMA & UPJOHN , INC.		

This International Search Report has been prepared by this International Searching Authority and is transmitted to the applicant according to Article 18. A copy is being transmitted to the International Bureau.

This International Search Report consists of a total of 7 sheets.

☐ It is also accompanied by a copy of each prior art document cited in this report.

1. Basis of the report

- a. With regard to the language, the international search was carried out on the basis of the international application in the language in which it was filed, unless otherwise indicated under this item.

☐ the international search was carried out on the basis of a translation of the international application furnished to this Authority (Rule 23.1(b)).

- b. With regard to any nucleotide and/or amino acid sequence disclosed in the international application, the international search was carried out on the basis of the sequence listing :

☒ contained in the international application in written form.

☒ filed together with the international application in computer readable form.

☐ furnished subsequently to this Authority in written form.

☐ furnished subsequently to this Authority in computer readable form.

☐ the statement that the subsequently furnished written sequence listing does not go beyond the disclosure in the international application as filed has been furnished.

☐ the statement that the information recorded in computer readable form is identical to the written sequence listing has been furnished

2. ☐ Certain claims were found unsearchable (See Box I).

3. ☒ Unity of invention is lacking (see Box II).

4. With regard to the title,

☒ the text is approved as submitted by the applicant.

☐ the text has been established by this Authority to read as follows:

5. With regard to the abstract,

☒ the text is approved as submitted by the applicant.

☐ the text has been established, according to Rule 38.2(b), by this Authority as it appears in Box III. The applicant may, within one month from the date of mailing of this international search report, submit comments to this Authority.

6. The figure of the drawings to be published with the abstract is Figure No.

☐ as suggested by the applicant.

☐ because the applicant failed to suggest a figure.

☐ because this figure better characterizes the invention.

☐ None of the figures.

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/09218

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N1/21 C07K14/285 A61K35/74 A61K39/02 C12N15/63
 C12N15/31 C07K16/12 C12Q1/18

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C07K A61K C12Q

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	WO 94 11024 A (UNIV MINNESOTA) 26 May 1994 (1994-05-26) examples 1-3	1-51
A	--- FERNANDEZ DE HENESTROSA A.R. ET AL.: "Importance of the galE gene on the virulence of Pasteurella multocida" FEMS MICROBIOLOGY LETTERS, vol. 154, 1997, pages 311-316, XP000864738 page 314, column 2, line 20 -page 316, column 1, line 18 --- -/--	1-51

☒ Further documents are listed in the continuation of box C.☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

T later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

X document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

Y document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art.

& document member of the same patent family

Date of the actual completion of the international search

19 July 2000

Date of mailing of the international search report

24. 10. 00

Name and mailing address of the ISA

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Authorized officer

Schönwasser, D

INTERNATIONAL SEARCH REPORT

International Application No

PCT/US 00/09218

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	FLEISCHMANN R D ET AL: "WHOLE-GENOME RANDOM SEQUENCING AND ASSEMBLY OF HAEMOPHILUS INFLUENZAE RD" SCIENCE, vol. 269, 28 July 1995 (1995-07-28), pages 496-512, XP002916664 ISSN: 0036-8075 the whole document	1-51
A	-& FLEISCHMANN R.D. ET AL.: "Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.; ATP SYNTHASE A CHAIN (EC 3.6.1.34.) (PROTEIN 6)" EMBL DATABASE ENTRY ATP6 HAEIN; ACCESSION NO. P43719, 1 November 1995 (1995-11-01), XP002142946	
P,A	--- FULLER T.E. ET AL.: "Identification of in vivo induced genes in Actinobacillus pleuropneumoniae" MICROBIAL PATHOGENESIS, vol. 27, no. 5, November 1999 (1999-11), pages 311-327, XP000864734 the whole document	1-51
T	--- FULLER T.E. ET AL.: "Identification of Actinobacillus pleuropneumoniae virulence genes in a swine infection model" MICROBIAL PATHOGENESIS, vol. 29, no. 1, July 2000 (2000-07), pages 39-51, XP000864735 the whole document -----	1-51

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/US 00/09218

Patent document cited in search report	Publication date	Patent family member(s)	Publication date
WO 9411024 A	26-05-1994	AU 5591694 A	08-06-1994
		CA 2148829 A	26-05-1994
		EP 0668779 A	30-08-1995
		JP 8503136 T	09-04-1996

[19] 中华人民共和国国家知识产权局

[51] Int. Cl⁷

[12] 发明专利申请公开说明书

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A61K 39/02 C12N 15/63
C12N 15/31 C07K 16/12
C12Q 1/18

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[32] 1999.9.10 [33] US [31] 60/153,453

[86] 国际申请 PCT/US00/09218 2000.4.6

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务所

代理人 樊卫民

权利要求书 6 页 说明书 310 页 附图页数 0 页

[54] 发明名称 抗细菌疫苗组合物

[57] 摘要

鉴定了革兰氏阴性菌毒力基因,从而允许鉴定针对
这些毒力基因 及其产物的新型抗菌剂,提供在疫苗中有
用的新型革兰氏阴性菌突变体。

ISSN 1008-4274

权 利 要 求 书

1. 一种革兰氏阴性菌，其在 SEQ ID NO:1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104, 108, 112, 116, 118, 120, 122, 124, 126, 128 和 130 任一所示的核苷酸序列或其物种同源物代表的基因中含有一个突变，该突变导致突变基因编码的基因产物的活性降低。

2. 权利要求 1 的革兰氏阴性菌，其中该突变导致突变基因编码的基因产物的表达降低。

3. 权利要求 1 的革兰氏阴性菌，其中该突变导致突变基因编码的无活性基因产物的表达。

4. 权利要求 1 的革兰氏阴性菌，其中该突变导致该基因全部或部分的缺失。

5. 权利要求 1 的革兰氏阴性菌，其中该突变导致该基因至少约 10%、至少约 20%、至少约 30%、至少约 40%、至少约 50%、至少约 60%、至少约 70%、至少约 80%、至少约 90%、至少约 95%、至少约 98%、至少约 99% 的缺失。

6. 权利要求 1 的革兰氏阴性菌，其中该突变导致基因中的插入，该插入使突变基因编码的基因产物的表达和/或突变基因编码的无活性基因产物的表达降低。

7. 一种减毒巴斯德氏菌科细菌，其在 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 和 164 任一所示的核苷酸序列或其物种同源物代表的基因中含有一个突变，该突变导致突变基因编码的基因产物的活性降低。

8. 权利要求 7 的巴斯德氏菌科细菌，其中该突变导致突变基因编

码的基因产物的表达降低。

9. 权利要求 7 的巴斯德氏菌科细菌，其中该突变导致突变基因编码的无活性基因产物的表达。

10. 权利要求 7 的巴斯德氏菌科细菌，其中该突变导致该基因全部或部分的缺失。

11. 权利要求 7 的巴斯德氏菌科细菌，其中该突变导致该基因至少约 10%、至少约 20%、至少约 30%、至少约 40%、至少约 50%、至少约 60%、至少约 70%、至少约 80%、至少约 90%、至少约 95%、至少约 98%、至少约 99% 的缺失。

12. 权利要求 7 的巴斯德氏菌科细菌，其中该突变导致基因中的插入，该插入使突变基因编码的基因产物的表达和/或突变基因编码的无活性基因产物的表达降低。

13. 权利要求 7 的巴斯德氏菌科细菌，其选自：溶血巴斯德氏菌、多杀巴斯德氏菌、大叶性肺炎放线杆菌和睡眠嗜血菌。

14. 权利要求 13 的巴斯德氏菌科细菌，其中该突变导致突变基因编码的基因产物的表达降低。

15. 权利要求 13 的巴斯德氏菌科细菌，其中该突变导致突变基因编码的无活性基因产物的表达。

16. 权利要求 13 的巴斯德氏菌科细菌，其中该突变导致该基因全部或部分的缺失。

17. 权利要求 13 的巴斯德氏菌科细菌，其中该突变导致该基因至少约 10%、至少约 20%、至少约 30%、至少约 40%、至少约 50%、至少约 60%、至少约 70%、至少约 80%、至少约 90%、至少约 95%、至少约 98%、至少约 99% 的缺失。

18. 权利要求 13 的巴斯德氏菌科细菌，其中该突变导致基因中的插入，该插入使突变基因编码的基因产物的表达和/或突变基因编码的无活性基因产物的表达降低。

19. 权利要求 13 的减毒巴斯德氏菌科细菌，它是多杀巴斯德氏菌。

20. 权利要求 19 的巴斯德氏菌科细菌，其中该突变导致突变基因

编码的基因产物的表达降低。

21. 权利要求 19 的巴斯德氏菌科细菌，其中该突变导致突变基因编码的无活性基因产物的表达。

22. 权利要求 19 的巴斯德氏菌科细菌，其中该突变导致该基因全部或部分的缺失。

23. 权利要求 19 的巴斯德氏菌科细菌，其中该突变导致该基因至少约 10%、至少约 20%、至少约 30%、至少约 40%、至少约 50%、至少约 60%、至少约 70%、至少约 80%、至少约 90%、至少约 95%、至少约 98%、至少约 99% 的缺失。

24. 权利要求 19 的巴斯德氏菌科细菌，其中该突变导致基因中的插入，该插入使突变基因编码的基因产物的表达和/或突变基因编码的无活性基因产物的表达降低。

25. 权利要求 13 的减毒巴斯德氏菌科细菌，它是大叶性肺炎放线杆菌。

26. 权利要求 25 的巴斯德氏菌科细菌，其中该突变导致突变基因编码的基因产物的表达降低。

27. 权利要求 25 的巴斯德氏菌科细菌，其中该突变导致突变基因编码的无活性基因产物的表达。

28. 权利要求 25 的巴斯德氏菌科细菌，其中该突变导致该基因全部或部分的缺失。

29. 权利要求 25 的巴斯德氏菌科细菌，其中该突变导致该基因至少约 10%、至少约 20%、至少约 30%、至少约 40%、至少约 50%、至少约 60%、至少约 70%、至少约 80%、至少约 90%、至少约 95%、至少约 98%、至少约 99% 的缺失。

30. 权利要求 25 的巴斯德氏菌科细菌，其中该突变导致基因中的插入，该插入使突变基因编码的基因产物的表达和/或突变基因编码的无活性基因产物的表达降低。

31. 一种免疫原性组合物，其含有根据权利要求 1-30 任一项的细菌。

32. 一种疫苗组合物，其含有根据权利要求 31 的免疫原性组合物和一种药学可接受的载体。

33. 根据权利要求 32 的疫苗组合物，其进一步含有一种佐剂。

34. 一种生产革兰氏阴性菌突变体的方法，包括以下步骤：向 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 和 164 任一所示的核苷酸序列或其物种同源物代表的基因中导入一个突变，该突变导致突变基因编码的基因产物的活性降低。

35. 一种生产减毒巴斯德氏菌科细菌的方法，包括以下步骤：向 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 和 164 任一所示的核苷酸序列或其物种同源物代表的基因中导入一个突变，该突变导致突变基因编码的基因产物的活性降低。

36. 一种纯化并分离的巴斯德氏菌科多核苷酸，其含有选自下列的核苷酸序列：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 和 164 任一所示的核苷酸序列。

37. 一种纯化并分离的巴斯德氏菌科多核苷酸，其含有选自下列的核苷酸序列：SEQ ID NO:1, 3, 7, 9, 21, 25, 27, 29, 39, 41, 51, 53, 55, 57, 58, 60, 68, 72, 74, 76, 78, 80, 82, 84, 104,

108, 112, 116, 118, 120, 122, 124, 126, 128 和 130 所示的核苷酸序列。

38. 一种纯化并分离的多核苷酸, 其编码巴斯德氏菌科毒力基因产物, 或其物种同源物, 选自:

- a) 根据权利要求 37 的多核苷酸,
- b) 编码由 (a) 的多核苷酸编码的多肽的多核苷酸, 和
- c) 在中度严格条件下可与 (a) 或 (b) 的多核苷酸的互补序列杂交的多核苷酸。

39. 一种纯化并分离的巴斯德氏菌科多核苷酸, 其编码具有选自 SEQ ID NO:2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161 和 165 所示氨基酸序列的多肽。

40. 权利要求 39 的多核苷酸, 它是一种 DNA。

41. 一种含有权利要求 40 的 DNA 的载体。

42. 权利要求 41 的载体, 它是一种表达载体, 其中 DNA 与一种表达控制 DNA 序列有效连接。

43. 以允许在宿主细胞中表达所编码多肽的方式, 用权利要求 40 的 DNA 稳定转化或转染的一种宿主细胞。

44. 一种生产重组多肽的方法, 包括在营养培养基中培养权利要求 43 的宿主细胞, 并从该宿主细胞或营养培养基中分离编码多肽。

45. 通过权利要求 44 的方法产生的一种纯化多肽。

46. 一种纯化多肽, 其含有选自具有 SEQ ID NO:2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151,

153, 155, 157, 159, 161 和 165 所示氨基酸序列的多肽的多肽。

47. 一种可与权利要求 46 的多肽特异反应的抗体。

48. 权利要求 47 的抗体, 它是一种单克隆抗体。

49. 一种使用权利要求 39 的单克隆抗体鉴定权利要求 1、7、13 或 19 的细菌的方法, 包括下列步骤: 使细菌提取物接触该单克隆抗体, 检测该单克隆抗体结合的缺乏。

50. 一种鉴定抗菌剂的方法, 包括下列步骤: 测定潜在药剂干扰 SEQ ID NO:2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161 和 165 任一所示氨基酸序列代表的基因产物表达或活性的能力, 并鉴定干扰所述基因产物表达或活性的药剂。

51. 一种鉴定抗菌剂的方法, 包括下列步骤:

a) 测定如 SEQ ID NO:2, 4, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 30, 32, 34, 38, 40, 42, 52, 54, 56, 59, 61, 69, 71, 73, 75, 77, 79, 81, 83, 85, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161 和 165 所示基因产物的表达或活性;

b) 使 (a) 的基因产物接触待测化合物;

c) 测定在待测化合物存在下基因产物的表达或活性; 和

d) 与不含待测化合物时的表达或活性相比, 在待测化合物存在下, 当基因产物的表达或活性降低时, 确定该待测化合物为一种抗菌剂。

说明书

抗细菌疫苗组合物

发明领域

本发明普遍涉及负责多杀巴斯德氏菌 (*Pasteurella multocida*) 和大叶性肺炎放线杆菌 (*Actinobacillus pleuropneumoniae*) 毒力的基因的鉴定, 从而允许生产在疫苗中有用的新型减毒突变株, 鉴定针对这些毒力基因及其产物的新型抗菌剂。

发明背景

巴斯德氏菌科 (*Pasteurellaceae*) 包括几种可感染多种动物的重要病原体。除了多杀巴斯德氏菌之外, 该科的主要成员包括溶血巴斯德氏菌 (*Pasteurella haemolytica*)、大叶性肺炎放线杆菌和睡眠嗜血杆菌 (*Haemophilus somnus*)。多杀巴斯德氏菌是一种革兰氏阴性、不活动的球杆菌, 在许多野生动物和家畜的正常菌群中发现, 已知可导致全世界多种动物种的疾病[Biberstein, 于: 《放线杆菌属》学院出版社, 伦敦, 61-73 页 (1981)]。感染后的疾病表现包括败血症、支气管肺炎、鼻炎和伤口感染[Shewen 等人, 于: C.L. Gyles 和 C.O. Thoen (编), 《动物细菌感染的致病机理》, 爱荷华州大学出版社, Ames, 216-225 页 (1993), 在此引用作为参考]。

多杀巴斯德氏菌感染一般由应激期间的侵害引起, 但也可通过气溶胶或接触暴露或通过蚤和蜱载体发生传播。在禽类, 多杀巴斯德氏菌感染引起急性到急性前败血症, 特别在与过高种群密度、产卵数、蜕皮或严重气候改变有关的应激条件下在家养火鸡和野生水鸟中流行。对于牛, 感染后有相似的出血性败血病, 并表现出包括高热和抑郁在内的症状, 随后一般很快死亡。传播是可能是通过气溶胶接触, 但也能在明显气候改变期间引起感染。对于兔, 感染引起复发性化脓性鼻炎, 随后一般有结膜炎、中耳炎、鼻窦炎、皮下脓疮和慢性支气

管肺炎。在重度感染中，兔死亡率由急性纤维化支气管肺炎、败血症或内毒素血症引起。病症一般在应激期间出现。对于猪，普通多杀巴斯德氏菌病症包括萎缩性鼻炎和细菌性肺炎。类似的肺炎症状也在狗、猫、山羊和绵羊中检出。多杀巴斯德氏菌一般可在许多动物的口腔菌群中检出，因此是咬伤和抓伤中的一种共同污染物。

多杀巴斯德氏菌株通常根据荚膜血清群和菌体血清型命名。根据特有的热稳定抗原的表达，可区分为 5 个荚膜血清群（A、B、D、E 和 F）和 16 个菌体血清型。大多数菌株是宿主特异的，极少感染一种或两种以上的动物。不同血清型的存在提出了一个关于接种的问题，因为用传统方法杀死的全细胞细菌通常只引起血清型特异的保护。然而，已经证明，自然感染一种血清型能导致对多种血清型的免疫保护 [Shewen 等人，于：C.L. Gyles 和 C.O. Thoen（编），《动物细菌感染的致病机理》，爱荷华州大学出版社，Ames，216-225 页（1993）]，使用灭活的体内生长的细菌也能刺激交叉保护 [Rimler 等人，美国兽医学研究杂志（Am J Vet Res.）42:2117-2121（1981）]。一种活的自发突变多杀巴斯德氏菌株已经被用作疫苗，显示可刺激强烈的免疫应答 [Davis，家禽文摘（Poultry Digest.）20:430-434（1987），Schlink 等人，鸟类疾病（Avian Dis.）31(1):13-21（1987）]。但是，如果疫苗接受者应激时，这种减毒株回复为毒性状态或导致死亡 [Davis，家禽文摘 20:430-434（1987），Schlink 等人，鸟类疾病 31(1):13-21（1987）]。

巴斯德氏菌科的另一个成员——大叶性肺炎放线杆菌，显示对猪的严格宿主特异性，是高传染性猪胸膜肺炎的病原体。感染通常在密集饲养条件下出现，被认为是以直接传播模式发生。该疾病通常是致死的，因此可导致猪生产工业的严重经济损失。大叶性肺炎放线杆菌感染可以是慢性或急性的，感染的特征在于出血性、坏死性支气管肺炎，并伴随有纤维蛋白性胸膜炎。迄今为止，已经将细菌毒力归因于结构蛋白，包括血清型特异荚膜多糖、脂多糖和表面蛋白，以及胞外溶细胞毒素。尽管纯化并在某些情况下克隆了这些毒力因子，但对这些毒力因子在大叶性肺炎放线杆菌感染中的实际作用了解极少。

根据荚膜多糖中的抗原差异和胞外毒素的产生,已经鉴定了大叶性肺炎放线杆菌的 12 个血清型。在美国,血清型 1、5 和 7 与大叶性肺炎放线杆菌感染最相关,而欧洲以血清型 1、2、5、7 和 9 为主。大叶性肺炎放线杆菌具有至少三种重要胞外毒素,它们是溶血素家族的成员,被称为 RTX 毒素。RTX 毒素由多种革兰氏阴性菌产生,包括大肠杆菌、普通变形菌 (*Proteus vulgaris*) 和溶血巴斯德氏菌,这些蛋白质一般共有结构和功能特征。然而,来自不同血清型的毒素在宿主特异性、靶细胞和生物活性方面不同。

主要的大叶性肺炎放线杆菌 RTX 毒素包括 ApxI、ApxII 和 ApxIII。ApxI 和 ApxII 具有溶血活性, ApxI 更强。ApxIII 不显示溶血活性,但对肺泡巨噬细胞和中性粒细胞有细胞毒性。大多数大叶性肺炎放线杆菌血清型产生这三种毒素中的两种。例如,血清型 1、5、9 和 11 表达 ApxI 和 ApxII, 血清型 2、3、4、6 和 8 表达 ApxII 和 ApxIII。但是,血清型 10 只产生 ApxI,而血清型 7 和 12 只表达 ApxII。产生 ApxI 和 ApxII 的这些大叶性肺炎放线杆菌血清型是最具毒性的菌株。

利用随机突变的野生型细菌,在鼠模型和猪感染中已经证明 Apx 毒素是毒力因子[Tascon 等人,分子微生物学 (*Mol. Microbiol.*) 14:207-216 (1994)]。也用定向诱变产生了其他大叶性肺炎放线杆菌突变体,以灭活编码 AopA 外膜毒力蛋白的基因[Mulks 和 Buysee, 基因 165:61-66 (1995)]。

在生产疫苗组合物的尝试中,用传统方法杀死的全细胞细菌只引起血清型特异的保护[MacInnes 和 Smart, 同上],但是,已经证明,自然感染一种高毒性血清型能刺激对多种血清型的强烈的保护性免疫[Nielsen, 北欧兽医学 (*Nord Vet Med.*) 31:407-13 (1979), Nielsen, 北欧兽医学 36:221-234 (1984), Nielsen, 加拿大兽医研究杂志 (*Can J Vet Res.*) 29:580-582 (1988), Nielsen, *ACTA Vet Scand.* 15:80-89 (1994)]。一种产生 ApxII 毒素灭活形式的确定的减毒活疫苗株在猪中具有交叉保护的希望[Prideaux 等人,感染与免疫 (*Infection &*

Immunity) 67:1962-1966 (1999)], 而其他未确定的减毒活突变体也有希望[Inzana 等人, 感染与免疫 61:1682-6 (1993), Paltineanu 等人, 国际猪兽医协会, 1992, 214 页, Utrera 等人, 国际猪兽医协会, 1992, 213 页]。

因为含有菌株的疫苗制剂具有菌株未确定的、自发突变的相关的问题, 本领域中需要合理构建在疫苗中使用的减毒活菌株, 它们应能安全地刺激对同源和异源的多杀巴斯德氏菌和大叶性肺炎放线杆菌血清型的保护性免疫。进一步需要鉴定减毒菌株和细菌毒力所需的基因, 从而促进鉴定抗菌剂之方法的发展。

发明概述

概括地说, 本发明提供用于生产和使用含减毒革兰氏阴性菌的疫苗组合物的材料与方法。一方面, 本发明的疫苗组合物含有巴斯德氏菌科细菌的减毒种, 其在本领域中周知, 并由 Dewhirst 等人, 细菌学杂志 (J. Bacteriol.) 174:2002-2013 (1992) 部分描述, 在此完整引用作为参考。该科中的种包括但不限于: 伴放线放线杆菌 (*A. actinomycetemcomitans*)、荚膜放线杆菌 (*A. capsulatus*)、马驹放线杆菌 (*A. equuli*)、李氏放线菌 (*A. lignieresii*)、大叶性肺炎放线杆菌(大叶性肺炎嗜血菌 (*H. pleuropneumoniae*))、种子放线杆菌 (*A. seminis*)、猪放线杆菌 (*A. suis*) (猪嗜血菌 (*H. Suis*))、豚放线杆菌 (*A. ureae*) (豚巴斯德氏菌 (*P. ureae*))、荚膜放线杆菌 (*A. capsulatus*)、Bisgaard 分类 11、埃及嗜血菌 (*H. aegyptius*)、嗜沫嗜血菌 (*H. aphrophilus*)、嗜沫嗜血菌(副流感嗜血菌 (*H. parainfluenzae*))、杜氏嗜血菌 (*H. ducreyi*)、嗜红血蛋白嗜血菌 (*H. haemoglobinophilus*)、溶血嗜血菌 (*H. haemolyticus*)、流感嗜血菌 (*H. influenzae*)、副兔嗜血菌 (*H. paracuniculus*)、副鸡嗜血菌 (*H. paragallinarum*)、副溶血嗜血菌 (*H. parahaemolyticus*)、副流感嗜血菌、(副嗜沫嗜血菌 (*H. paraphrophilus*))、副嗜沫溶血嗜血菌 (*H. paraphrohaemolyticus*)、副嗜沫嗜血菌、副猪嗜血菌 (*H. parasuis*)、5 型副猪嗜血菌、嗜性嗜血菌 (*H. segnis*)、睡眠嗜血菌 (*H. somnus*)、

嗜血菌属 (*Haemophilus*) 少数组、嗜血菌属分类 C、产气巴斯德氏菌 (*P. aerogenes*)、鸭巴斯德氏菌 (*P. anatis*)、鸟巴斯德氏菌 (*P. avium*) (鸟嗜血菌 (*H. avium*))、犬巴斯德氏菌 (*P. canis*)、达可马巴斯德氏菌 (*P. dagmatis*)、鸡巴斯德氏菌 (*P. gallinarum*)、溶血巴斯德氏菌 (*P. haemolytica*)、海藻巴斯德氏菌 (*P. trehalosi*) (溶血巴斯德氏菌生物型 T)、郎氏巴斯德氏菌 (*P. langaa*)、多杀巴斯德氏菌、侵肺巴斯德氏菌 (*P. pneumotropica*)、口巴斯德氏菌 (*P. stomatis*)、敏捷巴斯德氏菌 (*P. volantium*) (副流感嗜血菌)、敏捷巴斯德氏菌 (*P. volantium*)、巴斯德氏菌种 A、巴斯德氏菌种 B 和副嗜沫溶血嗜血菌 (*Haemophilus paraphrohaemolyticus*)。优选地，疫苗组合物含有减毒的溶血巴斯德氏菌、大叶性肺炎放线杆菌、睡眠嗜血菌或多杀巴斯德氏菌。在一个最优的实施方案中，本发明的疫苗组合物含有减毒的多杀巴斯德氏菌和大叶性肺炎放线杆菌菌株。

本发明的一个方面提供革兰氏阴性菌生物，其在 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 和 164 任一所示的基因序列或其物种同源物中含有一个功能突变，其中该突变抑制或消除了编码基因产物（即由一种基因编码的多肽）的表达和/或生物活性；该功能突变导致菌株的毒力减弱。如本领域所知，物种同源物包括在两种或多种不同物种中发现的基因，它们具有基本的多核苷酸序列同源性，并具有相同或类似的生物功能和/或性质。优选地，代表物种同源物的多核苷酸序列在中度严格条件下可以杂交，如此处实施例所述，并且具有相同或类似的生物活性和/或性质。另一方面，代表物种同源物的多核苷酸共有约 60% 以上的序列同源性，约 70% 以上的序列同源性，约 80% 以上的序列同源性，约 90% 以上的序列同源性，或约 95% 以上的序列同源性。调节（即增强或降低）一种基因产物的

表达和/或生物活性的功能突变包括该基因本身蛋白质编码区中，或负责或参与基因表达控制的序列中的插入或缺失。缺失突变包括其中所有或部分特异基因序列缺失的突变。一方面，该突变导致该基因至少约 10%、至少约 20%、至少约 30%、至少约 40%、至少约 50%、至少约 60%、至少约 70%、至少约 80%、至少约 90%、至少约 95%、至少约 98%、至少约 99% 的缺失。另一方面，该突变导致该基因中的插入，其中该插入使突变基因编码的基因产物的表达和/或突变基因编码的灭活基因产物的表达降低。本发明还构思了组合物，优选地疫苗组合物，其含有突变和减毒革兰氏阴性菌生物，任选地含有一种合适的佐剂和/或药学可接受的稀释剂或载体。为了使改变的菌株在疫苗组合物中有效，这种减毒必须足以防止病原体诱发严重临床症状，但也可足以使细菌在宿主中有限复制和生长。

本发明也提供编码革兰氏阴性菌毒力所需基因产物的多核苷酸。本发明的多核苷酸包括 DNA，如互补 DNA、基因组 DNA，包括互补或反义 DNA，和全部或部分合成的 DNA；RNA，包括有义和反义链；和肽核酸，如 Corey, TIBTECH 15:24-229 (1997) 所述。本发明的毒力基因多核苷酸包括 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 和 164 所示的，或其物种同源物，编码由 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 和 164 的多核苷酸或其物种同源物编码的毒力基因产物的多核苷酸，和在中度到高度严格条件下可与 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 和 164 所示任一多核苷酸及其物种同源物的非编码链（或互补链）杂交的多核苷酸。因此本发明包括 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 和 164 所示的来自巴斯德氏菌科的基因序列，以及来自其他革兰氏阴性菌生物的相关基因序列，包括其天然存在的（即物种同源物）和人工诱导的变体。本发明也包括编码由 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 和 164 所示任一多核苷酸和其物种同源物推断的多肽的多核苷酸。对本发明的多核苷酸序列的了解使得易于获得该多核苷酸的每种可能的片段。因此本发明提供本发明的多核苷酸的片段。

本发明还包括含有本发明的多核苷酸的表达构建体。也涉及用本发明的多核苷酸转化、转染或电穿孔的宿主细胞。本发明提供生产由本发明的多核苷酸编码的多肽的方法，包括下列步骤：在允许、优选地促进该多核苷酸编码的基因产物表达的条件下，培养本发明的宿主细胞，从宿主细胞或其生长培养基中分离基因产物。

本发明的多核苷酸的鉴定使得可以获得编码的多肽。本发明的多肽包括全长和片段或截短的蛋白质；其变体；融合或嵌合蛋白质；和

类似物，包括向野生型多肽中导入保守氨基酸置换的多肽。也提供可特异识别本发明的多肽的抗体，包括单克隆和多克隆抗体、单链抗体、嵌合抗体、人源化抗体、人抗体和互补决定区（CDR）-移植抗体，以及含有可特异识别本发明的多肽的 CDR 序列的化合物。本发明也提供对本发明的抗体有免疫特异性的抗独特型抗体。

根据本发明的另一方面，提供了鉴定可调节革兰氏阴性菌毒力基因或基因产物功能的新型抗菌剂的方法。本发明的方法包括：根据干扰由 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 和 164 任一所示 DNA 序列或其物种同源物编码的毒力基因产物表达的能力，筛选潜在制剂，或根据干扰由 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 和 164 任一所示 DNA 序列、其物种同源物或其互补链完整或部分编码的细菌基因产物生物功能的能力，筛选潜在制剂，随后鉴定在这些筛选试验中产生阳性结果的制剂。特别是，干扰毒力基因产物表达的制剂包括与毒力基因序列互补的反义多核苷酸和核酶。本发明还包括利用寡核苷酸指导的三股螺旋形成调节本发明基因产物转录的方法。

可干扰毒力基因产物功能的制剂包括毒力基因产物的变体，毒力基因产物的结合配偶体和这些结合配偶体的变体，和酶抑制剂（其中产物是一种酶）。

提供了用此处所述的方法鉴定的新型抗菌剂，以及治疗革兰氏阴性菌感染患者的方法，包括以有效降低细菌存在的量施用这些新型抗

菌剂。

在参考描述目前准备的实施方案的下列发明详述后，本领域技术人员将明白本发明的其他许多方面和优点。

发明详述

“毒力基因”在此使用时是指在宿主动物中成功建立和/或保持细菌感染需要其功能或产物的基因。因此，毒力基因和/或由其编码的蛋白质参与宿主生物的致病机理，但也可不是生长所必需的。

“签名标记诱变 (STM)”在此使用时是一种方法，在国际专利公开号 WO96/17951 中概述，在此引用作为参考，包括，例如，一种鉴定鼠菌血症模型毒力所需的细菌基因的方法。在该方法中，用转座子整合产生在其基因组中各含有一个随机突变的菌株；每一插入突变都带有不同的 DNA 签名标记，可使突变体彼此区别。该标记含有 40bp 可变中心区，其侧翼为 20bp 的不变“臂”，它使该中心部分能通过聚合酶链反应 (PCR) 共扩增。标记的突变株收集于微量平皿中，然后结合形成“接种物集合”用于感染研究。在接种后适当一段时间时，从动物中分离细菌，合并形成“回收集合”。单独扩增、标记回收集合中的标记和接种物集合中的标记，然后用它们来探查排列有代表接种物中突变体的全部不同标记的滤纸。毒力减弱的突变株是那些不能从被感染的动物中回收的菌株，即，当与接种物集合的标记杂交时产生杂交信号，而在与回收集合的标记杂交时不产生杂交信号的菌株。在该方法的一种变化中，可使用非放射性检测方法如化学发光法。

签名标记诱变允许在一个动物中同时筛查大量插入突变菌株的毒力丧失。筛查 19 个突变多杀巴斯德氏菌菌株集合鉴定出 60 个以上的毒力减弱的菌株，通过随后确定各突变体的近似 LD_{50} ，证实其中许多菌株毒力减弱。筛查大叶性肺炎放线杆菌突变体鉴定出在 35 个不同基因中含有突变的超过 100 个菌株。其中，22 个基因的突变产生显著减毒的大叶性肺炎放线杆菌菌株。转座子插入所打断的开放阅读框的核苷酸序列通过测序确定，并推断链和编码的氨基酸序列。核苷酸和氨

核酸序列的新颖性通过将该序列与 DNA 和蛋白质数据库比较而确定。

对细菌特别是多杀巴斯德氏菌和大叶性肺炎放线杆菌毒力基因的鉴定产生在疫苗中有用的显示毒力降低的微生物（即减毒株）。这些微生物包括巴斯德氏菌科突变体，其含有至少一种功能突变，该突变灭活 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 和 164 任一所示的基因。本领域技术人员应当理解，“功能突变”可在本发明的基因的蛋白质编码区中发生，并且可在调节毒力基因 RNA 转录的调节区中发生。

技术人员也应当理解，本发明的减毒多杀巴斯德氏菌和大叶性肺炎放线杆菌菌株包括含有一个以上功能突变的菌株。一个以上的突变可导致加和或协同的减毒程度。多个突变可按设计产生，或可由最初准备导入一个突变的缺失事件偶然引起。含有多个缺失的减毒株的一个例子是一种鼠伤寒沙门氏菌（*Salmonella typhimurium*）菌株，其中 *cya* 和 *crp* 基因功能缺失。该突变鼠伤寒沙门氏菌株具有作为活疫苗的前途。

对多杀巴斯德氏菌和大叶性肺炎放线杆菌毒力基因的鉴定能提供关于其他病原体物种中类似基因即物种同源物的信息。一个例子是，对 *aroA* 基因的鉴定导致鉴定出多种病原体中的保守基因，这些病原体包括：溶血巴斯德氏菌、嗜水气单胞菌（*Aeromonas hydrophila*）、杀鲑气单胞菌（*Aeromonas salmonicida*）、鼠伤寒沙门氏菌、肠炎沙门氏菌（*Salmonella enteritidis*）、都柏林沙门氏菌（*Salmonella dublin*）、鸡沙门氏菌（*Salmonella gallanum*）、副百日咳博德特氏菌（*Bordetella pertussis*）、小肠结肠炎耶尔森氏菌（*Yersinia enterocolitica*）、淋病奈瑟球菌（*Neisseria gonorrhoeae*）和炭疽芽孢杆菌（*Bacillus anthracis*）。在许多这类物种中，已经证明在 *aroA* 基因中含有突变的减毒菌株在疫

苗制剂中有效。利用在多杀巴斯德氏菌中鉴定的毒力基因序列，能在其他生物中，特别是巴斯德氏菌属内，以及大叶性肺炎放线杆菌和睡眠嗜血菌中鉴定出类似或同源基因。同样，对大叶性肺炎放线杆菌毒力基因的鉴定可允许鉴定其他生物中的相关基因。利用多杀巴斯德氏菌和大叶性肺炎放线杆菌基因作为探针的 Southern 杂交能在来自其他生物的染色体文库中鉴定这些相关基因。此外，PCR 在跨越物种界限的基因鉴定中同样有效。再另一种选择是，例如多杀巴斯德氏菌突变体与来自其他物种的染色体文库的互补，也能用于鉴定具有相同或相关毒性的基因。因此，对相关毒力基因的鉴定能导致产生另一种生物的减毒株，可用作另一种疫苗制剂。已经证明在其他物种（例如，溶血巴斯德氏菌、大叶性肺炎放线杆菌和睡眠嗜血菌）中存在的多杀巴斯德氏菌基因的例子包括基因 *exbB*、*atpG* 和 *pnp*。

用 STM 鉴定的减毒多杀巴斯德氏菌株是插入突变体，其中通过在开放阅读框或调节 DNA 序列中插入转座子序列使毒力基因无功能。因此，一方面，本发明的减毒多杀巴斯德氏菌株及其他革兰氏阴性突变菌株能带有一个或多个导致在基因中插入的突变，这种插入导致突变基因编码的基因产物表达和/或突变基因编码的灭活基因产物表达降低。这些插入突变体仍含有细菌毒力所需的所有遗传信息，并且通过插入转座子的缺失有可能回复为致病状态。因此，在制备疫苗制剂中，希望采用从减毒株搜集的信息，并产生一种缺失突变株，其中某些、大多数或全部毒力基因序列被去除，从而排除了细菌回复为毒性状态的可能性。因此本发明的减毒多杀巴斯德氏菌株及其他革兰氏阴性突变菌株包括含有一个或多个突变的菌株，该突变可导致毒力基因至少约 10%、至少约 20%、至少约 30%、至少约 40%、至少约 50%、至少约 60%、至少约 70%、至少约 80%、至少约 90%、至少约 95%、至少约 98%、至少约 99% 的缺失。

用 STM 鉴定的减毒插入突变体的疫苗性质预计与在相同基因中含有缺失的细菌相同或类似。然而，插入突变可能对连接基因序列发挥“极性”作用，因此，插入突变体可具有不同于在相同基因序列中

具有缺失的突变株的性质。缺失突变体能用本领域周知且常规实施的多种技术构建。

在一个实施例中，能应用使用反选择性标记的一种策略，其一般用来在许多细菌中删除基因。综述参见，例如，Reyrat 等人，感染与免疫 66:4011-4017 (1998)，在此引用作为参考。在该技术中，通常使用一种双选择策略，其中构建一种编码选择性标记和反选择性标记的质粒，其侧翼 DNA 序列来源于希望的缺失的两侧。选择性标记用来筛选质粒在适当位置、以适当方式整合到基因组中的细菌。反选择性标记用来筛选自发消除整合质粒的极少百分数的细菌。一小部分这些细菌于是只含有希望的缺失，而不含其他外源 DNA。应用这种技术的关键是合适的反选择性标记的可用性。

在另一种技术中，cre-lox 系统用于 DNA 的位点特异性重组。该系统由 34 个碱基对 lox 序列组成，它们可被细菌 cre 重组酶基因识别。如果在 DNA 中以适当方向存在 lox 位点，则侧翼为 lox 位点的 DNA 将被 cre 重组酶切下，导致除剩余的一拷贝 lox 序列外所有序列缺失。应用标准重组技术，能在多杀巴斯德氏菌或大叶性肺炎放线杆菌基因组中删除目的靶基因，并且将其替换为一种选择性标记（例如编码卡那霉素抗性的基因），其侧翼为 lox 位点。cre 重组酶的瞬时表达（通过自杀质粒的电穿孔，该质粒含有在多杀巴斯德氏菌或大叶性肺炎放线杆菌中起作用的启动子控制下的 cre 基因）将导致 lox 侧翼标记的有效去除。该方法将产生含有希望的缺失突变和一拷贝 lox 序列的突变体。

在另一种方法中，能直接将多杀巴斯德氏菌或大叶性肺炎放线杆菌基因组中的希望的缺失序列替换为一种标记基因，如绿色荧光蛋白（GFP）、 β -半乳糖苷酶或萤光素酶。在该技术中，侧翼为希望的缺失的 DNA 片段通过 PCR 制备，并克隆到用于多杀巴斯德氏菌或大叶性肺炎放线杆菌的自杀（非复制的）载体中。在侧翼序列之间克隆一种含有在多杀巴斯德氏菌或大叶性肺炎放线杆菌中有活性的启动子和合适的标记基因的表达盒。将该质粒导入野生型多杀巴斯德氏菌或大

叶性肺炎放线杆菌中。分离掺有并表达标记基因（也许以极低效率）的细菌，并检查合适的重组事件（即，野生型基因被标记基因的替换）。

这些生物的降低的毒力及其免疫原性可通过对受试动物施用来证实。尽管本发明的无毒微生物能单独施用，但优选地在含有合适的佐剂和药学可接受的稀释剂或载体的疫苗组合物中使用一种或多种这样的突变微生物。载体在与本发明的无毒微生物相容方面必须是“可接受的”，并且对所免疫的受试者无害。载体一般是水或盐水，是无菌的且不含致热原。将要免疫的受试者是需要保护免于罹患由多杀巴斯德氏菌、大叶性肺炎放线杆菌或其他致病微生物所致疾病的受试者。

应当理解，本发明的疫苗可用于人类医学和兽医学领域。因此，将要免疫的受试者可以是人或其他动物，例如农畜，包括母牛、绵羊、猪、马、山羊和家禽（例如鸡、火鸡、鸭和鹅）；宠物，如狗和猫；外来和/或动物园动物；和实验动物，包括小鼠、大鼠、兔、豚鼠和仓鼠。

本发明也提供多杀巴斯德氏菌或大叶性肺炎放线杆菌毒力所需的多肽和相应的多核苷酸。本发明包括自然存在的和非自然存在的多核苷酸和其产生的多肽。自然存在的毒性产物包括不同的基因和多肽种，以及在除多杀巴斯德氏菌或大叶性肺炎放线杆菌菌株之外的生物中表达的相应物种同源物。非自然存在的毒力产物包括自然存在的产物的变体，如类似物和含有共价修饰的毒性产物。在一个优选实施方案中，本发明提供含有 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 和 164 所示序列及其物种同源物的毒性多核苷酸，和具有由这些多核苷酸编码的氨基酸序列的多肽。

本发明提供纯化并分离的编码细菌毒力基因产物的新型多杀巴斯德氏菌或大叶性肺炎放线杆菌多核苷酸（例如 DNA 序列和 RNA 转录

物，有义和互补反义链)。本发明的 DNA 序列包括基因组和 cDNA 序列，以及完全或部分化学合成的 DNA 序列。本发明的基因组 DNA 包含本发明的多肽的蛋白质编码区，并且包括可在相同种其他菌株中发现的变体。在此使用时，如本领域所理解的，“合成的”是指产生多核苷酸的纯化学方法，不同于酶促方法。因此“完全”合成的 DNA 序列完全通过化学方法产生，而“部分”合成的 DNA 包括其中只是 DNA 的一部分通过化学法产生的 DNA。编码多杀巴斯德氏菌毒力基因产物的优选 DNA 序列在 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, 和 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163 和 164 及其物种同源物中列出。优选的编码毒力基因的大叶性肺炎放线杆菌 DNA 序列在 SEQ ID NO:122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163 和 164 及其物种同源物中列出。本领域技术人员可容易地理解，本发明优选的 DNA 包含双链分子，例如，具有 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 和 164 所示序列及其物种同源物的分子，以及具有根据 Watson-Crick DNA 碱基配对原则由 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 和 164 序列推

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断的序列的互补分子（“非编码链”或“互补序列”）。也优选编码由 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 和 164 所示任一种多核苷酸及其物种同源物编码的基因产物的多核苷酸。本发明还包括多杀巴斯德氏菌和大叶性肺炎放线杆菌 DNA 的物种、优选地细菌同源物。

本发明提供的多核苷酸序列信息使得通过众所周知的技术包括 Southern 和/或 Northern 杂交和聚合酶链反应（PCR）鉴定和分离编码相关细菌毒力分子的多核苷酸成为可能。相关多核苷酸的例子包括编码与 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 和 164 所示任一种多核苷酸及其物种同源物编码的毒力基因产物同源的多肽的多核苷酸，和编码共有本发明毒力基因产物的一种或多种生物和/或物理性质的结构相关多肽的多核苷酸。

本发明也包括编码细菌基因产物的 DNA 序列，这些基因产物在中度到高度严格条件下可与 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 和 164 所示任一种多核苷酸及其物种同源物的非编码链或互补链杂交。本发明涉及如果没有遗传密码简并性则与之杂交的编码毒性多肽的 DNA 序列。典型高严格条件包括最后

在 65℃-70℃ 下用含 0.2×SSC/0.1% SDS 的缓冲液洗涤, 典型中度严格条件包括最后在 35℃-45℃ 下用含 2×SSC/0.1% SDS 的缓冲液洗涤。本领域应当理解, 如 Ausubel 等人(编)《分子生物学方法》, John Wiley & Sons (1994) 6.0.3-6.4.10 页所述, 通过改变温度和缓冲液或盐浓度能达到相当的严格条件。杂交条件的改变能够根据经验确定, 或者根据探针鸟嘌呤/胞嘧啶 (GC) 碱基对的长度和百分比精确计算。杂交条件可如 Sambrook 等人(编)《分子克隆: 实验室》, 冷泉港实验室出版社: 冷泉港, 纽约 (1989), 第 9.47-9.51 页所述计算。

也提供了含有毒力基因序列的自主复制重组表达构建体如质粒和病毒 DNA 载体。也提供了其中毒力多肽编码多核苷酸与内源或外源表达控制 DNA 序列和转录终止子有效连接的表达构建体。利用多杀巴斯德氏菌基因组 DNA 作为模板, 通过 PCR 可克隆毒力基因。为便于向表达载体中插入基因, 选择 PCR 引物, 使得 PCR 扩增的基因在 5' 末端起始密码子 ATG 之前具有限制酶切位点, 并且在 3' 末端终止密码子 TAG、TGA 或 TAA 之后具有限制酶切位点。希望时, 根据 Grosjean 和 Fiers, 基因 18:199-209 (1982) 和 Konigsberg 和 Godson, 美国国家科学院院报 80:687-691 (1983) 所述的大肠杆菌密码子偏性, 可改变基因中的密码子, 而不改变氨基酸。密码子使用的优化可在大肠杆菌中产生时, 导致基因产物表达的增强。如果基因产物将在胞外产生, 在大肠杆菌或其他细菌周质中, 或向细胞培养基中产生, 则该基因在无起始密码子的情况下克隆, 并置于表达载体中信号序列之后。

根据本发明的另一方面, 提供了宿主细胞, 包括用本发明的多核苷酸序列以允许本发明的毒性多肽表达的方式稳定或瞬时转化、转染或电穿孔的原核和真核细胞。本发明的表达系统包括细菌、酵母、真菌、病毒、无脊椎动物和哺乳动物细胞系统。本发明的宿主细胞是免疫原的有价值来源, 用于产生可与毒力基因产物特异免疫反应的抗体。本发明的宿主细胞尤其可在大规模生产毒性多肽的方法中使用, 其中在合适的培养基中培养细胞, 并通过本领域周知和常规施行的如免疫亲和纯化或多种纯化技术中的任一种, 从细胞或培养细胞的培养基中

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分离希望的多肽产物。为了基因产物的表达，可利用本领域周知的合适的载体，使用任何合适的宿主细胞，如大肠杆菌，其他细菌，包括多杀巴斯德氏菌、芽孢杆菌和金黄色葡萄球菌（*S. aureus*），酵母，包括巴斯德毕赤酵母（*Pichia pastoris*）和酿酒酵母，昆虫细胞，或哺乳动物细胞，包括 CHO 细胞。通过胞内或胞外分泌到细菌细胞的周质间隙或细胞培养基中，蛋白质可直接产生，或与肽或多肽融合。蛋白质的分泌需要信号肽（也称作前序列）；已知来自原核和真核生物的许多信号序列可用于重组蛋白的分泌。在蛋白质分泌过程中，信号肽被信号肽酶去除，产生成熟蛋白质。

为了简化蛋白质纯化过程，可向基因编码序列的 5' 或 3' 端添加纯化标记。常用的纯化标记包括六组氨酸残基段（美国专利号 5,284,933 和 5,310,663），Schmidt 和 Skerra, 蛋白质工程（Protein engineering）6:109-122 所述的链霉亲和素亲和标记，FLAG 肽[Hopp 等人，生物技术（Biotechnology）6:1205-1210（1988）]，谷胱甘肽 S-转移酶[Smith 和 Johnson, 基因 67:31-40（1988）]和硫氧还蛋白[LaVallie 等人，生物/技术 11:187-193（1993）]。为了除去这些肽或多肽，可在融合接点处插入蛋白水解切割识别位点。常用的蛋白酶是因子 Xa、凝血酶和肠激酶。

本发明也提供纯化并分离的由本发明的多核苷酸编码的多杀巴斯德氏菌和大叶性肺炎放线杆菌毒性多肽。目前优选的是具有由 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 和 164 所示任一种多核苷酸及其物种同源物编码的氨基酸序列的多肽。本发明包括由选自下列的 DNA 编码的毒性多肽：a) 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 和 164 任一所示的 DNA 序列, 及其物种同源物; b) 编码由 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 和 164 任一及其物种同源物编码的多杀巴斯德氏菌或大叶性肺炎放线杆菌多肽的 DNA 分子; 和 c) 一种 DNA 分子, 其编码一种毒力基因产物, 在中度严格条件下可与 (a) 或 (b) 的 DNA 杂交。

本发明也包括多肽, 即物种同源物和类似物, 它们与本发明优选的多肽有至少约 99%、至少约 95%、至少约 90%、至少约 85%、至少约 80%、至少约 75%、至少约 70%、至少约 65%、至少约 60%、至少约 55%、至少约 50% 的同一性和/或同源性。对于本发明优选的多肽, 百分氨基酸序列“同一性”在此定义为: 将两种序列排比, 并在必要时引入缺口, 以达到最大百分序列同一性, 而不考虑作为序列同一性部分的任何保守置换之后, 与毒力基因产物中残基相同的候选序列中氨基酸残基的百分数。对于本发明优选的多肽, 百分氨基酸序列“同源性”在此定义为: 将序列排比, 并在必要时引入缺口, 以达到最大百分序列同一性, 也不考虑作为序列同一性部分的任何保守置换之后, 与毒力多肽序列之一中的残基相同的候选序列中氨基酸残基的百分数。保守置换可如表 A 和表 B 所示定义。

表 A
保守置换 I

侧链特征		氨基酸
脂族	非极性	G A P I L V
	极性——不带电	C S T M N Q
	极性——带电	D E K R
芳族		H F W Y
其他		N Q D E

本发明的多肽可从天然细菌细胞来源中分离，或者可以化学合成，但优选地通过包括本发明的宿主细胞的重组方法产生。本发明的毒力基因产物可以是全长多肽、生物活性片段或保留特异生物或免疫活性的变体。变体可含有毒力多肽类似物，其中一种或多种确定（即自然编码的）氨基酸缺失或被置换，或者其中加入一种或多种未确定氨基酸：（1）不丧失一种或多种对于毒力基因产物特异的生物活性或免疫特性；或（2）毒力基因产物特定生物活性的丧失。预期的缺失变体也包括缺乏非生物活性必需的多肽部分的片段，插入变体包括其中野生型多肽或其片段已与另一种多肽融合的融合多肽。

变异毒力多肽包括通过修饰编码本发明多肽的多核苷酸而引入保守置换的多肽。本领域中认为保守置换根据其有关物理性质将氨基酸分类，并且能如表 A 所示定义（来自 WO 97/09433，第 10 页，1997 年 3 月 13 日公布（PCT/GB96/02197，9/6/96 申请））。此外，保守氨基酸也可如 Lehninger[《生物化学》第二版；Worth Publishers, Inc. NY:NY（1975），第 71-77 页]所述如表 B 所示分组。

表 B
保守置换 II

侧链特征	氨基酸
非极性 (疏水)	
A. 脂族	A L I V P
B. 芳族	F W
C. 含硫	M
D. 临界	G
不带电——极性	
A. 羟基	S T Y
B. 酰胺	N Q
C. 巯基	C
D. 临界 (borderline)	G
带正电 (碱性)	K R H
带负电 (酸性)	D E

本发明的变异毒力产物包括成熟的毒力基因产物，即，其中前导序列或信号序列已经去除，含有其他的氨基酸残基。涉及在 1 位含有另一个甲硫氨酸残基的毒力基因产物，以及在 2 位和 1 位含有另外的甲硫氨酸和赖氨酸残基的毒力产物。这些类型的变体特别可用于在细菌细胞型中生产重组蛋白。本发明的变体也包括已经导入来源于其他蛋白质的氨基端序列的基因产物，以及含有未在天然存在的蛋白质中发现的氨基端序列的变体。

本发明也包括由于使用特异表达系统而含有其他氨基酸残基的变异多肽。例如，使用与谷胱甘肽-S-转移酶 (GST) 的融合蛋白形式表达希望的多肽的商品载体产生希望的多肽，其在从希望的多肽上切下 GST 组分之后，在 1 位含有另一个甘氨酸残基。也涉及由于使用其他载体系统表达而产生的变体。

本发明也包括抗体 (例如单克隆或多克隆抗体，单链抗体、嵌合抗体、人源化、人和 CDR 移植抗体，包括含有可特异识别本发明的多肽的 CDR 序列的化合物)，和对毒力基因产物或其片段特异的其他结合蛋白。术语“对……特异”是指本发明的抗体的可变区唯一地识别并结合一种毒力多肽 (即，能将一种毒力多肽与有关的毒力多肽相区别，尽管在多肽家族中发现序列同一性、同源性或相似性)，但也可

通过与抗体可变区之外、特别是分子恒定区中的序列相互作用，与其他蛋白质（例如，金黄色葡萄球菌蛋白 A 或 ELISA 技术中的其他抗体）相互作用。测定本发明抗体的结合特异性的筛查试验在本领域中公知并且常规施行。这些试验的综述，参见 Harlow 等人（编），《抗体：实验室手册》；冷泉港实验室；冷泉港，NY（1988），第 6 章。也涉及识别并结合本发明的毒力多肽的片段的抗体，只要抗体首先如上所述对产生该片段的本发明的毒力多肽特异。

本发明提供的 DNA 和氨基酸序列信息也使系统分析毒力基因及其编码的基因产物的结构和功能成为可能。对编码本发明的毒力基因产物的多核苷酸的了解也使可识别并杂交编码本发明毒力多肽的多核苷酸的反义多核苷酸可用。提供了全长和片段反义多核苷酸。技术人员应当理解，本发明的片段反义分子包括（i）特别识别并杂交特异 RNA 的（通过编码本发明毒力多肽的 DNA 与编码其他已知分子的 DNA 的序列对比确定），及（ii）识别并杂交编码毒力蛋白家族变体的 RNA 的。可与编码蛋白质毒力家族其他成员的 RNA 杂交的反义多核苷酸也是可以通过序列对比确定的，以鉴定分子家族的特征或签名、序列。

本发明还涉及利用核酶调节基因表达的方法。综述见 Gibson 和 Shillitoe，分子生物技术（Mol. Biotech.）7:125-137（1997）。核酶技术能用来以序列特异的方式抑制 mRNA 的翻译，是通过（i）互补 RNA 与靶 mRNA 的杂交，和（ii）利用互补链固有的核酸酶活性切割杂交的 mRNA。核酶可根据经验法确定，但更优选地是根据靶 mRNA 上的可接近位点特别设计[Bramlage 等人，生物技术趋势（Trends in Biotech）16:434-438（1998）]。核酶向靶细胞的输送能用本领域公知且常规使用的外源或源输送技术实现。外源输送方法可包括使用靶向脂质体或直接局部注射。内源方法包括使用病毒载体和非病毒质粒。

核酶在被设计为与编码毒力基因产物的多核苷酸的唯一区域互补时，能特异调节毒力基因的表达。“特异调节”因此是指，本发明的核酶只识别一种多核苷酸。类似地，核酶能被设计为调节所有或某些蛋白质家族的表达。这类核酶用来识别在编码该蛋白质家族的所有或

某些多核苷酸中保守的多核苷酸序列。

本发明还包括利用寡核苷酸指导的三股螺旋形成调节本发明的毒力基因转录的方法。综述见 Lavrovsky 等人, 生物化学与分子医学 (Biochem. Mol. Med.) 62:11-22 (1997)。使用可与双链 DNA 在 Watson-Crick 模型所定义的大沟中杂交的序列特异的寡核苷酸实现三股螺旋的形成。此后, 序列特异的寡核苷酸的杂交能调节 DNA 结合蛋白, 包括如转录因子和聚合酶的活性。为杂交优选的靶序列包括可调节毒力基因产物表达的转录调节区。能形成三股螺旋的寡核苷酸也可用于对靶 DNA 序列的位点特异的共价修饰。如 Lavrovsky 等人(同上)所述, 可用于共价修饰的寡核苷酸与不同 DNA 损坏剂偶联。

对多杀巴斯德氏菌和大叶性肺炎放线杆菌毒力基因的鉴定使基因和基因产物在鉴定抗菌剂的方法中 useful。这些方法包括: 测定潜在药剂干扰毒力基因产物表达的能力, 这些基因由 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, 和 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163 和 164 任一所示的 DNA 序列及其物种同源物代表(即, 由 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, 和 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163 和 164 的 DNA 序列所示的基因编码毒力基因产物, 或者 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, 和 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150,

152, 154, 156, 158, 160, 162, 163 和 164 的 DNA 序列与编码毒力基因产物的基因相邻, 或者参与毒力基因产物表达的调节), 或测定潜在药剂干扰细菌基因产物功能的能力, 该基因产物完全或部分由 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, 和 120, 122, 124, 126, 128, 130, 132, 134, 135, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 163 和 164 任一所示的 DNA 序列及其物种同源物或其互补序列编码, 随后鉴定在这些试验中为阳性的药剂。在这些试验中有用的多核苷酸和多肽不仅包括此处所述的基因和编码的多肽, 而且包括具有与野生型基因和多肽基本相同的活性的变体。

在高通量测定中用通过上述方法产生的毒力基因产物筛查抑制剂。将要筛选的潜在药剂的来源是化学化合物文库, 链霉菌发酵培养物, 其他细菌和真菌, 和植物和其他植被的细胞提取物。对于具有已知酶活性的蛋白质, 根据活性建立试验, 根据抑制该活性的能力筛选大量潜在药剂。对于与另一种蛋白质或核酸相互作用的蛋白质, 建立结合试验直接测定这些相互作用, 并根据抑制结合相互作用的能力筛选潜在药剂。

根据本发明该方面, 涉及本领域周知的不同测定法的应用。当毒力基因产物的功能已知或由与已知基因产物的序列相似性预测时, 能关键在于基因产物功能和/或性质的酶学或其他类型的生物和/或生物化学测定筛选潜在抑制剂。当毒力基因产物已知, 或由与可与另一种蛋白质或核酸相互作用的已知基因产物的序列相似性预测时, 能直接用结合试验筛选该相互作用的抑制剂。本发明涉及筛选和鉴定毒力基因产物结合抑制剂的多种试验。在一个实施例中, 在推断的抑制化合物存在或不存在的条件下, 固定毒力基因产物, 并估计与结合配偶体的相互作用。在另一个实施例中, 在推断的抑制化合物存在及不存在的情况下, 在溶液测定中估计毒力基因产物与其结合配偶体的相互

作用。在这两种试验中，抑制剂被确定为降低毒力基因产物与其结合配偶体结合的化合物。在毒力基因产物结合配偶体是蛋白质的情况中，也涉及其他测定法。例如，涉及双杂交测定的变化，其中如 1995 年 8 月 3 日公布的 PCT 公开号 WO 95/20652 所述，通过检测转化或转染的宿主细胞中的阳性信号鉴定蛋白质/蛋白质相互作用的抑制剂。

本发明涉及的候选抑制剂包括选自潜在抑制剂文库的化合物。有大量不同的文库用于小分子调节剂的鉴定，包括 (1) 化学文库，(2) 自然产物文库，和 (3) 由随机肽、寡核苷酸或有机分子组成的结合文库。化学文库由已知化合物的结构类似物或通过天然产物筛选确定为 “hits” 或 “leads” 的化合物组成。天然产物文库是微生物、动物、植物或海洋生物的集合，用来产生混合物，筛选方法包括：(1) 从土壤、植物或海洋微生物中发酵和提取培养液，或 (2) 植物或海洋生物的提取。天然产物文库包括 polyketide、非核糖体肽及其变体（非自然存在的）。综述参见科学 282:63-68 (1998)。组合文库由大量肽、寡核苷酸或有机化合物作为混合物组成。它们相对易于通过传统自动合成法、PCR、克隆或专利合成法制备。特别重要的是肽和寡核苷酸组合文库。其他目的文库包括肽、蛋白质、拟肽、多平行合成集合、重组和多肽文库。关于组合化学和由其产生的文库的综述参见 Myers, 生物技术现代观点 (Curr. Opin. Biotechnol.) 8:701-707 (1997)。利用此处所述的不同文库鉴定调节剂使得能修饰候选 “hit” (或 “lead”), 以优化 “hit” 调节活性的能力。

能设计本发明涉及的其他候选抑制剂，包括结合配偶体的溶液形式，以及为嵌合或融合蛋白的结合配偶体。此处使用的结合配偶体主要包括抗体、抗体片段，和修饰化合物，其包含对所鉴定的毒力基因表达产物有免疫特异性的抗体结构域。

当毒力基因产物的结合配偶体未知时，可使用其他测定法，包括通过测定待测结合配偶体与靶蛋白质的直接结合鉴定靶蛋白质的结合配偶体的测定法，通过亲和超滤与离子喷射质谱法/HPLC 法或其他物理和分析方法鉴定靶蛋白质的结合配偶体的测定法。此外，也可直接

用 Field 和 Song, 自然, 340:245-246 (1989) 和 Fields 和 Sternglanz, 遗传学趋势, 10:286-292 (1994) 所述的酵母双杂交系统评价这些结合作用, 这两篇文献在此引用作为参考。双杂交系统是一种检测两种蛋白质或多肽之间的相互作用的遗传测定法。它能用来鉴定可与已知目的蛋白质结合的蛋白质, 或描述对于该相互作用重要的结构域或残基。已经发展了该方法的变化, 来克隆编码 DNA 结合蛋白的基因, 鉴定可与一种蛋白质结合的肽, 并筛选药物。双杂交系统利用了一对相互作用蛋白质使转录激活域紧密靠近可与报道基因上游激活序列 (UAS) 结合的 DNA 结合域的能力, 并且一般在酵母中进行。该试验需要构建两种杂种基因, 它们编码 (1) 与第一种蛋白质融合的 DNA 结合域, 和 (2) 与第二种蛋白质融合的激活域。DNA 结合域针对将第一种杂种蛋白导向报道基因的 UAS; 然而, 因为大多数蛋白质缺乏激活域, 该 DNA 结合杂种蛋白不能激活报道基因的转录。含有激活域的第二种杂种蛋白不能自己激活报道基因的表达, 因为它不能结合 UAS。但是, 当存在两种杂种蛋白时, 第一种与第二种蛋白质的非共价相互作用使激活域限定于 USA, 激活报道基因的转录。当已知毒力基因产物 (例如第一种蛋白质) 可与另一种蛋白质或核酸相互作用时, 该试验能用来检测干扰结合作用的制剂。向系统中加入不同检测剂后监测报道基因的表达; 抑制剂的存在导致报道信号的缺乏。

当毒力基因产物的功能未知, 并且已知无配体可结合该基因产物时, 也能用酵母双杂交试验鉴定可与该基因产物结合的蛋白质。在鉴定可与第一种蛋白质 (靶蛋白) 结合的蛋白质的试验中, 在试验中产生并筛选编码不同第二种蛋白质的大量杂种基因。一般而言, 第二种蛋白质由总 cDNA 或基因组 DNA 与激活域连接的许多质粒编码。该系统适用于多种蛋白质, 甚至不需要知道第二种结合蛋白的名称或功能。该系统高度敏感, 能检测其他方法无法显示的相互作用; 甚至瞬时相互作用也可触发转录, 而产生一种稳定的 mRNA, 它能被重复翻译, 产生报道蛋白。

可以用其他试验寻找可与靶蛋白结合的制剂。美国专利号

5,585,277 描述了一种这样的筛选方法，其鉴定待测配体与靶蛋白质的直接结合，在此引用作为参考。该方法基于蛋白质通常作为折叠和非折叠状态的混合物存在，并且在两种状态之间不断交替的原理。当待测配体与折叠形式的靶蛋白质结合时（即，当待测配体是靶蛋白质的配体时），该配体结合的靶蛋白质分子仍为其折叠状态。因此，相比不存在配体的情况，在可结合靶蛋白质的待测配体存在下，折叠的靶蛋白以更高的程度存在。配体与靶蛋白的结合能通过可区别靶蛋白质折叠与非折叠状态的任何方法测定。为了进行此种测定，不需要知道靶蛋白的功能。实际上用该方法能评估任何试剂，作为待测配体，包括但不限于：金属、多肽、蛋白质、脂类、多糖、多核苷酸和有机小分子。

Wiebodlt 等人，分析化学 (Anal. Chem.) 69:1683-1691 (1997) 描述了鉴定靶蛋白配体的另一种方法，在此引用作为参考。该技术可在用于结合靶蛋白的溶液相中一次筛查 20-30 个试剂的组合文库。可与靶蛋白结合的试剂通过离心超滤与其他文库组分分离。保留在滤膜上的特别选择的分子随后从靶蛋白中释放，并通过 HPLC 和空气辅助电喷（离子喷射）电离质谱法分析。该方法筛选与靶蛋白具有最大亲和力的文库成分，特别可用于小分子文库。

评价最初筛选鉴定的抑制剂/结合剂对体内小鼠多杀巴斯德氏菌感染模型中的毒力的作用。可以使用菌血症、心内膜炎、脓毒性关节炎、软组织脓肿或肺炎。本发明也涉及包括使用其他动物的模型。例如，能在施用不同量的推断抑制剂/结合剂之前或之后，用野生型多杀巴斯德氏菌株攻击兔。只施用盐水代替推断的抑制剂/结合剂的对照动物提供了一种标准，根据它能确定待测动物的恶化。其他动物模型包括《动物与植物健康检查服务，USDA》，1994 年 1 月 1 日版，113.69-113.70 页；Panciera 和 Corstvet，美国兽医研究杂志 45:2532-2537；Ames 等人，加拿大比较医学杂志 (Can. J. Comp. Med.) 49:395-400 (1984)；和 Mukkur，感染与免疫 18:583-585 (1977) 所述的模型。干扰细菌毒力的抑制剂/结合剂能预防形成感染，或在形成后使感染的后果逆转。

在疫苗组合物中可使用本领域所知的任何佐剂，包括基于油的佐剂，如弗氏完全佐剂和弗氏不完全佐剂，基于梅菌酸的佐剂（例如海藻糖梅菌酸）、细菌脂多糖（LPS）、肽聚糖（即胞壁质、粘肽或糖蛋白，如 N-Opaca、胞壁酰二肽[MDP]或 MDP 类似物）、蛋白聚糖（例如，从肺炎克雷伯氏菌（*Klebsiella pneumoniae*）中提取的）、链球菌制剂（例如 OK432）、BiostimTM（例如 01K2）、EP 109 942, EP 180 564 和 EP 231 039 的 “Iscoms”、氢氧化铝、皂角苷、DEAE-葡聚糖、中性油（如 miglyol）、植物油（如花生油）、脂质体、Pluronic® 多元醇、Ribi 佐剂系统（参见，例如 GB-A-2 189 141），或白细胞介素，特别是刺激细胞介导的免疫的那些。美国专利号 4,877,612 描述了一种可供选择的佐剂，由无枝酸菌属（*Amycolata*）——放线菌目的一种细菌属——的提取物组成。另外，专利佐剂混合物可购得。使用的佐剂部分取决于接受的生物。施用的佐剂量取决于动物在类型和大小。最佳剂量可通过常规方法容易地确定。

疫苗组合物任选地可包含疫苗相容的、药学可接受的（即无菌且无毒的）液体、半固体或固体稀释剂，用作药学载体、赋形剂或基质。可使用本领域所知的任何稀释剂。代表性稀释剂包括但不限于：聚氧乙烯山梨聚糖一月桂酸酯、硬脂酸镁、羟基安息香酸甲基酯和羟基安息香酸丙基酯、滑石、藻酸盐、淀粉、乳糖、蔗糖、葡萄糖、山梨糖醇、甘露糖醇、阿拉伯树胶、磷酸钙、矿物油、可可脂和可可油。

疫苗组合物能以便于施用的形式包装。组合物能包装在胶囊、小胶囊、香袋、面囊、明胶、纸或其他容器中。当与向受体生物中加入免疫原性组合物相容时，特别是当以单位剂量形式施用免疫原性组合物时，优选这些施用形式。剂量单位能包装在，例如，片剂、胶囊、栓剂或面囊剂中。

疫苗组合物可通过任何常规方法输入欲免疫的受体中，这些方法包括，例如，静脉内、真皮内、肌内、乳房内、腹膜内或皮下注射；口服、舌下、鼻、肛门或阴道施用。治疗可由单次施用或一段时间内的多次施用组成。

本发明也包括使用本发明的减毒菌株，生产预防或缓解细菌感染和/或与之相关的症状的疫苗药物。本发明也提供使用本发明的抑制剂生产预防或缓解细菌感染和/或与之相关的症状的药物。

本发明通过下列实施例说明。实施例 1 描述了多杀巴斯德氏菌突变体的构建。实施例 2 涉及多杀巴斯德氏菌突变体的筛选。实施例 3 涉及测定多杀巴斯德氏菌突变体毒力的方法。实施例 4 描述多杀巴斯德氏菌毒力基因的克隆。实施例 5 涉及其他种中与多杀巴斯德氏菌毒力基因有关的基因的鉴定。实施例 6 描述大叶性肺炎放线杆菌突变体的构建。实施例 7 涉及减毒大叶性肺炎放线杆菌突变体的筛选。实施例 8 涉及大叶性肺炎放线杆菌毒力基因的鉴定。实施例 9 描述大叶性肺炎放线杆菌突变体和野生型细菌的竞争攻击。实施例 10 表征了鉴定的大叶性肺炎放线杆菌基因。实施例 11 涉及大叶性肺炎放线杆菌突变体保护对抗野生型细菌攻击的效能。

实施例 1

标记的转座子多杀巴斯德氏菌突变体文库的构建

在以前证明在多杀巴斯德氏菌中有功能且随机[Lee 等人，兽医微生物学 50:143-8 (1996)]的亲本载体 pLOF/Km 中[Herrero 等人，细菌学杂志 172:6557-67 (1990)]中构建标记的转座子突变体文库。质粒 pLOF/Km 构建为自杀载体 pGP704 的改变形式，包含一个在 Tac 启动子控制下的转座酶基因以及编码卡那霉素抗性的 mini-Tn10 转座元件。质粒 pTEF-1 如下所述构建，方法是修饰 pLOF/Km 以接受含有半随机[NK]₃₅ 序列的序列标记。

首先修饰质粒 pLOF/Km，在多克隆区中去除唯一 KpnI 限制位点，然后在 mini-Tn10 区中引入一个新的 KpnI 位点。用 KpnI 消化该质粒，按照厂商推荐的方法用 Klenow 聚合酶填平产生的突出端。此处所述的限制消化和连接按照按照厂商推荐的方法进行 (Gibco BRL, Gaithersburg, MD 和 Boehringer Mannheim, Indianapolis, IN)。平端产物自身连接，产生一种被命名为 pLOF/Km-KpnI 的质粒，用它转化大肠杆菌 DH5 α : λ pir 用于扩增。大肠杆菌 DH5 α : (λ pir

Φ80dlacZΔM15, recA1, endA1, gyrA96, thi-1, hsdR17(r_k⁻, m_k, supE44, relA1, deoR, Δ(lacZYA-argF)U169 在 37℃ 下在 Luria-Bertani (LB) 培养基中繁殖。质粒用来自 QIAGEN Inc. (Santa Clarita, CA) 的 QIAGEN SpinPreps 制备, 并用 SfiI 消化, 该酶在 mini-Tn10 转座元件内的唯一位点处切割。用退火寡核苷酸 TEF1 (SEQ ID NO:86) 和 TEF3 (SEQ ID NO:87) 制备 SfiI-KpnI-SfiI 接头, 产生的双链接头与 SfiI 位点连接, 产生质粒 pTEF-1。寡核苷酸 TEF1 和 TEF3 (以及此处所述的其他所有寡核苷酸) 由 Genosys Biotechnologies (The Woodlands, TX) 合成。

TEF1 5'-AGGCCGGTACCGGCCGCCT SEQ ID NO: 86

TEF3 5'-CGGCCGGTACCGGCCTAGG SEQ ID NO: 87

用于向 pTEF-1 的 KpnI 位点中插入的独特序列标记如下制备。用 GeneAmp XL PCR 试剂盒 (PE Applied Biosystems, Foster City, CA) 进行 PCR 产生双链 DNA 标记, 条件包括 250μM 每种 dNTP, 1.5mM Mg(OAc)₂, 100pmol 每种引物 TEF14 (SEQ ID NO:88) 和 TEF15 (SEQ ID NO:89), 1ng TEF26 (SEQ ID NO:90) 作为模板 DNA, 和 2.5 单位重组 Tth DNA 聚合酶 XL。

TEF14 5'-CATGGTACCCATTCTAAC SEQ ID NO: 88

TEF15 5'-CTAGGTACCTACAACCTC SEQ ID NO: 89

TEF26 SEQ ID NO: 90

5'-CTAGGTACCTACAACCTCAAGCTT-[NK]₃₅-

AAGCTTGGTTAGAATGGGTACCATG

反应条件包括开始在 95℃ 下温育 1 分钟，随后 95℃ 30 秒、45℃ 45 秒、72℃ 15 秒 30 个循环，最后 72℃ 温育 2 分钟。PCR 产物用 KpnI 消化，并用 QIAGEN 核苷酸消除试剂盒按照厂商推荐的方法（QIAGEN Inc., Chatsworth, GA）纯化。使用标准方法，将独特标记序列与预先用 KpnI 消化的线性化 pTEF-1 的 mini-Tn10 元件连接，用牛小肠碱性磷酸酶（Boehringer Mannheim）去磷酸化。产生的质粒文库转化大肠杆菌 DH5α:λpir。按照 DIG 用户指南（Boehringer Mannheim）进行菌落印迹分析，杂交和检测如下进行。

杂交基本按照 Genius 非放射性用户指南（Boehringer Mannheim Biochemicals）进行，用于 DIG-PCR 标记试剂盒（Boehringer Mannheim Biochemicals）的产物片段，和用于 CSPD（Boehringer Mannheim Biochemicals）的产物片段。为制备探针，用 Amplitaq PCR 缓冲液（PE Applied Biosystems）、200μM dNTP、140pmol 每种引物 TEF5（SEQ ID NO:91）和 TEF6（SEQ ID NO: 92）、2mM MgCl₂、2.5 单位 Amplitaq（PE Applied Biosystems）和 1ng 质粒 DNA 建立 100μl 主要 PCR 反应。

TEF5 5'-TACCTACAACCTCAAGCT SEQ ID NO: 91

TEF6 5'-TACCCATTCTAACCAAGC SEQ ID NO: 92

循环条件包括开始在 95℃ 下温育 2 分钟，随后 95℃ 30 秒、45℃ 50 秒、72℃ 15 秒 30 个循环，最后 72℃ 温育 3 分钟。用 2%-3:1 NuSieve GTG（FMC Bioproducts, Rockland, ME, USA）:琼脂糖凝胶电泳分离扩增产物，切下并纯化 109bp 产物。用 QIAGEN 凝胶提取试剂盒（QIAGEN）进行凝胶提取。用 DIG PCR 试剂盒，50pmol 每种引物 TEF24 和 TEF25，GID 探针合成混合液与 2mM dNTP 贮存液的混合物，在 50μl PCR 反应中标记约 15ng 初级产物。

TEF24 5'-TACCTACAACCTCAAGCTT SEQ ID NO: 93

TEF25 5'-TACCCATTCTAACCAAGCTT SEQ ID NO: 94

PCR 条件包括开始在 95℃ 下温育 4 分钟, 随后 95℃ 30 秒、50℃ 45 秒、72℃ 15 秒 25 个循环, 最后 72℃ 温育 3 分钟。标记的 PCR 产物在 90μl 总反应体积中用 HindIII 消化, 并用 2%-3:1 NuSieve GTG (FMC Bioproducts): 琼脂糖凝胶从固定引物臂中纯化。切下含有标记可变标记的区域, 完整凝胶切片在 10ml DIG EasyHyb 中 95℃ 溶解并变性 10 分钟。

斑点印迹用 Hybond®-N⁺ 膜 (Amersham-Pharmacia Biotech) 制备。用约 30ng PCR 产物在 96 孔板中制备每一标记的靶 DNA。加入等体积的 0.1N NaOH, 变性样品, 用 Schleicher 和 Schuell (Keene, NH, USA) 的 Minifold™ 斑点印迹装置以最低真空将每种样品加到膜上。每孔用 150μl 中和溶液 (0.5M Tris/3M NaCl, pH7.5) 和 150μl 2×SSC 洗涤。膜在 Stratalinker (Stratagene, La Jolla, CA, USA) 中 UV 交联, 并在 20ml DIG EasyHyb 缓冲液中 42℃ 预杂交 1 小时。加入变性探针, 在 42℃ 下杂交过夜。膜用含 0.1% SDS 的 2×SSC 洗涤两次, 每次 5 分钟。在 68℃ 下用 50ml 预温的含 0.1% SDS 的 0.1×SSC 缓冲液进行两次高严格洗涤 15 分钟, 之后进行标准 Genius 检测方法 (Genius Manual)。

为了安全、低成本、易用和减少有害物质, 希望使用非放射性检测系统。在使用以前描述类似方法的最初实验中 [Mei 等人, 分子生物学 26:399-407 (1997)], 在阴性对照中获得不可接受的杂交背景水平。为了降低背景, 标记长度提高 30bp, 至 70bp 的总长度, 延长扩增引物, 使之包含可变区侧翼的所有序列, 使用低浓度 dig-dUTP, 通过凝胶纯化去除序列标记区侧翼的保守序列。最重要的是, 在检测转

座子本身的背景杂交之后,用 PCR 产生[NK]₃₅ 序列标记,作为斑点印迹中的靶 DNA,而不用含有标记转座子的完整质粒。使用这些修饰,背景消除,使化学发光/非放射性筛选更加有效。

通过菌落印迹法筛选 pTEF-1 与 PCR 产生的序列标记连接产生的约 400 个不同转化子,将 96 个最强的杂交菌落集合于微量滴定板中进一步应用。尽管有复制标记极低的可能性,但彼此探查证实没有标记的主要标记平板的一半复制。纯化含有这些标记的质粒,并转化大肠杆菌 S17-1:λpir (pir, recA, thi, pro, hsd, (r-m⁺), RP4-2, (Tc::Mu), (Km::Tn7), [TmpR], [SMR]), 转化的细菌在 Luria-Bertani (LB) 培养基中 37℃ 繁殖。在接合中使用含有标记质粒 pTEF-1 的 96 个大肠杆菌 S17-1:λpir 转化子,产生多杀巴斯德氏菌的转座子突变体。多杀巴斯德氏菌株 TF5 是来源于一种牛临床分离株——UC6731 的自发萘啶酮酸抗性突变体。当在平板上生长时,多杀巴斯德氏菌株在 37℃ 和 5% CO₂ 下在脑心浸液 (BHI) 培养基 (Difco Laboratories, Detroit, MI, USA) 上生长。通过将每种大肠杆菌 S17-1:λpir/pTEF-1:[NK]₃₅ 克隆和 TF5 株培养到后对数期建立接合 (Mating)。每种标记-pTEF-1 克隆 50μl 培养液与 200μl TF5 培养液混合,50μl 每种接合混合液点样到预先置于含 100mM IPTG 和 10mM MgSO₄ 的 BHI 平板上的 0.22 μm 滤膜上。在 37℃ 和 5% CO₂ 下温育过夜后,将接合混合液从每一滤膜上洗脱到 3ml PBS 中,并将每种 25μl 涂板于 BHIN⁵⁰K¹⁰⁰ 平板上。选择过夜生长后,通过用牙签向 200μl BHIN⁵⁰K¹⁰⁰ 中转移,将菌落集合到微量滴定板中,确保微量滴定板的每孔中一直含有具有相同序列标记的转座子突变体。过夜生长后,向每孔中加入 50μl 75% 甘油,平板冻存于 -80℃ 下。

通过将转座子突变体转移到微量滴定板中形成 19 个集合,确保每孔含有具有适于该孔的标记的转座子突变体。换句话说,每个微量滴定板的特定孔一直含有具有相同序列标记的转座子突变体,虽然这些突变体中转座子的位置可能不同。

实施例 2

减毒多杀巴斯德氏菌突变体的鼠筛选

用败血症鼠模型筛选 19 个多杀巴斯德氏菌转座子突变体集合。从 -80°C 贮存中取出集合多杀巴斯德氏菌转座子突变体的冷冻平板，并通过将 $10\mu\text{l}$ 转移到新 96 孔圆底平板 (Corning Costar, Cambridge, MA, USA) 的每一孔中而传代培养，每孔含有 $200\mu\text{l}$ 脑心浸液 (DIFCO) 与 $50\mu\text{g/ml}$ 萘啶酮酸 (Sigma) 和 $50\mu\text{g/ml}$ 卡那霉素 (Sigma) ($\text{BHIN}^{50}\text{K}^{50}$)。平板不加振摇在 $5\% \text{CO}_2$ 中 37°C 温育过夜。过夜平板的传代培养包括：从每孔中转移 $10\mu\text{l}$ 到每孔含 $100\mu\text{l}$ BHI 的新平底 96 孔板 (Corning Costar) 中，并以约 150 转/分振摇在 37°C 下温育。用微量滴定板读数仪监测 OD_{540} 。在 OD_{540} 约为 0.2-0.25 时，集合每板，通过合并微量滴定板每孔 $100\mu\text{l}$ 形成“输入集合”。培养物用 BHI 适当稀释至约 10^4 、 10^5 、 10^6 CFU/ml 的剂量，用每一稀释度经腹膜施用感染雌性 14-16 克 BALB/C 小鼠。感染后第 2 天，使一只或两只存活小鼠安乐死，并收集脾脏。完整脾脏在 1.0ml 无菌 0.9% 盐水中匀浆。制备 10^{-2} - 10^{-5} 的匀浆稀释度，并接种于 $\text{BHIN}^{50}\text{K}^{50}$ 平板。过夜生长后，将至少 20000 个菌落集中于 10ml BHI 培养液中，形成“回收集合”，以 $3500\times\text{g}$ 离心 0.5ml 回收集合，按照以前描述的方法 (Wilson, 于: F.M. Ausubel 等人 (编)《现代分子生物学方法》第 1 卷, John Wiley and Sons, 纽约, 2.4.1-2.4.5 页 (1997) 用沉淀制备基因组 DNA。

最初使用毒性野生型多杀巴斯德氏菌的实验表明，能从显示真正败血症感染模型的脾脏、肺、肾脏和肝脏中回收生物。对“输入”和“回收”集合的斑点印迹如实施例 1 所述进行，并通过目测和半定量分析评估。杂交如实施例 1 所述进行，不同之处在于用来自输入和回收集合的 $5\mu\text{g}$ 基因组 DNA 作为模板。半定量分析显示是否发生单克隆的明显减少。如果突变体不能在宿主中存活，则回收信号与输入信号相比应当极低，产生高输入/回收比。大多数突变体在体内与在体外同样生长良好，因此其信号比应当约等于 1。选择经定量分析确定在回收集合中高度减少的克隆进行进一步研究。也可在目测由斑点印

迹制成的薄膜之后，选择具有可疑输入/回收比的其他克隆。

实施例 3

多杀巴斯德氏菌候选突变体毒力的测定

从最初集合平板中分离显示从脾组织回收减少的每种潜在突变体，并在攻击实验中个别使用，来证实并粗略估计转座子突变引起的减毒。由体内筛选获得的个别候选突变体在绵羊血琼脂平板上在 5% CO₂、37℃ 下生长过夜。将每种突变体约 6 个菌落接种于 BHI 培养液中，使之生长 6 个小时。进行稀释，如上所述分别用 10²、10³、10⁴ 和 10⁵ CFU 感染每组 5 只小鼠。通过将 6 天后的死亡率与野生型相比较，确定减毒。存活的小鼠假定受到保护，然后以比野生型菌株的 LD₅₀ 约高 200 倍的浓度用野生型多杀巴斯德氏菌制剂攻击。然后测定小鼠每一攻击组的存活率。

结果表明，120 个潜在转座子突变体中的 62 个减毒，具有比野生型菌株至少高 10 倍的近似 LD₅₀。克隆及其近似 LD₅₀ 值列于表 1 中。利用每组攻击平行进行使用野生型菌株的对照实验，在所有情况中，野生型攻击组的死亡率为 100%。

除了 LD₅₀ 值外，表 1 也提供了来自接种和攻击实验的数据。简言之，小鼠组 (n=5-10) 通过腹膜内注射接种表 1 所示的各种多杀巴斯德氏菌菌株，剂量约为野生型菌株毒力 LD₅₀ 的 200 倍。在计算死亡率数字后观察动物 28 天。

表 1
多杀巴斯德氏菌毒力基因

核苷酸 SEQ ID NO:	代表性 分离株	可能的基因 功能	接种#存活者 /总数	攻击#存活者/总数	LD ₅₀
--	野生型	-	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	vtaO (HI0146)	3/5		$>6 \times 10^5$
118	PM3G11	UnkO	4/5, 10/10	10/10	$>3 \times 10^5$
31	PM7B4	iroA (UnkB)	0/5		
17	PM4C6	fhaB (fhaB2)	2/5, 10/10, 9/10	10/10, 9/9	$>3 \times 10^6$
9	PM4G10-T9	dnaA	4/5		$>5 \times 10^5$
1	PM4D5-T5	atpB	5/5		$>4 \times 10^5$
53	PM4D5-T1	UnkC2	5/5		$>4 \times 10^5$
15	PM4F2	fhaB (fhaB1)	3/5, 6/10, 10/10	6/6, 10/10	$>3 \times 10^5$
41	PM5F7	mreB	4/5		1×10^3
7	PM5E2	devB	0/5, 3/10	2/3	?
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		-6×10^5
37	PM8C1-T3	mgIB	5/5		-6×10^5
58	PM8C1R1-T6	UnkD1	5/5		-6×10^5
45	PM10H7	purF (HI1207)	3/5, 8/10, 8/10	8/8, 8/8	$>3 \times 10^5$
25	PM10H10-T2	HI1501	5/5		$>1 \times 10^4$
72	PM11G8-T2	ygiK	5/5		$>2.4 \times 10^3$
21	PM11G8-T4	greA	5/5		$>2.4 \times 10^3$
84	PM12H6	yyam (HI0687)	3/5, 0/10		-2.2×10^3
33	PM15G8-T2	kdtB	5/5		$>1.2 \times 10^5$
116	PM15G8-T1	UnkK	5/5		$>1.2 \times 10^5$
104	PM16G11-T1	hmbR	3/5		$>1.9 \times 10^5$
29	PM16G11-T2	hxcC	3/5		$>1.9 \times 10^5$
35	PM16H8	lgtC	5/5, 10/10	10/10	$>2.4 \times 10^5$
80	PM16H3	vleA (HI0019)	5/5, 10/10		$>2.0 \times 10^5$
49	PM17H6-T1	sopE	4/5		-6×10^5
120	PM17H6	UnkP	4/5		-6×10^5
5	PM18F5-T8	cap5E	5/5		$>2.4 \times 10^5$
82	PM18F5-T10	vojB (HI0345)	5/5		$>2.4 \times 10^5$
13	PM19A1	exbB	5/5, 10/10	10/10	$>1.2 \times 10^5$
112	PM19D4	rcf	5/5, 8/10	8/8	-1.6×10^5
39	PM20A12	mioC (HI0669)	3/5, 8/10	8/8	-2×10^4
60	PM20C2	UnkD2	5/5, 10/10	10/10	$>8.2 \times 10^6$

实施例 4

多杀巴斯德氏菌毒力所需基因的克隆和鉴定

分析被证实减毒的每种转座子突变体, 进一步确定被打断的开放阅读框的性质。扩增每种突变体的 DNA, 纯化, 并用已知在转座子内不能酶切的限制酶消化, 通常产生可与该转座子杂交的 4-8kb 片段。利用对转座子编码的卡那霉素抗性的选择, 克隆每种转座子突变体的至少一个片段。

使用标记的来自 pLOF/Km 的 1.8kb MluI 片段作为探针, 对每种减毒突变体进行与多种限制酶的 Southern 杂交, 以确定用于克隆的适当大小的片段。将来自每种突变体的 mini-Tn10 元件和侧翼 DNA 克隆到 pUC19 中, 用内部引物 TEF32 和 TEF40、引物步移, 有时用通用 pUC-19 引物, 测定侧翼序列。

TEF-32 GGCAGAGCATTACGCTGAC SEQ ID NO: 95

TEF-40 GTACCGGCCAGGCGGCCACGCGTATTC SEQ ID NO: 96

使用 PE Applied Biosystems (Foster City, CA) 的 BigDye™ 染料终止化学试剂盒, 并在 ABI Prism 377 DNA 测序仪上进行测序反应。为每种克隆获得估计被打断的开放阅读框的双链序列。用 Sequencer 3.0 软件 (Genecodes, Corp., Ann Arbor, MI) 汇编并分析序列数据。用 GCG 程序 [Devereux 等人, 1997, Wisconsin Package 9.0 版, 9.0ed. Genetics Computer Group, Inc., Madison] 在当前可获得的数据库中检索同源序列。

在确定减毒的 37% 的克隆中, mini-Tn10 元件有多个插入。将包含其侧翼序列的每一插入分别克隆到 pGP704 中, 并与野生型菌株杂交, 产生新的多杀巴斯德氏菌突变体, 每种均只含有多种原始插入之一。分别重复检测各个突变体, 确定引起减毒表型的插入。通过测定两条链的序列确定被打断的、预测的开放阅读框的核苷酸序列, 并用

预测的氨基酸序列在当前可获得的数据库中检索类似序列。序列与已知基因、未知基因和以前测序的假定的开放阅读框匹配，或者不与以前鉴定的任何序列匹配。对于与以前鉴定的序列有同源性的那些基因，潜在的功能如表 1 所示分配。

实施例 5

其他种中相关基因的鉴定

在分别的实验中，也用大叶性肺炎放线杆菌（App）进行 STM。App 菌株之一在基因中含有插入，经测序（SEQ ID NO:97）确定为多杀巴斯德氏菌 atpG 基因的物种同源物。这一结果表明在其他细菌种中存在以前所知的多杀巴斯德氏菌基因的同源物，它们也能突变产生其他细菌种的减毒株，供疫苗组合物使用。为了确定在其他细菌种中是否存在其他多杀巴斯德氏菌基因的同源物，用大叶性肺炎放线杆菌 atpG 基因作为探针，对来自其他种的基因组 DNA 进行 Southern 杂交。

大叶性肺炎放线杆菌、溶血巴斯德氏菌（Ph）、多杀巴斯德氏菌和睡眠嗜血杆菌（Hs）基因组 DNA 用 CTAB 方法分离，并用 EcoRI 和 HindIII 在 37℃ 下消化 2 小时。消化的 DNA 用 0.7% 琼脂糖凝胶以 40V 在 TAE 缓冲液中分离过夜。凝胶相继浸于 0.1M HCl 中 30 分钟，0.5M NaOH/1.5M NaCl 中两次，每次 15 分钟，2.5M NaOH/1M Tris, pH7.5 中两次。用 20×SSC 缓冲液（3M NaCl/0.3M 柠檬酸钠）将 DNA 转移到硝酸纤维素膜（Amersham Hybond N⁺）上过夜。用 UV Stratalinker 以自动交联设置（120 毫焦耳）将 DNA 与该膜交联。该膜在 5×SSC/1% 封闭液/0.1% 月桂酰肌氨酸钠/0.02% SDS 中 50℃ 预杂交约 7 小时，并在含有 PCR 产生的 atgG 探针的相同溶液中 50℃ 杂交过夜。

使用 GeneAmp PCR 系统 2400 中的 GeneAmp XL PCR 试剂盒，用引物 DEL-1389（SEQ ID NO:98）和 TEF-46（SEQ ID NO:99）制备探针。模板是基因组大叶性肺炎放线杆菌 DNA。

DEL-1389 TCTCCATTCCCTTGCTGCGGCAGGG SEQ ID NO: 98

TEF-46 GGAATTACAGCCGGATCCGGG SEQ ID NO: 99

PCR 如下进行: 开始加热步骤 94℃ 5 分钟, 94℃ 变性 30 秒、50℃ 退火 30 秒、72℃ 延伸 3 分钟的 30 个循环, 最后延伸步骤 72℃ 5 分钟。用琼脂糖凝胶分离扩增产物, 用 QIAquick 凝胶纯化试剂盒 (QIAGEN) 纯化, 并用 DIG-高引物试剂盒 (Boehringer Mannheim) 标记。从杂交溶液中除去印迹, 用 2×SSC 漂洗, 并用相同缓冲液洗涤两次, 每次 5 分钟。然后在 60℃ 下用 0.5×SSC 洗涤印迹两次, 每次 15 分钟。用 DIG 核酸检测试剂盒 (Boehringer Mannheim) 显示相应带。

实施例 6

标记转座子多杀巴斯德氏菌突变体文库的构建

以前曾经报道使用 pLOF/Km 的转座子诱变在大叶性肺炎放线杆菌中有功能并且随机 [Tascon 等人, 细菌学杂志 175:5717-22(1993)]。为了构建标记的转座子大叶性肺炎放线杆菌突变体, 在接合中用含有预先选择的标记质粒 (pTEF-1:[NK]₃₅) 的 96 个 S17-1:λpir 转化子中的每一个产生大叶性肺炎放线杆菌 AP225 株的转座子突变体, 一种来源于体内传代的 ATCC 27088 株的血清型 1 自发萘啶酮酸抗性突变体。当在平板上生长时, 大叶性肺炎放线杆菌菌株在 37℃ 和 5% CO₂ 条件下在含有 10μg/ml B-烟酰胺腺嘌呤二核苷酸 (V¹⁰) (Sigma, St. Louis, Missouri) 的脑心浸液 (BHI) (Difco Laboratories, Detroit, MI, USA) 培养基上生长。大肠杆菌 S17-1:λpir (λpir, recA, thi, pro, hsdR(r_k, m_k+), RP4-2, (Tc^R::Mu), (Km^R::Tn7), [Tmp^R], [SM^R]) 在 Luria-Bertani (LB) 培养基中 37℃ 繁殖。必要时抗生素以 100μg/ml 氯霉素 (Sigma)、50μg/ml 萘啶酮酸 (N⁵⁰) (Sigma) 和 50 (K⁵⁰) 或 100 (K¹⁰⁰) μg/ml 卡那霉素 (Sigma) 使用。

通过将每种大肠杆菌 S17-1:λpir/pTEF-1:[NK]₃₅ 克隆和 AP225 株培养至后对数期建立接合。50μl 等份的每种标记 pTEF-1 克隆培养液与 150μl APP225 培养液混合，然后将 50μl 每种接合混合液点样到预先置于含 100μM IPTG 和 10mM MgSO₄ 的 BHIV¹⁰ 平板上的 0.22 滤膜上。在 37℃ 和 5% CO₂ 条件下温育过夜后，将接合混合液从每一滤膜上洗脱到 2ml PBS 中，并将每种 200μl 涂板于 BHIV¹⁰N⁵⁰K¹⁰⁰ 平板上。选择过夜生长后，通过用牙签向 200μl BHIV¹⁰N⁵⁰K¹⁰⁰ 中转移，将菌落集合到微量滴定板中，确保微量滴定板的每孔中一直含有具有相同序列标记的转座子突变体。过夜生长后，向每孔中加入 50μl 75% 甘油，平板冻存于 -80℃ 下。

APP 似乎不具有与多杀巴斯德氏菌相同的对 mini-Tn10 元件中多个插入的偏性。只有约 3% 的突变体确定含有多个插入，这与以前报道的一致 [Tascon 等人, 细菌学杂志 175:5717-22(1993)]。APP 的一个问题包括, 鉴定大量含有向 23S RNA 区中插入的突变体(以下所述): 28 个具有向 13 个独特位点中插入的总突变体。这可能表明 23S RNA 含有优先的插入位点, 而且这些插入足以影响 APP 的生长, 导致在宿主内的不同存活率。使用 APP 23S RNA 探针的 Southern 印迹分析表明, APP 可能只含有三个核糖体操纵子, 而与之不同, 在流感嗜血菌中有 5 个, [Fleischmann 等人, 科学 269:496-512 (1995)], 在大肠杆菌中有 7 个完整操纵子 [Blattner 等人, 科学 277:1453-1474 (1997)]。这种位点偏好及其对生长率的作用可能是“饱和诱变”的重要障碍, 因为相当数量的菌落将含有向这些 rRNA 中的插入, 大体积筛选对于获得其他独特减毒突变是必要的。

实施例 7

减毒大叶性肺炎放线杆菌突变体的猪筛选

用猪气管内感染模型筛选含有总共约 800 个突变体的 20 个大叶性肺炎放线杆菌转座子突变体集合。每一集合分别在两只动物中筛查。

从 -80℃ 贮存中取出集合大叶性肺炎放线杆菌转座子突变体的冷冻平板, 并通过将每孔 20μl 转移到新 96 孔圆底平板 (Corning Costar,

Cambridge, MA, USA) 中传代培养, 每孔含有 180 μ l BHIV¹⁰N⁵⁰K¹⁰⁰。平板不加振摇在 5% CO₂ 中 37℃ 温育过夜。过夜平板的传代培养包括: 将每孔 10 μ l 转移到每孔含 100 μ l BHIV¹⁰ 的新平底 96 孔板 (Corning Costar) 中, 并以约 150 转/分振摇在 37℃ 下温育。用微量滴定板读数仪监测 OD₅₆₂。在 OD₅₆₂ 约为 0.2-0.25 时, 集合每块板, 通过合并微量滴定板每孔 100 μ l 形成“输入集合”。培养物用 BHI 适当稀释至约 2 $\times$ 10⁶ CFU/ml。对于每种稀释的集合, 通过经气管气管内施用, 用 4.0ml 感染 10-20kg SPF 猪 (Whiteshire-Hamroc, Albion, IN)。感染后约 20 小时, 使所有存活动物安乐死, 并取出肺。通过向肺中灌注 150ml 无菌 PBS 进行灌洗, 回收存活的细菌, 该方法重复两次。灌洗液以 450 $\times$ g 离心 10 分钟析出大的碎片。然后以 2800 $\times$ g 离心上清液, 沉淀细菌。将沉淀重悬浮于 5ml BHI 中, 并以 10⁻²-10⁻⁵ 的稀释度置于 BHIV¹⁰N⁵⁰K⁵⁰ 平板上。过夜培养后, 至少 100000 个菌落集中于 10ml BHI 培养液中, 形成“回收集合”。通过 CTAB 方法 [Wilson, 于: Ausubel 等人 (编) 《现代分子生物学方法》第 1 卷, John Wiley and Sons, 纽约, 2.4.1-2.4.5 页 (1997)] 用每一回收集合的 0.7ml 部分制备基因组 DNA。

从动物中常规回收为从肺灌洗中 10⁸ CFU 的范围。

如以前所述进行斑点印迹, 并通过目测和半定量分析评估。所有杂交和检测均如述进行。简言之, 通过初始 PCR 扩增制备探针, 随后琼脂糖凝胶纯化希望的产物, 第二次 PCR 扩增引入 dig-dUTP。包括 TEF5、TEF6、TEF24、TEF25、TEF48 和 TEF62 在内的寡核苷酸由 Genosys Biotechnologies (The Woodlands, TX) 合成。引物 TEF69、TEF65 和 TEF66 也用于反向 PCR 反应, 并测序。

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

标记的 PCR 产物然后用 HindIII 消化, 将恒定引物臂与独特标记区分开。切下含有标记的可变标志的区域, 然后溶解完整凝胶切片, 并在 DIG EasyHyb 中变性。用标准 CSPD 检测方案制备并检测斑点印迹。进行薄膜暴露用于目测, 对每一斑点印迹样品测定每秒的发光计数 (LCPS)。用每一突变体的 $LCPS_{\text{输入}}/LCPS_{\text{回收}}$ 比确定可能减毒的突变体。

选择在输入集合中存在但回收集合中高度减少的克隆进行进一步研究。也可在目测由斑点印迹制成的薄膜之后, 选择具有可疑输入/回收比的其他克隆。

实施例 8

大叶性肺炎放线杆菌毒力基因的鉴定

对于 110 个突变体中的每一种, 通过反向 PCR 和直接产物测序测定部分侧翼序列。如上所述, 反向 PCR 用于产生侧翼 DNA 产物, 用于直接测序。测序反应用来自 PE Applied Biosystems (Foster City, CA) 的 BigDye™ 染料终止化学试剂盒进行, 并在 ABI Prism 377 DNA 测序仪上进行。用 Sequencer 3.0 软件 (Genecodes, Corp., Ann Arbor, MI) 汇编并分析序列数据。用 GCG 程序 [Devereux 和 Haeberli, Wisconsin Package 9.0 版, 9.0 ed. Genetics Computer Group, Inc., Madison(1997)] 在当前可获得的数据库中检索同源序列。

表 2 显示鉴定的大叶性肺炎放线杆菌基因和开放阅读框可确定的程度。为核苷酸序列及推断的氨基酸序列提供序列鉴定号。

表 2
大叶性肺炎放线杆菌开放阅读框

完整开放阅读框		无起始密码子-终止密码子	
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	无起始密码子-无终止密码子	
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
起始密码子-无终止密码子		RNA 或非编码序列	
lpdA	SEQ ID NO: 148	tRNA-leu	SEQ ID NO: 162
potD	SEQ ID NO: 156	tRNA-glu	SEQ ID NO: 163
yaeE	SEQ ID NO: 164		
apvC	SEQ ID NO: 128		

通过与细菌数据库比较, 分配表 3 (以下实施例 9) 列出的推断的身份。110 种突变体代表 35 类独特转座子插入。每个基因座不同突变的数量不同, 某些克隆在 ORF 单一位点处一直含有插入, 有些克隆在同一 ORF 的不同位点内含有插入。在通过产生多条 PCR 带并产生多个序列电泳图谱确定筛选的 110 种突变体中检测出三个多点插入。

实施例 9

大叶性肺炎放线杆菌突变体与野生型 APP225 的竞争攻击

从原始集合平板中分离一种代表性克隆, 其来自以上鉴定的每一个独特减毒突变组, 在回收群体中缺乏或高度降低, 并在与野生型菌株 (AP225) 的竞争攻击实验中使用, 证实由转座子突变引起的相对减毒。突变和野生型菌株在 BHIV¹⁰ 中生长至 OD₅₉₀ 为 0.6-0.9。将大约 5.0×10^6 CFU 的每种野生型和突变株加入到 4ml BHI 中。通过经气管气管内施用, 用 4ml 总剂量感染 10-20kg SPF 猪。感染约 20 小时后, 使所有存活动物安乐死, 并取出肺。肺灌洗如上所述进行。对

BHIV¹⁰N⁵⁰ 和 BHIV¹⁰N⁵⁰K¹⁰⁰ 进行平板计数, 以确定输入培养液与肺灌洗样品中野生型比突变体的相对数。竞争指数 (CI) 计算为 [突变 CFU/野生型 CFU]_{输入} / [突变 CFU/野生型 CFU]_{回收}。

在 35 个潜在转座子突变体中, 22 个明显减毒, 具有低于 0.2 的竞争指数 (CI)。从作为阳性对照的一种集合中选择根据 STM 筛查结果似乎不减毒的一种转座子突变体。该突变体具有约为 0.6 的体内 CI。也对该突变体进行体外竞争, 得到 0.8 的 CI。该突变体随后确定在两个苯丙氨酸 tRNA 之间含有插入。

独特减毒单点插入突变体的竞争指数在表 3 中列出。AtpG、pnp 和 exbB app 突变体的竞争指数表明, 这些突变体不能与野生型菌株有效竞争, 因此减毒。

表 3

大叶性肺炎放线杆菌突变体的毒力和建议功能

突变体	相似性	推断的或已知的功能	C.I.
AP20A6	atpH	ATP 合酶	.009
AP7F10	atpG	ATP 合酶	.013
AP17C6	lpdA	二氢硫辛酰胺脱氢酶	.039
AP11E7	exbB	铁化合物的转运	.003, .003, .006
AP3H7	potD	亚精胺/腐胺转运	.308
AP8H6	OmpP5	粘附素/OmpA 同源物	.184
AP18H8	OmpP5-2	粘附素/OmpA 同源物	.552
AP13E9	tig	肽酰-脯氨酸异构酶	.050
AP13C2	fkpA	肽酰-脯氨酸异构酶	<.001
AP15C11	pnp	多核苷酸磷酸化酶	.032
AP18F12	hupA	组蛋白样蛋白	.001
AP20F8	dksA	dnaK 突变的剂量依赖的抑制剂	.075
AP5G4	dnaK	热休克蛋白-陪伴分子	.376
AP17C9	tRNA-leu	蛋白质合成 (基因调节)	.059
AP5D6	tRNA-glu	蛋白质合成	.055
AP18B2	rpmF	蛋白质合成	.112
AP10E7	yaeA	未知	.001
AP19A5	HI0379	未知	.061
AP10C10	apvA	未知	.157
AP18F5	apvB	未知	.103
AP2A6	apvC	未知	.091
AP2C11	ApvD	未知	.014

CI 的精确性似乎极好, 因为 exbB 突变体在三种不同动物内竞争, 产生 0.003、0.003 和 0.006 和 CI。根据以下实施例 11 所述的用 7 种突变体 (n=8) 对猪预先接种的结果, 进一步证实了在大动物研究中根据一种竞争使用竞争指数确定减毒。

实施例 10

减毒大叶性肺炎放线杆菌毒力基因的表征

鉴定的大叶性肺炎放线杆菌基因代表 4 种广泛功能的类别：生物合成酶、细胞转运成分、细胞调节成分和未知的。

atpG 基因—— $F_0F_1 H^+-ATPase$ 复合体的 F_1 - γ 亚基，能在产生 ATP 或通过水解 ATP 转运质子中起作用。也在多杀巴斯德氏菌中鉴定了有关的 atpG 减毒突变体。也鉴定了另一种 atp 基因，atpH，其编码 $F_1\delta$ 亚基。atp 突变体的表型包括：不能适应的酸敏感表型[Foster, 细菌学杂志 173:6896-6902 (1991)]、鼠伤寒沙门氏菌 [Garcia del Portillo 等人, 感染与免疫 61:4489-4492 (1993)] 和多杀巴斯德氏菌 (同上) 中毒力的丧失、流感嗜血菌 Rd 的转化频率和竞争调节基因诱导的降低[Gwinn 等人, 细菌学杂志 179:7315-20 (1997)]。

LpdA 是一种二氢硫辛酰胺脱氢酶，是两种酶复合体——丙酮酸脱氢酶和 2-酮戊二酸脱氢酶的成分。尽管与毒力的关系不知，但当与来自人体的细菌蛋白质接触时，在鼠伤寒沙门氏菌中诱发 LpdA 的产生，这可能提示这种诱导可能参与修复外膜的尝试[Qi 等人, 分子微生物学 17:523-31 (1995)]。

生长和存活必需的稀有化合物的运输在体内是重要的。ExbB 是 TonB 转运复合体的一部分[Hantke 和 Zimmerman, 微生物学信件 (Microbiology letters) 49:31-35 (1981)]，至少以两种不同的方式与 TonB 相互作用[Karlsson 等人, 分子微生物学 8:389-96 (1993), Karlsson 等人, 分子微生物学 8:379-88 (1993)]。离子获取对于病原体是重要的。在这一工作中，已经在 APP 和多杀巴斯德氏菌中鉴定了减毒 exbB 突变体。在其他细菌中鉴定了几种 TonB 依赖的铁受体[Biswas 等人, 分子微生物学 24:169-179 (1997), Braun, FEMS 微生物学综述 (FEMS Microbiol Rev.) 16:295-307 (1995), Elkins 等人, 感染与免疫 66:151-160 (1998), Occhino 等人, 分子微生物学 29:1493-507 (1998), Stojiljkovic 和 Srinivasan, 细菌学杂志 179:805-12

(1997)]。大叶性肺炎放线杆菌产生两种转铁结合蛋白, 这可能依赖于 ExbB/ExbD/TonB 系统, 以获取铁。PotD 是亚精胺 (一种多胺) 转运所需的周质结合蛋白 [Kashiwagi 等人, 生物化学杂志 268:19358-63 (1993)]。巴斯德氏菌科的另一个成员, 溶血巴斯德氏菌, 含有 potD 的同源物 (Lpp38), 它是康复的或外膜蛋白接种的小牛中的主要免疫原 [Pandher 和 Murphy, 兽医微生物学 51:331-41 (1996)]。在溶血巴斯德氏菌中, PotD 似乎与内膜和外膜都有关。PotD 在毒力中或在与保护性抗体的关系中的作用还不知, 尽管以前的研究显示肺炎链球菌的 potD 突变株是减毒的 [Polissi 等人, 感染与免疫 66:5620-9 (1998)]。

鉴定了相对较少的 “经典毒力因子”, 如除流感嗜血菌 OMP P5 的同源物之外的粘附素或毒素。流感嗜血菌 OMP P5 是一种主要外膜蛋白, 与蛋白质 OmpA 孔蛋白家族有关 [Munson 等人, 感染与免疫 61:4017-20 (1993)]。不可分型的流感嗜血菌中的 OMP P5 编码一种表达为丝状结构的菌毛亚基蛋白 [Sirakova 等人, 感染与免疫 62:2002-20 (1994)], 该蛋白质引起粘蛋白和上皮细胞的毒力和结合 [Miyamoto 和 Bakaletz, 微生物病原体 (Microb Pathog.) 21:343-56 (1996), Reddy 等人, 感染与免疫 64:1477-9 (1996), Sirakova 等人, 感染与免疫 62:2002-20 (1994)]。一个重要的发现是鉴定了似乎编码 OMP P5 同源物的两种不同的 ORF。对于两种极其类似的蛋白质——来自杜氏嗜血菌的 MOMP 和 OmpA2 也是如此。仍需确定这两者是否在功能上参与菌毛的产生, 这两种 ORF 的存在是否代表具有多余或互补功能的分开复制。有趣的是, 两种 OMP P5 突变体似乎具有根本不同的 CI 值, 提示只对一个拷贝的重要性或功能性的不同。OMP P5 在慢性感染中显示经历分子变异 [Duim 等人, 感染与免疫 65:1351-1356 (1997)], 然而, 这似乎只限于经历点突变的一种基因, 由于多种基因的不同表达导致氨基酸改变而不是 “类型转变”。

蛋白质折叠酶对于周质和胞外蛋白质有效折叠是重要的附件, 已经鉴定了其产物具有肽酰-脯氨酰异构酶活性的两种基因: flkA 和 tig

（引发因子）。FkpA 是一种周质蛋白，它是 FK506 结合蛋白家族的一员 [Horne 和 Young, 微生物学报 (Arch Microbiol.) 163:357-65 (1995); Missiakas 等人, 分子微生物学 21:871-84 (1996)]。FkpA 显示有利于鼠伤寒沙门氏菌 [Horne 等人, 感染与免疫 65:806-10 (1997)] 的胞内存活, 嗜肺军团菌 (*Legionella pneumophila*) 同源物 mip [Engleberg 等人, 感染与免疫 57:1263-1270 (1989)] 负责毒力和巨噬细胞的感染 [Cianciotto 等人, 传染病杂志 162:121-6 (1990); Cianciotto 等人, 感染与免疫 57:1255-1262 (1989)]。Tig 或引发因子 [Crooke 和 Wickner, 美国国家科学院院报 84:5216-20 (1987), Guthrie 和 Wickner, 细菌学杂志 172:5555-62 (1990), Hesterkamp 和 Bukau., FEBS Lett. 389:32-4 (1996) 综述] 是一种含有典型 FKBP 区的肽酰脯氨酰异构酶 [Callebaut 和 Mornon, FEBS Lett. 374:211-215 (1995)], 但不受 FK506 影响 [Stoller 等人, EMBO J. 14:4939-48 (1995)]。Tig 显示与核糖体和新生多肽链有关 [Hesterkamp 等人, 美国国家科学院院报 93:4437-41 (1996), Stoller 等人, EMBO J. 14:4939-48 (1995)]。可能的作用包括在大肠杆菌中的一种未知的对细胞分裂的作用 [Guthrie 和 Wickner, 细菌学杂志 172:5555-62 (1990)], 酿脓链球菌 (*Streptococcus pyogenes*) 半胱氨酸蛋白酶分泌和激活的作用 [Lyon 等人, EMBO J. 17:6263-75 (1998)], 和枯草芽孢杆菌 (*Bacillus subtilis*) 在饥饿条件下的存活 [Gothel 等人, 生物化学 37:13392-9 (1998)]。

为了在多种宿主环境条件下存活, 细菌病原体利用多种机制协同调节基因表达。mRNA 稳定性的不同能调节原核生物中的基因表达 [Belasco 和 Higgins, 基因 72:15-23 (1988)]。例如, 例如, rnr (vacB) 是质粒携带的毒力基因在弗氏志贺氏菌 (*Shigella flexneri*) 中表达所需的 [Tobe 等人, 细菌学杂志 174:6359-67 (1992)], 并且编码 RnaseR 核糖核酸酶 [Cheng 等人, 生物化学杂志 273:14077-14080 (1998)]。PNP 是一种参与 mRNA 降解的多核苷酸磷酸化酶。无效 pnp/rnr 突变体是致死的, 提示可能的功能重叠。因此 rnr 和 pnp 两者都参与毒力

基因表达的调节是可能的。多杀巴斯德氏菌的 *pnp* 突变体在小鼠败血症模型中是无毒的（实施例 2）。其他 *pnp* 相关的表型包括枯草芽孢杆菌的能力缺陷和寒冷敏感性[Wang 和 Bechhofer, 细菌学杂志 178:2375-82 (1996)]。

HupA 是一种细菌组蛋白样蛋白质，它与 HupB 一起构成大肠杆菌的 HU 蛋白。有报道指出，*hupA* 和 *hupB* 单突变体不能证明有任何可观察到的表型[Huisman 等人, 细菌学杂志 171:3704-12 (1989), Wada 等人, 分子生物学杂志 204:581-91 (1988)]，然而，*hupA-hupB* 双突变体显示寒冷敏感，对热休克敏感，并能阻止多种形式的位点特异性 DNA 重组[Wada 等人, 分子生物学杂志 204:581-91 (1988), Wada 等人, 基因 76:345-52 (1989)]。以前的一组有限数据显示，*hupA* 直接参与毒力[Turner 等人, 感染与免疫 66:2099-106(1998)]。HupA 减毒的机制仍然不知。

DnaK 是一种众所周知的且高度保守的热休克蛋白，参与对不同应激环境改变的调节反应[Lindquist 和 Craig, 遗传学年述 (Annu Rev Genet) 22:631-77 (1988) 综述]。DnaK 也是在被巨噬细胞吞噬后小肠结肠炎耶尔森氏菌中最明显诱导的应激蛋白之一[Yamamoto 等人, 微生物学与免疫学(Microbiol Immunol.)38:295-300 (1994)]，猪布鲁氏杆菌 (*Brucella suis*) *dnaK* 突变体不能在巨噬细胞样细胞中增殖[Kohler 等人, 分子微生物学 20:701-12 (1996)]。相反，另一种胞内病原体，单核细胞增多性李斯特杆菌 (*Listeria monocytogenes*)，在吞噬作用后不显示 *dnaK* 的诱导[Hanawa 等人, 感染与免疫 63:4595-9 (1995)]。霍乱弧菌(*Vibrio cholera*)的 *dnaK* 突变体影响 ToxR 及其调节毒力因子的体外产生，但用体内生长的细胞未获得类似结果[Chakrabarti 等人, 感染与免疫 67:1025-1033 (1999)]。大叶性肺炎放线杆菌 *dnaK* 突变体的 CI 高于大多数减毒突变体，尽管仍有接近一半的阳性对照株。

DksA 是大肠杆菌 *dnaK* 突变体中丝状和温度敏感生长的一种剂量依赖的抑制剂[Kang 和 Craig, 细菌学杂志 172:2055-64 (1990)]。

DksA 目前没有确定的分子功能,但已经确定该基因对于鸡和新孵化的小鸡中鼠伤寒沙门氏菌的毒力是重要的[Turner 等人, 感染与免疫 66:2099-106 (1998)]。在该工作中,指出 dksA 突变体不能与葡萄糖或组氨酸一起良好生长,但以谷氨酰胺或谷氨酸作为唯一碳源可以生长良好。这一发现可以表明, dksA 突变体在谷氨酸生物合成方面不明原因地削弱[Turner 等人, 感染与免疫 66:2099-106 (1998)]。

鉴定了在蛋白质合成中具有作用的三种基因: tRNA-leu、tRNA-glu 和 rpmF。除了蛋白质合成之外, tRNA 在肽聚糖合成[Stewart 等人, 自然 230:36-38 (1971)]、卟啉环合成[Jahn 等人, 生物化学趋势 (Trends Biochem Sci.) 17:215-8 (1992)]、用于降解的蛋白质的导向[Tobias 等人, 科学 254:1374-7 (1991)]、氨基酸向蛋白质中的翻译后添加 [Leibowitz 和 Soffer, B.B.R.C. 36:47-53(1969)]和细菌-真核相互作用的介导[Gray 等人, 细菌学杂志 174:1086-98(1992), Hromockyj 等人, 分子微生物学 6:2113-24 (1992)]中也具有多种功能作用。更具体而言, tRNA-leu 与转录减弱 [Carter 等人, 美国国家科学院院报 83:8127-8131 (1986)]、丁香假单胞菌 (*Pseudomonas syringae*) 的损伤形成[Rich 和 Willis, 细菌学杂志 179:2247-58 (1997)]和尿路致病大肠杆菌的毒力[Dobrindt 等人, FEMS 微生物学信件 162:135-141 (1998), Ritter 等人, 分子微生物学 17:109-21(1995)]有关。还不知道我们已经鉴定的 tRNA 是否代表大叶性肺炎放线杆菌中 tRNA-leu 的少数种。无论如何, tRNA-leu 具有广泛功能中的任一种是可能的。RpmF 是大肠杆菌中的一种核糖体蛋白, 其基因也是含有脂肪酸生物合成酶的操纵子的部分。需要进一步的工作来说明在大叶性肺炎放线杆菌是否如此, 尽管在流感嗜血菌中发生相同的 fab 基因和 rpmF 聚簇。Fab 基因的表达不必依赖于 rpmF 上游的转录物起始, 因为在 rpmF 内确定有一个次级启动子[Zhang 和 Cronan, Jr., 细菌学杂志 180:3295-303 (1988)]。

最后一类减毒突变体包括未知功能的基因或以前未鉴定的基因内的突变。以前分别在大肠杆菌[Blattner 等人, 科学 277:1453-1474

(1997)]和流感嗜血菌[Fleischmann 等人, 科学 269:496-512(1995)]中鉴定了 yaeA 和 HI0379 的同源物。其余的未知物已经被命名为大叶性肺炎放线杆菌毒力基因 (apv)。apvC 基因显示与 HI0893 的显著相似性, 但是, 作为类似于脂肪酸应答调节剂 Bm3R1[Palmer, 生物化学杂志 273:1453-1474 (1997)]的转录抑制剂, 提出的 HI0893 的相似性受到怀疑。apvD 基因也最类似于来自大肠杆菌、具有未知功能的推断的膜蛋白(b0878)[Blattner 等人, 科学 277:1453-1474(1997)]。其他两种未知物, apvA 和 apvB 在公开数据库中沒有明显匹配。

实施例 11

大叶性肺炎放线杆菌突变体的安全性和效能

使用 9 组 (n=8) SPF 猪 (4-5 周龄, 3-10kg) 测定 7 株大叶性肺炎放线杆菌突变体作为减毒活疫苗株的安全性和效能。7 组在第一天鼻内感染 10^{10} CFU 每种突变体。一组在第 1 天和第 15 天接种商品获得的疫苗 Pleuromune (Bayer), 一个空白组不接种。在第 29 天, 所有组别都用每只猪 $1-5 \times 10^5$ CFU 的野生型 APP225 鼻内攻击。于研究的第 42 天使所有存活动物安乐死, 并进行尸体剖检。结果显示在表 4 中。

表 4

大叶性肺炎放线杆菌突变体的效能

疫苗	鼻内攻击后的%死亡率	
	接种	攻击
Pleuromune	0	37.5
exbB	0	0
tig	12.5	0
fkpA	12.5	0
HI0385	50.0	0
pnp	0	0
yaeE	0	0
atpG	0	0
无	N/A	50.0

当以 10^{10} CFU 的剂量鼻内施用, *exbB*、*atpG*、*pnp* 和 *yaeE* 突变体不导致死亡。*fkpA* 和 *tig* 突变体组每个有一只死亡, HI0379 组(如实施例 9 所示, 所检测的 7 个突变体的 CI 在 2000 年 4 月 6 日最高)有 4 只死亡。使用该模型的野生型 LD_{50} 一般为 1×10^7 CFU, 表明这些突变体中的每一种至少减毒 100 倍, 并且在 CI 与减毒之间存在合理相关性。

如以上说明性实施例所述, 预计本领域技术人员可想到本发明的大量修改和变化。因此, 只有所附权利要求书所示的这些限制才能对本发明施加。

序列表

<110> Lowery E., David
Fuller E., Troy
Kennedy J., Michael

<120> 抗菌疫苗组合物

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aacaatagtt ttaaacaata ttcttccatt ttttataagt aagtacttaa atataaagca 180

ttttcataaaa tatcaataaaa ggattagtt atg gca gca gag ett aca aca gcg 233

Met Ala Ala Glu Leu Thr Thr Ala

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5

gga tat att ggg cac cat tta gca ttc ttg aaa aca ggg gat tct ttc 281

Gly Tyr Ile Gly His His Leu Ala Phe Leu Lys Thr Gly Asp Ser Phe

10

15

20

tgg cat gtt cat tta gat acc ctt cta ttt tca att att tca ggt gca 329

Trp His Val His Leu Asp Thr Leu Leu Phe Ser Ile Ile Ser Gly Ala

25

30

35

40

att ttt ctt ttt gtt ttt tca aaa gtt gca aaa aaa gca acg ccg ggt 377

Ile Phe Leu Phe Val Phe Ser Lys Val Ala Lys Lys Ala Thr Pro Gly

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50

55

gtg cct agc aag atg caa tgt ttt gtt gag ata atg gtt gat tgg att 425

Val Pro Ser Lys Met Gln Cys Phe Val Glu Ile Met Val Asp Trp Ile

60

65

70

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 75 80 85

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 Pro Leu Ala Leu Thr Ile Phe Cys Trp Val Phe Ile Met Asn Ala Ile
 90 95 100

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 Asp Leu Ile Pro Val Asp Phe Leu Pro Gln Leu Ala His Leu Phe Gly
 105 110 115 120

att gaa tac tta aga gct gtt cca aca gca gat atc agt gga aca tta 617
 Ile Glu Tyr Leu Arg Ala Val Pro Thr Ala Asp Ile Ser Gly Thr Leu
 125 130 135

ggc tta tca att ggt gtc ttc ttc tta att att ttc tat aca atc aaa 665
 Gly Leu Ser Ile Gly Val Phe Phe Leu Ile Ile Phe Tyr Thr Ile Lys
 140 145 150

tca aaa ggt atg agt ggc ttt gtt aaa gaa tat acg ctt cat cct ttt 713
 Ser Lys Gly Met Ser Gly Phe Val Lys Glu Tyr Thr Leu His Pro Phe
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 Asn Asn Phe Ala Leu Asn Ser Met Gly Ile Phe Met His Leu Ala Trp
 220 225 230

gct att ttc cat att ctt gtg att acc tta caa gca ttt att ttt atg 953
 Ala Ile Phe His Ile Leu Val Ile Thr Leu Gln Ala Phe Ile Phe Met
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 35 40 45
 Val Ala Lys Lys Ala Thr Pro Gly Val Pro Ser Lys Met Gln Cys Phe
 50 55 60
 Val Glu Ile Met Val Asp Trp Ile Asp Gly Ile Val Lys Glu Asn Phe
 65 70 75 80
 His Gly Pro Arg His Ala Val Gly Pro Leu Ala Leu Thr Ile Phe Cys
 85 90 95
 Trp Val Phe Ile Met Asn Ala Ile Asp Leu Ile Pro Val Asp Phe Leu
 100 105 110
 Pro Gln Leu Ala His Leu Phe Gly Ile Glu Tyr Leu Arg Ala Val Pro
 115 120 125
 Thr Ala Asp Ile Ser Gly Thr Leu Gly Leu Ser Ile Gly Val Phe Phe
 130 135 140
 Leu Ile Ile Phe Tyr Thr Ile Lys Ser Lys Gly Met Ser Gly Phe Val
 145 150 155 160
 Lys Glu Tyr Thr Leu His Pro Phe Asn His Pro Leu Leu Ile Pro Val
 165 170 175
 Asn Leu Ala Leu Glu Ser Val Thr Leu Leu Ala Lys Pro Val Ser Leu
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 Ala Phe Arg Leu Phe Gly Asn Met Tyr Ala Gly Glu Leu Ile Phe Ile
 195 200 205
 Leu Ile Ala Val Met Tyr Met Ala Asn Asn Phe Ala Leu Asn Ser Met
 210 215 220
 Gly Ile Phe Met His Leu Ala Trp Ala Ile Phe His Ile Leu Val Ile
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 Met Arg Lys Thr Gln Glu Arg Met Ser Ser Ser Arg Pro Tyr Ser Glu
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 aca ata cgt aac gtg att agc cac gtt tcc aaa gca acg att ggt tac 552
 Thr Ile Arg Asn Val Ile Ser His Val Ser Lys Ala Thr Ile Gly Tyr
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 Lys His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile
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 Phe Lys Thr Val Leu Asn Glu Met Lys Glu Trp Lys Glu Lys Asp Val
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 Tyr Lys Lys Gly Glu Val Asp Val Val Tyr Leu Val Tyr Asn Lys Phe
 160 165 170 175
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 Ile Asn Thr Met Ser Gln Lys Pro Val Leu Glu Lys Leu Ile Pro Leu
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Tyr Ile Tyr Glu Pro Asp Ala Lys Val Leu Leu Asp Asn Leu Leu Val
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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

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 35 40 45
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 50 55 60
 His Pro Phe Leu Val Asp Arg Glu Val Lys Lys Val Gly Met Ile Val
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 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
 145 150 155 160
 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
 225 230 235 240
 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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Glu Phe Tyr Pro Leu Glu Ala Val Lys Thr Asn Ile Leu Gly Thr Ala	
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Asn Val Leu Glu Ala Ala Ile Gln Asn Gln Ile Lys Arg Val Val Cys	
35 40 45	
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Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser	
50 55 60	
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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	
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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	
ggg gaa cca aaa att acc gaa gtc acc gac tac aac tca cat aat act	720
Gly Glu Pro Lys Ile Thr Glu Val Thr Asp Tyr Asn Ser His Asn Thr	
225 230 235 240	

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 Glu Arg Leu Thr Val Lys Glu Met Lys Gln Leu Leu Leu Lys Leu Glu
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 Phe Ile Gln Lys Met Ile Glu Gly Glu Tyr Ile Ser Pro Glu Val
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 35 40 45
 Leu Ser Thr Asp Lys Ala Val Tyr Pro Ile Asn Ala Met Gly Ile Ser
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 Lys Ala Met Met Glu Lys Val Ile Ile Ala Lys Ser Arg Asn Leu Glu
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 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
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 Leu Glu Asp Ala Val Asp Leu Val Leu Tyr Ala Phe Lys Asn Gly Gln
 130 135 140

Asn Gly Asp Val Phe Val Gln Lys Ala Pro Ala Ala Thr Ile Gly Thr
 145_ 150 155 160
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 Ser Ile Ile Gly Thr Arg His Gly Glu Lys Ala Phe Glu Ala Leu Leu
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 Ser Arg Glu Glu Met Val His Ala Ile Asn Glu Gly Asn Tyr Tyr Arg
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 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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010100

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Glu Lys Ile Ala Gln Glu Leu Leu Ala Tyr Ser Leu Glu Gly Arg Pro
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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
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Thr Leu Ala Gln Ala Pro Tyr Asn Thr Glu Ile Gln Trp Lys Asn Leu

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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

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Glu Leu His Arg Phe Glu Gln Ala Leu Ser Ala Val Ile Pro Gly Gln
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145 150 155

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Ile Ala Lys His Pro Glu Thr Gly Gln Ile Arg Ile Ser Lys Thr Ala
160 165 170

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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

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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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Cys Leu Thr Gln Gln Phe Phe Tyr Ile Trp Gly Glu Gln Ser Ser Gly
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Lys Ser His Leu Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln
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His Gln Leu Asp Asp Glu Thr Leu Asp Asn Phe Tyr Pro Asp Asn Asn
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Leu Leu Leu Leu Asn Ser Leu Arg Lys Asn Phe Thr Cys Leu Thr Gln
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Leu Lys Gly Ile Thr His His Phe Phe Leu Leu Gln Arg Pro Ala Ile
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Tyr Val Pro Leu Glu Lys Ser Gln Tyr Phe Ser Pro Ala Val Leu Glu
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Ile Gly Asn Thr Glu Trp Glu Leu Ala Ile Phe Asp Leu Phe Asn Arg
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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
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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
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 Ala Leu Tyr Phe Gln His Gly Met Gly Leu Ala Pro Cys Val Met Cys
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 Ile Tyr Glu Arg Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu
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Val Ala Ile Leu Gly Ile Ala Phe Ser Gly Leu Leu Gly Leu Leu Tyr
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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
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Leu Tyr Pro Ala Pro Trp Lys Gln Cys Ser Ala Val Ala Glu Phe Pro
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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
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Gln Trp Ile Val Val Ile Phe Ala Leu Tyr Thr Leu Leu Leu Ala Leu
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 Gly Leu Leu Ala Phe Met Ser Phe Ile Met Val Trp Leu Val Ile Glu
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cgc ttt ctt ttc tta agt cgc gtc aac gtg gca tct tat gaa agc ata 2902
 Arg Phe Leu Phe Leu Ser Arg Val Asn Val Ala Ser Tyr Glu Ser Ile
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 His Glu Leu Asp Ile Asp Leu Gln Arg His Leu Thr Ala Ile Ser Thr
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 85 90 95

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 Gly Arg Lys Val Glu Val Asn Arg Leu Lys Trp Phe Ala Leu Asn Glu
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 Lys Lys Ala Lys Gln Ala
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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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Thr Ile Gly Ser Asn Ala Pro Tyr Val Gly Leu Leu Gly Thr Val Ile
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Gly Ile Leu Leu Thr Phe Tyr Glu Leu Gly His Ser Gly Gly Asp Ile
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Met
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Glu Asn Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu	
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Arg Ser Val Tyr Asn Ile Gly Asp Ile Tyr Ala Ser Lys Lys Leu Thr	
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Val His Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val	
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Ser Tyr Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val	
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Thr Phe Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe	
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Phe Gly Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn	
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01120

230	235	240	
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ttc ttt gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga Phe Phe Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly 450 455 460 465			1928
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0112

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aag aaa caa caa gaa gaa aaa cat tta tcc gag gag aaa aaa caa gct Lys Lys Gln Gln Glu Glu Lys His Leu Ser Glu Glu Lys Lys Gln Ala 595 600 605	2360
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att gaa caa cag aaa gcg tat gaa gaa atg gcg aag cga gag gca gag Ile Glu Gln Gln Lys Ala Tyr Glu Glu Met Ala Lys Arg Glu Ala Glu 630 635 640	2456
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Tyr	Val	Lys	Thr	Lys	Val	Lys	Gly	Lys	Asp	Val	Phe	Val	Pro	Lys	Val			
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tat	ttc	gct	tct	gaa	acg	ctc	gta	gaa	gcc	caa	aaa	tta	caa	ggg	tta	2936		
Tyr	Phe	Ala	Ser	Glu	Thr	Leu	Val	Glu	Ala	Gln	Lys	Leu	Gln	Gly	Leu			
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Gly	Thr	Gly	Thr	Ile	Arg	Val	Gly	Glu	Ala	Lys	Ile	Lys	Ala	Lys	Asp			
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tcg	ccg	agt	gca	cta	caa	gtt	gca	gaa	ctt	gat	gtg	gca	ggg	ctt	aaa	3368		
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 995 1000 1005

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Glu Tyr Asp Leu Ser Lys His Glu Leu Lys Lys Thr Ser Gly Glu Asn	
315 320 325	
gta tct aat gat gtt att gct atc acg gga tct agt aca ggc gca atg	2504
Val Ser Asn Asp Val Ile Ala Ile Thr Gly Ser Ser Thr Gly Ala Met	
330 335 340	
cat ggt aaa aat att aag ttg att gtg aca gat aaa ggt gca ggc gta	2552
His Gly Lys Asn Ile Lys Leu Ile Val Thr Asp Lys Gly Ala Gly Val	
345 350 355	
aaa cat gat gga att att ttg tct gaa aat gat att cag att gaa atg	2600
Lys His Asp Gly Ile Ile Leu Ser Glu Asn Asp Ile Gln Ile Glu Met	
360 365 370	
aat gaa ggt gac tta gaa ctt ggc aat acg att cag caa aca gtg gta	2648
Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr Ile Gln Gln Thr Val Val	
375 380 385 390	
aaa aaa gac cga aat att cga gcc aag aaa aaa att gaa gtg aaa aac	2696
Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys Lys Ile Glu Val Lys Asn	
395 400 405	
gct aat cgt gtt ttt gtt ggt agt caa acg aaa tca gat gaa att tcg	2744
Ala Asn Arg Val Phe Val Gly Ser Gln Thr Lys Ser Asp Glu Ile Ser	
410 415 420	
tta gag gcg aaa caa gtt aaa atc aga aaa aac gca gag att agg agt	2792
Leu Glu Ala Lys Gln Val Lys Ile Arg Lys Asn Ala Glu Ile Arg Ser	
425 430 435	
acg aca caa gcc aaa atc gta gca aag ggt gcc ctg tct att gag caa	2840
Thr Thr Gln Ala Lys Ile Val Ala Lys Gly Ala Leu Ser Ile Glu Gln	
440 445 450	
aat gcg aag ctc gtc gct aaa aag ata gat gtg gca aca gaa act cta	2888
Asn Ala Lys Leu Val Ala Lys Lys Ile Asp Val Ala Thr Glu Thr Leu	
455 460 465 470	
act aat gct ggg cgt att tat ggt cga gag gtt aag ctt gac act aat	2936
Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu Val Lys Leu Asp Thr Asn	
475 480 485	

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

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

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

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

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

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

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

<210> 18

<211> 589

<212> PRT

<213> 多杀巴斯德氏菌

<400> 18

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Leu Val Pro Val Ala Glu Cys Ile Asn Ser Ala Ile Ser Asn Gly Ser
 20 25 30

Ser Asp Ser Thr Ser Thr Ser Glu Gln Val Glu Glu Glu Pro Phe Leu
 35 40 45

Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
 50 55 60

Phe Asn Pro Val Ser Tyr Ala Met Gln Leu Thr Trp Lys Gln Leu Ser
 65 70 75 80

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

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

Lys Leu Asp Ala Ser Asn Leu Ala Gly Asn Asp Lys Thr Lys Ile Tyr
 115 120 125

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

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

Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala
 485 490 495
 Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile
 500 505 510
 Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg
 515 520 525
 Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser
 530 535 540
 Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu
 545 550 555 560
 Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu
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<210> 19
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 cat gct tac caa aac cag ccc cta tca aca aaa gtt gtt ttt caa tta 96
 His Ala Tyr Gln Asn Gln Pro Leu Ser Thr Lys Val Val Phe Gln Leu
 20 25 30
 gtg aaa gat ttg acg gaa gtt tta tac cgt tct ggc tac gtg aca agt 144
 Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
 35 40 45
 gca att ggt tta aaa aat tca aaa atc agc aat ggc gat ctt gaa ttt 192
 Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe
 50 55 60
 att gta ctg tgg gga aga act cgc gat ctg ttt gtg aat ggg gag aaa 240
 Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys
 65 70 75 80
 cca acc cgt ttt aga gat aaa aca atg tta tca gtc cta ccc aat tta 288
 Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
 85 90 95
 atc gga aat cgc tta agt att cac gac att gac cag ttg atc gaa atc 336
 Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
 100 105 110

tta aat act acg aat aaa aaa gcc aca gtg aat gtg gtt gca agt gaa	384
Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu	
115 120 125	
gaa aaa ggc agc tca aat cta aat att gaa aga caa tat gat gtt ttt	432
Glu Lys Gly Ser Ser Asn Leu Asn Ile Glu Arg Gln Tyr Asp Val Phe	
130 135 140	
ccg caa gtg agt gtc gga ttc aat aat tca ggt gct ggc aat aat gcc	480
Pro Gln Val Ser Val Gly Phe Asn Asn Ser Gly Ala Gly Asn Asn Ala	
145 150 155 160	
aat ggg cgt aat caa gct aca ttg aat att gct tgg agt gat cta tta	528
Asn Gly Arg Asn Gln Ala Thr Leu Asn Ile Ala Trp Ser Asp Leu Leu	
165 170 175	
ggc acg aat gat cgt tgg agt ttc tgc agt agt tac cgt tta tat aaa	576
Gly Thr Asn Asp Arg Trp Ser Phe Ser Ser Ser Tyr Arg Leu Tyr Lys	
180 185 190	
aat cat cat gct aac cag caa cgc aat tat act ttg tct tac agt cag	624
Asn His His Ala Asn Gln Gln Arg Asn Tyr Thr Leu Ser Tyr Ser Gln	
195 200 205	
cct ata ggc ttt tct aca gta gaa att aaa gca tgc gaa tct acg tat	672
Pro Ile Gly Phe Ser Thr Val Glu Ile Lys Ala Ser Glu Ser Thr Tyr	
210 215 220	
gaa aaa gaa ctt cgc ggt ata aat act cat tct tct cat ggg aaa acc	720
Glu Lys Glu Leu Arg Gly Ile Asn Thr His Ser Ser His Gly Lys Thr	
225 230 235 240	
caa agc tta gct gtc aag ctg atg cat gtg tta ttg cgt aat aag gag	768
Gln Ser Leu Ala Val Lys Leu Met His Val Leu Leu Arg Asn Lys Glu	
245 250 255	
agt att tta tct aca tat acc gag ttc gag ttt aaa aaa cgg att agt	816
Ser Ile Leu Ser Thr Tyr Thr Glu Phe Glu Phe Lys Lys Arg Ile Ser	
260 265 270	
tat ttt tct gat att ttg att ggg aaa tat cac aat aat aaa gtg agc	864
Tyr Phe Ser Asp Ile Leu Ile Gly Lys Tyr His Asn Asn Lys Val Ser	
275 280 285	
gta ggg tta tct tac atg act aat ttt gct tac ggg aag ctt tac agc	912
Val Gly Leu Ser Tyr Met Thr Asn Phe Ala Tyr Gly Lys Leu Tyr Ser	
290 295 300	
gac att gct tac gcg aat ggg ttg aga tgg ttt ggg gcg aat tat tca	960
Asp Ile Ala Tyr Ala Asn Gly Leu Arg Trp Phe Gly Ala Asn Tyr Ser	
305 310 315 320	
gca tat gat gca aat cgt gaa aaa acc tta aaa tta ttg tca gga agt	1008
Ala Tyr Asp Ala Asn Arg Glu Lys Thr Leu Lys Leu Leu Ser Gly Ser	
325 330 335	
att aat tgg cag cgt cca ata tcc ctg ttt gaa cgt gcg atg aat tat	1056
Ile Asn Trp Gln Arg Pro Ile Ser Leu Phe Glu Arg Ala Met Asn Tyr	
340 345 350	
caa tta cgt att ggt gcc caa tat ggt ttt gat agt ttg tat tct gaa	1104
Gln Leu Arg Ile Gly Ala Gln Tyr Gly Phe Asp Ser Leu Tyr Ser Glu	

355 360 365
 aat caa ttt tca att ggt gat gaa tat aca gta aga gga ttt aaa ggt 1152
 Asn Gln Phe Ser Ile Gly Asp Glu Tyr Thr Val Arg Gly Phe Lys Gly
 370 375 380
 ggt gcg gtt tct ggt gat agt ggt gcg tat tta tca caa aca ctg acg 1200
 Gly Ala Val Ser Gly Asp Ser Gly Ala Tyr Leu Ser Gln Thr Leu Thr
 385 390 395 400
 gtt cct ttt tat cca caa aaa gca tat tta tct cag gta tcc cct ttt 1248
 Val Pro Phe Tyr Pro Gln Lys Ala Tyr Leu Ser Gln Val Ser Pro Phe
 405 410 415
 att gga ttt gat atg ggt aaa gta cat att aaa tca aag cat aaa aca 1296
 Ile Gly Phe Asp Met Gly Lys Val His Ile Lys Ser Lys His Lys Thr
 420 425 430
 acc act tta gtc ggt ttt gcc cta ggc ttg aaa acg caa ata aag tta 1344
 Thr Thr Leu Val Gly Phe Ala Leu Gly Leu Lys Thr Gln Ile Lys Leu
 435 440 445
 ttt tca tta tca tta acc tat gca caa cca atg aat ggt gtg agt ggt 1392
 Phe Ser Leu Ser Leu Thr Tyr Ala Gln Pro Met Asn Gly Val Ser Gly
 450 455 460
 gtt acg caa cat cgt caa aaa ccg att tat tat ttc tca gga tca ctt 1440
 Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
 465 470 475 480
 tct ttt taatctcttt taagttaaag gattaactta atatgaacaa aaatcgttac 1496
 Ser Phe
 aaactcattt ttagtcaagt caaagggtgt ctcggtcctg tggcagaatg tattaactca 1556
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<211> 482

<212> PRT

<213> 多杀巴斯德氏菌

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Val Lys Asp Leu Thr Glu Val Leu Tyr Arg Ser Gly Tyr Val Thr Ser
35 40 45

Ala Ile Gly Leu Lys Asn Ser Lys Ile Ser Asn Gly Asp Leu Glu Phe
50 55 60

Ile Val Leu Trp Gly Arg Thr Arg Asp Leu Phe Val Asn Gly Glu Lys
65 70 75 80

Pro Thr Arg Phe Arg Asp Lys Thr Met Leu Ser Val Leu Pro Asn Leu
85 90 95

Ile Gly Asn Arg Leu Ser Ile His Asp Ile Asp Gln Leu Ile Glu Ile
100 105 110

Leu Asn Thr Thr Asn Lys Lys Ala Thr Val Asn Val Val Ala Ser Glu
115 120 125

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

Val Thr Gln His Arg Gln Lys Pro Ile Tyr Tyr Phe Ser Gly Ser Leu
465 470 475 480

Ser Phe

<210> 21
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ttaagttttt agccacaaaa cctaggtctg tcccttcggg taaatgagcg ttgatttcag 360
caagatcaat ctacgcataa ctgaaatgac tgacgagtaa actacatata agtatcggtc 420
gtttgaaaag gcgtaaaagc gtggcagtaa aaaaagaaga tatttttatac ataattggct 480
cgagcagttg ctattttttt attgtcgaac aataatagta tttgaaccct cgagagtaaa 540
tcctttttctc gttaaactact tatttttttta ttcaactacg gcattgtttt tacaatgttg 600

tggttttggt tttatctaaa aaggaagaaa aaacgatt atg aaa cag att cca atg 656
Met Lys Gln Ile Pro Met
1 5

act ata cgt ggt gcg gaa caa tta aga caa gaa ctc gat ttt ttg aaa 704
Thr Ile Arg Gly Ala Glu Gln Leu Arg Gln Glu Leu Asp Phe Leu Lys
10 15 20

aac act cgt cgc cca gaa att att aat gct atc gca gaa gct cgt gaa 752
Asn Thr Arg Arg Pro Glu Ile Ile Asn Ala Ile Ala Glu Ala Arg Glu
25 30 35

cat ggc gat cta aaa gaa aat gca gaa tac cat gct gcg cgt gaa cag 800
His Gly Asp Leu Lys Glu Asn Ala Glu Tyr His Ala Ala Arg Glu Gln
40 45 50

caa gga ttt tgt gaa gga cga atc caa gaa att gaa ggg aaa tta gcg 848
Gln Gly Phe Cys Glu Gly Arg Ile Gln Glu Ile Glu Gly Lys Leu Ala
55 60 65 70

asc agt caa att att gat gtc aca aag atc cca aat aat ggc aaa gtg 896
 Asn Ser Gln Ile Ile Asp Val Thr Lys Ile Pro Asn Asn Gly Lys Val
 75 80 85
 att ttt ggt gcc aca att ttg tta ctg aat att gac acg gaa gaa gaa 944
 Ile Phe Gly Ala Thr Ile Leu Leu Asn Ile Asp Thr Glu Glu Glu
 90 95 100
 gtc tcg tac caa att gta ggc gat gat gaa gcc aat att aaa gca ggg 992
 Val Ser Tyr Gln Ile Val Gly Asp Asp Glu Ala Asn Ile Lys Ala Gly
 105 110 115
 cta att tca gtt aac gcc acg cga ttg aat tagagaaagc taaatggatt 1042
 Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
 120 125
 gcccaagatc ttggcgtaac acaaacgtta attgacactt ccgtcattaa agcgattacg 1102
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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
 Pro Asn Asn Gly Lys Val Ile Phe Gly Ala Thr Ile Leu Leu Leu Asn
 85 90 95
 Ile Asp Thr Glu Glu Glu Val Ser Tyr Gln Ile Val Gly Asp Asp Glu
 100 105 110
 Ala Asn Ile Lys Ala Gly Leu Ile Ser Val Asn Ala Thr Arg Leu Asn
 115 120 125

<210> 23
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 <213> 多杀巴斯德氏菌

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 <222> (980)..(2440)

<220>

<223> guaB

<400> 23

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gcgatcaatt tattccgata aatcgtttgt aatacttcaa tcagctctgc ccaagggtga 180
tcaatttgct gtgtttgttt tgggaaagac aaattaatgc caaagccaat cacgagatta 240
tggtgattat tctgacgatt ggcgatttcg accaaaatcc ctgctaattt gcgccccatgt 300
aatagcacat catttgggca ttttaatcca atgttcaaag cacctgcttg ctttagcggt 360
tctgcgattg ccataccac tactaaactc aagccttcta aattgacctt ttggtcacat 420
gcccaataca aatcataat cacttggtca gcaaaaggag aaagccattg acgaccacgt 480
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ggcgctaacg cttgcgtcaa ataagattca tttaagcgac ttaattgagg tatgagacga 660
aaatgttgga cttgctgttc tatttgatc ccttggtgtt tcaatttttc gatattgtgt 720
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agcaacgaaa tctgtataat gcgaccgcaa tattttttac ccttttattt tccatatcaa 960
cctaagagag aatattgca atg tta cga gta ata aaa gaa gca tta acc ttc 1012
Met Leu Arg Val Ile Lys Glu Ala Leu Thr Phe
1 5 10
gat gat gtt ttg ctt gtc cca gca cat tct act gtg ctc cca aat acc 1060
Asp Asp Val Leu Leu Val Pro Ala His Ser Thr Val Leu Pro Asn Thr
15 20 25
gca gac ctt tcc act caa ctc acc aaa act atc cgc ctc aat atc cca 1108
Ala Asp Leu Ser Thr Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro
30 35 40
atg tta tcc gcc gcc atg gat acc gtg aca gaa act aaa ctg gca atc 1156
Met Leu Ser Ala Ala Met Asp Thr Val Thr Glu Thr Lys Leu Ala Ile
45 50 55
tct ctt gca caa gaa ggt ggc atc ggg ttt att cat aaa aat atg tct 1204
Ser Leu Ala Gln Glu Gly Gly Ile Gly Phe Ile His Lys Asn Met Ser
60 65 70 75
att gag cgt caa gcg gaa cgt gtc cgc aaa gtg aaa aaa ttt gag agc 1252
Ile Glu Arg Gln Ala Glu Arg Val Arg Lys Val Lys Lys Phe Glu Ser
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ggc 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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gtt	gat	gat	gaa	aaa	aat	ctt	gtc	ggg	atc	att	act	ggg	cgt	gat	aca	1396
Val	Asp	Asp	Glu	Lys	Asn	Leu	Val	Gly	Ile	Ile	Thr	Gly	Arg	Asp	Thr	
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cgc	ttt	gtc	acg	gat	tta	aat	aaa	aca	gtg	gcg	gac	ttt	atg	acc	cct	1444
Arg	Phe	Val	Thr	Asp	Leu	Asn	Lys	Thr	Val	Ala	Asp	Phe	Met	Thr	Pro	
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aaa	gct	cgt	ctt	gtc	acg	gtg	aaa	cgc	aat	gca	agt	cgc	gat	gaa	att	1492
Lys	Ala	Arg	Leu	Val	Thr	Val	Lys	Arg	Asn	Ala	Ser	Arg	Asp	Glu	Ile	
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Phe	Gly	Leu	Met	His	Thr	His	Arg	Val	Glu	Lys	Val	Leu	Val	Val	Ser	
175					180					185						
gac	gat	ttc	aaa	tta	aaa	ggc	atg	atc	acc	tta	aaa	gac	tac	caa	aaa	1588
Asp	Asp	Phe	Lys	Leu	Lys	Gly	Met	Ile	Thr	Leu	Lys	Asp	Tyr	Gln	Lys	
190					195					200						
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Ser	Glu	Gln	Lys	Pro	Gln	Ala	Cys	Lys	Asp	Glu	Phe	Gly	Arg	Leu	Arg	
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Val	Gly	Ala	Ala	Val	Gly	Ala	Gly	Pro	Gly	Asn	Glu	Glu	Arg	Ile	Asp	
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gca	tta	gtg	aaa	gca	ggg	gtc	gat	gtg	tta	ttg	att	gac	tca	tca	cac	1732
Ala	Leu	Val	Lys	Ala	Gly	Val	Asp	Val	Leu	Leu	Ile	Asp	Ser	Ser	His	
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Gly	His	Ser	Glu	Gly	Val	Leu	Gln	Arg	Val	Arg	Glu	Thr	Arg	Ala	Lys	
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tac	cca	gat	ttg	cca	att	gtt	gca	ggg	aat	gtg	gca	acc	gct	gaa	ggc	1828
Tyr	Pro	Asp	Leu	Pro	Ile	Val	Ala	Gly	Asn	Val	Ala	Thr	Ala	Glu	Gly	
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gca	att	gcg	ttg	gct	gat	gca	ggg	gca	agt	gca	gtg	aaa	gtg	ggg	att	1876
Ala	Ile	Ala	Leu	Ala	Asp	Ala	Gly	Ala	Ser	Ala	Val	Lys	Val	Gly	Ile	
285					290					295						
ggg	cct	ggg	tca	att	tgt	aca	aca	cgt	att	gtc	aca	ggc	gtg	ggc	gtt	1924
Gly	Pro	Gly	Ser	Ile	Cys	Thr	Thr	Arg	Ile	Val	Thr	Gly	Val	Gly	Val	
300					305					310					315	
cca	caa	att	aca	gcg	att	gcc	gat	gcg	gca	gaa	gca	cta	aaa	gat	cgg	1972
Pro	Gln	Ile	Thr	Ala	Ile	Ala	Asp	Ala	Ala	Glu	Ala	Leu	Lys	Asp	Arg	
320					325					330						
ggg	att	cct	gtg	att	gca	gat	ggc	ggg	atc	cgt	ttc	tct	ggg	gat	att	2020
Gly	Ile	Pro	Val	Ile	Ala	Asp	Gly	Gly	Ile	Arg	Phe	Ser	Gly	Asp	Ile	
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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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ttt gca ggt aca gaa gaa gca cca ggt gaa atc gaa ctt tat caa ggt 2116
 Phe Ala Gly Thr Glu Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly
 365 370 375

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

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

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

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

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

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

act atc aca aaa gaa gcc cct aat tat cgt atg ggt taaacattgc 2450
 Thr Ile Thr Lys Glu Ala Pro Asn Tyr Arg Met Gly
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<213> 多杀巴斯德氏菌

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Val Pro Ala His Ser Thr Val Leu Pro Asn Thr Ala Asp Leu Ser Thr
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Gln Leu Thr Lys Thr Ile Arg Leu Asn Ile Pro Met Leu Ser Ala Ala

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

Glu Ala Pro Gly Glu Ile Glu Leu Tyr Gln Gly Arg Ala Phe Lys Ser
 -370 375 380
 Tyr Arg Gly Met Gly Ser Leu Gly Ala Met Ser Lys Gly Ser Ser Asp
 385 390 395 400
 Arg Tyr Phe Gln Ser Asp Asn Ala Ala Asp Lys Leu Val Pro Glu Gly
 405 410 415
 Ile Glu Gly Arg Ile Pro Tyr Lys Gly Phe Leu Lys Glu Ile Ile His
 420 425 430
 Gln Gln Met Gly Gly Leu Arg Ser Cys Met Gly Leu Thr Gly Cys Ala
 435 440 445
 Thr Ile Asp Glu Leu Arg Thr Lys Ala Gln Phe Val Arg Ile Ser Gly
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 Ala Pro Asn Tyr Arg Met Gly
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 aattgacggc gatttagggc gtgatgaatt tgatgacggc gatttataca gtatttgggc 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 ggc tta gat aca caa aca aat gag gcg cgt gtc acg gag 277
 Val Gln Val Gly Leu Asp Thr Gln Thr Asn Glu Ala Arg Val Thr Glu
 15 20 25

aca gga aga att att tct gat cac cca agc aat aaa att acc ccc gca 325
 Thr Gly Arg Ile Ile Ser Asp His Pro Ser Asn Lys Ile Thr Pro Ala
 30 35 40 45

aag tta aaa ggg att tta gaa gat gct gaa ggt ggt gat att acc gcg 373
 Lys Leu Lys Gly Ile Leu Glu Asp Ala Glu Gly Gly Asp Ile Thr Ala
 50 55 60

caa cat gag ctt ttc atg gat att gaa gaa cgc gac agt tgc atc ggg 421
 Gln His Glu Leu Phe Met Asp Ile Glu Glu Arg Asp Ser Cys Ile Gly

65	70	75	
gca aat att caa acc cgt aag cgt gcg att tta acc ctt gac tgg cgc Ala Asn Ile Gln Thr Arg Lys Arg Ala Ile Leu Thr Leu Asp Trp Arg 80 85 90			469
att gca gag cca cgt aat gcc aca ccg caa gaa gaa aaa ctg caa gtc Ile Ala Glu Pro Arg Asn Ala Thr Pro Gln Glu Glu Lys Leu Gln Val 95 100 105			517
gaa att gac gag ctt ttc tat caa ttc cca atg cta gaa gat tta atg Glu Ile Asp Glu Leu Phe Tyr Gln Phe Pro Met Leu Glu Asp Leu Met 110 115 120 125			565
gtg gat atg atg gat gcg gta gga cat ggt ttt tcg gcg tta gaa att Val Asp Met Met Asp Ala Val Gly His Gly Phe Ser Ala Leu Glu Ile 130 135 140			613
gaa tgg aag caa gct gaa agt aaa tgg att cca gtt aat ttt atc gca Glu Trp Lys Gln Ala Glu Ser Lys Trp Ile Pro Val Asn Phe Ile Ala 145 150 155			661
cgt ccg cag tcg tgg ttt aaa cta gac aag gat gat aat tta ctg ctt Arg Pro Gln Ser Trp Phe Lys Leu Asp Lys Asp Asp Asn Leu Leu Leu 160 165 170			709
aaa acg cca gat aat caa gac ggt gag ccg ttg aga caa tat ggc tgg Lys Thr Pro Asp Asn Gln Asp Gly Glu Pro Leu Arg Gln Tyr Gly Trp 175 180 185			757
gta gtg cat acc cac aaa tca aga aca gta cag ctt gct cgt atg ggt Val Val His Thr His Lys Ser Arg Thr Val Gln Leu Ala Arg Met Gly 190 195 200 205			805
tta ttt aga acg ctc gca tgg ctt tat atg ttt aaa cac tac tcg gtg Leu Phe Arg Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val 210 215 220			853
cat gat ttt gcc gaa ttt cta gag ctt tat ggt atg ccg att cgt att His Asp Phe Ala Glu Phe Leu Glu Leu Tyr Gly Met Pro Ile Arg Ile 225 230 235			901
ggt aaa tac cca ttt ggg gca acg aat gac gaa aag cgc aca tta ttg Gly Lys Tyr Pro Phe Gly Ala Thr Asn Asp Glu Lys Arg Thr Leu Leu 240 245 250			949
cgt gca ctt gct caa atc gga cat aac gca gca ggg att atg cca gaa Arg Ala Leu Ala Gln Ile Gly His Asn Ala Ala Gly Ile Met Pro Glu 255 260 265			997
gga atg aat gtt gag ttg cat aat gtg aca aac act act ggc tcg gct Gly Met Asn Val Glu Leu His Asn Val Thr Asn Thr Thr Gly Ser Ala 270 275 280 285			1045
gga agc aac ccg ttt ttg caa atg gtg gac tgg tgt gaa aag tcc gcc Gly Ser Asn Pro Phe Leu Gln Met Val Asp Trp Cys Glu Lys Ser Ala 290 295 300			1093
gca cgt ttg att cta ggg caa aca tta aca agc ggt gca gat ggt aaa Ala Arg Leu Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys 305 310 315			1141

act tca act aat gcc ctt gga caa gtg cat aat gaa gtc aga cgt gac 1189
 Thr Ser Thr Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp
 320 325 330

ttg ctt gtg tct gat gct aaa cag att gca caa act att aca caa cag 1237
 Leu Leu Val Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln
 335 340 345

att att ctg cca tat ctt caa att aac att gat ccg aat att ttg cct 1285
 Ile Ile Leu Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro
 350 355 360 365

tct cgt gtg ccg tat ttc gag ttt gac acg aaa gaa tat gct gat tta 1333
 Ser Arg Val Pro Tyr Phe Glu Phe Asp Thr Lys Glu Tyr Ala Asp Leu
 370 375 380

agt gtc cta gcg gat gct att cct aag ctt gtg agc gta gga gtg cgc 1381
 Ser Val Leu Ala Asp Ala Ile Pro Lys Leu Val Ser Val Gly Val Arg
 385 390 395

att cct gaa aat tgg gtg cgt gat aaa gcg ggc att cca gaa ccg cag 1429
 Ile Pro Glu Asn Trp Val Arg Asp Lys Ala Gly Ile Pro Glu Pro Gln
 400 405 410

gaa aat gaa acg att tta agt gcg gtt caa cat gat ttt aaa aca gat 1477
 Glu Asn Glu Thr Ile Leu Ser Ala Val Gln His Asp Phe Lys Thr Asp
 415 420 425

tta aac gat gtt gaa aat ccg aaa aaa cag acc gca ctt tct gta caa 1525
 Leu Asn Asp Val Glu Asn Pro Lys Lys Gln Thr Ala Leu Ser Val Gln
 430 435 440 445

aat cac gtg aca ggt tgt cag tgt gat ggc tgt cgt ggt gtt gca tta 1573
 Asn His Val Thr Gly Cys Gln Cys Asp Gly Cys Arg Gly Val Ala Leu
 450 455 460

tct gcg aat aat aac agt tct act gcg cag ggc gtg cta gat ggt gga 1621
 Ser Ala Asn Asn Asn Ser Ser Thr Ala Gln Gly Val Leu Asp Gly Gly
 465 470 475

ctt gcg caa gca ttt aat gag cct gat ttt aat aaa caa tta aat cca 1669
 Leu Ala Gln Ala Phe Asn Glu Pro Asp Phe Asn Lys Gln Leu Asn Pro
 480 485 490

atg gta aag aaa gct gtt gcg gta ctc atg gca tgt gac tct tac gat 1717
 Met Val Lys Lys Ala Val Ala Val Leu Met Ala Cys Asp Ser Tyr Asp
 495 500 505

gag gcg gca gaa aaa ctc gct gaa gca tac cca gaa att tca agt cac 1765
 Glu Ala Ala Glu Lys Leu Ala Glu Ala Tyr Pro Glu Ile Ser Ser His
 510 515 520 525

gaa cac gaa cag tat ctc tca aat gcg ctg ttt tta gct gat tta ctt 1813
 Glu His Glu Gln Tyr Leu Ser Asn Ala Leu Phe Leu Ala Asp Leu Leu
 530 535 540

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

gccattgagt ttttacataa taaaaaatta cttgcaacga aagtgtttaa aaaatcactg 1928

catgatagtg ccacgcaag agctacaaca atcgcgagat tatctagtct tgagatgacg 1988
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<212> PRT

<213> 多杀巴斯德氏菌

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		20						25					30		
Ile	Ile	Ser	Asp	His	Pro	Ser	Asn	Lys	Ile	Thr	Pro	Ala	Lys	Leu	Lys
		35					40					45			
Gly	Ile	Leu	Glu	Asp	Ala	Glu	Gly	Gly	Asp	Ile	Thr	Ala	Gln	His	Glu
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Leu	Phe	Met	Asp	Ile	Glu	Glu	Arg	Asp	Ser	Cys	Ile	Gly	Ala	Asn	Ile
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			85					90						95	
Pro	Arg	Asn	Ala	Thr	Pro	Gln	Glu	Glu	Lys	Leu	Gln	Val	Glu	Ile	Asp
		100						105					110		
Glu	Leu	Phe	Tyr	Gln	Phe	Pro	Met	Leu	Glu	Asp	Leu	Met	Val	Asp	Met
		115					120					125			
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Gln	Ala	Glu	Ser	Lys	Trp	Ile	Pro	Val	Asn	Phe	Ile	Ala	Arg	Pro	Gln
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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
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Thr Leu Ala Trp Leu Tyr Met Phe Lys His Tyr Ser Val His Asp Phe
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 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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 Ile Leu Gly Gln Thr Leu Thr Ser Gly Ala Asp Gly Lys Thr Ser Thr
 305 310 315 320
 Asn Ala Leu Gly Gln Val His Asn Glu Val Arg Arg Asp Leu Leu Val
 325 330 335
 Ser Asp Ala Lys Gln Ile Ala Gln Thr Ile Thr Gln Gln Ile Ile Leu
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 Pro Tyr Leu Gln Ile Asn Ile Asp Pro Asn Ile Leu Pro Ser Arg Val
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Gly Leu Ser Asp Ala Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu
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Arg Tyr Gly Ile Glu Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr
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Val Lys Leu Phe Leu Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu
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 Trp Asp His Tyr Asn Tyr Lys Pro Leu Leu Asn Ser Gln His Asn Ile
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gcgctcagca ccgcctgttc cgaaaatcgt ttcttgatga ccacaattgc taaaaatatg 8512

catcgacata ttttcgataa tgccataaac gggtagagaa acacgctcaa acatcgccac 8572

acctttaatc gcatccagta aagcaatata ttgtgggtgt gtcaccacga ccgcccccg 8632

cactggaatt tgttgagaaa gggtcagctg gatatccctt gtaccggtg gcataatcaat 8692

gactaaataa tctaaatcag gccataaggt ttcttgcaaa agctgactta aggcactgct 8752

tgccattgga ccgcgccaaa tcgtagcatt gtcgggttcc attaagaaac caatggaatt 8812
 ggcaaaaata tgatgtgctt gaattgggggt aatgtgctgg ttatctggcg aagttgggcg 8872
 ttgatcagca acccctaaca tgtgtggaat agatggacca taaatatcgg catctaaaat 8932
 tccaacacga gcaccttgtc tttgtaaggc aagagcaaga ttgacggaaa tagtagattt 8992
 tcttacacca cctttaccgg atgtcacggc aataatattt ttaccctt ttacgggtgg 9052
 gtggctatta gcgcgtttta atgtcgcgat ttgataattt aattgccatt tgatgtcttt 9112
 gcattctgct aatgtgagaa gttctgtgga gagagcgctc ttgagttgtt cgaatgcagt 9172
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 tttgatagca tttaggctga cgagatcttt ttgtaagcta ggatgttgaa attgttgaaa 9292
 tgtgttttgg atagcttgtt tttgactgtc cgtaaactg tcagaaaata aaattcccat 9352
 tgattttatc cgtttatttt tgggtggctaa ttaaagccct agttaatcac tcaactatat 9412
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 aaaatactgc gaataaggta acataagcgc caattttttg atgaaaaata ggaatgataa 9532
 catggcaaat tcggcacgcg atatttttgg cacttgcgcc ttaccttatg caaatgggtgc 9592
 aattcattta gggcatttat tagaacatat tcaagcagat atttgggtgc gttccaacgt 9652
 atgcgtgggc ataaagtgc ttttatttgg gcagatgatg cccatggcac accaatcatg 9712
 ttaaattgca taaattaggt attacacca agcattaatt gctcctcgaa agcagaacat 9772
 gtggcggatt tgaaggctta atattagcta tgataatatc at 9814

<210> 32

<211> 967

<212> PRT.

<213> 多杀巴斯德氏菌

<400> 32

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

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

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

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

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

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

100 105 110

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

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

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

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

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

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

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

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

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

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

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

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

Asp Leu Thr Lys Arg Lys Asn Val Ser Phe Thr Tyr Glu Asn Tyr Thr
305 310 315 320

Val Thr Pro Phe Trp Asp Thr Leu Lys Leu Ser Tyr Ser Gln Gln Arg
325 330 335

Ile Thr Thr Arg Ala Arg Thr Glu Asp Tyr Cys Asp Gly Asn Glu Leu
340 345 350

Cys Asp Ser Tyr Lys Asn Pro Leu Gly Leu Gln Phe Lys Asp Gly Gln
355 360 365

Ile Leu Asp Pro Ala Gly Asn Lys Ile Lys Leu Gln Gly Ser Gly Leu
370 375 380

Ser Thr Gln Ile Val Asp Glu Asn Gly Lys Pro Phe Pro Thr Thr Thr
385 390 395 400

Gly Thr Asn Asn Ala Ala Phe Ser Asn Asn Leu Arg Leu Arg Pro Thr
405 410 415

Gly Phe Trp Leu Asp Cys Ser Val Phe Asp Cys Asn Lys Pro Phe Thr
420 425 430

80

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

<210> 33
 <211> 2990
 <212> DNA
 <213> 多杀巴斯德氏菌

<220>
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 <222> (1106)..(1564)

<220>
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 ttcttcgtca gggcgatcaa tataaggggg caatggcata tgcccaattt gctgtaaacac 180
 gtctaaaagt gcggtctggt ttgcgcgat ttctaattca aataaggtat catggcgcg 240
 aaccatgatc attttgacac catgatgttc acctaaactta tcttcgcta accacagttc 300

tgccctctct	ttcggtgctt	ttgaggagcg	cacatgggct	aaaaagcg	tgctggataa	360										
aatcgctcg	accaacactt	ccacettacc	gccactggct	ttacgtccaa	acatccttgc	420										
aggaatcacg	cgcgtgttat	taaaaattaa	taagtcgcct	tcatagaattt	gatcaaggat	480										
atcagcaaaa	gtgcgggtggg	taatctcacc	attttcgccg	ttaagttgta	ataagcgact	540										
agcgggtgca	tccgggttttg	ggtaacgagc	aatcagctca	tccgggtaaat	caaaataaaa	600										
gtcagaaaca	cgcataaata	gggtttataaa	aagttatcta	aaaaatcgtg	ggcgtaaagtc	660										
tagtgtgaat	tccgctcttg	cacaaggaaa	aatccagatt	ttgtttgttta	gtatcgaatt	720										
gagatgattt	tggacaaaaa	aaaagccctt	tcaagaaaga	cgaaagggcg	aaaatatatt	780										
tggagtcata	cttttttaggg	tatgtgtcgg	attatacaca	caaaaataac	aaatgcaaca	840										
tttttttaac	aatcatatgt	aagcgtattg	tgtgagaacg	agcgtaaaaa	tgaacgcatt	900										
ctaaaggatg	atttattttag	cctatttaaaa	aaacacatga	gatgagagtt	tgcgagagcg	960										
gtaataaaaag	tgccggtgggt	tttagaaaag	ttttgaatag	gatcacaaat	taaacaaagt	1020										
ttgtgaaata	ccaagtagta	gtttttaagt	atatgatgaa	tcatatgcta	aagttttaaac	1080										
ccgttaaata	accaagaggt	ggaag	atg	aca	gaa	gaa	aat	aaa	gga	aag	aga	1132				
			Met	Thr	Glu	Glu	Asn	Lys	Gly	Lys	Arg					
			1					5								
tat	ttt	tta	tgg	ttc	ata	ttg	ttt	atc	ctt	tca	atc	tat	tta	ttt	att	1180
Tyr	Phe	Leu	Trp	Phe	Ile	Leu	Phe	Ile	Leu	Ser	Ile	Tyr	Leu	Phe	Ile	
10					15					20					25	
acc	ata	caa	gaa	aga	cga	ggg	tat	tgt	ttt	gac	aaa	cgt	gca	tat	att	1228
Thr	Ile	Gln	Glu	Arg	Arg	Gly	Tyr	Cys	Phe	Asp	Lys	Arg	Ala	Tyr	Ile	
				30					35						40	
cat	gag	ctt	tat	act	gag	caa	gag	tta	att	gat	cgg	ggg	att	gaa	tat	1276
His	Glu	Leu	Tyr	Thr	Glu	Gln	Glu	Leu	Ile	Asp	Arg	Gly	Ile	Glu	Tyr	
			45					50					55			
gtg	gta	tcc	acc	atg	ccg	tca	ggg	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	ggg	tat	gtc	aga	att	gaa	tat	tta	aga	1468
Tyr	Pro	Asp	Asp	Asp	Gly	Tyr	Gly	Tyr	Val	Arg	Ile	Glu	Tyr	Leu	Arg	
				110					115					120		
cat	tat	gtt	gag	aat	cta	aaa	cct	tat	cat	aga	gtg	att	tat	ctt	gaa	1516
His	Tyr	Val	Glu	Asn	Leu	Lys	Pro	Tyr	His	Arg	Val	Ile	Tyr	Leu	Glu	
			125					130					135			

tat acg ccc tgt gga gag tta agg gaa gag gcg gct ttt tca aaa aat 1564
 Tyr Thr Pro Cys Gly Glu Leu Arg Glu Glu Ala Ala Phe Ser Lys Asn
 - 140 145 150

taagagtgag gtgaagaaat ggcattacca acagcaacaa taatgaggaa tttatcttta 1624
 tctaaaaatc aattcactct gaaagggatg gaatgcgtag attccctatt tcaagcatgc 1684
 agtaatatgg atcatgggta ctgaggtgga agatggcaga agaaaataaa ggaaagagat 1744
 attttttatg gttcatattg tttatccttt caatctatctt atttattacc atacaagaaa 1804
 gacgaggtta ttgttttgac aaatgggaat atatccataa cttttataacc gagcaagagt 1864
 tgatcgatag aggggttgaa tatgtggtat ccaccatgcc gtcaggtggt tttgaaccag 1924
 atggcacaac aaccgaaata aaacgttatg ctagtgttga ggagtttaaa cagatgaacc 1984
 ctgattgttg taaattaaca agatttatta atgaaggaat agatggctat ccagatgatg 2044
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 atcatagagt gctttatctc gaataacgc cttgtggaga attaaggga gaggtttctt 2164
 tttaaaaaat aaataatagt gaggtgaaga aatggcatta ccaacagcaa cagaaatcac 2224
 aatgcatat ttatataaaa ataaattaac tcctaaagcg gaggaagag tagattcaat 2284
 acaaattctt gaaaaaggag atgaacattt cgaagtaaatt ttaattgat caaagtactc 2344
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 aaacaggtaa acgcagtgtg ttagattact tatttagccc attaaaaacc acaaaaataat 2464
 attaaggaga ataatatgtc gtataataaaa tatactgttg ctttgattac gttctcaaca 2524
 gggatctgta ttccggcaat atgctacgct cttaaattcgc tgggatacag atcctgtttg 2584
 agactatgta gaaaagacta aactttgtgt ggttaactgg gcttcggtaa aattctggaa 2644
 acaaatgggc ttaaccgcg tgatcttacc ccgtgagctt tcgcttgatg aaattgccga 2704
 aattcgtcag caagtgccag aaatggaaat tgaagtgttc gtgcatgggg cattatgcat 2764
 ggcgtattct ggacgttggt tattatcagg ctatattaat aaacgtgatc caaatcaagg 2824
 cacctgtacc aatgcgtgcc gttgggaata cagtgtaac gaagccaaag aagatgagat 2884
 cggcaacatt gtgaatgtgg gtgaagaaat tccagtgaat aatgtagcac cgacacttgg 2944
 cgaaggcgac accaaccagta aagtattttt attagcagaa agtcga 2990

<210> 34

<211> 153

<212> PRT

<213> 多杀巴斯德氏菌

<400> 34

Met Thr Glu Glu Asn Lys Gly Lys Arg Tyr Phe Leu Trp Phe Ile Leu
 1 5 10 15

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

<210> 35

<211> 1683

<212> DNA

<213> 多杀巴斯德氏菌

<220>

<221> CDS

<222> (325)..(1230)

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<223> lgtC

<400> 35

atatcaaaagt ctcatggcaa gaaaattaga aaagagcgat caattattat ttgcaagatt 60

tgggtattat tcataggcta ggtgaaagat atatttttcc atgatattaa aacgattcag 120

gcagaactgg ctagcttatac acttttagat aattgtatta ttaaaagaag ctgtatgatt 180

gttattctat cattagtggg taataaatat tctttatttt ttgagagata aaaacaattc 240

atattttcaat agaaaacaga aaataaagat tatcaaaaga attatccgtc cttataaata 300

tgagtctgta ttgtgagatg atat atg aat att tta ttt gtt tct gat gat 351

Met Asn Ile Leu Phe Val Ser Asp Asp
1 5

gtt tat gct aaa cat ctg gtg gtt gcg att aaa agc att ata aat cat 399

Val Tyr Ala Lys His Leu Val Val Ala Ile Lys Ser Ile Ile Asn His
10 15 20 25

aat gaa aaa ggt att tca ttt tat att ttt gat ttg ggt ata aag gat 447

Asn Glu Lys Gly Ile Ser Phe Tyr Ile Phe Asp Leu Gly Ile Lys Asp
30 35 40

gaa aat aag aga aat att aat gat att gtt tct tct tat gga agt gaa	495
Glu Asn Lys Arg Asn Ile Asn Asp Ile Val Ser Ser Tyr Gly Ser Glu	
45 50 55	
gtc aac ttt att gct gtg aat gag aaa gaa ttt gag agt ttt cct gtt	543
Val Asn Phe Ile Ala Val Asn Glu Lys Glu Phe Glu Ser Phe Pro Val	
60 65 70	
caa att agt tat att tct tta gca aca tat gca agg cta aaa gcg gca	591
Gln Ile Ser Tyr Ile Ser Leu Ala Thr Tyr Ala Arg Leu Lys Ala Ala	
75 80 85	
gag tat ttg ccg gat aat tta aat aaa att att tat tta gat gtt gat	639
Glu Tyr Leu Pro Asp Asn Leu Asn Lys Ile Ile Tyr Leu Asp Val Asp	
90 95 100 105	
gtt ttg gtt ttt aac tca tta gaa atg tta tgg aat gtt gat gtt aat	687
Val Leu Val Phe Asn Ser Leu Glu Met Leu Trp Asn Val Asp Val Asn	
110 115 120	
aat ttt ctt acc gca gcc tgt tat gat tct ttc atc gaa aat gaa aag	735
Asn Phe Leu Thr Ala Ala Cys Tyr Asp Ser Phe Ile Glu Asn Glu Lys	
125 130 135	
tct gag cat aaa aaa tcg att tca atg tca gat aag gaa tat tat ttt	783
Ser Glu His Lys Lys Ser Ile Ser Met Ser Asp Lys Glu Tyr Tyr Phe	
140 145 150	
aat gca gga gta atg cta ttt aat tta gat gaa tgg cgg aag atg gat	831
Asn Ala Gly Val Met Leu Phe Asn Leu Asp Glu Trp Arg Lys Met Asp	
155 160 165	
gta ttc tca aga gct tta gac ctg tta gct atg tat cct aat caa atg	879
Val Phe Ser Arg Ala Leu Asp Leu Leu Ala Met Tyr Pro Asn Gln Met	
170 175 180 185	
att tat cag gat caa gat ata ttg aat atc ctt ttt agg aat aaa gtc	927
Ile Tyr Gln Asp Gln Asp Ile Leu Asn Ile Leu Phe Arg Asn Lys Val	
190 195 200	
tgt tat tta gat tgc aga ttt aat ttc atg cca aat caa ctt gaa aga	975
Cys Tyr Leu Asp Cys Arg Phe Asn Phe Met Pro Asn Gln Leu Glu Arg	
205 210 215	
ata aan caa tac cat aaa gga aaa ntg agc aac tta cat tct tta gaa	1023
Ile Xaa Gln Tyr His Lys Gly Lys Xaa Ser Asn Leu His Ser Leu Glu	
220 225 230	
aaa aca acg atg cct gtc gtt att tca cat tat tgt ggt cca gaa aaa	1071
Lys Thr Thr Met Pro Val Val Ile Ser His Tyr Cys Gly Pro Glu Lys	
235 240 245	
gcg tgg cat gcg gat tgt aaa cat ttt aat gta tat ttc tat cag aaa	1119
Ala Trp His Ala Asp Cys Lys His Phe Asn Val Tyr Phe Tyr Gln Lys	
250 255 260 265	
ata tta gca naa atn tcg aga ggc ncg gat aaa gaa cgc gta tta tct	1167
Ile Leu Ala Xaa Xaa Ser Arg Gly Xaa Asp Lys Glu Arg Val Leu Ser	
270 275 280	
ata aaa act tat ctc aag gcc ttg att aga agg att aga tat aaa ttc	1215
Ile Lys Thr Tyr Leu Lys Ala Leu Ile Arg Arg Ile Arg Tyr Lys Phe	

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

tgatttcttc aaagcgaaaa ggaggaaata gcttgttcta atttattaca ataatgggtg 1330
 tattcatctt gattttgaag gaaagagagt gttttttgta taaaagcatt ttcgtcacct 1390
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 tccatggata ttacaggtgt accgcaagcc atgctttcta ggataactgt cggtaacccc 1510
 tctttcaaag aggtgtgtaa aaatagctta gcatttttta ttaatggata cggattatct 1570
 ttatttccta aaagaaaaca atcttcttgt agattgagtg attctatttg tttctctaata 1630
 tttctctgac actcaccatc ccaaacaata tatancnttt ctggatacc tcc 1683

<210> 36

<211> 302

<212> PRT

<213> 多杀巴斯德氏菌

<400> 36

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 Xaa Gln Tyr His Lys Gly
 210 215 220
 Lys Xaa Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val
 225 230 235 240
 Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys
 245 250 255
 His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Xaa Xaa Ser Arg
 260 265 270
 Gly Xaa Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala
 275 280 285
 Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr
 290 295 300

<210> 37
 <211> 2029
 <212> DNA
 <213> 多杀巴斯德氏菌

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

<220>
 <223> mglB

<400> 37
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 Leu Asn Lys Ala Gly Lys Ile Gln Tyr Val Leu Leu Lys Gly Asn Gln
 1 5 10 15

gga cac cca gat gca gaa gct cgt aca aaa ttc gtc att aaa gaa tta 97
 Gly His Pro Asp Ala Glu Ala Arg Thr Lys Phe Val Ile Lys Glu Leu
 20 25 30

nat aat aaa ggc att caa gat gag caa tta ttc atc gac acg ggg atg 145
 Xaa Asn Lys Gly Ile Gln Asp Glu Gln Leu Phe Ile Asp Thr Gly Met
 35 40 45

tgg gat gcc gct tta gcg aaa gat aaa atg gat gca tgg tta tct agc 193
 Trp Asp Ala Ala Leu Ala Lys Asp Lys Met Asp Ala Trp Leu Ser Ser
 50 55 60

tct aaa gca aat caa att gaa gtg atc atc gct aac aac gat ggt atg 241
 Ser Lys Ala Asn Gln Ile Glu Val Ile Ile Ala Asn Asn Asp Gly Met
 65 70 75 80

gcg atg ggg gca ttg gaa gcc acg aaa gca cat ggt aaa aaa tta cca 289
 Ala Met Gly Ala Leu Glu Ala Thr Lys Ala His Gly Lys Lys Leu Pro
 85 90 95

atc ttc ngc gta nat gcg tta cca gaa gtc ctc caa tta atc aaa aaa 337
 Ile Phe Xaa Val Xaa Ala Leu Pro Glu Val Leu Gln Leu Ile Lys Lys
 100 105 110

ggt gaa att gca ggt acg gtg tta aat gac ggt gtg aac caa ggt aaa 385
 Gly Glu Ile Ala Gly Thr Val Leu Asn Asp Gly Val Asn Gln Gly Lys
 115 120 125

gcc gtt gtt caa tta agt aat aat ctt gca aaa gga aaa cct gcc act 433
 Ala Val Val Gln Leu Ser Asn Asn Leu Ala Lys Gly Lys Pro Ala Thr
 130 135 140

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

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

tataacaaaa caagamgttg taattctcgg ggaggtatac cctccccctt tttatgtgag 589
 gttggatatg acaactcaaa ttccaaatca agacagtga atactgctca caatgaccaa 649
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<210> 38
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<213> 多杀巴斯德氏菌

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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
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Cys Trp Cys Gly Cys Gly
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attacgcagt gaaaatgaac aactaaagag tgagcaccaa aactggcaag aacgtttacg	240
ctcattatta ggcaaaattg ataacgtata attcacttct tattaaggct tagtttttct	300
aagccttatt ttttaggaga aatta atg aaa aca aaa att tgt att atc act	352
Met Lys Thr Lys Ile Cys Ile Ile Thr	
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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	
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gtg gaa caa tta ctg cta agc aaa gat gct tta caa ctg tgt gaa tcg	688
Val Glu Gln Leu Leu Leu Ser Lys Asp Ala Leu Gln Leu Cys Glu Ser	
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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	
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Gln Trp Leu Pro Gln Phe Leu Ser Gln Leu	
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<211> 147

<212> PRT

<213> 多杀巴斯德氏菌

<400> 40

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 20 25 30

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

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

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Val Arg Lys Thr Phe Gly Ser Ile Ile Gly Glu Pro Thr Ala Glu Arg			
205	210	215	
atc aaa caa gag att ggt agt gcg ttt att caa gaa ggc gat gaa gtc	3904		
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220	225	230	
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<210> 42

<211> 351

<212> PRT

<213> 多杀巴斯德氏菌

<400> 42

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Val	Leu	Asp	Glu	Pro	Ser	Val	Val	Ala	Ile	Arg	Gln	Glu	Arg	Ser	Gly
		35					40					45			
Ala	Leu	Lys	Ser	Ile	Ala	Ala	Val	Gly	Arg	Asp	Ala	Lys	Leu	Met	Leu
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Gly	Arg	Thr	Pro	Lys	Ser	Ile	Ala	Ala	Ile	Arg	Pro	Met	Lys	Asp	Gly
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Val	Ile	Ala	Asp	Phe	Phe	Val	Thr	Glu	Lys	Met	Leu	Gln	Tyr	Phe	Ile
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Lys	Gln	Val	His	Ser	Ser	Asn	Phe	Met	Arg	Pro	Ser	Pro	Arg	Val	Leu
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Pro	Met	Ala	Ala	Ala	Ile	Gly	Ala	Lys	Leu	Pro	Val	Ser	Thr	Ala	Thr
145					150					155					160
Gly	Ser	Met	Val	Ile	Asp	Ile	Gly	Gly	Gly	Thr	Thr	Glu	Val	Ala	Val
				165					170					175	
Ile	Ser	Leu	Asn	Gly	Ile	Val	Tyr	Ser	Ser	Ser	Val	Arg	Ile	Gly	Gly
			180					185					190		
Asp	Arg	Phe	Asp	Glu	Ala	Ile	Ile	Ser	Tyr	Val	Arg	Lys	Thr	Phe	Gly
		195					200					205			
Ser	Ile	Ile	Gly	Glu	Pro	Thr	Ala	Glu	Arg	Ile	Lys	Gln	Glu	Ile	Gly
	210					215					220				

Ser Ala Phe Ile Gln Glu Gly Asp Glu Val Arg Glu Ile Glu Val His
 225 230 235 240
 Gly His Asn Leu Ala Glu Gly Ala Pro Arg Ser Phe Lys Leu Thr Ser
 245 250 255
 Arg Asp Val Leu Glu Ala Ile Gln Ala Pro Leu Asn Gly Ile Val Ala
 260 265 270
 Ala Val Arg Thr Ala Leu Glu Glu Cys Gln Pro Glu His Ala Ala Asp
 275 280 285
 Ile Phe Glu Arg Gly Met Val Leu Thr Gly Gly Gly Ala Leu Ile Arg
 290 295 300
 Asn Ile Asp Val Leu Leu Ser Lys Glu Thr Gly Val Pro Val Ile Ile
 305 310 315 320
 Ala Asp Asp Pro Leu Thr Cys Val Ala Arg Gly Gly Gly Glu Ala Leu
 325 330 335
 Glu Met Ile Asp Met His Gly Gly Asp Ile Phe Ser Asp Asp Ile
 340 345 350

<210> 43
 <211> 2172
 <212> DNA
 <213> 多杀巴斯德氏菌

<220>
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 <222> (1)..(1464)
 <220>
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 Thr Arg Val Gly Ile Gly Trp His Leu Asn Pro Asn Thr Ala Leu Ile
 1 5 10 15
 gaa aaa gtg aaa gcg att gca gaa gcg cgt tta ggc gaa gca tac cgt 96
 Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
 20 25 30
 atc act gaa aac aag cac gtt atg aac aaa att gat gcg att aaa gct 144
 Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
 35 40 45
 gat gtg att gca caa atc aca gct gaa gta gca gaa ggc gaa gac atc 192
 Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
 50 55 60
 agt gaa ggg aaa att gtc gat att ttc acc gca ctt gaa agc caa atc 240
 Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
 65 70 75 80
 gta cgt agc cgt atc att gct ggt gaa cca cgt att gat ggt cgt aca 288
 Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
 85 90 95

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

aca cac ggt tct gcg att ttc acc cgt ggt gaa aca cag gcg tta gct 384
Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
115 120 125

gtc gcg aca tta ggt aca gaa cgt gat gca caa att att gat gaa tta 432
Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
130 135 140

aca ggt gag cgt tca gat cac ttc tta ttc cac tac aac ttc ccg cca 480
Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
145 150 155 160

tat tct gtg ggt gaa acc ggt atg att ggt tca cca aaa cgt cgt gaa 528
Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
165 170 175

att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct gca gtg atg cca 576
Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro
180 185 190

aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc tct gaa atc aca 624
Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr
195 200 205

gaa tca aat ggt tct tct tct atg gca tgc gtt tgt ggt gcg tct tta 672
Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys Gly Ala Ser Leu
210 215 220

gca tta atg gat gcg ggt gta cca att aaa gcg gcg gtt gca ggt att 720
Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala Val Ala Gly Ile
225 230 235 240

gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg gtg ctt tca gac 768
Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp
245 250 255

atc tta ggt gat gaa gat cac tta ggt gac atg gac ttc aaa gtc gcg 816
Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala
260 265 270

ggt aca cgt acg ggt gtg acg gca tta caa atg gat atc aaa atc gaa 864
Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu
275 280 285

ggt atc aca gca gaa atc atg caa att gcg tta aac caa gcg aaa agc 912
Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser
290 295 300

gca cgt tta cac att tta ggt gtg atg gag caa gcg atc cca gcg cca 960
Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
305 310 315 320

cgt gcg gat att tct gat ttt gca ccg cgt att tac act atg aaa att 1008
Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
325 330 335

gat ccg aag aaa atc aaa gat gtg atc ggt aaa ggt ggt gca acc att 1056
Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile

340	345	350	
cgt gcc tta aca gaa gaa aca ggt acc tca att gat atc gat gat gat 1104 Arg Ala Leu Thr Glu Glu Thr Gly Thr Ser Ile Asp Ile Asp Asp Asp 355 360 365			
ggt acg gtg aag att gct gcg gtt gat ggc aat tca gca aaa gag gtg 1152 Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val 370 375 380			
atg gcg cgt att gaa gat att act gca gaa gtt gaa gcg ggt gca gtg 1200 Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val 385 390 395 400			
tat aaa ggt aaa gtt act cgt tta gct gat ttt ggt gcc ttc gtt tct 1248 Tyr Lys Gly Lys Val Thr Arg Leu Ala Asp Phe Gly Ala Phe Val Ser 405 410 415			
atc gta ggt aac aaa gaa gcg 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			
aaagggcggt ggtgtgcatg ttgataagta caatttgtgc tttaaggcga agcgaaatga 1554			
agcaatttca tccgtgggta aagtgcctgc taattttccc attttgggta tgttggttaa 1614			
cagcttgtgt taatcatgaa caagtttttc tttcaaaaga gaaattaatg ttagcagagc 1674			
aacatccgaa tgatcatctt gagcatgagg tgatgggtgc gcaaattagc gaattgttac 1734			
ttgttaaagg gttaaaaaaa gaagaacgtg cgattttaca ttttgagcga ggcgtgctgt 1794			
acgatagctt aggattgtgg gcattggcgc gttatgattt tgaccaaaaca ttagcgttgt 1854			
atccaaagt ggcagcagcg ttaattatt taggtttata tttattgtta gaggaagatt 1914			
acagcgcata tctagatata ttaattgtgt tgtttgaact tgatcctcaa tatgagtatg 1974			
cattcctaaa tagagggcta aatttttatt acgtcggacg ttatgaatta gctcagcggg 2034			
attttcttca attttatcaa gccgataaat cagatccata ccgcacttta tggctttatt 2094			
taaatgaatt aaagcataat cctcaggatg cttctaaaaa tcttgctcaa cgagcaatgg 2154			
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<210> 44

<211> 488

<212> PRT

<213> 多杀巴斯德氏菌

<400> 44

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Glu Lys Val Lys Ala Ile Ala Glu Ala Arg Leu Gly Glu Ala Tyr Arg
20 25 30

Ile Thr Glu Asn Lys His Val Met Asn Lys Ile Asp Ala Ile Lys Ala
35 40 45

Asp Val Ile Ala Gln Ile Thr Ala Glu Val Ala Glu Gly Glu Asp Ile
50 55 60

Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu Glu Ser Gln Ile
65 70 75 80

Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile Asp Gly Arg Thr
85 90 95

Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly Val Leu Pro Arg
100 105 110

Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr Gln Ala Leu Ala
115 120 125

Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile Ile Asp Glu Leu
130 135 140

Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr Asn Phe Pro Pro
145 150 155 160

Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro Lys Arg Arg Glu
165 170 175

Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala Ala Val Met Pro
180 185 190

Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val Ser Glu Ile Thr
195 200 205

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

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

Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val Val Leu Ser Asp
245 250 255

Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp Phe Lys Val Ala
260 265 270

Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp Ile Lys Ile Glu
275 280 285

Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn Gln Ala Lys Ser
290 295 300

Ala Arg Leu His Ile Leu Gly Val Met Glu Gln Ala Ile Pro Ala Pro
305 310 315 320

Arg Ala Asp Ile Ser Asp Phe Ala Pro Arg Ile Tyr Thr Met Lys Ile
325 330 335

Asp Pro Lys Lys Ile Lys Asp Val Ile Gly Lys Gly Gly Ala Thr Ile
340 345 350

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

Gly Thr Val Lys Ile Ala Ala Val Asp Gly Asn Ser Ala Lys Glu Val
370 375 380

Met Ala Arg Ile Glu Asp Ile Thr Ala Glu Val Glu Ala Gly Ala Val
385 390 395 400

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

Ile Val Gly Asn Lys Glu Gly Leu Val His Ile Ser Gln Ile Ala Glu
420 425 430

Glu Arg Val Glu Lys Val Ser Asp Tyr Leu Ala Val Gly Gln Glu Val
435 440 445

Thr Val Lys Val Val Glu Ile Asp Arg Gln Gly Arg Ile Arg Leu Thr
450 455 460

Met Lys Glu Val Ala Pro Lys Gln Glu His Val Asp Ser Val Val Ala
465 470 475 480

Asp Val Ala Ala Glu Glu Asn Ala
485

<210> 45

<211> 633

<212> DNA

<213> 多杀巴斯德氏菌

<220>

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<222> (2)..(631)

<220>

<223> purF

<400> 45

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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

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

<210> 46

<211> 210

<212> PRT

<213> 多杀巴斯德氏菌

<400> 46

Asp Gly Val Ser Val Tyr Ala Ala Arg Val His Met Gly Gln Arg Leu
 1 5 10 15

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

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

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

Val Gly Arg Thr Phe Ile Met Pro Gly Gln Ala Leu Arg Val Ser Ser
 65 70 75 80
 Val Arg Arg Lys Leu Asn Thr Ile Ala Ser Glu Phe Lys Asp Lys Asn
 85 90 95
 Val Leu Leu Val Asp Asp Ser Ile Val Arg Gly Thr Thr Ser Glu Gln
 100 105 110
 Ile Val Glu Met Ala Arg Ala Ala Gly Ala Lys Lys Ile Tyr Phe Ala
 115 120 125
 Ser Ala Ala Pro Glu Ile Arg Tyr Pro Asn Val Tyr Gly Ile Asp Met
 130 135 140
 Pro Thr Lys Asn Glu Leu Ile Ala Tyr Gly Arg Asp Val Asp Glu Ile
 145 150 155 160
 Ala Asn Leu Ile Gly Val Asp Lys Leu Ile Phe Gln Asp Leu Asp Ala
 165 170 175
 Leu Thr Gly Ser Val Gln Gln Glu Asn Pro Ser Ile Gln Asp Phe Asp
 180 185 190
 Cys Ser Val Phe Thr Gly Val Tyr Val Thr Gly Asp Ile Thr Pro Glu
 195 200 205
 Tyr Leu
 210

<210> 47
 <211> 4788
 <212> DNA
 <213> 多杀巴斯德氏菌

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<220>
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<400> 47
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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	
ggt aga cgt gag ctt gtt act ata tct 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 tct gca gaa aga aaa gaa cga tat tca gaa cag gac att	384			
Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile				
115	120	125		
aaa aca ata tta gaa aca gct aga tat tgt gaa gat aaa cta ccc ata	432			
Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile				
130	135	140		
aca ctc aaa caa aga gta gca att gca atg tta ttt gct att gaa acc	480			
Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr				
145	150	155	160	
gct atg cgt gct ggt gag att gct agt ata aaa tgg gat aat gtt ttt	528			
Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys Trp Asp Asn Val Phe				
165	170	175		
ctt gaa aag aga ata gta cat tta ccg aca act aaa aac ggg cac tct	576			
Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser				
180	185	190		
aga gat gtg ccg ctt tct 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 cgccttttgc cacttgatta	916			
Asn Leu Leu Asp				
290				
catcgccagc cttatatctt ttactttcat tacttccttt ttctaatagaa actggggatg	976			
gaaagtcttg gcgggtaata atatgacgag atgtgttaatt gtaagaacga ttaatcatga	1036			

tagaaatgtc ttcaatacta agaagaactg gactatcttc ttttaagttga gctaaggttc 1096
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ttaatgcttt ttctaagtca aatgctttca ttttttactc tccagcttgc tcatcaataa 1996
gtcatcaat ccattctcga atttcagatt ggaaattttc taacgaatta ttttcattaa 2056
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gcttttcttc aaacaaatca tcttttgaga ttgcgcatac ttttcctacg cctctatac 2176
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accgcatttc tgcggttatt ctgtgtattt atttaaaata ttacttatag tttcagcatc 2356
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actgaagata gatggtaagt acgaagagac ataaagaaaa catcatctcg ccacgcgatt 2776
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 aaaaattttt tttctgtttc tatcatagtt aaattccctta ttcttttatt aatgggcgag 3196
 gaatcggttg ccagtgtgta acgttaatag ctagatcata aattggacca ttctgattta 3256
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 ctgctaaaag actttcatat tctgcttttg tgattgttac tgtttctgtc atagttaaatt 3616
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 cggcgttagt tttctaacaa ctgattctac tgataaagca acgcaaggaa cattattacc 3916
 accagttccc attcttgctt ttaagggttg tgaaatatca tcgtgaatac gacaagcttc 3976
 ttcacctta acctcaaata gaatattttc caatcctcca tttcttccaa tgcaatgcgc 4036
 tgtattttta gaaatgattg gatcttgtga accgtgaaca acaaaagttt cactaccgcc 4096
 agcaagaact ccacgcgttg ctcttaatgt tcccgaaca tcggatttgc gatattgagc 4156
 aaagcttgtc tcaataaagg cggaatatc ttttgctgc gttccgctct gttcaatatt 4216
 cctcgcacg cttttggact caatgagtat ttgtgcaaca cttcgtttcc tagcacttgc 4276
 cacaagaaac actcttttac gacgttgggc aactccgaag tattgagcat cgagaactcg 4336
 ccagcagatt gttcggattg aatgcacata accagcgttc gtccatcttc tccctgtgtg 4396
 ctgcaatggc tcacactctt gaaccagtc agccagaagg tgtccgaatg cgttgctcca 4456
 ggtggatagc acaccggaa cgttttccca cacgagaatg cacggtggtt tgttgtcatt 4516
 gaatctaaca tagtcgateg cttctaaaat ttaattaaa actaacgtga gatttccctg 4576
 ctcatcgtct aaactttgac gattgccagc aactgaaaaa gattgacaag gaggaccacc 4636
 aactaaaacg tctggtgccg gaatttcacg atctaattt ttctgttgca attcagtcac 4696
 atcaccaaga ttgggaacgt tagggtaatg gtaagctaatt actgcgcttg ggaattgctc 4756

aatttcagaa aaccagagtg gctctgcgaa tt

4788

<210> 48

<211> 292

<212> PRT

<213> 多杀巴斯德氏菌

<400> 48

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

Ile Ile Phe Arg Asp Val Ile Glu Arg Tyr Gln Asn Glu Val Ser Ile
20 25 30

Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg Leu Asn Arg Phe Leu
35 40 45

Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp Leu Arg Lys Glu Asp
50 55 60

Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu Val Ser Asp Ala Ser
65 70 75 80

Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val Leu Thr Thr Ala Ile
85 90 95

Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met Thr Gly Ile Glu Lys
100 105 110

Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr Ser Glu Gln Asp Ile
115 120 125

Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu Asp Lys Leu Pro Ile
130 135 140

Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu Phe Ala Ile Glu Thr
145 150 155 160

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

Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr Lys Asn Gly His Ser
180 185 190

Arg Asp Val Pro Leu Ser Gln Arg Ala Val Ala Leu Ile Leu Lys Met
195 200 205

Lys Glu Val Glu Asn Gly Asp Leu Val Phe Gln Thr Thr Pro Glu Ser
210 215 220

Leu Ser Thr Thr Phe Arg Val Leu Lys Lys Glu Cys Gly Leu Glu His
225 230 235 240

Leu His Phe His Asp Thr Arg Arg Glu Ala Leu Thr Arg Leu Ser Lys
245 250 255

Lys Val Asp Val Met Thr Leu Ala Lys Ile Ser Gly His Arg Asp Leu
260 265 270

Arg Ile Leu Gln Asn Thr Tyr Tyr Ala Pro Asn Met Ser Glu Val Ala
275 280 285

Asn Leu Leu Asp
290

<210> 49
<211> 1618
<212> DNA
<213> 多杀巴斯德氏菌

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

<220>
<223> sopE

<400> 49

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

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

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

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

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

aat tgc aaa gtg att gtt gtg cga gtg caa gaa agt gcg caa gaa gac 289
Asn Cys Lys Val Ile Val Val Arg Val Gln Glu Ser Ala Gln Glu Asp
85 90 95

gaa gaa aca aaa gca agt gaa atg aac acg gca att att ggc aca atc 337
Glu Glu Thr Lys Ala Ser Glu Met Asn Thr Ala Ile Ile Gly Thr Ile
100 105 110

aca gaa gaa ggg cag tac aca ggc ttg aag gcg tta ttg att gcg aaa 385
Thr Glu Glu Gly Gln Tyr Thr Gly Leu Lys Ala Leu Leu Ile Ala Lys
115 120 125

aac aaa ttc ggt atc aaa cca cgt att tta tgt gtg cca aaa ttc gac 433
Asn Lys Phe Gly Ile Lys Pro Arg Ile Leu Cys Val Pro Lys Phe Asp
130 135 140

aca aaa gaa gtc gcc aca gag ctt gca agt atc gcc gcc aaa ctc aac 481
Thr Lys Glu Val Ala Thr Glu Leu Ala Ser Ile Ala Ala Lys Leu Asn
145 150 155 160

gca ttt gct tac att tca tgt caa ggg tgt aaa acg aaa gaa caa gcg 529
Ala Phe Ala Tyr Ile Ser Cys Gln Gly Cys Lys Thr Lys Glu Gln Ala
165 170 175

gtg caa tat aaa cgc aac ttc tca caa cgt gaa gtc atg ctg atc atg 577

Val Gln Tyr Lys Arg Asn Phe Ser Gln Arg Glu Val Met Leu Ile Met
180 185 190

ggc gat ttt ctg tca ttt aat gtc aac aca tca aaa gtt gag att gac 625
Gly Asp Phe Leu Ser Phe Asn Val Asn Thr Ser Lys Val Glu Ile Asp
195 200 205

tat gcc gtc act cgt gcg gcg gca atg cgt gca tat ctt gat aaa gaa 673
Tyr Ala Val Thr Arg Ala Ala Ala Met Arg Ala Tyr Leu Asp Lys Glu
210 215 220

cag ggc tgg cat acg tct att tca aat aaa ggc att aat ggc gtg agc 721
Gln Gly Trp His Thr Ser Ile Ser Asn Lys Gly Ile Asn Gly Val Ser
225 230 235 240

ggt gtc aca caa cca ctc tat ttt gac att aac gac agc tcg act gat 769
Gly Val Thr Gln Pro Leu Tyr Phe Asp Ile Asn Asp Ser Ser Thr Asp
245 250 255

gtg aac tat ctc aat gaa caa ggc atc acg tgt tgc gtg aat cat aat 817
Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
260 265 270

ggc ttt cgt ttt tgg ggc tta cgc acg act gca gaa gat cca tta ttc 865
Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
275 280 285

aag ttt gaa gtg tac acc cgc act gca caa atc tta aaa gat acg att 913
Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
290 295 300

gca ggg gcg ttt gat tgg gca gtg gat aaa gat att tct gtc acg cta 961
Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
305 310 315 320

gtg aaa gat att att gaa gca atc aat gcg aag tgg cgt gat tac acc 1009
Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
325 330 335

aca aaa ggc tac tta att ggc ggt aaa gcg tgg ctt aat aaa gag ctt 1057
Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
340 345 350

aac agt gca acg aat tta aaa gat gcg aag ttg ttg atc tct tat gat 1105
Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
355 360 365

tat cac cca gta cca ccg ctc gaa cag cta ggc ttt aat cag tac att 1153
Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
370 375 380

tct gat gaa tac ctt gtt gat ttt tca aat cgt tta gca tcg 1195
Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385 390 395

taaggggtag aaaatggctt taccacgcaa acttaaattg atgaatttaa tcatcgacgg 1255

taacaaatat ctccggcgaag tcacggaagt gactcaacca aaattagcaa tgaaaatcga 1315

agaatttcgc gcgggcggta tgattggttc ggtggatgtc aatctcgggc ttgaaaagct 1375

cgaagcggaa tttaaagccg gtggctacat ggtcgaatta attaaaaaat tcggcgggtc 1435

aatcaacggc attccattgc gttttcttgg ctcatatcag cgtgatgaca cagaagaagt 1495
cacatctgtt gagcttgtga tgcaaggctcg atttactgaa attgacagcg gaaacagcaa 1555
agtgggcgat gacactgaac aaacattcaa agtgccttta acgtattaca aaatcattgt 1615
tga 1618

<210> 50
<211> 398
<212> PRT
<213> 多杀巴斯德氏菌

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

Val Asn Tyr Leu Asn Glu Gln Gly Ile Thr Cys Cys Val Asn His Asn
260 265 270

Gly Phe Arg Phe Trp Gly Leu Arg Thr Thr Ala Glu Asp Pro Leu Phe
275 280 285

Lys Phe Glu Val Tyr Thr Arg Thr Ala Gln Ile Leu Lys Asp Thr Ile
290 295 300

Ala Gly Ala Phe Asp Trp Ala Val Asp Lys Asp Ile Ser Val Thr Leu
305 310 315 320

Val Lys Asp Ile Ile Glu Ala Ile Asn Ala Lys Trp Arg Asp Tyr Thr
325 330 335

Thr Lys Gly Tyr Leu Ile Gly Gly Lys Ala Trp Leu Asn Lys Glu Leu
340 345 350

Asn Ser Ala Thr Asn Leu Lys Asp Ala Lys Leu Leu Ile Ser Tyr Asp
355 360 365

Tyr His Pro Val Pro Pro Leu Glu Gln Leu Gly Phe Asn Gln Tyr Ile
370 375 380

Ser Asp Glu Tyr Leu Val Asp Phe Ser Asn Arg Leu Ala Ser
385 390 395

<210> 51

<211> 353

<212> DNA

<213> 多杀巴斯德氏菌

<220>

<221> CDS

<222> (1)..(351)

<220>

<223> 未知的 C1

<400> 51

atg aca tta ttt gat gaa tgt aaa tta gct ctt aga gac gat ttt aat 48
Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
1 5 10 15

cta att tgt gat gaa gag aag gat tgt gta atg gat aag ttt tat ttc 96
Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
20 25 30

tat ttc ttg gaa aag aaa gag gaa ttt aat ttt caa gat tat tca ttt 144
Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
35 40 45

gaa gaa atg tat ata ttt tca aaa atg gaa cct gtg tat gtt tta tgt 192
Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
50 55 60

gat agc tct aat ata cct ttg ttt agg agt aat tgg gaa ttg att atc 240
Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
65 70 75 80

aat aat ata tat gat gtt gtc tgt tta tct aca aaa gta ttt ttt cta 288

Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95

gat gat gaa aag tta atg atg gaa tta ttt cct gaa gat aaa gta aga 336
 Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110

gtc atc tat aaa aga ta 353
 Val Ile Tyr Lys Arg
 115

<210> 52
 <211> 117
 <212> PRT
 <213> 多杀巴斯德氏菌

<400> 52
 Met Thr Leu Phe Asp Glu Cys Lys Leu Ala Leu Arg Asp Asp Phe Asn
 1 5 10 15

Leu Ile Cys Asp Glu Glu Lys Asp Cys Val Met Asp Lys Phe Tyr Phe
 20 25 30

Tyr Phe Leu Glu Lys Lys Glu Glu Phe Asn Phe Gln Asp Tyr Ser Phe
 35 40 45

Glu Glu Met Tyr Ile Phe Ser Lys Met Glu Pro Val Tyr Val Leu Cys
 50 55 60

Asp Ser Ser Asn Ile Pro Leu Phe Arg Ser Asn Trp Glu Leu Ile Ile
 65 70 75 80

Asn Asn Ile Tyr Asp Val Val Cys Leu Ser Thr Lys Val Phe Phe Leu
 85 90 95

Asp Asp Glu Lys Leu Met Met Glu Leu Phe Pro Glu Asp Lys Val Arg
 100 105 110

Val Ile Tyr Lys Arg
 115

<210> 53
 <211> 509
 <212> DNA
 <213> 多杀巴斯德氏菌

<220>
 <221> CDS
 <222> (1) .. (507)

<220>
 <223> 未知的 C2

<400> 53
 atg aaa aat ttt agg aat ata aat att tat agt gat tat gga aag gtt 48
 Met Lys Asn Phe Arg Asn Ile Asn Ile Tyr Ser Asp Tyr Gly Lys Val
 1 5 10 15

gat aag gaa att ata tta gaa ttc gaa aat gaa ttt aat ata aag ctt 96
 Asp Lys Glu Ile Ile Leu Glu Phe Glu Asn Glu Phe Asn Ile Lys Leu

20										25					30					
cct	tct	tta	tac	ata	gat	tta	att	acg	gcg	cat	aat	gct	ccg	aag	agt	144				
Pro	Ser	Leu	Tyr	Ile	Asp	Leu	Ile	Thr	Ala	His	Asn	Ala	Pro	Lys	Ser					
35					40					45										
gaa	gag	aat	tgc	ttt	gaa	tat	tac	aat	gag	cgt	aat	gag	ccc	acg	ttt	192				
Glu	Glu	Asn	Cys	Phe	Glu	Tyr	Tyr	Asn	Glu	Arg	Asn	Glu	Pro	Thr	Phe					
50					55					60										
tct	tcc	ttt	gga	ttt	gaa	ggg	ttt	gag	aca	gag	cgg	tct	agc	gcc	tct	240				
Ser	Ser	Phe	Gly	Phe	Glu	Gly	Phe	Glu	Thr	Glu	Arg	Ser	Ser	Ala	Ser					
65					70					75					80					
ctt	gaa	aat	ata	tat	gct	cag	tat	att	tat	gat	gat	cca	atc	tat	ggg	288				
Leu	Glu	Asn	Ile	Tyr	Ala	Gln	Tyr	Ile	Tyr	Asp	Asp	Pro	Ile	Tyr	Gly					
85					90					95										
tat	gaa	cat	gtg	tat	tct	ttt	ggg	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	ggg	gat	gaa	ccc	aaa	atc	tgt	384				
Cys	Phe	Asp	Tyr	Arg	Asp	Asp	Pro	Lys	Gly	Asp	Glu	Pro	Lys	Ile	Cys					
115					120					125										
atc	gtg	att	cac	gat	gaa	tat	gat	gaa	aaa	aca	ggg	aaa	atg	cga	ctg	432				
Ile	Val	Ile	His	Asp	Glu	Tyr	Asp	Glu	Lys	Thr	Gly	Lys	Met	Arg	Leu					
130					135					140										
ttt	cct	ata	gca	gag	aat	ttt	gaa	gcg	ttt	tta	gat	agt	ttg	aaa	tca	480				
Phe	Pro	Ile	Ala	Glu	Asn	Phe	Glu	Ala	Phe	Leu	Asp	Ser	Leu	Lys	Ser					
145					150					155					160					
ttt	gat	gaa	atg	ata	gag	aag	tat	tcg	ta							509				
Phe	Asp	Glu	Met	Ile	Glu	Lys	Tyr	Ser												
165																				

<210> 54

<211> 169

<212> PRT

<213> 多杀巴斯德氏菌

<400> 54

Met	Lys	Asn	Phe	Arg	Asn	Ile	Asn	Ile	Tyr	Ser	Asp	Tyr	Gly	Lys	Val
1				5					10					15	

Asp	Lys	Glu	Ile	Ile	Leu	Glu	Phe	Glu	Asn	Glu	Phe	Asn	Ile	Lys	Leu
			20					25					30		

Pro	Ser	Leu	Tyr	Ile	Asp	Leu	Ile	Thr	Ala	His	Asn	Ala	Pro	Lys	Ser
35					40					45					

Glu	Glu	Asn	Cys	Phe	Glu	Tyr	Tyr	Asn	Glu	Arg	Asn	Glu	Pro	Thr	Phe
50					55					60					

Ser	Ser	Phe	Gly	Phe	Glu	Gly	Phe	Glu	Thr	Glu	Arg	Ser	Ser	Ala	Ser	
65					70					75					80	

Leu	Glu	Asn	Ile	Tyr	Ala	Gln	Tyr	Ile	Tyr	Asp	Asp	Pro	Ile	Tyr	Gly
85					90					95					

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

<210> 55
 <211> 443
 <212> DNA
 <213> 多杀巴斯德氏菌

<220>
 <221> CDS
 <222> (1) .. (441)
 <220>
 <223> 未知的 C3

<400> 55
 atg ata aaa tat tta gag gga aat att aac tcg ttt ata tcg gca tta 48
 Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
 1 5 10 15
 ggt aaa aac gaa agt aat aaa gat att tta aaa tta gta gaa ata gtt 96
 Gly Lys Asn Glu Ser Asn Lys Asp Ile Leu Lys Leu Val Glu Ile Val
 20 25 30
 tct tca gat ttt gaa gtg gat gaa cta agt cat aaa gat gaa cac gag 144
 Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
 35 40 45
 ata tat tat ttg ttt tat aag agg ggt gtt gaa ttt tgt ttt aaa aga 192
 Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
 50 55 60
 ata gat gaa gag tat gtc tta tat tcg gtt ttc ttt ttc ttg gta gag 240
 Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
 65 70 75 80
 gtt gat aat tat ttt tca tgc cca ttt att cat gaa tta ata tgt gat 288
 Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
 85 90 95
 ctt aaa cac gga ttc tca ata gag gat att ata agg ttt tta ggg gag 336
 Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
 100 105 110
 cca aat ttt aaa ggt agt ggc tgg gta aga tat tct tat aat gga aga 384
 Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
 115 120 125
 aat att cat ttc gaa ttt aat gaa tct aat gaa tta tcc cag att agc 432

Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
 -130 135 140

att ttt att ta
 Ile Phe Ile
 145

443

<210> 56
 <211> 147
 <212> PRT
 <213> 多杀巴斯德氏菌

<400> 56
 Met Ile Lys Tyr Leu Glu Gly Asn Ile Asn Ser Phe Ile Ser Ala Leu
 1 5 10 15

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

Ser Ser Asp Phe Glu Val Asp Glu Leu Ser His Lys Asp Glu His Glu
 35 40 45

Ile Tyr Tyr Leu Phe Tyr Lys Arg Gly Val Glu Phe Cys Phe Lys Arg
 50 55 60

Ile Asp Glu Glu Tyr Val Leu Tyr Ser Val Phe Phe Phe Leu Val Glu
 65 70 75 80

Val Asp Asn Tyr Phe Ser Cys Pro Phe Ile His Glu Leu Ile Cys Asp
 85 90 95

Leu Lys His Gly Phe Ser Ile Glu Asp Ile Ile Arg Phe Leu Gly Glu
 100 105 110

Pro Asn Phe Lys Gly Ser Gly Trp Val Arg Tyr Ser Tyr Asn Gly Arg
 115 120 125

Asn Ile His Phe Glu Phe Asn Glu Ser Asn Glu Leu Ser Gln Ile Ser
 130 135 140

Ile Phe Ile
 145

<210> 57
 <211> 8498
 <212> DNA
 <213> 多杀巴斯德氏菌

<220>
 <223> 未知的 C

<400> 57
 gaattcgaat taagcgagaa aattgctgaa acactagaac aaagtcaatt aaatattagt 60
 caattatcaa ttgttgaaat ttatcctttc aatgaagaac aagggatagc ttttcataat 120
 aaaagtgtgg tacaacttaa accagaagag gtggaatggt catcaatcca ttatcttttc 180
 tttgctggcg atattcagca agtcgctcat ctcgcgaaag ccgcagaaat gggttgcgtg 240

gtgattgata tgaaagggat ttgtgccagc ttgcaagacg tccctgtggt gataccggga 300
 gtaaatcagg aaaaattggg agatttacgt cagcgtaata ttgtgtcctt agccgatcca 360
 caagtgcac aacttgcat agtcacgcc tcgttgatgt caaatcacga aatcaaagac 420
 attgccgtaa cctcgttatt acctgcactt tatactaacy gagaaacggg aggtaaatta 480
 gcgggacaaa cagcgcgatt gttaaatggc attccacttg atgaaggcga acaacgttta 540
 gcttttgatg tttccctac gcctgcacgc catttaaata tgcaaattca caagatcttt 600
 ccacaattag ataatgtcgt atttcattct atccaagtgc ctgttttcta cgggatgggg 660
 caaatggtga gcgtattatc ggattatgca ttagatcctc aatcttgctt agcgagctgg 720
 actgacaatc cgttgatgac ttatcatgca gaaaaatatt gcacccagc gacgaatggc 780
 gaacaggaaa tggcagaaga gcaagcagca aaattacata taagtgggtt aagtgcgggtg 840
 gaaaatgggc tacaattttg gtcgggtgca gatgaacagc gctttaatct tgctttattg 900
 agtgttacgc ttgcagagtt aatttactcg caagggttatt aatttaaattg tgtttttgca 960
 cgatattttt atcttgaact ttgagagcgc actcgttttt gacgagtgcg tttttgttaa 1020
 aacattcgtt tgaaagacag tgaatgaata gcggagttat tgataagaat caattttatc 1080
 aaaagcaact gaatgttatt aatcgaggca ataaacctat tgatagtttt agttggcgcc 1140
 ataatacata aactgtactt aataatatgc aatcaatacc tagaaatatt catgacgtaa 1200
 tccaacatat cggggagggg attttaagtg atggtagaaa aaacatttag aaatctaaaa 1260
 atatatgatg attatgggtc tgcctctcag gaaattattt ttaattttga aaaagagttt 1320
 gatataaaac tccctttatc ctatatctca cttgtgaaaa agtataatgg cgtttgggtt 1380
 aaggaaaagtg attttgaata tttatctcaa aatgggaaaa gaataataag ctcatagagt 1440
 tttgatagtt ttgagacaaa agataatatc gaaccaatga ataatatatt aagacaatat 1500
 atttatgatg atgaaattta tggatataag aatgtttatt ctttgggtta cactggaaat 1560
 ggtgactttg tctgttttga ttatcgtgat gacccaaaag gtgatgagcc caaaatctgt 1620
 atcgtgattc atgatgaata tgatgaaaaa acaggcaagc gtttgttatt gcctgtggca 1680
 gaaaattttg aggcattttt agatatgctt tacgattttg atgaacgcta tccgaatggg 1740
 tatgaatagg tatttgttta aataatgtgt tgtatttttt aagcattatt tacaactaac 1800
 attttaagtg cgttcaattt tgaaaaagtt ttgggctttg agaattgggc gcattttttt 1860
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 65 70 75 80
 Gly Asp Val Asn Arg Gln Val Val Ser Pro Gln Asp Lys Ala Lys Phe
 85 90 95
 Gly Gly Asn Glu Phe Met Ala Lys Gln Glu Lys Arg Asn Gln Glu Leu
 100 105 110
 Ile Gln Gly Ile Ala Lys Leu Tyr Leu Arg Ser Glu Asn Ala Asn Ala
 115 120 125
 Ser Ser Asp Ala Pro Ile Thr Ile Asp Lys Pro Phe His Tyr Ser Cys
 130 135 140
 Glu Glu Leu Asp Leu Pro Thr Ala Asn Glu Tyr Ala Arg Arg Lys Pro
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 Ile Val Cys Glu Val Gln Gly Gly Val Asn Arg Lys Phe Trp Leu Pro
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 Val Ser Glu Ser Leu Val Ser Glu Asp Lys Leu Lys Lys Asp Arg Val
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 Arg Leu Glu Ser Asp Thr Ser Tyr Ala Ile Lys Glu Lys Gly Ile Val

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Glu	Asp	Val	Ser	Glu	Gly	Val	Ser	Pro	Phe	Asn	Arg	Ile	Gly	Phe	Thr
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Thr	Phe	Ser	Gly	Gly	Val	Arg	Gln	Arg	Asp	Val	Thr	Glu	Gly	Cys	Val
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Arg	Trp	Glu	Arg	Ser	Thr	Val	Ser	Phe	Gln	Glu	His	Tyr	Lys	Gly	Tyr
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Tyr	Asp	Lys	Phe	His	Ser	Ser	Thr	Cys	Arg	Gly	Ser	Gly	Ser	Ser	Arg
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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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Arg	Arg	Tyr	Asp	Met	Val	Phe	Thr	Asp	Glu	Glu	Arg	Cys	Leu	Gly	Gly
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Asn	Ile	Gly	Arg	Arg	Thr	Thr	Arg	Ala	Trp	Phe	Asp	Gln	Lys	Asn	Lys
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Asp	Ile	Thr	Arg	Glu	Leu	Asn	Ile	Val	Arg	Pro	Ser	Gly	Trp	Thr	Ser
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Lys	Asn	Pro	Asp	Ala	Gln	Pro	Ser	Lys	Leu	Gly	Thr	Asn	Ile	Gln	Arg
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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
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Ala Trp Lys Lys Cys Val Gly Asp Gln Tyr Tyr Thr Ala Tyr Ser Lys
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<211> 5798

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 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
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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
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Ser Ser Leu Leu Tyr Leu Thr Pro Leu Leu Asn Asp Asn Thr Lys Leu			
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Pro Asn Glu Gly Glu Val Tyr Asn Leu Arg Gly Ile Ala Tyr Ala Gln			
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Asn Gly Asn Leu Val Asn Ala Arg Asn Asp Ile Asn Lys Ala Arg Glu			
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Tyr Leu Asn Gly Val Lys Asn Ser Arg Leu Ile His Asn Leu Val Phe			
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gct tta gtt aaa aat ggt gat ctt gat tat gca aaa gat atc att gtt			1387
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Lys Glu Arg Leu Asn Thr Ser Pro Asp Leu Ile Asn Ala Leu Lys			
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<212> PRT

<213> 多杀巴斯德氏菌

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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
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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

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240

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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
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 Phe Val Asn Tyr Gly Thr Leu Ala Ser Ala Gln Asn Leu Thr Ile Asn
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 Thr Glu Gln Gly Ser Ile Tyr Asn Ile Gly Gly Ile Leu Gly Ala Gly
 85 90 95

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 Lys Ser Leu Asn Leu Ser Ala Lys Arg Gly Glu Asn Gln Gly Gly Tyr
 100 105 110

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 115 120 125

ctc aca gcg gat cgc acg gtg 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

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 Gly Asp Ala Thr Ile Asn Ala Asn Ala Leu Ile Asn Asp Val Thr Leu
 145 150 155 160

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 Thr Gly Arg Leu Glu Tyr Gln Asp Leu Lys Lys Asp Tyr Thr Arg Tyr
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 Tyr Arg Ile Asn Glu Thr Ala Lys His Gly Trp His Asn Asn Phe Tyr
 180 185 190

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 195 200

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 aagttcttca ttcgttgga tcaccatggc aacaggcgta ttgtctgctg taatcaccoc 1710
 ttcatgacca aagcgagccg ctttgttttt atctgaatcc acttgataac cgaacagttt 1770
 taaatgggtt aaggttga 1788

<210> 63

<211> 200

<212> PRT

<213> 多杀巴斯德氏菌

<400> 63

Val Asn Thr Gly Leu Ile His Ser Asn Gly Asn Ala Lys Leu Thr Phe
 1 5 10 15

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

<210> 64
 <211> 278
 <212> DNA
 <213> 多杀巴斯德氏菌

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<220>
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<400> 64
 gaattccaac caaatctcac accagagcaa gaacgctaca tagtggaatg gttggcagaa 60
 cattacccaa atggaaataa accttaacca tagcaagaga gaagaaa atg aaa att 116
 Met Lys Ile
 1
 act att aca cga aat cat cca gaa gta ttt caa gaa tcc gct cgt tta 164
 Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser Ala Arg Leu
 5 10 15
 gta gcc gaa aag ttc att aaa gcc caa tgt gta gaa gca tta aca ttg 212
 Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala Leu Thr Leu

_ 20 25 30 35
 gct ttg att gag ggt gtc gag cac ttt gtg ctg gaa ggt gag gag gaa 260
 Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly Glu Glu Glu
 40 45 50
 agc aaa agg gga cat agt 278
 Ser Lys Arg Gly His Ser
 55
 <210> 65
 <211> 57
 <212> PRT
 <213> 多杀巴斯德氏菌
 <400> 65
 Met Lys Ile Thr Ile Thr Arg Asn His Pro Glu Val Phe Gln Glu Ser
 1 5 10 15
 Ala Arg Leu Val Ala Glu Lys Phe Ile Lys Ala Gln Cys Val Glu Ala
 20 25 30
 Leu Thr Leu Ala Leu Ile Glu Gly Val Glu His Phe Val Leu Glu Gly
 35 40 45
 Glu Glu Glu Ser Lys Arg Gly His Ser
 50 55
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 <222> (1) .. (597)
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 Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
 1 5 10 15
 gca atg cgt gca tat ctt gat aaa gaa cag gcc tgg cat acg tct att 96
 Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
 20 25 30
 tca aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat 144
 Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
 35 40 45
 ttt gac att aac gac agc tgc act gat gtg aac tat ctc aat gaa caa 192
 Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
 50 55 60
 ggc atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta 240
 Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
 65 70 75 80

cgc acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc 288
 Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
 85 90 95

act gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca 336
 Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
 100 105 110

gtg gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca 384
 Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
 115 120 125

atc aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc 432
 Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
 130 135 140

ggt aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa 480
 Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
 145 150 155 160

gat gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc 528
 Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
 165 170 175

gaa cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat 576
 Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
 180 185 190

ttt tca aat cgt tta gca tgc taaggggtag aaaatggctt taccacgcaa 627
 Phe Ser Asn Arg Leu Ala Ser
 195

acttaaattg atgaatttaa tcatcgacgg taacaaatat ctcggcgaag tcacggaagt 687

gactcaacca aaattagcaa tgaaaaatcga agaatttcgc gcgggcggta tgattgggttc 747

ggtggatgtc aatctcgggc ttgaaaagct cgaagcggaa tttaaagccg gtggctacat 807

ggtcgaatta attaaaaaat tcggcgggtc aatcaacggc attccattgc gttttcttgg 867

ctcatatcag cgtgatgaca cagaagaagt cacatctgtt gagcttgtga tgcaaggctcg 927

atttactgaa attgacagcg gaaacagcaa agtgggcgat gacactgaac aaacattcaa 987

agtgccctta acgtattaca aaatcattgt tga 1020

<210> 67

<211> 199

<212> PRT

<213> 多杀巴斯德氏菌

<400> 67

Val Asn Thr Ser Lys Val Glu Ile Asp Tyr Ala Val Thr Arg Ala Ala
 1 5 10 15

Ala Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile
 20 25 30

Ser Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr
 35 40 45

Phe Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln
 - 50 55 60
 Gly Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu
 65 70 75 80
 Arg Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg
 85 90 95
 Thr Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala
 100 105 110
 Val Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala
 115 120 125
 Ile Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly
 130 135 140
 Gly Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys
 145 150 155 160
 Asp Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu
 165 170 175
 Glu Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp
 180 185 190
 Phe Ser Asn Arg Leu Ala Ser
 195

<210> 68
 <211> 2584
 <212> DNA
 <213> 多杀巴斯德氏菌

<220>
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 <222> (1042)..(2286)

<220>
 <223> xylA

<400> 68
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 taccattatt ttatggaatc tctctggacc gatgaccatt gccaatattg aaattcctca 120
 cgcgatggtc tttttggtct ttatttacgt gctgtttagc agtattgtgg catttaaaat 180
 cggtcgcccc ttaattcagc tcaattttgc caatgaacgc ttaaacgcca actaccgtta 240
 ttcacttata cgtctgaaag aatatgctga aagcattgct ttttatcgtg gtgaaaaaat 300
 ggaaaaacgt ctattgacca cacaatttaa tcaggtgatt gataacgttt ggcaagtaat 360
 ctaccgcacc ttgaaattat ccggttttaa cttaatcatt acgcagattt cgggtggttt 420
 tccgctggtg attcaagtga cacgttattt tcgtcgacaa taggtgcata tgagggtgtt 480
 agaatagcga tactttctgt tggaaaagta aactctttta tataaataga aatcgcttga 540

atgattctcg	ggcaaaaaat	aatgtactca	tttgcgatct	catactgata	atggcgaaagt	600										
aaatatcttc	tracaatatt	atggtaatta	tcaggtaata	ccgtatagcc	atagattcca	660										
gttctatfff	gttttgctaa	ataattgatg	agcatttgag	gcgcaggtaa	atccatatct	720										
gcaacagaca	ttgaaatcat	atccttgccg	tattttacgag	taattgcccc	tttagcacta	780										
tgacaatctg	atctatcagt	aaaaacatca	aacaaattat	ccgtcataca	tgttctccaa	840										
tattggattt	atataaactt	tagaacttga	ggtagattgt	tggaattggt	aaatctggta	900										
tttctattac	gttttttctt	ttttgtgata	taagccacaa	taaccaataa	tcttaattgt	960										
taagtgaaat	aacgtaattg	atcctcccat	tgttttacta	aattatgtct	ctgaaactta	1020										
tttgttcagg	agaaatcatt	t	atg	tcc	act	tac	ttc	gac	aaa	att	gaa	aaa	1071			
			Met	Ser	Thr	Tyr	Phe	Asp	Lys	Ile	Glu	Lys				
			1					5				10				
gta	aat	tat	gaa	ggg	gta	act	tca	tct	aat	ccg	ttt	gca	tat	aag	cat	1119
Val	Asn	Tyr	Glu	Gly	Val	Thr	Ser	Ser	Asn	Pro	Phe	Ala	Tyr	Lys	His	
			15						20					25		
tat	gat	gct	aat	caa	gtt	att	tta	ggg	aag	acg	atg	gct	gaa	cac	tta	1167
Tyr	Asp	Ala	Asn	Gln	Val	Ile	Leu	Gly	Lys	Thr	Met	Ala	Glu	His	Leu	
			30					35					40			
cgt	tta	gcc	gtc	tgt	tat	tgg	cac	act	ttc	tgt	tgg	aca	ggg	aat	gat	1215
Arg	Leu	Ala	Val	Cys	Tyr	Trp	His	Thr	Phe	Cys	Trp	Thr	Gly	Asn	Asp	
		45					50					55				
atg	ttc	ggg	gtc	ggg	tct	ttc	gat	cgt	tgt	tgg	cag	aag	gcg	agt	gat	1263
Met	Phe	Gly	Val	Gly	Ser	Phe	Asp	Arg	Cys	Trp	Gln	Lys	Ala	Ser	Asp	
	60					65					70					
tca	tta	gca	ggg	gca	aaa	caa	aaa	gca	gat	atc	gct	ttt	gaa	ttt	ttc	1311
Ser	Leu	Ala	Gly	Ala	Lys	Gln	Lys	Ala	Asp	Ile	Ala	Phe	Glu	Phe	Phe	
	75				80					85					90	
agt	aaa	tta	ggc	ata	cct	tat	tat	tgt	ttt	cat	gat	gtt	gat	gtt	gcg	1359
Ser	Lys	Leu	Gly	Ile	Pro	Tyr	Tyr	Cys	Phe	His	Asp	Val	Asp	Val	Ala	
				95					100					105		
cca	gaa	ggg	cat	tca	ttt	aaa	gaa	tat	ttg	tcg	aac	ttt	aat	aca	atg	1407
Pro	Glu	Gly	His	Ser	Phe	Lys	Glu	Tyr	Leu	Ser	Asn	Phe	Asn	Thr	Met	
			110					115					120			
atc	gat	gtt	tta	gcg	cag	aaa	caa	gaa	gaa	aca	ggc	gtc	aaa	ttg	ttg	1455
Ile	Asp	Val	Leu	Ala	Gln	Lys	Gln	Glu	Glu	Thr	Gly	Val	Lys	Leu	Leu	
		125				130						135				
tgg	ggg	act	gca	aat	tgt	ttt	aca	cac	cct	cgt	tat	atg	tct	ggg	gct	1503
Trp	Gly	Thr	Ala	Asn	Cys	Phe	Thr	His	Pro	Arg	Tyr	Met	Ser	Gly	Ala	
	140					145					150					
gca	aca	aat	ccg	aat	cca	gaa	att	ttt	gct	tgg	gct	gct	gca	caa	gta	1551
Ala	Thr	Asn	Pro	Asn	Pro	Glu	Ile	Phe	Ala	Trp	Ala	Ala	Ala	Gln	Val	
155					160					165					170	
ttt	act	gcc	atg	ggg	gca	act	cag	cgt	tta	ggg	ggg	gaa	aat	tat	gtt	1599

	175	180	185	
ttg tgg gga gga cgt gaa gga tat gaa acg tta tta aat acc aat tta				1647
Leu Trp Gly Gly Arg Glu Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu				
	190	195	200	
aaa cag gag cga gag caa att gga cgt ttc atg caa atg gtg gtt gag				1695
Lys Gln Glu Arg Glu Gln Ile Gly Arg Phe Met Gln Met Val Val Glu				
	205	210	215	
cat aaa tat aaa atc ggt ttt aac ggg act ttg ctg att gaa cca aag				1743
His Lys Tyr Lys Ile Gly Phe Asn Gly Thr Leu Ile Glu Pro Lys				
	220	225	230	
cca caa gag cca acg aaa cat caa tat gac tat gat gtg gcg acc gtt				1791
Pro Gln Glu Pro Thr Lys His Gln Tyr Asp Tyr Asp Val Ala Thr Val				
	235	240	245	250
tat ggc ttt tta aag cag ttt ggt tta gaa aaa gaa att aaa gtg aat				1839
Tyr Gly Phe Leu Lys Gln Phe Gly Leu Glu Lys Glu Ile Lys Val Asn				
	255	260	265	
att gaa gct aat cac gca aca tta gct gga cac act ttc cag cat gaa				1887
Ile Glu Ala Asn His Ala Thr Leu Ala Gly His Thr Phe Gln His Glu				
	270	275	280	
gtc gcc atg gct aca gcg tta gat att ttt ggt tct att gat gca aat				1935
Val Ala Met Ala Thr Ala Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn				
	285	290	295	
cgt ggt gat cca caa tta ggt tgg gat acc gat caa ttc cct aat agc				1983
Arg Gly Asp Pro Gln Leu Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser				
	300	305	310	
gta gaa gaa aat act ttg gtc ata tat gaa att ctc aaa gca ggg ggc				2031
Val Glu Glu Asn Thr Leu Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly				
	315	320	325	330
ttt aca acc ggt ggt ttt aat ttt gat gct aaa atc cgt cgg cag agt				2079
Phe Thr Thr Gly Gly Phe Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser				
	335	340	345	
acg gat cct tac gat tta ttt cat gga cat att ggc gcg att gat gta				2127
Thr Asp Pro Tyr Asp Leu Phe His Gly His Ile Gly Ala Ile Asp Val				
	350	355	360	
ctt gcc tta tca cta aaa tgt gcg gcg aaa atg ctt gaa gag caa gct				2175
Leu Ala Leu Ser Leu Lys Cys Ala Ala Lys Met Leu Glu Glu Gln Ala				
	365	370	375	
tta caa aaa gtc gtc aat caa cgt tat gct ggt tgg aca tca tca ctt				2223
Leu Gln Lys Val Val Asn Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu				
	380	385	390	
ggt caa ctt gtt caa atc cgg tcc tac cac gcg tgt ctg caa tac aga				2271
Gly Gln Leu Val Gln Ile Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg				
	395	400	405	410
cta aca aaa gtg ctt taaaacgttc cggttacgc cagacatcta gacgattgaa				2326
Leu Thr Lys Val Leu				
	415			

taatttcaat attgtctcgc cacgtaattc aaaggctttg tgtatgtgcg aatgatattc 2386
acaacaaagt tctgcaaaat cttgaattgc gtgaggtaat ttaaagcgct gacataagcg 2446
tcttgctcgc atgacaccag ctttttcatg tccataatga tgtggcaata tttcttttgg 2506
tgttaaggct tttcctaaat catgacaaat tgcagcaaaa cgtaccgcac ttttgtcact 2566
gtccgtgttt tctgtcga 2584

<210> 69
<211> 415
<212> PRT
<213> 多杀巴斯德氏菌

<400> 69
Met Ser Thr Tyr Phe Asp Lys Ile Glu Lys Val Asn Tyr Glu Gly Val
1 5 10 15
Thr Ser Ser Asn Pro Phe Ala Tyr Lys His Tyr Asp Ala Asn Gln Val
20 25 30
Ile Leu Gly Lys Thr Met Ala Glu His Leu Arg Leu Ala Val Cys Tyr
35 40 45
Trp His Thr Phe Cys Trp Thr Gly Asn Asp Met Phe Gly Val Gly Ser
50 55 60
Phe Asp Arg Cys Trp Gln Lys Ala Ser Asp Ser Leu Ala Gly Ala Lys
65 70 75 80
Gln Lys Ala Asp Ile Ala Phe Glu Phe Phe Ser Lys Leu Gly Ile Pro
85 90 95
Tyr Tyr Cys Phe His Asp Val Asp Val Ala Pro Glu Gly His Ser Phe
100 105 110
Lys Glu Tyr Leu Ser Asn Phe Asn Thr Met Ile Asp Val Leu Ala Gln
115 120 125
Lys Gln Glu Glu Thr Gly Val Lys Leu Leu Trp Gly Thr Ala Asn Cys
130 135 140
Phe Thr His Pro Arg Tyr Met Ser Gly Ala Ala Thr Asn Pro Asn Pro
145 150 155 160
Glu Ile Phe Ala Trp Ala Ala Ala Gln Val Phe Thr Ala Met Gly Ala
165 170 175
Thr Gln Arg Leu Gly Gly Glu Asn Tyr Val Leu Trp Gly Gly Arg Glu
180 185 190
Gly Tyr Glu Thr Leu Leu Asn Thr Asn Leu Lys Gln Glu Arg Glu Gln
195 200 205
Ile Gly Arg Phe Met Gln Met Val Val Glu His Lys Tyr Lys Ile Gly
210 215 220
Phe Asn Gly Thr Leu Leu Ile Glu Pro Lys Pro Gln Glu Pro Thr Lys
225 230 235 240

His Gln Tyr Asp Tyr Asp Val Ala Thr Val Tyr Gly Phe Leu Lys Gln
 245 250 255
 Phe Gly Leu Glu Lys Glu Ile Lys Val Asn Ile Glu Ala Asn His Ala
 260 265 270
 Thr Leu Ala Gly His Thr Phe Gln His Glu Val Ala Met Ala Thr Ala
 275 280 285
 Leu Asp Ile Phe Gly Ser Ile Asp Ala Asn Arg Gly Asp Pro Gln Leu
 290 295 300
 Gly Trp Asp Thr Asp Gln Phe Pro Asn Ser Val Glu Glu Asn Thr Leu
 305 310 315 320
 Val Ile Tyr Glu Ile Leu Lys Ala Gly Gly Phe Thr Thr Gly Gly Phe
 325 330 335
 Asn Phe Asp Ala Lys Ile Arg Arg Gln Ser Thr Asp Pro Tyr Asp Leu
 340 345 350
 Phe His Gly His Ile Gly Ala Ile Asp Val Leu Ala Leu Ser Leu Lys
 355 360 365
 Cys Ala Ala Lys Met Leu Glu Glu Gln Ala Leu Gln Lys Val Val Asn
 370 375 380
 Gln Arg Tyr Ala Gly Trp Thr Ser Ser Leu Gly Gln Leu Val Gln Ile
 385 390 395 400
 Arg Ser Tyr His Ala Cys Leu Gln Tyr Arg Leu Thr Lys Val Leu
 405 410 415

<210> 70
 <211> 3501
 <212> DNA
 <213> 多杀巴斯德氏菌

<220>
 <221> CDS
 <222> (298) .. (1905)

<220>
 <223> yabk

<400> 70
 gaattcgagg aagggggcgt attacaaatt gaaacggctg cacgtgtagc acaacatgat 60
 aatgcctgtg cggatcattt ccttgccctt ttacttcac cagaagcaca agggcattta 120
 gtcaagaata atgtgatgtt accggtgatt aataccaata ttgaaccgca ctttgatgcc 180
 cttagagcca cccaaatgaa cacgaaagt ctcgatacct caaaagtgaa tgccgaacaa 240
 gtcaaaaaat ggattgctgt ttggcaaacg accctaaccc aataattgtt tgtcttg 297
 atg ttt aag cga ttt cgt gca ttc aca tac cgt ccc gcc agt tat ctt 345
 Met Phe Lys Arg Phe Arg Ala Phe Thr Tyr Arg Pro Ala Ser Tyr Leu
 1 5 10 15
 ggc ggg atg ttg gtg att gtt ttt ctg agc gct ttt tat gcg ttc gcc 393

Gly Gly Met Leu Val Ile Val Phe Leu Ser Ala Phe Tyr Ala Phe Ala	
- 20 25 30	
tta ggg gcg gtt ttt tcg ctc cct ttt gcg cgc agt tgg aca gcg ttg	441
Leu Gly Ala Val Phe Ser Leu Pro Phe Ala Arg Ser Trp Thr Ala Leu	
35 40 45	
ttg agt gat cag tat tta caa cac gtg atc atc ttt agc ttt tgg caa	489
Leu Ser Asp Gln Tyr Leu Gln His Val Ile Ile Phe Ser Phe Trp Gln	
50 55 60	
gcc ttt ctg tcg gcg gta ctt gcg gtc ctc ttt ggt gcc att gta gca	537
Ala Phe Leu Ser Ala Val Leu Ala Val Leu Phe Gly Gly Ile Val Ala	
65 70 75 80	
cga gcc ttt ttt tat caa ccg ttt gtg gcc aag aaa ctg atc ctc aaa	585
Arg Ala Phe Phe Tyr Gln Pro Phe Val Gly Lys Lys Leu Ile Leu Lys	
85 90 95	
tta ttt tca ctg act ttt gtg tta cct gcc tta gtg gcg att ttt ggt	633
Leu Phe Ser Leu Thr Phe Val Leu Pro Ala Leu Val Ala Ile Phe Gly	
100 105 110	
tta tta gcc gtg tat gcc gct tct gcc tgg tta gcg atg tta agc cag	681
Leu Leu Gly Val Tyr Gly Ala Ser Gly Trp Leu Ala Met Leu Ser Gln	
115 120 125	
ttt ttc gct tgg gat tgg act cct aat att tac gcc tta aca ggt att	729
Phe Phe Ala Trp Asp Trp Thr Pro Asn Ile Tyr Gly Leu Thr Gly Ile	
130 135 140	
tta ctg gcg cat ctt ttt ttt aat gtc cca tta gct tgt cgc ctg ttt	777
Leu Leu Ala His Leu Phe Phe Asn Val Pro Leu Ala Cys Arg Leu Phe	
145 150 155 160	
tta caa ggt ttg caa gca att ccg gtg caa caa cgt cag ctc gcg gca	825
Leu Gln Gly Leu Gln Ala Ile Pro Val Gln Gln Arg Gln Leu Ala Ala	
165 170 175	
caa ctc aat tta cgt ggt tgg cat ttt ata cgt ctg att gag tgg ccc	873
Gln Leu Asn Leu Arg Gly Trp His Phe Ile Arg Leu Ile Glu Trp Pro	
180 185 190	
tat tta cgc cag caa ttg tta cct gca ttt act ttg att ttc atg ctg	921
Tyr Leu Arg Gln Gln Leu Leu Pro Ala Phe Thr Leu Ile Phe Met Leu	
195 200 205	
tgt ttt acc agt ttt gcg att gtg ctc act tta ggt gcc gga ccg aaa	969
Cys Phe Thr Ser Phe Ala Ile Val Leu Thr Leu Gly Gly Gly Pro Lys	
210 215 220	
tat acc acg ttg gaa gtg gct atc tat caa gcg att tta ttt gag ttt	1017
Tyr Thr Thr Leu Glu Val Ala Ile Tyr Gln Ala Ile Leu Phe Glu Phe	
225 230 235 240	
gat gta ccg aaa gcc gcc tta ttt gcg tta tta caa ttt gtt ttt tgt	1065
Asp Val Pro Lys Ala Gly Leu Phe Ala Leu Leu Gln Phe Val Phe Cys	
245 250 255	
ttt ctg tta ttc acg ctg agt agc ttt ttt tct cca gcc ccc gcc acg	1113
Phe Leu Leu Phe Thr Leu Ser Ser Phe Phe Ser Pro Ala Pro Ala Thr	
260 265 270	

aca tta cac agt caa cct act tgg ttt gcg ccc caa tcg tat tgg gtt	1161
Thr Leu His Ser Gln Pro Thr Trp Phe Ala Pro Gln Ser Tyr Trp Val	
275 280 285	
aaa tta tgg caa cgt atg atc att gtg tgt gcg aca gta ttt atc tta	1209
Lys Leu Trp Gln Arg Met Ile Ile Val Cys Ala Thr Val Phe Ile Leu	
290 295 300	
tta ccg cta ctc aat acg cta gtt tct gct ttg ctt tcg tct cag ttt	1257
Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe	
305 310 315 320	
ttt acc ttg tgg tta caa cct caa tta tgg aaa gca tta ggt tac tcg	1305
Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser	
325 330 335	
ctc acc atc gcc ccc act tct gca ttg ctc gct tta gta ctg tct ttt	1353
Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe	
340 345 350	
gcc tta tta ttg ctt gcc aga gaa tta cat tgg cga cat tat cgc agc	1401
Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser	
355 360 365	
tta tcc cat gtg att tta aat atc ggt gcg acc att tta gcc att cca	1449
Leu Ser His Val Ile Leu Asn Ile Gly Ala Thr Ile Leu Ala Ile Pro	
370 375 380	
acg tta gtg tta gct att ggt tta ttc att tta tta cgt gag atc gat	1497
Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp	
385 390 395 400	
ttt tct cca tac cat ctt ttt ggg gtt gtg gta tgc tgt aac gcg tta	1545
Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu	
405 410 415	
gct gct atg cct ttt gtg ttg cgt att ttg gct tta ccg atg cat aac	1593
Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn	
420 425 430	
aat atg att tat tat gaa aaa tta tgc caa tca ctt aac ctg cgt ggt	1641
Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly	
435 440 445	
tgg caa cgt ttt cga ttg att gaa tgg cac aag ctt cgt gcg cca atg	1689
Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met	
450 455 460	
aaa tac gcc ttt gca ctg gct tgt gcg tta tca tta ggc gat ttc acc	1737
Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr	
465 470 475 480	
gca atc gcg tta ttt ggt cag gct gac ttc aca tcg tta ccg cat ttg	1785
Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu	
485 490 495	
ttg tat caa caa ttg ggg cat tat cgt agt cag gaa gcg gca gta aca	1833
Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr	
500 505 510	
gcg ttt att tta ttg gtt ttt tgt ttg agt gtt ttt atg att att gaa	1881
Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu	

515

520

525

cga cat cag gaa ccg cgt gat gat taatttaaac ggtgttcagt tttcctataa 1935
 Arg His Gln Glu Pro Arg Asp Asp
 530 535

tacctttact tttgagctgg atttgcagat tctgtctcaa caaaaagttg ctattattgg 1995
 cgccagtggc gcagggaaga gtaccttatt aaatttgatt gcgggttttg cattgccaca 2055
 gcaaggggaa atttggttga atggtgaaaa tcatagccaa actcaacctt atgaacgtcc 2115
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 aaagagcagg attaatgtct agcttagcta atttagacct gcaaccgaa tcggtgccga 3315
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 cagaatttgt gcgcactatt gcgggtggcg gtattaccat gccgaaaagc tatgtacgtt 3435
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<210> 71

<211> 536

<212> PRT

<213> 多杀巴斯德氏菌

<400> 71

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

Leu Pro Leu Leu Asn Thr Leu Val Ser Ala Leu Leu Ser Ser Gln Phe
305 310 315 320

Phe Thr Leu Trp Leu Gln Pro Gln Leu Trp Lys Ala Leu Gly Tyr Ser
325 330 335

Leu Thr Ile Ala Pro Thr Ser Ala Leu Leu Ala Leu Val Leu Ser Phe
340 345 350

Ala Leu Leu Leu Leu Ala Arg Glu Leu His Trp Arg His Tyr Arg Ser
355 360 365

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

Thr Leu Val Leu Ala Ile Gly Leu Phe Ile Leu Leu Arg Glu Ile Asp
385 390 395 400

Phe Ser Pro Tyr His Leu Phe Gly Val Val Val Cys Cys Asn Ala Leu
405 410 415

Ala Ala Met Pro Phe Val Leu Arg Ile Leu Ala Leu Pro Met His Asn
420 425 430

Asn Met Ile Tyr Tyr Glu Lys Leu Cys Gln Ser Leu Asn Leu Arg Gly
435 440 445

Trp Gln Arg Phe Arg Leu Ile Glu Trp His Lys Leu Arg Ala Pro Met
450 455 460

Lys Tyr Ala Phe Ala Leu Ala Cys Ala Leu Ser Leu Gly Asp Phe Thr
465 470 475 480

Ala Ile Ala Leu Phe Gly Gln Ala Asp Phe Thr Ser Leu Pro His Leu
485 490 495

Leu Tyr Gln Gln Leu Gly His Tyr Arg Ser Gln Glu Ala Ala Val Thr
500 505 510

Ala Phe Ile Leu Leu Val Phe Cys Leu Ser Val Phe Met Ile Ile Glu
515 520 525

Arg His Gln Glu Pro Arg Asp Asp
530 535

<210> 72

<211> 3182

<212> DNA

<213> 多杀巴斯德氏菌

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<222> (1544) .. (2809)

<220>

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<400> 72

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tgcaggagaa aaagtttatg aaatccaaaa agaatggact gacaatattg aaaaagcttc 180
 caatgggaga ataagtatag agttattacc tctcgactca gtcttaaaat ctagtacat 240
 gctttctggt gtccgaaata aaattattga tggagcgggt gcaacagcgg caatgtatgc 300
 aggcactgac cctggattcg gattaattgg tgatactatt tctgcttgga accatgacga 360
 agatatttta aatttttact ataatggagg tggttttgaa gttgttgata atattttcca 420
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 tatccaaaaa ttgtttgcaa gattaggagc cgctcctggt ggtcttctctg gttcagaaat 600
 ctatactagt ttagaaaaag gtattattga tgctgccgat ttctcaacgt ttgcaaataa 660
 tcaagcaciaa ggagtcctatg atattgcaaa atatccaatc tatccgggaa ttcattcttc 720
 accagccgtt catatgatta tgaatcataa aacttgaggat agcttaactc catcggatca 780
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 ttgttgctcg gtatttatcc tctagcccaa cactttgggt tcatgaagta acaacatttt 1260
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 gagaagcatt atttactcca tcaggaaaat tcaaaatgca aacttctgga agtgtattag 1500
 acatgccatt tccagcaatt gaaaaaagtt tcttctttat ttc atg cct cat cat 1555
 Met Pro His His

1
 tgt tgt tct ttc agt act aca tat att ccg tca cat cta tac aaa ata 1603
 Cys Cys Ser Phe Ser Thr Thr Tyr Ile Pro Ser His Leu Tyr Lys Ile
 5 10 15 20
 tca gga gga att atc atg ata agt gca ttt ggg ata ggt att gga act 1651
 Ser Gly Gly Ile Ile Met Ile Ser Ala Phe Gly Ile Gly Ile Gly Thr
 25 30 35
 ctt att atc ttt tta atg atg att tcc ctt tta ttt att gga atg cca 1699
 Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe Ile Gly Met Pro
 40 45 50

tta ggt ttt ctc act ggg tta atc gct tta gtt att tca tat ctt tgg	1747
Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile Ser Tyr Leu Trp	
55 60 65	
ttt gat act acc gca ata atg caa atg ata gct tca cgt gtc act gat	1795
Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser Arg Val Thr Asp	
70 75 80	
ttc aca tca tct tac act ttt gta gct gtg cct atg ttt gtt ctt atg	1843
Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met Phe Val Leu Met	
85 90 95 100	
gca aca tta ctt gat aag act gga att gct aga gat ctc tac aac gca	1891
Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp Leu Tyr Asn Ala	
105 110 115	
atg cga gtc att ggc ggt cga tta cga ggt gga att gca att caa tgg	1939
Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile Ala Ile Gln Ser	
120 125 130	
atg ttt gtt gca gtt cta ctt gct acg atg tca ggt att atc ggt gga	1987
Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly Ile Ile Gly Gly	
135 140 145	
gaa act gtt tta tta ggc atg ttg gca tta cca caa atg tta cgc tta	2035
Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln Met Leu Arg Leu	
150 155 160	
ggc tat aat aaa aac tta gct ata gga act gtt gta gca gga gga gca	2083
Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val Ala Gly Gly Ala	
165 170 175 180	
ttg ggt aca atg gtt cct cca agt atc gtg ttg att att tac gga atg	2131
Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile Ile Tyr Gly Met	
185 190 195	
acc gca aat gtt tct att gga gaa cta ttt ctt gca gca att cca gcc	2179
Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala Ala Ile Pro Ala	
200 205 210	
tcc tta cta ctt tct aca ttc tat att tta tat att cta gta ctt tgc	2227
Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile Leu Val Leu Cys	
215 220 225	
tac ttc aaa cct agc tat ggc cct gca atg cct agc tca gaa aat cat	2275
Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser Ser Glu Asn His	
230 235 240	
aca tta acg aaa gaa gat att aaa aaa att att cat gat att gca att	2323
Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His Asp Ile Ala Ile	
245 250 255 260	
cca gta gct atc gcc aca tgg att tta gga agt att tat ggc ggg ata	2371
Pro Val Ala Ile Ala Thr Trp Ile Leu Gly Ser Ile Tyr Gly Gly Ile	
265 270 275	
gca tca atc act gaa tct gcc tgt gtt ggt gta gtt ggg gta ata tta	2419
Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val Gly Val Ile Leu	
280 285 290	
gca gca ttc tat cga aaa gaa tta aat ttc aaa ata gta caa gaa tca	2467
Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile Val Gln Glu Ser	

011000

295	300	305	
cta aaa cat aca atc aat act gtt ggt atg ata atc tgg gtc ggc att	2515		
Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile Trp Val Gly Ile			
310	315	320	
ggc gca aca atg att ata ggt att tat aat cta atg ggt ggg gac cga	2563		
Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met Gly Gly Asp Arg			
325	330	335	340
ttt ata gct aac tta ttc gct agc tta gat gcc tct cca att tat act	2611		
Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser Pro Ile Tyr Thr			
345	350	355	
atc att att atg atg gtt att tta tta ata ctt ggt atg ttc tta gat	2659		
Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly Met Phe Leu Asp			
360	365	370	
tgg att ggt gtt gcc atg ttg act ttc ctc aag aca agt aaa gcg aca	2707		
Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr Ser Lys Ala Thr			
375	380	385	
atc aat ttg tgt ttt gac ata gtc agg tac agt att tgg cgt ggt ccc	2755		
Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile Trp Arg Gly Pro			
390	395	400	
tcc ttc cac agt acc aat gtt cat cgt ggt acc ttt gtc ggg cgc ggt	2803		
Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe Val Gly Arg Gly			
405	410	415	420
act ttt tagtaaatct tgcgcgatac gaataaacgc attgatggca tttgctcgt	2859		
Thr Phe			
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tcccttttct ttcgttaacg tttccactta gattgccccag aagccgatct gtctgaatgg	2979		
gaacaagtgt tataccaaga agcgaatcca acaggtgaag tggtgatcgg tatggtgggt	3039		
aaatacactg aattaccgga tgccatacaa tcggttaatg aagccttgaa acacgcaggc	3099		
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 <211> 422
 <212> PRT
 <213> 多杀巴斯德氏菌

<400> 73
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 20 25 30
 Gly Ile Gly Thr Leu Ile Ile Phe Leu Met Met Ile Ser Leu Leu Phe
 35 40 45
 Ile Gly Met Pro Leu Gly Phe Leu Thr Gly Leu Ile Ala Leu Val Ile

50 55 60

Ser Tyr Leu Trp Phe Asp Thr Thr Ala Ile Met Gln Met Ile Ala Ser
65 70 75 80

Arg Val Thr Asp Phe Thr Ser Ser Tyr Thr Phe Val Ala Val Pro Met
85 90 95

Phe Val Leu Met Ala Thr Leu Leu Asp Lys Thr Gly Ile Ala Arg Asp
100 105 110

Leu Tyr Asn Ala Met Arg Val Ile Gly Gly Arg Leu Arg Gly Gly Ile
115 120 125

Ala Ile Gln Ser Met Phe Val Ala Val Leu Leu Ala Thr Met Ser Gly
130 135 140

Ile Ile Gly Gly Glu Thr Val Leu Leu Gly Met Leu Ala Leu Pro Gln
145 150 155 160

Met Leu Arg Leu Gly Tyr Asn Lys Asn Leu Ala Ile Gly Thr Val Val
165 170 175

Ala Gly Gly Ala Leu Gly Thr Met Val Pro Pro Ser Ile Val Leu Ile
180 185 190

Ile Tyr Gly Met Thr Ala Asn Val Ser Ile Gly Glu Leu Phe Leu Ala
195 200 205

Ala Ile Pro Ala Ser Leu Leu Leu Ser Thr Phe Tyr Ile Leu Tyr Ile
210 215 220

Leu Val Leu Cys Tyr Phe Lys Pro Ser Tyr Gly Pro Ala Met Pro Ser
225 230 235 240

Ser Glu Asn His Thr Leu Thr Lys Glu Asp Ile Lys Lys Ile Ile His
245 250 255

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

Tyr Gly Gly Ile Ala Ser Ile Thr Glu Ser Ala Cys Val Gly Val Val
275 280 285

Gly Val Ile Leu Ala Ala Phe Tyr Arg Lys Glu Leu Asn Phe Lys Ile
290 295 300

Val Gln Glu Ser Leu Lys His Thr Ile Asn Thr Val Gly Met Ile Ile
305 310 315 320

Trp Val Gly Ile Gly Ala Thr Met Ile Ile Gly Ile Tyr Asn Leu Met
325 330 335

Gly Gly Asp Arg Phe Ile Ala Asn Leu Phe Ala Ser Leu Asp Ala Ser
340 345 350

Pro Ile Tyr Thr Ile Ile Ile Met Met Val Ile Leu Leu Ile Leu Gly
355 360 365

Met Phe Leu Asp Trp Ile Gly Val Ala Met Leu Thr Phe Leu Lys Thr
370 375 380

Ser Lys Ala Thr Ile Asn Leu Cys Phe Asp Ile Val Arg Tyr Ser Ile
385 _ 390 395 400

Trp Arg Gly Pro Ser Phe His Ser Thr Asn Val His Arg Gly Thr Phe
405 410 415

Val Gly Arg Gly Thr Phe
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<210> 74

<211> 2787

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<222> (463) .. (936)

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<223> yhcJ

<400> 74

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ggcgttgcaa tctgttggcg ttgtttctatt ttgccgtctg ttacaatagc cgaggcaatt 180
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taatccgggtt cagctggaat ttcaccgccca gtataaccag ac atg gtg cta cca 474
Met Val Leu Pro
1

ata att tct acc cct aag ttg tgg caa tac atc cct tct tca aaa tta 522
Ile Ile Ser Thr Pro Lys Leu Trp Gln Tyr Ile Pro Ser Ser Lys Leu
5 10 15 20

gaa caa tcc gcc atg gct aaa caa cct aat tct ttg att cgt tta ata 570
Glu Gln Ser Ala Met Ala Lys Gln Pro Asn Ser Leu Ile Arg Leu Ile
25 30 35

atg gct tca cgt gta gtt gga cgg acg cga tcg gta cca tca aaa gca 618
Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val Pro Ser Lys Ala
40 45 50

ata ata tcg gcg cct gct gcg gct aac tct tca atg tct tgt aaa aat 666
Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met Ser Cys Lys Asn
55 60 65

ggg cta ata cga acg gga ctg tca ggt aaa tcg cgt tta acg ata cca 714
Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg Leu Thr Ile Pro
70 75 80

ata atc ggt aca ttg acg acg tta cgc gtg gct ttt aaa ttt tcg atc 762

Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe Lys Phe Ser Ile
 85 90 95 100
 cct tca ata cgt aac ccg gca gca cca ccg ata acg gat gct tgc gcc 810
 Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr Asp Ala Cys Ala
 105 110 115
 atg gcg gca aca att tct ggc gag tcc att ggc cca tta tct acg ggc 858
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 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 taaatttattc aaaagaagat 956
 Cys Asp Ser Phe Asp Ile Leu Thr Pro Val
 150 155
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<211> 158
<212> PRT
<213> 多杀巴斯德氏菌

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Ile Arg Leu Ile Met Ala Ser Arg Val Val Gly Arg Thr Arg Ser Val
      35             40             45

Pro Ser Lys Ala Ile Ile Ser Ala Pro Ala Ala Ala Asn Ser Ser Met
      50             55             60

Ser Cys Lys Asn Gly Leu Ile Arg Thr Gly Leu Ser Gly Lys Ser Arg
  65             70             75             80

Leu Thr Ile Pro Ile Ile Gly Thr Leu Thr Thr Leu Arg Val Ala Phe
      85             90             95

Lys Phe Ser Ile Pro Ser Ile Arg Asn Pro Ala Ala Pro Pro Ile Thr
      100             105             110

Asp Ala Cys Ala Met Ala Ala Thr Ile Ser Gly Glu Ser Ile Gly Pro
      115             120             125

Leu Ser Thr Gly Trp Gln Asp Ala Ile Lys Pro Tyr Leu Ile Cys Ser
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Lys Thr Cys Gly Cys Asp Ser Phe Asp Ile Leu Thr Pro Val
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<222> (1949)...(2785)

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<400> 76

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caacgtaacc aatagaggag aactcata atg aaa ttt aaa aaa cta cta ctt 1972
Met Lys Phe Lys Lys Leu Leu Leu
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gca tct tta tgt tta ggt gtt tca gct tct gta ttt gca gca gat tac 2020
Ala Ser Leu Cys Leu Gly Val Ser Ala Ser Val Phe Ala Ala Asp Tyr
10 15 20
gat ctt aaa ttc ggt atg gtt gcg ggt cca agc tca aac gaa tat aaa 2068
Asp Leu Lys Phe Gly Met Val Ala Gly Pro Ser Ser Asn Glu Tyr Lys
25 30 35 40
gca gta gaa ttc ttt gcg aaa gaa gtg aaa gaa aaa tcc aat ggc aaa 2116
Ala Val Glu Phe Phe Ala Lys Glu Val Lys Glu Lys Ser Asn Gly Lys
45 50 55
att gat gtg gct att ttc cct agc tca cag tta ggt gat gac cgt gtg 2164
Ile Asp Val Ala Ile Phe Pro Ser Ser Gln Leu Gly Asp Asp Arg Val
60 65 70
atg att aaa caa tta aaa gac ggt gca tta gac ttt acg tta ggt gaa 2212
Met Ile Lys Gln Leu Lys Asp Gly Ala Leu Asp Phe Thr Leu Gly Glu
75 80 85
tca gca cgt ttc caa att tac ttc cca gaa gca gaa gta ttt gcg ttg 2260
Ser Ala Arg Phe Gln Ile Tyr Phe Pro Glu Ala Glu Val Phe Ala Leu
90 95 100
cct tat atg att cct aat ttt gaa acc tct aaa aaa gcg ttg ctc gac 2308
Pro Tyr Met Ile Pro Asn Phe Glu Thr Ser Lys Lys Ala Leu Leu Asp
105 110 115 120
aca aaa ttt ggt caa ggt tta ttg aaa aaa att gat aaa gag tta aac 2356
Thr Lys Phe Gly Gln Gly Leu Leu Lys Lys Ile Asp Lys Glu Leu Asn
125 130 135
gta caa gtg tta tct gtg gcg tat aac ggt aca cgt caa aca act tct 2404
Val Gln Val Leu Ser Val Ala Tyr Asn Gly Thr Arg Gln Thr Thr Ser
140 145 150
aac cgt gca atc aac agc att gaa gac atg aaa ggg tta aaa tta cgt 2452
Asn Arg Ala Ile Asn Ser Ile Glu Asp Met Lys Gly Leu Lys Leu Arg
155 160 165
gta cct aac gcg gca acc aac ctt gct tat gca aaa tac gtg ggt gca 2500
Val Pro Asn Ala Ala Thr Asn Leu Ala Tyr Ala Lys Tyr Val Gly Ala
170 175 180
gcg cca aca cca atg gca ttc tct gaa gtt tac ctt gcg ctt caa aca 2548
Ala Pro Thr Pro Met Ala Phe Ser Glu Val Tyr Leu Ala Leu Gln Thr
185 190 195 200
aac tct gtg gat ggt caa gaa aac cca tta ccg aca atc caa gca caa 2596
Asn Ser Val Asp Gly Gln Glu Asn Pro Leu Pro Thr Ile Gln Ala Gln

205 210 215

aaa ttc tat gaa gta caa aaa tac tta gcg tta act aac cac atc tta 2644
 Lys Phe Tyr Glu Val Gln Lys Tyr Leu Ala Leu Thr Asn His Ile Leu
 220 225 230

aat gac caa ctt tac tta atc agt aac gat acg ttg gca gat tta cca 2692
 Asn Asp Gln Leu Tyr Leu Ile Ser Asn Asp Thr Leu Ala Asp Leu Pro
 235 240 245

gaa gat tta caa aaa gtg gtt aaa gat gca gca gcg aaa gcc gct gaa 2740
 Glu Asp Leu Gln Lys Val Val Lys Asp Ala Ala Ala Lys Ala Ala Glu
 250 255 260

tat cac act aaa ctc ttc gtt gac ggt gag aac agc tta gtt gaa tt 2787
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<210> 77

<211> 279

<212> PRT

<213> 多杀巴斯德氏菌

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 35 40 45

Val Lys Glu Lys Ser Asn Gly Lys Ile Asp Val Ala Ile Phe Pro Ser
 50 55 60

Ser Gln Leu Gly Asp Asp Arg Val Met Ile Lys Gln Leu Lys Asp Gly
 65 70 75 80

Ala Leu Asp Phe Thr Leu Gly Glu Ser Ala Arg Phe Gln Ile Tyr Phe
 85 90 95

Pro Glu Ala Glu Val Phe Ala Leu Pro Tyr Met Ile Pro Asn Phe Glu
 100 105 110

Thr Ser Lys Lys Ala Leu Leu Asp Thr Lys Phe Gly Gln Gly Leu Leu
 115 120 125

Lys Lys Ile Asp Lys Glu Leu Asn Val Gln Val Leu Ser Val Ala Tyr
 130 135 140

Asn Gly Thr Arg Gln Thr Thr Ser Asn Arg Ala Ile Asn Ser Ile Glu
 145 150 155 160

Asp Met Lys Gly Leu Lys Leu Arg Val Pro Asn Ala Ala Thr Asn Leu
 165 170 175

Ala Tyr Ala Lys Tyr Val Gly Ala Ala Pro Thr Pro Met Ala Phe Ser
 180 185 190

Glu Val Tyr Leu Ala Leu Gln Thr Asn Ser Val Asp Gly Gln Glu Asn

195

200

205

Pro^r Leu Pro Thr Ile Gln Ala Gln Lys Phe Tyr Glu Val Gln Lys Tyr
 210 215 220

Leu Ala Leu Thr Asn His Ile Leu Asn Asp Gln Leu Tyr Leu Ile Ser
 225 230 235 240

Asn Asp Thr Leu Ala Asp Leu Pro Glu Asp Leu Gln Lys Val Val Lys
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Gly Glu Asn Ser Leu Val Glu
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<210> 78

<211> 2590

<212> DNA

<213> 多杀巴斯德氏菌

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<222> (908)..(1294)

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<223> yigF

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Met Thr Lys Val Ile His Thr Asp Asn Ala Pro Ala Ala Ile
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ggg cct tat gta caa gcg gta gat tta ggt aat atg ctg tta acc tct 997
Gly Pro Tyr Val Gln Ala Val Asp Leu Gly Asn Met Leu Leu Thr Ser
15 20 25 30

ggg caa att cca gtg aat cca aaa acc ggt gaa gtg cca gcg gat atc 1045
Gly Gln Ile Pro Val Asn Pro Lys Thr Gly Glu Val Pro Ala Asp Ile
35 40 45

gta gca caa gca cgt caa tcg tta gaa aac gtg aaa gcg att gtg gaa 1093
Val Ala Gln Ala Arg Gln Ser Leu Glu Asn Val Lys Ala Ile Val Glu
50 55 60

caa gcg gga tta caa gtc gca aat atc gtg aaa acc acg gtg ttt gtg 1141
Gln Ala Gly Leu Gln Val Ala Asn Ile Val Lys Thr Thr Val Phe Val
65 70 75

aaa gat tta aat gac ttt gca gcg gtc aat gcg gag tat gaa cgt ttc 1189
Lys Asp Leu Asn Asp Phe Ala Ala Val Asn Ala Glu Tyr Glu Arg Phe
80 85 90

ttt aaa gag aac aat cac cct agc ttc cct gct cgt tca tgt gtg gaa 1237
Phe Lys Glu Asn Asn His Pro Ser Phe Pro Ala Arg Ser Cys Val Glu
95 100 105 110

gtg gca cgt ttg ccg aaa gat gtg ggg att gaa atc gag gca atc gct 1285
Val Ala Arg Leu Pro Lys Asp Val Gly Ile Glu Ile Glu Ala Ile Ala
115 120 125

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Val Lys Ala

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<211> 129

<212> PRT

<213> 多杀巴斯德氏菌

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	20						25						30		
Ile	Pro	Val	Asn	Pro	Lys	Thr	Gly	Glu	Val	Pro	Ala	Asp	Ile	Val	Ala
	35						40					45			
Gln	Ala	Arg	Gln	Ser	Leu	Glu	Asn	Val	Lys	Ala	Ile	Val	Glu	Gln	Ala
	50					55					60				
Gly	Leu	Gln	Val	Ala	Asn	Ile	Val	Lys	Thr	Thr	Val	Phe	Val	Lys	Asp
65					70				75					80	
Leu	Asn	Asp	Phe	Ala	Ala	Val	Asn	Ala	Glu	Tyr	Glu	Arg	Phe	Phe	Lys
			85						90					95	
Glu	Asn	Asn	His	Pro	Ser	Phe	Pro	Ala	Arg	Ser	Cys	Val	Glu	Val	Ala
			100					105					110		
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<210> 80

<211> 6642

<212> DNA

<213> 多杀巴斯德氏菌

<220>

<221> CDS

<222> (463) .. (1884)

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<223> yleA

<400> 80

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Met Thr Gln Lys
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tta cat att aaa acg tgg ggt tgt cag atg aat gaa tat gat tca tct 522
Leu His Ile Lys Thr Trp Gly Cys Gln Met Asn Glu Tyr Asp Ser Ser
5 10 15 20
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Lys Met Ala Asp Leu Leu Asn Ser Thr His Gly Leu Glu Leu Thr Glu
25 30 35
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Ile Pro Glu Glu Ala Asp Val Leu Leu Leu Asn Thr Cys Ser Ile Arg
40 45 50
gaa aaa gca caa gaa aaa gtt ttc cat caa tta gga cgt tgg aaa gaa 666
Glu Lys Ala Gln Glu Lys Val Phe His Gln Leu Gly Arg Trp Lys Glu
55 60 65
tta aag aaa cat aag ccg gga ctg gtt atc ggt gtt ggg ggc tgt gtt 714
Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val Gly Gly Cys Val
70 75 80
gcc tca caa gaa gga gaa cac att cgt act cgt gct cct tat gtc gat 762
Ala Ser Gln Glu Gly Glu His Ile Arg Thr Arg Ala Pro Tyr Val Asp
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Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro Glu Met Ile Asn
105 110 115
cag atc aga ggt ggt aaa agc tca gta gtc gat gtc agt ttt cca gaa 858
Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val Ser Phe Pro Glu
120 125 130
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Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala Glu Gly Pro Thr
135 140 145
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Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr Cys Ser Phe Cys
150 155 160
gtc gtg cct tat acg cgt ggt gaa gaa gtc agt cgt cca gtg gat gat 1002
Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg Pro Val Asp Asp
165 170 175 180

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Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly Ala Thr His Asp	
200 205 210	
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Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu Val Ala Ala Ile	
215 220 225	
gat ggt att gac cgt tta cgt ttt acc acc agt cac cca att gag ttc	1194
Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His Pro Ile Glu Phe	
230 235 240	
act gat gac att att gat gtg tac cgt gat acg cca gag ttg gtg agt	1242
Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro Glu Leu Val Ser	
245 250 255 260	
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Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg Val Leu Ser Met	
265 270 275	
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Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser Ile Ile Arg Lys	
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Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser Asp Phe Ile Val	
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ggg ttc ccg ggc gaa aca gca gaa gat ttc gag caa acc atg aat tta	1434
Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln Thr Met Asn Leu	
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Ile Ala Gln Val Asn Phe Asp Met Ser Phe Ser Phe Ile Tyr Ser Ala	
325 330 335 340	
cgt cca ggc acg cca gca gca gat atg cct gat gat gtg aca gaa gaa	1530
Arg Pro Gly Thr Pro Ala Ala Asp Met Pro Asp Asp Val Thr Glu Glu	
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Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg Ile Asn Asn Gln	
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Ala Ala Gln Phe Ser Arg Ala Met Leu Gly Thr Glu Gln Arg Val Leu	
375 380 385	
gtg gaa gga ccc tcg aaa aaa gat tta atg gaa ctc aca ggg cgt aca	1674
Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu Thr Gly Arg Thr	
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gaa act aat cgt atc gtc aat ttt gtg ggc acg cct gat atg att ggg	1722
Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro Asp Met Ile Gly	
405 410 415 420	
aag ttt gtt gat atc aag atc acg gat gtg ttt act aac tca ctg cgt	1770
Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr Asn Ser Leu Arg	

425	430	435	
ggg gaa gtc gtt aga act gaa gaa caa atg gga ctt cgc gtt gtt caa			1818
Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu Arg Val Val Gln			
440	445	450	
tcg cca caa atg gtg att aat cgt act cgt aaa gaa gat gaa ctc ggc			1866
Ser Pro Gln Met Val Ile Asn Arg Thr Arg Lys Glu Asp Glu Leu Gly			
455	460	465	
gtg gga cgt tat cac gcg tagtcgtgct atcccttcaa atatttaacc			1914
Val Gly Arg Tyr His Ala			
470			
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<400> 81

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		20						25						30	

Glu	Leu	Thr	Glu	Ile	Pro	Glu	Glu	Ala	Asp	Val	Leu	Leu	Leu	Asn	Thr

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 50 55 60
 Arg Trp Lys Glu Leu Lys Lys His Lys Pro Gly Leu Val Ile Gly Val
 65 70 75 80
 Gly Gly Cys Val Ala Ser Gln Glu Gly Glu His Ile Arg Thr Arg Ala
 85 90 95
 Pro Tyr Val Asp Ile Ile Phe Gly Pro Gln Thr Leu His Arg Leu Pro
 100 105 110
 Glu Met Ile Asn Gln Ile Arg Gly Gly Lys Ser Ser Val Val Asp Val
 115 120 125
 Ser Phe Pro Glu Ile Glu Lys Phe Asp Arg Leu Pro Glu Pro Arg Ala
 130 135 140
 Glu Gly Pro Thr Ala Phe Val Ser Ile Met Glu Gly Cys Asn Lys Tyr
 145 150 155 160
 Cys Ser Phe Cys Val Val Pro Tyr Thr Arg Gly Glu Glu Val Ser Arg
 165 170 175
 Pro Val Asp Asp Val Leu Phe Glu Ile Ala Gln Leu Ala Glu Gln Gly
 180 185 190
 Val Arg Glu Val Asn Leu Leu Gly Gln Asn Val Asn Ala Tyr Arg Gly
 195 200 205
 Ala Thr His Asp Asp Gly Ile Cys Thr Phe Ala Glu Leu Leu Arg Leu
 210 215 220
 Val Ala Ala Ile Asp Gly Ile Asp Arg Leu Arg Phe Thr Thr Ser His
 225 230 235 240
 Pro Ile Glu Phe Thr Asp Asp Ile Ile Asp Val Tyr Arg Asp Thr Pro
 245 250 255
 Glu Leu Val Ser Phe Leu His Leu Pro Val Gln Ser Gly Ser Asp Arg
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 Val Leu Ser Met Met Lys Arg Asn His Thr Ala Leu Glu Tyr Lys Ser
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 Ile Ile Arg Lys Leu Arg Ala Val Arg Pro Glu Ile Gln Ile Ser Ser
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 Asp Phe Ile Val Gly Phe Pro Gly Glu Thr Ala Glu Asp Phe Glu Gln
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 Thr Met Asn Leu Ile Ala Gln Val Asn Phe Asp Met Ser Phe Ser Phe
 325 330 335
 Ile Tyr Ser Ala Arg Pro Gly Thr Pro Ala Ala Asp Met Pro Asp Asp
 340 345 350
 Val Thr Glu Glu Glu Lys Lys Gln Arg Leu Tyr Val Leu Gln Gln Arg
 355 360 365

Ile Asn Asn Gln Ala Ala Gln Phe Ser Arg Ala Met Leu Gly Thr Glu
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Gln Arg Val Leu Val Glu Gly Pro Ser Lys Lys Asp Leu Met Glu Leu
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Thr Gly Arg Thr Glu Thr Asn Arg Ile Val Asn Phe Val Gly Thr Pro
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Asp Met Ile Gly Lys Phe Val Asp Ile Lys Ile Thr Asp Val Phe Thr
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Asn Ser Leu Arg Gly Glu Val Val Arg Thr Glu Glu Gln Met Gly Leu
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aca gtt gtg aat cct gaa cgt cgt cga ttt ttt aaa gag gct acg cgc 463
 Thr Val Val Asn Pro Glu Arg Arg Arg Phe Phe Lys Glu Ala Thr Arg
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 Lys Gln Ser Leu Ala Arg Glu Gly Val Ala Leu Arg Pro Pro Phe Ala
 40 45 50

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 Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro Met Ala Leu
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<213> 多杀巴斯德氏菌

<400> 83

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 65 70 75 80
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 85 90 95
 Asp Lys Pro Cys Glu Met Cys Val Asp Ile Pro Cys Ala Lys Ala Cys
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 Pro Thr Gly Ala Leu Asp Asn Gln Ala Thr Glu Ile Asp Asp Ala Arg
 115 120 125
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 Gly Leu Arg Cys Asp Val Cys Tyr Arg Val Cys Pro Leu Ile Asn Lys
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 Ala Ile Thr Leu Val Met His Arg Asn Glu Arg Thr Gly Lys His Ala
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 Val Phe Ile Pro Thr Val His Ser Glu Ala Cys Thr Gly Cys Gly Lys
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 Cys Glu Glu Ala Cys Val Leu Glu Glu Ala Ala Ile Lys Val Leu Pro
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 Met Ala Leu Ala Lys Gly Met Leu Gly Lys His Tyr Arg Leu Gly Trp
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 gaaattattg gtcgtggggg aagggagttt aaataccgct cagctggagc aaaaagttgg 2220
 tgggtggccat ttggctcgtgc tgaaggcagt agcggactga aaacaggtac ctattttatg 2280
 cagttaagcg ccttagggaa gcaaagtgcg gtggtgatga ccgatgatga tggcaatgcg 2340
 ttatctgggg agcaagctca ggcgctttat caagcattac aaaatctctt agcgaaataa 2400
 tacagtcaag atg act aaa ctc agt atc cag cga gat aac ttg att tgt 2449
 Met Thr Lys Leu Ser Ile Gln Arg Asp Asn Leu Ile Cys
 1 5 10
 ttg agt tat gtc gca tta atg gga ttc ggc ttt ccc att atg cgt tat 2497
 Leu Ser Tyr Val Ala Leu Met Gly Phe Gly Phe Pro Ile Met Arg Tyr
 15 20 25
 atg agt att cat ttt gat aca tta aat aat aac gct gtt cgc ttt ctc 2545
 Met Ser Ile His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu
 30 35 40 45
 tca ggg ggc agc gtt ttt att tta gcc tgt ttt ttt tat tat cgc gct 2593
 Ser Gly Gly Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala
 50 55 60
 gag tta aca tct tcg ggg gct ggc gtc cag tcc gtt gcg atg ttg cgc 2641
 Glu Leu Thr Ser Ser Gly Ala Gly Val Gln Ser Val Ala Met Leu Pro
 65 70 75
 agt tca agt tta ggt ttc tta ata ttg aaa act gta cca tct ttt tca 2689
 Ser Ser Ser Leu Gly Phe Leu Ile Leu Lys Thr Val Pro Ser Phe Ser
 80 85 90
 tac gtt aca atc tca aca ctt aat cgc gtt tgaccttcg atttttgata 2739
 Tyr Val Thr Ile Ser Thr Leu Asn Arg Val
 95 100
 gtcaaagact actgagtaac gctttagtc gcgtgaatcg actgttacat aagccgatat 2799
 gtcagaataa gtactgccgg tatatcgtct taatctaaga ttaagcttgc cacttttggt 2859
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 aagtgaagcc acttcatctt tgctagcttt cgtttctttt aagtcagaaa tgccactagt 3279
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 gctagccgtt ttttgaatta gctgtatttc actttcgtc aatccaactc tagcagttag 3399

actgtctagc ttgtcagcag tagatttatt cacagtcgct tgtgattgct tgtgttgaat 3459

aatatccgcg cttacttccg agatagccac gtcca 3494

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<211> 103

<212> PRT

<213> 多杀巴斯德氏菌

<400> 85

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1 5 10 15

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

His Phe Asp Thr Leu Asn Asn Asn Ala Val Arg Phe Leu Ser Gly Gly
35 40 45

Ser Val Phe Ile Leu Ala Cys Phe Phe Tyr Tyr Arg Ala Glu Leu Thr
50 55 60

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

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

Ile Ser Thr Leu Asn Arg Val
100

<210> 86

<211> 19

<212> DNA

<213> 人工序列

<220>

<223> 人工序列描述: 引物

<400> 86

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<210> 87

<211> 19

<212> DNA

<213> 人工序列

<220>

<223> 人工序列描述: 引物

<400> 87

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<210> 88

<211> 18

<212> DNA

<213> 人工序列

<220>
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<400> 88
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18

<210> 89
<211> 18
<212> DNA
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<220>
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18

<210> 90
<211> 119
<212> DNA
<213> 人工序列

<220>
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<400> 90
ctaggtacct acaacctcaa gcttnknknk nknknknknk nknknknknk nknknknknk 60
nknknknknk nknknknknk nknknknknk nknkaagctt ggtagaatg ggtaccatg 119

<210> 91
<211> 18
<212> DNA
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<220>
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tacctacaac ctcaagct

18

<210> 92
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<400> 92
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18

<210> 93
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<210> 94
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<220>
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 <400> 94
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<210> 95
 <211> 19
 <212> DNA
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<220>
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 <400> 95
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<210> 96
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 <212> DNA
 <213> 人工序列

<220>
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 <400> 96
 gtaccggcca ggcggccacg cgtattc 27

<210> 97
 <211> 531
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> atpG
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 cgtgagatct caagtaacgg gattaggcga taatccggaa atggaacgta tcgtgggcgc 120
 agttaatgaa atgattaatg cgttccgaaa cggagaagtg gatgcggttt acgtcgctta 180
 caaccgtttt gaaaatacga tgtcacaaaa acctgttatt gcacagttac ttccgttacc 240
 taaactagat gacgatgaat tagatacgaa aggttcatgg gattatattt atgaaccgaa 300

tccacaagtt ttattggata gtttacttgt tcgttattta gaaactcagg tataccaagc 360
 agttgtagat aacctagctt ctgaacaagc cgctcgaatg gtagcgatga aagccgcaac 420
 agataatgcg ggtacattaa tcgatgaatt acaattagtg tataacaaag ctgcgcaagc 480
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<210> 98
 <211> 25
 <212> DNA
 <213> 人工序列

<220>
 <223> 人工序列描述: 引物

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<210> 99
 <211> 20
 <212> DNA
 <213> 人工序列

<220>
 <223> 人工序列描述: 引物

<400> 99
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<210> 100
 <211> 1034
 <212> DNA
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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 Thr Thr Asp	
180 185 190	
cct gag atg aca cgc ttt atg atg aca ttg gaa gat gct gtg gat tta	624
Pro Glu Met Thr Arg Phe Met Met Thr Leu Glu Asp Ala Val Asp Leu	
195 200 205	
gtc cta tat gca ttt aaa aat ggt caa aat ggt gat gtt ttt gta caa	672
Val Leu Tyr Ala Phe Lys Asn Gly Gln Asn Gly Asp Val Phe Val Gln	
210 215 220	
aaa gcc ccc gca gca acc att ggt acc ctt gcc aaa gca att acc gaa	720
Lys Ala Pro Ala Ala Thr Ile Gly Thr Leu Ala Lys Ala Ile Thr Glu	
225 230 235 240	
tta tta tct gtc cca aat cac cct att tcc att ata ggt acg cgt cat	768
Leu Leu Ser Val Pro Asn His Pro Ile Ser Ile Ile Gly Thr Arg His	
245 250 255	
gga gag aaa gca ttc gaa gct tta tta agc cgt gaa gaa atg gtt cat	816
Gly Glu Lys Ala Phe Glu Ala Leu Leu Ser Arg Glu Glu Met Val His	
260 265 270	
gca att aat gaa 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	

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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 325 330 335
 Gly Glu Tyr Ile Ser Pro Glu Val
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<210> 102
 <211> 4931
 <212> DNA
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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
 20 25 30
 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
 35 40 45
 cta gaa caa tat tca ctt tcc tcc gtg tct tta tta gta aaa agc acg 192
 Leu Glu Gln Tyr Ser Leu Ser Ser Val Ser Leu Leu Val Lys Ser Thr
 50 55 60
 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
 65 70 75 80
 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 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
Asp Gly Leu Lys Tyr Leu Asp Ile Ile Ala Lys Lys Ile Glu Gln Lys	
275 280 285	
caa tca att aca tca ggg gat aat tca gaa gca aaa aca gat gtc act	912
Gln Ser Ile Thr Ser Gly Asp Asn Ser Glu Ala Lys Thr Asp Val Thr	
290 295 300	
ctt att gcg ggt tcc agt gaa tat gat tta agc aaa cat gag ctg aaa	960
Leu Ile Ala Gly Ser Ser Glu Tyr Asp Leu Ser Lys His Glu Leu Lys	
305 310 315 320	
aaa acg agc ggt gaa aat gta tct aat gat gtt att gct atc acg gga	1008
Lys Thr Ser Gly Glu Asn Val Ser Asn Asp Val Ile Ala Ile Thr Gly	
325 330 335	
tct agt aca ggc gca atg cat ggt aaa aat att aag ttg att gtg aca	1056
Ser Ser Thr Gly Ala Met His Gly Lys Asn Ile Lys Leu Ile Val Thr	
340 345 350	
gat aaa ggt gca ggc gta aaa cat gat gga att att ttg tct gaa aat	1104
Asp Lys Gly Ala Gly Val Lys His Asp Gly Ile Ile Leu Ser Glu Asn	

001123

355	360	365	
gāt att cag ātt gaa atg aat gaa ggt gac tta gaa ctt ggc aat acg Asp Ile Gln Ile Glu Met Asn Glu Gly Asp Leu Glu Leu Gly Asn Thr 370 375 380			1152
att cag caa aca gtg gta aaa aaa gac cga aat att cga gcc aag aaa Ile Gln Gln Thr Val Val Lys Lys Asp Arg Asn Ile Arg Ala Lys Lys 385 390 395 400			1200
aaa att gaa gtg aaa aac gct aat cgt gtt ttt gtt ggt agt caa acg Lys Ile Glu Val Lys Asn Ala Asn Arg Val Phe Val Gly Ser Gln Thr 405 410 415			1248
aaa tca gat gaa att tcg tta gag gcg aaa caa gtt aaa atc aga aaa Lys Ser Asp Glu Ile Ser Leu Glu Ala Lys Gln Val Lys Ile Arg Lys 420 425 430			1296
aac gca gag att agg agt acg aca caa gcc aaa atc gta gca aag ggt Asn Ala Glu Ile Arg Ser Thr Thr Gln Ala Lys Ile Val Ala Lys Gly 435 440 445			1344
gcc ctg tct att gag caa aat gcg aag ctc gtc gct aaa aag ata gat Ala Leu Ser Ile Glu Gln Asn Ala Lys Leu Val Ala Lys Lys Ile Asp 450 455 460			1392
gtg gca aca gaa act cta act aat gct ggg cgt att tat ggt cga gag Val Ala Thr Glu Thr Leu Thr Asn Ala Gly Arg Ile Tyr Gly Arg Glu 465 470 475 480			1440
gtt aag ctt gac act aat aat ttg att aat gat aaa gaa att tat gct Val Lys Leu Asp Thr Asn Asn Leu Ile Asn Asp Lys Glu Ile Tyr Ala 485 490 495			1488
gaa cgg aaa ttg agt att ttg acg aaa gga aaa gat ctt gaa att att Glu Arg Lys Leu Ser Ile Leu Thr Lys Gly Lys Asp Leu Glu Ile Ile 500 505 510			1536
caa gat aga tat ttg tct cca ctg atg cgc gta aaa agt agt gtc cgc Gln Asp Arg Tyr Leu Ser Pro Leu Met Arg Val Lys Ser Ser Val Arg 515 520 525			1584
ttt tta ggc tct ccg ttt ttc tca ata tct ccg tcg atg ctc gca agc Phe Leu Gly Ser Pro Phe Phe Ser Ile Ser Pro Ser Met Leu Ala Ser 530 535 540			1632
ctt agt gca cag ttt aag cct ggt ttt gtg aat aag gga ctc att gaa Leu Ser Ala Gln Phe Lys Pro Gly Phe Val Asn Lys Gly Leu Ile Glu 545 550 555 560			1680
agt gcg ggg agt gca gaa tta act ttt aaa gaa aaa acc agt ttt tta Ser Ala Gly Ser Ala Glu Leu Thr Phe Lys Glu Lys Thr Ser Phe Leu 565 570 575			1728
aca gag ggc aat aat ttt att aga gct aaa gat gcg tta act att aac Thr Glu Gly Asn Asn Phe Ile Arg Ala Lys Asp Ala Leu Thr Ile Asn 580 585 590			1776
gcc caa aat att gaa att gat aaa aat caa gat att caa ttg ggt gct Ala Gln Asn Ile Glu Ile Asp Lys Asn Gln Asp Ile Gln Leu Gly Ala 595 600 605			1824

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

aag cct atc ggt tca agt cgt gat tat gat atc agt cgt gtt gcg gta 2208
 Lys Pro Ile Gly Ser Ser Arg Asp Tyr Asp Ile Ser Arg Val Ala Val
 725 730 735

cat ggt tgg cac aat aat gtt tat aag ctc aac tta aat ctg caa gaa 2256
 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
 740 745 750

caa gat aaa acc gat att aaa gtt gtg aaa atg ggg gct atc cgt tct 2304
 Gln Asp Lys Thr Asp Ile Lys Val Val Lys Met Gly Ala Ile Arg Ser
 755 760 765

gat ggt gat ttt gac ttt aag gga ata aag gcg aca tca tca gaa tca 2352
 Asp Gly Asp Phe Asp Phe Lys Gly Ile Lys Ala Thr Ser Ser Glu Ser
 770 775 780

aaa ccg cag tta att aat cat gga tta att aat gtc aaa gga aca ttt 2400
 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
 785 790 795 800

aat gcg gaa gct gat caa gtg gtg aac caa atg aaa gcg ttt aac caa 2448
 Asn Ala Glu Ala Asp Gln Val Val Asn Gln Met Lys Ala Phe Asn Gln
 805 810 815

aat gca tta gca agc gtg ttt aag aat cca gcg aaa atc acg atg tac 2496
 Asn Ala Leu Ala Ser Val Phe Lys Asn Pro Ala Lys Ile Thr Met Tyr
 820 825 830

tat caa cca ctt act cgt tat att tgg aca cca tta tcg ggt aat gca 2544
 Tyr Gln Pro Leu Thr Arg Tyr Ile Trp Thr Pro Leu Ser Gly Asn Ala
 835 840 845

tcg cgt gaa ttt aac aat tta gag tct ttc ctc gat gcc ttg ttt ggc 2592
 Ser Arg Glu Phe Asn Asn Leu Glu Ser Phe Leu Asp Ala Leu Phe Gly

850	855	860	
tca aca aca atc tta aaa tca agt ttc tat agt acg gaa aat ttt agt Ser Thr Thr Ile Leu Lys Ser Ser Phe Tyr Ser Thr Glu Asn Phe Ser 865 870 875 880			2640
gct tat cag ctt cta tct cat att cag cat tca cca atg tac caa aaa Ala Tyr Gln Leu Leu Ser His Ile Gln His Ser Pro Met Tyr Gln Lys 885 890 895			2688
gcg atg gca caa gtg ttt ggt gca gag tgg cat agt aaa tcc tat gat Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp 900 905 910			2736
gag atg cga aac aaa tgg aaa agc ttt aaa gaa aat cca aca gat ttc Glu Met Arg Asn Lys Trp Lys Ser Phe Lys Glu Asn Pro Thr Asp Phe 915 920 925			2784
att tat tac cca tca gaa aaa gca aaa atc cta gcg gga aaa cta gaa Ile Tyr Tyr Pro Ser Glu Lys Ala Lys Ile Leu Ala Gly Lys Leu Glu 930 935 940			2832
ggt aag ctt aca acg cta caa aat ggt gaa tat gcc gaa cgt ggt aag Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys 945 950 955 960			2880
ttt gat gag agt atc caa att ggt aaa cac caa tta tcg cta cca tca Phe Asp Glu Ser Ile Gln Ile Gly Lys His Gln Leu Ser Leu Pro Ser 965 970 975			2928
gta gag ctt aaa gcg gag ttt agt gat aaa gaa cgt ttg gaa gag gac Val Glu Leu Lys Ala Glu Phe Ser Asp Lys Glu Arg Leu Glu Glu Asp 980 985 990			2976
ggg gta gat tta tcc tcg atc gcc gaa ctc tta gaa atg cca aac tta Gly Val Asp Leu Ser Ser Ile Ala Glu Leu Leu Glu Met Pro Asn Leu 995 1000 1005			3024
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gag gat cta gat gaa gaa cca cgt aaa aat ctg gat ata gaa gaa agc Glu Asp Leu Asp Glu Glu Pro Arg Lys Asn Leu Asp Ile Glu Glu Ser 1025 1030 1035 1040			3120
cat tct aat tca tcg gat gac gtg ctt agc atg aat gat gat gag tct His Ser Asn Ser Ser Asp Asp Val Leu Ser Met Asn Asp Asp Glu Ser 1045 1050 1055			3168
gat aca gac gat agc aag tgg agt atg ggc aat gat gag aaa gag atg Asp Thr Asp Asp Ser Lys Trp Ser Met Gly Asn Asp Glu Lys Glu Met 1060 1065 1070			3216
ccc gat gat aag ctg ggt ata agt cgt gat gat cgt gga aat aaa cca Pro Asp Asp Lys Leu Gly Ile Ser Arg Asp Asp Arg Gly Asn Lys Pro 1075 1080 1085			3264
cct cgt act gat cct aca gtt gat tat ctt aac cct gat gaa ttc ttt Pro Arg Thr Asp Pro Thr Val Asp Tyr Leu Asn Pro Asp Glu Phe Phe 1090 1095 1100			3312

gaa aat ggt tat ctc ttg aat gag cta cta cag gag ctt gga gaa gag 3360
 Glu Asn Gly Tyr Leu Leu Asn Glu Leu Leu Gln Glu Leu Gly Glu Glu
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ccg tta cta aaa gaa ggg gaa gat cat ttt aaa cgt tct acc aat cta 3408
 Pro Leu Leu Lys Glu Gly Glu Asp His Phe Lys Arg Ser Thr Asn Leu
 1125 1130 1135

gtc cgt cta ggc gag aga gat agg caa aat aga gaa aag aga gaa aaa 3456
 Val Arg Leu Gly Glu Arg Asp Arg Gln Asn Arg Glu Lys Arg Glu Lys
 1140 1145 1150

gag ggg tat ttt gat ctg cct ggt aca tta gat atg aaa ctg cag gag 3504
 Glu Gly Tyr Phe Asp Leu Pro Gly Thr Leu Asp Met Lys Leu Gln Glu
 1155 1160 1165

tta ttc gaa aaa aga aaa caa aaa cac gaa gca gaa cag aaa gca aga 3552
 Leu Phe Glu Lys Arg Lys Gln Lys His Glu Ala Glu Gln Lys Ala Arg
 1170 1175 1180

ata gaa aaa gca ctt cta caa aaa tca gaa caa caa gaa aaa cgt gtt 3600
 Ile Glu Lys Ala Leu Leu Gln Lys Ser Glu Gln Gln Glu Lys Arg Val
 1185 1190 1195 1200

gaa gaa cgt aag caa gag gaa aaa cgt caa gcg caa gat aaa att gct 3648
 Glu Glu Arg Lys Gln Glu Glu Lys Arg Gln Ala Gln Asp Lys Ile Ala
 1205 1210 1215

aag caa gta gaa att gca aaa gaa atg caa cgg gta gaa gaa att cgc 3696
 Lys Gln Val Glu Ile Ala Lys Glu Met Gln Arg Val Glu Glu Ile Arg
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cag aga gaa aaa caa ctt gcg atc caa ctg caa gaa gaa gag aag aaa 3744
 Gln Arg Glu Lys Gln Leu Ala Ile Gln Leu Gln Glu Glu Lys Lys
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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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 Tyr Ala Gly Ala Asn Tyr Phe Phe Asn Lys Val Gly Leu Asn Thr Lys
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ggt cat caa aaa gta aat gtg tta ggg gat aac tat ttt gat cat caa 4080
 Gly His Gln Lys Val Asn Val Leu Gly Asp Asn Tyr Phe Asp His Gln

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Val Ile Thr Arg Ser Ile Glu Lys Lys Val Asp Asn His Leu Asn Gln				
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Lys Tyr Asn Leu Ser Asp Val Glu Leu Val Lys Gln Leu Met Asp Asn				
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Ser Thr Thr Gln Ala Gln Glu Leu Asp Leu Lys Leu Gly Ala Ala Leu				
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act aaa gaa caa caa gct aac ttg acc caa gat atc gtt tgg tat gtc				4272
Thr Lys Glu Gln Gln Ala Asn Leu Thr Gln Asp Ile Val Trp Tyr Val				
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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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aat acc ggg aca tta gct ggg aga aaa ctc aat gtt gaa gcg agt aat				4464
Asn Thr Gly Thr Leu Ala Gly Arg Lys Leu Asn Val Glu Ala Ser Asn				
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Lys Ile Lys Asn Gln Gly Ser Ile Leu Ser Thr Thr Gln Glu Thr Arg Leu				
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Val Gly Arg Lys Gly Ile Glu Asn Val Ser Arg Ser Phe Ala Asn Asp				
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Glu Leu Gly Val Thr Ala Gln Arg Ser Glu Ile Lys Thr Glu Gly His				
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Leu His Leu Glu Thr Asp Lys Asp Ser Thr Ile Asp Val Gln Ala Ser				
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Asp Ile Lys Ala Lys Thr Ser Phe Val Lys Thr Gly Asp Val Asn Leu				
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Lys Asn Thr Tyr Asn Thr Lys His Ala Tyr Arg Glu Lys Phe Ser Pro				
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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
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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
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Lys Gly Ile Ser Asp Asn Arg Phe Glu Lys Phe Asn Ile Pro Asn Ser
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Gln Asn Gly Ile Thr Leu Asn Gly Val Arg Thr Ile Asn Ser Asp Arg

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 Phe Val Ala Thr Thr Ser Glu Leu Ile Asp Pro Asn Gln Met Met Leu
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 Gly Leu Phe His Thr Leu Gly Asn Met Met Leu Glu Ala Glu Arg Ser
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 Thr His Asn Leu Ile Asn Asp Val Arg Leu Ser Gly Asn Val Ser Tyr
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 His Gly Trp His Asn Asn Val Tyr Lys Leu Asn Leu Asn Leu Gln Glu
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 Lys Pro Gln Leu Ile Asn His Gly Leu Ile Asn Val Lys Gly Thr Phe
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Ala Met Ala Gln Val Phe Gly Ala Glu Trp His Ser Lys Ser Tyr Asp
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Gly Lys Leu Thr Thr Leu Gln Asn Gly Glu Tyr Ala Glu Arg Gly Lys
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 Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
 100 105 110
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 115 120 125
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Tyr	Lys	Pro	Leu	Leu	Asn	Ser	Gln	His	Asn	Ile	Asn	Arg	Thr	Gln	Arg	
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tta	cct	tat	cca	aaa	aca	tca	tcc	aaa	ttt	tgc	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 tgc gca 1536
 Ala Val Ile Lys Gly Val Glu Val Ser Gly Ala Leu Asn Gly Ser Ala
 500 505 510

ttc gga ctt tcc gac ggt tta act ttc cgt ctc aaa ggg agc tac agc 1584
 Phe Gly Leu Ser Asp Gly Leu Thr Phe Arg Leu Lys Gly Ser Tyr Ser
 515 520 525

aaa ggt caa aat cat gac ggc gat ccg tta aaa tct att caa cca tgg 1632
 Lys Gly Gln Asn His Asp Gly Asp Pro Leu Lys Ser Ile Gln Pro Trp
 530 535 540

aca gtg gta acc ggt att gat tac gaa act gaa ggg tgg agc gtg agt 1680
 Thr Val Val Thr Gly Ile Asp Tyr Glu Thr Glu Gly Trp Ser Val Ser
 545 550 555 560

ttg agc ggg cgt tat agt gcg gct aaa aaa gcc aaa gat gcg ata gaa 1728
 Leu Ser Gly Arg Tyr Ser Ala Ala Lys Lys Ala Lys Asp Ala Ile Glu
 565 570 575

acg gaa tac aca cat gat aaa aag gtt gtc aaa caa tgg ccg cat tta 1776
 Thr Glu Tyr Thr His Asp Lys Lys Val Val Lys Gln Trp Pro His Leu
 580 585 590

agt cca tcc tac ttt gtt gtt gat ttt acg ggg caa gtt aac ctc agt 1824
 Ser Pro Ser Tyr Phe Val Val Asp Phe Thr Gly Gln Val Asn Leu Ser
 595 600 605

aaa aat gtc att ttg aat atg ggg gta ttt aac ttg ttc aat cgt gat 1872
 Lys Asn Val Ile Leu Asn Met Gly Val Phe Asn Leu Phe Asn Arg Asp
 610 615 620

tat atg acg tgg gac agt gca tat aac ttg ttt act agg ggg tat act 1920
 Tyr Met Thr Trp Asp Ser Ala Tyr Asn Leu Phe Thr Arg Gly Tyr Thr

625 630 635 640

tcc cgt tct gtc cgt gct aac agc cca ggc att aat egg ttt acc gca 1968
 Ser Arg Ser Val Arg Ala Asn Ser Pro Gly Ile Asn Arg Phe Thr Ala
 645 650 655

cca aaa cgt aat ttt gct gcc tcg gtg gaa att cgt ttt ta 2009
 Pro Lys Arg Asn Phe Ala Ala Ser Val Glu Ile Arg Phe
 660 665

<210> 105
 <211> 669
 <212> PRT
 <213> 多杀巴斯德氏菌

<400> 105
 Ile Arg Gly Val Asp Lys Asp Arg Val Ala Val Ile Val Asp Gly Ile
 1 5 10 15

Pro Gln Ala Glu Ser Thr Ile Ser Thr Ser Ala Arg Tyr Ser Thr Glu
 20 25 30

Arg His Asn Gly Asn Ile Asn Asn Ile Glu Tyr Glu Asn Val Ser Ser
 35 40 45

Leu Lys Val Gln Lys Gly Ala Ala Ser Val Met Tyr Gly Ser Gly Ala
 50 55 60

Leu Gly Gly Thr Val Glu Phe Thr Thr Lys Asp Ile Glu Asp Phe Val
 65 70 75 80

Glu Pro Gly Arg His Leu Gly Phe Leu Ser Lys Thr Gly Tyr Thr Ser
 85 90 95

Lys Asn Arg Glu Tyr Arg Gln Val Ile Gly Val Gly Gly Lys Gly Glu
 100 105 110

His Phe Phe Gly Phe Val Gln Leu Thr Lys Arg Trp Gly His Glu Thr
 115 120 125

Ile Asn Asn Gly Lys Gly Thr Asp Ile Leu Gly Glu His Arg Gly Lys
 130 135 140

Pro Asn Pro Leu Asn Tyr Tyr Thr Thr Ser Trp Leu Thr Lys Val Gly
 145 150 155 160

Tyr Asp Ile Asn Asn Thr His Arg Phe Thr Leu Phe Leu Glu Asp Arg
 165 170 175

Arg Glu Lys Lys Leu Thr Glu Glu Lys Thr Leu Gly Leu Ser Asp Ala
 180 185 190

Val Arg Phe Ala Asn Asp Gln Thr Pro Tyr Leu Arg Tyr Gly Ile Glu
 195 200 205

Tyr Arg Tyr Asn Gly Leu Ser Trp Leu Glu Thr Val Lys Leu Phe Leu
 210 215 220

Ala Lys Gln Lys Ile Glu Gln Arg Ser Ala Leu Gln Glu Phe Asp Ile
 225 230 235 240

Asn Asn Arg Asn Lys Leu Asp Ser Thr Met Ser Phe Val Tyr Leu Gln
 245 250 255
 Arg Gln Asn Ile Ala Arg Gly Glu Phe Ser Thr Ser Pro Leu Tyr Trp
 260 265 270
 Gly Pro Ser Arg His Arg Leu Ser Ala Lys Phe Glu Phe Arg Asp Lys
 275 280 285
 Phe Leu Glu Asn Met Asn Lys His Phe Thr Phe Arg Pro Trp Gln Ile
 290 295 300
 Asn Arg Phe Arg Gln Gln Gly Arg Asn Asn Tyr Thr Glu Val Phe Pro
 305 310 315 320
 Val Lys Ser Arg Glu Phe Ser Phe Ser Leu Met Asp Asp Ile Lys Ile
 325 330 335
 Gly Glu Leu Leu His Leu Gly Leu Gly 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> 多杀巴斯德氏菌

<220>
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<220>
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 <222> (1)..(906)

<400> 106
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 Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
 1 5 10 15
 gtt gcg att aaa agc att ata aat cat aat gaa aaa ggt att tca ttt 96
 Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
 20 25 30
 tat att ttt gat ttg ggt ata aag gat gaa aat aag aga aat att aat 144
 Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
 35 40 45
 gat att gtt tct tct tat gga agt gaa gtc aac ttt att gct gtg aat 192
 Asp Ile Val Ser Ser Tyr Gly Ser Glu Val Asn Phe Ile Ala Val Asn
 50 55 60
 gag aaa gaa ttt gag agt ttt cct gtt caa att agt tat att tct tta 240
 Glu Lys Glu Phe Glu Ser Phe Pro Val Gln Ile Ser Tyr Ile Ser Leu
 65 70 75 80
 gca aca tat gca agg cta aaa gcg gca gag tat ttg ccg gat aat tta 288
 Ala Thr Tyr Ala Arg Leu Lys Ala Ala Glu Tyr Leu Pro Asp Asn Leu
 85 90 95
 aat aaa att att tat tta gat gtt gat gtt ttg gtt ttt aac tca tta 336
 Asn Lys Ile Ile Tyr Leu Asp Val Asp Val Leu Val Phe Asn Ser Leu
 100 105 110
 gaa atg tta tgg aat gtt gat gtt aat aat ttt ctt acc gca gcc tgr 384
 Glu Met Leu Trp Asn Val Asp Val Asn Asn Phe Leu Thr Ala Ala Cys

00110

115	120	125	
tat gat tct ttc atc gaa aat gaa aag tct gag cat aaa aaa tgc att Tyr Asp Ser Phe Ile Glu Asn Glu Lys Ser Glu His Lys Lys Ser Ile 130 135 140			432
tca atg tca gat aag gaa tat tat ttt aat gca gga gta atg cta ttt Ser Met Ser Asp Lys Glu Tyr Tyr Phe Asn Ala Gly Val Met Leu Phe 145 150 155 160			480
aat tta gat gaa tgg cgg aag atg gat gta ttc tca aga gct tta gac Asn Leu Asp Glu Trp Arg Lys Met Asp Val Phe Ser Arg Ala Leu Asp 165 170 175			528
ctg tta gct atg tat cct aat caa atg att tat cag gat caa gat ata Leu Leu Ala Met Tyr Pro Asn Gln Met Ile Tyr Gln Asp Gln Asp Ile 180 185 190			576
ttg aat atc ctt ttt agg aat aaa gtc tgt tat tta gat tgc aga ttt Leu Asn Ile Leu Phe Arg Asn Lys Val Cys Tyr Leu Asp Cys Arg Phe 195 200 205			624
aat ttc atg cca aat caa ctt gaa aga ata aaa caa tac cat aaa gga Asn Phe Met Pro Asn Gln Leu Glu Arg Ile Lys Gln Tyr His Lys Gly 210 215 220			672
aaa ttg agc aac tta cat tct tta gaa aaa aca acg atg cct gtc gtt Lys Leu Ser Asn Leu His Ser Leu Glu Lys Thr Thr Met Pro Val Val 225 230 235 240			720
att tca cat tat tgt ggt cca gaa aaa gcg tgg cat gcg gat tgt aaa Ile Ser His Tyr Cys Gly Pro Glu Lys Ala Trp His Ala Asp Cys Lys 245 250 255			768
cat ttt aat gta tat ttc tat cag aaa ata tta gca gaa ata acg aga His Phe Asn Val Tyr Phe Tyr Gln Lys Ile Leu Ala Glu Ile Thr Arg 260 265 270			816
ggc acg gat aaa gaa cgc gta tta tct ata aaa act tat ctc aag gcc Gly Thr Asp Lys Glu Arg Val Leu Ser Ile Lys Thr Tyr Leu Lys Ala 275 280 285			864
ttg att aga agg att aga tat aaa ttc aaa tat caa gtc tat ta Leu Ile Arg Arg Ile Arg Tyr Lys Phe Lys Tyr Gln Val Tyr 290 295 300			906

<210> 107

<211> 302

<212> PRT

<213> 多杀巴斯德氏菌

<400> 107

Met Asn Ile Leu Phe Val Ser Asp Asp Val Tyr Ala Lys His Leu Val
1 5 10 15

Val Ala Ile Lys Ser Ile Ile Asn His Asn Glu Lys Gly Ile Ser Phe
20 25 30

Tyr Ile Phe Asp Leu Gly Ile Lys Asp Glu Asn Lys Arg Asn Ile Asn
35 40 45

01110

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

<210> 108
<211> 2054
<212> DNA
<213> 多杀巴斯德氏菌

<220>
<223> pnp

<220>
<221> CDS
<222> (1) .. (2052)

<400> 108

01121

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Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys	
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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 Gly Glu Asp Ile Ser Glu Gly Lys Ile Val Asp Ile Phe Thr Ala Leu 260 265 270			816
gaa agc caa atc gta cgt agc cgt atc att gct ggt gaa cca cgt att Glu Ser Gln Ile Val Arg Ser Arg Ile Ile Ala Gly Glu Pro Arg Ile 275 280 285			864
gat ggt cgt aca gtg gat act gtt cgt gca tta gat att tgt act ggt Asp Gly Arg Thr Val Asp Thr Val Arg Ala Leu Asp Ile Cys Thr Gly 290 295 300			912
gtt tta cca cgt aca cac ggt tct gcg att ttc acc cgt ggt gaa aca Val Leu Pro Arg Thr His Gly Ser Ala Ile Phe Thr Arg Gly Glu Thr 305 310 315 320			960
cag gcg tta gct gtc gcg aca tta ggt aca gaa cgt gat gca caa att Gln Ala Leu Ala Val Ala Thr Leu Gly Thr Glu Arg Asp Ala Gln Ile 325 330 335			1008
att gat gaa tta aca ggt gag cgt tca gat cac ttc tta ttc cac tac Ile Asp Glu Leu Thr Gly Glu Arg Ser Asp His Phe Leu Phe His Tyr 340 345 350			1056
aac ttc ccg cca tat tct gtg ggt gaa acc ggt atg att ggt tca cca Asn Phe Pro Pro Tyr Ser Val Gly Glu Thr Gly Met Ile Gly Ser Pro 355 360 365			1104
aaa cgt cgt gaa att ggt cat ggt cgt tta gcg aaa cgc ggt gta gct Lys Arg Arg Glu Ile Gly His Gly Arg Leu Ala Lys Arg Gly Val Ala 370 375 380			1152
gca gtg atg cca aca ctt gcc gag ttc ccg tat gtg gta cgt gtt gtc Ala Val Met Pro Thr Leu Ala Glu Phe Pro Tyr Val Val Arg Val Val 385 390 395 400			1200
tct gaa atc aca gaa tca aat ggt tct tct tct atg gca tgc gtt tgt Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala Ser Val Cys 405 410 415			1248
ggt gcg tct tta gca tta atg gat gcg ggt gta cca att aaa gcg gcg Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile Lys Ala Ala 420 425 430			1296
gtt gca ggt att gca atg ggc tta gtc aaa gaa gac gaa aaa ttt gtg Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Asp Glu Lys Phe Val 435 440 445			1344
gtg ctt tca gac atc tta ggt gat gaa gat cac tta ggt gac atg gac Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly Asp Met Asp 450 455 460			1392
ttc aaa gtc gcg ggt aca cgt acg ggt gtg acg gca tta caa atg gat Phe Lys Val Ala Gly Thr Arg Thr Gly Val Thr Ala Leu Gln Met Asp 465 470 475 480			1440
atc aaa atc gaa ggt atc aca gca gaa atc atg caa att gcg tta aac Ile Lys Ile Glu Gly Ile Thr Ala Glu Ile Met Gln Ile Ala Leu Asn 485 490 495			1488

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 gcc 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> 多杀巴斯德氏菌

<400> 109

Met Ala Ser Met Asp Asp Thr Thr Val Phe Val Thr Val Val Ala Lys
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Lys Asp Val Lys Glu Gly Gln Asp Phe Phe Pro Leu Thr Val Asn Tyr
20 25 30

Gln Glu Arg Thr Tyr Ala Ala Gly Arg Ile Pro Gly Gly Phe Phe Lys

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

Lys Arg Arg Glu Ile Gly 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
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 <213> 多杀巴斯德氏菌

<220>
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 atg tgt ggt att gtt ggt att gtt agc caa agc ccc gtt aac caa tca 48
 Met Cys Gly Ile Val Gly Ile Val Ser Gln Ser Pro Val Asn Gln Ser
 1 5 10 15

att tat gat gcg tta acc tta ttg caa cac cgc ggg caa gac gcc gcc 96
 Ile Tyr Asp Ala Leu Thr Leu Leu Gln His Arg Gly Gln Asp Ala Ala
 20 25 30

ggg att gta acc gta gat gat gaa aac cga ttc cgc ttg cgt aaa gcg 144
 Gly Ile Val Thr Val Asp Asp Glu Asn Arg Phe Arg Leu Arg Lys Ala
 35 40 45

aac ggg tta gtc agc gat gta ttt gaa caa gtt cat atg tta cgt tta 192
 Asn Gly Leu Val Ser Asp Val Phe Glu Gln Val His Met Leu Arg Leu
 50 55 60

caa ggc aat gct ggc att gga cat gtt cgt tat cct acg gct ggg agc 240
 Gln Gly Asn Ala Gly Ile Gly His Val Arg Tyr Pro Thr Ala Gly Ser
 65 70 75 80

tca agt gtc tct gaa gcg caa cct ttt tat gta aat tcg cct tat ggc 288
 Ser Ser Val Ser Glu Ala Gln Pro Phe Tyr Val Asn Ser Pro Tyr Gly
 85 90 95

tta acc tta gtg cat aat ggt aac ttg acc aat tca agt gaa tta aaa 336
 Leu Thr Leu Val His Asn Gly Asn Leu Thr Asn Ser Ser Glu Leu Lys
 100 105 110

gaa aag tta ttt cgt ctc gca cgt cgc cat gta aat acc aat tca gat 384
 Glu Lys Leu Phe Arg Leu Ala Arg Arg His Val Asn Thr Asn Ser Asp
 115 120 125

tct gaa tta tta ctc aat atc tta gcc aat cac ctt gat cac ttc gaa 432
 Ser Glu Leu Leu Leu Asn Ile Leu Ala Asn His Leu Asp His Phe Glu
 130 135 140

aaa tac caa tta gat ccg caa gat gta ttc agt gct gtc aaa caa acg 480
 Lys Tyr Gln Leu Asp Pro Gln Asp Val Phe Ser Ala Val Lys Gln Thr
 145 150 155 160

cat cag gat att cgt ggt gct tat gct tgt atc gcc atg att att ggt 528
 His Gln Asp Ile Arg Gly Ala Tyr Ala Cys Ile Ala Met Ile Ile Gly
 165 170 175

cat ggt atg gtc gcg ttt cgt gat ccg aac ggt atc cgt ccg tta gtg 576
 His Gly Met Val Ala Phe Arg Asp Pro Asn Gly Ile Arg Pro Leu Val
 180 185 190

tta ggg aaa cgc gag gaa aat ggc aaa aca gag tat atg ttt gcc tcc 624
 Leu Gly Lys Arg Glu Glu Asn Gly Lys Thr Glu Tyr Met Phe Ala Ser

195	200	205	
gaa agt atc gca tta gat Glu Ser Ile Ala Leu Asp 210	aca gtg ggt ttt gag ttt Thr Val Gly Phe Glu Phe 215	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 gaa tac Gln Gln Cys Ala Asp Lys Pro Thr Leu Thr Pro Cys Ile Phe Glu Tyr 245			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 tct 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
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<210> 111

<211> 504

<212> PRT

<213> 多杀巴斯德氏菌

<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
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<400> 112

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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 gaagtg tct ata act aaa aaa ggc gcg cga aat gaa att ata aga	240
Asn Glu Val Ser Ile Thr Lys Lys Gly Ala Arg Asn Glu Ile Ile Arg	
65 70 75 80	
tta aac cgc ttt tta aga tat gat att tct aat ctg tat att cgt gat	288
Leu Asn Arg Phe Leu Arg Tyr Asp Ile Ser Asn Leu Tyr Ile Arg Asp	
85 90 95	
tta aga aaa gaa gat ttt gag gag tgg atc aga att cgc cta acc gaa	336
Leu Arg Lys Glu Asp Phe Glu Glu Trp Ile Arg Ile Arg Leu Thr Glu	
100 105 110	
gta tcg gat gct agc gtt aga cgt gag ctt gtt act ata tcg tca gtg	384
Val Ser Asp Ala Ser Val Arg Arg Glu Leu Val Thr Ile Ser Ser Val	
115 120 125	
ctg aca aca gca ata aat aag tgg gga tat att tca agg cat cca atg	432
Leu Thr Thr Ala Ile Asn Lys Trp Gly Tyr Ile Ser Arg His Pro Met	
130 135 140	
act ggt att gaa aaa cca aaa aac tcg gca gaa aga aaa gaa cga tat	480
Thr Gly Ile Glu Lys Pro Lys Asn Ser Ala Glu Arg Lys Glu Arg Tyr	
145 150 155 160	
tca gaa cag gac att aaa aca ata tta gaa aca gct aga tat tgt gaa	528
Ser Glu Gln Asp Ile Lys Thr Ile Leu Glu Thr Ala Arg Tyr Cys Glu	
165 170 175	
gat aaa cta ccc ata aca ctc aaa caa aga gta gca att gca atg tta	576
Asp Lys Leu Pro Ile Thr Leu Lys Gln Arg Val Ala Ile Ala Met Leu	
180 185 190	
ttt gct att gaa acc gct atg cgt gct ggt gag att gct agt ata aaa	624
Phe Ala Ile Glu Thr Ala Met Arg Ala Gly Glu Ile Ala Ser Ile Lys	
195 200 205	
tgg gat aat gtt ttt ctt gaa aag aga ata gta cat tta ccg aca act	672
Trp Asp Asn Val Phe Leu Glu Lys Arg Ile Val His Leu Pro Thr Thr	

210	215	220	
aaa aac ggg cac tct	aga gat gtg ccg ctt	tcg caa aga gct gtt gcg	720
Lys Asn Gly His Ser	Arg Asp Val Pro Leu	Ser Gln Arg Ala Val Ala	
225	230	235 240	
cta att tta aaa atg	aaa gag gta gaa aat	gga gat ctt gtg ttt cag	768
Leu Ile Leu Lys Met	Lys Glu Val Glu Asn	Gly Asp Leu Val Phe Gln	
245	250	255	
acc acg cct gaa tca	tta agc acc acg ttt	aga gtg tta aag aaa gag	816
Thr Thr Pro Glu Ser	Leu Ser Thr Thr Phe	Arg Val Leu Lys Lys Glu	
260	265	270	
tgt gga ctt gaa cat	ctc cat ttt cat gat	acg aga agg gaa gcg ttg	864
Cys Gly Leu Glu His	Leu His Phe His Asp	Thr Arg Arg Glu Ala Leu	
275	280	285	
acg aga tta tct aag	aaa gta gat gta atg	act cta gcc aaa att agc	912
Thr Arg Leu Ser Lys	Lys Val Asp Val Met	Thr Leu Ala Lys Ile Ser	
290	295	300	
gga cat aga gat tta	aga att tta caa aac	aca tat tac gca ccg aat	960
Gly His Arg Asp Leu	Arg Ile Leu Gln Asn	Thr Tyr Tyr Ala Pro Asn	
305	310	315 320	
atg agt gaa gtg gca	aac ttg ttg gat ta		989
Met Ser Glu Val Ala	Asn Leu Leu Asp		
325			

<210> 113

<211> 329

<212> PRT

<213> 多杀巴斯德氏菌

<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

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	ggc	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	ggc	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						160	
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	ggc	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	ggc	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	ggc	gtg	agc	ggg	gtc	720
Trp	His	Thr	Ser	Ile	Ser	Asn	Lys	Gly	Ile	Asn	Gly	Val	Ser	Gly	Val	
	225					230				235					240	
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	ggc	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> 多杀巴斯德氏菌

<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> 多杀巴斯德氏菌

<220>

<223> unkK

<220>

<221> CDS

<222> (1) .. (2202)

<400> 116

atg aat aaa aat cgc tat aaa ctc att ttt agt aaa act aaa ggc tgt 48
 Met Asn Lys Asn Arg Tyr Lys Leu Ile Phe Ser Lys Thr Lys Gly Cys
 1 5 10 15

ctt gta cct gtt gct gaa acg att aat tct gca gta gga aat gcc tca 96
 Leu Val Pro Val Ala Glu Thr Ile Asn Ser Ala Val Gly Asn Ala Ser
 20 25 30

tca aaa gac gtt tct gac acc gag ata agt gct tct caa cca gcg ctc 144
 Ser Lys Asp Val Ser Asp Thr Glu Ile Ser Ala Ser Gln Pro Ala Leu
 35 40 45

aac tcg ccg ctt tcg acc ctt tct gta tta gtc aaa acc gca ttt aat 192
 Asn Ser Pro Leu Ser Thr Leu Ser Val Leu Val Lys Thr Ala Phe Asn
 50 55 60

ccg gtt tca aca ttg atg tcg ttg act tgg aaa gaa tac gcc gtt tta 240
 Pro Val Ser Thr Leu Met Ser Leu Thr Trp Lys Glu Tyr Ala Val Leu
 65 70 75 80

tta tta agt gtg gtg tct ttt cct ctt atg gca caa gcc tct gat aca 288
 Leu Leu Ser Val Val Ser Phe Pro Leu Met Ala Gln Ala Ser Asp Thr
 85 90 95

gat tca gtg gta caa aga aaa cct gaa tta act gat gtg acg aat agc 336
 Asp Ser Val Val Gln Arg Lys Pro Glu Leu Thr Asp Val Thr Asn Ser
 100 105 110

aac agc tat cat gtg gaa tta gat aga gag cat cat aaa ggg gag cat 384
 Asn Ser Tyr His Val Glu Leu Asp Arg Glu His His Lys Gly Glu His
 115 120 125

caa aca aaa atc aaa cat act gag aat aat gtc atc att gtt gat att 432
 Gln Thr Lys Ile Lys His Thr Glu Asn Asn Val Ile Ile Val Asp Ile
 130 135 140

gca aaa cca aac caa aag ggc att tca gat aac cgt ttt aaa cac ttc 480
 Ala Lys Pro Asn Gln Lys Gly Ile Ser Asp Asn Arg Phe Lys His Phe
 145 150 155 160

aac atc cca aat ggg gcg gta ttt aac aat agc gcc aag gaa aaa cgc 528
 Asn Ile Pro Asn Gly Ala Val Phe Asn Asn Ser Ala Lys Glu Lys Arg
 165 170 175

tca cag tta gtg ggg tat ttg cca ggt aac cag aat tta acg gaa ggt 576
 Ser Gln Leu Val Gly Tyr Leu Pro Gly Asn Gln Asn Leu Thr Glu Gly
 180 185 190

agt gaa gca aaa gcg atc tta aat cag gtg act gga ccg gat gcc agt 624
 Ser Glu Ala Lys Ala Ile Leu Asn Gln Val Thr Gly Pro Asp Ala Ser
 195 200 205

aaa att gaa ggc gcc ctt gaa att tta ggg caa aaa gcc gat ttg gtg 672
 Lys Ile Glu Gly Ala Leu Glu Ile Leu Gly Gln Lys Ala Asp Leu Val
 210 215 220

att gcg aac caa aat ggc att gtg ctt aat ggg gta aaa acc att aat 720
 Ile Ala Asn Gln Asn Gly Ile Val Leu Asn Gly Val Lys Thr Ile Asn
 225 230 235 240

gcc aat cgt ttt gtg gca aca acc agt agt acc att gat cct gag caa 768
 Ala Asn Arg Phe Val Ala Thr Thr Ser Ser Thr Ile Asp Pro Glu Gln

245										250					255					
atg	cag	tta	aat	gtc	acg	caa	ggg	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	ggg	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	ggg	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	ggg	gcg	agt	acc	ggg	gca	atg	tac	ggg	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	ggg	aag	cac	gtt	att	att	ggg	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	ggg	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> 多杀巴斯德氏菌

<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> 多杀巴斯德氏菌

<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 45
 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> 多杀巴斯德氏菌

<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> 多杀巴斯德氏菌

<220>
 <223> unkP
 <220>
 <221> CDS
 <222> (1) .. (546)

<400> 120
 atg cgt gca tat ctt gat aaa gaa cag ggc tgg cat acg tct att tca 48
 Met Arg Ala Tyr Leu Asp Lys Glu Gln Gly Trp His Thr Ser Ile Ser
 1 5 10 15
 aat aaa ggc att aat ggc gtg agc ggt gtc aca caa cca ctc tat ttt 96
 Asn Lys Gly Ile Asn Gly Val Ser Gly Val Thr Gln Pro Leu Tyr Phe
 20 25 30
 gac att aac gac agc tcg act gat gtg aac tat ctc aat gaa caa ggc 144
 Asp Ile Asn Asp Ser Ser Thr Asp Val Asn Tyr Leu Asn Glu Gln Gly
 35 40 45
 atc acg tgt tgc gtg aat cat aat ggc ttt cgt ttt tgg ggc tta cgc 192
 Ile Thr Cys Cys Val Asn His Asn Gly Phe Arg Phe Trp Gly Leu Arg
 50 55 60
 acg act gca gaa gat cca tta ttc aag ttt gaa gtg tac acc cgc act 240
 Thr Thr Ala Glu Asp Pro Leu Phe Lys Phe Glu Val Tyr Thr Arg Thr
 65 70 75 80
 gca caa atc tta aaa gat acg att gca ggg gcg ttt gat tgg gca gtg 288
 Ala Gln Ile Leu Lys Asp Thr Ile Ala Gly Ala Phe Asp Trp Ala Val
 85 90 95
 gat aaa gat att tct gtc acg cta gtg aaa gat att att gaa gca atc 336
 Asp Lys Asp Ile Ser Val Thr Leu Val Lys Asp Ile Ile Glu Ala Ile
 100 105 110
 aat gcg aag tgg cgt gat tac acc aca aaa ggc tac tta att ggc ggt 384
 Asn Ala Lys Trp Arg Asp Tyr Thr Thr Lys Gly Tyr Leu Ile Gly Gly

115 120 125

aaa gcg tgg ctt aat aaa gag ctt aac agt gca acg aat tta aaa gat 432
 Lys Ala Trp Leu Asn Lys Glu Leu Asn Ser Ala Thr Asn Leu Lys Asp
 130 135 140

gcg aag ttg ttg atc tct tat gat tat cac cca gta cca ccg ctc gaa 480
 Ala Lys Leu Leu Ile Ser Tyr Asp Tyr His Pro Val Pro Pro Leu Glu
 145 150 155 160

cag cta ggc ttt aat cag tac att tct gat gaa tac ctt gtt gat ttt 528
 Gln Leu Gly Phe Asn Gln Tyr Ile Ser Asp Glu Tyr Leu Val Asp Phe
 165 170 175

tca aat cgt tta gca tcg ta 548
 Ser Asn Arg Leu Ala Ser
 180

<210> 121
 <211> 182
 <212> PRT
 <213> 多杀巴斯德氏菌

<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> 大叶性肺炎放线杆菌

<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 69
 Asp Lys Phe Lys Ile Leu Ser
 20

<210> 123
 <211> 23
 <212> PRT
 <213> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<400> 127
 Leu Ile Ser Phe Pro Phe Ile Thr Phe Ala Ser Asn Val Asn Gly Ala
 1 5 10 15
 Glu Ile Gly Leu Gly Gly Ala Arg Glu Ser Ser Ile Tyr Tyr Ser Lys
 20 25 30
 His Lys Val Ala Thr Asn Pro Phe Leu Ala Leu Asp Leu Ser Leu Gly
 35 40 45
 Asn Phe Tyr Met Arg Gly Thr Ala Gly Ile Ser Glu Ile Gly Tyr Glu
 50 55 60
 Gln Ser Phe Thr Asp Asn Phe Ser Val Ser Leu Phe Val Asn Pro Phe
 65 70 75 80
 Asp Gly Phe Ser Ile Lys Gly Lys Asp Leu Leu Pro Gly Tyr Gln Ser
 85 90 95
 Ile Gln Thr Arg Lys Thr Gln Phe Ala Phe Gly Trp Gly Leu Asn Tyr
 100 105 110
 Asn Leu Gly Gly Leu Phe Gly Leu Asn Asp Thr Phe Ile Ser Leu Glu
 115 120 125
 Gly Lys Ser Gly Lys Arg Gly Ala Ser Ser Asn Val Ser Leu Leu Lys
 130 135 140
 Ser Phe Asn Met Thr Lys Asn Trp Lys Val Ser Pro Tyr Ile Gly Ser
 145 150 155 160
 Ser Tyr Tyr Ser Ser Lys Tyr Thr Asp Tyr Tyr Phe Gly Ile Lys Gln
 165 170 175
 Ser Glu Leu Gly Asn Lys Ile Thr Ser Val Tyr Lys Pro Lys Ala Ala
 180 185 190
 Tyr Ala Thr His Ile Gly Ile Asn Thr Asp Tyr Ala Phe Thr Asn Asn
 195 200 205
 Leu Gly Met Gly Leu Ser Val Gly Trp

210

215

<210> 128
 <211> 242
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> apvC

<220>
 <221> CDS
 <222> (1) .. (240)

<400> 128
 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
 ggt 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> 大叶性肺炎放线杆菌

<400> 129
 Met Trp Arg Met Gly Asp Phe Met Ser Lys Lys Glu Arg Leu Asn Asp
 1 5 10 15
 Met Ala Arg Gln Ile Leu Ser Ala Ala Glu Leu Leu Ile Ala Lys Glu
 20 25 30
 Gly Leu Gln Asn Leu Ser Met Arg Lys Ile Ala Ser Glu Ala Gly Ile
 35 40 45
 Ala Thr Gly Thr Leu Tyr Leu Tyr Phe Lys Thr Lys Asp Glu Leu Leu
 50 55 60
 Asp Cys Leu Ala Glu Gln Leu His Glu Arg Tyr Tyr Arg Tyr Leu Asn
 65 70 75 80

<210> 130

<211> 527
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> apvD

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

<400> 130
 aat att caa aaa aca gtt att gct agc ggc aca ttg caa gcg act gaa 48
 Asn Ile Gln Lys Thr Val Ile Ala Ser Gly Thr Leu Gln Ala Thr Glu
 1 5 10 15
 caa gta gat att ggt gca caa gta tct ggg cag att aag cat att tta 96
 Gln Val Asp Ile Gly Ala Gln Val Ser Gly Gln Ile Lys His Ile Leu
 20 25 30
 gta caa gaa gga cag aag gtt aaa aaa ggt gag cta tta gct gta att 144
 Val Gln Glu Gly Gln Lys Val Lys Lys Gly Glu Leu Leu Ala Val Ile
 35 40 45
 gat cca cgt ctg gct gaa acg gaa tta aaa cta gca aaa gct gag cta 192
 Asp Pro Arg Leu Ala Glu Thr Glu Leu Lys Leu Ala Lys Ala Glu Leu
 50 55 60
 gca aat gct tct gct aat ttg gat aca aaa aaa att aat ctt aag caa 240
 Ala Asn Ala Ser Ala Asn Leu Asp Thr Lys Lys Ile Asn Leu Lys Gln
 65 70 75 80
 ctg caa tca gat tgg gaa cgt cat caa cgt ttg ata cga acc aat gcg 288
 Leu Gln Ser Asp Trp Glu Arg His Gln Arg Leu Ile Arg Thr Asn Ala
 85 90 95
 aca agc caa aag gaa aca gaa gaa gca aaa agt aga tta aat acg gcc 336
 Thr Ser Gln Lys Glu Thr Glu Glu Ala Lys Ser Arg Leu Asn Thr Ala
 100 105 110
 aaa gca gaa ctt caa att gcg caa aat aat cta gat atc gct aaa atc 384
 Lys Ala Glu Leu Gln Ile Ala Gln Asn Asn Leu Asp Ile Ala Lys Ile
 115 120 125
 aga gtg gaa aaa gct gaa acc gaa cta gga tat aca gaa att cgt tct 432
 Arg Val Glu Lys Ala Glu Thr Glu Leu Gly Tyr Thr Glu Ile Arg Ser
 130 135 140
 cca ctt gat gca aca gta att tca gta ttt gcg caa aat ggt caa act 480
 Pro Leu Asp Ala Thr Val Ile Ser Val Phe Ala Gln Asn Gly Gln Thr
 145 150 155 160
 tta gtc acc acc caa caa gta cca gtg ctg atg aaa tta gct aat at 527
 Leu Val Thr Thr Gln Gln Val Pro Val Leu Met Lys Leu Ala Asn
 165 170 175

<210> 131
 <211> 175
 <212> PRT
 <213> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<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
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
caa gcc gct cga atg gta gcg atg aaa gcc gca aca gat aat gcg ggt			768
Gln Ala Ala Arg Met Val Ala Met Lys Ala Ala Thr Asp Asn Ala Gly			
	245	250	255
aca tta atc gat gaa tta caa tta gtg tat aac aaa gct cgc caa gca			816
Thr Leu Ile Asp Glu Leu Gln Leu Val Tyr Asn Lys Ala Arg Gln Ala			
	260	265	270
agc att aca aat gaa tta aac gaa att gtt gcg ggt gcc gca gca att			864
Ser Ile Thr Asn Glu Leu Asn Glu Ile Val Ala Gly Ala Ala Ala Ile			
	275	280	285
taa			867

<210> 133

<211> 288
 <212> PRT
 <213> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<220>

<223> atpH

<220>

<221> CDS

<222> (1) .. (531)

<400> 134

atg tca gaa tta agt aca gta gct cgc ccc tac gct aaa gca gct ttt	48
Met Ser Glu Leu Ser Thr Val Ala Arg Pro Tyr Ala Lys Ala Ala Phe	
1 5 10 15	
gat ttt gct tta gaa caa ggt cag ttg gac aaa tgg caa gaa atg tta	96
Asp Phe Ala Leu Glu Gln Gly Gln Leu Asp Lys Trp Gln Glu Met Leu	
20 25 30	
cag ttt tcg gca ttc gtt gct gaa aac gaa caa gtg gcg gaa tat att	144
Gln Phe Ser Ala Phe Val Ala Glu Asn Glu Gln Val Ala Glu Tyr Ile	
35 40 45	
aat tct tcc ctt gca agc ggt cag att tct gaa act ttt atc aaa atc	192
Asn Ser Ser Ser Leu Ala Ser Gly Gln Ile Ser Glu Thr Phe Ile Lys Ile	
50 55 60	
tgc ggc gac caa ctt gat caa tat ggg caa aat ttt att cgt gta atg	240
Cys Gly Asp Gln Leu Asp Gln Tyr Gly Gln Asn Phe Ile Arg Val Met	
65 70 75 80	
gct gaa aat aaa cgt ctg gct gtg ttg cct atg gtt ttt gat act ttc	288
Ala Glu Asn Lys Arg Leu Ala Val Leu Pro Met Val Phe Asp Thr Phe	
85 90 95	
gta tca tta cga gcg gaa cat gaa gcg gta aaa gat gta aca att gtt	336
Val Ser Leu Arg Ala Glu His Glu Ala Val Lys Asp Val Thr Ile Val	
100 105 110	
tcg gca aac gaa tta agt caa gca caa gaa gat aaa atc gca aaa gcg	384
Ser Ala Asn Glu Leu Ser Gln Ala Gln Glu Asp Lys Ile Ala Lys Ala	
115 120 125	
atg gaa aaa cgc tta ggt caa aaa gtt cgt tta acc aac caa atc gat	432
Met Glu Lys Arg Leu Gly Gln Lys Val Arg Leu Thr Asn Gln Ile Asp	
130 135 140	
aac agc ctg att gca ggc gta att att aaa tac gat gat gtt gtt att	480
Asn Ser Leu Ile Ala Gly Val Ile Ile Lys Tyr Asp Asp Val Val Ile	
145 150 155 160	
gat ggt agt agc cgc ggt cag tta aat cgc tta gcg tca gcg ttg agc	528
Asp Gly Ser Ser Arg Gly Gln Leu Asn Arg Leu Ala Ser Ala Leu Ser	
165 170 175	
ttg taa	534
Leu	

<210> 135

<211> 177

<212> PRT

<213> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<220>
 <223> dnaK

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

<400> 138
 gct gag ttt gaa gaa gtg aaa gat aat aaa taa 33

Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
 1 5 10

<210> 139
 <211> 10
 <212> PRT
 <213> 大叶性肺炎放线杆菌

<400> 139
 Ala Glu Phe Glu Glu Val Lys Asp Asn Lys
 1 5 10

<210> 140
 <211> 453
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> exbB

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

<400> 140
 atg gaa caa atg ctt gaa ctt tta caa ggt cat gtt gat tat att att 48
 Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
 1 5 10 15

tta ggc tta tta cta tta atg agt gtt gtg ttg gta tgg aaa att att 96
 Leu Gly Leu Leu Leu 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
Ala Arg Lys Ala Asn Gln
145 150

453

<210> 141
<211> 150
<212> PRT
<213> 大叶性肺炎放线杆菌

<400> 141
Met Glu Gln Met Leu Glu Leu Leu Gln Gly His Val Asp Tyr Ile Ile
1 5 10 15
Leu Gly Leu Leu Leu Leu Met Ser Val Val Leu Val Trp Lys Ile Ile
20 25 30
Glu Arg Val Leu Phe Tyr Lys Gln Leu Asp Val Thr Lys Tyr Asp Thr
35 40 45
Leu Gln Asp Leu Glu Ile Asp Thr Thr Arg Asn Leu Thr Thr Ile Ser
50 55 60
Thr Ile Gly Ala Asn Ala Pro Tyr Ile Gly Leu Leu Gly Thr Val Leu
65 70 75 80
Gly Ile Leu Leu Thr Phe Tyr His Leu Gly His Ser Gly Gly Asp Ile
85 90 95
Asp Ala Ala Ser Ile Met Val His Leu Ser Leu Ala Leu Lys Ala Thr
100 105 110
Ala Ala Gly Ile Leu Val Ala Ile Pro Ala Met Met Phe Tyr Ser Gly
115 120 125
Phe Asn Arg Lys Val Asp Glu Ser Lys Leu Lys Trp Gln Ala Ile Gln
130 135 140
Ala Arg Lys Ala Asn Gln
145 150

<210> 142
<211> 720
<212> DNA
<213> 大叶性肺炎放线杆菌

<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
gtt 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	
gtt 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> 大叶性肺炎放线杆菌

<400> 143

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

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

<210> 144
 <211> 290
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> HI0379

<220>
 <221> CDS
 <222> (3) .. (287)

<400> 144
 tg cat agc gtg aga ggt ccg ggc ggc ggt tat caa ctc ggt aag caa 47
 His Ser Val Arg Gly Pro Gly Gly Gly Tyr Gln Leu Gly Lys Gln
 1 5 10 15
 cct gaa gag att agt gtg ggg atg att att gcg gcg gtg aat gaa aat 95
 Pro Glu Glu Ile Ser Val Gly Met Ile Ile Ala Ala Val Asn Glu Asn

	20	25	30	
ctc gac gta acc aaa tgt aaa ggt agc ggc aac tgt agc aaa aac tct				142
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> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<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	ggc	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	ggc	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	
						70					75				80	
gca	ggc	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> 太叶性肺炎放线杆菌

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<400> 147
Met Asn Lys Thr Glu Leu Ile Asp Ala Ile Ala Ala Gly Ala Glu Leu
  1                      5                      10                      15

Ser Lys Lys Asp Ala Lys Ala Ala Leu Glu Ala Thr Leu Asn Ala Ile
  20                      25                      30

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

Thr Phe Lys Val Asn Glu Arg Asn Ala Arg Thr Gly Arg Asn Pro Arg
  50                      55                      60

Thr Gly Glu Glu Ile Lys Ile Ala Ala Ser Lys Val Pro Ala Phe Val
  65                      70                      75                      80

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

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<210> 148
<211> 551
<212> DNA
<213> 大叶性肺炎放线杆菌

<220>
<223> 1pdA

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<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
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gcc ggt tat tca gcg gca ttc cgt tgt gcc gac tta ggc tta gaa aca 96
 Ala Gly Tyr Ser Ala Ala Phe Arg Cys Ala Asp Leu Gly Leu Glu Thr
 20 25 30

gta att gtc gaa cgt tat tca act ttg ggc ggt gta tgc tta aac gta 144
 Val Ile Val Glu Arg Tyr Ser Thr Leu Gly Gly Val Cys Leu Asn Val
 35 40 45

ggt tgt att ccg tct aaa gca tta tta cac gtt gca aaa gtt atc gaa 192
 Gly Cys Ile Pro Ser Lys Ala Leu Leu His Val Ala Lys Val Ile Glu
 50 55 60

gaa gca aaa cac gca gag aaa aac ggt att act ttc ggt gag ccc aac 240
 Glu Ala Lys His Ala Glu Lys Asn Gly Ile Thr Phe Gly Glu Pro Asn
 65 70 75 80

att gat tta gat aaa gtg cgt gcg ggt aaa gaa gcg gtt gtt tct aaa 288
 Ile Asp Leu Asp Lys Val Arg Ala Gly Lys Glu Ala Val Val Ser Lys
 85 90 95

tta acc ggc ggt tta gcg ggt atg gct aaa gca cgt aaa gta aca gta 336
 Leu Thr Gly Gly Leu Ala Gly Met Ala Lys Ala Arg Lys Val Thr Val
 100 105 110

gtg gaa ggt tta gcg gcg ttt acc gat ccg aat act tta gta gct cgt 384
 Val Glu Gly Leu Ala Ala Phe Thr Asp Pro Asn Thr Leu Val Ala Arg
 115 120 125

gac cgt gac ggt aat ccg aca acg att aaa ttt gat tat gca att att 432
 Asp Arg Asp Gly Asn Pro Thr Thr Ile Lys Phe Asp Tyr Ala Ile Ile
 130 135 140

gca gcc ggt tct cgt ccg att cag ctt ccg ttc att cca cac gaa gat 480
 Ala Ala Gly Ser Arg Pro Ile Gln Leu Pro Phe Ile Pro His Glu Asp
 145 150 155 160

ccg cgt gtg tgg gat tct acg gat gca ctt aaa tta aaa gaa gta ccc 528
 Pro Arg Val Trp Asp Ser Thr Asp Ala Leu Lys Leu Lys Glu Val Pro
 165 170 175

gaa aaa att act cat tat ggg cc 551
 Glu Lys Ile Thr His Tyr Gly
 180

<210> 149

<211> 183

<212> PRT

<213> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<220>
 <223> Omp5-2

<220>
 <221> CDS
 <222> (1)..(1092)

<400> 150
 atg aaa aaa tca tta gtt gct tta aca gta tta tcg gct gca gcg gta 48
 Met Lys Lys Ser Leu Val Ala Leu Thr Val Leu Ser Ala Ala Val
 1 5 10 15
 gct caa gca gcg cca caa caa aat act ttc tac gca ggt gcg aaa gca 96
 Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Ala
 20 25 30
 ggt tgg gcg tca ttc cat gat ggt atc gaa caa tta gat tca gct aaa 144
 Gly Trp Ala Ser Phe His Asp Gly Ile Glu Gln Leu Asp Ser Ala Lys
 35 40 45
 aac aca gat cgc ggt aca aaa tac ggt atc aac cgt aat tca gta act 192
 Asn Thr Asp Arg Gly Thr Lys Tyr Gly Ile Asn Arg Asn Ser Val Thr
 50 55 60
 tac ggc gta ttc ggc ggt tac caa att tta aac caa gac aaa tta ggt 240
 Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asp Lys Leu Gly
 65 70 75 80
 tta gcg gct gaa tta ggt tat gac tat ttc ggt cgt gtg cgc ggt tct 288
 Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Phe Gly Arg Val Arg Gly Ser
 85 90 95

gaa aaa cca aac ggt aaa gcg gac aag aaa act ttc cgt cac gct gca 336
 Glu Lys Pro Asn Gly Lys Ala Asp Lys Lys Thr Phe Arg His Ala Ala
 100 105 110

cac ggt gcg aca atc gca tta aaa cct agc tac gaa gta tta cct gac 384
 His Gly Ala Thr Ile Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp
 115 120 125

tta gac gtt tac ggt aaa gta ggt atc gca tta gta aac aat aca tat 432
 Leu Asp Val Tyr Gly Lys Val Gly Ile Ala Leu Val Asn Asn Thr Tyr
 130 135 140

aaa aca ttc aat gca gca caa gag aaa gtg aaa act cgt cgt ttc caa 480
 Lys Thr Phe Asn Ala Ala Gln Glu Lys Val Lys Thr Arg Arg Phe Gln
 145 150 155 160

agt tct tta att tta ggt gcg ggt gtt gag tac gca att ctt cct gaa 528
 Ser Ser Leu Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro Glu
 165 170 175

tta gcg gca cgt gtt gaa tac caa tgg tta aac aac gca ggt aaa gca 576
 Leu Ala Ala Arg Val Glu Tyr Gln Trp Leu Asn Asn Ala Gly Lys Ala
 180 185 190

agc tac tct act tta aat cgt atg ggt gca act gac tac cgt tcg gat 624
 Ser Tyr Ser Thr Leu Asn Arg Met Gly Ala Thr Asp Tyr Arg Ser Asp
 195 200 205

atc agt tcc gta tct gca ggt tta agc tac cgt ttc ggt caa ggt gcg 672
 Ile Ser Ser Val Ser Ala Gly Leu Ser Tyr Arg Phe Gly Gln Gly Ala
 210 215 220

gca ccg gtt gca gct ccg gca gtt gaa act aaa aac ttc gca ttc agc 720
 Ala Pro Val Ala Ala Pro Ala Val Glu Thr Lys Asn Phe Ala Phe Ser
 225 230 235 240

tct gac gta tta ttc gca ttc ggt aaa tca aac tta aaa ccg gct gcg 768
 Ser Asp Val Leu Phe Ala Phe Gly Lys Ser Asn Leu Lys Pro Ala Ala
 245 250 255

gca aca gca tta gat gca atg caa acc gaa atc aat aac gca ggt tta 816
 Ala Thr Ala Leu Asp Ala Met Gln Thr Glu Ile Asn Asn Ala Gly Leu
 260 265 270

tca aat gct gcg atc caa gta aac ggt tac acg gac cgt atc ggt aaa 864
 Ser Asn Ala Ala Ile Gln Val Asn Gly Tyr Thr Asp Arg Ile Gly Lys
 275 280 285

gaa gct tca aac tta aaa ctt tca caa cgt cgt gcg gaa aca gta gct 912
 Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg Ala Glu Thr Val Ala
 290 295 300

aac tac atc gtt tct aaa ggt gct ccg gca gct aac gta act gca gta 960
 Asn Tyr Ile Val Ser Lys Gly Ala Pro Ala Ala Asn Val Thr Ala Val
 305 310 315 320

ggt tac ggt gaa gca aac cct gta acc ggc gca aca tgt gac aaa gtt 1008
 Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala Thr Cys Asp Lys Val
 325 330 335

aaa ggt cgt aaa gca tta atc gct tgc tta gca ccg gat cgt cgt gtt 1056
 Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala Pro Asp Arg Arg Val

340 345 350 1095
gaa gtt caa gtt caa ggt act aaa gaa gta act atg taa
Glu Val Gln Val Gln Gly Thr Lys Glu Val Thr Met
355 360

<210> 151
<211> 364
<212> PRT
<213> 大叶性肺炎放线杆菌

<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> 大叶性肺炎放线杆菌

<220>
<223> Omp5

<220>
<221> CDS
<222> (1) .. (1107)

<400> 152

atg	aaa	aaa	tca	tta	ggt	gct	tta	gca	gta	tta	tcg	gct	gca	gca	gta	48
Met	Lys	Lys	Ser	Leu	Val	Ala	Leu	Ala	Val	Leu	Ser	Ala	Ala	Ala	Val	
1				5					10						15	
gct	caa	gca	gct	cca	caa	caa	aat	act	ttc	tac	gca	ggt	gcg	aaa	ggt	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	ggt	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	ggt	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 Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp 115 120 125	384
gtt tac ggt aaa gta ggt att gcg gtt gtt cgt aat gac tat aaa aaa Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys 130 135 140	432
tat ggt gcg gaa aac act aac gaa tca aca aca aaa ttc cac aaa tta Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu 145 150 155 160	480
aaa gca tca act att tta ggt gca ggt gtt gag tac gca att ctt cct Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro 165 170 175	528
gaa tta gcg gca cgt gtt gaa tac caa tac tta aac aaa gcg ggt aac Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn 180 185 190	576
tta aat aaa gca tta gtt cgt tca ggc aca caa gat gtg gac ttc caa Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln 195 200 205	624
tat gct cct gat atc cac tct gta aca gca ggt tta tca tac cgt ttc Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe 210 215 220	672
ggt caa ggc gct gta gca cca gtt gtt gag cca gaa gtt gta act aaa Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys 225 230 235 240	720
aac ttc gca ttc agc tca gac gtt tta ttt gat ttc ggt aaa tca agc Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser 245 250 255	768
tta aaa cca gca gca gca aca gct tta gac gca gct aac act gaa atc Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile 260 265 270	816
gct aac tta ggt tta gca act cca gct atc caa gtt aac ggt tat aca Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr 275 280 285	864
gac cgt atc ggt aaa gaa gct tca aac tta aaa ctt tca caa cgc cgt Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg 290 295 300	912
gca gaa act gta gct aac tac tta gtt tct aaa ggt caa aac cct gca Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala 305 310 315 320	960
aac gta act gca gta ggt tac ggt gaa gca aac cca gta acc ggc gca Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala 325 330 335	1008
aca tgt gat gca gtt aaa ggt cgt aaa gca tta atc gct tgc tta gca Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala 340 345 350	1056
ccg gat cgt cgt gtt gaa gtt caa gta caa ggt gct aaa aac gta gct Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala	1104

355

360

365

atg taa
Met

1110

<210> 153

<211> 369

<212> PRT

<213> 大叶性肺炎放线杆菌

<400> 153

Met Lys Lys Ser Leu Val Ala Leu Ala Val Leu Ser Ala Ala Ala Val
1 5 10 15

Ala Gln Ala Ala Pro Gln Gln Asn Thr Phe Tyr Ala Gly Ala Lys Val
20 25 30

Gly Gln Ser Ser Phe His His Gly Val Asn Gln Leu Lys Ser Gly His
35 40 45

Asp Asp Arg Tyr Asn Asp Lys Thr Arg Lys Tyr Gly Ile Asn Arg Asn
50 55 60

Ser Val Thr Tyr Gly Val Phe Gly Gly Tyr Gln Ile Leu Asn Gln Asn
65 70 75 80

Asn Phe Gly Leu Ala Ala Glu Leu Gly Tyr Asp Tyr Tyr Gly Arg Val
85 90 95

Arg Gly Asn Val Asp Glu Phe Arg Thr Val Lys His Ser Ala His Gly
100 105 110

Leu Asn Leu Ala Leu Lys Pro Ser Tyr Glu Val Leu Pro Asp Leu Asp
115 120 125

Val Tyr Gly Lys Val Gly Ile Ala Val Val Arg Asn Asp Tyr Lys Lys
130 135 140

Tyr Gly Ala Glu Asn Thr Asn Glu Ser Thr Thr Lys Phe His Lys Leu
145 150 155 160

Lys Ala Ser Thr Ile Leu Gly Ala Gly Val Glu Tyr Ala Ile Leu Pro
165 170 175

Glu Leu Ala Ala Arg Val Glu Tyr Gln Tyr Leu Asn Lys Ala Gly Asn
180 185 190

Leu Asn Lys Ala Leu Val Arg Ser Gly Thr Gln Asp Val Asp Phe Gln
195 200 205

Tyr Ala Pro Asp Ile His Ser Val Thr Ala Gly Leu Ser Tyr Arg Phe
210 215 220

Gly Gln Gly Ala Val Ala Pro Val Val Glu Pro Glu Val Val Thr Lys
225 230 235 240

Asn Phe Ala Phe Ser Ser Asp Val Leu Phe Asp Phe Gly Lys Ser Ser
245 250 255

Leu Lys Pro Ala Ala Ala Thr Ala Leu Asp Ala Ala Asn Thr Glu Ile
260 265 270

Ala Asn Leu Gly Leu Ala Thr Pro Ala Ile Gln Val Asn Gly Tyr Thr
 275 280 285
 Asp Arg Ile Gly Lys Glu Ala Ser Asn Leu Lys Leu Ser Gln Arg Arg
 290 295 300
 Ala Glu Thr Val Ala Asn Tyr Leu Val Ser Lys Gly Gln Asn Pro Ala
 305 310 315 320
 Asn Val Thr Ala Val Gly Tyr Gly Glu Ala Asn Pro Val Thr Gly Ala
 325 330 335
 Thr Cys Asp Ala Val Lys Gly Arg Lys Ala Leu Ile Ala Cys Leu Ala
 340 345 350
 Pro Asp Arg Arg Val Glu Val Gln Val Gln Gly Ala Lys Asn Val Ala
 355 360 365

Met

<210> 154
 <211> 1076
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> pnp new

<220>
 <221> CDS
 <222> (1)..(1074)

<400> 154
 aat att aaa gaa ttc gta aaa gaa gcg ggt aaa ccg cgt tgg gat tgg 48
 Asn Ile Lys Glu Phe Val Lys Glu Ala Gly Lys Pro Arg Trp Asp Trp
 1 5 10 15
 gtt 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 gcg 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	
ggg 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	
ggg 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	
ggg gta tta gcg gta atg ccg act gct gaa gaa ttc ccg tat gta gtg	624
Gly Val Leu Ala Val Met Pro Thr Ala Glu Glu Phe Pro Tyr Val Val	
195 200 205	
cgc gta gta tct gaa att acc gaa tca aac ggt tct tct tca atg gct	672
Arg Val Val Ser Glu Ile Thr Glu Ser Asn Gly Ser Ser Ser Met Ala	
210 215 220	
tcc gta tgc ggc gca tct tta gcg tta atg gac gca ggc gta ccg att	720
Ser Val Cys Gly Ala Ser Leu Ala Leu Met Asp Ala Gly Val Pro Ile	
225 230 235 240	
aaa gcg gcg gtt gcg ggt atc gca atg ggc tta gtg aaa gaa gaa gaa	768
Lys Ala Ala Val Ala Gly Ile Ala Met Gly Leu Val Lys Glu Glu Glu	
245 250 255	
aaa ttt gtg gtg ctt tca gac atc tta ggt gac gaa gac cat tta ggc	816
Lys Phe Val Val Leu Ser Asp Ile Leu Gly Asp Glu Asp His Leu Gly	
260 265 270	
gat atg gac ttc aaa gta gcc ggt acg cgt gaa ggt gta acc gca ctt	864
Asp Met Asp Phe Lys Val Ala Gly Thr Arg Glu Gly Val Thr Ala Leu	
275 280 285	
caa atg gat att aaa atc gaa ggt atc acg cct gaa att atg caa atc	912
Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile	
290 295 300	
gca tta aat caa gcg aaa ggt gcg cgt atg cac atc tta agc gtg atg	960
Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met	
305 310 315 320	
gaa caa gcg att cct gca cct cgt gcc gat att tcc gat ttt gcg cct	1008
Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro	
325 330 335	
cgt att cat acg atg aag atc gat ccg aag aaa atc aaa gac gtg atc	1056
Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile	
340 345 350	
ggg aaa ggc ggt gcg gtt at	1076
Gly Lys Gly Gly Ala Val	

<210> 155

<211> 358

<212> PRT

<213> 大叶性肺炎放线杆菌

<400> 155

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

Gln Met Asp Ile Lys Ile Glu Gly Ile Thr Pro Glu Ile Met Gln Ile
 290 295 300

Ala Leu Asn Gln Ala Lys Gly Ala Arg Met His Ile Leu Ser Val Met
 305 310 315 320

Glu Gln Ala Ile Pro Ala Pro Arg Ala Asp Ile Ser Asp Phe Ala Pro
 325 330 335

Arg Ile His Thr Met Lys Ile Asp Pro Lys Lys Ile Lys Asp Val Ile
 340 345 350

Gly Lys Gly Gly Ala Val
 355

<210> 156

<211> 1055

<212> DNA

<213> 大叶性肺炎放线杆菌

<220>

<223> potD

<220>

<221> CDS

<222> (1)..(1053)

<400> 156

atg aaa aaa tta gcg ggt tta ttt gca gca ggt tta gcg aca gtt gca 48
 Met Lys Lys Leu Ala Gly Leu Phe Ala Ala Gly Leu Ala Thr Val Ala
 1 5 10 15

tta aca gcg tgt aat gaa gaa aag cca aaa gcg gct gaa gca gcg gct 96
 Leu Thr Ala Cys Asn Glu Glu Lys Pro Lys Ala Ala Glu Ala Ala Ala
 20 25 30

caa ccg gca gca gcg gga aca gtt cac ctt tat act tgg act gaa tat 144
 Gln Pro Ala Ala Ala Gly Thr Val His Leu Tyr Thr Trp Thr Glu Tyr
 35 40 45

gtg cct gaa ggc ttg tta gat gaa ttt aca aag caa acc ggt atc aaa 192
 Val Pro Glu Gly Leu Leu Asp Glu Phe Thr Lys Gln Thr Gly Ile Lys
 50 55 60

gta gag gtt tca agc ctt gaa tct aac gaa acc atg tat gcg aaa tta 240
 Val Glu Val Ser Ser Leu Glu Ser Asn Glu Thr Met Tyr Ala Lys Leu
 65 70 75 80

aaa tta caa ggt aaa gac ggc ggt tac gat gtt atc gca cct tct aac 288
 Lys Leu Gln Gly Lys Asp Gly Gly Tyr Asp Val Ile Ala Pro Ser Asn
 85 90 95

tac ttc gtt tca aaa atg gcg aaa gaa ggt atg tta gcg gaa tta gat 336
 Tyr Phe Val Ser Lys Met Ala Lys Glu Gly Met Leu Ala Glu Leu Asp
 100 105 110

cac gca aaa ctt cct gta atc aaa gag tta aac caa gat tgg tta aac 384
 His Ala Lys Leu Pro Val Ile Lys Glu Leu Asn Gln Asp Trp Leu Asn
 115 120 125

aaa cct tat gac caa ggt aac aaa tac tct tta ccg caa tta tta ggt 432

Lys	Pro	Tyr	Asp	Gln	Gly	Asn	Lys	Tyr	Ser	Leu	Pro	Gln	Leu	Leu	Gly		
-	130					135					140						
gca	ccg	ggg	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	ggg	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				
ggg	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	ggg	gaa	gta	tct	gta	ggg	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	ggg	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	ggg	cct	gta	ctt	tgg	gtt	gat	acg	tta	gcc	816	
Met	Val	Phe	Pro	Lys	Glu	Gly	Pro	Val	Leu	Trp	Val	Asp	Thr	Leu	Ala		
			260					265					270				
att	ccg	gcg	aat	gcg	aaa	aac	aaa	gaa	aat	gcg	cat	aag	tta	atc	aac	864	
Ile	Pro	Ala	Asn	Ala	Lys	Asn	Lys	Glu	Asn	Ala	His	Lys	Leu	Ile	Asn		
		275					280					285					
tac	tta	tta	agc	gca	ccg	gtt	gcg	gaa	aaa	tta	acg	tta	gaa	atc	ggg	912	
Tyr	Leu	Leu	Ser	Ala	Pro	Val	Ala	Glu	Lys	Leu	Thr	Leu	Glu	Ile	Gly		
	290					295					300						
tat	ccg	act	tca	aac	gta	gaa	gcg	tta	aaa	aca	tta	cca	aaa	gag	att	960	
Tyr	Pro	Thr	Ser	Asn	Val	Glu	Ala	Leu	Lys	Thr	Leu	Pro	Lys	Glu	Ile		
305					310				315						320		
acc	gaa	gat	ccg	gca	atc	tat	ccg	aca	gct	gat	gtg	tta	aaa	gcg	gca	1008	
Thr	Glu	Asp	Pro	Ala	Ile	Tyr	Pro	Thr	Ala	Asp	Val	Leu	Lys	Ala	Ala		
				325					330					335			
caa	tgg	caa	gac	gat	gta	ggg	aat	gca	atc	gaa	ctt	tac	gaa	aaa	ta	1055	
Gln	Trp	Gln	Asp	Asp	Val	Gly	Asn	Ala	Ile	Glu	Leu	Tyr	Glu	Lys			
			340					345					350				

<210> 157

<211> 351

<212> PRT

<213> 大叶性肺炎放线杆菌

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

Gln Trp Gln Asp Asp Val Gly Asn Ala Ile Glu Leu Tyr Glu Lys
 - 340 345 350

<210> 158
 <211> 525
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> rpmF

<220>
 <221> CDS
 <222> (1) .. (522)

<400> 158
 atg caa aag gta aaa cta ccc ctc acc att gac cca tat aaa gac gct 48
 Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala
 1 5 10 15
 cag cgt cga atg gat tac gaa ggc tac atc tca cgt agt ctg ctt aat 96
 Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
 20 25 30
 cgt ttg 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 ggt 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 ggt aac ccg ttt 240
 Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
 65 70 75 80
 aca caa acg ctt gac tgt tcg ttt tgt ttc agt ccg gtg tcc aat atg 288
 Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
 85 90 95
 gat cag gcg gac aat ttg ccc gaa att tat gaa cca atc gaa gta aac 336
 Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
 100 105 110
 gag ttc ggt gaa gta aat tta cta gat atg atc gaa gat gga ttt atc 384
 Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
 115 120 125
 atc gaa ttg cct cta gtc ccg atg cat agt gaa gaa cac tgt gaa gtg 432
 Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
 130 135 140
 tcc gtg agt gaa cag gtg ttt ggc gaa ttg cct gaa gaa ttg gcg aaa 480
 Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
 145 150 155 160
 aaa cct aac ccg ttc gct gta tta gct aat tta aag aaa aac tag 525
 Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
 165 170

<210> 159
 <211> 174
 <212> PRT
 <213> 大叶性肺炎放线杆菌

<400> 159
 Met Gln Lys Val Lys Leu Pro Leu Thr Ile Asp Pro Tyr Lys Asp Ala
 1 5 10 15
 Gln Arg Arg Met Asp Tyr Glu Gly Tyr Ile Ser Arg Ser Leu Leu Asn
 20 25 30
 Arg Leu Gly Glu Ser Val Ser Asn Val Leu Ser Asp Ala Gln Val Thr
 35 40 45
 Leu Ser Leu Tyr Ile Asp Pro Gln Arg Leu Thr Val Ile Lys Gly Thr
 50 55 60
 Ala Thr Val Glu Val Glu Phe Asp Cys Gln Arg Cys Gly Asn Pro Phe
 65 70 75 80
 Thr Gln Thr Leu Asp Cys Ser Phe Cys Phe Ser Pro Val Ser Asn Met
 85 90 95
 Asp Gln Ala Asp Asn Leu Pro Glu Ile Tyr Glu Pro Ile Glu Val Asn
 100 105 110
 Glu Phe Gly Glu Val Asn Leu Leu Asp Met Ile Glu Asp Gly Phe Ile
 115 120 125
 Ile Glu Leu Pro Leu Val Pro Met His Ser Glu Glu His Cys Glu Val
 130 135 140
 Ser Val Ser Glu Gln Val Phe Gly Glu Leu Pro Glu Glu Leu Ala Lys
 145 150 155 160
 Lys Pro Asn Pro Phe Ala Val Leu Ala Asn Leu Lys Lys Asn
 165 170

<210> 160
 <211> 1302
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> tig

<220>
 <221> CDS
 <222> (1) .. (1299)

<400> 160
 atg tca att tct att gaa act tta gaa ggc tta caa cgc cgc gta act 48
 Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
 1 5 10 15
 att acc gta gct gct gat aaa atc gaa gcg gct tac aaa gag caa tta 96
 Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
 20 25 30
 aaa ggc tat gcg aaa aac gct cgt gta gac ggt ttc cgt aaa ggt aaa 144

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

gta atc aac ggt tta atc gca caa aat gaa att gaa gtg ccg gct gca 912
 Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
 290 295 300

gcg gta gcg gaa gaa gtg gac gta tta cgt cgt caa gcg gtt caa cgt 960
 Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
 305 310 315 320

ttc ggt ggt aaa ccg gaa atg gct gca caa tta ccg gcg gaa tta ttc 1008
 Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
 325 330 335

gaa gcg gat gca aaa cgt cgt gtt caa gta ggt tta tta ctt tca acc 1056
 Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
 340 345 350

gta atc ggt act aac gaa tta aaa gtt gat gaa aaa cgt gtt gaa gaa 1104
 Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
 355 360 365

acg att gca gaa atc gct tca gct tac gaa caa ccg gcg gaa gtt gtt 1152
 Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
 370 375 380

gct cat tat gcg aaa aac cgt caa tta acc gaa aat atc cgt aac gta 1200
 Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
 385 390 395 400

gtg tta gaa gag caa gcg gtt gaa gtt gta ctt gcg aaa gca aaa gta 1248
 Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
 405 410 415

act gaa aaa gcg act tct ttt gat gaa gta atg gct caa caa gct caa 1296
 Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
 420 425 430

ggc taa 1302
 Gly

<210> 161

<211> 433

<212> PRT

<213> 大叶性肺炎放线杆菌

<400> 161

Met Ser Ile Ser Ile Glu Thr Leu Glu Gly Leu Gln Arg Arg Val Thr
 1 5 10 15

Ile Thr Val Ala Ala Asp Lys Ile Glu Ala Ala Tyr Lys Glu Gln Leu
 20 25 30

Lys Gly Tyr Ala Lys Asn Ala Arg Val Asp Gly Phe Arg Lys Gly Lys
 35 40 45

Val Pro His Ala Ile Ile Glu Gln Arg Phe Gly Leu Ala Ala Arg Gln
 50 55 60

Asp Val Leu Ser Asp Glu Met Gln Arg Ala Phe Phe Asp Ala Val Ile
 65 70 75 80

Ala Glu Lys Ile Asn Leu Ala Gly Arg Pro Thr Phe Thr Pro Asn Asn

85 90 95

Tyr Gln Pro Ser Gln Glu Phe Ser Phe Thr Ala Thr Phe Glu Val Phe
100 105 110

Pro Glu Val Glu Leu Lys Gly Leu Glu Asn Ile Glu Val Glu Lys Pro
115 120 125

Val Val Glu Ile Thr Glu Ala Asp Leu Asp Lys Met Ile Asp Val Leu
130 135 140

Arg Lys Gln Gln Ala Thr Trp Ala Glu Ser Gln Ala Ala Ala Gln Ala
145 150 155 160

Glu Asp Arg Val Val Ile Asp Phe Val Gly Ser Val Asp Gly Glu Glu
165 170 175

Phe Glu Gly Gly Lys Ala Thr Asp Phe Thr Leu Ala Met Gly Gln Ser
180 185 190

Arg Met Ile Pro Gly Phe Glu Glu Gly Ile Val Gly His Lys Ala Gly
195 200 205

Glu Gln Phe Asp Ile Asp Val Thr Phe Pro Glu Glu Tyr His Ala Glu
210 215 220

Asn Leu Lys Gly Lys Ala Ala Lys Phe Ala Ile Thr Leu Lys Lys Val
225 230 235 240

Glu Asn Ile Val Leu Pro Glu Leu Thr Glu Glu Phe Val Lys Lys Phe
245 250 255

Gly Ser Ala Lys Thr Val Glu Asp Leu Arg Ala Glu Ile Lys Lys Asn
260 265 270

Met Gln Arg Glu Leu Lys Asn Ala Val Thr Ala Arg Val Lys Asn Gln
275 280 285

Val Ile Asn Gly Leu Ile Ala Gln Asn Glu Ile Glu Val Pro Ala Ala
290 295 300

Ala Val Ala Glu Glu Val Asp Val Leu Arg Arg Gln Ala Val Gln Arg
305 310 315 320

Phe Gly Gly Lys Pro Glu Met Ala Ala Gln Leu Pro Ala Glu Leu Phe
325 330 335

Glu Ala Asp Ala Lys Arg Arg Val Gln Val Gly Leu Leu Leu Ser Thr
340 345 350

Val Ile Gly Thr Asn Glu Leu Lys Val Asp Glu Lys Arg Val Glu Glu
355 360 365

Thr Ile Ala Glu Ile Ala Ser Ala Tyr Glu Gln Pro Ala Glu Val Val
370 375 380

Ala His Tyr Ala Lys Asn Arg Gln Leu Thr Glu Asn Ile Arg Asn Val
385 390 395 400

Val Leu Glu Glu Gln Ala Val Glu Val Val Leu Ala Lys Ala Lys Val
405 410 415

Thr Glu Lys Ala Thr Ser Phe Asp Glu Val Met Ala Gln Gln Ala Gln
 - 420 425 430
 Gly

<210> 162
 <211> 316
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> tRNA-glu

<400> 162
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 ggccctaggac atcgcccttt cacggcggta accgggggttc gaatccccgt ggggaacgcca 120
 tttaaagatg acttttggtg tctgaattgt tctttaaaaa attggaaaca agctgaaaac 180
 tgagagattt tcgaaagaaa gtctgagtag taaaagataa gtaattatct tgaaaatctt 240
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<210> 163
 <211> 85
 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
 <223> tRNA-leu

<400> 163
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 gagttcgagt ctgccccaga gcacc 85

<210> 164
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 <212> DNA
 <213> 大叶性肺炎放线杆菌

<220>
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<220>
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<400> 164
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 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														
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<210> 165

<211> 207

<212> PRT

<213> 大叶性肺炎放线杆菌

<400> 165

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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