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(54) **VETERINARY VACCINES AND METHODS  
FOR THE TREATMENT OF PASTEURELLA  
MULTOCIDA INFECTIONS IN FOOD  
PRODUCTION ANIMALS**

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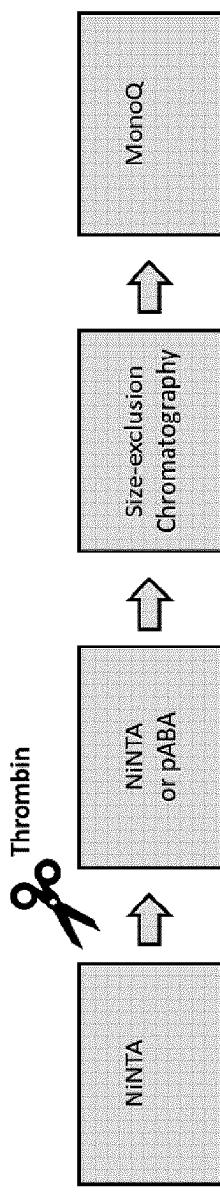
(52) **U.S. Cl.**

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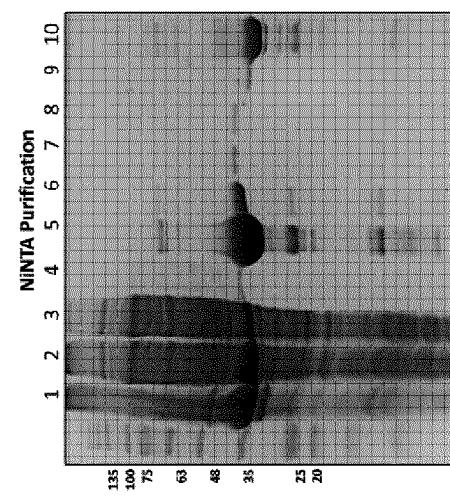
(57) **ABSTRACT**

Disclosed are novel veterinary vaccine compositions comprising a *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof. The vaccine compositions may be used to ameliorate, treat or prevent pathogenic infections of food production animals, such as bovine and porcine animals, caused by *Pasteurella multocida*. Related methods and uses are also disclosed.

**Specification includes a Sequence Listing.**

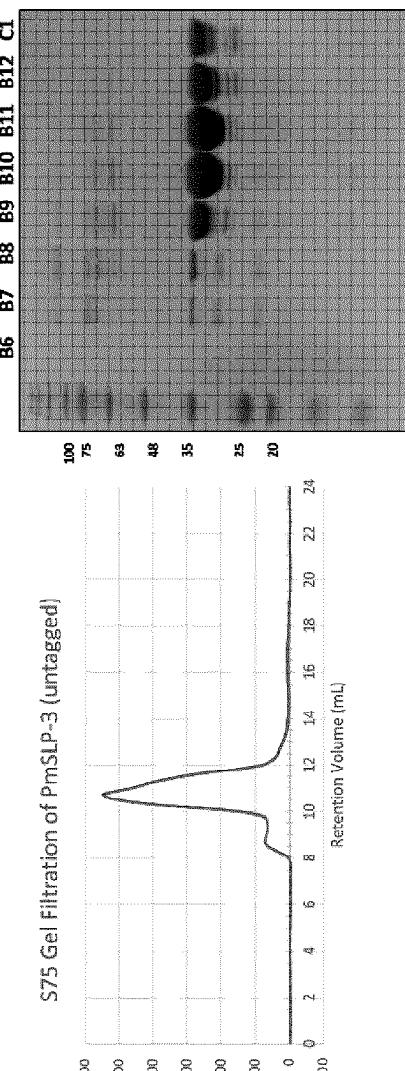


**FIG. 1A**



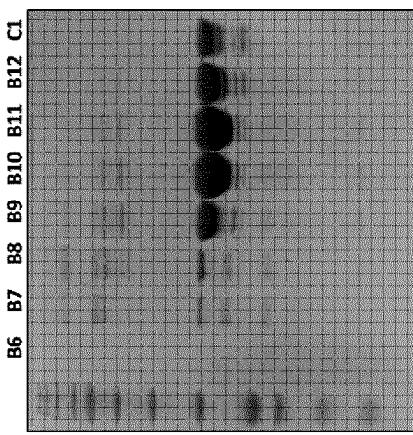
- 1: Cell pellet
- 2: Input
- 3: Flow-through
- 4: Wash
- 5 – 8: Elution fractions
- 9: empty
- 10: Post-thrombin digest

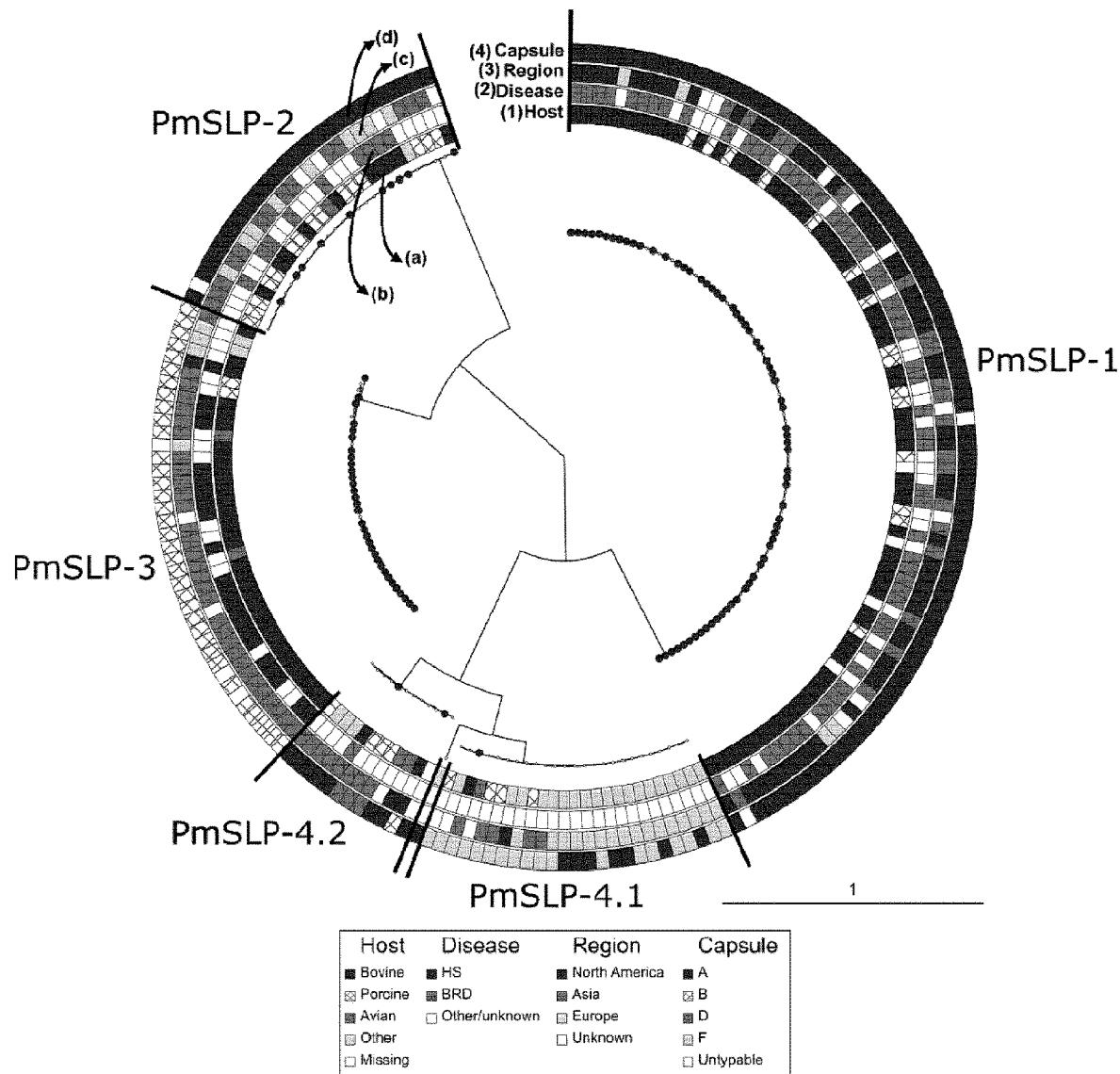
**FIG. 1B**



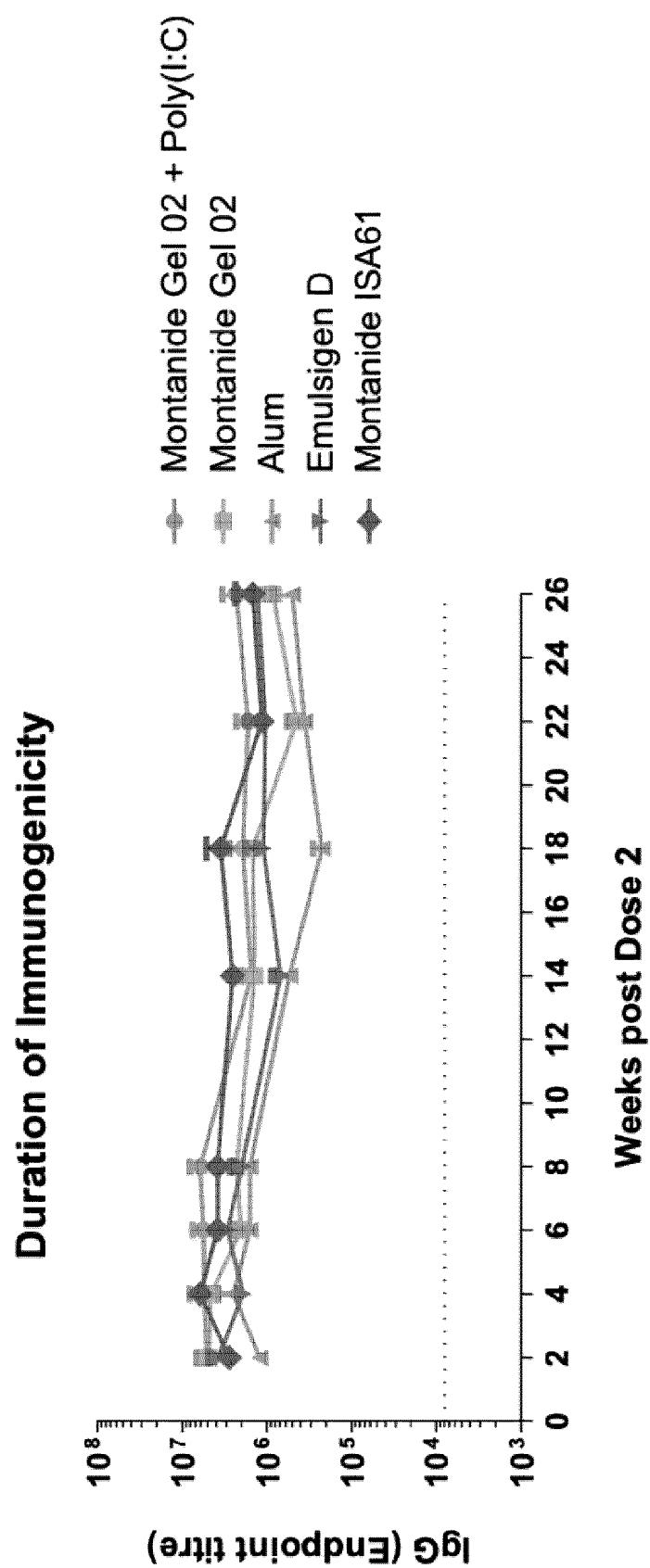
**FIG. 1C**

**FIG. 1D**

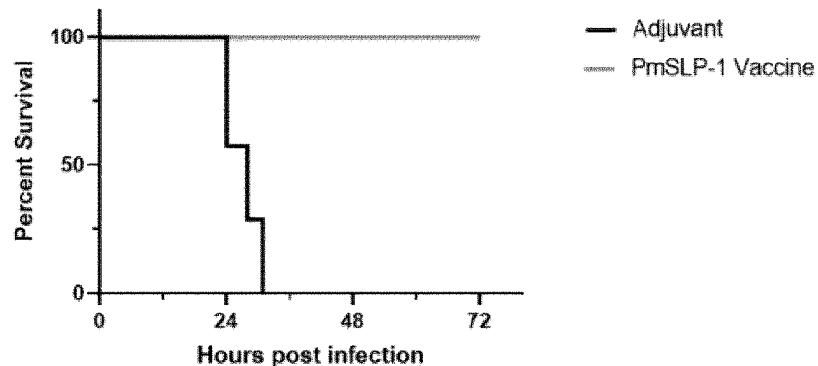




**FIG. 2**

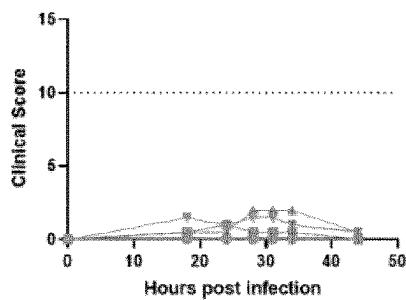
**FIG. 3**

**Survival after infection with a matched BRD strain**



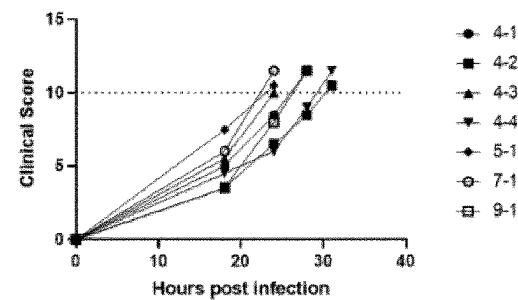
**FIG. 4A**

PmSLP-1 Vaccinated Group - Clinical Score



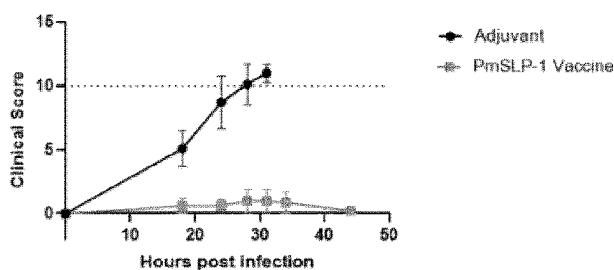
**FIG. 4B**

Adjuvant Group - Clinical Score



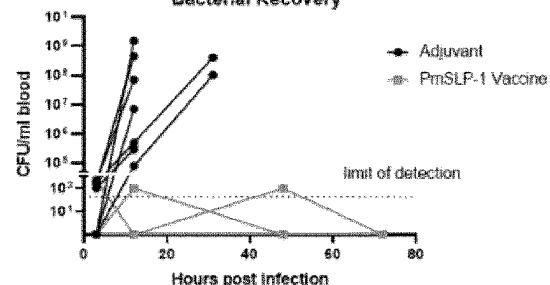
**FIG. 4C**

Combined Clinical Score

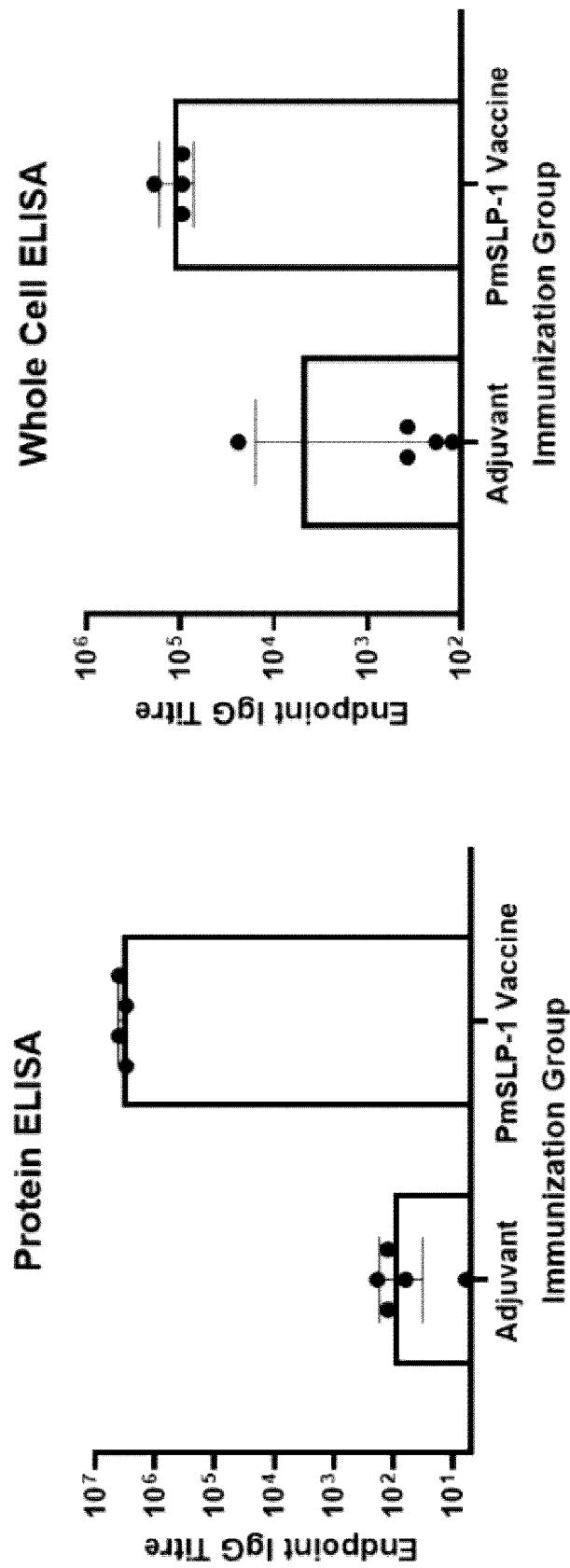


**FIG. 4D**

Bacterial Recovery

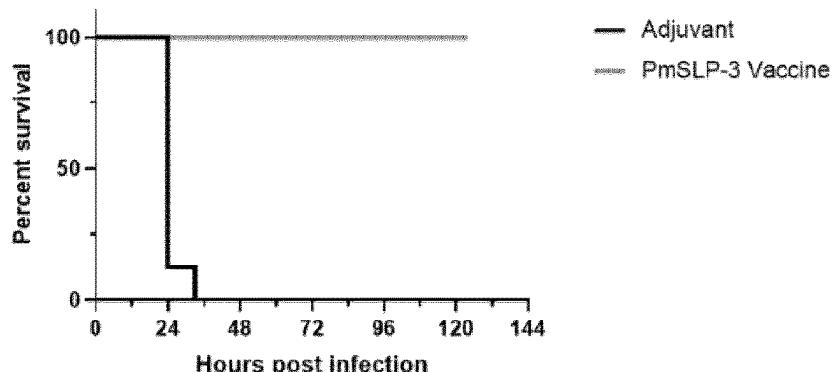


**FIG. 4E**



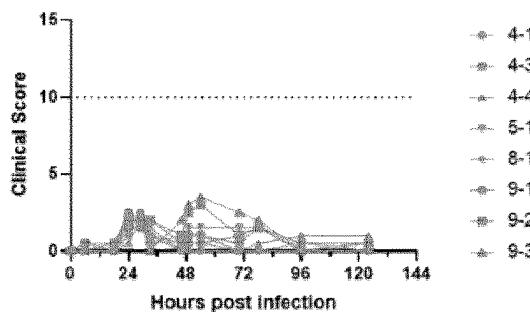
**FIG. 5A**  
**FIG. 5B**

**Survival after infection with a matched porcine strain**



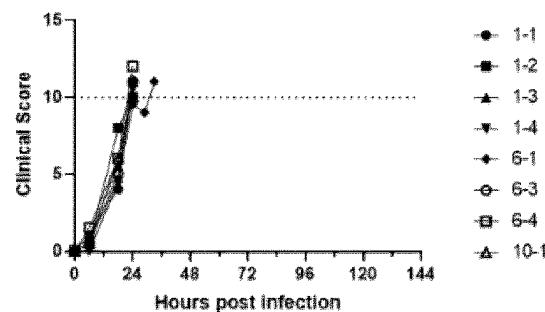
**FIG. 6A**

**PmSLP-3 Vaccinated Group - Clinical Score**



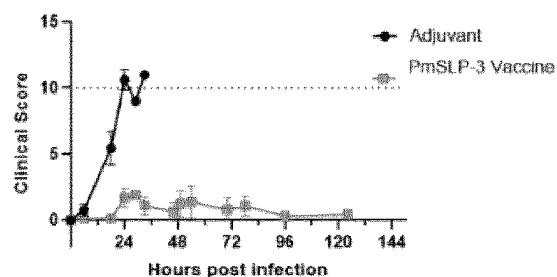
**FIG. 6B**

**Adjuvant Group - Clinical Score**



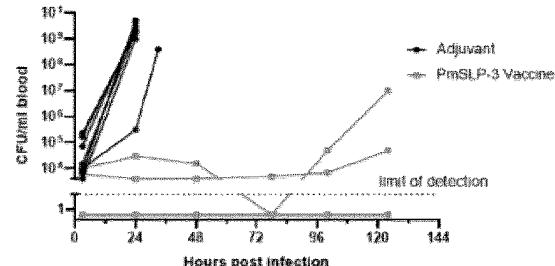
**FIG. 6C**

**Combined Clinical Score**



**FIG. 6D**

**Bacterial Recovery**



**FIG. 6E**

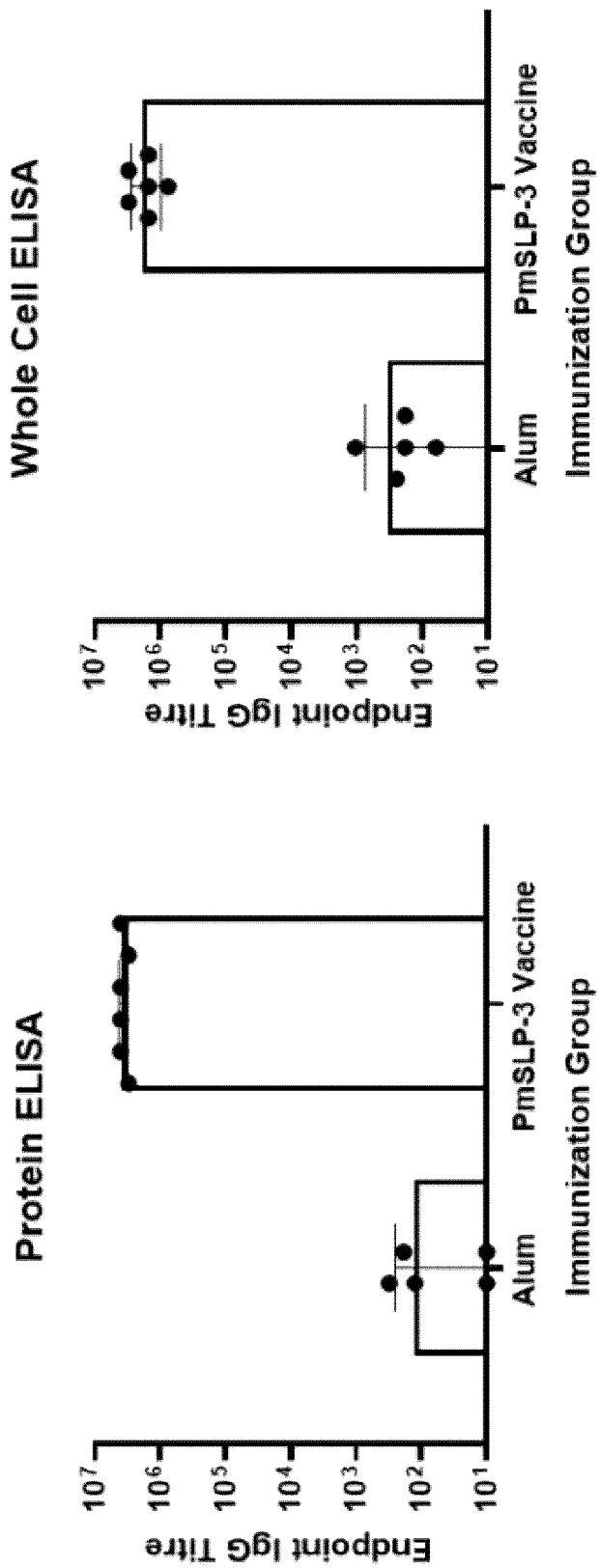
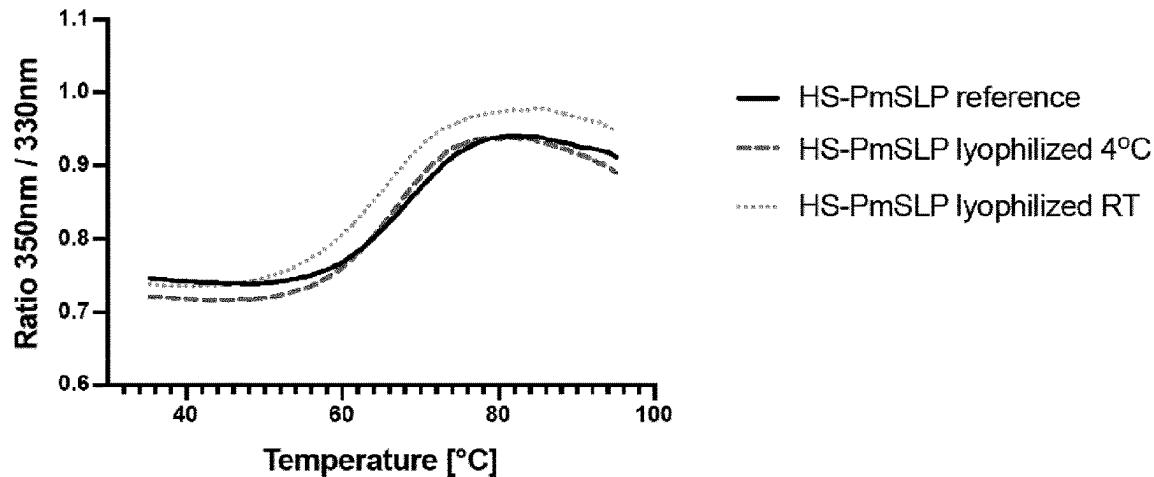


FIG. 7B

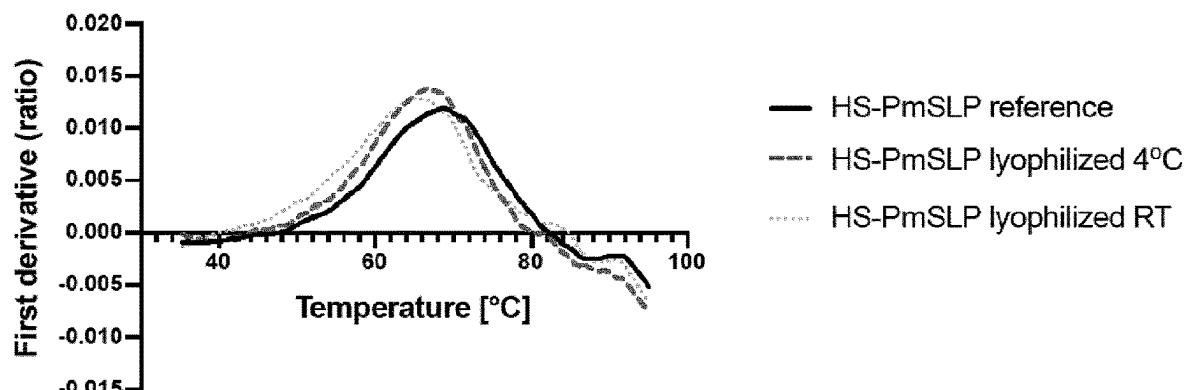
FIG. 7A

**Ratio 350 nm / 330 nm**



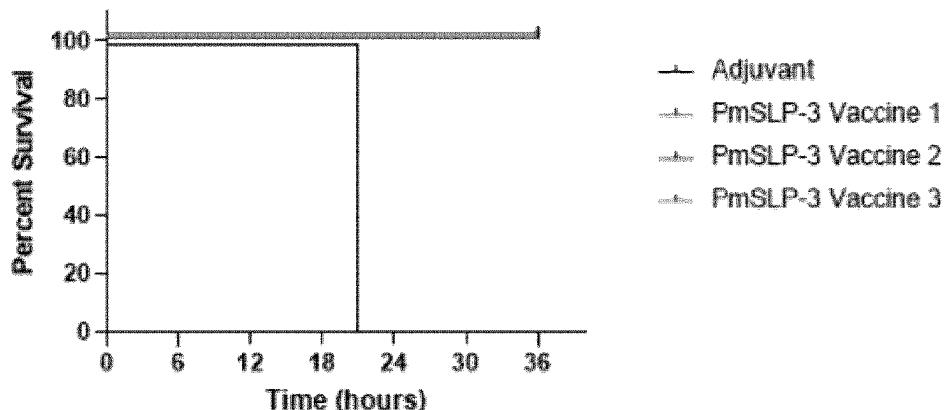
**FIG. 8A**

**First derivative**



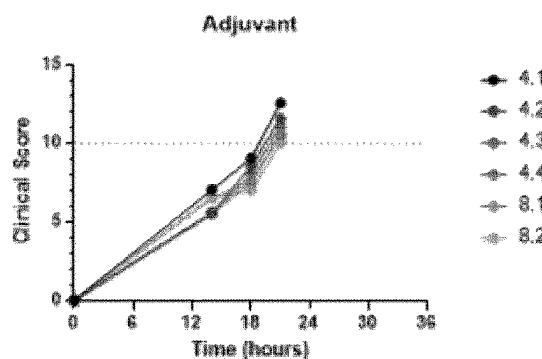
**FIG. 8B**

**Survival after challenge with a matched P. mult.**

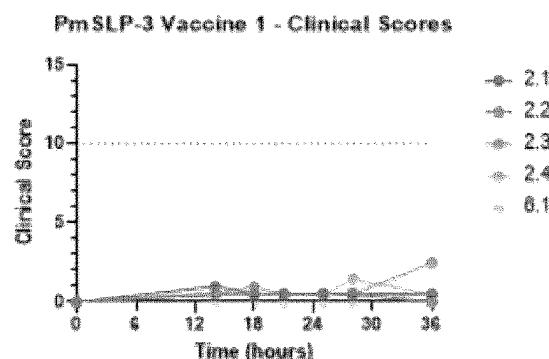


Vaccine 1: Fresh formulation prepared prior to each dose using protein stored at -80°C  
 Vaccine 2: Fresh formulation prepared prior to each dose using lyophilized protein stored at 4°C  
 Vaccine 3: Formulation prepared during Dose 1 and stored at 4°C until Dose 2

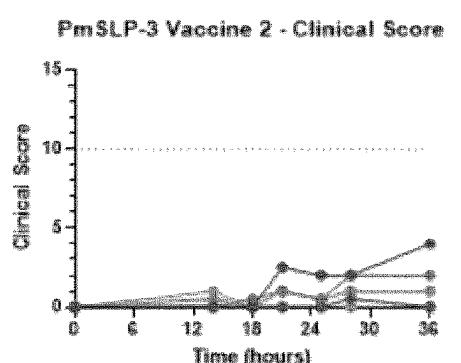
**FIG. 9A**



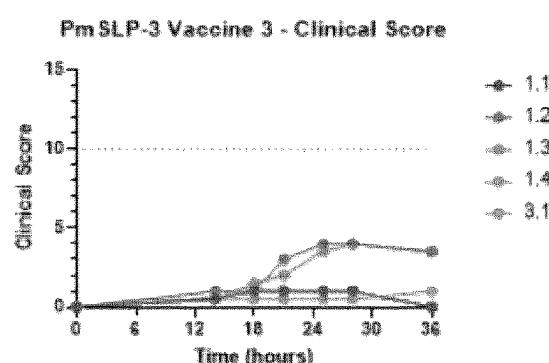
**FIG. 9B**



**FIG. 9C**



**FIG. 9D**



**FIG. 9E**

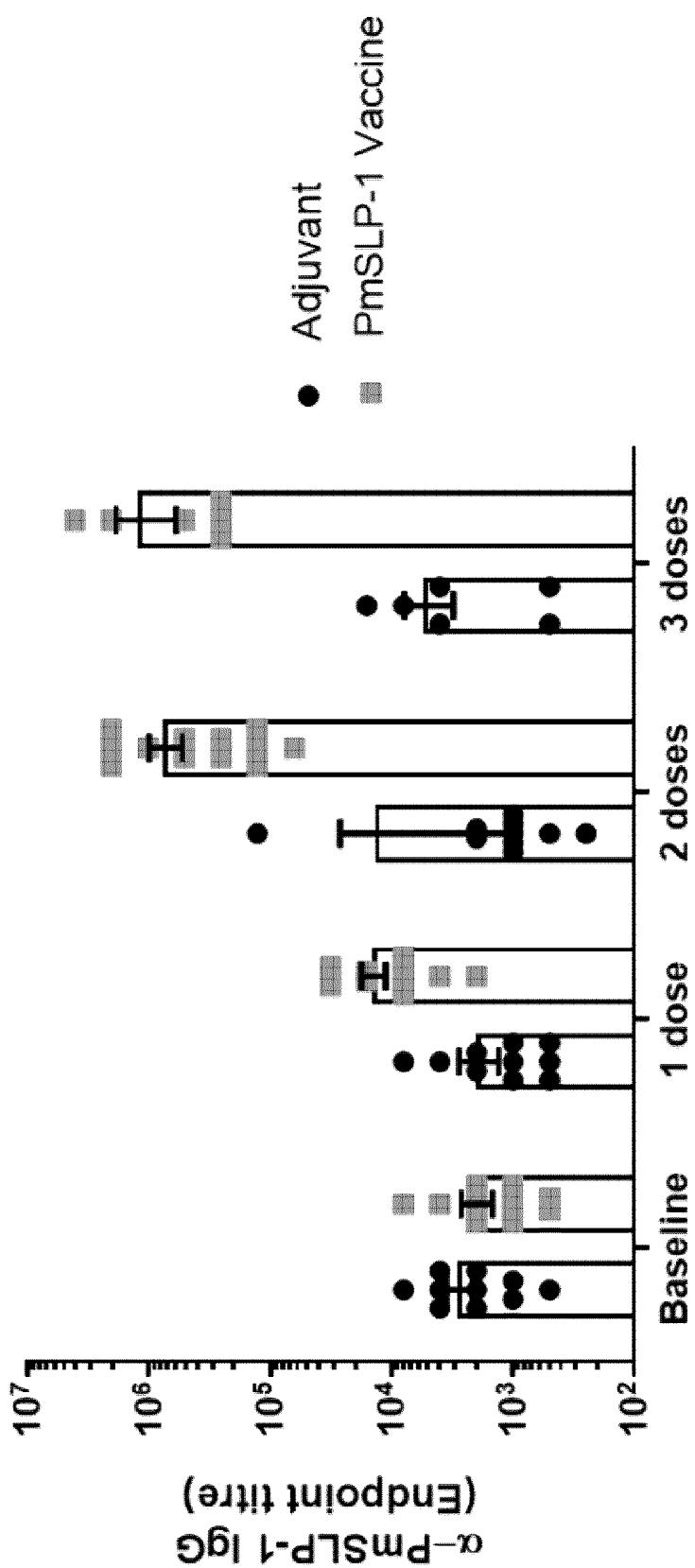


FIG. 10

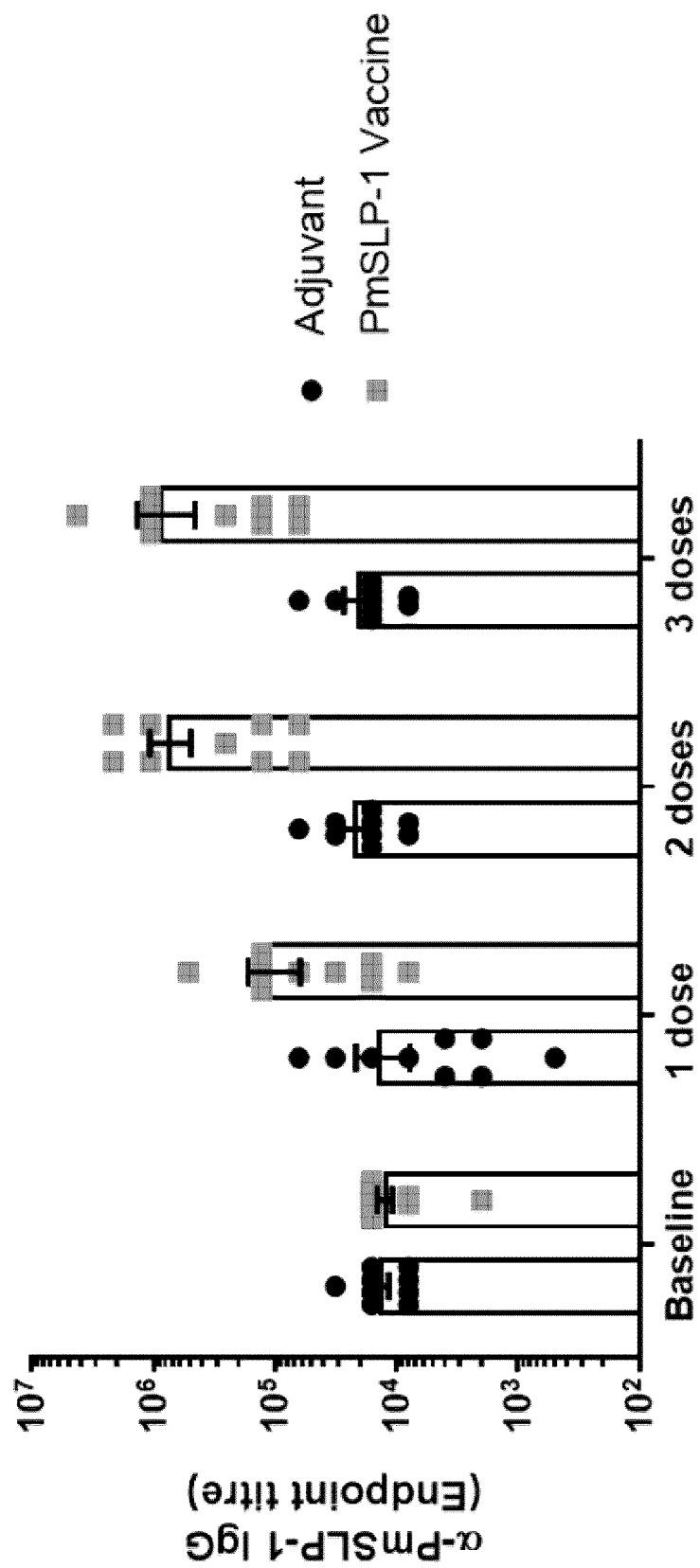
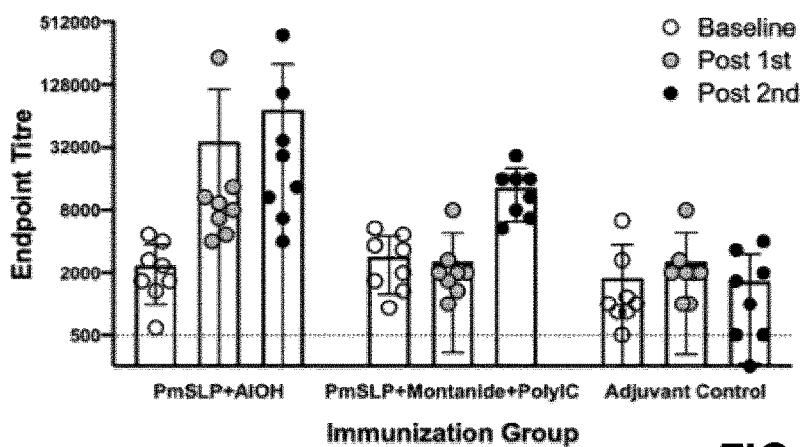
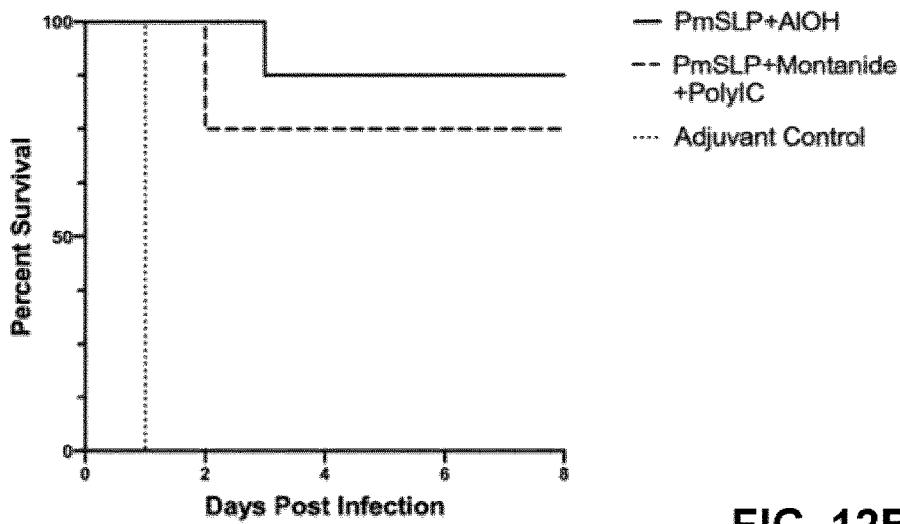


FIG. 11



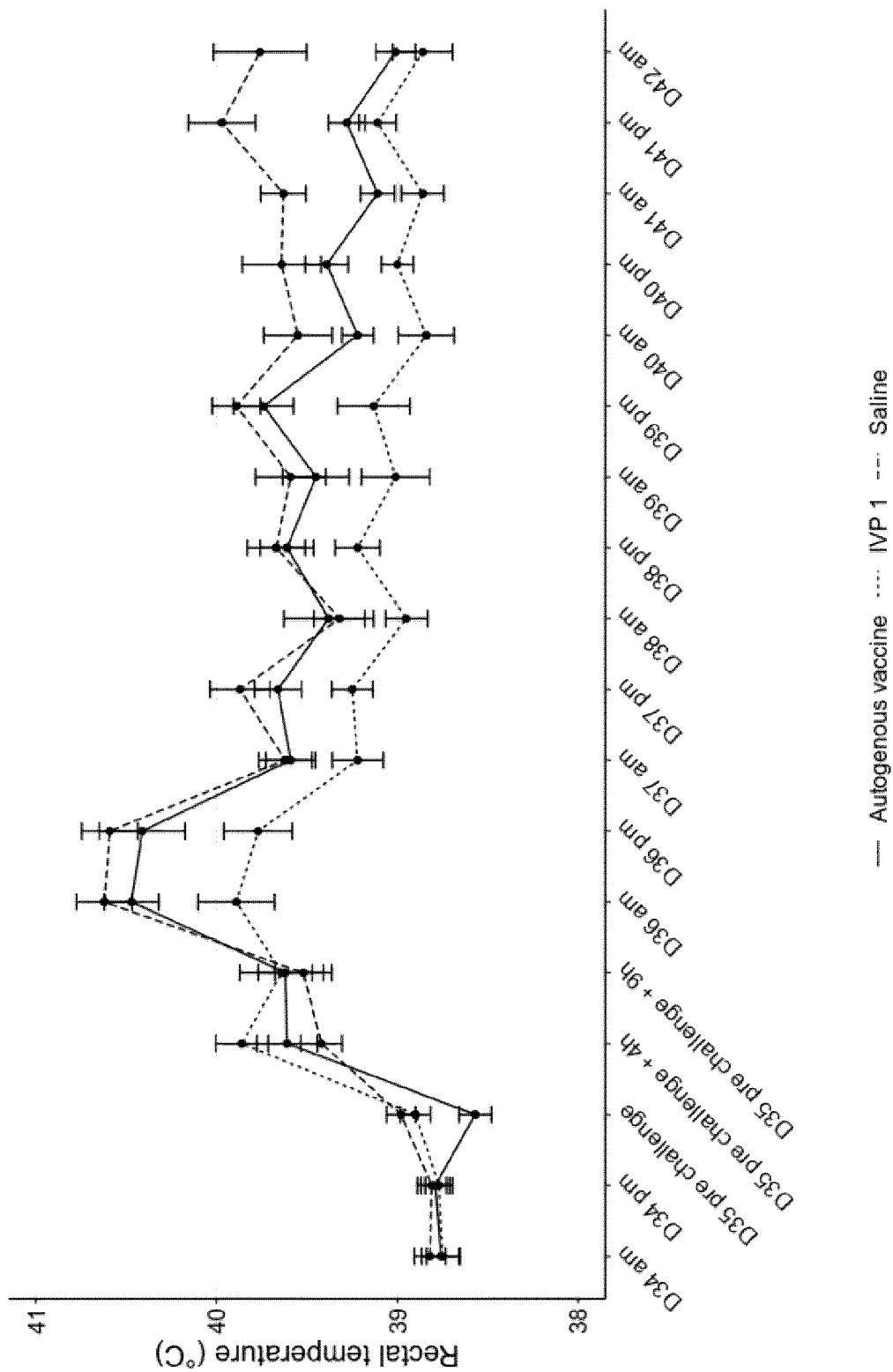
**FIG. 12A**



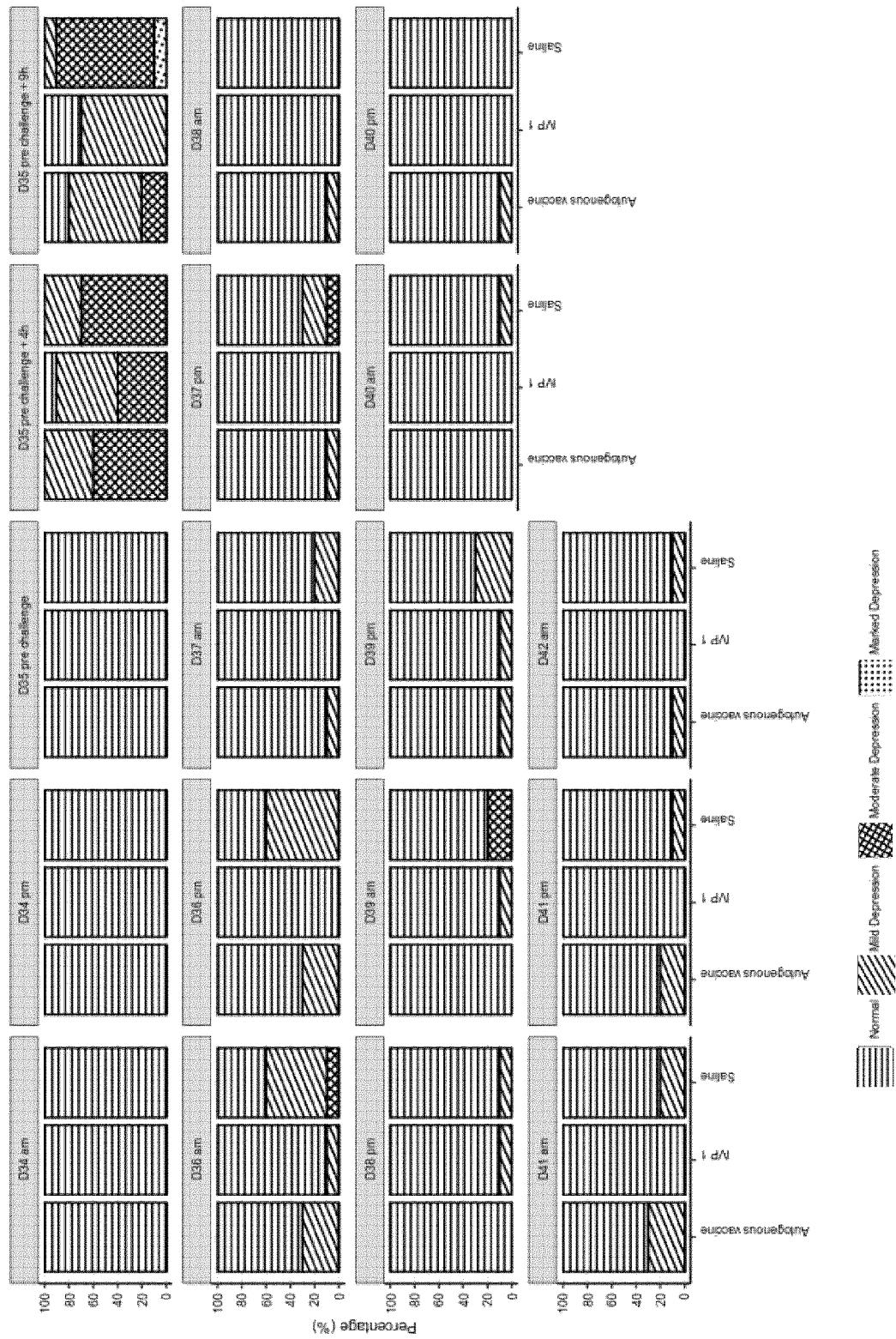
**FIG. 12B**

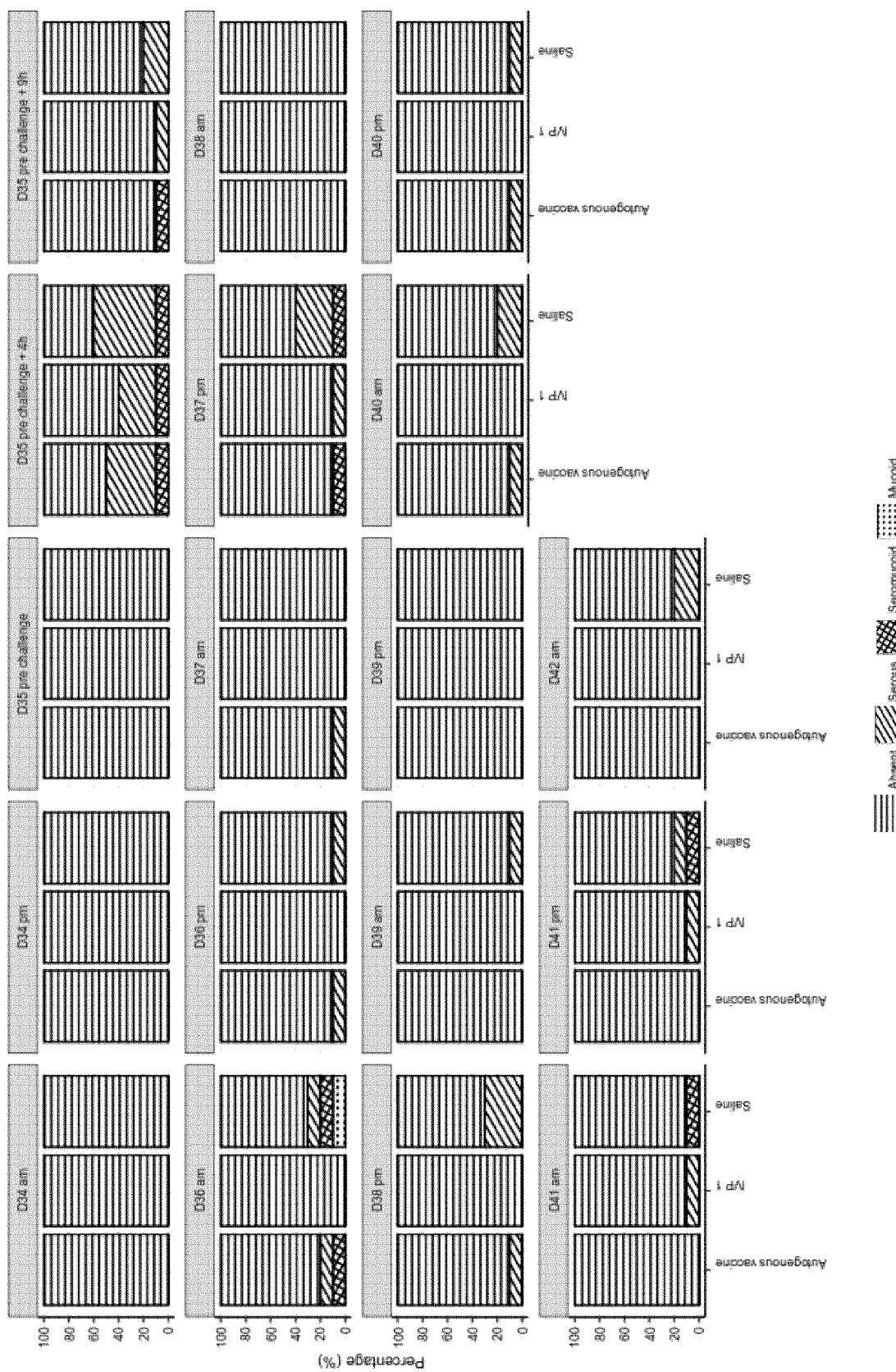
Vaccine	Reaction after primary dose	Reaction after booster dose
PmSLP + AIOH	None	None
Montanide Gel Only	50% with swelling at injection site	None
PmSLP + Montanide Gel + Poly(I:C)	50% with swelling at injection site	None

**FIG. 12C**

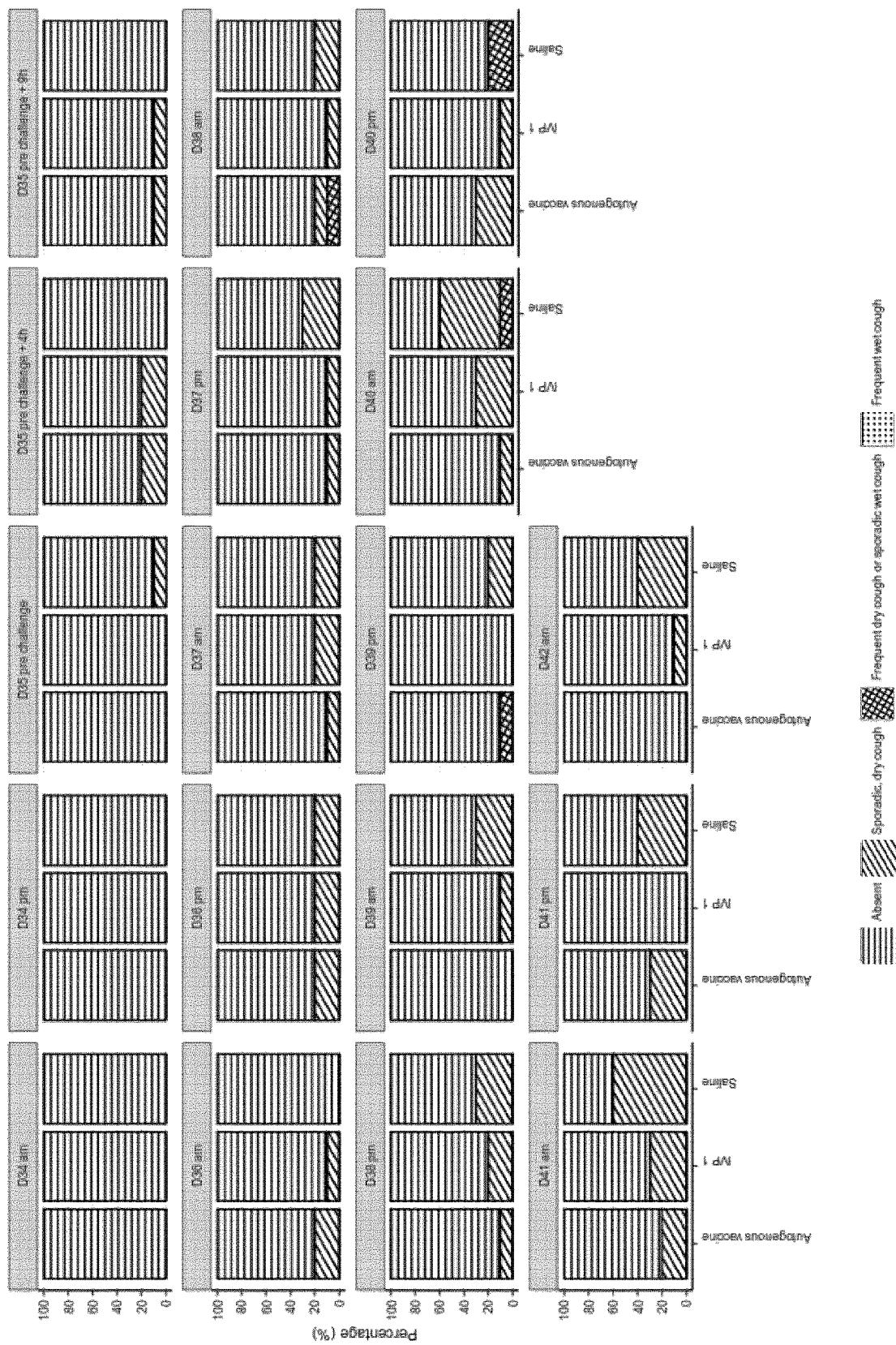


**FIG. 13A**

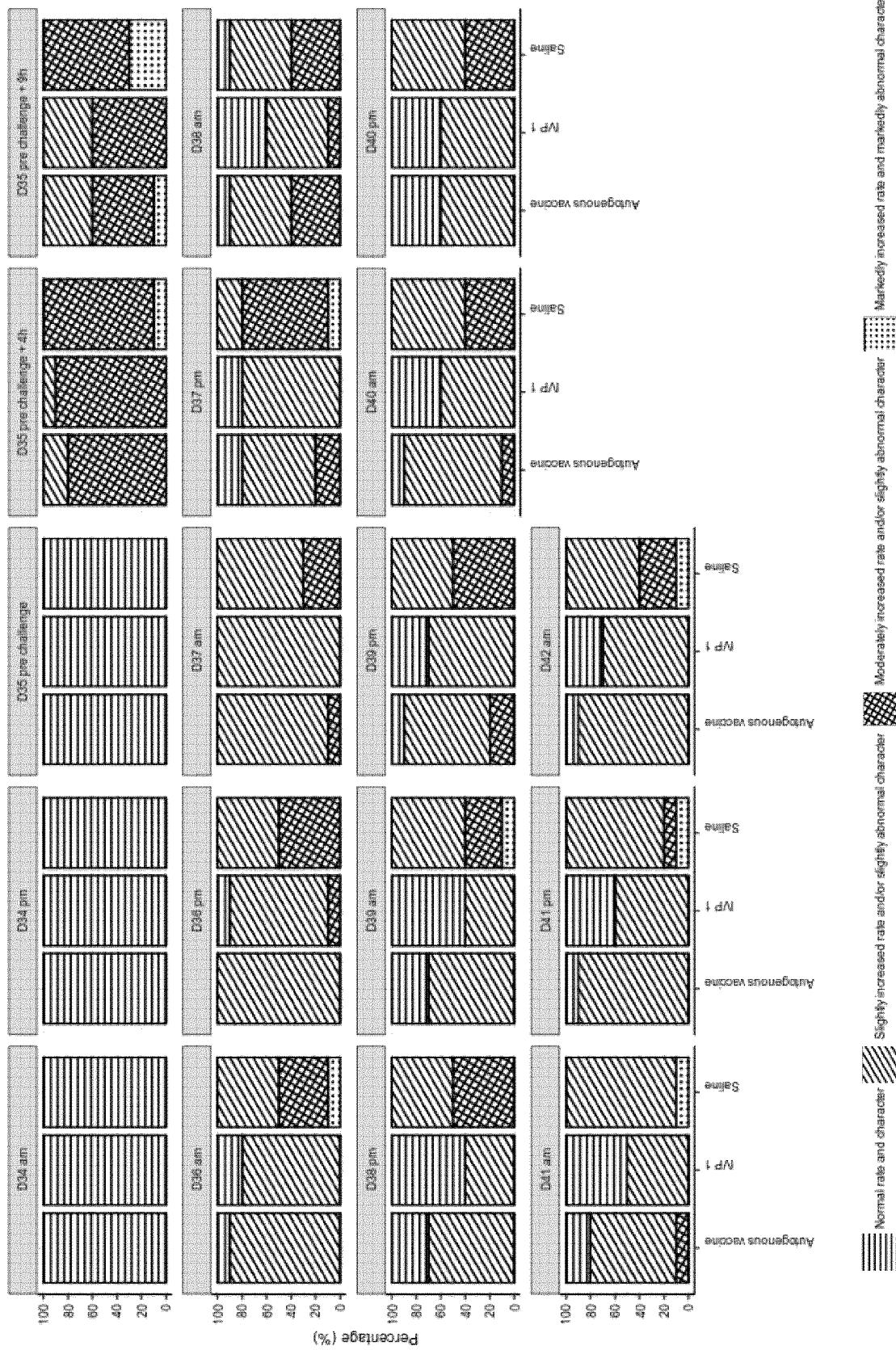




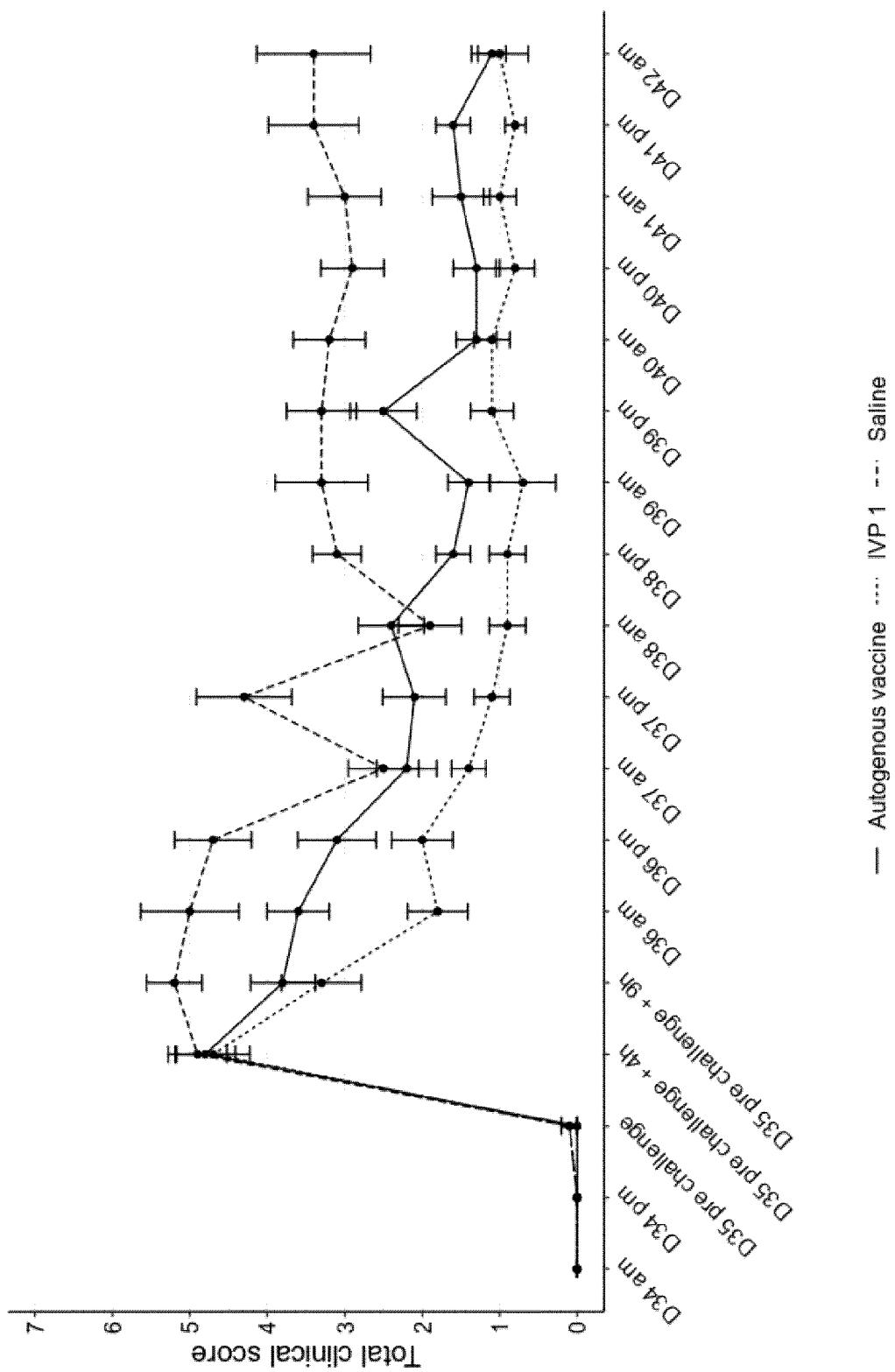
**FIG. 13C**



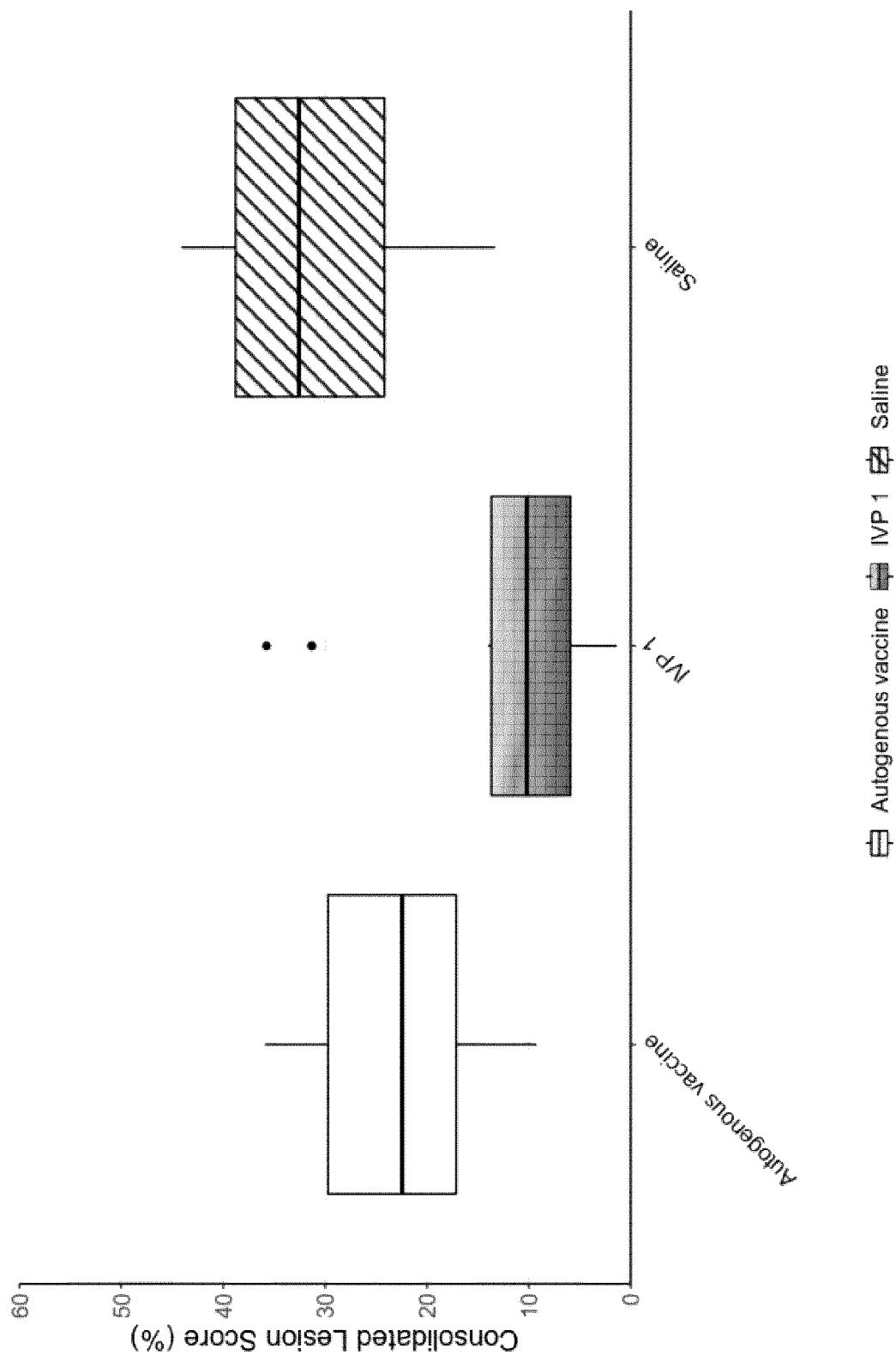
**FIG. 13D**



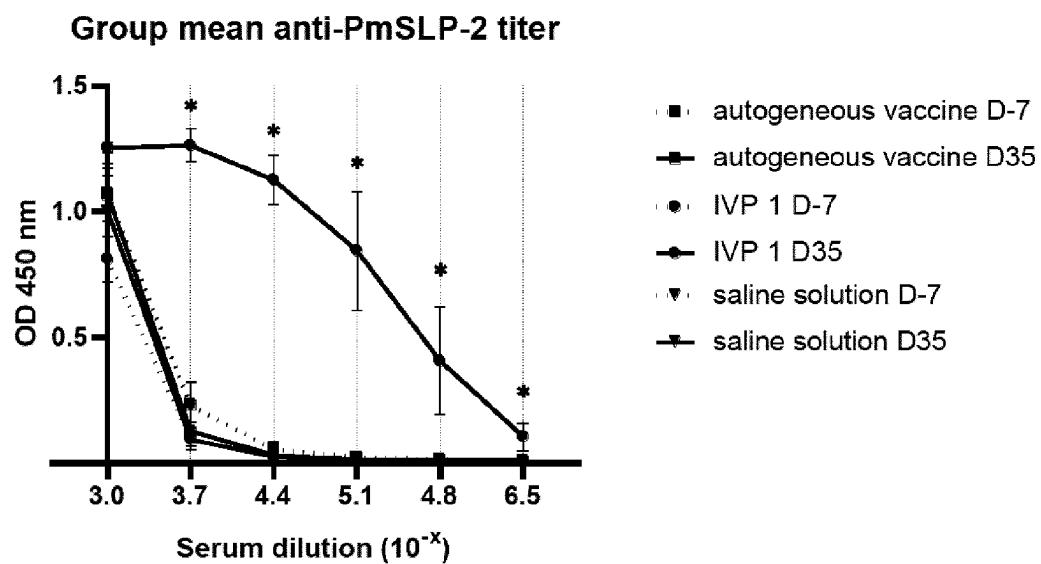
**FIG. 13E**



**FIG. 13F**



**FIG. 13G**



**FIG. 13H**

**VETERINARY VACCINES AND METHODS  
FOR THE TREATMENT OF PASTEURELLA  
MULTOCIDA INFECTIONS IN FOOD  
PRODUCTION ANIMALS**

RELATED APPLICATION

[0001] This application claims the benefit of priority U.S. Provisional Application No. 63/332,966 filed Apr. 20, 2022; the entire contents of U.S. Provisional Application No. 63/332,966 are hereby incorporated by reference.

INCORPORATION OF SEQUENCE LISTING

[0002] A computer readable form of the Sequence Listing “21806-P64683PC00\_SequenceListing.xml” (149,526 bytes), was created on Apr. 19, 2023, is filed herewith by electronic submission and is incorporated by reference herein.

FIELD OF THE DISCLOSURE

[0003] The methods, uses and compositions disclosed herein relate to the treatment of infectious diseases. In particular, the methods, uses and compositions disclosed herein relate to veterinary vaccines to prevent, treat or ameliorate infections in food production animals caused by the infectious Gram-negative bacterium *Pasteurella multocida*.

BACKGROUND OF THE DISCLOSURE

[0004] The following paragraphs are provided by way of background to the present disclosure. They are not however an admission that anything discussed therein is prior art or part of the knowledge of persons skilled in the art.

[0005] *Pasteurella multocida* is a Gram-negative bacterium that is able to colonize and infect a large array of different animals, including mammals and birds. The resultant diseases vary by animal species and include respiratory tract diseases in ruminants, bovine respiratory disease (BRD) and hemorrhagic septicemia (HS) in cattle and *Bovinae* species, porcine pneumonic pasteurellosis and porcine atrophic rhinitis (PAR) in swine, and fowl cholera in avian species.

[0006] *P. multocida* is a rod-shaped, non-flagellated bacterium frequently found in the oral, nasal, and respiratory tract of animals. However, disease is often associated with further organic or systemic dissemination of the bacterium and can include symptoms such as pneumonia, atrophic rhinitis, dermonecrosis, cellulitis, abscesses, meningitis, and hemorrhagic septicemia. Furthermore, *P. multocida* infections can be either chronic or acute (Harper M. et al., 2006, FEMS Microbiol. Letters, 265(1), 1-10. doi:10.1111/j.1574-6968.2006.00442.x; Wilson, B. & Ho, M., 2013, Clinical Microbiol. Rev., 26(3), 631. doi:10.1128/CMR.00024-13).

[0007] Taxonomically, *P. multocida* can be subdivided into three subspecies: *P. multocida* subspecies *multocida*, *P. multocida* subspecies *gallicida*, and *P. multocida* subspecies *septica* (Mutters R. et al., 1985, Intern. J. of Syst. Evol. Microbiol., 35(3), 309-322. doi.org/10.1099/00207713-35-3-309). Furthermore, *P. multocida* can be classified in accordance with serogroups, representing different types of extracellular capsular polysaccharides. In this respect, five serogroups (serogroup A, B, D, E, and F) are commonly distinguished (Carter, G. 1955, Rev Sci Tech, 19(2), 626-637. doi:10.20506/rst.19.2.1236). *P. multocida* strains can

yet further be stratified into 16 serotypes (serotype 1-16) based on the antigenic membrane lipopolysaccharide (LPS) constituents different *P. multocida* strains may exhibit (Hedleston, K., 1972, Avian Dis, 16(4), 925-936).

[0008] Bovine-associated diseases caused by *P. multocida* include bovine respiratory disease complex (BRD) and hemorrhagic septicemia (HS), with BRD being common in feedlots across North America and Europe, while HS is a frequent cause of disease in smallholder farmers across Asia and Africa. BRD, alternatively known as “shipping fever” in feedlot cattle, is overall considered the leading cause of cattle morbidity and mortality in feedlots and has been estimated to cause between 45-55% of all feedlot deaths (Johnson, K. & Pendell, D., 2017, Frontiers in Vet. Sci., 4(189). doi:10.3389/fvets.2017.00189). Furthermore, BRD has been estimated to be one of the costliest diseases in commercial North American feedlots (Griffin, D., 1997, Vet. Clin. North Am. Food Animal Practice, 13(3), 367-377. doi:10.1016/s0749-0720(15)30302-9. In this respect, BRD is commonly associated with infections of the lungs, causing pneumonia in recently weaned and feedlot cattle, nursing beef calves, housed dairy calves, and lactating dairy cows. BRD is more common among herds kept in tight quarters such as feedlots or in large herds kept on a small number of acres. BRD is additionally more typical among stressed animals and in animals with pre-existing infections, for example, pre-weaned calves and calves shortly following weaning, shipped to new locations (Wilson et al., B. K. 2017 J. Animal Sci., 95(5), 2170-2182. doi:10.2527/jas.2016.1006; Dubrovsky, S. et al., J Dairy Sci., 2019, 102(8): 7320-7328. doi: 10.3168/jds.2018-15463).

[0009] Hemorrhagic septicemia (HS) is a rapidly progressing, highly fatal septicemic disease of cattle and buffaloes. HS causes significant economic losses in tropical regions of the world, especially in low and middle-income countries in Africa and Asia. HS is particularly devastating to smallholder farmers where husbandry and preventive practices are often inadequate. HS causing *P. multocida* can colonize the tonsils of a small proportion of healthy water buffalo and cattle (carriers) and can be shed during periods of stress, such as high temperature and humidity (Shivachandra, S. et al., 2011, Animal Health Res. Rev., 12(1), 67-82. doi:10.1017/S146625231100003X). Outbreaks of disease are most prevalent during the rainy season. Infection occurs by contact with infected oral or nasal secretions from either healthy carrier animals or animals with disease, or possibly by ingestion of contaminated feed or water (OIE Manual of Diagnostic Tests and Vaccines for Terrestrial Animals, 8<sup>th</sup> Edition, 2018, Chapter 3.4.10, 1125-1138). The development of disease from colonized cattle is incompletely understood but typically there is a combination of local involvement in the neck region and systemic spread which culminates in dissemination to various organs, tissue injury, cytokine storm, and toxic shock. Clinical signs can appear 1-3 days after the organism is first detected, and death can occur as rapidly as within 8-24 hours after the onset of symptoms. The economic loss due to HS has been estimated at almost \$800 million USD per year in India (Singh, B. et al., 2014, Agric. Econ. Res. Rev., 27(347-2016-17135), 271-279).

[0010] Current veterinary vaccines available for ruminant-associated *P. multocida* infections are limited and mainly focused on traditional bacterin formulations (killed whole bacteria) or live attenuated bacteria (streptomycin-depen-

dent mutant strains). Both of these vaccines have unreliable efficacy profiles due to limited protection, partially due to bacterial polysaccharide capsule specificity of these vaccines, and the potential of unmatched circulating strains, but even when the capsule is matched the efficacy is incomplete and not well documented in the literature (Dabo, S. et al., 2007, *Anim. Health Res. Rev.*, 8(2), 129-150). Moreover, due to the limited effectiveness of existing vaccines against *P. multocida* and other BRD causing bacteria, prophylactic and metaphylactic use of antimicrobials is pervasive in cattle farming and is a potential important source of the development of antimicrobial resistance in pathogens (Cameron, A. & McAllister T., 2016, *J. Animal Sci. and Biotechn.*, 7(1), 68. doi:10.1186/s40104-016-0127-3).

[0011] *P. multocida* infections in swine can cause porcine pneumonic pasteurellosis and progressive atrophic rhinitis (PAR) infections which are of considerable economic importance worldwide (Adlam C. & Rutter J, 1989, *Pasteurella multocida*: molecular biology, toxins and infection (Vol. 361): Springer Science & Business Media). PAR is associated with certain toxigenic strains of *P. multocida*, which are frequently serogroup D and, to a lesser extent, serogroup A (Eamens G. et al., 1988, *Aust. Vet. J.*, 65(4), 120-123. doi:10.1111/j.1751-0813.1988.tb14430.x; Foged N. et al., 1989, *Vet. Rec.*, 125, 7-11; Fussing, V. et al., *Vet. Microbiol.*, 65(1), 61-74. doi:10.1016/s0378-1135(98)00288-0; and Sakano T. et al., 1992, *J. Vet. Med. Sci.*, 54(3), 403-407. doi:10.1292/jvms.54.403), while pneumonic pasteurellosis is generally caused by non-toxigenic strains but also encompasses serogroups A and D (Djordjevic, S. et al., 1998, *J. Med. Microbiol.*, 47(8), 679-688. doi.org/10.1099/00222615-47-8-679; Pijoan, C. et al., 1983, *J. Clin. microbiol.*, 17(6), 1074-1076; and Zhao, G. et al., 1992, *Infect. Immun.*, 60(4), 1401-1405). *P. multocida*-associated swine infections occur globally, including in North America, Europe, and Asia (VanderWaal D. & Deen J., 2018, *PNAS* 115(45), 11495. doi:10.1073/pnas.1806068115). As is the case in cattle rearing, *P. multocida*-associated infections are of significant economic burden and management of these infections leads to increased antibiotic usage. Swine vaccines against *P. multocida* are generally either bacterins of toxigenic and non-toxigenic strains or toxoid-based vaccines (OIE Manual of Diagnostic Tests and Vaccines for Terrestrial Animals, 8<sup>th</sup> Edition, 2018, Chapter 3.8.2, 1540-1550). Vaccines against pneumonic pasteurellosis in swine do not appear to be widely available.

[0012] *P. multocida* is also the causative agent of fowl cholera and is associated with a wide variety of infections. Acute infections can progress rapidly, and often sudden death of birds within flocks is the only sign that infection is occurring within a facility, however other symptoms can include discharge from the mouth and nose, cyanosis, general depression, and diarrhea (Christensen, J. & Bisgaard, M. 2000, *Rev. Sci. Tech.*, 19(2), 626-637. doi:10.20506/rst.19.2.1236). Fowl cholera can effect a variety of avian species, with chicken, turkey, duck, and quail being of the most economic importance (Glisson, J. 1998, *Poultry Science*, 77(8), 1139-1142. doi.org/10.1093/ps/77.8.1139). Fowl cholera is mostly caused by serogroup A strains of *P. multocida*, however serogroups F and D have also been reported (Dziva, F. et al., 2008, *Vet. Microbiol.*, 128(1-2), 1-22. doi:10.1016/j.vetmic.2007.10.018). Available vaccines include inactivated bacterins and live attenuated vaccines. Inactivated vaccines elicit a serotype specific

response, thus offering limited protection. On the other hand, live inactivated vaccines do appear to elicit a broad, cross-serotype response. However live attenuated vaccines have the potential to induce chronic fowl cholera in chickens and turkeys (Glisson, J. 1998, *Poultry Science*, 77(8), 1139-1142. doi.org/10.1093/ps/77.8.1139).

[0013] In light of the foregoing, there exists a need in the art for improved methods and compositions to treat *P. multocida* infections. In particular, there is a need in the art for improved vaccines to prevent disease caused by *Pasteurella multocida* infections in food production animals, including but not limited to ruminant such as bovine, porcine, and avian food production animals.

#### SUMMARY OF THE DISCLOSURE

[0014] The following paragraphs are intended to introduce the reader to the more detailed description, not to define or limit the claimed subject matter of the present disclosure.

[0015] In one aspect, the present disclosure relates to vaccine formulations.

[0016] In another aspect, the present disclosure relates to vaccine formulations to prevent or ameliorate diseases in food production animals that are caused by the bacterial pathogen *Pasteurella multocida* (*P. multocida*).

[0017] The inventors have discovered that the veterinary vaccine formulations of the present disclosure can provide protection to food production animals against infection by multiple *P. multocida* strains, including in a cross-protective manner, using a single immunogenic active agent. The immunogenic agents discovered to be effective when administered to a food production animal in a veterinary vaccine formulation are, in particular, proteins selected from a class of *P. multocida* proteins, known as PmSLP proteins.

[0018] Accordingly, the present disclosure provides, in accordance with the teachings herein, in at least one embodiment, a veterinary vaccine formulation for the prevention or amelioration of *P. multocida* infection in a food production animal susceptible to *P. multocida* infection, the vaccine formulation comprising an effective amount of at least one PmSLP protein, or an immunogenically equivalent portion thereof.

[0019] In at least one embodiment, in an aspect, the vaccine formulation can comprise at least one *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof selected from the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0020] In at least one embodiment, in an aspect, the vaccine formulation can comprise a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0021] In at least one embodiment, in an aspect, the food production animal can be a ruminant animal susceptible to infection by a *P. multocida* strain causing a respiratory tract disease, and the vaccine formulation comprises a *P. multocida* PmSLP protein from a respiratory tract disease causing *P. multocida* strain, or an immunogenically equivalent portion thereof, wherein the PmSLP protein is selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, PmSLP-3, and PmSLP-4.2, wherein the selected

*P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0022] In at least one embodiment, in an aspect, the food production animal can be a bovine animal susceptible to infection by a *P. multocida* strain causing BRD, and the vaccine formulation comprises a *P. multocida* PmSLP protein from a BRD causing *P. multocida* strain, or an immunogenically equivalent portion thereof, wherein the PmSLP protein is selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0023] In at least one embodiment, in an aspect, the food production animal can be a bovine animal susceptible to infection by a *P. multocida* strain causing HS, and the vaccine formulation comprises a *P. multocida* PmSLP protein from an HS causing *P. multocida* strain, or an immunogenically equivalent portion thereof, wherein the PmSLP protein is selected from the phylogenetic cluster PmSLP-3 wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0024] In at least one embodiment, in an aspect, the food production animal can be a porcine animal susceptible to infection by a *P. multocida* strain causing porcine atrophic rhinitis (PAR), and the vaccine formulation comprises a *P. multocida* PmSLP protein from a PAR causing *P. multocida* strain, or an immunogenically equivalent portion thereof, wherein the PmSLP protein is selected from the group of phylogenetic clusters consisting of PmSLP-2, PmSLP-4.1, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0025] In at least one embodiment, in an aspect, the food production animal can be a porcine animal susceptible to infection by a *P. multocida* strain causing pneumonic pasteurellosis, and the vaccine formulation comprises a *P. multocida* PmSLP protein from a pneumonic pasteurellosis causing *P. multocida* strain, or an immunogenically equivalent portion thereof, wherein the PmSLP protein is selected from the group of phylogenetic clusters consisting of PmSLP-2, PmSLP-4.1, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0026] In at least one embodiment, in an aspect, the food production animal can be an avian animal susceptible to infection by a *P. multocida* strain causing fowl cholera, and the vaccine formulation comprises a *P. multocida* PmSLP protein from a fowl cholera causing *P. multocida* strain, or an immunogenically equivalent portion thereof, wherein the PmSLP protein is selected from the group of phylogenetic clusters consisting of PmSLP-3 and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0027] In at least one embodiment, in an aspect, the vaccine formulation can comprise a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain, and wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, further is of a *P. multocida* strain belonging to a serogroup selected from the group consisting of serogroup A, B, D, E, and F, wherein the serogroup is the same as the serogroup of the infecting *P. multocida* strain.

[0028] In at least one embodiment, in an aspect, the at least one PmSLP protein, or immunologically equivalent portion thereof, can be a protein expressed by a nucleic acid sequence selected from the group of nucleic acid sequences consisting of:

[0029] (a) SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID. NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID. NO: 19, SEQ.ID. NO: 21, SEQ.ID. NO: 23, SEQ.ID. NO: 25, SEQ.ID. NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ. ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ. ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96;

[0030] (b) a nucleic acid sequence having at least 70% identity with any one of the nucleic acid sequences of (a);

[0031] (c) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a) but for the degeneration of the genetic code;

[0032] (d) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

[0033] (e) a chimeric nucleic acid obtained by a fusion between at least two nucleic acid sequences of (a), (b), (c), and (d), or a portion thereof;

[0034] (f) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

[0035] (g) a nucleic acid sequence encoding a polypeptide having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93,

SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;

[0036] (h) a nucleic acid sequence that encodes a functional variant of any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereto; and

[0037] (i) a nucleic acid sequence that hybridizes under stringent conditions to any one of the nucleic acid sequences set forth in (a), (b), (c), (d), (e), (f), (g), or (h).

[0038] In at least one embodiment, in an aspect, the at least one *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, can comprise any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing the respiratory tract disease.

[0039] In at least one embodiment, in an aspect, the food production animal can be a ruminant species, and the *P. multocida* infection causes respiratory tract disease.

[0040] In at least one embodiment, in an aspect, the food production animal can be a bovine species, and the *P. multocida* infection causes bovine respiratory disease (BRD) or hemorrhagic septicemia (HS).

[0041] In at least one embodiment, in an aspect, the food production animal can be a porcine species and the *P. multocida* infection causes porcine pneumonic pasteurellosis or porcine atrophic rhinitis (PAR).

[0042] In at least one embodiment, in an aspect, the food production animal can be an avian species, and the *P. multocida* infection causes fowl cholera.

[0043] In at least one embodiment, in an aspect, the food production animal can be a ruminant species, wherein the *P. multocida* infection causes a respiratory tract disease, and wherein the PmSLP protein comprises SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38,

SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing the respiratory tract disease.

[0044] In at least one embodiment, in an aspect, the food production animal can be a bovine species, wherein the *P. multocida* infection causes BRD, and wherein the PmSLP protein comprises SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 22, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 77, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing BRD.

[0045] In at least one embodiment, in an aspect, the food production animal can be a bovine species, wherein the *P. multocida* infection causes HS, and wherein the PmSLP protein comprises SEQ.ID NO: 6, SEQ.ID NO: 20, SEQ.ID NO: 24, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 53, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, or SEQ.ID NO: 89, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing HS.

[0046] In at least one embodiment, in an aspect, the food production animal can be a porcine species, and the *P. multocida* infection causes pneumonic pasteurellosis, and wherein the PmSLP protein comprises SEQ.ID NO: 4, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 75, SEQ.ID NO: 77, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing pneumonic pasteurellosis.

[0047] In at least one embodiment, in an aspect, the food production animal can be a porcine species, wherein the *P. multocida* infection causes PAR, and wherein the PmSLP protein comprises SEQ.ID NO: 4, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 75, SEQ.ID NO: 77, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing PAR.

[0048] In at least one embodiment, in an aspect, the food production animal can be an avian species, wherein the *P. multocida* infection causes fowl cholera, and wherein the PmSLP protein comprises SEQ.ID NO: 6, SEQ.ID NO: 10, SEQ.ID NO: 20, SEQ.ID NO: 24, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 40, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 61, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, or SEQ.ID NO: 89, or an

immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing pneumonic pasteurellosis.

[0049] In at least one embodiment, in an aspect, the PmSLP protein, or immunogenically equivalent portion thereof, can be recombinantly produced in a microbial host organism.

[0050] In at least one embodiment, in an aspect, the veterinary vaccine formulation can be a cross-protective vaccine formulation comprising a PmSLP protein, or immunogenically equivalent portion thereof, obtained from a first *P. multocida* strain, and the vaccine formulation is a formulation for the administration to the food production animal to prevent or ameliorate an infection caused by another *P. multocida* strain.

[0051] In at least one embodiment, in an aspect, the vaccine formulation can be substantially free of other *P. multocida* constituents.

[0052] In at least one embodiment, in an aspect, the PmSLP protein, or immunologically equivalent portion thereof, can be a recombinantly produced protein, wherein the vaccine formulation is substantially free of host cell constituents.

[0053] In at least one embodiment, in an aspect, wherein the vaccine formulation further can comprise a veterinary pharmaceutically acceptable adjuvant.

[0054] In at least one embodiment, in an aspect, wherein the vaccine formulation can further comprise a veterinary pharmaceutically acceptable excipient, carrier, or diluent.

[0055] In at least one embodiment, in an aspect, wherein the vaccine formulation can comprise from about 0.001% to about 20% by weight of the PmSLP protein or the immunogenically equivalent portion thereof, and a veterinary pharmaceutically acceptable adjuvant constituting from about 0.1% to about 60% by weight or volume of the vaccine formulation.

[0056] In at least one embodiment, in an aspect, the vaccine formulation can comprise a second *P. multocida* PmSLP protein, or immunologically equivalent portion thereof.

[0057] In at least one embodiment, in an aspect, the vaccine formulation can comprise a fusion polypeptide comprising the first and second *P. multocida* PmSLP protein, or immunologically equivalent portion thereof.

[0058] In at least one embodiment, in an aspect, the second *P. multocida* PmSLP protein, or immunologically equivalent portion thereof, can belong to the same or a different phylogenetic cluster as the first *P. multocida* PmSLP protein, or immunologically equivalent portion thereof.

[0059] In at least one embodiment, in an aspect, the fusion polypeptide can comprise a fusion polypeptide selected from the group consisting of a (i) PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 1 and a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 3; (ii) PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 1 and a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 2; (iii) a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 1 and a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 4.1; and (iv) a PmSLP protein, or

immunologically equivalent portion thereof, belonging to phylogenetic cluster 1 and a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 4.2.

[0060] In at least one embodiment, in an aspect, the second *P. multocida* PmSLP protein, or immunologically equivalent portion thereof, can be obtained from a *P. multocida* strain belonging to the same or a different serogroup as the *P. multocida* strain of the first *P. multocida* PmSLP protein, or immunologically equivalent portion thereof.

[0061] In another aspect, the present disclosure provides, in accordance with the teachings herein, in at least one embodiment, a use of a veterinary vaccine formulation for the prevention, treatment or amelioration of *P. multocida* infection in a food production animal susceptible to *P. multocida* infection, the vaccine formulation comprising an effective amount of at least one PmSLP protein, or an immunogenically equivalent portion thereof. In another embodiment, the present disclosure provides a veterinary vaccine formulation for use in the prevention, treatment or amelioration of *P. multocida* infection in a food production animal susceptible to *P. multocida* infection, the vaccine formulation comprising an effective amount of at least one PmSLP protein, or an immunogenically equivalent portion thereof.

[0062] In at least one embodiment, in an aspect, the vaccine formulation can cause an improved trending towards normal of one or more clinical parameters selected from the group consisting of (i) rectal temperature, (ii) animal demeanor, (iii) nasal discharge pattern, (iv) coughing pattern, (v) respiratory pattern, and (vi) overall clinical health, relative to an animal production animal not having been administered the veterinary vaccine formulation.

[0063] In at least one embodiment, in an aspect, the vaccine formulation can be capable of eliciting an immune response in the food production animal, wherein anti-PmSLP antibodies are detectable in the blood serum of the food production animal at least in the period starting 7 days and ending 52 weeks from the date of use of the vaccine formulation.

[0064] In another aspect, the present disclosure provides, in accordance with the teachings herein, in at least one embodiment, a method for prevention, treatment or amelioration of *P. multocida* infection in a food production animal susceptible to *Pasteurella multocida* (*P. multocida*) infection, the method comprising administering to the food production animal a veterinary vaccine formulation comprising a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, wherein the vaccine formulation is administered in an effective amount to prevent, treat or ameliorate the *P. multocida* infection.

[0065] In at least one embodiment, in an aspect, the amelioration of the *P. multocida* infection can comprise the reduction of clinical signs of any disease caused by the *P. multocida* infection.

[0066] In at least one embodiment, in an aspect, the clinical signs can be selected from the group consisting of: (i) rectal temperature, (ii) animal demeanor, (iii) nasal discharge pattern, (iv) coughing pattern, (v) respiratory pattern, and (vi) overall clinical health, relative to an animal production animal not having been administered the veterinary vaccine formulation.

[0067] In at least one embodiment, in an aspect, the food production animal susceptible to *Pasteurella multocida*

infection can be selected from the group consisting of ruminant, porcine, and avian species.

[0068] In at least one embodiment, in an aspect, the disease caused by *Pasteurella multocida* infection can be selected from the group consisting of respiratory tract disease, bovine respiratory disease (BRD), hemorrhagic septicemia (HS), porcine atrophic rhinitis (PAR), and fowl cholera.

[0069] In at least one embodiment, in an aspect, the food production animal can be a ruminant susceptible to *P. multocida* infection, and wherein the veterinary vaccine formulation administered in an effective amount to the ruminant comprises at least one PmSLP protein from a *P. multocida* strain causing respiratory tract disease, or an immunogenically equivalent portion thereof.

[0070] In at least one embodiment, in an aspect, the food production animal susceptible to *P. multocida* infection can be a bovine species, and wherein the veterinary vaccine formulation administered in an effective amount to the bovine species comprises at least one PmSLP protein from a *P. multocida* strain causing BRD, or an immunogenically equivalent portion thereof.

[0071] In at least one embodiment, in an aspect, the food production animal susceptible to *P. multocida* infection can be a ruminant, and wherein the veterinary vaccine formulation administered in an effective amount to the ruminant comprises at least one PmSLP protein from a *P. multocida* strain causing HS, or an immunogenically equivalent portion thereof.

[0072] In at least one embodiment, in an aspect, the food production animal susceptible to infection by a *P. multocida* strain can be a porcine animal, and wherein the veterinary vaccine formulation administered in an effective amount to the porcine animal comprises at least one PmSLP protein from a *P. multocida* causing porcine atrophic rhinitis (PAR), or an immunogenically equivalent portion thereof.

[0073] In at least one embodiment, in an aspect, the food production animal susceptible to infection by a *P. multocida* strain can be an avian animal, and wherein the veterinary vaccine formulation administered in an effective amount to the avian animal comprises at least one PmSLP protein from a fowl cholera causing *P. multocida* strain, or an immunogenically equivalent portion thereof.

[0074] In at least one embodiment, in an aspect, the vaccine formulation administered in an effective amount to the food production animal can comprise at least one *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, and PmSLP-4.2.

[0075] In at least one embodiment, in an aspect, the veterinary vaccine formulation can comprise at least one *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, which confers to the food production animal susceptible to infection by *P. multocida* a homologous protection against a *P. multocida* strain, possessing a PmSLP protein from the same phylogenetic cluster.

[0076] In at least one embodiment, in an aspect, the veterinary vaccine formulation can comprise at least one *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, which confers to the food animal susceptible to infection by *P. multocida* heterologous protection against a *P. multocida* strain, possessing a PmSLP protein from a different phylogenetic cluster.

[0077] In at least one embodiment, in an aspect, the vaccine formulation can comprise at least one *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, selected from a protein encoded by a nucleic acid sequence selected from the group of nucleic acid sequences consisting of:

[0078] (a) SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID NO: 19, SEQ.ID NO: 21, SEQ.ID NO: 23, SEQ.ID NO: 25, SEQ.ID NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ.ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ.ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96;

[0079] (b) a nucleic acid sequence having at least 70% identity with any one of the nucleic acid sequences of (a);

[0080] (c) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a) but for the degeneration of the genetic code;

[0081] (d) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

[0082] (e) a chimeric nucleic acid obtained by a fusion between at least two nucleic acid sequences of (a), (b), (c), and (d) or portion thereof;

[0083] (f) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

[0084] (g) a nucleic acid sequence encoding a polypeptide having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14, SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;

[0085] (h) a nucleic acid sequence that encodes a functional variant of any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14, SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69,

SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereto, and

[0086] (i) a nucleic acid sequence that hybridizes under stringent conditions to any one of the nucleic acid sequences set forth in (a), (b), (c), (d), (e), (f), (g), or (h).

[0087] In at least one embodiment, in an aspect, the vaccine formulation can comprise at least one *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, having any one of amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ. ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, or a chimeric protein obtained by a fusion between any one of said sequences or portion thereof.

[0088] In at least one embodiment, in an aspect, the PmSLP protein, or immunogenically equivalent portion thereof can be recombinantly produced in a microbial host organism.

[0089] In at least one embodiment, in an aspect, the PmSLP protein, or immunologically equivalent portion thereof, can be substantially free of other *P. multocida* constituents.

[0090] In at least one embodiment, in an aspect, the PmSLP protein, or immunologically equivalent portion thereof, can be a recombinantly produced protein, wherein the PmSLP protein, or immunologically equivalent portion thereof, is substantially free of host cell constituents.

[0091] In at least one embodiment, in an aspect, the vaccine formulation further can comprise a veterinary pharmaceutically acceptable adjuvant.

[0092] In at least one embodiment, in an aspect, the vaccine formulation can comprise a veterinary pharmaceutically acceptable excipient, carrier, or diluent.

[0093] In another aspect, the present disclosure provides, in accordance with the teachings herein, in at least one embodiment, a method for preparing a veterinary vaccine formulation for the prevention or amelioration of *P. multocida* infection in a food production animal susceptible to *P. multocida* infection, the method comprising:

[0094] (i) diagnosing a *P. multocida* infection in a food production animal;

[0095] (ii) identifying the phylogenetic cluster to a which a PmSLP protein present in the infecting *P. multocida* belongs, the phylogenetic cluster being selected from PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1 or PmSLP-4.2; and

[0096] (iii) preparing a vaccine formulation comprising a *P. multocida* PmSLP protein, or immunogenically equivalent portion thereof, which belongs to the identified phylogenetic cluster together with a veterinary

pharmaceutically acceptable adjuvant to form a veterinary vaccine formulation comprising an effective amount of the *P. multocida* PmSLP protein or the immunogenically equivalent portion thereof to treat a food production animal susceptible to *P. multocida* infection.

[0097] In at least one embodiment, in an aspect, the method additionally can comprise identifying the serogroup of the infecting *P. multocida* strain, the serogroup being selected from the group consisting of serogroup A, B, D, E, and F, and the vaccine being prepared using a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, from the same or another *P. multocida* strain belonging to the selected serogroup.

[0098] In another aspect, the present disclosure provides, in accordance with the teachings herein, in at least one embodiment, a method for preparing a veterinary vaccine formulation comprising a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, the method comprising:

[0099] (a) providing a chimeric nucleic acid sequence comprising as operably linked components:

[0100] (i) a nucleic acid sequence encoding a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof; and

[0101] (ii) one or more nucleic acid sequences capable of controlling expression of the nucleic acid sequence encoding the PmSLP protein, or an immunogenically equivalent portion thereof in a host cell;

[0102] (b) introducing the chimeric nucleic acid sequence into a host cell;

[0103] (c) growing the host cell to produce the *P. multocida* PmSLP protein or the immunogenically equivalent portion thereof; and

[0104] (d) recovering the *P. multocida* PmSLP protein or the immunogenically equivalent portion thereof; and

[0105] (e) formulating the *P. multocida* PmSLP protein or the immunogenically equivalent portion thereof together with a veterinary pharmaceutically acceptable adjuvant to form a veterinary vaccine formulation comprising an effective amount of the *P. multocida* PmSLP protein or the immunogenically equivalent portion thereof to treat a food production animal susceptible to *P. multocida* infection.

[0106] In at least one embodiment, in an aspect, the nucleic acid sequence can be a nucleic acid sequence selected from the group of nucleic acid sequences consisting of:

[0107] (a) SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID. NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID. NO: 19, SEQ.ID. NO: 21, SEQ.ID. NO: 23, SEQ.ID. NO: 25, SEQ.ID. NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ. ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ. ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96;

- [0108] (b) a nucleic acid sequence having at least 70% identity with any one of the nucleic acid sequences of (a);
- [0109] (c) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a) but for the degeneration of the genetic code;
- [0110] (d) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);
- [0111] (e) a chimeric nucleic acid obtained by a fusion between at least two nucleic acid sequences of (a), (b), (c), and (d), or a portion thereof;
- [0112] (f) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);
- [0113] (g) a nucleic acid sequence encoding a polypeptide having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;
- [0114] (h) a nucleic acid sequence that encodes a functional variant of any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereto; and
- [0115] (i) a nucleic acid sequence that hybridizes under stringent conditions to any one of the nucleic acid sequences set forth in (a), (b), (c), (d), (e), (f), (g), or (h).
- [0116] In another aspect, the present disclosure provides, in accordance with the teachings herein, in at least one embodiment, an expression vector comprising:
- [0117] (a) a nucleic acid sequence encoding a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof; and
- [0118] (b) a nucleic acid sequence capable of controlling expression of the nucleic acid sequence encoding the *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof in a host cell.
- [0119] In at least one embodiment, in an aspect, the nucleic acid sequence can be a nucleic acid sequence selected from the group of nucleic acid sequences consisting of:
- [0120] (a) SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID. NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID. NO: 19, SEQ.ID. NO: 21, SEQ.ID. NO: 23, SEQ.ID. NO: 25, SEQ.ID. NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ. ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ. ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96;
- [0121] (b) a nucleic acid sequence having at least 70% identity with any one of the nucleic acid sequences of (a);
- [0122] (c) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a) but for the degeneration of the genetic code;
- [0123] (d) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);
- [0124] (e) a chimeric nucleic acid obtained by a fusion between any nucleic acid sequence of (a), (b), (c), and (d) or portion thereof;
- [0125] (f) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);
- [0126] (g) a nucleic acid sequence encoding a polypeptide having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;
- [0127] (h) a nucleic acid sequence that encodes a functional variant of any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;

SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereto; and

[0128] (i) a nucleic acid sequence that hybridizes under stringent conditions to any one of the nucleic acid sequences set forth in (a), (b), (c), (d), (e), (f), (g), or (h).

[0129] In another aspect, the present disclosure provides, in accordance with the teachings herein, in at least one embodiment, a host cell comprising a chimeric nucleic acid comprising:

[0130] (a) a nucleic acid sequence encoding a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof; and

[0131] (b) a nucleic acid sequence capable of controlling expression of the nucleic acid sequence encoding the *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof in a host cell.

[0132] In at least one embodiment, in an aspect, the nucleic acid sequence can be a nucleic acid sequence selected from the nucleic acid sequences consisting of:

[0133] (a) SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID NO: 19, SEQ.ID NO: 21, SEQ.ID NO: 23, SEQ.ID NO: 25, SEQ.ID NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ.ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ.ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96;

[0134] (b) a nucleic acid sequence having at least 70% identity with any one of the nucleic acid sequences of (a);

[0135] (c) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a) but for the degeneration of the genetic code;

[0136] (d) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

[0137] (e) a chimeric nucleic acid obtained by a fusion between any nucleic acid sequence of (a), (b), (c), and (d) or portion thereof;

[0138] (f) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

[0139] (g) a nucleic acid sequence encoding a polypeptide having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereto; and

SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;

[0140] (h) a nucleic acid sequence that encodes a functional variant of any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereto; and

[0141] (i) a nucleic acid sequence that hybridizes under stringent conditions to any one of the nucleic acid sequences set forth in (a), (b), (c), (d), (e), (f), (g), or (h).

[0142] In another aspect, the present disclosure provides, in accordance with the teachings herein, in at least one embodiment, a use of a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, to prepare a veterinary vaccine formulation comprising the P protein or an immunogenically equivalent portion thereof together with a veterinary pharmaceutically acceptable adjuvant.

[0143] Other features and advantages will become apparent from the following detailed description. It should be understood, however, that the detailed description, while indicating preferred implementations of the disclosure, are given by way of illustration only, since various changes and modifications within the spirit and scope of the disclosure will become apparent to those of skill in the art from the detailed description.

#### BRIEF DESCRIPTION OF THE DRAWINGS

[0144] The disclosure is in the hereinafter provided paragraphs described, by way of example, in relation to the attached figures. The figures provided herein are provided for a better understanding of the example embodiments and to show more clearly how the various embodiments may be carried into effect. The figures are not intended to limit the present disclosure.

[0145] FIGS. 1A, 1B, 1C, and 1D depict certain aspects of an example production and purification workflow for recombinant PmSLP proteins and example analytical data and results obtained during different steps in the performance of an example process for the purification of PmSLP-3. FIG. 1A is a flowchart showing a schematic workflow for the purification of recombinant PmSLP. FIG. 1B is a photographic image of a sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) gel in which sample material collected at different stages (1-6) of nickel nitrilotriacetic acid (NTA) purification of his-tagged PmSLP-3 (SEQ.ID NO: 12) from *E. coli* lysate are shown. FIG. 1C is a S75 gel filtration chromatogram of size exclusion chromatography after removal of the poly-histidine tag of PmSLP-3

(SEQ.ID NO: 14). FIG. 1D is a photographic image of an SDS-PAGE gel of purified PmSLP-3 after the performance of a polishing step with the MonoQ. It is noted that PmSLP-3 migrates in the gel at approximately 35 kDa after tag removal.

[0146] FIG. 2 is a phylogenetic tree of PmSLP protein sequences collected from a certain local collection of PmSLP sequences combined with publicly available sequences from online databases, and certain information related to the phylogenetic tree. Annotations regarding host species, confirmed disease status, geographical region, and serotype, for each PmSLP variant, are based on information available in the National Center for Biotechnology Information (NCBI) BioSample database, literature searches and genomic sequence analysis. Black circles on the phylogenetic branches of the tree indicate sequences originating from bovine species; small light grey shaded dots represent other hosts. Further depicted, peripheral to the phylogenetic tree, are four ring structures, representing: (1) host (species), (2) disease, (3) (geographical) region, and (4) capsule. Each ring structure is constituted of multiple rectangular pieces, each corresponding with a single PmSLP variant of the phylogenetic tree. Thus, moving directly outwardly from a specific selected rectangular piece on the inner most ring structure, representing a specific PmSLP variant sequence, are: (1) host species (the selected rectangular piece of the inner ring structure, for example, rectangular piece (a)); (2) disease (the rectangular piece moving directly outward and immediately adjacent to the piece selected under (1), for example, rectangular piece (b)); (3) geographic region (the rectangular piece moving further directly outward and immediately adjacent to the piece identified under (2), for example, rectangular piece (c)); and (4) capsule (the rectangular piece moving further directly outward and immediately adjacent to the piece identified under (3), for example, rectangular piece (d)). Grey scale indicators for the rectangular pieces are as follows, in the innermost ring structure, representing host species: black, bovine species (including rectangular piece (a)); hatched, porcine species; intermediate grey shade, avian species; light grey shade, other species; and white, missing. For the ring structure immediately peripheral relative to the most centrally positioned ring, representing disease, grey scale indicators for the rectangular pieces are as follows: black, bovine hemorrhagic septicemia (HS); intermediate grey shade, bovine respiratory disease (BRD) (including rectangular piece (b)); and white, disease status unconfirmed/unknown. For the ring structure immediately central relative to the most peripherally positioned ring, representing the geographical region from which the samples were obtained, grey scale indicators for the rectangular pieces are as follows: black, North America; intermediate grey shade, Asia; light grey shade, Europe (including rectangular piece (c)); and white, unknown region. For the most peripherally positioned ring structure, indicating the capsular serogroup of *P. multocida* (where known), grey scale indicators are as follows: black, serogroup A (including rectangular piece (d)); hatched pattern, serogroup B; intermediate grey shade, serogroup D; light grey shade, serogroup F; and white, untypable. Thus, the example selected PmSLP sequence corresponding with example rectangular pieces (a), (b), (c), (d) corresponds with a bovine PmSLP isolated from a *P. multocida* strain causing BRD in Europe, the *P. multocida* strain having serogroup A. It is noted that the phylogenetic tree of PmSLP variants can

be seen to separate into five phylogenetic clusters (PmSLP-1, PmSLP-2, PmSLP-3, and PmSLP-4.1, and PmSLP-4.2).

[0147] FIG. 3 is a graph depicting results obtained in the performance of a certain experiment, notably an experiment to evaluate antibody responses in mice having been administered a PmSLP vaccine formulation. In the graph endpoint IgG titre is plotted as a function of time. Serum IgG titre from mice having received 2 doses of vaccine was measured in serum samples collected over a 26-week period. Data points in the graph represent mean, error bars depict standard error. The dotted line at the 8,000 endpoint IgG titre signifies the limit of detection, which is the lowest serum dilution assayed. The IgG titre remained stable for the entire duration of the experiment and none of the groups showed any significant signs of waning. The experimental results demonstrate that long-lived antibody responses can be elicited using PmSLP-1 (SEQ.ID NO: 14) containing vaccine formulations.

[0148] FIGS. 4A, 4B, 4C, 4D, and 4E are further graphs depicting results obtained in the performance of certain experiments, notably an experiment to evaluate immune responses in mice having been administered a PmSLP vaccine formulation. In this example experiment, the efficacy of a PmSLP-1 (SEQ.ID NO: 14) vaccine formulation was evaluated against a bovine respiratory disease (BRD) isolate of *P. multocida* strain H246 that harbours a pmSLP gene from the same phylogenetic cluster. The graph shown in FIG. 4A depicts the percentage survival as a function of time, notably the percentage survival of mice after infection with *P. multocida* BRD strain H246 (the confirmed sequence of the PmSLP in this strain is defined in SEQ.ID NO: 22). PmSLP-1 vaccinated mice were 100% protected. The graph shown in FIG. 4B depicts clinical score as a function of time, notably the clinical score of mice immunized with PmSLP-1 vaccine separated by individual animal. The graph shown in FIG. 4C depicts clinical score as a function of time, notably the clinical score of mice immunized with adjuvant only separated by individual animal. The graph shown in FIG. 4D shows clinical score as a function of time, notably the mean clinical score of mice from both groups, error bars depict standard error. For FIGS. 4B, 4C, and 4D, a clinical score cut off of 10 is considered the humane endpoint at which point animals are euthanized. The graph shown in FIG. 4E shows bacterial recovery as a function of time, notably bacterial recovery from tail vein bleeds during the infection separated by individual animal. The experimental results demonstrate PmSLP vaccines can be efficacious against relevant bovine *P. multocida* disease isolates in an acute mouse infection model.

[0149] FIGS. 5A and 5B are further graphs depicting results obtained in the performance of certain experiments, notably an experiment to evaluate the immune response in mice having been administered a PmSLP vaccine formulation. Serum samples were obtained from mice immunized with two doses of either PmSLP-1 (SEQ.ID NO: 14) vaccine or adjuvant prior to being challenged. The graph shown in FIG. 5A depicts  $\alpha$ -PmSLP-1 IgG titre against the purified antigen as measured by protein ELISA. The graph shown in FIG. 5B depicts  $\alpha$ -PmSLP-1 IgG titre against whole bacteria as measured by heat inactivated whole cell ELISA. *P. multocida* BRD strain H246 (containing a PmSLP defined in SEQ.ID NO: 22, which harbours a pmSLP gene from the same phylogenetic cluster as the vaccine antigen was used. For both FIG. 5A and FIG. 5B, individual points depict

individual animals. Bars depict mean, error bars depict standard error. The experimental results demonstrate that  $\alpha$ -PmSLP-1 antibodies elicited in vaccinated mice can bind purified antigen as well as the antigen on the bacterial surface.

[0150] FIGS. 6A, 6B, 6C, 6D, and 6E are further graphs depicting results obtained in the performance of certain experiments, notably an experiment to evaluate the immune response in mice having been administered a PmSLP vaccine formulation. In this example, the efficacy of a PmSLP-3 (SEQ.ID NO: 20) vaccine was evaluated against a porcine disease isolate that harbours a pmSLP gene from the same phylogenetic cluster. The graph shown in FIG. 6A depicts percentage survival as a function of time, notably the percentage survival of mice after infection with *P. multocida* porcine strain H229 (containing a PmSLP with the sequence defined in SEQ.ID NO: 24). PmSLP-3 vaccinated mice were 100% protected. The graph shown in FIG. 6B depicts the clinical score as a function of time, notably the clinical score of mice immunized with PmSLP-3 vaccine separated by individual animal. The graph shown in FIG. 6C depicts the clinical score as a function of time, notably the clinical score of mice immunized with adjuvant only separated by individual animal. The graph shown in FIG. 6D depicts the clinical score as a function of time, notably the mean clinical score of mice from both groups, error bars depict standard error. For FIGS. 6B, 6C, and 6D, a clinical score cut off of 10 is considered the humane endpoint at which point animals are euthanized. The graph shown in FIG. 6E depicts bacterial recovery as a function of time, notably bacterial recovery from tail vein bleeds during the infection separated by individual animal. The experimental results demonstrate that PmSLP containing vaccines can be efficacious against relevant porcine *P. multocida* disease isolates in an acute mouse infection model.

[0151] FIGS. 7A and 7B are further graphs depicting results obtained in the performance of certain experiments, notably an experiment to evaluate the immune response in mice having been administered a PmSLP vaccine formulation. Serum samples were obtained from mice immunized with two doses of either PmSLP-3 (SEQ.ID NO: 20) vaccine or adjuvant prior to being challenged. The graph shown in FIG. 7A depicts  $\alpha$ -PmSLP-3 IgG titre against the purified antigen as measured by protein ELISA. The graph shown in FIG. 7B depicts  $\alpha$ -PmSLP-3 IgG titre against whole bacteria as measured by heat inactivated whole cell ELISA. *P. multocida* porcine isolate of *P. multocida* strain H229, which harbours a pmSLP gene from the same phylogenetic cluster as the vaccine antigen was used (the confirmed sequence of the PmSLP in this strain is defined in SEQ.ID NO: 24). For both FIG. 7A and FIG. 7B, individual points depict individual animals. Bars depict mean, error bars depict standard error. The experimental results demonstrate that  $\alpha$ -PmSLP-3 antibodies elicited in vaccinated mice can bind purified antigen as well as the antigen on the bacterial surface.

[0152] FIGS. 8A and 8B are further graphs depicting results obtained in the performance of certain experiments, notably an experiment to evaluate the stability of a PmSLP polypeptide. The intrinsic fluorescence given off by tryptophan and tyrosine residues (Ratio 350 nm/330 nm) (graphs shown in FIG. 8A) was measured to generate thermal profiles and calculate the thermal inflection temperatures (Ti) (graph shown in FIG. 8B) for PmSLP-1 protein samples stored under the indicated storage conditions. The results

demonstrate that purified PmSLP-3 protein (SEQ.ID NO: 20) can be stable under various storage conditions after lyophilization for one year.

[0153] FIGS. 9A, 9B, 9C, 9D, and 9E are further graphs depicting results obtained in the performance of certain experiments, notably an experiment to evaluate the protection from lethal challenge in mice having been administered PmSLP vaccine formulations. The graph shown in FIG. 9A depicts the percentage survival as a function of time, notably the percentage survival of mice after infection with antigen-matched *P. multocida* porcine strain H229 (the confirmed sequence of the PmSLP of this strain is defined in SEQ.ID NO: 24) wherein all mice that received PmSLP-3 vaccine formulations were fully protected from lethal challenge. The graphs shown in FIGS. 9B, 9C, 9D, and 9E show the clinical score for individual mice as a function of time, notably the clinical scores of mice immunized with Adjuvant, Vaccine 1 (freshly formulated vaccine with protein stored at -80° C. until formulation), Vaccine 2 (freshly formulated vaccine with lyophilized protein stored at 4° C. until formulation), and Vaccine 3 (formulated vaccine prepared prior to dose 1 and stored at 4° C. until dose 2) respectively. Each line depicts the clinical score of an individual mouse over the duration of the experimental challenge with clinical monitoring performed at multiple timepoints over the 36 hours post infection. The dotted line at clinical score 10 depicts clinical score cut off which is considered the humane endpoint at which point animals are euthanized. The experimental results demonstrate that PmSLP-3 (SEQ.ID NO: 20) vaccine preparations, stored under various conditions, can be efficacious in a mouse model.

[0154] FIG. 10 is a further graph depicting results obtained in the performance of certain experiments, notably an experiment to evaluate the immune response in a ruminant (bovine) species having been administered a PmSLP vaccine formulation. In this example, Zebu cattle were immunized sub-cutaneously with either PmSLP-1 (SEQ.ID NO: 14) vaccine or adjuvant. Serum samples obtained at baseline or 2-3 weeks after the indicated dose and assayed using protein-based ELISA. Data points represent individual animal, bars represent the mean  $\alpha$ -PmSLP-1 IgG titre, error bars represent standard error. The experimental results demonstrate that a PmSLP vaccine can be immunogenic in an animal host species that is relevant in the food production industry and affected by *P. multocida* infections.

[0155] FIG. 11 is a further graph depicting results obtained in the performance of certain experiments, notably an experiment to evaluate the immune response in a ruminant (bovine species) having been administered a PmSLP vaccine formulation. In this example, beef cattle were immunized via intramuscular route with either PmSLP-1 (SEQ.ID NO: 14) vaccine or adjuvant. Serum samples obtained at baseline or 2-3 weeks after the indicated dose and assayed using protein-based ELISA. Data points represent individual animal, bars represent the mean  $\alpha$ -PmSLP-1 IgG titre, error bars represent standard error. The experimental results demonstrate that a PmSLP vaccine can be immunogenic in an animal host species that is relevant in the food production industry and affected by *P. multocida* infections.

[0156] FIGS. 12A, 12B, and 12C are further graphs depicting results obtained in the performance of certain experiments, notably an experiment to evaluate the immune response in a ruminant (bovine) species having been administered a PmSLP vaccine formulation. In this example, zebu

cattle were immunized sub-cutaneously with PmSLP-3 (SEQ.ID NO: 20) formulated with two different adjuvants in a prime-boost schedule. The graph shown in FIG. 12A demonstrates serum samples obtained at baseline, prior to the booster dose, and prior to challenge and assayed using protein-based ELISA. Data points represent individual animals, bars represent the mean  $\alpha$ -PmSLP-3 IgG titre, and error bars represent the standard error. The graph shown in FIG. 12B shows animal survival as a function of time, notably animal survival following lethal challenge. The graph shown in FIG. 12C documents any local reactogenicity that was evaluated following administration of either vaccine dose. The example experimental results demonstrate that a PmSLP vaccine can be immunogenic and safe in an animal host species that is relevant in the food production industry and affected by *P. multocida* infections, as well as that those vaccine formulations can be protective against experimental challenge of a lethal dose of *P. multocida*.

[0157] FIGS. 13A, 13B, 13C, 13D, 13E, 13F, 13G, and 13H are further graphs depicting results obtained in the performance of a certain experiment, notably an experiment to evaluate a PmSLP vaccine administered to ruminant (bovine) animals. The graphs show, in particular, the assessment results of multiple clinical parameters which were tracked during the course of the experiment. The graph shown in FIG. 13A depicts a plot of rectal temperature as a function of time in animals having been administered an IVP 1 vaccine (containing PmSLP-2), an autogenous vaccine (positive control), and a saline solution (negative control) following challenge with a pathogenic *P. multocida* strain. FIG. 13B depicts multiple bar graphs of animal demeanor scores at different time points in the experiment (day 34 (D34)-day 42 (D42)) in animals having been administered an IVP 1 vaccine (containing PmSLP-2), an autogenous vaccine (positive control), and a saline solution (negative control) following challenge with a pathogenic *P. multocida* strain. FIG. 13C depicts multiple bar graphs of nasal discharge scores at different time points in the experiment (day 34 (D34)-day 42 (D42)) in animals having been administered an IVP 1 vaccine (containing PmSLP-2), an autogenous vaccine (positive control), and a saline solution (negative control) following challenge with a pathogenic *P. multocida* strain. FIG. 13D depicts multiple bar graphs of cough scores at different time points in the experiment (day 34 (D34)-day 42 (D42)) in animals having been administered an IVP 1 vaccine (containing PmSLP-2), an autogenous vaccine (positive control), and a saline solution (negative control) following challenge with a pathogenic *P. multocida* strain. FIG. 13E depicts multiple bar graphs of respiration scores at different time points in the experiment (day 34 (D34)-day 42 (D42)) in animals having been administered an IVP 1 vaccine (containing PmSLP-2), an autogenous vaccine (positive control), and a saline solution (negative control) following challenge with a pathogenic *P. multocida* strain. FIG. 13F depicts a plot of total clinical score as a function of time in animals having been administered an IVP 1 vaccine (containing PmSLP-2), an autogenous vaccine (positive control), and a saline solution (negative control) following challenge with a pathogenic *P. multocida* strain. FIG. 13G depicts a plot of lung lesion scores in animals having been administered an IVP 1 vaccine (containing PmSLP-2), an autogenous vaccine (positive control), and a saline solution (negative control) following challenge with a pathogenic *P. multocida* strain. FIG. 13H

depicts a plot of anti-body titre at two different experimental time points (Day 7 (D-7) (prior to vaccination), and day 35 (D35) (day of challenge)) in animals having been administered an IVP 1 vaccine (containing PmSLP-2), an autogenous vaccine (positive control), and a saline solution (negative control) following challenge with a pathogenic *P. multocida* strain. The example experimental results further demonstrate that a PmSLP vaccine can be immunogenic and safe in an animal host species that is relevant in the food production industry and affected by *P. multocida* infections, as well as that those vaccine formulations can be protective against experimental challenge with a dose of *P. multocida*. [0158] The figures together with the following detailed description make apparent to those skilled in the art how the disclosure may be implemented in practice.

#### DETAILED DESCRIPTION

[0159] Various compositions, methods, or processes will be described below to provide an example of an embodiment of each claimed subject matter. No embodiment described below limits any claimed subject matter and any claimed subject matter may cover processes, compositions or methods that differ from those described below. The claimed subject matter is not limited to compositions, processes or methods having all of the features of any one composition, method or process described below or to features common to multiple or all of the compositions, methods or processes described below. It is possible that a composition, method, or process described below is not an embodiment of any claimed subject matter. Any subject matter disclosed in a composition, method, or process described below that is not claimed in this document may be the subject matter of another protective instrument, for example, a continuing patent application, and the applicant(s), inventor(s) or owner(s) do not intend to abandon, disclaim or dedicate to the public any such subject matter by its disclosure in this document.

[0160] As used herein and in the claims, the singular forms, such as "a", "an" and "the" include the plural reference and vice versa unless the context clearly indicates otherwise. Throughout this specification, unless otherwise indicated, "comprise," "comprises" and "comprising" are used inclusively rather than exclusively, so that a stated integer or group of integers may include one or more other non-stated integers or groups of integers. The term "or" is inclusive unless modified, for example, by "either".

[0161] When ranges are used herein for physical properties, such as molecular weight, or chemical properties, such as chemical formulae, all combinations and sub-combinations of ranges and specific embodiments therein are intended to be included. Other than in the operating examples, or where otherwise indicated, all numbers expressing quantities of ingredients or reaction conditions used herein should be understood as modified in all instances by the term "about." The term "about" when referring to a number or a numerical range means that the number or numerical range referred to is an approximation within experimental variability (or within statistical experimental error), and thus the number or numerical range may vary between 1% and 15% of the stated number or numerical range, as will be readily recognized by context. Furthermore, any range of values described herein is intended to specifically include the limiting values of the range, and any intermediate value or sub-range within the given range, and

all such intermediate values and sub-ranges are individually and specifically disclosed (e.g., a range of 1 to 5 includes 1, 1.5, 2, 2.75, 3, 3.90, 4, and 5). Similarly, other terms of degree such as “substantially” and “approximately” as used herein mean a reasonable amount of deviation of the modified term such that the end result is not significantly changed. These terms of degree should be construed as including a deviation of the modified term if this deviation would not negate the meaning of the term it modifies.

[0162] Unless otherwise defined, scientific and technical terms used in connection with the formulations described herein shall have the meanings that are commonly understood by those of ordinary skill in the art. The terminology used herein is for the purpose of describing particular embodiments only and is not intended to limit the scope of the present invention, which is defined solely by the claims.

[0163] All publications, patents and patent applications are herein incorporated by reference in their entirety to the same extent as if each individual publication, patent, or patent application was specifically and individually indicated to be incorporated by reference in its entirety.

#### Terms and Definitions

[0164] The terms “nucleic acid”, or “nucleic acid sequence”, as used herein, refer to a sequence of nucleoside or nucleotide monomers, consisting of naturally occurring bases, sugars and intersugar (backbone) linkages. The term also includes modified or substituted sequences comprising non-naturally occurring monomers or portions thereof. The nucleic acids of the present disclosure may be deoxyribonucleic nucleic acids (DNA) or ribonucleic acids (RNA) and may include naturally occurring bases including adenine, guanine, cytosine, thymidine, and uracil. The nucleic acids may also contain modified bases. Examples of such modified bases include aza and deaza adenine, guanine, cytosine, thymidine and uracil, and xanthine and hypoxanthine. A sequence of nucleotide or nucleoside monomers may be referred to as a polynucleotide sequence, nucleic acid sequence, a nucleotide sequence, or a nucleoside sequence.

[0165] The terms “polypeptide” and “protein”, as may be used interchangeably herein, in conjunction with a reference SEQ.ID NO, refer to any and all polypeptides and proteins comprising a sequence of amino acid residues which is (i) substantially identical to the amino acid sequence constituting the polypeptide having such reference SEQ.ID NO, or (ii) encoded by a nucleic acid sequence capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding the polypeptide having such reference SEQ.ID NO, but for the use of synonymous codons. A sequence of amino acid residues may be referred to as an amino acid sequence, or polypeptide sequence.

[0166] The terms “nucleic acid sequence encoding a polypeptide” and “nucleic acid sequence encoding a protein”, as used herein in conjunction with a reference SEQ.ID NO, refer to any and all nucleic acid sequences encoding a polypeptide or protein having such reference SEQ.ID NO. Nucleic acid sequences encoding a polypeptide, in conjunction with a reference SEQ.ID NO, further include any and all nucleic acid sequences which (i) encode polypeptides that are substantially identical to the polypeptide having such reference SEQ.ID NO; or (ii) hybridize to any nucleic acid sequences encoding polypeptides having such reference SEQ.ID NO under at least moderately stringent hybridiza-

tion conditions or which would hybridize thereto under at least moderately stringent conditions but for the use of synonymous codons.

[0167] The terms “nucleic acid sequence encoding PmSLP”, and “nucleic acid sequence encoding a “PmSLP polypeptide”, “nucleic acid sequence encoding a PmSLP protein” as may be used interchangeably herein, refer to any and all nucleic acid sequences encoding a PmSLP polypeptide, including, for example, SEQ.ID NO: 1. Nucleic acid sequences encoding a PmSLP polypeptide further include any and all nucleic acid sequences which (i) encode polypeptides that are substantially identical to the PmSLP polypeptide sequences set forth herein; or (ii) hybridize to any PmSLP nucleic acid sequences set forth herein under at least moderately stringent hybridization conditions or which would hybridize thereto under at least moderately stringent conditions but for the use of synonymous codons.

[0168] The terms “PmSLP protein” or “PmSLP polypeptide”, as may be used herein, interchangeably refer to any and all protein comprising a sequence of amino acid residues which is (i) substantially identical to the amino acid sequences constituting any PmSLP polypeptide set forth herein, including, for example, SEQ.ID NO: 2, or (ii) encoded by a nucleic acid sequence capable of hybridizing under at least moderately stringent conditions to any nucleic acid sequence encoding any PmSLP protein set forth herein, but for the use of synonymous codons. PmSLP proteins may also be numbered in order to facilitate distinguishing different PmSLP proteins referred to herein, e.g., PmSLP-1, PmSLP-2, PmSLP-3, and so on.

[0169] By the term “substantially identical” it is meant that two amino acid sequences preferably are at least 70% identical, and more preferably are at least 85% or 90% identical, and most preferably at least 95% identical, for example 96%, 97%, 98%, 99%, 99.5%, 99.6%, 99.7%, 99.8%, or 99.9% identical. In order to determine the percentage of identity between two amino acid sequences the amino acid sequences of such two sequences are aligned, using for example the alignment method of Needleman and Wunsch (J. Mol. Biol., 1970, 48: 443), as revised by Smith and Waterman (Adv. Appl. Math., 1981, 2: 482) so that the highest order match is obtained between the two sequences and the number of identical amino acids is determined between the two sequences. Methods to calculate the percentage identity between two amino acid sequences are generally well recognized and include, for example, those described by Carillo and Lipton (SIAM J. Applied Math., 1988, 48:1073) and those described in Computational Molecular Biology, Lesk, e.d. Oxford University Press, New York, 1988, Biocomputing: Informatics and Genomics Projects. Generally, computer programs will be employed for such calculations. Computer programs that may be used in this regard include, but are not limited to, GCG (Devereux et al., Nucleic Acids Res., 1984, 12: 387) BLASTP, BLASTN and FASTA (Altschul et al., J. Mol. Biol., 1990: 215:403). A particularly preferred method for determining the percentage identity between two polypeptides involves the Clustal W algorithm (Thompson, J. D., Higgins, D. G. and Gibson T. J., 1994, Nucleic Acid Res 22(22): 4673-4680 together with the BLOSUM 62 scoring matrix (Henikoff S & Henikoff, J G, 1992, Proc. Natl. Acad. Sci. USA 89: 10915-10919 using a gap opening penalty of 10 and a gap extension penalty of 0.1, so that the highest order match

obtained between two sequences wherein at least 50% of the total length of the two sequences is involved in the alignment.

[0170] By “at least moderately stringent hybridization conditions” it is meant that conditions are selected which promote selective hybridization between two complementary nucleic acid molecules in solution. Hybridization may occur to all or a portion of a nucleic acid sequence molecule. The hybridizing portion is typically at least 15 (e.g., 20, 25, 30, 40 or 50) nucleotides in length. Those skilled in the art will recognize that the stability of a nucleic acid duplex, or hybrids, is determined by the Tm, which in sodium containing buffers is a function of the sodium ion concentration and temperature ( $T_m = 81.5^\circ C - 16.6 (\log 10 [Na^+]) + 0.41(G+C) - 600/I$ , or similar equation). Accordingly, the parameters in the wash conditions that determine hybrid stability are sodium ion concentration and temperature. In order to identify molecules that are similar, but not identical, to a known nucleic acid molecule a 1% mismatch may be assumed to result in about a  $1^\circ C$ . decrease in Tm, for example if nucleic acid molecules are sought that have a >95% identity, the final wash temperature will be reduced by about  $5^\circ C$ . Based on these considerations those skilled in the art will be able to readily select appropriate hybridization conditions. In preferred embodiments, stringent hybridization conditions are selected. By way of example the following conditions may be employed to achieve stringent hybridization: hybridization at 5× sodium chloride/sodium citrate (SSC)/5×Denhardt's solution/1.0% SDS at Tm (based on the above equation)- $5^\circ C$ , followed by a wash of 0.2×SSC/0.1% SDS at  $60^\circ C$ . Moderately stringent hybridization conditions include a washing step in 3×SSC at  $42^\circ C$ . It is understood however that equivalent stringencies may be achieved using alternative buffers, salts, and temperatures. Additional guidance regarding hybridization conditions may be found in: Current Protocols in Molecular Biology, John Wiley & Sons, N.Y., 1989, 6.3.1.-6.3.6 and in: Sambrook et al., Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 1989, Vol. 3.

[0171] The term “functional variant”, as used herein in reference to polynucleotides or polypeptides, refers to polynucleotides or polypeptides capable of performing the same function as a noted reference polynucleotide or polypeptide. Thus, for example, a functional variant of the polypeptide set forth in SEQ.ID NO: 2, refers to a polypeptide capable of performing the same function as the polypeptide set forth in SEQ.ID NO: 2. Functional variants include modified a polypeptide wherein, relative to a noted reference polypeptide, the modification includes a substitution, deletion, or addition of one or more amino acids. In some embodiments, substitutions are those that result in a replacement of one amino acid with an amino acid having similar characteristics. Such substitutions include, without limitation (i) glutamic acid and aspartic acid; (ii) alanine, serine, and threonine; (iii) isoleucine, leucine, and valine, (iv) asparagine and glutamine, and (v) tryptophan, tyrosine, and phenylalanine.

[0172] The term “chimeric”, as used herein in the context of nucleic acids, refers to at least two linked nucleic acids which are not naturally linked. Chimeric nucleic acids include linked nucleic acids of different natural origins. For example, a nucleic acid constituting a microbial promoter linked to a nucleic acid encoding a plant polypeptide is considered chimeric. Chimeric nucleic acids also may comprise nucleic acids of the same natural origin, provided they

are not naturally linked. For example, a nucleic acid constituting a promoter obtained from a particular cell-type may be linked to a nucleic acid encoding a polypeptide obtained from that same cell-type, but not normally linked to the nucleic acid constituting the promoter. Chimeric nucleic acids also include nucleic acids comprising any naturally occurring nucleic acids linked to any non-naturally occurring nucleic acids.

[0173] The term “phylogenetic cluster” refers to a group of evolutionary related polypeptide sequences. In order to determine whether two polypeptides belong to the same phylogenetic cluster, an evolutionary tree containing multiple branches (for example, at least 5, 7, 10, 15, or 20 branches), can be constructed using multiple more or less similar polypeptide sequences (for example, preferably at least 25, at least 50, at least 100, or at least 1,000, polypeptide sequences). Upon inspection of the phylogenetic tree, the evolutionary relationship of the polypeptide sequences can be evaluated. Polypeptides belonging to the same phylogenetic cluster are polypeptides located on a particular branch descended from a common ancestor on a phylogenetic tree. Those skilled in the art will be familiar with software programs to assist in the automated generation of phylogenetic trees based on polypeptide sequence input. Suitable phylogenetic tree construction software includes, for example, sequence alignment software such as MAFFT (v7.450) (Katoh, K. et al., 2002, Nucleic Acids Research, 30 (14), 3059-3066) which can, for example, be using the G-INS-I algorithm; evolutionary modeling software to identify an appropriate evolutionary model such as ProtTest (v3.4.2) (Darriba D, Taboada G L, Doallo R, Posada D. ProtTest 3: fast selection of best-fit models of protein evolution. Bioinformatics, 27:1164-1165, 2011); and phylogenetic tree assembly software such as PhyML (v3.3. 20190909) (Guindon S., et al., 2010, Systematic Biology, 59(3):307-21, 2010) and RAxML (Stamatakis, A. Bioinformatics, Volume 30, Issue 9, May 2014, Pages 1312-1313, doi.org/10.1093/bioinformatics/btu033). An example phylogenetic tree of PmSLP polypeptide sequences showing example phylogenetic clusters PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, and PmSLP-4.2 includes the phylogenetic tree shown in FIG. 2. Example phylogenetic cluster PmSLP-1 includes, for example, at least a PmSLP polypeptide sequence having SEQ.ID NO: 2. Example phylogenetic cluster PmSLP-2 includes, for example, at least a PmSLP polypeptide sequence having SEQ.ID NO: 4. Example phylogenetic cluster PmSLP-3 includes, for example, at least a PmSLP polypeptide sequence having SEQ.ID NO: 6. Example phylogenetic cluster PmSLP-4.1 includes, for example, at least a PmSLP polypeptide sequence having SEQ.ID NO: 8. Example phylogenetic cluster PmSLP-4.2 includes, for example, at least a PmSLP polypeptide sequence having SEQ.ID NO: 10.

[0174] The term “animal”, as used herein, refers to all species belonging to the kingdom Animalia, excluding humans.

[0175] The term “avian”, as used herein, refers to any animal species belonging to the class Aves, including, for example, poultry, such as chickens, turkeys, geese, ducks, and quails.

[0176] The term “bovine”, as used herein, refers to any animal species belonging to the subfamily Bovinae including, for example, cows, cattle, oxen, bison, and buffalo.

[0177] The term "porcine", as used herein, refers to any animal species belonging to the family Suidae including, for example, pigs, hogs, and boars.

[0178] The term "ruminant", as used herein, refers to herbivorous mammalian animals having a digestive system comprising multi-compartment stomach system, including typically a rumen, reticulum, omasum, and abomasum, capable of digesting plant materials through microbial fermentation processes. Ruminants include cows, cattle, oxen, goats, sheep, bison, and buffalo.

[0179] The term "food production animal", as used herein, refers to animals raised and farmed by humans for human food production. Food production animals include, without limitation, ruminant species, bovine species, porcine species, and avian species.

[0180] The terms "*Pasteurella multocida*" or "*P. multocida*", as used herein, refer to any bacteria belonging the bacterial species taxonomically classified as such and include any subspecies thereof, including *P. multocida* subspecies *multocida*, *P. multocida* subspecies *gallicida*, and *P. multocida* subspecies *septica*, and further include any *P. multocida* strains, variants, serogroups (including serogroups A, B, D, E and F), serotypes (including serotypes 1-16), or genotypes. It is noted that *P. multocida* strains may be referred to by serogroup and serotype. Thus, for example, a strain referred to as *P. multocida* A:3, denotes a *P. multocida* strain of serogroup A and serotype 3.

[0181] The term "effective amount", as used herein, refers to an amount of an active agent or veterinary pharmaceutical formulation, including a veterinary vaccine formulation, sufficient to induce a desired biological or therapeutic effect, including a prophylactic effect. Such effect can include an effect with respect to the signs, symptoms or causes of a disorder, or disease or any other desired alteration of a biological system. The effective amount can vary depending, for example, on the health condition, injury stage, disorder stage, or disease stage, of the animal being treated, timing of the administration, manner of the administration, age of the animal, size of the animal, and the like, all of which can be determined by those of skill in the art.

[0182] The term "immunologically equivalent", as used herein, refers to a molecule that is capable of eliciting a humoral immune response in the form of the production of native polyclonal antibodies in a subject animal when administered thereto, wherein the binding specificity to the native polyclonal antibodies is comparable to the specificity of native polyclonal antibodies produced when a reference molecule is administered to the subject animal. For example, immunologically equivalent portions of a reference full length PmSLP polypeptide include immunogenic portions of a PmSLP polypeptide which when administered to a subject animal elicit a humoral immune response in the form of the production of native antibodies with a specificity to a PmSLP polypeptide which is comparable to the binding specificity for a PmSLP polypeptide of native antibodies obtained when the reference full length PmSLP is administered to the animal. Immunologically equivalent portions of full length PmSLP polypeptides can vary in length and may, for example, include polypeptides comprising or consisting of at least 10, at least or up to 15, at least or up to 20, at least or up to 30, at least or up to 50, or at least or up to 60 consecutive amino acid residues which are identical to a portion of a PmSLP polypeptide. Furthermore, immunologically equivalent portions of full length PmSLP polypeptides

include polypeptides which are at least 90%, at least 95%, at least 96%, at least 97%, at least 98%, or at least 99%, at least 99.5%, at least 99.6%, at least 99.7%, at least 99.8%, at least 99.9% identical to a full length PmSLP polypeptide. To compare binding specificity between a reference molecule and an immunologically equivalent molecule a radioimmunoassay (RIA) may be used, and the extent of binding may be measured. The dissociation constant of an immunologically equivalent molecule is preferably at least 50%, at least 60%, at least 70%, at least 80%, at least 90%, or at least 95% of the dissociation constant of a reference molecule.

[0183] The term "cross-protective", as used herein, refers to a vaccine formulation capable of providing protection against infection by multiple strains (e.g., 2, 3, 4, 5, or more strains) of a pathogenic microbial organism, for example, strains belonging to multiple serogroups or serotypes. A cross-protective vaccine formulation may comprise multiple antigenic substances, or a single antigenic substance, for example, multiple immunogenic polypeptides or a single immunogenic polypeptide. To evaluate cross-protection, a vaccine formulation comprising an immunogenic substance obtained from a selected strain of a microbial organism, a PmSLP protein, for example, may be used to immunize a subject animal. The subject animal then may be exposed to (challenged with) another pathogenic strain of the pathogenic microbial organism, and the immunological response and the development of disease symptoms of the animal may be evaluated. In the event the infection results in the development of an improved immune response, or less severe or no disease symptoms in the infected animal than in an unvaccinated animal exposed to the same infection, the vaccine formulation can be said to be cross-protective.

[0184] The term "veterinary pharmaceutically acceptable", as used herein, refers to materials, including carriers, diluents, or auxiliary agent that are compatible with other materials in a veterinary pharmaceutical formulation, including a veterinary vaccine formulation, and within the scope of reasonable medical judgement suitable for use in contact with animals without excessive toxicity, allergic response, irritation, or other adverse response commensurate with a reasonable risk/benefit ratio.

[0185] The terms "treating" and "treatment", and the like, as used herein, are intended to mean obtaining a desirable physiological, pharmacological, or biological effect. The effect may result in the prevention (i.e., prophylactic treatment), inhibition, amelioration, attenuation, reversal of a sign, symptom or cause of a disorder, or disease, attributable to the disorder, or disease. Clinical evidence of the treatment may vary with the disorder, or disease, the animal, and the selected treatment. In the context of the treatment of an indication a physiological effect may include, for example, an improved respiratory capacity or lung function, reduced hemorrhaging, reduced mucoid nasal or oral discharge, improved rectal temperatures, improved animal demeanor, reduced coughing, or a reduction in lung lesions.

[0186] The term "respiratory disease", as used herein refers to the accepted veterinary medical definition of a respiratory disease and includes any disease involving invasion and colonization by *P. multocida* species of the respiratory tract, including the upper and lower respiratory tract of an animal, and includes, for example, BRD and HS.

[0187] The terms "bovine respiratory disease" or "BRD", as used herein, refer to the accepted medical veterinary

definition of bovine respiratory disease, and include, in general, a respiratory disease state in a bovine animal caused by a pathogenic *P. multocida* infection.

[0188] The terms “hemorrhagic septicemia” or “HS”, as used herein, refer to refer to the accepted medical veterinary definition of hemorrhagic septicemia, and include, in general, a respiratory disease state in a bovine animal caused by a pathogenic *P. multocida* infection.

[0189] The term “porcine atrophic rhinitis” or “PAR”, as used herein, refer to refer to the accepted medical veterinary definition of porcine atrophic rhinitis and includes, in general, a respiratory disease state in a porcine animal caused by a pathogenic *P. multocida* infection.

[0190] The term “pneumonic pasteurellosis”, as used herein, refers to the accepted medical veterinary definition of as used herein, refer to refer to the accepted medical veterinary definition of pneumonic pasteurellosis and includes, in general, a respiratory disease state in a porcine animal caused by a pathogenic *P. multocida* infection.

[0191] The term “fowl cholera”, as used herein, refers to refer to the accepted medical veterinary definition of fowl cholera, and includes, in general, a respiratory disease state in an avian animal caused by a pathogenic *P. multocida* infection.

[0192] The terms “vaccine”, “vaccine formulation”, “veterinary vaccine”, and “veterinary vaccine formulation” as used herein, refer to a veterinary pharmaceutically acceptable preparation that may be administered to an animal to induce a humoral immune response (including eliciting a soluble antibody response) and/or cell-mediated immune response (including eliciting a cytotoxic T lymphocyte (CTL) response).

[0193] The term “homologous protection”, as used herein, refers to protection conferred by a vaccine against infection by a strain of a microbial species, wherein the infecting strain possesses an antigen, for example a PmSLP protein antigen, which belongs to the same phylogenetic cluster as an antigen, for example, a PmSLP protein antigen, or an immunologically equivalent portion thereof, included in the vaccine formulation.

[0194] The term “heterologous protection”, as used herein, refers to protection conferred by a vaccine against infection by a strain of a microbial species, wherein the infecting strain possesses an antigen, for example a PmSLP protein antigen, which belongs to a different phylogenetic cluster as an antigen, for example, a PmSLP protein antigen, or an immunologically equivalent portion thereof, included in the vaccine formulation.

[0195] The terms “substantially pure” and “isolated”, as may be used interchangeably herein describe a compound, e.g., a polypeptide, which has been separated from components that naturally accompany it. Typically, a compound is substantially pure when at least 60%, more preferably at least 75%, more preferably at least 90%, 95%, 96%, 97%, or 98%, and most preferably at least 99% of the total material (by volume, by wet or dry weight, or by mole percent or mole fraction) in a sample is the compound of interest. Purity can be measured by any appropriate method, e.g., in the case of polypeptides, by chromatography, gel electrophoresis or HPLC analysis.

#### General Implementation

[0196] As hereinbefore mentioned, the present disclosure relates to veterinary vaccine formulations. In general, the

herein provided methods and compositions can be used to prevent or ameliorate *Pasteurella multocida* infections in food production animals, including ruminant animal species, bovine animal species, porcine animal species, and avian animal species. In this respect, the methods, and compositions of the present disclosure, in particular, may be used to treat bovine respiratory disease or hemorrhagic septicemia in bovine species, pneumonic pasteurellosis or progressive atrophic rhinitis in swine, or fowl cholera in poultry. The veterinary vaccine formulations of the present disclosure can provide long-term, effective protection against *P. multocida* infections.

[0197] The inventors have discovered that the veterinary vaccine formulations of the present disclosure are cross-protective and can provide protection to food production animals against infection by multiple *P. multocida* strains. Surprisingly, the veterinary vaccine formulations of the present disclosure can be cross-protective using a single immunogenic active agent.

[0198] Furthermore, the vaccine formulations of the present disclosure can provide long-term protection, with antibodies against the immunizing agent being detectable in the blood serum of a subject food production animal, for example, at least 26 weeks from administration of the vaccine formulation.

[0199] Furthermore, the vaccine formulations of the present disclosure involve the use of polypeptide-based immunogenic active agents, and as such, the compositions and methods of the present disclosure do not involve the use of live attenuated microbial species, and thus avoid infection risks associated with the use of live vaccines.

[0200] Furthermore, the vaccine formulations of the present disclosure can limit the administration of antibiotics to food production animals, and thus limit the development of antibiotic resistant microbial strains. In addition, some consumers have a preference for food products obtained from animals which have not been treated with antibiotics.

[0201] Furthermore, the polypeptide-based immunogenic active agents included in the vaccine formulations of the present disclosure may be prepared using a convenient recombinant production system, and the immunogenic active agents may be stably stored.

[0202] The present inventors have discovered, in particular, that proteins selected from a class of proteins known as PmSLP proteins may be used as immunogenic active agents in the formulation of veterinary vaccines to prevent or ameliorate *P. multocida* infections in food production animals. The PmSLP proteins can be selected and obtained from a *P. multocida* strain. The *P. multocida* strain from which the PmSLP protein is selected preferably is a *P. multocida* strain which belongs to the same phylogenetic cluster as the *P. multocida* strain causing the infection in the food production animal. Thus, the PmSLP protein does not need to be selected from the same *P. multocida* strain as the infecting *P. multocida* infecting strain provided however, said another strain belongs to the same phylogenetic cluster.

[0203] In what follows example embodiments of the compositions and methods of the present disclosure are described.

[0204] Thus, the present disclosure provides, in at least one aspect, and in at least one embodiment, a veterinary vaccine formulation for the prevention or amelioration of *P. multocida* infection in a food production animal susceptible to *P. multocida* infection, the vaccine formulation compris-

ing an effective amount of a PmSLP protein or an immunogenically equivalent portion thereof.

[0205] In another aspect, and in at least one other embodiment, the present disclosure further provides a method for treatment of a food production animal susceptible to *P. multocida* infection, the method comprising administering to the food production animal a veterinary vaccine formulation comprising a PmSLP protein or an immunogenically equivalent portion thereof, wherein the vaccine formulation is administered in an effective amount to prevent or ameliorate the *P. multocida* infection.

[0206] In general, according to an aspect, veterinary vaccine formulations comprising a selected PmSLP protein or an immunogenically equivalent portion thereof are prepared or obtained. These formulations are administered in effective amounts to a food production animal in need thereof. Thus, in what follows next suitable preparations comprising a selected PmSLP protein, or an immunogenically equivalent portion thereof, will be described, as well as methods of making a selected PmSLP protein, or an immunogenically equivalent portion thereof. Thereafter, veterinary vaccine formulations comprising a selected PmSLP protein or an immunogenically equivalent portion thereof, and methods of preparing veterinary vaccine formulations and administering the same to a food production animal in need thereof will be described.

[0207] Thus, initially, considering PmSLP protein preparations, in an aspect, preparations containing a selected PmSLP protein or an immunogenically equivalent portion thereof can be prepared biosynthetically using a host cell system. In this respect, an isolated nucleic acid encoding an amino acid sequence corresponding with a PmSLP protein or an immunogenically equivalent portion thereof can be introduced in host cells and expressed therein.

[0208] In general, any PmSLP protein may be used in accordance herewith. PmSLP proteins can be obtained from *P. multocida* bacteria, including any PmSLP comprising strain thereof, including any PmSLP comprising *P. multocida* strain belonging to any serogroup or serotype. In this respect, it is noted, as is known to those of skill in the art, that *P. multocida* strains may be classified as belonging to different serogroups and/or serotypes. Serogroups in this respect include serogroups A, B, D, E, and F, and serotypes include 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, and 16. When referring to different *P. multocida* strains, serogroups and serotypes may be referred to accordingly. For example, *P. multocida* strain A:3 can be classified as belonging to serogroup A and serotype 3, *P. multocida* strain E:2 strain can be classified as belonging to serogroup E and serotype 2, and so on. Thus, in accordance herewith the PmSLP protein can be a PmSLP protein obtained from a *P. multocida* strain selected from serogroup A, B, D, E, and F *P. multocida* strains. Furthermore, the PmSLP protein can be a PmSLP protein obtained from a *P. multocida* strain selected from serotype 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, and 16 *P. multocida* strains. Thus, it is to be understood that the PmSLP protein, in accordance herewith, can be selected from PmSLP proteins obtainable or obtained from a *P. multocida* strain belonging to any serogroup or any serotype, or any combination thereof.

[0209] According to an aspect, in an example embodiment, a nucleic acid sequence encoding a PmSLP protein may be selected, wherein such nucleic acid includes SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID NO: 7,

SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID NO: 19, SEQ.ID NO: 21, SEQ.ID NO: 23, SEQ.ID NO: 25, SEQ.ID NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ.ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ.ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96 set forth herein. Selected example PmSLP proteins include SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, which are polypeptides encoded by SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID NO: 19, SEQ.ID NO: 21, SEQ.ID NO: 23, SEQ.ID NO: 25, SEQ.ID NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ.ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ.ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96, respectively.

[0210] In some embodiments, the PmSLP protein can be a protein expressed by a nucleic acid sequence selected from the group of nucleic acid sequences consisting of

[0211] (a) SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID NO: 19, SEQ.ID NO: 21, SEQ.ID NO: 23, SEQ.ID NO: 25, SEQ.ID NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ.ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ.ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96;

[0212] (b) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a);

[0213] (c) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a) but for the degeneration of the genetic code;

[0214] (d) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

[0215] (e) a nucleic acid sequence encoding a polypeptide having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;

[0216] (f) a nucleic acid sequence that encodes a functional variant of any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof; and

[0217] (g) a nucleic acid sequence that hybridizes under stringent conditions to any one of the nucleic acid sequences set forth in (a), (b), (c), (d), (e) or (f).

[0218] PmSLP proteins that may be used in accordance herewith include naturally occurring PmSLP proteins, as well as PmSLP proteins that may have been modified. Modifications in this respect include modifications made to the amino acid sequence of a PmSLP polypeptide, including for example, a modification in one or more specific individual amino acids, which may be referred to as "site-directed mutations", such as for example a PmSLP protein having SEQ.ID NO: 65 and SEQ.ID NO: 67.

[0219] Further modifications that may be made to PmSLP proteins include modifications which diminish binding of the PmSLP protein to a native host protein, (i.e., a protein in a food production animal susceptible to *P. multocida* infection). Such diminished binding can generally be assessed by evaluating the affinity of a PmSLP protein for a native host protein. The affinity may be quantitatively evaluated by experimentally determining the dissociation constant (Kd) between the PmSLP protein and the native host protein. Thus, for example, in this respect, the Kd between a native PmSLP protein and a native host protein, for example between PmSLP-1 and bovine complement factor I, may be compared with the Kd between a modified PmSLP protein and the same native host protein. In general, the higher the Kd value the weaker the affinity of the PmSLP protein for the native host protein. In some embodiments, the Kd

between a modified PmSLP and a native host protein may exceed the Kd between the native non-modified PmSLP and the native host protein by a factor of at least 2x, at least 5x, at least 10x, at least 25x, at least 50x, at least 100x, at least 250x, or at least 500x. Techniques to determine the Kd between two proteins are well known to those of skill in the art and include, for example isothermal calorimetry, surface plasmon resonance and biolayer interferometry (see further, for example, Rich R. et al. 2007, Anal. Biochem 361: 1-6; Abdiche, Y. et al., 2008, Anal. Biochem. 377: 209-217; and Velazquez-Campoy, A. et al., 2004, Methods Mol. Biol. 261: 35-54).

[0220] Examples of PmSLP polypeptides that may be used in this respect include PmSLP polypeptides having SEQ.ID NO: 65 and SEQ.ID NO: 67 (encoded by nucleic acid sequences having SEQ.ID NO: 64 and SEQ.ID NO: 66, respectively). In this respect, the PmSLP polypeptides having SEQ.ID NO: 65, and SEQ.ID NO: 67 encode PmSLP-1 polypeptides (SEQ.ID NO: 2) comprising a V214D mutation (substitution of valine amino acid residue 214 by an aspartic acid amino acid residue), and E240A mutation (substitution of glutamic acid amino acid residue 240 by an alanine acid amino acid residue). The Kd between each modified PmSLP having SEQ.ID NO: 65, and SEQ.ID NO: 67 and a native host protein was determined to be less than 2,000 nM, with the Kd between the wild type PmSLP-1 protein (SEQ.ID NO: 2) and the native host protein being 30 nM $\pm$ 10 nM. Thus, the Kd between these two example modified PmSLP proteins and a native host protein exceeds the Kd between the native non-modified PmSLP and the native host protein by a factor of at least 500x.

[0221] According to an aspect, suitable nucleic acid sequences include nucleic acid sequences encoding an immunogenically equivalent portion of a PmSLP polypeptide, notably, in particular, PmSLP polypeptide portions which are at least immunologically equivalent to full length PmSLP polypeptides, including the polypeptides set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97. Thus, further example nucleic acid sequences that may be used in selected embodiments include nucleic acid sequences encoding an amino acid sequence which is at least immunologically equivalent to a PmSLP polypeptide, the amino acid sequence corresponding with at least 10 consecutive amino acids and up to 150 amino acids, including 10, 20, 30, 40, 50, 55, 60, 70, 80, 90, 100, 110, 120, 130, 140, or 150 amino acids of a full length PmSLP polypeptide, including the PmSLP polypeptides set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ.ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 57, SEQ.ID NO: 59,

SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97.

[0222] In a further embodiment, the PmSLP protein or immunogenically equivalent portion thereof may be linked to another polypeptide to form a hybrid polypeptide, including, for example a carrier protein or extension to facilitate detection or purification, such as a polyhistidine extension (HIS-tag) or a FLAG-tag peptide extension, or another immunogenic polypeptide, including, further a second PmSLP or an immunogenically equivalent portion thereof. [0223] Further examples of hybrid polypeptides, are hybrid polypeptides comprising a first and second PmSLP polypeptide, for example, PmSLP-1 and PmSLP-3, and PmSLP-1 and PmSLP-2, such as set forth in SEQ.ID NO: 51 (PmSLP-1 and PmSLP-2 hybrid), SEQ.ID NO: 53 (PmSLP-1, PmSLP-2, PmSLP-3 hybrid), and SEQ.ID NO: 55 (PmSLP-1, PmSLP-2, PmSLP-4.2 hybrid), which can be encoded by the nucleic acid sequences set forth in SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO; and SEQ.ID NO: 54, respectively.

[0224] Yet further examples of hybrid polypeptides are hybrid polypeptides comprising a first, second, and third PmSLP polypeptide, for example, PmSLP-1, PmSLP-2, and PmSLP-3, and PmSLP-1, PmSLP-2, and PmSLP-4, such as set forth in SEQ. ID NO: 53 (PmSLP-1, PmSLP-2, and PmSLP-3 hybrid polypeptide) and SEQ.ID NO: 55 (PmSLP-1, PmSLP-2, and PmSLP-3 hybrid polypeptide), which can be encoded by the nucleic acid sequences set forth in SEQ. ID. NO: 52 and SEQ. ID NO: 54, respectively.

[0225] As is known to those of skill in the art, expression of nucleic acids in a host cell, to produce a protein thereby biosynthetically, can be achieved by providing one or more nucleic acids capable of controlling expression in a host cell, and operably linking the one or more nucleic acids capable of controlling expression in a host cell to the nucleic acid one wishes to express. Such operable linking of a nucleic acid controlling expression generally involves linking in the 5' to 3' direction of expression the nucleic acid capable of controlling expression in a host cell to the nucleic acid one wishes to express, i.e., within the context of the instant disclosure, a PmSLP protein. Nucleic acid sequences capable of controlling expression in host cells that may be used herein include any transcriptional promoter capable of controlling expression of polypeptides in host cells. Generally, promoters obtained from bacterial cells are used when a bacterial host cell is selected, while a yeast promoter will be used when a yeast host cell is selected, a plant promoter will be used when a plant cell is selected, and so on. The obtained nucleic acid comprising a promoter and the nucleic acid expressing a PmSLP protein is generally a chimeric nucleic acid. Further nucleic acid elements capable elements of controlling expression in a host cell include transcriptional terminators, enhancers and the like, all of which may be included in the chimeric nucleic acid sequences of the present disclosure.

[0226] In accordance with the present disclosure, the chimeric nucleic acid sequences can be integrated into a recombinant expression vector which ensures good expression in the host cell, wherein the recombinant expression vector is suitable for expression in a host cell. The term

“suitable for expression in a host cell” means that the recombinant expression vector comprises the chimeric nucleic acid linked to genetic elements required to achieve expression in a cell. As noted, such genetic elements can include transcriptional promoters, terminators, and enhancers, and the like. Further genetic elements that may be included in the expression vector are one or more nucleic acid sequences encoding marker genes, and one or more origins of replication. In some embodiments, the expression vector can freely replicate in the host cell. In other embodiments, the chimeric nucleic acid can be integrated into the host cell's genomic DNA. In some embodiments, the expression vector further can comprise genetic elements required for the integration of the vector or a portion thereof in the host cell's genome, for example, if a plant host cell is used the T-DNA left and right border sequences which facilitate the integration into the plant's nuclear genome can be included in the vector.

[0227] Marker genes that may be used in accordance with the present disclosure include all genes that allow the distinction of transformed cells from non-transformed cells, including all selectable and screenable marker genes. A marker gene may be a resistance marker such as an antibiotic resistance marker against, for example, kanamycin, chloramphenicol, methotrexate, or ampicillin. In other instances, a marker gene may be a gene which allows a cell to produce an essential nutrient, for example amino acids.

[0228] Thus, in an aspect, the present disclosure provides, in an example embodiment, an expression vector comprising:

[0229] (a) a nucleic acid sequence encoding a PmSLP protein or an immunogenically equivalent portion thereof; and

[0230] (b) a nucleic acid sequence capable of controlling expression of the nucleic acid sequence encoding the PmSLP protein or an immunogenically equivalent portion thereof in a host cell.

[0231] In example embodiments, the expression vector can comprise a chimeric nucleic acid comprising a nucleic acid sequence encoding a promoter linked to a nucleic acid sequence encoding a PmSLP protein or an immunogenically equivalent portion thereof.

[0232] Turning now to the host cell, it is noted, initially, that any host cell which upon cultivation expresses the chimeric nucleic acid can be selected and used in accordance with the present disclosure. Suitable host cells in this respect include, for example, microbial cells, such as bacterial cells, yeast cells, for example, and algal cells or plant cells. A variety of techniques and methodologies to manipulate host cells to introduce nucleic acid sequences in cells and attain expression exists and are well known to the skilled artisan. These methods include, for example, cation-based methods, for example, lithium ion or calcium ion-based methods, electroporation, biolistics, and glass beads-based methods. As will be known to those of skill in the art, depending on the host cell selected, the methodology to introduce nucleic acid material in the host cell may vary, and, furthermore, methodologies may be optimized for uptake of nucleic acid material by the host cell, for example, by comparing uptake of nucleic acid material using different conditions. Detailed guidance can be found, for example, in Sambrook et al., Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2012, Fourth Ed. It is noted that the

chimeric nucleic acid is a non-naturally occurring chimeric nucleic acid sequence and can be said to be heterologous to the host cell.

[0233] One example host cell that conveniently may be used is *Escherichia coli*. The preparation of the *E. coli* vectors may be accomplished using commonly known techniques such as restriction digestion, ligation, gel electrophoresis, DNA sequencing, the polymerase chain reaction (PCR) and other methodologies. A wide variety of cloning vectors is available to perform the necessary steps required to prepare a recombinant expression vector. Among the vectors with a replication system functional in *E. coli*, are vectors such as pBR322, the pUC series of vectors, the M13 mp series of vectors, pBluescript etc. Suitable promoter sequences for use in *E. coli* include, for example, the T7 promoter, the T5 promoter, tryptophan (trp) promoter, lactose (lac) promoter, tryptophan/lactose (lac) promoter, lipoprotein (lpp) promoter, and λ phage PL promoter. Typically, cloning vectors contain a marker, for example, an antibiotic resistance marker, such as ampicillin or kanamycin resistance marker, allowing selection of transformed cells. Nucleic acid sequences may be introduced in these vectors, and the vectors may be introduced in *E. coli* by preparing competent cells, electroporation or using other well-known methodologies to a person of skill in the art. *E. coli* may be grown in an appropriate medium, such as Luria-Broth medium and harvested. Recombinant expression vectors may readily be recovered from cells upon harvesting and lysing of the cells.

[0234] Another example host cell that may be conveniently used is a yeast cell. Example yeast host cells that can be used are yeast cells belonging to the genus *Candida*, *Kluyveromyces*, *Saccharomyces*, *Schizosaccharomyces*, *Pichia*, *Hansenula*, and *Yarrowia*. In specific example embodiments, the yeast cell can be a *Saccharomyces cerevisiae* cell, a *Yarrowia lipolytica* cell, or *Pichia pastoris* cell.

[0235] A number of vectors exist for the expression of recombinant proteins in yeast host cells. Examples of vectors that may be used in yeast host cells include, for example, Yip type vectors, YEpl type vectors, YRp type vectors, YCp type vectors, pGPD-2, pAO815, pGAPZ, pGAPZα, pHIL-D2, pHIL-S1, pPIC3.5K, pPIC9K, pPICZ, pPICZα, pPIC3K, pHWO10, pPUZZLE and 2 μm plasmids. Such vectors are known to the art and are, for example, described in Cregg et al., Mol Biotechnol. (2000) 16(1): 23-52. Suitable promoter sequences for use in yeast host cells are also known and described, for example, in Matanovich et al., Methods Mol. Biol., 2012, 824:329-58, and in Romanos et al., 1992, Yeast 8: 423-488. Examples of suitable promoters for use in yeast host cells include promoters of glycolytic enzymes, like triosephosphate isomerase (TPI), phosphoglycerate kinase (PGK), glyceraldehyde-3-phosphate dehydrogenase (GAPDH or GAP) and variants thereof, lactase (LAC) and galactosidase (GAL), *P. pastoris* glucose-6-phosphate isomerase promoter (PPGI), the 3-phosphoglycerate kinase promoter (PPGK), the glyceraldehyde phosphate dehydrogenase promoter (PGAP), translation elongation factor promoter (PTEF), *S. cerevisiae* enolase (ENO-1), *S. cerevisiae* galactokinase (GAL1), *S. cerevisiae* alcohol dehydrogenase/glyceraldehyde-3-phosphate dehydrogenase (ADH1, ADH2/GAP), *S. cerevisiae* triose phosphate isomerase (TPI), *S. cerevisiae* metallothionein (CUP1), and *S. cerevisiae* 3-phosphoglycerate kinase (PGK), and the maltase gene promoter (MAL). Marker

genes suitable for use in yeast host cells are also known to the art. Thus, antibiotic resistance markers, such as ampicillin resistance markers, can be used in yeast, as well as marker genes providing genetic functions for essential nutrients, for example, leucine (LEU2), tryptophan (TRP1 and TRP2), uracil (URA3, URA5, URA6), histidine (HIS3), and the like. Methods for introducing vectors into yeast host cells can, for example, be found in S. Kawai et al., 2010, Bioeng. Bugs 1(6): 395-403.

[0236] Yet other example host cells that may be used in accordance herewith are plant cells. Methods for introducing nucleic acids in plant cells are known to those of skill in the art. *Agrobacterium* mediated plant cell transformation methods are described, for example, by Gelvin S. in Microbiol. Mol. Biol. Rev., 2003, 67(1): 16-37, and physical transformation-based methods for plant cells are described by Rivera A. L. et al., 2012, Phys. Life Rev. 9(3): 308-345. Plant selectable marker genes are known to those of skill in the art and include antibiotic resistance genes, for example kanamycin resistance genes, and herbicide resistance genes, such as the bar and pat genes (Wohlleben et al., 1988, Gene 70:25-37). Screenable markers that may be employed to identify plant transformants through visual inspection include β-glucuronidase (GUS) (U.S. Pat. Nos. 5,268,463 and 5,599,670) and green fluorescent protein (GFP) (Niedz et al., 1995, Plant Cell Rep., 14: 403). Plant promoters are also known to those in the art and include, for example, constitutive promoters, such as the 35S cauliflower mosaic virus (CaMV) promoter (Rothstein et al., 1987, Gene 53: 153-161), the rice actin promoter (McElroy et al., 1990, Plant Cell 2:163-171; U.S. Pat. No. 6,429,357), a ubiquitin promoter, such as the corn ubiquitin promoter (U.S. Pat. Nos. 5,879,903 and 5,273,894), and the parsley ubiquitin promoter (Kawalleck, P. et al., 1993, Plant Mol. Biol. 21:673-684), and organ specific promoters, such as seed specific promoters, for example, a phaseolin promoter (Sengupta-Gopalan et al., 1985, Proc. Natl. Acad. Sci. USA 82: 3320-3324), or an oleosin promoter (U.S. Pat. No. 5,792, 922).

[0237] Further, guidance with respect to the preparation of expression vectors and introduction thereof into host cells, including in *E. coli* cells, yeast cells, and other host cells, may be found in, for example: Sambrook et al., Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2012, Fourth Ed.

[0238] Thus, in another aspect, the present disclosure provides, one example embodiment, a host cell comprising a chimeric nucleic acid comprising:

[0239] (a) a nucleic acid sequence encoding a PmSLP protein or an immunogenically equivalent portion thereof; and

[0240] (b) a nucleic acid sequence capable of controlling expression of the nucleic acid sequence encoding the PmSLP protein or an immunogenically equivalent portion thereof in a host cell.

[0241] In example embodiments, the expression vector can comprise a chimeric nucleic acid comprising a nucleic acid sequence encoding a promoter linked to a nucleic acid sequence encoding a PmSLP protein or an immunogenically equivalent portion thereof.

[0242] Thus, to briefly recap, a host cell comprising a chimeric nucleic acid comprising (i) a nucleic acid sequence encoding a PmSLP protein or an immunogenically equivalent portion thereof; and (ii) a nucleic acid sequence capable

of controlling expression of the nucleic acid sequence encoding a PmSLP protein or an immunogenically equivalent portion thereof in a host cell can be prepared in accordance with the present disclosure.

[0243] In accordance herewith, host cells are grown to multiply and to express a chimeric nucleic acid. Expression of the chimeric nucleic acid results in the biosynthetic production in the host cell of a PmSLP protein of an immunogenically equivalent portion thereof. Growth media and growth conditions can vary depending on the host cell that is selected, as will be readily appreciated to those of ordinary skill in the art. Growth media typically contain a carbon source, one or several nitrogen sources, essential salts including salts of potassium, sodium, magnesium, phosphate and sulphate, trace metals, water soluble vitamins, and process aids including but not limited to antifoam agents, protease inhibitors, stabilizers, ligands and inducers. Typical carbon sources are e.g., mono- or disaccharides. Typical nitrogen sources are, e.g., ammonia, urea, amino acids, yeast extract, corn steep liquor and fully or partially hydrolyzed proteins. Typical trace metals are e.g., Fe, Zn, Mn, Cu, Mo and H<sub>3</sub>BO<sub>3</sub>. Typical water-soluble vitamins are e.g., biotin, pantothenate, niacin, thiamine, p-aminobenzoic acid, choline, pyridoxine, folic acid, riboflavin, and ascorbic acid. Further, specific example media include liquid culture media for the growth of yeast cells and bacterial cells including, Luria-Bertani (LB) broth for bacterial cell cultivation, and yeast extract peptone dextrose (YEFD or YPD), for yeast cell cultivation. Further media and growth conditions can be found in Sambrook et al., Molecular Cloning, a Laboratory Manual, Cold Spring Harbor Laboratory Press, 2012, Fourth Ed.

[0244] Upon production by the host cells of a PmSLP protein or an immunogenically equivalent portion thereof, the PmSLP protein or the immunogenically equivalent portion thereof may be recovered from the host cells, and separated from other constituents, such as cellular debris, or media constituents, for example. Separation techniques will be known to those of skill in the art and include a variety of different protein purification techniques including, e.g., ion-exchange chromatography, size exclusion chromatography, affinity chromatography, hydrophobic interaction chromatography, reverse phase chromatography, gel filtration, etc. Further general guidance with respect to protein purification may for example be found in: Cutler, P. Protein Purification Protocols, Humana Press, 2004, Second Ed. Thus, substantially pure preparations of PmSLP proteins or immunogenically equivalent portions thereof may be obtained. The recovered PmSLP proteins may be obtained in a more or less pure form, for example, a preparation of a PmSLP protein or immunogenically equivalent portion thereof having a purity of at least about 60% (w/v), about 70% (w/v), about 80% (w/v), about 90% (w/v), about 95% (w/v), or about 99% (w/v) may be obtained.

[0245] Furthermore, it is noted that the recombinant production of the PmSLP proteins or immunogenically equivalent portions thereof in host cell system permits the production thereof in a manner in which the PmSLP proteins or immunogenically equivalent portions are substantially free from other *P. multocida* constituent materials, such as other *P. multocida* proteins, membrane materials, lipopolysaccharides, and the like, naturally associated with PmSLP proteins.

[0246] It is noted that the cells, in some embodiments, may secrete a portion of the produced PmSLP protein or immunogenically equivalent portion thereof in the cell growth medium, thus a portion of the produced PmSLP protein or immunogenically equivalent portion thereof may be recovered from the cells and a further portion of the PmSLP protein or immunogenically equivalent portion thereof may be recovered from the growth medium.

[0247] It is further noted that the veterinary vaccine formulations of the present disclosure may comprise PmSLP proteins or an immunogenically equivalent portion thereof in more or less pure form. Thus, in accordance herewith, a substantially pure PmSLP protein or immunogenically equivalent portion thereof may be obtained and used to prepare veterinary vaccine formulations. Thus, for example, in some embodiments, the PmSLP protein may be substantially free of other host cell constituent materials, such as host cell proteins, membrane materials, lipopolysaccharides, and the like. In other embodiments, more crude preparations comprising PmSLP protein or immunogenically equivalent portion thereof may be obtained and used to prepare vaccine formulations. Thus, for example, in such embodiments, host cells, host cell lysates or host cell fractions comprising the PmSLP protein or immunogenically equivalent portion thereof may be used to prepare the vaccine formulations.

[0248] It is noted that any PmSLP or immunogenically equivalent portion thereof may be used to formulate the veterinary vaccine formulations of the present disclosure, including a PmSLP protein having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof.

[0249] Furthermore, in an aspect of the present disclosure, when preparing a vaccine formulation, preferably consideration is given to the *P. multocida* strain causing the infection in the food production animal, when a PmSLP protein is selected.

[0250] In particular, in preparing a vaccine formulation to treat an animal infected by a *P. multocida* strain possessing a PmSLP protein belonging to a specific phylogenetic cluster, the vaccine is preferably prepared by selecting a PmSLP polypeptide belonging to the same phylogenetic cluster, including the same PmSLP polypeptide or another PmSLP polypeptide belonging to the same phylogenetic cluster, and including the thus selected PmSLP polypeptides in the vaccine formulation. Thus, for example, referring to FIG. 2, in preparing a vaccine formulation, preferably, to treat an animal infected by a *P. multocida* strain possessing a PmSLP polypeptide belonging to a phylogenetic cluster PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, or PmSLP-4.2, a PmSLP polypeptide from the same phylogenetic cluster is selected to prepare the vaccine. Thus, by way of example, if the

animal is infected by a *P. multocida* strain possessing a PmSLP polypeptide belonging to phylogenetic cluster PmSLP-1, for example, SEQ.ID NO: 2, the vaccine formulation preferably is prepared by selecting a PmSLP polypeptide or an immunogenically equivalent portion thereof belonging to phylogenetic cluster PmSLP-1, for example, SEQ.ID NO: 2, or another PmSLP polypeptide belonging to phylogenetic cluster PmSLP-1, and included the same in the vaccine preparation; and, by way of further example, if the animal is infected by a *P. multocida* strain possessing a PmSLP protein belonging to a phylogenetic cluster PmSLP-3, for example, SEQ.ID NO: 6, the vaccine formulation preferably is prepared by selecting a PmSLP polypeptide or an immunogenically equivalent portion thereof, belonging to phylogenetic cluster PmSLP-3, for example SEQ.ID NO: 6, for example, SEQ.ID NO: 6, or another PmSLP polypeptide belonging to phylogenetic cluster PmSLP-3, and included the same in the vaccine preparation. The strain from which the PmSLP protein is selected can be the same *P. multocida* strain, or another strain than the *P. multocida* infecting strain, provided however, said another strain belongs to the same phylogenetic cluster. Thus, the PmSLP protein does not need to be selected from the same *P. multocida* strain as the infecting *P. multocida* infecting strain provided however, said another strain belongs to the same phylogenetic cluster.

[0251] Furthermore, preferably, in selecting a PmSLP polypeptide consideration is given to the host and clinical indication. In particular, in preparing a vaccine formulation to treat an animal host infected by a *P. multocida* strain causing a particular indication, the vaccine is preferably prepared by selecting a PmSLP polypeptide from a *P. multocida* strain capable of causing the indication in the host, including the same PmSLP polypeptide or another PmSLP polypeptide, isolated from a *P. multocida* strain capable of causing the indication in the host, and including the thus selected PmSLP polypeptides in the vaccine formulation. Thus, for example, referring again to FIG. 2, in preparing a vaccine formulation, preferably, to treat an animal infected by a *P. multocida* strain possessing a PmSLP polypeptide belonging to a phylogenetic cluster PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, or PmSLP-4.2, a PmSLP polypeptide from the same phylogenetic cluster is selected to prepare the vaccine, wherein furthermore the PmSLP is obtainable from a *P. multocida* strain, known to cause the indication to be treated in the host species to be treated. Thus, by way of example, if a bovine animal is diagnosed with BRD caused by infection of a *P. multocida* strain possessing a PmSLP polypeptide belonging to phylogenetic cluster PmSLP-2, for example, SEQ.ID NO: 4, the vaccine formulation preferably is prepared by selecting a PmSLP polypeptide or an immunogenically equivalent portion thereof belonging to phylogenetic cluster PmSLP-2, for example, SEQ.ID NO: 4, or another PmSLP polypeptide belonging to phylogenetic cluster PmSLP-2, wherein further the PmSLP-2 polypeptide further preferably is obtainable from a *P. multocida* strain known to cause BRD in bovine animals, and not, for example, from porcine animals, which also can be infected by *P. multocida* strains contain PmSLP-2, as can be appreciated from FIG. 2.

[0252] In one example embodiment, the food production animal can be a ruminant animal susceptible to infection by a *P. multocida* strain causing a respiratory tract disease, and the vaccine formulation is prepared to comprise at least one

*P. multocida* PmSLP protein or an immunogenically equivalent portion thereof selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, PmSLP-3, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0253] In one example embodiment, the food production animal can be a bovine animal susceptible to infection by a *P. multocida* strain causing BRD, and the vaccine formulation is prepared to comprise at least one *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP2, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0254] In one example embodiment, the food production animal can be a bovine animal susceptible to infection by a *P. multocida* strain causing HS, and the vaccine formulation is prepared to comprise at least one *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof selected from the group of phylogenetic clusters consisting of PmSLP-3, wherein the selected *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0255] In one example embodiment, the food production animal can be a porcine animal susceptible to infection by a *P. multocida* strain causing porcine atrophic rhinitis (PAR), and the vaccine formulation is prepared to comprise at least one *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof selected from the group of phylogenetic clusters consisting of PmSLP-2, PmSLP-4.1, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0256] In one example embodiment, the food production animal can be a porcine animal susceptible to infection by a *P. multocida* strain causing pneumonic pasteurellosis, and the vaccine formulation is prepared to comprise at least one *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof selected from the group of phylogenetic clusters consisting of PmSLP-2, PmSLP-4.1, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0257] In one example embodiment, the food production animal can be an avian animal susceptible to infection by a *P. multocida* strain causing fowl cholera, and the vaccine formulation is prepared to comprise a *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof selected from the group of phylogenetic clusters consisting of PmSLP-3, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

[0258] It is noted that a *P. multocida* strain may be isolated from infected food production animals and cultured in order to identify the *P. multocida* strain, and the sequence of the PmSLP polypeptide present therein may be determined

using techniques known to those of ordinary skill in the art, see e.g., Pasteurellaceae: Biology, Genomics and Molecular Aspects. Publisher: Caister Academic Press Edited by: Peter Kuhnert (1) and Henrik Christensen (2). Institute of Veterinary Bacteriology, Vetsuisse Faculty University of Bern, Langgass-Str. 122, 3001 Bern, Switzerland (1) and Department of Veterinary Pathobiology, Faculty of Life Science, Copenhagen University, Dyrlaegevej 88, 1870 Frederiksberg, Denmark (2).

[0259] Furthermore, in an example embodiment, in preparing a vaccine formulation, in order to treat an animal infected by a *P. multocida* strain belonging to a specific serogroup, the vaccine is preferably prepared using a PmSLP polypeptide obtained from a *P. multocida* strain belonging to the same serogroup. Thus, for example, in preparing a vaccine formulation, preferably, in order to treat an animal infected by a *P. multocida* strain belonging to serogroup A, B, C, D, E, or F, a vaccine formulation comprising a PmSLP polypeptide obtained from a *P. multocida* strain from the same serogroup is selected for inclusion in the vaccine. Thus, by way of example, if the animal is infected by a *P. multocida* strain of serogroup A, the vaccine formulation preferably is prepared by selection and inclusion in the formulation of a PmSLP polypeptide or an immunogenically equivalent portion thereof, obtained from *P. multocida* strain of serogroup A; and, by way of further example, if the animal is infected by a *P. multocida* strain belonging to serogroup F, the vaccine formulation preferably is prepared by selection and inclusion in the formulation of a PmSLP polypeptide or an immunogenically equivalent portion thereof, obtained from a *P. multocida* strain belonging to serogroup F. The strain can be the same strain, or another strain, provided said another strain belongs to the same serogroup.

[0260] In further preferred example embodiments, consideration is given to both phylogenetic cluster and serogroup. Thus, preferably, in preparing a vaccine formulation, in order to treat an animal infected by a *P. multocida* strain containing a PmSLP polypeptide belonging to a specific phylogenetic cluster and a specific serogroup, the vaccine formulation is preferably prepared by selecting and using a PmSLP polypeptide belonging to the same phylogenetic cluster and a strain belonging to the same serogroup as the infectious strain. Thus, referring again to FIG. 2, for example, in preparing a vaccine formulation, preferably, in order to treat an animal infected by a *P. multocida* strain containing PmSLP protein belonging to phylogenetic cluster PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, or PmSLP-4.2 and the *P. multocida* strain belonging to serogroup A, B, D, E, or F, a vaccine formulation comprising a PmSLP polypeptide from the same phylogenetic cluster and obtained from strain of the same serogroup is selected for inclusion in the vaccine. The PmSLP polypeptide can be identical to the PmSLP contained in the infectious strain, or different, provided however, the PmSLP polypeptide belongs to the same phylogenetic cluster and is obtained from a strain of the same serogroup as the infectious strain. Thus, by way of example, if the animal is infected by a *P. multocida* strain containing a PmSLP polypeptide belonging to phylogenetic cluster PmSLP-2 and the infectious strain belongs to serogroup A, the vaccine formulation preferably is prepared to include a PmSLP polypeptide or an immunogenically equivalent portion thereof, obtained from *P. multocida* strain containing a PmSLP polypeptide belonging to phylogenetic

cluster PmSLP-2 and a strain belonging to serogroup A; if the animal is infected by a *P. multocida* strain containing a PmSLP polypeptide belonging to phylogenetic cluster PmSLP-3 and the strain belongs to serogroup F, the vaccine formulation preferably is prepared to include a PmSLP polypeptide or an immunogenically equivalent portion thereof, obtained from a *P. multocida* strain containing a PmSLP polypeptide belonging to phylogenetic cluster PmSLP-3, and a strain belonging to serogroup F. The strain can be the same strain, or another strain, provided said another strain belongs to the same phylogenetic cluster and the same serogroup.

[0261] Thus, it will now be clear one embodiment, the vaccine formulation can comprises a *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof elected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain, wherein the selected *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof further is of a *P. multocida* strain belonging to a serogroup selected from the group consisting of serogroup A, B, D, E, and F, wherein the serogroup is the same as the serogroup of the infecting *P. multocida* strain.

[0262] Additionally, the PmSLP protein can be a PmSLP protein obtained from a *P. multocida* strain selected from serotype 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, and 16 *P. multocida* strains, the food production animal is susceptible to infection by a *P. multocida* strain of the selected serotype. Thus, in one embodiment, in preparing a vaccine formulation, in order to treat an animal infected by a *P. multocida* strain containing a PmSLP protein belonging to a specific phylogenetic cluster, and a specific serogroup, and a specific serotype, the vaccine is preferably prepared using a PmSLP polypeptide belonging to the same phylogenetic cluster, the same serogroup, and the same serotype. Thus, for example, when a *P. multocida* infection causes hemorrhagic septicemia among bovine species, and the strain is a B:2 strain, the PmSLP protein may be obtained from the B:2 strain; or, for example, when a *P. multocida* infection causes progressive atrophic rhinitis among porcine species, and the strain belongs to serogroup D, the PmSLP protein may be obtained from a *P. multocida* strain belonging to serogroup D, and so on. It is noted that specific *P. multocida* strains can be obtained (e.g., from a collection of microbial species, such as the American Type Culture Collection (ATCC)) or isolated, for example, from infected food production animals, and the serogroup and/or serotype of a strain, can be determined using methods known to those of skill in the art (see: for example, Wilson, M. et al., 1992, J. Clin. Microbiol. 1518-1524; Arumugam, N., et al. 2011, Tropical Biomed. 28(1) 55-63).

[0263] In a further example embodiment, the food production animal can be selected to be a ruminant species, and a vaccine formulation can be prepared for administration to the ruminant species, wherein the *P. multocida* infection causes a respiratory tract disease, and wherein the PmSLP protein comprises SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34,

SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing the respiratory tract disease.

[0264] In a further example embodiment, the food production animal can be selected to be bovine species, and a vaccine formulation can be prepared for administration to the bovine species, wherein the *P. multocida* infection causes BRD, and wherein the PmSLP protein comprises SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 22, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 77, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing BRD.

[0265] In a further example embodiment, the food production animal can be selected to be a bovine species, and a vaccine formulation can be prepared for administration to the bovine species, wherein the *P. multocida* infection causes HS, and wherein the PmSLP protein comprises SEQ.ID NO: 6, SEQ.ID NO: 20, SEQ.ID NO: 24, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 53, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, or SEQ.ID NO: 89, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing HS.

[0266] In a further example embodiment, the food production animal can be selected to be a porcine species, and a vaccine formulation can be prepared for administration to the porcine species, wherein the *P. multocida* infection causes pneumonic pasteurellosis, and wherein the PmSLP protein comprises SEQ.ID NO: 4, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 75, SEQ.ID NO: 77, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing pneumonic pasteurellosis.

[0267] In a further example embodiment, the food production animal can be a porcine species, and a vaccine formulation can be prepared for administration to the porcine species, wherein the *P. multocida* infection causes PAR, and wherein the PmSLP protein comprises SEQ.ID NO: 4, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 75, SEQ.ID NO: 77, or SEQ.ID NO: 91, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing PAR.

[0268] In yet a further example embodiment, the food production animal can be an avian species, and the vaccine formulation can be prepared for administration to the avian species, wherein the *P. multocida* infection causes fowl cholera, and wherein the PmSLP protein comprises SEQ.ID

NO: 6, SEQ.ID NO: 10, SEQ.ID NO: 20, SEQ.ID NO: 24, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 40, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 61, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, or SEQ.ID NO: 89, or an immunogenically equivalent portion thereof, to prevent or ameliorate a *P. multocida* infection causing pneumonic pasteurellosis.

[0269] It is noted, however, that the vaccine formulations of the present disclosure can be used to ameliorate or prevent infections by *P. multocida* strains, other than the strains from which the PmSLP protein included in a veterinary vaccine formulation is selected. Thus, the vaccine formulations of the present disclosure, surprisingly, do not necessarily need to include PmSLPs from a plurality of *P. multocida* strains in order to be used for the treatment of a food production animal, even if the food production animal can be or has been exposed to, or can be or has been infected by a plurality of *P. multocida* strains. Thus, for example, a vaccine formulation comprising a PmSLP protein obtained from a *P. multocida* strain of a first serotype, may be used to treat a food production animal for an infection caused by a *P. multocida* strain of another serotype. In this respect, the veterinary vaccine formulations, even if they include a single PmSLP or immunogenically equivalent portion thereof, can be said to be cross-protective, and may confer homologous or heterologous protection.

[0270] Notwithstanding the foregoing, in some embodiments, vaccine formulations may comprise two or more PmSLP proteins. Thus, in example embodiments, vaccine formulations may comprise PmSLP proteins obtained from two or more *P. multocida* strains, each belonging to a single serogroup selected from serogroup A, B, D, E, or F, or veterinary vaccine formulations may comprise PmSLP proteins obtained from two *P. multocida* strains, belonging to two or more serogroups selected from A, B, D, E, or F. In such embodiments, the vaccine can prevent or ameliorate infection by strains of two or more *P. multocida* strains, and such vaccines can be said to be cross-protective.

[0271] In further example embodiments, vaccine formulations may comprise two or more PmSLP proteins belonging to two or more strains, each belonging to a single phylogenetic cluster PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, and PmSLP-4.2, or veterinary vaccine formulations may comprise PmSLP proteins obtained from two or more *P. multocida* strains, belonging to two or more phylogenetic clusters PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, and PmSLP-4.2. In such embodiments, the vaccine can prevent or ameliorate infection by strains of two or more *P. multocida* strains, and such vaccines can be said to be cross-protective.

[0272] In further example embodiments, vaccine formulations may comprise two or more PmSLP proteins obtained from two *P. multocida* strains, each belonging to a single serotype selected from serotype 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16, or veterinary vaccine formulations may comprise PmSLP proteins obtained from two or more *P. multocida* strains, belonging to two or more serotypes selected from 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, or 16. In such embodiments, the vaccine can prevent or ameliorate infection by strains of two or more *P. multocida* strains, and such vaccines can be said to be cross-protective.

[0273] In further example embodiments, vaccine formulations may comprise at 2 or least 2, 3 or at least 3, 4 or at

least 4, 5 or at least 5 PmSLP proteins protein having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID. NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID. NO: 20, SEQ.ID. NO: 22, SEQ. ID. NO: 24, SEQ.ID. NO: 26, SEQ.ID. NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ. ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or immunogenically equivalent portions thereof.

[0274] Thus, to briefly recap, in accordance with the present disclosure *P. multocida* PmSLP polypeptides or an immunogenically equivalent portion thereof, may be selected for inclusion in veterinary vaccine formulations to treat food production animals infected by *P. multocida*. Preferably, the selected *P. multocida* PmSLP polypeptide belongs to the same phylogenetic cluster as a PmSLP polypeptide contained by the infecting *P. multocida* strain.

[0275] Turning next to the preparation of vaccine formulations, in an aspect hereof, in order to prepare a vaccine formulation, a preparation comprising a PmSLP protein or immunogenically equivalent portion thereof may be combined with at least one other veterinary pharmaceutically acceptable in ingredient, including, but not limited to, a diluent, an excipient, a carrier, an adjuvant, or mixtures thereof, whereby the PmSLP protein or immunogenically equivalent portion thereof and at least one other ingredient are mixed together or blended or homogenized or otherwise prepared until the vaccine formulation is formed.

[0276] The amount of PmSLP protein or immunogenically equivalent portion thereof in the veterinary vaccine formulation may vary. In general, consideration is given to the dose to be administered to an animal. Doses for the PmSLP protein or an immunogenically equivalent portion thereof may be formulated to include PmSLP protein or an immunogenically equivalent portion thereof, in quantities ranging from about 1 µg/kg of animal body weight to about 0.25 mg/kg of animal body weight, preferably about 1 µg/kg of animal body weight to about 100 µg/kg of animal body weight. Furthermore, vaccine formulations are preferably formulated so that a dose comprises at least about 0.001% by weight or volume, at least 0.025% or about 0.025%, at least 0.05% or about 0.05%, at least 0.1% or about 0.1%, at least 0.5 or about 0.5%, at least 1% or about 1%, at least 5% or about 5%, at least 10% or about 10%, at least 15% or about 15%, at least 20% or about 20%, or at least 25% or about 25%, by weight of the PmSLP protein, so that the ratio of PmSLP to other vaccine constituents (e.g., adjuvants, diluents, carriers, excipients) of the vaccine formulation by weight or volume is at least 0.001:99.999, 0.025:99.975, 0.05: 99, 95, 0.01:99.99, 0.5:99.5, 1:99, 5:95, 15:85, 20:80, or 25:75, respectively, by weight or volume. The exact amount necessary, however, will vary depending on the species, age, and general condition of the recipient animal to be treated, the severity of the condition being treated, the particular preparation delivered, the site of administration, the subject biological species, as well as other factors. In this respect, veterinary vaccine formulations may, in particular,

vary with respect to the quantity of PmSLP protein or immunogenically equivalent portion thereof included in a dose, depending on the species of the food production animal to which the vaccine formulation is administered. A suitable effective amount can be readily determined by one of skill in the art. Thus, a therapeutically effective amount of the PmSLP protein or immunogenically equivalent portion to be included in the veterinary vaccine formulations of the present disclosure will be an amount sufficient to bring about amelioration or prevention of disease or condition symptoms and will fall in a relatively broad range that can be determined through routine trials.

[0277] Veterinary vaccine formulations comprising the PmSLP protein or immunogenically equivalent portion thereof of the present disclosure preferably further are prepared by combining the PmSLP protein or immunogenically equivalent portion thereof with e.g., carriers, excipients, diluents, and auxiliary substances, such as wetting or emulsifying agents, pH buffering substances and the like. These carriers, excipients, diluents, and auxiliary substances are veterinary pharmaceutically acceptable ingredients. Veterinary pharmaceutically acceptable excipients include, but are not limited to, liquids such as water, saline, polyethylene glycol, hyaluronic acid, glycerol, and ethanol. Veterinary pharmaceutically acceptable salts can also be included in the formulation, for example, mineral acid salts such as hydrochlorides, phosphates, sulfates, and the like, and the salts of organic acids such as acetates, propionates, benzoates, and the like. It is also preferred, although not required, that the vaccine formulation will contain a veterinary pharmaceutically acceptable carrier that serves as a stabilizer, particularly in order to stabilize the polypeptides of the present disclosure. Examples of suitable carriers that also act as stabilizers for peptides include, without limitation, veterinary pharmaceutical grades of dextrose, sucrose, lactose, sorbitol, inositol, dextran, and the like. Other suitable carriers include, again without limitation, starch, cellulose, sodium or calcium phosphates, citric acid, glycine, polyethylene glycols (PEGs), and combinations thereof. Carriers, excipients, diluents, may constitute, for example, from about 10% to about 95% by weight or volume of the vaccine formulation.

[0278] Further, auxiliary agents such as freeze-drying stabilizers, wetting or emulsifying agents, pH buffering agents, gelling or viscosity enhancing additives, and preservatives may also be included in the vaccine formulations of the present disclosure. Vaccine formulations generally comprise less than about 5% by weight of such auxiliary agents.

[0279] In order to augment an immune response in an animal, the veterinary vaccine formulations provided herein further preferably include one or more adjuvants, such as pharmacological agents, cytokines, or the like. Suitable adjuvants include any substance that enhances the immune response of the recipient animal to the immunogenic PmSLP protein or immunogenically equivalent portion thereof of the disclosure. Non-limiting examples of adjuvants include cytokines, e.g., IL-1, IL-2, IL-12, IL-6, and further include inorganic salts, e.g., aluminum hydroxide, aluminum phosphate, and calcium phosphate; oil emulsions, e.g., mineral oil, MF59, QS-21, Montanide™ ISA51, Montanide™ ISA61, Montanide™ ISA 61 VG, Montanide™ Gel 02, Montanide™ ISA-720, or Emulsigen D®; Isocombs, e.g., ISCOMATRIX; microbial derivatives, e.g., monophosphoryl lipid A (MPLA), macrophage-activating protein-2, viro-

somes, LT/CT, CpG; natural polymers, e.g., polysaccharides; and synthetic polymers, e.g., polyanhydrides and polyesters, or nucleic acid analogs, such as Poly I:C. Adjuvants may be administered, for example, as proteins or other macromolecules at the same time (e.g., by inclusion in the vaccine formulation), prior to, or subsequent to, administration of the polypeptide antigens. When included in a vaccine formulation, adjuvants may constitute, for example, from 0.1% or about 0.1% to 50% or about 50%, from 0.1% or about 0.1% to 20% or about 20%, or from 1% or about 1% to 10% or about 10% by weight or volume of a vaccine formulation.

[0280] In light of the foregoing, it will be understood that the present disclosure provides, in another aspect, methods for preparing vaccine formulations. In this respect, the present disclosure provides, in one example embodiment, a method for preparing a veterinary vaccine formulation for the prevention or amelioration of *P. multocida* infection in a food production animal susceptible to *P. multocida* infection, the method comprising:

[0281] (i) diagnosing a *P. multocida* infection in a food production animal;

[0282] (ii) identifying the phylogenetic cluster to which a PmSLP protein contained in the infecting *P. multocida* belongs, the phylogenetic cluster being selected from PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1 or PmSLP-4.2; and

[0283] (iii) preparing a vaccine formulation comprising a *P. multocida* PmSLP protein or immunogenically equivalent portion thereof which belongs to the identified phylogenetic cluster together with a veterinary pharmaceutically acceptable adjuvant to form a veterinary vaccine formulation comprising an effective amount of the *P. multocida* PmSLP protein or the immunogenically equivalent portion thereof to treat a food production animal susceptible to *P. multocida* infection.

[0284] In one embodiment, in an aspect, the method additionally can comprise identifying the serogroup of the infecting *P. multocida* strain, the serogroup being selected from the group consisting of serogroup A, B, D, E, and F, and the vaccine being prepared using a *P. multocida* PmSLP protein or an immunogenically equivalent portion thereof from the same or another *P. multocida* strain belonging to the selected serogroup.

[0285] In a further example embodiment, the present disclosure provides a method for preparing a veterinary vaccine formulation comprising a PmSLP protein or an immunogenically equivalent portion thereof, the method comprising:

[0286] (a) providing a chimeric nucleic acid sequence comprising as operably linked components:

[0287] (i) a nucleic acid sequence encoding a PmSLP protein or an immunogenically equivalent portion thereof; and

[0288] (ii) one or more nucleic acid sequences capable of controlling expression in a host cell;

[0289] (b) introducing the chimeric nucleic acid sequence into a host cell;

[0290] (c) growing the host cell to produce the PmSLP protein or the immunogenically equivalent portion thereof; and

[0291] (d) recovering the PmSLP protein or the immunogenically equivalent portion thereof; and

[0292] (e) formulating the PmSLP protein or the immunogenically equivalent portion thereof together with an adjuvant to form a veterinary vaccine formulation comprising an effective amount of the PmSLP protein or the immunogenically equivalent portion thereof to treat a food production animal susceptible to *P. multocida* infection.

[0293] The vaccine formulations of the present disclosure may be used to prevent infection or disease caused by pathogenic infectious *P. multocida* in food production animals. The vaccine formulations may be used to immunize any food production animal, including any bovine species, porcine species, or avian species.

[0294] The veterinary vaccine formulations of the present may be administered to a food production animal using any convenient administration means. Thus, for example, the veterinary vaccine formulations may be injected, for example, intramuscularly or subcutaneously, or the vaccine formulations may be orally administered to the animal, for example, as a feed supplement. It will be understood that, in this respect, the administration means and techniques, such as, for example, in the case of injections, the gauge of the injection needle, may vary depending on the animal. The dosage of the veterinary vaccine formulation will be dependent upon the disease, the route of administration, the animal species, body weight, and other standard factors. In this respect, a person of ordinary skill in the art can readily titrate the appropriate dosage for an effective amount as well as select a suitable method of administration.

[0295] It is further noted that the veterinary vaccine formulations of the present disclosure may be administered prophylactically, i.e., in order to prevent *P. multocida* infection in a food production animal, or in order to ameliorate symptoms associated with *P. multocida* infection following the occurrence of an infection in a food production animal.

[0296] The administration of the veterinary vaccine formulations of the present disclosure generally elicits an immune response in the subject food production animal. Thus, antibodies against the PmSLP protein included in the vaccine formulation may be formed by the food production animal. In some embodiments, anti-PmSLP antibodies can be detected in the blood serum of the food production animal at least 7 days, at least 2 weeks, at least 5 weeks, at least 10 weeks, at least 13 weeks, at least 26 weeks, or at least 52 weeks following administration of the vaccine formulation.

[0297] In light of the foregoing, it will now be understood that, in another aspect, the present disclosure provides, in an example embodiment, a use of PmSLP protein or an immunogenically equivalent portion thereof to prepare a veterinary vaccine formulation comprising the PmSLP protein or an immunogenically equivalent portion thereof together with a veterinary pharmaceutically acceptable adjuvant.

[0298] In light of the foregoing, it will now be understood that, in another aspect, the present disclosure provides, in an example embodiment, a use of a veterinary vaccine formulation comprising a PmSLP protein or an immunogenically equivalent portion thereof together with a veterinary pharmaceutically acceptable adjuvant to ameliorate or prevent a *P. multocida* infection in a food production animal susceptible to *P. multocida* infection.

[0299] As can now be understood, veterinary vaccine formulations comprising a PmSLP protein, or an immunogenically equivalent portion thereof may be prepared. The

veterinary vaccine formulations can be administered to a food production animal to ameliorate or prevent infection of the animal by *P. multocida*.

[0300] Of course, the above-described example embodiments of the present disclosure are intended to be illustrative and in no way limiting. The embodiments are susceptible to many modifications or composition, details, and order of operation. The invention and this disclosure are intended to encompass all such modifications within its scope, as defined by the claims, which should be given a broad interpretation consistent with the description as a whole.

#### Summary of Sequences

[0301] SEQ.ID NO: 1 and SEQ.ID NO: 2 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-1 of *P. multocida* (belonging to phylogenetic cluster 1).

[0302] SEQ.ID NO: 3 and SEQ.ID NO: 4 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-2 of *P. multocida* (belonging to phylogenetic cluster 2).

[0303] SEQ.ID NO: 5 and SEQ.ID NO: 6 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-3 of *P. multocida* (belonging to phylogenetic cluster 3).

[0304] SEQ.ID NO: 7 and SEQ.ID NO: 8 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-4 of *P. multocida* (belonging to phylogenetic cluster 4.1).

[0305] SEQ.ID NO: 9 and SEQ.ID NO: 10 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-4 of *P. multocida* (belonging to phylogenetic cluster 4.2).

[0306] SEQ.ID NO: 11 and SEQ.ID NO: 12 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 of *P. multocida* with a 14-residue anchor truncation of PmSLP, a thrombin cleavage site, and a C terminal polyhistidine tag (belonging to phylogenetic cluster 1).

[0307] SEQ.ID NO: 13 and SEQ.ID NO: 14 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 of *P. multocida* with a 14-residue anchor truncation (belonging to phylogenetic cluster 1).

[0308] SEQ.ID NO: 15 and SEQ.ID NO: 16 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 of *P. multocida* with a 126-residue anchor truncation, a thrombin cleavage site, and C terminal polyhistidine tag (belonging to phylogenetic cluster 1).

[0309] SEQ.ID NO: 17 and SEQ.ID NO: 18 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 of *P. multocida* with a 94-residue anchor truncation, introduced SERp1 mutations, a thrombin cleavage site, and C terminal polyhistidine tag (belonging to phylogenetic cluster 1).

[0310] SEQ.ID NO: 19 and SEQ.ID NO: 20 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-3 with a 15-residue anchor truncation and a mutation of the 16<sup>th</sup> residue from valine to methionine of *P. multocida* (belonging to phylogenetic cluster 3).

[0311] SEQ.ID NO: 21 and SEQ.ID NO: 22 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* challenge strain H246 (belonging to phylogenetic cluster 1).

[0312] SEQ.ID NO: 23 and SEQ.ID NO: 24 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-3 from *P. multocida* challenge strain H229 (belonging to phylogenetic cluster 3).

[0313] SEQ.ID NO: 25 and SEQ.ID NO: 26 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 with a C-terminal FLAG tag from *P. multocida* (belonging to phylogenetic cluster 1).

[0314] SEQ.ID NO: 27 and SEQ.ID NO: 28 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* with a 14-residue anchor truncation, a thrombin cleavage site, and C terminal polyhistidine tag from *P. multocida* (belonging to phylogenetic cluster 1).

[0315] SEQ.ID NO: 29 and SEQ.ID NO: 30 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-3 from *P. multocida* with a 15-residue anchor truncation, a mutation of the 16<sup>th</sup> residue from valine to methionine, a thrombin cleavage site, and C terminal polyhistidine tag from *P. multocida* (belonging to phylogenetic cluster 3).

[0316] SEQ.ID NO: 31 and SEQ.ID NO: 32 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1) with a 14-residue anchor truncation as a fusion protein to PmSLP-3 (belonging to phylogenetic cluster 3) with a 15-residue anchor truncation and a mutation of the 16<sup>th</sup> residue from valine to methionine. This construct lacks a signal peptide and contains a thrombin cleavage site between the two PmSLP proteins, as well as a second thrombin cleavage site on the C terminus, followed by a polyhistidine tag.

[0317] SEQ.ID NO: 33 and SEQ.ID NO: 34 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1) with a 14-residue anchor truncation as a fusion protein to PmSLP-3 (belonging to phylogenetic cluster 3) with a 15-residue anchor truncation and a mutation of the 16<sup>th</sup> residue from valine to methionine. This construct lacks a signal peptide, contains a serine-alanine linker peptide between the two PmSLP proteins, a C terminal thrombin cleavage site, followed by a polyhistidine tag.

[0318] SEQ.ID NO: 35 and SEQ.ID NO: 36 set forth the polynucleotide sequence and deduced amino acid, respectively, of a full length PmSLP-1 protein from *P. multocida* belonging to phylogenetic cluster 1), including the endogenous signal peptide as a fusion protein to PmSLP-3 (belonging to phylogenetic cluster 3) with a 15-residue anchor truncation and a mutation of the 16<sup>th</sup> residue from valine to methionine. This construct contains a serine-alanine linker peptide between the two PmSLP proteins, a C terminal thrombin cleavage site, followed by a polyhistidine tag.

[0319] SEQ.ID NO: 37 and SEQ.ID NO: 38 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP from *P. multocida* (belonging to phylogenetic cluster 1) from strain 1500E.

[0320] SEQ.ID NO: 39 and SEQ.ID NO: 40 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-4 from *P. multocida* (belonging to phylogenetic cluster 4.2) from strain HS-Canada1.

[0321] SEQ.ID NO: 41 sets forth a thrombin cleavage site contained once within SEQ.ID NO: 12, SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID

NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, and contained twice within SEQ.ID NO: 32.

[0322] SEQ.ID NO: 42 sets forth the endogenous signal sequence contained within SEQ.ID NO: 36.

[0323] SEQ.ID NO: 43 sets forth a polypeptide portion contained within SEQ.ID NO: 34 and SEQ.ID NO: 36 comprising a serine-alanine (SA) linker.

[0324] SEQ.ID NO: 44 sets forth a first nucleic acid primer sequence.

[0325] SEQ.ID NO: 45 sets forth a second nucleic acid primer sequence.

[0326] SEQ.ID NO: 46 sets forth a third nucleic acid primer sequence.

[0327] SEQ.ID NO: 47 sets forth a fourth nucleic acid primer sequence.

[0328] SEQ.ID NO: 48 sets forth a fifth nucleic acid primer sequence.

[0329] SEQ.ID NO: 49 sets forth a sixth nucleic acid primer sequence.

[0330] SEQ.ID NO: 50 and SEQ.ID NO: 51 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1) with a 14-residue anchor truncation as a fusion protein to PmSLP-2 (belonging to phylogenetic cluster 2) with a 14-residue anchor truncation and a mutation of the 15<sup>th</sup> residue from lysine to methionine. This construct lacks a signal peptide, contains a serine-alanine linker peptide between the two PmSLP proteins, a C terminal thrombin cleavage site, followed by a polyhistidine tag.

[0331] SEQ.ID NO: 52 and SEQ.ID NO: 53 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1) with a 14-residue anchor truncation as a fusion protein to PmSLP-2 (belonging to phylogenetic cluster 2) with a 14-residue anchor truncation and a mutation of the 15<sup>th</sup> residue from lysine to methionine, as a fusion protein to the PmSLP-3 (belonging to phylogenetic cluster 3) with a 15-residue anchor truncation and a mutation of the 16<sup>th</sup> residue from valine to methionine. This construct contains a serine-alanine linker peptide between each of the three PmSLP proteins, a C terminal thrombin cleavage site, followed by a polyhistidine tag.

[0332] SEQ.ID NO: 54 and SEQ.ID NO: 55 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1) with a 14-residue anchor truncation as a fusion protein to PmSLP-2 (belonging to phylogenetic cluster 2) with a 14-residue anchor truncation and a mutation of the 15<sup>th</sup> residue from lysine to methionine, as a fusion protein to the PmSLP-4 (belonging to phylogenetic cluster 4.2) with a 41-residue N-terminal truncation and a mutation of the 42<sup>nd</sup> residue from alanine to methionine. This construct contains a serine-alanine linker peptide between each PmSLP protein, a C terminal thrombin cleavage site, followed by a polyhistidine tag.

[0333] SEQ.ID NO: 56 and SEQ.ID NO: 57 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-2 from *P. multocida* (belonging to phylogenetic cluster 2) of *P. multocida* with a 14-residue anchor truncation and a mutation of the 15<sup>th</sup> residue from lysine to methionine. This construct contains a C terminal thrombin cleavage site followed by a polyhistidine tag.

[0334] SEQ.ID NO: 58 and SEQ.ID NO: 59 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-2 from *P. multocida* (belonging to phylogenetic cluster 2) with a 14-residue anchor truncation and a mutation of the 15<sup>th</sup> residue from lysine to methionine.

[0335] SEQ.ID NO: 60 and SEQ.ID NO: 61 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-4 from *P. multocida* (belonging to phylogenetic cluster 4.2) with a 15-residue anchor truncation.

[0336] SEQ.ID NO: 62 and SEQ.ID NO: 63 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-4 from *P. multocida* (belonging to phylogenetic cluster 4.1 with a 15-residue anchor truncation.

[0337] SEQ.ID NO: 64 and SEQ.ID NO: 65 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1) with a 14-residue anchor truncation, a mutation of the 214<sup>th</sup> residue from valine to aspartic acid, a C terminal thrombin cleavage site, followed by a polyhistidine tag.

[0338] SEQ.ID NO: 66 and SEQ.ID NO: 67 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1) with a 14-residue anchor truncation, a mutation of the 240<sup>th</sup> residue from glutamic acid to alanine, a C terminal thrombin cleavage site, followed by a polyhistidine tag.

[0339] SEQ.ID NO: 68 and SEQ.ID NO: 69 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-4 from *P. multocida* (belonging to an unclassified phylogenetic cluster).

[0340] SEQ.ID NO: 70 and SEQ.ID NO: 71 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1).

[0341] SEQ.ID NO: 72 and SEQ.ID NO: 73 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1).

[0342] SEQ.ID NO: 74 and SEQ.ID NO: 75 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-4 from *P. multocida* (belonging to phylogenetic cluster 4.1).

[0343] SEQ.ID NO: 76 and SEQ.ID NO: 77 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-4 from *P. multocida* (belonging to phylogenetic cluster 4.2).

[0344] SEQ.ID NO: 78 and SEQ.ID NO: 79 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-3 from *P. multocida* (belonging to phylogenetic cluster 3).

[0345] SEQ.ID NO: 80 and SEQ.ID NO: 81 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-3 from *P. multocida* (belonging to phylogenetic cluster 3).

[0346] SEQ.ID NO: 82 and SEQ.ID NO: 83 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-3 from *P. multocida* (belonging to phylogenetic cluster 3).

[0347] SEQ.ID NO: 84 and SEQ.ID NO: 85 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-3 from *P. multocida* (belonging to phylogenetic cluster 3).

[0348] SEQ.ID NO: 86 and SEQ.ID NO: 87 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-3 from *P. multocida* (belonging to phylogenetic cluster 3).

[0349] SEQ.ID NO: 88 and SEQ.ID NO: 89 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-3 from *P. multocida* (belonging to phylogenetic cluster 3).

[0350] SEQ.ID NO: 90 and SEQ.ID NO: 91 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-2 from *P. multocida* (belonging to phylogenetic cluster 2).

[0351] SEQ.ID NO: 92 and SEQ.ID NO: 93 set forth the polynucleotide sequence and deduced amino acid, respectively, of a PmSLP-1 from *P. multocida* (belonging to phylogenetic cluster 1).

[0352] SEQ.ID NO: 94 and SEQ.ID NO: 95 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-2 from *P. multocida* (belonging to phylogenetic cluster 2).

[0353] SEQ.ID NO: 96 and SEQ.ID NO: 97 set forth the polynucleotide sequence and deduced amino acid, respectively, of a mature PmSLP-4 from *P. multocida* (belonging to phylogenetic cluster 4.2).

[0354] Hereinafter are provided examples of specific implementations for performing the methods of the present disclosure, as well as implementations representing the compositions of the present disclosure. The examples are provided for illustrative purposes only and are not intended to limit the scope of the present disclosure in any way.

## EXAMPLES

### Example 1—Genetic Cloning, Protein Production, and Purification of PmSLP

[0355] This Example illustrates a general workflow involved in the production of recombinant PmSLP proteins in *E. coli*.

#### Cloning and Site Directed Mutagenesis

[0356] Amino-terminal truncations of PmSLP (SEQ.ID NO: 12) for protein expression and purification were designed based on key structural residues as predicted by XtalPred (Slabinski et al., 2007) and synthesized by restriction-free cloning (van den Ent & Lowe, 2006). All primers were synthesized from Sigma Aldrich and Taq DNA polymerase (Thermo Fisher Scientific) was used in PCR reactions in conditions as recommended by the manufacturers. Forward primers (15 amino acid truncation amplified with primer (SEQ.ID NO: 44), 95 amino acid truncation amplified with primer (SEQ.ID NO: 45), and 121 amino acid truncation amplified with primer (SEQ.ID NO: 46) with complementarity to the truncated amino-terminus and reverse primers (reverse primer (SEQ.ID NO: 47) to the vector plasmid pET52b were used to amplify megaprimer from pET52b containing PmSLP with a carboxy-terminal thrombin cleavage site and decahistidine tag. Megaprimer were subsequently purified by gel electrophoresis and excision following manufacturer instructions (Geneaid). Purified gene fragments were used in a linear amplification reaction around empty pET52b plasmids template. The reaction was incubated with 1 U DpnI (Thermo Fisher Scientific) at 37° C. for 1 hr to degrade the methylated template. 5 µL of the

reaction was used to transform *E. coli* MM294 cells by heat shock and 1 hr recovery in LB at 37° C. shaking. Transformants were selected on LB agar with 100 µg/mL ampicillin and grown overnight at 37° C. Single colonies were used to inoculate 5 mL LB cultures and were incubated at 37° C. overnight shaking. Plasmids were subsequently purified using MiniPrep kit following manufacturer instructions (Geneaid). Charged residues to mutate in PmSLP were predicted by the UCLA MBI SERp server (Goldschmidt, Cooper, Derewenda, & Eisenberg, 2007). Megaprimer with the mutations were amplified using forward primers (SEQ.ID NO: 48) with 10 nt complementarity flanking the mutation and reverse primers (SEQ.ID NO: 49) to the vector. Secondary PCR was performed with purified megaprimer and construct-containing pET52b templates. Constructs were transformed into and propagated in *E. coli* MM294 and were extracted by MiniPrep kit, as described above. Mutagenesis was confirmed by Sanger sequencing (TCAG) with T7 forward and reverse primers. The SERp1 mutant form of PmSLP-1<sup>94</sup> is presented in SEQ.ID NO: 17.

#### Expression and Purification of Recombinant PmSLP

[0357] Plasmids containing the PmSLP construct were transformed into *E. coli* T7 express via 45 second heat shock and 1 hr recovery in LB at 37° C. shaking. Transformants were selected on LB agar with 100 µg/mL ampicillin. Multiple colonies were used to inoculate starter cultures in 20 mL LB with 100 µg/mL ampicillin and grown at 37° C. shaking for 16 hrs. These overnight cultures were centrifuged at 4,500×g for 4 min and the pelleted cells were used to inoculate 2 L of LB and this larger culture was grown at 37° C. while shaking for approximately 3 hrs or until OD<sub>600</sub>=0.5. Protein expression was induced with the addition of Isopropyl β-D-1-thiogalactopyranoside (IPTG) to a final concentration of 5 mM and cells continued to grow overnight, shaking at 20° C. Cells were pelleted at 4500×g and resuspended in 40 mL of lysis buffer (50 mM Tris-HCl [pH 8.0], 300 mM NaCl) with 10 mM imidazole, 1 mM phenylmethylsulfonyl fluoride (PMSF), 1 mM benzamidine, 1 mg/mL lysozyme, 0.03 mg/mL DNase I. Cells are lysed by sonication (Branson) for 2.5 minutes and centrifuged for 45 min at 30,000×g to remove cell debris. The supernatant was passed through a 0.45 µm syringe filter and was incubated at 4° C. overnight shaking with 2 mL HisPur Ni-NTA resin (ThermoFisher Scientific). Beads were pelleted for 2 min at 700×g, loaded onto a gravity flow column (Econo-Pac® Bio Rad), and washed with 100 mL cold wash buffer (lysis buffer with 20 mM imidazole). Protein was eluted in 12 mL cold elution buffer (lysis buffer with 400 mM imidazole) and incubated with 2U bovine thrombin (Sigma Aldrich, cat #T4648) in dialysis against 500 mL of 25 mM Tris-HCl [pH 8.0] and 100 mM NaCl at 4° C. overnight. Dialysed sample was incubated with 100 µL HisPur Ni-NTA resin (Thermo Fisher Scientific) and 100 µL p-aminobenamidine-agarose (Sigma Aldrich) for 1 hr shaking at 22° C. Cleaved proteins were 0.22 µm syringe filtered, concentrated to 20 mg/mL by 10K MWCO concentrator (Thermo Fisher Scientific), and purified by size exclusion chromatography (Superdex 75 10/300 GL, GE Healthcare). For antigen studies, PmSLP protein was further purified on a strong anion exchange chromatography column (MonoQ 5/50 GL, GE Healthcare) to remove endotoxins (for workflow, see: FIG. 1A).

[0358] Selenomethionine incorporated PmSLP was expressed and purified as above, with a notable difference in

the growth medium. The starter culture was inoculated in 50 mL of 0.02 mg/ml methionine supplemented minimal media (M9 with final 0.2% glucose, 1 mM MgSO<sub>4</sub>, 1 mM thiamin, 0.02 mg/mL essential L-amino acids) with 100 µg/mL ampicillin, which was pelleted and subcultured into 2 L of minimal media supplemented with 0.02 mg/ml of selenomethionine (ACROS, Thermo Fisher Scientific).

[0359] FIG. 1 shows a production and purification workflow for PmSLP proteins along with example gels of purified PmSLP-3. In particular, FIG. 1A depicts a flowchart showing a schematic workflow for the purification of recombinant PmSLP. FIG. 1B depicts a SDS PAGE gel in which samples collected at different stages of Nickel NTA purification of his-tagged PmSLP-3 (SEQ.ID NO: 12) from *E. coli* lysate are shown (lane 1: whole cell lysate; lane 2: cell pellet; lane 3: soluble fraction; lane 4: flow through fraction; lane 5: wash fraction; lane 6: elution fraction). FIG. 1C shows a S75 gel filtration chromatogram of size exclusion chromatography after removal of the poly-histidine tag of PmSLP-3 (SEQ.ID NO: 14). FIG. 1D shows an SDS-PAGE gel of different fractions (B9, B10, B11, B12, C1, C2) of purified PmSLP-3 after the performance of a polishing step with the MonoQ column. PmSLP-3 migrates within the gel at approximately 35 kDa after tag removal.

#### Example 2—Phylogenetic Analysis of PmSLP Clusters and Associated Disease Types

[0360] This Example illustrates the PmSLP sequence variability in *P. multocida* isolates from bovine respiratory disease, bovine hemorrhagic septicemia, swine pasteurellosis and fowl cholera infections in birds, as well as from other host species, by constructing phylogenetic tree based on multiple PmSLP sequences. By evaluation of the phylogenetic tree, PmSLP polypeptides or immunogenic fragments, can be selected for inclusion in a veterinary vaccine formulation.

[0361] pmSLP genes were obtained from 263 publicly available assembled *P. multocida* genomes obtained from public repositories on Jun. 24, 2020 that originated from China (n=45), the USA (n=56), Iran (n=1), India (n=9), the UK (n=6), Thailand (n=3), Pakistan (n=9), Bangladesh (n=1), Canada (n=1), France (n=16), Sri Lanka (n=1), Kazakhstan (n=3), and Myanmar (n=1). Where available, information about what host animal the *P. multocida* strain was obtained from was included, including cattle (n=87), bison/buffalo (n=17), alpaca (n=2), chicken (n=10), duck (n=11), turkey (n=10), dog (n=1), human (n=12), sheep (n=4), goat (n=2), rabbit (n=20), rodent (n=2), wolf (n=2), cat (n=2), horse (n=2), boar (n=2), pig (n=59), and goose/Anatidae/avian (n=8). For sequences originating from bovine samples, sequences were stratified by disease where available (BRD vs HS) as well as by capsular serotype where annotated.

[0362] PmSLP protein sequences were aligned with MAFFT (v7.450) using the G-INS-1 algorithm. ProtTest (v3.4.2) was used to identify the most appropriate model of evolution, which was found to be WAG+I+G+F. A phylogenetic tree was generated using PhyML (v3.3.20190909) and is shown in FIG. 2.

[0363] Referring to FIG. 2, the phylogenetic tree of PmSLP variants can be seen to separate into five discrete clusters (PmSLP-1, PmSLP-2, PmSLP-3, and PmSLP-4.1, and PmSLP-4.2). On the phylogenetic tree, variants originating from bovine species are shown as the larger dark

circles. Furthermore, indicated in the four ring structures in FIG. 2, are from inner to outer ring structure: (1) host species, (2) disease, (3) geographical region, and (4) capsule type. As can be seen, BRD-PmSLP variants represent two of the four major clusters (PmSLP-1 and PmSLP-2) while HS-PmSLP variants represent a single cluster (PmSLP-3). BRD-PmSLP variants were predominantly isolated from samples originating from North America or Europe, while HS-PmSLP variants were primarily isolated from samples originating from Asia and Africa. PmSLP sequences for each cluster include PmSLP-1 (e.g., SEQ.ID NO: 2) from cluster PmSLP-1, PmSLP-2 (e.g., SEQ.ID NO: 4) from cluster PmSLP-2, PmSLP-3 (e.g., SEQ.ID NO: 6) from cluster PmSLP-3, PmSLP-4.1 (e.g., SEQ.ID NO: 8) from cluster PmSLP-4.1, and PmSLP-4.2 (e.g., SEQ.ID NO: 10) from cluster PmSLP-4.2. PmSLP-1 is at minimum 99.7% identical to the cluster PmSLP-1 sequences. PmSLP-2 is at minimum 99.7% identical to the cluster PmSLP-2 sequences and on average 100.0% identical to the cluster PmSLP-2 sequences. PmSLP-3 is at minimum 93.9% identical to cluster PmSLP-3 sequences and on average 99.4% identical to the cluster PmSLP-3 sequences. PmSLP-4.1 is at minimum 99.7% identical to the cluster PmSLP-4.1 sequences and on average 99.8% identical to the cluster PmSLP-4.1 sequences. PmSLP-4.2 is at minimum 96.8% identical to the cluster PmSLP-4.2 sequences and on average 97.2% identical to the cluster PmSLP-4.2 sequences.

#### Example 3—Evaluation of IgG Responses and Duration of Immunogenicity Using Various PmSLP-1 Containing Vaccine Formulations in Mice

[0364] This Example demonstrates that PmSLP proteins are immunogenic in a mammalian host and can be formulated with various types of vaccine adjuvants to elicit robust, long term antibody responses.

[0365] Vaccine formulations consisting of purified PmSLP-1 protein (SEQ.ID NO: 14) formulated with various adjuvants were administered to 4-6-week-old C57BL/6 mice (Charles River) to assess immunogenicity. Each formulation had a total volume of 100 µL/dose and consisted of 20 µg of PmSLP-1 protein formulated with (i) 20% (v/v) Montanide™ Gel 02 (Seppic)+3 µg Poly(I:C) (Invivogen), (ii) 20% (v/v) Montanide™ Gel 02 (Seppic), (iii) 100 µg Aluminum Hydroxide (Invivogen), (iv) 20% (v/v) Emulsigen D® (MVP Adjuvants), (v) 50% (v/v) Montanide™ ISA61 (Seppic). Two doses of each vaccine were administered via sub-cutaneous injection, 21 days apart. Serum samples were collected 20 days post Dose 1, 2 weeks post Dose 2, and at regular intervals for up to 26 weeks post Dose 2.

[0366] Serum antibody titre against PmSLP-1 protein was measured using ELISA (enzyme linked immunosorbent assay). Total anti-PmSLP-1 IgG, as well as anti-PmSLP-1 IgG subclasses (IgG1, IgG2b, IgG2c) were measured in samples collected after administering one dose and two doses of vaccine (FIG. 9). All five vaccine formulations were able to elicit PmSLP-1 specific IgG in serum after just one dose, and the IgG titre was further augmented after the second dose. PmSLP-1 specific IgG was not detected in unvaccinated naive control mice. This suggests that PmSLP-1 antigen is immunogenic in vivo and can be used in conjunction with a wide variety of adjuvants. Antibody subclass analysis showed that the predominant subclass elicited in mice is IgG1, followed by IgG2b, while IgG2c antibodies were only consistently elicited in groups that

received vaccines containing Montanide™ Gel02+Poly (I:C) or Montanide™ ISA61 adjuvants. Since different IgG subclasses have different effector functions, this suggests that the type of immune response elicited by PmSLP-1 vaccines can be further regulated through adjuvant selection.

**[0367]** The duration of immunogenicity after administering two doses of the five different PmSLP-1 formulations was assessed for up to 26 weeks (FIG. 3). PmSLP-1 specific IgG titre in serum had remained stable over the duration assessed for all groups, without any significant signs of waning. This suggests that long-lasting antibody responses can be elicited by a PmSLP-1 based vaccine.

**Example 4—Evaluation of PmSLP-1 Efficacy in a Mouse Model of Invasive Infection Against an Antigen-Matched Bovine *P. multocida* Isolate**

**[0368]** This Example illustrates the efficacy of a vaccine formulation comprising PmSLP-1. The vaccine formulation was used to immunize and then challenge mice with a *P. multocida* isolate that harbours a different PmSLP gene but from the same phylogenetic cluster as the PmSLP-1 protein included in the vaccine. In this Example, a bovine respiratory disease (BRD) *P. multocida* isolate was used for the challenge. This example further illustrates vaccine formulations can be prepared that are cross-protective against *P. multocida* infections by different strains.

**[0369]** PmSLP-1 (SEQ.ID NO: 14) was formulated as a vaccine using 20 µg of protein mixed with Montanide™ Gel 02 (Seppic) combined with Poly (I:C) (Invivogen) to a final volume of 100 µl per dose. 4-6-week-old male C57Bl/6 mice (Charles River) were given two doses of vaccine at three-week intervals via sub-cutaneous injection. Pre-challenge bleeds were collected prior to infection.

**[0370]** Two weeks after the second dose, anaesthetized animals were challenged via intra-peritoneal injection with approximately 10<sup>4</sup> CFU of log-phase *P. multocida* strain H246 (antigen-matched BRD isolate, the confirmed sequence of the PmSLP in this strain is defined in SEQ.ID NO: 22. Strain H246 is a serogroup A strain.). It is noted that SEQ.ID NO: 14 and SEQ.ID NO: 22 exhibit a sequence identity of 100% over the portion of the antigen contained in the immunizing protein. Mice were monitored every 6-12 hours post infection for clinical symptoms including lethargy, breathing, movement, dehydration, diarrhea, posture, and weight loss. A combined clinical score of 10 or higher was considered as clinical endpoint, at which point mice were humanely euthanized (FIGS. 4B, 4C and 4D). Tail vein bleeds were taken at 3, 24, 48, and 72 hours post infection, or at clinical endpoint, and bacteria was enumerated by plating on selective media (FIG. 4E). All mice that received the PmSLP-1 vaccine survived the infection, compared to all animals that received only adjuvant which reached endpoint between 24 and 32 hours post infection (FIG. 4A). Mice that were immunized with adjuvant alone were highly bacteremic, whereas mice that received PmSLP-1 either never had detectable bacteremia or were able to clear any bacteremia by 72 hours post infection.

**[0371]** Pre-challenge serum samples were evaluated against purified PmSLP-1 (FIG. 5A) or against heat killed whole *P. multocida* strain H246 (FIG. 5B). All mice that received PmSLP-1 vaccine had high levels of anti-PmSLP-1 and anti-*P. multocida* serum IgG prior to the challenge,

while mice that received only adjuvant had low levels of serum IgG against either the protein antigen or the whole bacteria.

**[0372]** These results suggest that purified PmSLP-1 protein is a highly effective vaccine antigen against *P. multocida* strains that harbour the PmSLP gene from the same phylogenetic cluster.

**Example 5—PmSLP-3 Protection in an Acute Mouse Infection Model Against an Antigen-Matched Porcine *P. multocida* Isolate**

**[0373]** This Example illustrates the efficacy of a vaccine formulation comprising PmSLP-3. The vaccine formulation was used to immunize and then challenge mice with a *P. multocida* isolate that harbours a different PmSLP gene but from the same phylogenetic cluster as the PmSLP-3 protein included in the vaccine. In this Example, a porcine *P. multocida* isolate was used for the challenge. This example further illustrates vaccine formulations can be prepared that are cross-protective against *P. multocida* infections by different strains. PmSLP-3 (SEQ.ID NO: 20) was formulated as a vaccine using 20 µg of protein mixed with Montanide™ Gel 02 (Seppic) combined with Poly (I:C) (Invivogen) to a final volume of 100 µl per dose. 4-6-week-old male C57Bl/6 mice (Charles River) were given two doses of vaccine at three-week intervals via sub-cutaneous injection. Pre-challenge bleeds were collected prior to infection.

**[0374]** Two weeks after the second dose, anaesthetized animals were challenged via intra-peritoneal injection with approximately 10<sup>4</sup> CFU of log-phase *P. multocida* strain H229 (antigen-matched porcine isolate, the confirmed sequence of the PmSLP in this strain is defined in SEQ.ID NO: 24. H229 is a serogroup A strain). It is noted that SEQ.ID NO: 20 and SEQ.ID NO: 24 exhibit a sequence identity of 99.4% over the portion of the antigen contained in the immunizing protein. Mice were monitored every 6-12 hours post infection for clinical symptoms including lethargy, breathing, movement, dehydration, diarrhea, posture, and weight loss. A combined clinical score of 10 or higher was considered as clinical endpoint, at which point mice were humanely euthanized (FIGS. 6B, 6C, and 6D). Tail vein bleeds were taken at 3, 24, 48, 78, 100 and 124 hours post infection, or at clinical endpoint, and bacteria was enumerated by plating on selective media (FIG. 13E). All mice that received PmSLP-3 vaccine survived the infection, compared to all animals that received only adjuvant which reached endpoint between 24 and 32 hours post infection (FIG. 6A). Mice that were immunized with adjuvant alone were highly bacteremic, whereas mice that received PmSLP-3 vaccine either never had detectable bacteremia, or only subclinical bacteremia.

**[0375]** Pre-challenge serum samples were evaluated against purified PmSLP-3 (FIG. 7A) or against heat killed whole *P. multocida* strain H229 (FIG. 7B). All mice that received PmSLP-3 vaccine had high levels of anti-PmSLP-3 and anti-*P. multocida* serum IgG prior to challenge, while mice that received only adjuvant had low levels of serum IgG against either the protein antigen or the whole bacteria.

**[0376]** These results suggest that purified PmSLP-3 protein is a highly effective vaccine antigen against *P. multocida* strains that harbour the PmSLP gene from the same phylogenetic cluster.

Example 6—Stability and Efficacy of PmSLP Antigens Under Different Storage Conditions

[0377] This Example takes into consideration practical aspects of utilizing PmSLPs as vaccine antigens and examines the effect of different storage conditions and lyophilization of the protein. Stability and efficacy of PmSLP antigens were evaluated by using both biophysical methods as well as in protection studies in a mouse model.

[0378] For the biophysical approach, stability of purified PmSLP-3 protein (SEQ.ID NO: 20) stored for one year after lyophilization at either 4° C. or at room temperature was evaluated by thermal denaturation utilizing the Tycho (NanoTemper) and compared to reference antigen. This approach involves measuring the intrinsic fluorescence (detected at both 350 nm and 330 nm) given off by tryptophan and tyrosine residues as a thermal ramp is applied to the sample and the proteins begin to unfold. Changes in fluorescence signal (Ratio 350 nm/330 nm) indicate transitions in the folding status of a protein and the temperature at which a transition occurs is called the inflection temperature (Ti). Comparison of the thermal denaturation profile and Ti of samples stored under different conditions provides a rapid biophysical assessment of the structural integrity of the protein.

[0379] PmSLP-3 protein that was lyophilized and stored at 4° C. or room temperature (RT) for one year was compared to reference PmSLP-3 protein, a freshly prepared sample at a concentration of 100 µg/mL in buffer (phosphate buffered saline, pH 7.4). Lyophilized proteins were reconstituted at 100 µg/mL in the same buffer prior to analysis. The thermal denaturation profiles and Tis showed no appreciable change after storage at either room temperature or 4° C. for one year when evaluating the fluorescence signals (FIG. 8A; FIG. 8B), indicating that the lyophilized proteins maintained structural integrity for this duration.

[0380] The effect of antigen lyophilization and storage at 4° C. was further evaluated *in vivo* in a mouse infection model. PmSLP-3 protein (SEQ.ID NO: 20) was formulated as a vaccine using 20 µg of protein mixed with Montanide™ Gel 02 (Seppic) combined with Poly (I:C) (Invivogen) to a final volume of 100 µL per dose. 4-6-week-old male C57BL/6 mice (Charles River) were given two doses of vaccine at three-week intervals via sub-cutaneous injection. Vaccine group 1 received formulation that was prepared fresh prior to each dose using PmSLP-3 protein aliquots that had been stored at -80° C. Vaccine group 2 received formulation that was prepared fresh prior to each dose using PmSLP-3 protein aliquots that had been lyophilized and stored at 4° C. Vaccine group 3 received formulation that was prepared fresh prior to the first dose using PmSLP-3 protein that had been stored at -80° C.; the mixed formulation was then stored at 4° C. for three weeks and administered again during the second dose.

[0381] Six weeks after the second dose, anaesthetized animals were challenged via intra-peritoneal injection with approximately 10<sup>4</sup> CFU of log-phase *P. multocida* strain H229 (antigen-matched porcine isolate, the confirmed sequence of the PmSLP in this strain is defined in SEQ.ID NO: 24). Mice were monitored every 6-12 hours post infection for clinical symptoms including lethargy, breathing, movement, dehydration, diarrhea, posture, and weight loss. A combined clinical score of 10 or higher was considered as clinical endpoint, at which point mice were humanely euthanized (FIG. 9). All mice that received any of

the PmSLP-3 vaccines were fully protected from infection, compared to all animals that received only adjuvant which reached endpoint at 21 hours post infection (FIG. 9A). Clinical scores for individual mice that received adjuvant only (FIG. 9B), Vaccine 1 (freshly prepared vaccine with protein that was stored at -80° C. until immediately prior to each dose; FIG. 9C), Vaccine 2 (freshly prepared vaccine with protein that was lyophilized and stored at 4° C. until immediately prior to each dose; FIG. 9D), or Vaccine 3 (vaccine formulated prior to dose 1 with protein stored at -80° C. and then remaining vaccine stored at 4° C. for three weeks until the second dose; FIG. 9E).

Example 7—Immunogenicity of PmSLP-1 in Cattle

[0382] This Example illustrates the immunogenicity of PmSLP vaccine in a food production animal that is impacted by *P. multocida* infection. In this Example, two different breeds of cattle were used to evaluate the immunogenicity of a PmSLP-1 vaccine. A PmSLP-1 vaccine was chosen for this Example in the cattle host since this variant is expressed by the vast majority of bovine respiratory disease (BRD) causing *P. multocida* isolates.

[0383] Healthy zebu breed cattle (age 4-6 months old) that were seronegative against all serotypes of *P. multocida* were randomized into two groups. 200 µg of lyophilized PmSLP-1 protein (SEQ.ID NO: 14) was reconstituted with PBS directly prior to vaccination and formulated with 30 µg of Poly (I:C) (Invivogen) and 20% v/v Montanide™ Gel 02 (Seppic) in a final volume of 2 mL per dose. Animals were randomized into groups and received three doses, three weeks apart, of either PmSLP-1 vaccine or adjuvant alone via sub-cutaneous injection. Blood was collected prior to vaccination (baseline), and approximately 2-3 weeks after the first, second and third dose. Serum samples were evaluated for the presence a-PmSLP-1 IgG using ELISA (enzyme linked immunosorbent assay). FIG. 10 shows the endpoint titre of cattle immunized with either PmSLP-1 vaccine or adjuvant. As shown, there is a detectable increase in PmSLP-1 specific antibody after one dose, which is substantially increased after two doses. There is minimal boosting effect with a third dose.

[0384] A second cattle immunization was performed with healthy beef cattle (age approximately 10 months old) that were seronegative against all serotypes of *P. multocida*. Animals were randomized into two groups of 9 animals each. Animals received either three doses of PmSLP-1 (SEQ.ID NO: 14) vaccine or adjuvant. Vaccine was prepared prior to each immunization by mixing 200 µg of PmSLP-1 protein that was stored at -80° C. with 30 µg of Poly (I:C) (Invivogen) and 20% v/v Montanide™ Gel 02 (Seppic) in a final volume of 2 mL per dose. Animals were vaccinated in three-week intervals intra-muscularly and bleeds were taken prior to the first immunization (baseline) and 2-3 weeks after the first, second and third dose. Serum was evaluated for the presence of a-PmSLP-1 IgG. FIG. 11 shows the endpoint titre of cattle immunized with either PmSLP-1 vaccine or adjuvant at baseline and after one, two, or three doses of vaccine. As shown, there is a detectable increase in specific antibody after one dose, which is substantially increased after two doses, with again very minimal boosting effect of a third dose.

**[0385]** Overall, the PmSLP-1 vaccine was immunogenic in both cattle breeds, with titres peaking after 2 doses of vaccine administered either intramuscularly or subcutaneously with this formulation.

Example 8—Protection of PmSLP-3 in Cattle Against a Serogroup B Strain of *P. multocida*

**[0386]** This Example illustrates the immunogenicity, safety, and protective efficacy of PmSLP vaccine in a food production animal that is impacted by *P. multocida* infection. In this Example, zebu breed cattle were used to evaluate the immunogenicity and safety of two PmSLP-3 vaccine formulations, as well as to evaluate the protective efficacy of this vaccine against lethal challenge of Serogroup B *P. multocida*. A PmSLP-3 vaccine was chosen for this Example in the cattle host since this variant is expressed by all of the known hemorrhagic septicemia (HS) causing *P. multocida* isolates.

**[0387]** Healthy zebu breed cattle (aged 4-6 months old) that were seronegative against all serotypes of *P. multocida* were randomized into three groups. 200 µg of PmSLP-3 (SEQ.ID NO 20) was reconstituted in PBS directly prior to vaccination and formulated with either 1 mg of aluminum hydroxide (Alhydrogel, Sigma-Aldrich) or with 30 µg of Poly (I:C) (Invivogen) and 20% v/v Montanide™ Gel 02 (Seppic) in a final volume of 2 mL per dose. A control group that received only adjuvant was used as the negative control. Animals were vaccinated twice in three-week intervals sub-cutaneously and bleeds were taken prior to the first immunization (baseline), prior to the second immunization (post first dose), and prior to challenge (post second dose). Serum was evaluated for the presence of a-PmSLP-1 IgG. Injection sites were monitored for local reactions after vaccination. 14 days after the booster dose, cattle were challenged sub-cutaneously with  $4.4 \times 10^4$  CFU/mL of a serogroup B strain of *P. multocida* and monitored for 8 days after infection.

**[0388]** FIG. 12A shows the endpoint titre of cattle immunized with PmSLP-3 formulated with aluminum hydroxide, PmSLP-3 formulated with Montanide Gel 02+Poly (I:C), or with adjuvant alone. As shown, there is detectable serum IgG against PmSLP-3 after two doses of vaccine with both PmSLP-3 vaccine formulations, while PmSLP-3 formulated with aluminum hydroxide elicited detectable serum IgG against PmSLP-3 after the first dose. FIG. 12B shows survival of cattle after challenge of serogroup B *P. multocida*. As shown, zebu cattle that received adjuvant only were fully vulnerable to infection and succumbed one day post infection. In comparison, 87.5% of cattle (7/8) vaccinated with PmSLP-3 formulated with aluminum hydroxide survived challenge, and 75% of cattle (6/8) vaccinated with PmSLP-3 formulated with Montanide Gel 02+Poly (I:C) survived challenge. FIG. 12C shows a table containing reactogenicity after one or two doses of vaccines. As shown, PmSLP-3 formulated with aluminum hydroxide showed no local reactions following either dose, while PmSLP-3 formulated with Montanide Gel 02+Poly (I:C) or Montanide Gel 02 alone caused local swelling in 50% of animals after the first dose.

**[0389]** Overall, PmSLP-3 vaccines formulated with either aluminum hydroxide or Montanide Gel 02+Poly (I:C) were safe, immunogenic, and protective in zebu cattle after two doses of vaccine when delivered sub-cutaneously.

Example 9—Evaluation of Efficacy of a PmSLP-2 Containing Vaccine in Ruminants

**[0390]** This Example illustrates the efficacy of a vaccine formulation comprising PmSLP-2. The vaccine formulation was used to immunize and then challenge ruminant animals with a *P. multocida* isolate. In this Example, a bovine respiratory disease (BRD) *P. multocida* isolate was used for the challenge.

Vaccine and Control Formulations

**[0391]** PmSLP-2 (SEQ.ID NO: 4) was formulated as a vaccine using 200 µg of protein in phosphate buffered saline (PBS) mixed with Montanide™ ISA 61 VG (60% v/v) to a final volume of 2,000 µl per dose and a final antigen concentration of 100 µg/mL. The vaccine formulation containing PmSLP-2 is further referred to herein as IVP 1.

**[0392]** Negative and positive controls were a saline solution and an autogenous vaccine corresponding to the challenge strain *Pasteurella multocida* A:3 strain 671/90 (Lainson F. et al., Genome Announc. 2013 Oct. 3; 1(5):e00803-13. doi: 10.1128/genomeA.00803-13), formulated with adjuvant VAP #07, respectively. *Pasteurella multocida* A:3 strain 671/90 contains a PmSLP-2 polypeptide identical to the PmSLP-2 polypeptide included in the IVP 1 formulation.

Ruminant Animals and Vaccination

**[0393]** A total of 30, three- to four-week-old healthy bovine calves from commercial animal farms, which were seronegative, or low positive for antibodies to *P. multocida*, and which were not previously vaccinated against *P. multocida*, were included in the evaluation.

**[0394]** Calves were separated into three groups: a first group of 10 calves received the IVP1 vaccine formulation, a second group of 10 calves received the autogenous vaccine, and a third group of 10 calves received a saline solution. All product administrations were performed by intramuscular injection at the left side of the neck of the animals. The animals were administered each product (i.e., IVP 1, or the autogenous vaccine, or saline solution) twice, a first time at the start of the evaluation (DO), and a second time, twenty-one days later (D21). It is noted that for purposes of this evaluation, the day an animal was first administered a product is referred to as day 0 (DO). Similarly other time points may be referred to herein, for example, as D10, or D35, meaning the 10<sup>th</sup> day or 35<sup>th</sup> day, following the first administration, respectively.

Challenge Test

**[0395]** On D35, all calves were challenged by intra-tracheal deposition of 300 ml of *P. multocida* A:3 (strain 671/90) diluted broth culture with an anticipated challenge dose concentration of  $1 \times 10^9$  Colony Forming Units (CFU) per calf (acceptable range  $5 \times 10^8$  to  $5 \times 10^9$  CFU) to the bifurcation of the main bronchus by means of a fibre-optic bronchoscope.

Safety Assessment

**[0396]** Injection site assessment was carried out on all animals prior to administration on DO and D21 then once daily for four days (D1 to D4 and from D22 to D25).

**[0397]** The injection site area was examined and scored as swelling present (Yes/No) and if present the length, breadth

and height was measured using a calibrated ruler. An assessment of pain, heat and firmness was also made for all detected swellings. No substantive swelling disqualifying animals from further participation in the evaluation was identified in any of the animals.

#### Clinical Assessment

**[0398]** Clinical observations were conducted twice on D34, pre-challenge on D35, and then approximately 4 and 9 hours later ( $\pm 1$  hour) on D35, twice daily from D36 to D41, and once on D42.

**[0399]** Each clinical observation includes assessments of demeanour, nasal discharge, coughing and respiration according to a scoring system, as set out in Table 1, as well as rectal temperature ( $^{\circ}$  C.).

TABLE 1

Parameter	Score				
	0	1	2	3	4
Rectal Temperature	37.5° C. to 39.5° C.	39.6° C. to 40.0° C.	40.1° C. to 40.9° C.	$\geq 41.0^{\circ}$ C. < 37.5° C.	N/A
Demeanour	Normal	Mild Depression	Moderate Depression	Marked Depression	Moribund/severe depression (euthanasia on welfare grounds)
Nasal Discharge	Absent	Serous	Seromucoid	Mucoid	N/A
Coughing	Absent	Sporadic, dry cough	Frequent dry cough or sporadic wet cough	Frequent wet cough	N/A
Respiration	Normal rate and character	Slightly increased rate and/or slightly abnormal character	Moderately increased rate and/or slightly abnormal character	Markedly increased rate and markedly abnormal character	Respiratory distress (euthanasia on welfare grounds)

N/A = not applicable

**[0400]** On D42, the animals were euthanized by lethal injection. The lungs were removed from each animal and the percentage lung damage, as evidenced by the presence of lesions, for each lung lobe, was recorded.

**[0401]** To enable quantitative assessment of clinical severity of the pathology developing in each animal, the observed clinical parameters at each monitoring occasion was transformed to scores. These individual scores for each clinical symptom were summed and recorded to give the total clinical score for each animal on each observation. This allowed assessment of temporal progression of pathology.

**[0402]** Clinical observation parameters were scored throughout the evaluation period in accordance with Table 1 and clinical parameter scores were statistically evaluated and used to develop bar plots, box plots, and graphs showing clinical parameter scores for the time period immediately preceding (D34) and following challenge (D35-D42) as described below.

#### Clinical Assessment Results—Rectal Temperature

**[0403]** FIG. 13A is a graph showing results of animal rectal temperature measurements upon administration of

three products, IVP 1, the autogenous vaccine, and saline solution from D34 to D42, following administration of a challenge strain to the animals on D35.

**[0404]** As can be seen in FIG. 13A, following an initial increase rectal temperature immediately following administration of the pathogenic challenge strain, the average rectal temperatures trended strongly downwards in animals having been administered the autogenous vaccine and IVP 1, recovering gradually by D42 to average or near average rectal temperatures recorded prior to administration of the challenge strain. By contrast, the rectal temperature of non-vaccinated animals (i.e., the animals having been administered saline solution) remained higher than the average rectal temperatures recorded prior to administration of the challenge strain. It is noteworthy that rectal temperatures

return to baseline (i.e., temperature prior to the challenge) faster in animals having been administered IVP 1 than in animals having been administered the autogenous vaccine.

#### Clinical Assessment Results—Demeanour

**[0405]** FIG. 13B is a bar plot showing results of animal demeanour scores upon administration of three products, IVP 1, the autogenous vaccine, and saline solution from D34 to D42, following administration of a challenge strain to the animals on D35.

**[0406]** As can be seen in FIG. 13B, following an initial reaction of depression immediately following administration of the pathogenic challenge strain of all animals, average animal demeanor recovered to relatively normal in all animal groups. However, animal demeanor in animals having been administered the IVP 1 vaccine formulation recovered somewhat faster than non-vaccinated animals (i.e., the animals having been administered saline solution).

#### Clinical Assessment Results—Nasal Discharge

**[0407]** FIG. 13C is a bar plot showing results of nasal discharge scores upon administration of three products, IVP

1, the autogenous vaccine, and saline solution from D34 to D42, following administration of a challenge strain to the animals on D35.

**[0408]** As can be seen in FIG. 13C, following an initial nasal discharge reaction immediately following administration of the pathogenic challenge strain of all animals, average animal nasal discharge recovered to relatively normal in all animal groups. However, animal nasal discharge in animals having been administered the IVP 1 vaccine formulation recovered somewhat faster than non-vaccinated animals (i.e., the animals having been administered saline solution), which exhibited lingering nasal discharge effects on D42.

#### Clinical Assessment Results—Coughing

**[0409]** FIG. 13D is a bar plot showing results of cough scores upon administration of three products, IVP 1, the autogenous vaccine, and saline solution from D34 to D42, following administration of a challenge strain to the animals on D35.

**[0410]** As can be seen in FIG. 13D, at least a sporadic dry coughing persisted in all animal groups through to D42, however coughing scores remained somewhat higher in non-vaccinated animals during the time period clinical observations were performed.

#### Clinical Assessment Results—Respiration

**[0411]** FIG. 13E is a bar plot showing results of respiration scores upon administration of three products, IVP 1, the autogenous vaccine, and saline solution from D34 to D42, following administration of a challenge strain to the animals on D35.

**[0412]** As can be seen in FIG. 13E, following an initial clear moderately increased and/or slightly abnormal respiration score immediately following administration of the pathogenic challenge strain of all animals, respiration recovered albeit never to a fully normal score in any animal groups during the time period clinical observations were performed. However, respiration in animals having been administered the IVP 1 vaccine formulation or the autogenous vaccine formulation appeared to be on a faster path to recovery towards normal respiration than non-vaccinated animals (i.e., the animals having been administered saline solution), with the animal group having received the saline formulation still exhibiting moderately or markedly increased respiration scores on D42, while these levels of

deviation from normal were not seen in animals having received the IVP 1 vaccine formulation or the autogenous vaccine formulation.

#### Clinical Assessment Results—Total Clinical Score

**[0413]** FIG. 13F is a graph showing results of total clinical score upon administration of three products, IVP 1, the autogenous vaccine, and saline solution from D34 to D42, following administration of a challenge strain to the animals on D35.

**[0414]** As can be seen in FIG. 13F following an initial sharp increase occurring immediately after administration of the pathogenic challenge strain in all animals, the total clinical score evolved to almost fully normal score (i.e., score 1) in animals having been administered the autogenous vaccine and IVP1. However, animals having received the saline formulation still exhibited moderately or markedly increased total clinical scores on D42. Of note, the total clinical score reduced faster in animals having been administered IVP 1 than in animals having been administered the autogenous vaccine.

#### Clinical Assessment Results—Total Lesion Score

**[0415]** FIG. 13G is a box plot showing results of total lung lesion scores upon administration of three products, IVP 1, the autogenous vaccine, and saline solution from D34 to D42, following administration of a challenge strain to the animals on D35.

**[0416]** As can be seen in FIG. 13G, following challenge with the pathogenic *P. multocida* strain, on D42 a statistically significantly higher consolidated lung lesion score was observed in animals having been administered the saline solution (mean % [SD]=30.90% [10.24]), than in animals having been administered the autogenous vaccine (mean % [SD]=23.25% [8.70]; p=0.049) or IVP 1 (mean % [SD]=13.29% [11.44]).

#### Serological Results

**[0417]** FIG. 13H is showing the mean group results of serum samples in a PmSLP-2 ELISA collected prior to first vaccination (D7) and at day of challenge (D35). A significant increase in serum titres against PmSLP-2 is observed only in the IVP 1 group at D35 compared to the average result of the same group at D7 and to the saline vaccinated and autogenous vaccine group at D7 and D35.

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CSGGGGNNNN VPHPPVEKRT VATTQQVAAK PTTPPSESLVK RVLNNSENNPN PSRESEKKAS	60
QTPPQTDSAK STIQSTPAVI PDRNTSLTSK KGQIQMSPEW IGKEEKKYAQ YSWEHTPESI	120
PVFKLIENNQ YYKVDDKYFT LESINLNLTK ENQVKEGSYQ FSLLDSCVYY GHYLSNDGI	180
HPEYNFVIAF DKNREYTLKD ITAEYYNSEG FNYAISDRMK GDYIWQVGDV RLFYTNGSVH	240
GEIVEVNDGS KTALFRFENT ADRNPNQIVI VPERDNRHGL SPRGDRMIMD MHFINGSDGE	300
KYKYVVGHN SDRYYGTLFA TKKDKE	326

SEQ ID NO: 7	moltype = DNA length = 933
FEATURE	Location/Qualifiers
source	1..933
	mol_type = genomic DNA
	organism = Pasteurella multocida

SEQUENCE: 7	
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caagtgcctg cgccccactt tcatgtcgtt gcaaaaaccac aacaacatgt tgaacaagaa	120
gttatttggaa agaaaacctcc agtttcagtg actagaacag caagtcaatc tagttctat	180
tcagcaaaag cggccatcaca agtatctcac gataaaaatg cggtacactg gaaaggagaa	240
tcagttctgtt aaaaagaaaca ttcttgcactt tcttacagta aagatgcgtt atttaccctg	300
cattttggtaa caaatccaaa cgctgtttat agcaactgtt ctaacctgtat tagtaaagac	360
attaaatata ttacattaac cactactgga tataatcaag ataataaagag cggtccaaac	420
tatgagttaa atttgcgtca tgaaaatatt tattacggt actatcgtt ttcacaagat	480
atgaatcatg tttttttttt ctatgtatg gggttcaaaa aagatgcaga aaatcaagat	540
aatcttcaat ttcttgcacg aatttaccaaa ggagaattttt tattctcaac ggcaacaaac	600
ccaaatgtgc cggtacttgg taaaactgttca taaaatttaca aagaaggaaa agctaaaggc	660
gaaatttctag aacgagatag caattacaaa ttatttgcata ttatgtttaa tgagccct	720
aatcaagcaa tttttttttt tgtagctgtt agactaccc cctctgtatc tattatgtat	780
acacgtaaaaa attcaccaga ccgtgttcaaa atagattttac actttttttt ggggtcaagat	840
aaccaagaaa ataaatataat tttttttttt ggggtttttt ggggtttttt ggggtttttt	900
ggtttagaga aaaaagagac caaggcagaa aaa	933

SEQ ID NO: 8	moltype = AA length = 311
FEATURE	Location/Qualifiers
source	1..311
	mol_type = protein
	organism = Pasteurella multocida

SEQUENCE: 8	
CSGGGGGGGS NSNHQAHPVN QVPAPVLHVA AKPQQHVEQE VIEKKPPPV TRTASQSSFY	60
SAKAPSQSH DKRSVHWKGE SVSEKEHLD SYSKDAVFTR HLVTNPNAVY STDPMNLSKQ	120
IKYITLTGTY YNQDNKSGPN YELNLLDENI YYGYYRDSQD MNHVENIYVY GFKKDAENQD	180
NLQFLTANYQ GEFLFSTATN PNVPVLGKAV LNYKEGKAKG EILERDSNYK LFDIYVNERP	240
NQAILNPVAE RLPTSDLIMN TRKNSPDRVT IDLHFIKGQD NQENKYIVGQ GGNEKYWGVL	300
GLEKKETKAE K	311

SEQ ID NO: 9	moltype = DNA length = 945
FEATURE	Location/Qualifiers
source	1..945
	mol_type = genomic DNA
	organism = Pasteurella multocida

SEQUENCE: 9	
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caagtgcctg cgccccactt tcatgtcgtt gcaaaaaccac aacaacatgt tgaagaatc	120
caagcccaag aaaaatgtt tgatgttgg cctctgttca atgtgttca accaatcgaa	180
tcatcaaaatt tttttttttt agaatcaccc aaaaaccacg cagacaataa gatttcaaaa	240
caatggaaatgg gggaaatccat tgccaaatgg agaaaaacacg acttttacta tagtaaagac	300
gcccgttttta cacgttccactt agtggaaaaat cccaaacgtt ttttacgacac agacccaaat	360
ctgatttagca aagaaatccca gtatataatccca ctacaaacttgc ggcataatgt tgataatgt	420
gtatgttccaa atatgttcaaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa	480
gattcacaag atatgttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa	540
gaaaaccatg aaaaatccca atcccaatccca gcaaaatccca gcaaaatccca gcaaaatccca	600
actgtgttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa	660
aaaggtttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa	720
gataagaaatccca atatgttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa	780
ataaaacttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa	840
aagggtttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa atatgttccaa	900
tggggcgtttaga gaaaaatccca accaggccatg aaaaaaaa	945

SEQ ID NO: 10	moltype = AA length = 315
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FEATURE	Location/Qualifiers
source	1..315
	mol_type = protein
	organism = <i>Pasteurella multocida</i>
<b>SEQUENCE: 10</b>	
CSGGGGGGSN NSNHQAHPVN QVPAPVHLVA AKPQQHVEEI QAEEKVVELE PLVNAQPIE 60	
SSNLSLTESTP KKPADNKISK QWEGESIAKW RKTDFNYSKD AVFTRHLVEN PKAIYDTPN 120	
LISKEIQYIK LQLGDNVNDN DAPNYELNL NENAYYGFYR DSQDMNNHVEN IYVYGFKDKA 180	
ENHENLQSLT ANYEGEFLFS TATNLNVTVT GRVVLKYQEG KAKGEILERD IDYKLFDISV 240	
DKKPQNQALN PVVEALPGSN IKLVNRPNSP DRITVDLHFI KGQDNQENKY IVGQGNGNEKY 300	
WGVLGLEKKE TRAEK	315
SEQ ID NO: 11	moltype = AA length = 975
FEATURE	Location/Qualifiers
source	1..975
	mol_type = protein
	organism = <i>Pasteurella multocida</i>
<b>SEQUENCE: 11</b>	
ATGGAAAAAC GTACCGTAAC TATACCACAA GCACAAAAAG TAGCAGAAAA ACCAGCGCTA 60	
ACAAATACAAA CAGTGGTAAC TTCACCAACT ACACCAATTAA AGCGCCCTC ACTCGCTCCG 120	
ACTATTGATA CTGCGCTAA ACAAAATCCC GTGCCGACAG CGCAAATAAC GGCTACTTTA 180	
CCAGCGAAC CTGTAAAGT GCCAGTTCTG ATTCGGAAAG TAAACAAAAC ACTTTTAGAA 240	
ACATCAACTA ATCCAGTAA AGATCTTAT AATAAAGATG CTGTATTAC ATACGAATTAA 300	
ATCGCAAACT CAGATGCAGA TTATAGCGAT CAAAATTTGA TTCTTTAAAAG AGAAATTAGT 360	
TATATCAAAC TTAATCTAGG CATAAAATCAA GACAATAAAA ATGCACCAAG CTATATTTT 420	
AATTACTAG ATGACAATGT CTATATTGTT TTTTATCGTG ATACTCAAGA TATGAACAGA 480	
ATAGAAATAA ATATATCTA TGCTTTCAA AAAAGAACCTG AAAATTTGA TAACCTTCAA 540	
AAATTAAATG CGACTTATGA AGGTCAATT TGTTTCTCTA GTATAGATAC TCCAATGTA 600	
CCTACTGTTG CAAGAGCATT CTTAACATAT AACAATGGTA GAGTGGATGG TGAAATATTG 660	
GCTAAACATT CGGAATGAAA ATTGTTTCAG ATTACTGGAT TTGATAATAA TCCTCGTAAA 720	
GTAGAAATTTC TTCTCTACTGT AGAATATTAA CCTAATTCCG GAACAAAGACT AACAAAAGGA 780	
GCCACATCAC CTCATCGTT CCAAATGGAC TTACATTCTA TCAATAGTAC AAATGGTGAA 840	
AAAAACAAAT ATCTGTCGG CCAAGGTAGT ACTGAGCAGT ACTGGGGTGT TTTAGGTATG 900	
GAGAAAAAAC AAGAGCTGC TCTGGTGCCA CGCGGTAGTT CCGCTCATCA CCACCATCAT 960	
CACCATCAC ACCAC	975
SEQ ID NO: 12	moltype = AA length = 325
FEATURE	Location/Qualifiers
source	1..325
	mol_type = protein
	organism = <i>Pasteurella multocida</i>
<b>SEQUENCE: 12</b>	
MKRRTVITPQ AQKVAEKPAL TIQTVTSPPT TPIKAPS LAP TIDTAKQNP VPTAQITATL 60	
PAEPVKVPVL IPEVNKTLLE TSTNPVKDSY NKDAFTVYEL IANPDADYSQ QKLILKKEIS 120	
YIKLNLGINQ DNKNAPSYIF NLDDDNVYYG FYRDTQDMNR IENKYTYAFK KEAENFDNLQ 180	
KFNATYEGQF WFSSIDTPNV PTVARAFLTY NNGRVDGEIL AKHWNEKLFQ ITGFDNNPRK 240	
VEIFPTVEYL PNSGTRLTKG ATSPHRFQMD LHFinSTMGE KNKYLVQGQS TEQYWGVLM 300	
EKKQELALVP RGSSAHHHHH HHHHH	325
SEQ ID NO: 13	moltype = DNA length = 912
FEATURE	Location/Qualifiers
source	1..912
	mol_type = genomic DNA
	organism = <i>Pasteurella multocida</i>
<b>SEQUENCE: 13</b>	
atggaaaaac gtaccgtaac tataccacaa gcacaaaaag tagcagaaaa accagcgcta 60	
acaatataaaa cagtggtac ttccaccaact acaccaattaa agcgccctc actcgctccg 120	
actattgata ctgcccctaa acaaaatccc gtgccgacag cgcaaataac ggctacttt 180	
ccagccgaac ctgttaagt gccagttctg attcggaaag taaacaaaac acttttagaa 240	
acatcaacta atccagtaaa agatcttata aataaagatg ctgtattac atacgaattaa 300	
atcgcaaaatc cagatgcaga ttatagcgat caaaatttga ttctttaaaag agaaatttt 360	
tatatacaac ttaatctagg cataaaatcaa gacaataaaa atgcaccaag ctatatTTT 420	
aatttactag atgacaatgt ctatattggt ttttattcgtg atactcaaga tatgaacaga 480	
atagaaaaata aataatactta tgctttcaaa aaagaagctg aaaatTTGA taaccttcaa 540	
aaatTTAAATG CGACTTATGA AGGTCAATT TGTTTCTCTA GTATAGATAC TCCAATGTA 600	
cctactgttg caagagcatt cttAACATAT AACAATGGTA GAGTGGATGG TGAAATATTG 660	
gctaaacatt ggaatgaaaa attgTTTCAG ATTACTGGAT TTGATAATAA TCCTCGTAAA 720	
gtagaaaattt tcctactgtt agaataattta CCTAATTCCG GAACAAAGACT AACAAAAGGA 780	
ccccacatcac CTCATCGTTT CCAAATGGAC TTACATTCTA TCAATAGTAC AAATGGTGAA 840	
aaaaacaaat atcttgcgg ccaaggtagt actgagcagt actggggtgtt ttttaggtatg 900	
gagaaaaaac aa	912
SEQ ID NO: 14	moltype = AA length = 304
FEATURE	Location/Qualifiers
source	1..304
	mol_type = protein

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atggaaaaac gtaccgttgc aaccacacag cagggttcgca caaaaccgcac accgccttagc  
gaaagcctgg ttaaacgttg tctgtaatac agccggaaaata atccgcctag ccgtgaaagc  
gaaaaaaaaaag caagtccagac ccctccgcag accgatagcg caaaagcac cattcagac  
acaccggcag ttatcccgta tctgttaccaat agctgttaca gaaaaaaagg tcatgttac  
atgagtcgg aatggattttg taaaagaagag aaaaaatacgc cccagtatag ctgggaacat  
acaccggaaa gtatccgggt ttttaactcg atccggaaaata accgatcacaat gtagctggat  
gacaaatattat tccatccgtt aagcattaaat ctgttacaatcg cggaaagaaaaa ccagggtgaaa  
ggaggtagct atcgatcttgc tctgttgcgtt agccgtgtt attatgttca ttatgttgc  
agcaacgtatgttcatcc cgtatataac tttgtgtatcg ctttgcataa aaaccgttg  
tatatacttgc aagatatacgc cggatataatcataatcg agggtttttatcgatcc  
agcgtatcg tggaaaggcgtt ttatattttgc cagggttgcgtt atgttgcgtt gttttatacc  
atggtagcgc tgcatgttgc aattttgttgcgtt gttatgttgcgtt atgttgcgtt  
cgctttgaaa ataccgcaga tcgtatccgc aatcagatgc ttatgttgcgtt ggaacgttg  
aatcgtatcg gtctgttgcgtt gctgttgcgtt cgtatgttgcgtt tggatgttgcgtt  
ggcagegcgc gcgagaaataa aatataatgtt gttgttgcgtt gtaacacgcgc  
ggcaccctgtt tttgttgcgtt aaaaatggatataa gag

**SEQ ID NO: 20** moltype = AA length = 311  
**FEATURE** Location/Qualifiers  
**source** 1..311  
**mol\_type** = protein  
**organism** = Pasteurella multocida

**SEQUENCE: 20**  
MEKRTVATTQ QVAAKPTPPS ESLVKRVLNN SENNPPSRES EKKASQTTPQ TDSAKSTIQS  
TPAVIPDRTN SLTSKKGQIQ MSPEWIGKEE KKYAQYSWEH TPESIPVFKL IENNQYKYVD  
DKYFTLESIN LNLTKENQVK EGSYQFSLLD SGVYYGHYLS SNDGIGHPEYN FVIAPDKNR  
YTLKIDITAYPE YNSEGFNYAI SDRMKGDYIW QVGDVRLFYNT NGSVHGEIVE VNDGSKTALF  
FRENTADRNPN QNQIVIVPERD NRHGLSPRGD RMIMDMHFIN GSDGEKYKYV VGHGNDSRY  
GTLFATKKDK E

**SEQ ID NO: 21** moltype = DNA length = 954  
**FEATURE** Location/Qualifiers  
**source** 1..954  
**mol\_type** = genomic DNA  
**organism** = Pasteurella multocida

**SEQUENCE: 21**  
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actataccac aagcacaaaaa agtagcagaa aaaccagcgc taacaatata aacagtggta  
acttccacca ctacaccaataa taaacgcgc tcaactcgctc cgactatcgta tactcgccatt  
aaaaacaaaatc cccgtggcgc acgcgcataa acggcttaccatc taccagccga acctgtttaaa  
gtgccagttc tgatccccgtt aagttacaaaa acacttttagt aacatcaac taatccgtta  
aaagattctt ataataaaaga tgctgttattt acatcagaat taatcgaaaaa tccagatgc  
gattatagcg atcaaaaaattt gattttttttt aaaaatggatataatccatataatcta  
ggcataatc aagacaatataa aatgcacca agtataattt ttaatttttactt agatgacata  
gtctttttatcg gttttttatcg tttactacta gataatggatataatccatataatcta  
tatgccttca aaaaagaagc tgaaaattttt gataacccttc aaaaattttgcgttactt  
gaaggatcaat ttgggttctc tagatgtat actccaaatg tacctactgt tgcaagacga  
ttcttcaatcataaataatgg tagatgttgcgttggaaatataatggcttaaaaaatggatataat  
aaatgttttccatcataatgg tagatgttgcgttggaaatataatggcttaaaaaatggatataat  
gttagatataatgg tacctaattc gggacaacaaga ctaacaaaaag gagccacatc accttcatcgt  
ttccaaatgg actttacattt catcaatgtt acaaataatggt aaaaaaaacaa atatcttgc  
ggcacaaggatcgttactgttgcgttgggggtt gtttttaggtt aaaaatggatataatggatataat

**SEQ ID NO: 22** moltype = AA length = 318  
**FEATURE** Location/Qualifiers  
**source** 1..318  
**mol\_type** = protein  
**organism** = Pasteurella multocida

**SEQUENCE: 22**  
CSGGGGNNNP SHSPMKEKRTV TIPQAQKVAE KPALTQITV TSPTTPIKAP SLAPTIIDTAP  
KQNPPVTAQI TATLPAEPVK VPVLIPEVNK TLEETSTNPV KDSYNKDAVF TYELIANPDA  
DYSDQKLILK KEISYIKLNL GINQDNKNAP SYIFNLLDDN VYYGFYRDTQ DMNRIENKY  
YAFKKEAENF DNLQKPFNATY EGQFWFSSID TPNVPTVARA FLTYNNGRVD GEILAKHWNE  
KLFQITGFDN NPKRVEIFPT VEYLPNNGSTR LTKGATSPHR PQMDLHFIINS TNGEKKNKYLV  
QQGSTEQYWVG VLGMEEKKQ

**SEQ ID NO: 23** moltype = DNA length = 978  
**FEATURE** Location/Qualifiers  
**source** 1..978  
**mol\_type** = genomic DNA  
**organism** = Pasteurella multocida

**SEQUENCE: 23**  
tgtatgttgcgttgggggttaa taataacaatgttaccacacc ctcctgttgcgtt aaaaacgtact  
gtggggcgcacaa cacaacaaatgttaccacacc ccaactccgc cttctgttgcgtt aaaaacgtact  
cgatctactca ataataatccgtt gataatccgtt ccatcaatcg aatgttgcgtt aaaaacgtact  
cacaatccac cacaacaaatgttgcgtt aaaaacgtactcc cccgttccatcataatggatataat

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ccagatagta	caaactctt	aacatctaag	aaaggacaaa	ttcaaatgtc	tccagaatgg	300
attggaaag	aagaaaaaaaa	gtatgcgca	tattcatgg	aacatacgcc	agaacttt	360
ccagtattta	aattaatttg	aaataaccac	tacaatatg	ttaatgataa	gtactttaca	420
ctttagatcaa	tcaatcttaa	tttgactaaa	gaaaatccag	ttaaagaagg	ttctttatcaa	480
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catccagaat	ataactttgt	gattgcgttt	gacaaaaaaca	gagaatacac	actgaaaagat	600
atcacagct	aatactataa	tctgggggt	tccaattatg	ctataatgt	tagataatgg	660
ggtgactata	tctggcaagt	gggtatgt	cgtttttatc	ataacaatgg	ttctgtgcatt	720
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gcagatagaa	acccaaatca	aatttgttatt	gtccccagaaa	gagataatcg	tcatggattat	840
tctcttcggag	gagatccgat	gataatggat	atgcatttt	ttaatggtag	tgatggagaa	900
aaataacaat	atgtatgttgg	tcacggtaat	tcagatcgat	actacggctac	actatttgcac	960
acccaaaaaa	ataaaagaa					978

SEQ ID NO: 24 moltype = AA length = 326  
FEATURE Location/Qualifiers  
source 1..326  
mol\_type = protein  
organism = Pasteurella multocida

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SEQUENCE: 24
CSGGGGNNN VPHPPVEKRT VATTQQVAAK PTPPSESLVK RVLNNSENNP PSRESEKKAS 60
QTPPQTDASAK STIQSTPAVI PDSTNSLTSK KQGQIPEW IGKEEKYYAQ YSWEHTPESI 120
PVFKLIENNN YKVYNDKYFT LESINLTLK ENQVKEGSYQ FSLLDGSVYQ GHYLSNSNDGI 180
HEPYENVIASF DKNRTEYTLKD ITAYEYNSEG FNYAISDRMK GDYIWIQVGDV RLFTYNTGSVH 240
GEIVEVNDDGS KTALEFRFENT ADRNPQNQIVI VPERDNRHGL SPRGDRMIMD MHFINGSDGE 300
KYKVYVGHGNS DRYYGTLLFA TKKDKE 326

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SEQUENCE: 26
MEKRTVTIPQ AQKVAEKPAL TIQTVVTSP TPIKAPSAPL TIDTAPKQNP VPTAQITATL 60
PAPEPVKVPV L IPEVNKTLLIE TSTMPVKDSY NKDAVFTYEL IANPDPADYSD QKLILKKEIS 120
YIKLNLGINQ DNKNAPSYIF NLDDNNVYYG FYRDTQDMNR IENKYTYAFK KEAENFDNLQ 180
KFNATYEGQW WFSSIDTPNV PTVARAFLTY NNGRVDGEIL AKHWNEKLFFQ ITGFDNNPRK 240
VEIFPTVEYL PNSGTRLTKG ATSPHRFQMD LHPINSTNGE KNKYLVGQGS TEQYWGVLM 300
EKKQDYKDDD DK 312

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SEQ ID NO: 27 moltype = DNA length = 975  
FEATURE Location/Qualifiers  
source 1..975  
mol\_type = genomic DNA  
organism = Pasteurella multocida

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SEQUENCE: 27
atggaaaaac gtaccgtaac tataccacaa gcacaaaaag tagcagaaaa accagcgta 60
acaatacaca cagtggtaac ttccaccaact acacccaatta aaggcccttc actcgctccg 120
actatttgata ctgcgcctaa acaaattccc gtgcgcagac cgcaataaac ggctacttta 180
ccagcgcgaac ctgtttaagt gcccgttctg atccccggaa taaaacaaaac acttttttagaa 240
acatcaacta atcccgatata agatctttt aataaaatggatc ctgttattttc atacgaaatta 300
atcgcaaatc cagatgcgcga ttatgcgtttt aaaaatggatc ttctttttttt aaaaatgtt 360
tatatacaac ttaatcttagg cataaatcaa gacaataaaa atgcaccaag ctatattttt 420

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aatatttaatg	cgacttatga	aggtaattt	tggttctcta	gtatagatac	tccaaatgt	600
cctactgtt	caagagcatt	cttaacat	aacaatggta	gagtggatgg	tgaaatattt	660
gtaaacat	ggaatggaaa	attgtttcag	attactggat	ttgataataa	tccctcgtaa	720
gttagaaattt	ttccactgtt	agaatattta	cctaatttcg	gaacaagact	aacaaaaggd	780
gccacatcac	ctcatcgtt	ccaaatggac	ttacatttca	tcaatagta	aaatgggtaa	840
aaaaacaaat	atcttgtcgg	ccaaaggtagt	actggcaggt	actggggtgt	tttagtgat	900
gagaaaaaaac	aagagctcgc	tctggtggca	ccgggttagt	ccgtatggga	aaaacgtacc	960
gttgcaccca	cacacgggt	tgccgaaaaa	ccgacaccgc	ctacggaaag	ctcggttaaa	1020
cgtgttctga	ataaacagcga	aaataatccg	cctagccgt	aaagcggaaa	aaaagcaagt	1080
cagacccccc	cgcgacacgg	tgccgaaaaa	agacccat	agacccaccc	ggcgttattt	1140
ccggatgtca	ccaaatagct	gaccggaaaa	aaaggccaga	ttccatgttag	tccggaaatgg	1200
attggtaaag	aagagaaaaaa	atacgcccc	tatagtcggg	aacataccacc	ggaaatgttatt	1260
ccgggtttta	aactgtatcga	aaacaaccag	tacaagtagc	tggatgacaa	atatttcacc	1320
ctggaaaggca	ttaatctggaa	cctggacggaa	gaaaaccagg	tgaagaagg	tagttatccg	1380
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ggcgattata	tctggcagggt	tggtgatgtt	cgtctgtttt	ataccatgg	tagctgtttt	1620
ggtggaaattt	tggaaaggtaa	tgatgtgtt	aaaaccgcac	tgtttcgctt	tgaaaatacc	1680
cgacatcgta	atccgaatca	gattgtttat	gtgcggaaac	tggtatatac	tcatgttctg	1740
agtcccgctg	gtgatcgat	gattatggat	atgcatttca	ttaatggcag	cgacggcgg	1800
aaatacaataat	atgttgttttgg	tcatgtgtaa	agcgatcggt	attatggcac	cctgtttgc	1860
acccaaaaaaag	ataaaagagga	gctcgcttgc	gtccacccgc	gtatgtccgc	tcatcaccac	1920
catcatcacc	atccacca	c				1941

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SEQUENCE: 33
atggaaaaac gtaccgttaac tataccacaa gcacaaaaag tagcagaaaa accagcgcta 60
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atatttgata ctgcgcttaa acaaaaatccc gtgcggacag cgcaataaac ggctacttta 180
ccagccgaac ctgttaaagt gccagttctg attccccagaag taaacaaaac acttttagaa 240
acatcaacta atccagtaaa agatttctat aataaagatg ctgttatttc atacaattta 300
atcgcaatcc cagatgcaga ttatagcgat caaaaaaaaa ttctttaaaaaa agaaatttagt 360
tatatacaac ttaatcttagg cataaaatcc gacaataaaa atgcaccaag ctatattttt 420
aattttactag atgacaatgt ctattatggt ttatctcgat atactcaaga tatgaacaga 480
atagaaaata aataatactta tgctttcaaa aaagaacatg aaaattttga taaccttcaa 540
aaattttaatc cgacttataa aggttcaattt tggttctta gtatagatc tccaaatcg 600
ctctacttttgc caagaggattt cttaaacat aacaatggta gagttgatgg tttaaatattt 660
gctaaacattt ggaatgaaaaa attgtttcag attactggat ttgataataa tcctcgtaa 720
gtagaaattt ttccactatgtt agaataatcc cttaaatccg gaacaagact aacaaaaggaa 780
gccacatcatc ctcatcgat cccaaatggac ttatccatca tcaatagatc aatagggttgc 840
aaaacaaatatttcttgc ccaaggatgt actggaggatc actgggggtt tttatgtatg 900
gagaaaaaaac aatccgtcat gggaaaaacatc accgttgcac ccacacgcg ggttgcacgaa 960
aaaccgcacac cgccttagcga aaggctgggtt aaacgtgttc tgaataacag cgaaaataat 1020
ccgccttagcc gtgaaaacgcg aaaaaaaagca agtcagaccc ctccgcacac cgatagcgca 1080
aaaagcacca ttccagacac accggcggat attccggatc gtacaaatcg ctgcacccgg 1140
aaaaaaaggtc agatccatg gatgttggaa ttggatggta aagaagagaaa aataatcgcc 1200
cagtagatcgtt gggaaacatcc accggaaatc attccgggtt tttaactgtat cgaaaacaaac 1260
cagtagatcgtt accgtggatga caaatatttc accctggaaa gcattaaatct gaaactcgacg 1320
aaagaaaacc aggtgaaaga aggttagctt cagtttagtc tgctggatag cgggttttat 1380
tatggtcatt atctgacgcg caacgcgtgtt attccatccgg aataataactt tttatgtatgc 1440
ttccgtataaaa accgttgatgtt taccctggaa gatataccgg cagaatatttta caatagcgag 1500
gggttttaactt atgcattttcg cgtatcgatc aaaggcgat attatctggca ggttggatgt 1560
tttcgtgtgtt ttatccaa ttggatcgatc catggtaaaa ttgttggaaatgtaatgtatgtt 1620

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-continued

agtaaaaccg	cactgtttcg	cttgaaat	accgcagatc	gtaatccgaa	tcagattgtt	1680
attgtgccgg	aacgtgataa	tcgtcatgtt	ctgagttccgc	gtggtgatcg	catgattatg	1740
gatatgtatc	tcaattatgg	cagcgcaggc	gagaataaca	aatatgttgc	tggtcatgtt	1800
aacagcgatc	gttattatgg	caccctgttg	gcaacaaaaa	agataaaaga	ggagtcgcgt	1860
ctgggtcccc	cgccgttagtc	cgctcatcac	ccccatcatc	accatccacca	ccac	1914

SEQ ID NO: 34 moltype = AA length = 638

## FEATURE Location/Qualifiers

source 1..638

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mol_type = protein
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SEQ ID NO: 35 moltype = DNA length = 2016

**FEATURE** Location/Qualifiers

source 1..2016

mol type = genomic DNA

organism = *Pasteurella multocida*

SEQUENCE : 35

atgcagtatt ttgacatcaa aaaatctct cctgtttttt gttcttctt gattaccgtc 60  
tgttagtggtg gtgggggtaa taacaatcca tctcacatct ctagggaaaa acgtaccgtta 120  
actataccac aagcacaaaa agtagcaga aaaccaggcg taacaataca aacagtggta 180  
atttcaccaa ctaccaaat taaggccgg tcactcgct cgactatgtt tactcgccct 240  
aaacaaatcc cccgtggccac agcgcaata acggcttact taccaggccga accgtttaaa 300  
gtgccagttc tgattcccgta agttaaacaaa acacttttag aaacatcaac taatccagta 360  
aaagattttc ataataaaaga tgctgttattt acatacaatgta taatccggaa tcccgatgtc 420  
gattatagcg atcaaaaattt gattttaaa aagaagattt gtatataatca acttaatctt 480  
ggccataatc aagacaataa aatgdcacca agctatattt ttaatattact agatgacaata 540  
gtctattatg gtttttatcg tgataactaa gatatgaaca gaatagaaaaa taaaataact 600  
tatgttttca aaaaagaagc tgaaaatttt gataaccctt aaaaattttt tgccgacttt 660  
gaaggatccat tttggtttcc tagtatagat actccaaatg tacctactgt tgcagagca 720  
ttcttaacat atacaatagg tagatggat ggtgaaaattt tgctttaaca tttggatgtaa 780  
aaattgtttc agattactgg atttgataat aatcctcgta aagtagaaaat ttttcttact 840  
gttgaatatt tacctaattt gggacaaga ctaacaatgg gggccacatc acccttactgt 900  
ttccaaatgg acttacatcatcataatgta aaaaatggt gaaaaaaacaa atatcttgc 960  
ggccaaatggta gtactggaca gtactggggt gtttttaggtg tggagaaaaaa acatcccggt 1020  
atggaaaaac gtaccgttgc aaccacacag cagggttgcag caaaaccggc accgccttagc 1080  
gaaaggctgg ttaaacctgt tctgaaataac aecgaaaaata atcccgcttg ccgtgaaaggc 1140  
gaaaaaaaaaa caagtccagac cccctccggcag ccggatagcg caaaaggac cattccagac 1200  
acaccggcag tattccggta tcgttaccaat agccgttggca gaaaaaaaagg tcaggatcc 1260  
atgagtcgg aatggatgg taaagaagag aaaaataacg cccagttatag ctgggaacat 1320  
acaccggaaa gtattccggt ttttaaactg atcgaaaaaca accagttacaa gtactgttgat 1380  
gacaatattt tcaccctgttga aacgatataat ctgaaacctga cggaaaaaaa ccaggtgaaa 1440  
gaagggtagct atcgttttag tctgttgat agccgttggttt attatgtca ttatctgagc 1500  
agcaacatgtt gtattccatcc cgaatataac ttgtgtatcg ccttcgataa aaaccgttag 1560  
tataccctgta aagatatacc cgcagaatatac tacaatagcg agggttttaa ctatggcatt 1620  
agccgtatgtc tgaaaggccga ttatctgg cagggttgggt atgttctgtt gttttatacc 1680  
aatggtagcg tgcattggta aatttgtgaa gttaatgtat gttagaaaaac cgcactgttt 1740  
cgcttggaaa ataccggcaga tcgttaatcc aatcagatgtt ttatggcc gggacgtgt 1800  
aatcgtcatg gtctgatgtcc gctgtggat cgcgttggatc tggatatgc tttcatataat 1860  
ggcaggccggc ggcgaaaaata caaatatgtt gttggccatg gtaacagcgta tggatatttt 1920  
ggccatgtt gttcaacccaa aaaaatggat gggatgtcc tcctggcc gacgggttagt 1980  
tcccgatccatc accccatcatc tcaccatcc caccac 2016

SEQ ID NO: 36 moltype = AA length = 672

SEQ ID NO: 38 Moltype = AA Length = 100  
FEATURE Location/Qualifiers

FEATURE SOURCE Location  
1 672

mol time = protein

organism = *Pasteurella multocida*

SEQUENCE: 36  
MOVENDI KUKI - B

MQYFDIKSL PVFCSSLITA CSGGGNNNP SHSPMEKRTV TIPQAQKVAE KPALTIQTVV	60
TSPTPIKAQ SLAPTIDTAP KQNPVPTAQI TATLPAPEVK VPVLIVEPNK TLLETSTNPV	120
KDSYKDAVF TYELIANPDA YADFQKLILK KEISYIKLNL GINQDNKNAP SYIFNLLDDN	180
VYYGFYRDTQ DMNRNIENKT YADFKKEAENF DNLKQKFNATL EGQFWFSSID TPVNPTVARA	240
FLTYNNGRVD GEILAKHWNIE KLFQITGFDN NPKVEIFPT VEYLPNMSGTR LTKGATSPHR	300

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FQMDLHFI NS	TNGEKNKYLV	GQGSTEQYW G	VLGMEKIQSA	MEKRTVATT Q	QVAAKPTPP S	360
ESLVKRVLNI	SENNPPSRE	EKKASQTPPC	TDSAKSTIQS	TPAVIPDRTR	SLTSKKGQIQ	420
MSPEWIGKEE	KKYAQSYWEH	TEPESIPVFKL	ENNQYQKVVD	DKYFTLESIN	LNLTKENQVK	480
EGSYQFSLLD	SGVYGGHYLS	SNDGHIPEYN	FVIAFDKNRTE	YTLKDITAEY	UNSEGFYNAI	540
SDRMKGDIYH	QVGDVRLFYI	NGSVHGEIVE	VNDGSKTA LF	RFENTADRNP	NQIVIVPERD	600
NRHGGLSFRGD	RMIIMDMHFI N	GSDGEKYKV	VGHGNSDRY Y	GTLFATKKDK	EELALVPRGS	660
SAHHHHHHHH	HH					672

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SEQ ID NO: 38 moltype = AA length = 235
FEATURE Location/Qualifiers
source 1..235
mol_type = protein
organism = Pasteurella multocida
SEQUENCE: 38
CSGGGGNNNP SHSPMEKRTV TIPQAQKVAE KPALTIQTVV TSPTTPIKAP SLAPТИDTAP 60
KQNPVPTAAQI TATLPAEPVK VPVLPIPEVNV TLLETSTPNV KDSYNDKDAFV TYELIANPDA 120
DYSDQKLILK KEISYIKLNL GINQDNKNAP SYIFNLLDDN VYYGFYRDTQ DMNRRIENKYT 180
YAFKEKAEEFN DNLOKENNATY EGOFWESSSS TPNVPTVARA ELTYNNNGRVD GEILE 235

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SEQ ID NO: 40 moltype = AA length = 315  
FEATURE Location/Qualifiers  
source 1..315  
mol\_type = protein  
organism = Pasteurella multocida

SEQUENCE: 40	60
CSGGGGGGSN NSNHQAHPVN QVPAPVLHVA AKPQOHVEEI QVEEKVVELE PLVNAQPIE	60
SSNLSLTESTP KKPADNKISK QWEGESIAKW RKTDFNYSKD AVFTRHLVEN PKAIYDTPN	120
LISKEIQYIK LQLGDVNVDNV DAPNYELNLL NENAYYGFYR DSQDMNHVEN IYVYGFKKDA	180
ENHENQLSLT ANYEGEFLS TATNLNVTVT GRVULKYQEG KAKGEILERD IDYKLFDISV	240
WCKPNQNALN PVVEALPGSN IKLVLNRPNSP DRITVDLHFI KGQDNQENKY IVGQGGNEKY	300
WGVLGLKEKKF TKAEK	315

SEQ ID NO: 41 moltype = AA length = 11  
FEATURE Location/Qualifiers

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source	1..11	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 41		
ELALVPRGSS A		11
SEQ ID NO: 42	moltype = AA length = 20	
FEATURE	Location/Qualifiers	
source	1..20	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 42		
MQYFDIJKSL PVFCSSLITA		20
SEQ ID NO: 43	moltype = AA length = 14	
FEATURE	Location/Qualifiers	
source	1..14	
	mol_type = protein	
	organism = synthetic construct	
SEQUENCE: 43		
VLGMEKKQSA MEKR		14
SEQ ID NO: 44	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 44		
taactttaag aaggagatat acatatggaa aaacgtaccg taactatacc		50
SEQ ID NO: 45	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 45		
taactttaag aaggagatat acatatgaca tcaactaattc cagtaaaaaga		50
SEQ ID NO: 46	moltype = DNA length = 48	
FEATURE	Location/Qualifiers	
source	1..48	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 46		
taactttaag aaggagatat acatatggat tatagcgatc aaaaatttg		48
SEQ ID NO: 47	moltype = DNA length = 53	
FEATURE	Location/Qualifiers	
source	1..53	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 47		
actaccgcgt ggcaccagag cgagcttcttg tttttctcc atacctaaaa cac		53
SEQ ID NO: 48	moltype = DNA length = 50	
FEATURE	Location/Qualifiers	
source	1..50	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 48		
ggtgttttag gtatggcgcc agcacaagag ctgcgtctgg tgccacgcgg		50
SEQ ID NO: 49	moltype = DNA length = 52	
FEATURE	Location/Qualifiers	
source	1..52	
	mol_type = other DNA	
	organism = synthetic construct	
SEQUENCE: 49		
caccagagcg agctcttgcg ctgcggccat acctaaaaca ccccaagtact gc		52
SEQ ID NO: 50	moltype = DNA length = 1818	
FEATURE	Location/Qualifiers	
source	1..1818	
	mol_type = genomic DNA	
	organism = Pasteurella multocida	
SEQUENCE: 50		

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atggaaaaac gtaccgtAAC tataccacAA gcacaaaaAG tagcagaaaa accagcgCTA	60
acaatacAA cagtggtaAC ttccaccaACT acaccaATTAA aagcgccCTC actcgctCCG	120
actattgata ctgcgcctAA acaaaatccc gtgcgcagAG cgcaaaataAC ggctactTTA	180
ccagccGAAC ctgttaaAGT gccagttCTG attccCGAAG taaacAAAC acTTTtagAA	240
acatcaACTA atccAGtAA agattCTTA aataaAGATG ctgtatttAC atacGAATTa	300
atcgcaaaTC cagatgcAGA ttatAGCgAT caaaaATTGA ttcttAAAAA agaaaATTAGT	360
tatatacAAAC ttaatCTTAGG cataAAATCAA gacaATAAAAt ATGCAACAG CTatATTT	420
aatttactAG atgacaATGT ctattatGGT ttttATCGTg ATACTCAAGA tatGAACAGA	480
atagaaaATA aataAACTTA tgcttCAAA aaAGAAGCTG AAAATTGTA taacCTTCA	540
aaatttAAATG cgacttATGA aggtCAATTG ttGTTCTCTA gtatAGATAC tccAAATGTA	600
cctactGTGtA caagAGCATT cttAACATAT aacaATGGTA gagTGGatGG tgaAAATTG	660
gctaaacATT ggaatgAAAC attgttCAG attactGGAT ttGATAATAA tcctCGTAA	720
gtagaAAATT ttccTACTGT agaataTTTA cctaATTcGG gaacaAGACT aacAAAGGA	780
gccacatCAC ctcATCGTTT ccaaATGGAC ttacATTcA tcaATAGTAC AAATGGTGA	840
aaaacAAACAT atcttGTCGG ccaaggTAGT actgAGCAGT actGGGGGTG tttAGGTATG	900
gagaaaaAAAC aatccGCTAT ggaatgACG cctgtGGTA ctGAACAAGC cAAACAGCT	960
aaagaAGTGA ttttACCTAC accCTCTATT ggatCAGAAC agtcatCTCA aaACGTATA	1020
gctaaAGATG ctttCAATGT gaggcAAAAAC acgcATCACAC actCCAAACC agaaaaAAATT	1080
gcaAAAGATG ttaattGGAC aggtAGTGTCTA taggCTCTAC ttggTGGCA	1140
cataAAACCA AATAATTCC ttttttACCA ctaattCTTA atgaaaACCA aatttACTCC	1200
gatgaaaaAA ACTTCACTCT agaACAAAAA catATTGATC ttacAAAGAA taatTTTG	1260
gatgaaaaAGT actttCATTT cacATTAA gactCCGGAA ttTATATTGG aaATTATTAA	1320
agttcatacG atcAGATGAA cgcAGATCTT aattATGTTT ttGATTTGA taAGATCTG	1380
gaatatacAG gaaAGATAT CACCGCAAT TATTATGGTA atGAAGGATT TAATATTCT	1440
gtAAAATTAG gtaatacATA CCTATCACAG GTGGGTGATG ttCACTTAAT CTATCGAGAA	1500
gggaaAGATG caggAGAAAT ttTTGTCAA aataACGTAA AACACCTTA CGTATTAAT	1560
agoaataAAAT ttGACCAAA tagCATTGTt ATTGTCCCAG aagaAGCACA TCGATATCTA	1620
tccAGAAATG atAAATGTT CTTAGAAATG CATTTCATTA atGGGGAAA TGGAGAAA	1680
tataAAATATA ttGTGGTAG TGGTAAACG gacaAAATACT acGGCGCATT ATTGCAACT	1740
aaacaAGAAA accAGGAGCT CGCTCTGGT CCACGCGGTa GtCCGCTCA tcaccACCAT	1800
catcacCCATC accACCCAC	1818

SEQ ID NO: 51	moltype = AA length = 606
FEATURE	Location/Qualifiers
source	1..606
	mol_type = protein
	organism = Pasteurella multocida
SEQUENCE: 51	
MEKRTVTIPQ AQKVAEKPAL TIQTVVTSP TPIKAPSLAP TIDTAPKQNP VPTAQITATL	60
PAEPVKVPVL IPEVNLKLL E TSTNPVKDSY NKDAVFTYEL IANPDADYSQ QKLILKKEIS	120
YIKLNLGINQ DNKNAPSYIF NLLDDNVYYG FYRDTQDMNR IENKYTYAFK KEAENFDNLQ	180
KFNATYEGQF WFSSIDTPNV PTVARAFLTY NNGRVDGEIL AKHWNEKLFQ ITGFDNPNRK	240
VEIFPPTVEYL PNSGTRTLKG ATSPHRFQMD LHFINSTNGE KNKYLVGQGS TEQYWGVGLM	300
EKKQSAMEVR PVVTEQAKTA KEVILTPPSI GSEQSSQNVI AKDAFNVSEK THQHSKPEKI	360
AKDINWTGSA VSSIGSTWWQ HKPNNIPVPT LILNENQIYS DEKNFTLEQK HIDLTKNNIL	420
DEKYFHFTLL DSGIYYGNYL SSYDQMNAES NYVFADFDR EYTGKDITAN YYGNEGFKYS	480
VKLGNNTYLSQ VGDVHLIYRE GKVSGEIFQO NNVKHFSFMN SNKIDPNSIV IVPEBAHRYL	540
SRNDKMPLEM HFINGENGEK KYIIVGSGKT DKYYGALPAT KOENQELALV PRGSSAHHHH	600
HHHHHH	606

SEQ ID NO: 52	moltype = DNA length = 2757
FEATURE	Location/Qualifiers
source	1..2757
	mol_type = genomic DNA
	organism = Pasteurella multocida
SEQUENCE: 52	
atggaaaaAC gtaccgtAAC tataccacAA gcacaaaaAG tagcagaaaa accagcgCTA	60
acaatacAA cagtggtaAC ttccaccaACT acaccaATTAA aagcgccCTC actcgctCCG	120
actattgata ctgcgcctAA acaaaatccc gtgcgcagAG cgcaaaataAC ggctactTTA	180
ccagccGAAC ctgttaaAGT gccagttCTG attccCGAAG taaacAAAC acTTTtagAA	240
acatcaACTA atccAGtAA agattCTTA aataaAGATG ctgtatttAC atacGAATTa	300
atcgcaaaTC cagatgcAGA ttatAGCgAT caaaaATTGA ttcttAAAAA agaaaATTAGT	360
tatatacAAAC ttaatCTTAGG cataAAATCAA gacaATAAAAt ATGCAACAG CTatATTT	420
aatttactAG atgacaATGT ctattatGGT ttttATCGTg ATACTCAAGA tatGAACAGA	480
atagaaaATA aataAACTTA tgcttCAAA aaAGAAGCTG AAAATTGTA taacCTTCA	540
aaatttAAATG cgacttATGA aggtCAATTG ttGTTCTCTA gtatAGATAC tccAAATGTA	600
cctactGTGtA caagAGCATT cttAACATAT aacaATGGTA gagTGGatGG tgaAAATTG	660
gctaaacATT ggaatgAAAC attgttCAG attactGGAT ttGATAATAA tcctCGTAA	720
gtagaAAATT ttccTACTGT agaataTTTA cctaATTcGG gaacaAGACT aacAAAGGA	780
gccacatCAC ctcATCGTTT ccaaATGGAC ttacATTcA tcaATAGTAC AAATGGTGA	840
aaaacAAACAT atcttGTCGG ccaaggTAGT actgAGCAGT actGGGGGTG tttAGGTATG	900
gagaaaaAAAC aatccGCTAT ggaatgACG cctgtGGTA ctGAACAAGC cAAACAGCT	960
aaagaAGTGA ttttACCTAC accCTCTATT ggatCAGAAC agtcatCTCA aaACGTATA	1020
gctaaAGATG ctttCAATGT gaggcAAAAAC acgcATCACAC actCCAAACC agaaaaAAATT	1080
gcaAAAGATG ttaattGGAC aggtAGTGTCTA taggCTCTAC ttggTGGCA	1140
cataAAACCA AATAATTCC ttttttACCA ctaattCTTA atgaaaACCA aatttACTCC	1200

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gataaaaaaaaa	acttcactct	agaacaaaaaa	catattgtac	ttacaagaa	taatatttt	1260
gatggaaaagt	actttcattt	cacatttata	gactccggaa	tttatattgg	aaattattta	1320
agtctcatacg	atccatgttt	cgccgaaat	aattatgttt	ttgcatttg	taaagatcgt	1380
gaatatacag	gaaaagat	caccgcata	tattatggta	atgaaggatt	taataatgtt	1440
gtaaaattag	gtatacata	cctatccacag	gtgggtatg	ttcaactta	ctatcgagaa	1500
gggaaagtat	caggagaaat	tttttgttcaa	aataacgtaa	aacacatttg	ctttatgtaa	1560
agcaataaaaa	tttgccccaa	tagcatgtt	attgtcccg	aagaagcaca	tcgatata	1620
tccagaaatg	ataaaatgtt	cttagaaat	cattttcatta	atggggaaaa	tggagaaaaa	1680
tataataata	tttgtggtag	tggtaaaacg	gacaataact	acggccatt	atttgcact	1740
aaacaagaaa	accagtccgc	tatggaaaaaa	cgtacccttg	caaccacaca	gcaggttgca	1800
gcaaaaaacg	caccgcctag	cgaaaaacgtc	gttaaacatgt	ttctgtataaa	caggaaaaat	1860
aatccgcctt	gcccgtaaag	cgaaaaaaa	caaggtcaga	ccccccgc	gaccgtatgc	1920
gcaaaaaacg	ccatcccgag	cacacccgg	gttattcccg	atcgatccaa	tagccgtacc	1980
agcaaaaaag	gtcagatttca	gatggatcc	gaatggattt	gttaagaaga	aaaaaaatac	2040
gccctgat	tgtgggaaaca	tacacccggaa	agttatccgg	tttttaatct	gatcgaaaaa	2100
aaccgtata	agtaatgttca	tgacaaaat	ttcacccctgg	aaagacttta	tctgaaacctt	2160
acggaaaaaa	accagggttga	agaagggtac	tatcaggta	gtctgtctgg	tagccgttgg	2220
tattatggtc	attatctgag	cagcaacgt	ggtatttcatc	ccgaatataa	ctttgtgtac	2280
gccttcgata	aaaacccgtt	gtataccctg	aaagatatac	ccgcagaata	ttacaatagc	2340
gagggtttta	actatccat	tagcgtatgt	atgaaaggcg	attatatctg	cgagggttgtt	2400
gtatgtcg	tgttttatac	caatgttgc	gtgcattgtt	aaatttgttga	agttaatgt	2460
ggtagtaaaa	ccgcactgtt	tcgtttgaa	aatacccgag	atcgtaatcc	gaatcgatt	2520
gttattgtgc	cggaacgtt	taatcgtcat	ggtctgagtc	cgccgttgta	tcgcattgt	2580
atggatcatgc	atttcattaa	tggcagcgac	ggcgagaaaat	acaataatgt	ttgttgttcat	2640
ggttaacagcg	atcggttata	tggccacctt	tttgcaccca	aaaaagataa	agagggtcct	2700
gcttcgtgc	cacgcgtgtt	tcgtccgtct	caccacccat	atcaccatca	ccaccac	2757

SEQ ID NO: 53 moltype = AA length = 919  
FEATURE Location/Qualifiers  
source 1..919  
mol\_type = protein  
organism = Pasteurella multocida

SEQUENCE :	53	ORGANISM : <i>Escherichia coli</i>
MEKRTVTIPO	AQKVAAEKPAL	TIQTVTUVTSPT
PAEPVKVPKV	IPEVNVKTLLE	TSTNPVKDSY
YIKLNLINQIN	DNKNAPSYIF	NKDAVFTYEL
KFNATYEGQF	WFSSIDTPNV	IANPADDYSQ
VEIFPTVEYL	PNSGTRLTKG	QKLILRKKEIS
EKKQSAMEVR	PPVTEQAKTA	TKDFTQDMNR
AKDINWTGSA	VSSIGSTWQ	IENKYTYAFK
DEKYFHFTLL	DSGIYYGNYL	KEAEFNDLNQ
VKLGNNTYLSQ	VGDVHLIYRE	ITGFDNNPRK
SRNDKMFLEM	GKVSGEIFGQ	18
AKPTPPSES	HFGINGENGEK	19
SKKGQIQMSP	YKIVIGSGKT	20
TKENQVKEGS	DKYYGALFAT	21
EGFNYAISDR	KVRFVLNNSEN	22
VIVPERDNRH	NPPSRESEKK	23
ALVPRGSSAH	ASQTPQPTDS	24
GLSPRGDRMI	SIPVFKLIEN	25
MDMHFIGNSD	QNYKVVDDKY	26
GEKYKVVGH	FTLESINLNL	27
GNSDTRYGTL	TKTLEQHK	28
FATKDKHEEL	HIDLTKNNIL	29
90	DEKFNTLEQK	30
91	RTVATTCQQA	31
92	RTVATTCQQA	32
93	RTVATTCQQA	33
94	RTVATTCQQA	34
95	RTVATTCQQA	35
96	RTVATTCQQA	36
97	RTVATTCQQA	37
98	RTVATTCQQA	38
99	RTVATTCQQA	39
100	RTVATTCQQA	40

SEQUENCE:	54	Organism - Pasteurellia mitocida				
atggaaaaac	gtaccgtaac	tataccacaa	gcacaaaaag	tagcagaaaa	accagcgcta	60
acaatataaa	cagtggtaac	tttcccaact	acaccaatta	aaggcccttc	actcgctccg	120
actattgtta	ctgcgcctaa	acaaaatccc	gtgccgacag	cgcaaaaaac	ggtactttta	180
ccagccgaaac	ctgtttaaagt	gccagttctg	atccccaaag	taaaaaaaac	acttttagaa	240
acatcaacta	atccagtaaa	agattcttat	aataaaagatg	ctgttattac	atagaattta	300
atcgcaaatc	catatgcaga	ttatagcgat	caaaaaattga	ttctttaaaaa	agaaatttagt	360
tatataaacc	ttatattttag	catataatcaa	gacaataaaaa	atgcaccaag	ctatattttt	420
aattttactag	atgacaatgt	cttattatgtt	ttttatctgt	atactcaaga	tatgaacaga	480
atagaaaaata	aatatactta	tgctttccaa	aaagaqaatgt	aaaattttga	taaccccttaa	540
aaatttaatgt	cgactttatga	aggtcaattt	tggttctcta	gtatagatac	tccaaatgtta	600
cctactgttg	caagagcatt	cttaacatat	aacaatgttta	gagtggatgg	tgaatatttgg	660
gctaaacattt	ggaatgtaaaa	attgtttccat	attacttgtt	ttgtatataaa	tccctgttaaa	720
gttagaaaaattt	ttcttactgt	agaatattta	cctaaatccg	gaacaagact	aacaaaggaa	780
ccacatcac	ctcatcggtt	ccaaaatggac	tttacatttca	ctaatatgtac	aaatgttggaa	840
aaaaacaaat	atcttgcgg	ccaaaggatgt	actgagcagt	actgggggtgt	tttaggtatg	900
gagaaaaaaaaac	aatccgctat	ggaaggtaacgc	cctgtgtttaa	ctgaacaacgc	caaaacagct	960
aaagaagtgta	tttttacctac	acccttattt	ggatccaaac	agtcatctca	aaaacgtata	1020
gctaaatggat	ctttcaatgt	gagcggaaaaa	acgcatcaac	actccaaacc	agaaaaaaatt	1080
gaaaaatgtata	ttatggac	aggatgttgt	gtgtcgctta	taggtcttac	ttttggccaa	1140
cataaaaccaaa	ataatattcc	tgtttttaca	ctaattttta	atgaaaccca	aattttactcc	1200



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MEVRPVVTEQ	AKTAKEVILP	TPSIGSEQSS	QNIAKDAFN	VSEKTHQHSK	PEKIAKDINW	60
TGSAVSSIGS	TWWQHPKNNI	PVFTFLILNEN	QIYSDEKFT	LEQKHIDLTK	NNILEDKYFHH	120
FTLLEDSGIYY	GNYLSSDYMM	NAESNYVFAF	DKDREYTGKD	ITANYGYNEG	FKYVKLGFH	180
LTSQVGDFVHL	TYIREKGVSGE	I FGQNNVVKH	SDFMNSNKIDP	NSIVIPEEEA	HRYLSRNDKM	240
FLEMHFINGE	NGEKYKYIVG	SGKTDKYGA	LFATKQENQE	LALVPRGSSA	HHHHHHHHHH	300

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SEQ ID NO: 58          moltype = DNA    length = 837
FEATURE                Location/Qualifiers
source                 1..837
                      mol_type = genomic DNA
                      organism = Pasteurella multocida
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SEQUENCE : 58

atggaaatgc	gcccgttgtt	aactgaacaa	gccaaaaacag	ctaaagaagt	gattttacct	60
acaccctcta	ttggatcaga	acagtcatct	caaacaacgtt	tagctaaaga	tgtcttcataat	120
gtgaggcgaaa	aaacggcatac	acactccaaa	ccagaaaaaa	ttgcaaaaaa	tattaattgg	180
acaggatgtg	ctgtgtcgtc	tataggctt	acttgggtgc	aacataaaacc	aaataatatt	240
ctgtttttta	cactaatttc	taatggaaaac	caaatttatc	ccgtatggaaa	aaacttccat	300
cttagaacaaa	aaacatatttg	tcttacaaag	aataatattt	ttggatggaaa	gtactttcat	360
ttcacattat	tagactccgg	attttttt	ggaaatattt	taagttcata	cgatcagatg	420
aacgcagaat	ctaattatgt	ttttgcattt	gataaaggatc	tggtatatac	aggaaaagat	480
atccacggcaa	attttatgg	taatggagga	ttaaatat	ctgtaaaaatt	aggttaataca	540
taccttatcac	agggtgggtg	tgttcaactt	atctatcgag	aaggggaaatg	atcaggagaa	600
atttttggtc	aaaataacgt	aaaacactt	agctttatga	atagcaataa	aattgaccca	660
aataggatgg	ttatgttcc	aaagagaagca	catcgatatac	tatccggaaaa	tgataaaatg	720
ttcttagaaaa	tgcatttcat	taatggggaa	aatggggaaaa	aatataaaaat	tatgtgggt	780
agtggaaaaa	cggacaaaata	ctacggcgca	ttatggcaat	ctaaacaaga	aaaccagg	837

SEQ ID NO: 59 moltype = AA length = 279  
FEATURE Location/Qualifiers  
source 1..279  
mol\_type = protein  
organism = Pasteurella multocida

SEQUENCE: 59

MEVRPVVTEQ	AKTAKEVILP	TPSIGSEQQ	QNIKADAFN	VSEKTHQHSK	PEKIADINW	60
TGSAVSSIGS	TWWQHPKNNI	PVFTFLILNEF	QIYSDEKFT	LEQKHIDLT	NNILDEKYFH	120
FTLLDGSIYY	GNYLLSDYQDN	NAESNYVFCAF	DKDREYTGKD	ITANYYGNEG	FKYSVKLGN	180
LTSQVGDVHL	TYIREKGVSGE	IFGQNQNVKHF	SFMNSNPKLDM	NSIVIVPEEA	HRYLSRNDKM	240
FLEMHFINGE	NGEKYKYIVG	SGKTDKYVGA	LFATKQENQ			279

SEQUENCE : 60

gctcatcgtt	ttaatcaagt	gcgtcgcccc	gtacttcatg	tttgtctaaa	accacaacaa	60
catgttgaag	aatccaagc	cgaagaaaaa	gttgtttagt	tagaacctct	agtcaatgt	120
gctcaaccaa	tgcgtatcc	aaattttcc	ctaacaaggat	caccctaaaa	accacgac	180
aataaggatt	caaaacatg	ggaaaggggaa	tccatggaaa	aatggagaaa	aacagactt	240
aactatagta	aagacccgtt	ttttcacatgt	cacttagtgg	aaaatccaa	agtctttac	300
gacacagacc	caaatactgtat	tagcaaagaa	atccagttata	ttaaaactaca	actaggcgt	360
aacgttggata	atgtggatgc	tccaaactat	gaattaatt	tactcaatgt	aatgttttac	420
tatgttttct	atcgttgatcc	aaaagatgtat	accatgttg	aaaatatctt	tgtgtatggaa	480
ttttaaaaaa	atgcgaaaaaa	ccatgaaaaat	cttcaatctt	taaccgcaaa	ttatggaa	540
gaatttttat	tttcaatctg	gacaaattttt	aatgtgtactt	tttacaggaa	agtctgtactt	600
aaatatcaag	agggttaaagg	taaagggtttaa	attcttagaa	gagatatcg	ttacaaaatttt	660
tttggatataat	ctgttgatataa	gaaaacctaa	caagcttattt	ttaatccctt	tgttagaggcc	720
tttacagggtt	caataatataaa	acttggtaat	cgtccaaattt	caccagaccc	tatcccggtt	780
gattttactt	ttttaaagggg	tcaagataat	caagaaaaaa	aatatattgt	agggtcaagggg	840
ggtaatggaa	aatattgggg	cgtttaggtt	tttagagaaaa	aagagaccaa	ggcagaaaaaa	900

SEQ ID NO: 61 moltype = AA length = 300  
FEATURE Location/Qualifiers  
source 1..300  
mol\_type = protein  
organism = Pasteurella multocida

SEQUENCE: 61  
 AHPVNQVPAP VLHVAAKPQQ HVVEIQAEEK VVELEPLVNV AQPIESSNLS LTESPKKPAD 60  
 NKISKQWEGE SIAKWRKTDF NYSKDAVFTL HLVENPKAIY DTDPNLISKE IQYIKLQLGD 120  
 NVNDNVDPNLY ELNNLLNENAY YGFYRDSQDM NHVENIVYVG FKKDAAHENH LQSLTANYEG 180  
 EFLFSTATNLY NVTYITGRVVL KYQBGKAGE ILERIDYIKL FDISDDKPN QAILNPVVEA 240  
 IEGCNCWVHLI DPGCDBDRLT DHEUICGDN CPTKUWJCS CPEKUWJCS G LEKPCWJCS

SEQ ID NO: 62 moltype = DNA length = 888  
FEATURE Location/Qualifiers  
SOURCE 1 888

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mol_type = genomic DNA
organism = Pasteurella multocida

SEQUENCE: 62
gtccatcctg ttaatcaagt gcctgcgccg gtacttcatg tcgctgcggaaa accacaacaa 60
catgttgaac aagaagttat tgagaagaaa cctccagttc gaggacttag aacagcaagt 120
caatctagg ttctattcage aaaagcgcca tcacaaggat ctcacgatcaa aagatcggt 180
cactggaaag gagaatcagt ttctgaaaaa gaacatcttg acttcttca cagtaaagat 240
ggcgatatta cccgtcattt ggtaacaaaat ccaaacgcgtt tttatgcac tgatccta 300
ctgatttagta aagacattaa atatattaca ttaaccacta ctggatataa tcaagataat 360
aagagcggtc caaaatcatgaa gttaaatttt ctcgatgaaa atatattata cggttactat 420
ctgttatttttca aagatatacg ttcatgttggaa aatattctatgatatgggtt caaaaaaagat 480
gcgaaaaatc aagataatct tcaatttcta acagcaaat accaaggaga atttttattt 540
tcaacggcaa caaacccaa tttgtccggta cttagttaaag ctgttctttaa ttacaagaa 600
ggaaaagctt aaggcgaaat tcttagaaacgat gatagcaat aacaattttt tgatatttt 660
gttaatgagc gcccattatca agcaattttt aatccctgttag ctgaaagact acctacctt 720
gatcttattt tgaatcacg taaaattca ccagaccgtt tcacaataga ttacactt 780
attaagggtc aagataacca agaaaataaa tatattgttag gtcaaggggg taatgaaaaa 840
tattgggctc tatttaggttt agagaaaaaa gagaccaagg cagaaaaaa 888

SEQ ID NO: 63      moltype = AA length = 296
FEATURE           Location/Qualifiers
source            1..296
mol_type = protein
organism = Pasteurella multocida

SEQUENCE: 63
AHPVNQVPAP VLHVAAKPQQ HVEQEVIKKK PPVRVTRTAS QSSFYSAKAP SQVSHDKRSV 60
HWKGESVSEK BHLDPSYSKD AVFTRHLVTN PNAVYSTDPN LISKDIKYIT LTTTGYNQDN 120
KSGPNYELNL LDENIYYGYY RDSQDMNHBV NIIVYGFKKD AENQDNLQFL TANYGEFLF 180
STATNPNVPV LGKAVALNYKE GKAKGEILER DSNYKLPDIY VNERPNQAIL NPVAERLPTS 240
DLIMNTRKNS PDRVTIDLHF IKGQDNQENK YIVGQGGNEK YWGVLGLEKK ETKAEK 296

SEQ ID NO: 64      moltype = DNA length = 975
FEATURE           Location/Qualifiers
source            1..975
mol_type = genomic DNA
organism = Pasteurella multocida

SEQUENCE: 64
atggaaaaac gtaccgtAAC tataccacAA gcacaaaaAG tagcagaaaa accagcgctA 60
acaaatccAAA cagtggttaAC ttccacaATT acaccaATT aagcgccCTC actcgctCC 120
actattttttCA ctgcgtcCAA aaaaaATCCC gtgcccAGAC cgcaaaATAAC ggctactttA 180
ccagccGAAC ctgtttAAAGT gccaGTTCTG attccCGAAG taaacaaaaAC acttttagAA 240
acatcaACTA atccAGTAAAG agatttttA aataaaAGATG ctgttatttAC atacGAATTA 300
atcgcaAACTC cagatGcGAAT ttatcgCAt caaaaaaaaAGAAGAAATTAGT 360
tatatacAAC ttaatctAGG cattaaACG aacaataAAAt atgcaccaAG ctatatttt 420
aattttactAG atgacAAatGT ctattttAGT ttttAtcGtGt atactcAAGA tatgaaACAGA 480
atagaaaaAA AATATACTTA tgctttCAAAG aaagaAGCTG AAAATTGTA taacCttCAA 540
aaatTTAAAG CGACTCTTA AGGCTTAATG ttggttCtCTA gtatAGATAC tccaaATGAT 600
ctcaactGTTG caagAGCATT CttaaACATAT aacaatGTTG gaggGatGTT tgaaatATTG 660
gtctaaACATT GGAATGAAAA ATTGTTCAgG attactGgttG ttgataatTA tcctcgtaAA 720
gttagaaATTt TTCTCTACTGT agaaatTTTA cctaattCggG gaacaAGACT aacAAAGGA 780
cccacatCAC CTCATGTTT CCAAATGGAC ttacatttCA tcaatAGTAC aaatGTTGAA 840
aaaacaaatATCttGTCGG ccaaggTAGT actggacGATG actgggggtGT tttaggttG 900
gagaaaaaaAC aagacGTCGc tctggtgccA cgcggtagt ccgctcatca ccaccatcat 960
caccatCAC ACCAC 975

SEQ ID NO: 65      moltype = AA length = 325
FEATURE           Location/Qualifiers
source            1..325
mol_type = protein
organism = Pasteurella multocida

SEQUENCE: 65
MEKRTVTIPQ AKVVAEKPAL TIQTVTSPT TPIKAPSLAP TIDTAPKQNP VPTAQITATL 60
PAEPVKVPVL IPEVNKTLLIE TSTNPVKDSY NKDAVFTYEL IANPDADYSD QKLILKKEIS 120
YIKLNLGINQ DNKNAPSYIF NLLEDDNVYVG FYRDTQDMNR IENKYTYAFK KEAENFDNLQ 180
KFNATYEGQF WFSIDTPND PTVARAFLYTY NNGRVDGEIL AKHWNEKLFQ ITGFDNNPRK 240
VEIFPTVEYL PNSGTRLTKG ATSPHRFQMD LHFINSTNGE KNKYLVGQGS TEQYWGVGLM 300
EKKQELALVP RGSSAHHHHH HHHHH 325

SEQ ID NO: 66      moltype = DNA length = 975
FEATURE           Location/Qualifiers
source            1..975
mol_type = genomic DNA
organism = Pasteurella multocida

SEQUENCE: 66
atggaaaaac gtaccgtAAC tataccacAA gcacaaaaAG tagcagaaaa accagcgctA 60
acaaatccAAA cagtggttaAC ttccacaATT acaccaATT aagcgccCTC actcgctCC 120

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actattgata ctgcgcctaa acaaataccc gtccgacag cgaaataac ggctacttta 180
ccagccgaac ctgttaaagt gccagttcg atccccgaag taaaacaaac acttttagaa 240
acatcaacta atccgtaaa agattttat aataaaagatg ctgttattac atacgaatta 300
atcgcaaatc cagatgcaga ttatgcgt caaaaattga ttcttaaaaa agaaattagt 360
tatatacaac ttaatctagg cataaataca gacaataaaa atgcaccaag ctatatttt 420
aatttactag atgacaatgt ctattatgtt ttttategtt atactcaaga tatgaacaga 480
atagaaaaata aataactta tgcttc当地 aaaaagatg 540
aaattnaaatg cgactttagt aggtcaattt tggttctctt gtatagatc tccaaatgt 600
cctactgttg caagagcatt cttaacatata aacaatggta gagtggatgg tgaaatattg 660
gctaaacattt ggaatgcattt attgtttcgat attactggat ttgataataa tcctcgtaaa 720
gtagaaaaattt ttcctactgtt agaatattc cttaaatccgg gaacaagact aacaaaagga 780
gccccatcac ctcatcgat cccaaatggat ttacatttc tcaatagatc aatgtgtgaa 840
aaaaacaaat atcttgcgg ccaaggatgt actgagcagt actgggggtgt ttttaggtatg 900
gaaaaaaaaac aagagctcgc tctggtgcca cggcttagt ccgctcatca ccaccatcat 960
caccatcacc accac 975

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SEQ ID NO: 67 moltype = AA length = 325
FEATURE Location/Qualifiers
source 1..325
mol_type = protein
organism = Pasteurella multocida
SEQUENCE: 67
MEKRTVTIPQ AQKVAEKPAL TIQTVVTSPT TPIKAPSLAP TIDTAPKQNP VPTAQITATL 60
PAEPVKVPVL IPEVNKTLL E TSTNPVKDSY NKDAVFTYEL IANPDADYSQ QKLILKKEIS 120
YIKLNLGINQ DNKNAPSYIF NLLDDNVYYG FYRDTQDMNR IENKYTYAFK KEAENFDNLQ 180
KFNATYEQOF WFSSIDTPNV PTVARAFLTY NNGRVDGEIL AKHWNNAKLFO ITGFDFNNPRK 240
VEIFPTEVEYL PNSGTRLTKG ATSPHRFQMD LHFINSTNGE KNKYLVGQGS TEQYWGVLM 300
EKKQELALVP RGSSAHHHHH HHHHH 325

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SEQ ID NO: 68 moltype = DNA length = 966
FEATURE Location/Qualifiers
source 1..966
mol_type = genomic DNA
organism = Pasteurella multocida
SEQUENCE: 68
tgttagtgggg aaggtggatgg aagtaataac agcaatcatc aagctcatcc tggtaatcaa 60
gtcgctactc caatgcctgc taccgtatca aaaacctgaat tacccaaacc agtagcactt 120
attgaagaaa cagtcgaagc tgaagaaaaa gtcgtggaa agaaacacctt agttggccact 180
ggcactattc aaccacggatc tcaatccaaat atcttattccca aaaaagcacc aacacaaaca 240
tctgataataaaaatc aacttgcggaa ggagagtctt tttcagaaaaa gggaaatcgc 300
gacttcttccatc acaataaaaa tgctgttattt actctgttccat tagtaacaaa tccaaatgcc 360
gtttatgaca cagatcctaa cctgtttagt aaagatattaa aatataattac attaacggat 420
ggatacaacc aagataataaaatc gaatgttca aactatgtt aatatttgc tggatggaaat 480
gttttattatg tctactatcg tgattcacaa gatatacgatc atgttggaaaaa tatctatgt 540
taagggttca aaaaagatgc aaaaatccaaatc gataacttccca aatttttaac agcaaaat 600
caaggtgatgtt ttttattttc aacagcgaca aacccaaatttgc tggctatattt aggtttaagct 660
atctttaattt acaaaagatgc aaaaatccaaatc ggttggaaatttgc tagaaacgaga taacaattac 720
aaatattttatgtt taatgttcaatccaaatc cttatccaaatc ttttgc ttttgc 780
gaaaatggatc cccgttctgtt aattttatgtt gatatacgatc aaaaatccaaatc agacccatc 840
tcaatagatc tgcacttcat caaaatgttca gataatccaaatc aaaaatataatc ttttgc 900
caaggtgatgtt acaaaatccaaatc ctggggcgatgtt ttttgc ttttgc agaaaaaaatc tacaccaatc 960
gcaaaaa 966

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SEQ ID NO: 69 moltype = AA length = 322
FEATURE Location/Qualifiers
source 1..322
mol_type = protein
organism = Pasteurella multocida
SEQUENCE: 69
CSGGSGGSNN SNHQAHPVNQ VRTPMPATVA KPELPKPVAL IEETVQAEK VVEEKPLVAT 60
ATIQPAVQSN IYSEKAPTQT SDNKKSVNWQ GESISEKGNR DFSYNKNAVF TRHLVTPNPA 120
VYDTPNLLIS KDIKYITLTD GYNQDNKNGP NYELNLLDEN VYYGYYRDSQ DMNHVENIYV 180
YGFKKDAEQQ DTLQFLTANY QGEFLFSTAT NPNVPILGKA ILNYKEGKAK GEILERDNNY 240
KLFDIYVNER PNQAILSPVA ERLPASDIIM DTRKNSSDRI SIDLHFIKSK DNQENKYIVG 300
QGGNEKYWGV LGLEKKDPTK AK 322

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SEQ ID NO: 70 moltype = DNA length = 954
FEATURE Location/Qualifiers
source 1..954
mol_type = genomic DNA
organism = Pasteurella multocida
SEQUENCE: 70
tgttagtgggg aaggtggatgg aagtaataac tctcaacttccatc ttttgc ttttgc 60
actataccac aagcacaaaaa agtagcagaa aaaccacggcc taacaataca aacatgttca 120
atcttccatc aatgttcaatccaaatc ttttgc ttttgc 180
aaacacaaaaatc ccgtggccatc aacccatc acgttcaatccaaatc ttttgc ttttgc 240

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gtgccagttc tgattccgaa	agtaaacaaa acacttttag	aaacatcaac taatccagta	300
aaagatttttataaaga	tgcgtgtatt	acatacgaaat taatcgaaa	360
gattatcgatccaaattt	gattttaaa	aaagaaattha gttatcatca	420
ggcataaaatc aagacaataa	aatgcacca	agctatattt ttaatttact	480
gtcttattatg gttttatcg	tgataactca	gatatgaaca gaatagaaaa	540
tatgcttc aaaaagaagc	tgaaaatttt	gataaccctt aaaaatttta	600
gaaggctcaat ttgggtctc	tagtatagat	actccaaatg tactactgt	660
ttcttaacat ataacaatgg	tagtgat	ggtaaatat tggctaaaca	720
aaattgttca agattactgg	atttgataat	aatcctcgta aagtagaaat	780
gtagaatatt tacctaattc	gggaacaaga	ctaacaaaag gagccacatc	840
ttccaaatgg atttacattt	catcaatagt	acaatatggt aaaaaaacaa	900
ggccaaggta gtactgggt	gtactgggt	gttttaggt tggagaaaaa	954

SEQ ID NO: 71	moltype = AA	length = 318	
FEATURE	Location/Qualifiers		
source	1..318		
	mol_type = protein		
	organism = Pasteurella multocida		
SEQUENCE: 71			
CSGGGNNNP SHSPMEKRTV	TIPQAQKVAE KPALTIQTVV	TSPTTPIKAP SLAPTTDAP	60
KQNPVPVTAQI TATFPAPVK	VPVLIPEVNK TLLETSTNPV	KDSYNKDAVF TYELIANPDA	120
DYSDQKLILK KEISYIKLNL	GINQDNKNAP SYIFNLLDDN	VYYGFYRDTQ DMNRIENKYT	180
YAFKKEAENF DNLQKPNATY	EGQFWFSSID TPNVPTVARA	FLTYNNGRVD GEILAKHWNE	240
KLQITGFDN NPKVEIFPT	VEYLPNSGTR LTKGATSPHR	FQMDLHFINS TNGEKNKYLV	300
GQGSTEQYWG VLGMEKKQ			318

SEQ ID NO: 72	moltype = DNA	length = 954	
FEATURE	Location/Qualifiers		
source	1..954		
	mol_type = genomic DNA		
	organism = Pasteurella multocida		
SEQUENCE: 72			
tgttgtgtt gttggggtaa	taacaatcca tctcactctc	ctatggaaaa acgttaccgt	60
actataccac aagcacaaaaa	agtagcagaa	aaaccagcgc taacaataca	120
acttcaccaa ataccaat	taaaagcggcc	tcaactcgctc cgactattga	180
aaacaaaatc ccgtgcgcac	agcgttactt	acggccgcga acctgttaaa	240
gtgccagttc tgattccgaa	agtaaacaaa	acacttttag aaacatcaac	300
aaagatttttataaaga	tgcgtgtatt	acatacgaaat taatcgaaa	360
gattatcgatccaaattt	gattttaaa	aaagaaattha gttatcatca	420
ggcataaaatc aagacaataa	aatgcacca	agctatattt ttaatttact	480
gtcttattatg gttttatcg	tgataactca	gatatgaaca gaatagaaaa	540
tatgcttc aaaaagaagc	tgaaaatttt	gataaccctt aaaaatttta	600
gaaggctcaat ttgggtctc	tagtatagat	actccaaatg tacctactgt	660
ttcttaacat ataacaatgg	tagtgat	ggtaaatat tggctaaaca	720
aaattgttca agattactgg	atttgataat	aatcctcgta aagtagaaat	780
gtagaatatt tacctaattc	gggaacaaga	ctaacaaaag gagccacatc	840
ttccaaatgg atttacattt	catcaatagt	acaatatggt aaaaaaacaa	900
ggccaaggta gtactgggt	gtactgggt	gttttaggt tggagaaaaa	954

SEQ ID NO: 73	moltype = AA	length = 318	
FEATURE	Location/Qualifiers		
source	1..318		
	mol_type = protein		
	organism = Pasteurella multocida		
SEQUENCE: 73			
CSGGGNNNP SHSPMEKRTV	TIPQAQKVAE KPALTIQTVV	TSPTTPIKAP SLAPTTDAP	60
KQNPVPVTAQI TATFPAPVK	VPVLIPEVNK TLLETSTNPV	KDSYNKDAVF TYELIANPDA	120
DYSDQKLILK KEISYIKLNL	GINQDNKNAP SYIFNLLDDN	VYYGFYRDTQ DMNRIENKYT	180
YAFKKEAENF DNLQKPNATY	EGQFWFSSID TPNVPTVARA	FLTYNNGRVD GEILAKHWNE	240
KLQITGFDN NPKVEIFPT	VEYLPNSGTR LTKGATSPHR	FQMDLHFINS TNGEKNKYLV	300
GQGSTEQYWG VLGMEKKQ			318

SEQ ID NO: 74	moltype = DNA	length = 933	
FEATURE	Location/Qualifiers		
source	1..933		
	mol_type = genomic DNA		
	organism = Pasteurella multocida		
SEQUENCE: 74			
tgttgtgtt gttggggagg	tggaaat aacagcaatc	atcaagctca tcctgttaat	60
caagtgcctg cggccgtact	tcatgtgtc	gcaaaaaccac aacaacatgt	120
gttatttgcata agaaacctcc	agttcgatgt	actagaacag caagtcattc tagttctat	180
tccatggaaatc cggccatcaca	agtatctca	gataaaaatg cggtacactg	240
tccatggaaatc tcttgacttc	tcttacgt	aaagatccgtt atttaccgt	300
cattttgttataa cttatccaa	cgctgtttat	agcactgatc ctaacctgtat	360
attaaatataa ttatccaa	cactactgtt	tataatcaag ataataagag	420
tatggatataa ttatccgtt	tttacgtt	tttacgttataa	480

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atgaatcatg ttgaaaatat ctatgtataat gggttcaaaa aagatgcaga aaatcaagat	540
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mol_type = protein	
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IKYITLTNTTG YNQDNKSGPN YELNLILDENI YYGYYRDSQD MNHVENIYVV GFKKDAENQD	180
NLQFLTANYQ GEFLFSTATN PNVPVLGKAV LNYKEKGAKG EILERDSNYK LFDIYVNERP	240
NQAILNVAE RLPTSDLIMN TRKNSPDRVT IDLHFIIKGQD NQENKYIVGQ GGNEYKVGVL	300
GLEKKETKAE K	311
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mol_type = genomic DNA	
organism = Pasteurella multocida	
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caagtgcag aaaaatgtgt tgagtttagaa cctcttagtc atgttagctca accaatcgaa	180
tcatcaattt tattccaaac aagatcacct aaaaaccacg cagacaataa gatttcaaaa	240
caatggaaag gggaaatccat tgccaaatgg agaaaaacac actttaacta tagtaaagac	300
gccgtttta cacgtcactt agtgaaaaat cccaaagctca ttacgacac agaccataat	360
ctgatttagca aagaaatccca gtatattaaa ctacaaactagc gcgataaactgt tgataatgtg	420
gatgtctccaa actatgaaattt aatattactc aatgaaaaatg ttactatgg ttctatctgt	480
gattcacaag atatgaaatca tggtaaaat atctatgtt atggattttaa aaaatgtca	540
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actgcgacaa atttaatgtt gactgttaca ggaagagtcg tactcaataa tcaagagggt	660
aaagctaaag gtgaaatctt agaagcgatg atcgattaca aattatttga tatatctgtt	720
gataagaaac ctaatcaagc tatttttaat cctgtttagt aggcattacc aggttcaat	780
ataaaaacttg tcaatcttcc aaattccacca gaccgtatca ctgttagattt acactttatt	840
aagggtcaag ataaccatgaa aaataatattt attgtagtca aagggggtaa tgaaaatata	900
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mol_type = protein	
organism = Pasteurella multocida	
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SSNLSLTEST KKPADNKISK QWEGESIAKWL RKTDFNYSKD AVFTRHLVEN PKAIYDTDPN	120
LISKEIQYIK LQLGDNVNDN DAPNYELNLL NENAYYGFYR DSQDMNHVEN IYVYGFKKDA	180
ENHENLQSLT ANYEGEFLFS TATNLNVTVT GRVVLKYQEG KAKGEILERD IDYKLFDISV	240
DKKPNQAILN PVVEALPGSN IKLVRNRPNSP DRITVDLHFI KGQDNQENKY IVGQGGNEKY	300
WGVLGLEKKE TKAEK	315
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organism = Pasteurella multocida	
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cgagttactca ataattcaga gaataaccca ccatcaagag agttagagaa aaaaatgtca	180
caaactccac cacaacacaga tagcgcgaaa tcaacaatac aatctactcc cgctgttata	240
ccagatgttataa aacatcttaa aaggacaaa ttcaaatgtc tccaaatgtt	300
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accaaaaaaag ataaagaa	978
 SEQ ID NO: 79 moltype = AA length = 326	
FEATURE Location/Qualifiers	
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mol_type = protein	
organism = Pasteurella multocida	
 SEQUENCE: 79	
CSGGGGNNN VPHPPVEKRT VATTQVAAK PTPPSESLVK RVLNNEENNPs PSRESEKKAS 60	
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PVFKLIENNQ KYVNDKYFT LESINLNLTQ ENQVKEGSYQ FSLLDSGVYY GHYLSSNDGI 180	
HPEYNFVIAF DKNREYTLKD ITAEYNSSEG FNYAISDRMK GDYIWQVGDV RLFYTNGSVH 240	
GEIVEVNDSG KTALFRFENT ADRNPQNQIVI VPERNNRHGL SPRGDRMIMD MHFINGSDGE 300	
KYKVVVGHGN SDRYYGTLFA TKKDKE 326	
 SEQ ID NO: 80 moltype = DNA length = 978	
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mol_type = genomic DNA	
organism = Pasteurella multocida	
 SEQUENCE: 80	
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cttgaatcaa tcaatcttaa ttgtactaaa gaaaatcaag ttaaagaagg ttcttatcaa 480	
tttagtctat tagactctgg agtcttattt ggccattact taagctcaa cgtatggatt 540	
catccagaat ataactttgt gattgctttt gacaaaaacaa gagaatacac actgaaagat 600	
atcacagctg aataactataa ttccggagggt ttcaattatgt cttataatgtg tagaatgaaa 660	
ggtgactata tctggcaagt gggtgatgtg cgtttattctt atacaatggg ttctgtgcat 720	
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gcagatagaa acccaaatc aatttgttattt gtcccgaaaa gagaataatcg tcatggatta 840	
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accaaaaaaag ataaagaa	978
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FEATURE Location/Qualifiers	
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mol_type = protein	
organism = Pasteurella multocida	
 SEQUENCE: 81	
CSGGGGNNN VPHPPVEKRT VATTQVAAK PTPPSESLVK RVLNNEENNPs PSRESEKKAS 60	
QTPPQTDSAK STIQSTPAVI PDSTSLSLTK KGOIQMSPEW IGKEEKYYAQ YSWEHTPESI 120	
PVFKLIENNQ KYVNDKYFT LESINLNLTQ ENQVKEGSYQ FSLLDSGVYY GHYLSSNDGI 180	
HPEYNFVIAF DKNREYTLKD ITAEYNSSEG FNYAISDRMK GDYIWQVGDV RLFYTNGSVH 240	
GEIVEVNDSG KTALFRFENT ADRNPQNQIVI VPERDNRHGL SPRGDRMIMD MHFINGSDGE 300	
KYKVVVGHGN SDRYYGTLFA TKKDKE 326	
 SEQ ID NO: 82 moltype = DNA length = 978	
FEATURE Location/Qualifiers	
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mol_type = genomic DNA	
organism = Pasteurella multocida	
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cgagacttca ataattcaga gataaaccca ccatcaagag agtcagagaa aaaaggctca 180	
caaactccac cacaacacaga tagcgcgaaa tcaacaatac aatctactcc cgctgttata 240	
ccagatagta caaaactcttt aacatctaag aaaggacaaa ttcaatgtc tccagaatgg 300	
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accaaaaaaag ataaagaa	978
SEQ ID NO: 83 moltype = AA length = 326	
FEATURE Location/Qualifiers	
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mol_type = protein	
organism = Pasteurella multocida	
 SEQUENCE: 83	
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QTPPQTDASK STIQSTPAVI PDSTNSLTSK KQIQMSPWEW IGKEEKYQAQ YSWEHTPESI 120	
PVFKLIENNQ YKVNDKYFT LESINLNLTQ ENQVKEGSYQ FSLLDSGVYY GHYLSSNDGI 180	
HPEYNFVIAF DKNREYTLKD ITAEYYNSEG FNYAISDRMK GDYIWQVGDV RLFYTNGSVH 240	
GEIVEVNDGS KTALFRFENT ADRNPQIVI VPERDNRHGL SPRGDRMIMD MHFINGSDGE 300	
KYKVVVGHGN SDRYYGTFLA TKDKDE 326	
 SEQ ID NO: 84 moltype = DNA length = 978	
FEATURE Location/Qualifiers	
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mol_type = genomic DNA	
organism = Pasteurella multocida	
 SEQUENCE: 84	
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cggactactca ataattcaga gaataaccca ccatcaagag agtcagagaa aaaaggctca 180	
caaactccac cacaacgaga tagccgcggaa tcaacaatac aatctactcc cgctgttata 240	
ccagatagta caaaactctt aacatctaag aaaggacaaa ttcaaatgtc tccagaatagg 300	
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ccagatatta aattaattga aaataaccca tacaatata ttaatgataa gtactttaca 420	
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tctcctcgag gagatcgcat gataatggat atgcattta ttaatggtag tgatggagaa 900	
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FEATURE Location/Qualifiers	
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mol_type = protein	
organism = Pasteurella multocida	
 SEQUENCE: 85	
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QTPPQADSASK STIQSTPAVI PDSTNSLTSK KQIQMSPWEW IGKEEKYQAQ YSWEHTPESI 120	
PVFKLIENNQ YKVNDKYFT LEPINLNLTQ ENQVKEGSYQ FSLLDSGVYY GHYLSSNDGI 180	
HPEYNFVIAF DKNREYTLKD ITAEYYNSEG FNYAISDRMK GDYIWQVGDV RLFYTNGSVH 240	
GEIVEVNDGS KTALFRFENT ADRNPQIVI VPERDNRHGL SPRGDRMIMD MHFINGSDGE 300	
KYKVVVGHGN SDRYYGTFLA TKDKDE 326	
 SEQ ID NO: 86 moltype = DNA length = 978	
FEATURE Location/Qualifiers	
source 1..978	
mol_type = genomic DNA	
organism = Pasteurella multocida	
 SEQUENCE: 86	
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cggactactca ataattcaga gaataaccca ccatcaagag agtcagagaa aaaaggctca 180	
caaactccac cacaacgaga tagccgcggaa tcaacaatac aatctactcc cgctgttata 240	
ccagatagta caaaactctt aacatctaag aaaggacaaa ttcaaatgtc tccagaatagg 300	
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ccagatatta aattaattga aaataaccca tacaatata ttaatgataa gtactttaca 420	
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tctcctcgag gagatcgcat gataatggat atgcattta ttaatggtag tgatggagaa 900	
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acaaaaaaag ataaagaa SEQ ID NO: 87 moltype = AA length = 326  
 FEATURE Location/Qualifiers  
 source 1..326  
 mol\_type = protein  
 organism = Pasteurella multocida

SEQUENCE: 87 CSGGGGNKVK VPHPPVEKRT VATTOQVAAK PTTPPSESLVK RVLNNSENNPs PSRESEKKAS QTTPQTDsAK STIQSTPAVI PDRTNLSLTK KGQIQMSPEW IGKEEKKYAQ YSWEHTPESI PVFKLIENNQ YKVYVNDKVFPT LESINLNLTk ENQVKEGSYQ FSLLDGSVYY GHYLSSNDGI HPEYNFVIAF DKNREYTLKD ITAEYYNSEG FNYAISDRMK GDYIWQVGDV RLIFYTNGSVH GEIEEVNDGS KTALFRFENT ADRNPQNIVI VPERNNRHL SPRGDRMIMD MHFINGSDGE KYKVVGHGN SDRYYGTLFA TKKDKE 60 120 180 240 300 326

SEQ ID NO: 88 moltype = DNA length = 978  
 FEATURE Location/Qualifiers  
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 mol\_type = genomic DNA  
 organism = Pasteurella multocida

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 attggaaag aagaaaaaaa gtatgcgca tattcatggg aacatacgcc agaacttatt  
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 ggtgactata tctggcaagt gggtgatgtg cgtttattt acataatgg ttctgtcgt  
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 accaaaaaaag ataaagaa

SEQ ID NO: 89 moltype = AA length = 326  
 FEATURE Location/Qualifiers  
 source 1..326  
 mol\_type = protein  
 organism = Pasteurella multocida

SEQUENCE: 89 CSGGGGNNNV VPHPPVEKRT VATTOQVAAK PTTPPSESLVK RVLNNSENNPs PSRESEKKAS QTTPQTDsAK STIQSTPAVI PDRTNLSLTK KGQIQMSPEW IGKEEKKYAQ YSWEHTPESI PVFKLIENNQ YKVYVDDKCFPT LESINLNLTk ENQVKEGSYQ FSLLDGSVYY GHYLSSNDGI HPEYNFVIAF DKNREYTLKD ITAEYYNSEG FNYAISDRMK GDYIWQVGDV RLIFYTNGSVH GEIEEVNDGS KTALFRFENT ADRNPQNIVI VPERDNRHL SPRGDRMIMD MHFINGSDGE KYKVVGHGN SDRYYGTLFA TKKDKE 60 120 180 240 300 326

SEQ ID NO: 90 moltype = DNA length = 879  
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 mol\_type = genomic DNA  
 organism = Pasteurella multocida

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 caaacactcca aaccagaaaa aattgcaaaa gatattaattt ggacaggttag tgctgtgtcg  
 tctataggct ccacttgggt gcaacataaaa ccaataata ttccgttta tacactaatt  
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 gatcttacaa agataatTTTGTGATGA aagtactttt atttcacattttagactcc  
 ggaattttt atggaaatTTTAAAGTTCTAGATCAGA tgaacgcaaga atcttaattt  
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 gtaaaaacact ttagctttat gaatagcaat aaaaatttggcc aataatcgat tgTTTGTGTC  
 ccagaacaaacatccatgtatccca qataatggaaa ttgtttttaga aatcgatcc  
 attaatggggg aaaaatggaaa aaaaataaaa tatattgtgg gtagtggtaa aacggacaaa  
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SEQ ID NO: 91 moltype = AA length = 293  
 FEATURE Location/Qualifiers

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source 1..293  
mol\_type = protein  
organism = Pasteurella multocida

SEQUENCE: 91  
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QHSKPEKIAK DINWTGSAVS SIGSTWWQHK PNNIPVFTLI LNENQIYSDE KNFTLEQKHI 120  
DLTKNNILDE KYFHTLLDS GIYGNLYLS YDQMNAESNY VFAFDKDREY TGKDITANY 180  
GNEGFKYSVK LGNTYLSQVG DVHLTYREGK VSGEIFGQNN VKHFSEMFNSN KIDPNSIVIV 240  
PEEAHRYLRSR NDKMFLEMHF INGENGEKYK YIVGSGKTDK YYGALFATKQ ENQ 293

SEQ ID NO: 92  
moltype = DNA length = 680  
FEATURE Location/Qualifiers  
source 1..680  
mol\_type = genomic DNA  
organism = Pasteurella multocida

SEQUENCE: 92  
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aaatttagtta tatcaaactt aatctaggca taaatcaaga caataaaaat gcaccaagct 180  
atatttttaa ttacttagt gacaatgtt attatgtt ttatctgtat actcaagat 240  
tgaacagaat agaaaataaa tatacttata ctttc当地 aqaaagctgaa aatttgtata 300  
acccatcaaaa atttaatggc actttatggc gtcattttt gttctctagt atagatactc 360  
caaattgtacc tactgttgc agagcattt taacatataa caatggtaga gtggatggtg 420  
aaatattggc taaacatgg aatggaaaat tgtttccatg tactgttgcatt gataataatc 480  
ctcgtaaagt agaaaattttt cttatgttgc aatatttttccatgataatc aaaaagactaa 540  
caaaaggaggc cacatcaccc catgttttccatgataatc aatattttccatgataatc 600  
atggtgaaaa aaacaaatat cttgtcgccc aaggtagtac tgacgactac tggggatgttt 660  
taggtatgga gaaaaaaacaa 680

SEQ ID NO: 93  
moltype = AA length = 227  
FEATURE Location/Qualifiers  
source 1..227  
mol\_type = protein  
organism = Pasteurella multocida

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mol\_type = genomic DNA  
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GNEGFKYSVK KLGNNTYLSQVG GDVHLTYREGK KVSGEIFGQNN NVKHFSEMFNSN KIDPNSIVI 180  
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moltype = DNA length = 801  
FEATURE Location/Qualifiers  
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mol\_type = genomic DNA  
organism = Pasteurella multocida

SEQUENCE: 96

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gaacatcttg acttcttta cagtaaagat gcccgttta cccgtcattt ggtaacaaat 180
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ccagaccgtg tcaacaataga ttatcactt attaagggtt aagataacca agaaaataaa 720
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gagaccaagg cagaaaaataa g 801

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FEATURE          Location/Qualifiers
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organism = Pasteurella multocida

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NIYVYGFKPD AENQDNLQFL TANYQGEFLF STATNPVNVP LGKAVLNYKE GKAKGEILER 180
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YIVGQGGNEK YWGVLGLEKK ETKAEK 266

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**1.** A veterinary vaccine formulation for the prevention, treatment or amelioration of *P. multocida* infection in a ruminant animal susceptible to *P. multocida* infection, the vaccine formulation comprising an effective amount of at least one PmSLP protein, or an immunogenically equivalent portion thereof, together with a veterinary pharmaceutically acceptable excipient, carrier or diluent, and, optionally a veterinary pharmaceutically acceptable adjuvant.

**2.** (canceled)

**3.** A veterinary vaccine formulation according to claim **1**, wherein the vaccine formulation comprises a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

**4.** (canceled)

**5.** A veterinary vaccine formulation according to claim **1**, wherein the ruminant animal is a bovine animal susceptible to infection by a *P. multocida* strain causing BRD, and the vaccine formulation comprises a *P. multocida* PmSLP protein from a BRD causing *P. multocida* strain, or an immunogenically equivalent portion thereof, wherein the PmSLP protein is selected from the group of phylogenetic clusters consisting of PmSLP-1, PmSLP-2, and PmSLP-4.2, wherein the selected *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

**6.** A veterinary vaccine formulation according to claim **1**, wherein the ruminant animal is a bovine animal susceptible to infection by a *P. multocida* strain causing HS, and the vaccine formulation comprises a *P. multocida* PmSLP protein from an HS causing *P. multocida* strain, or an immunogenically equivalent portion thereof, wherein the PmSLP protein is selected from the phylogenetic cluster PmSLP-3 wherein the selected *P. multocida* PmSLP protein, or an

immunogenically equivalent portion thereof, belongs to the same phylogenetic cluster as a PmSLP protein present in the infecting *P. multocida* strain.

**7.** (canceled)

**8.** (canceled)

**9.** (canceled)

**10.** A veterinary vaccine formulation according to claim **1**, wherein the vaccine formulation comprises a *P. multocida* strain belonging to a serogroup selected from the group consisting of serogroup A, B, D E, and F, wherein the serogroup is the same as the serogroup of the infecting *P. multocida* strain.

**11.** A veterinary vaccine formulation according to claim **1**, wherein the at least one PmSLP protein, or immunologically equivalent portion thereof, is a protein expressed by a nucleic acid sequence selected from the group of nucleic acid sequences consisting of:

(a) SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID. NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID. NO: 19, SEQ.ID. NO: 21, SEQ.ID. NO: 23, SEQ.ID. NO: 25, SEQ.ID. NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ. ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ. ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96;

(b) a nucleic acid sequence having at least 70% identity with any one of the nucleic acid sequences of (a);

(c) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a) but for the degeneration of the genetic code;

- (d) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);
  - (e) a chimeric nucleic acid obtained by a fusion between at least two nucleic acid sequences of (a), (b), (c), and (d), or a portion thereof;
  - (f) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);
  - (g) a nucleic acid sequence encoding a polypeptide having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;
  - (h) a nucleic acid sequence that encodes a functional variant of any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereto; and
  - (i) a nucleic acid sequence that hybridizes under stringent conditions to any one of the nucleic acid sequences set forth in (a), (b), (c), (d), (e), (f), (g), or (h).
- 12.** (canceled)
- 13.** A veterinary vaccine formulation according to claim 1, wherein the *P. multocida* infection causes respiratory tract disease, bovine respiratory disease (BRD) or hemorrhagic septicemia (HS).
- 14.** (canceled)
- 15.** (canceled)
- 16.** (canceled)
- 17.** (canceled)
- 18.** (canceled)
- 19.** (canceled)
- 20.** (canceled)
- 21.** (canceled)
- 22.** (canceled)
- 23.** (canceled)
- 24.** A veterinary vaccine formulation according to claim 1, wherein the veterinary vaccine formulation is a cross-protective vaccine formulation comprising a PmSLP protein, or

immunogenically equivalent portion thereof, obtained from a first *P. multocida* strain, and the vaccine formulation is a formulation for the administration to the food production animal to prevent or ameliorate an infection caused by another *P. multocida* strain.

**25.** A veterinary vaccine formulation according to claim 1, wherein the vaccine formulation is substantially free of other *P. multocida* constituents.

**26.** (canceled)

**27.** (canceled)

**28.** (canceled)

**29.** A veterinary vaccine formulation according to claim 1, wherein the vaccine formulation comprises from about 0.001% to about 20% by weight of the PmSLP protein or the immunogenically equivalent portion thereof, and a veterinary pharmaceutically acceptable adjuvant constituting from about 0.1% to about 60% by weight or volume of the vaccine formulation.

**30.** A veterinary vaccine formulation according to claim 1, wherein the vaccine formulation comprises a second *P. multocida* PmSLP protein, or immunologically equivalent portion thereof.

**31.** (canceled)

**32.** A veterinary vaccine formulation according to claim 30, wherein the second *P. multocida* PmSLP protein, or immunologically equivalent portion thereof, belongs to the same or a different phylogenetic cluster as the first *P. multocida* PmSLP protein, or immunologically equivalent portion thereof or optionally the same phylogenetic cluster as the first *P. multocida* PmSLP protein, or immunologically equivalent portion thereof.

**33.** A veterinary vaccine formulation according to of claim 32, wherein the vaccine formulation comprises a fusion polypeptide selected from the group consisting of a (i) PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 1 and a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 3; (ii) PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 1 and a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 2; (iii) a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 1 and a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 4.1; and (iv) a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 1 and a PmSLP protein, or immunologically equivalent portion thereof, belonging to phylogenetic cluster 4.2.

**34.** A veterinary vaccine formulation according to claim 33, wherein the second *P. multocida* PmSLP protein, or immunologically equivalent portion thereof, is obtained from a *P. multocida* strain belonging to the same or a different serogroup as the *P. multocida* strain of the first *P. multocida* PmSLP protein, or immunologically equivalent portion thereof.

**35.** (canceled)

**36.** (canceled)

**37.** (canceled)

**38.** A method for prevention, treatment or amelioration of *Pasteurella multocida* (*P. multocida*) infection in ruminant animal susceptible to *P. multocida* infection, the method comprising administering to the ruminant animal a veterinary vaccine formulation comprising a *P. multocida* PmSLP

protein, or an immunogenically equivalent portion thereof, wherein the vaccine formulation is administered in an effective amount to prevent, treat or ameliorate the *P. multocida* infection.

**39.** (canceled)

**40.** (canceled)

**41.** (canceled)

**42.** (canceled)

**43.** The method according to claim **38**, wherein 1) the ruminant is susceptible to *P. multocida* infection, and wherein the veterinary vaccine formulation administered in an effective amount to the ruminant comprises at least one PmSLP protein from a *P. multocida* strain causing respiratory tract disease, or an immunogenically equivalent portion thereof; 2) the ruminant is a bovine species, and wherein the veterinary vaccine formulation administered in an effective amount to the bovine species comprises at least one PmSLP protein from a *P. multocida* strain causing BRD, or an immunogenically equivalent portion thereof, or 3) the veterinary vaccine formulation administered in an effective amount to the ruminant comprises at least one PmSLP protein from a *P. multocida* strain causing HS, or an immunogenically equivalent portion thereof.

**44.** (canceled)

**45.** (canceled)

**46.** (canceled)

**47.** (canceled)

**48.** (canceled)

**49.** (canceled)

**50.** (canceled)

**51.** A method according to claim **38**, wherein the vaccine formulation comprises at least one *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, selected from a protein encoded by a nucleic acid sequence selected from the group of nucleic acid sequences consisting of:

(a) SEQ.ID NO: 1, SEQ.ID NO: 3, SEQ.ID NO: 5, SEQ.ID NO: 7, SEQ.ID NO: 9, SEQ.ID NO: 11, SEQ.ID NO: 13, SEQ.ID NO: 15, SEQ.ID NO: 17, SEQ.ID NO: 19, SEQ.ID NO: 21, SEQ.ID NO: 23, SEQ.ID NO: 25, SEQ.ID NO: 27, SEQ.ID NO: 29, SEQ.ID NO: 31, SEQ.ID NO: 33, SEQ.ID NO: 35, SEQ.ID NO: 37, SEQ.ID NO: 39, SEQ.ID NO: 50, SEQ.ID NO: 52, SEQ.ID NO: 54, SEQ.ID NO: 56, SEQ.ID NO: 58, SEQ.ID NO: 60, SEQ.ID NO: 62, SEQ.ID NO: 64, SEQ.ID NO: 66, SEQ.ID NO: 68, SEQ.ID NO: 70, SEQ.ID NO: 72, SEQ.ID NO: 74, SEQ.ID NO: 76, SEQ.ID NO: 78, SEQ.ID NO: 80, SEQ.ID NO: 82, SEQ.ID NO: 84, SEQ.ID NO: 86, SEQ.ID NO: 88, SEQ.ID NO: 90, SEQ.ID NO: 92, SEQ.ID NO: 94, or SEQ.ID NO: 96;

(b) a nucleic acid sequence having at least 70% identity with any one of the nucleic acid sequences of (a);

(c) a nucleic acid sequence that is substantially identical to any one of the nucleic acid sequences of (a) but for the degeneration of the genetic code;

(d) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

(e) a chimeric nucleic acid obtained by a fusion between at least two nucleic acid sequences of (a), (b), (c), and (d), or a portion thereof;

(f) a nucleic acid sequence that is complementary to any one of the nucleic acid sequences of (a);

(g) a nucleic acid sequence encoding a polypeptide having any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereof;

(h) a nucleic acid sequence that encodes a functional variant of any one of the amino acid sequences set forth in SEQ.ID NO: 2, SEQ.ID NO: 4, SEQ.ID NO: 6, SEQ.ID NO: 8, SEQ.ID NO: 10, SEQ.ID NO: 12, SEQ.ID NO: 14 SEQ.ID NO: 16, SEQ.ID NO: 18, SEQ.ID NO: 20, SEQ.ID NO: 22, SEQ.ID NO: 24, SEQ.ID NO: 26, SEQ.ID NO: 28, SEQ.ID NO: 30, SEQ.ID NO: 32, SEQ.ID NO: 34, SEQ.ID NO: 36, SEQ.ID NO: 38, SEQ.ID NO: 40, SEQ.ID NO: 51, SEQ.ID NO: 53, SEQ.ID NO: 55, SEQ.ID NO: 57, SEQ.ID NO: 59, SEQ.ID NO: 61, SEQ.ID NO: 63, SEQ.ID NO: 65, SEQ.ID NO: 67, SEQ.ID NO: 69, SEQ.ID NO: 71, SEQ.ID NO: 73, SEQ.ID NO: 75, SEQ.ID NO: 77, SEQ.ID NO: 79, SEQ.ID NO: 81, SEQ.ID NO: 83, SEQ.ID NO: 85, SEQ.ID NO: 87, SEQ.ID NO: 89, SEQ.ID NO: 91, SEQ.ID NO: 93, SEQ.ID NO: 95, or SEQ.ID NO: 97, or an immunogenically equivalent portion thereto; and

(i) a nucleic acid sequence that hybridizes under stringent conditions to any one of the nucleic acid sequences set forth in (a), (b), (c), (d), (e), (f), (g), or (h).

**52.** (canceled)

**53.** (canceled)

**54.** (canceled)

**55.** (canceled)

**56.** (canceled)

**57.** A method according to claim **38**, wherein the vaccine formulation comprises a veterinary pharmaceutically acceptable excipient, carrier, or diluent and, optionally, a veterinary pharmaceutically acceptable adjuvant.

**58.** A method for preparing a veterinary vaccine formulation for the prevention, treatment or amelioration of *P. multocida* infection in a ruminant animal susceptible to *P. multocida* infection, the method comprising:

(i) diagnosing a *P. multocida* infection in a ruminant animal;

(ii) identifying the phylogenetic cluster to which a PmSLP protein present in the infecting *P. multocida* belongs, the phylogenetic cluster being selected from PmSLP-1, PmSLP-2, PmSLP-3, PmSLP-4.1 or PmSLP-4.2; and

(iii) preparing a vaccine formulation comprising a *P. multocida* PmSLP protein, or immunogenically equivalent portion thereof, which belongs to the identified phylogenetic cluster together with a veterinary pharmaceutically acceptable adjuvant to form a veterinary

vaccine formulation comprising an effective amount of the *P. multocida* PmSLP protein or the immunogenically equivalent portion thereof to treat a food production animal susceptible to *P. multocida* infection.

**59.** A method according to claim **58**, wherein the method additionally comprises identifying the serogroup of the infecting *P. multocida* strain, the serogroup being selected from the group consisting of serogroup A, B, D, E, and F, and the vaccine being prepared using a *P. multocida* PmSLP protein, or an immunogenically equivalent portion thereof, from the same or another *P. multocida* strain belonging to the selected serogroup.

- 60.** (canceled)
- 61.** (canceled)
- 62.** (canceled)
- 63.** (canceled)
- 64.** (canceled)
- 65.** (canceled)
- 66.** (canceled)

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