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(54) Title: *EHRlichia CANIS* DIVA (DIFFERENTIATE INFECTED FROM VACCINATED ANIMALS)

(57) Abstract: *Ehrlichia canis* antigens that can be used to differentiate *E. canis* infected animals from animals that have been challenged with *E. canis*, e.g., vaccinated against *E. canis*, are disclosed. The invention also provides compositions and methods for determining the presence of *E. canis* antigens and antibodies.



Title: *Ehrlichia canis* DIVA (Differentiate Infected from Vaccinated Animals)

Priority

5 This application claims the benefit of U.S. Appl. No. 60/668,205, filed on April 4, 2005, which is incorporated herein by reference in its entirety.

Background of the Invention

10 The *Ehrlichia* are obligate intracellular pathogens that infect circulating white blood cells in mammalian hosts. *Ehrlichia canis* can infect canines and humans and cause canine monocytic ehrlichiosis (CME) and human monocytic ehrlichiosis (HME), respectively. The canine disease is characterized by fever, lymphadenopathy, weight loss, and pancytopenia. In humans the disease is characterized by fever, headache, myalgia, and leukopenia. Early detection and treatment are important for treating both canine and human ehrlichiosis.

15 **Summary of the Invention**

 In one embodiment the invention provides a method for determining whether an animal is infected with *Ehrlichia canis*, or is either not infected or is vaccinated with an *E. canis* vaccine. The method comprises contacting a biological sample from the animal with a first purified *E. canis* polypeptide that is not an element of the *E. canis* vaccine; and detecting whether an antibody in the sample specifically binds to the first purified *E. canis* polypeptide. If an antibody in the sample specifically binds to the first purified *E. canis* polypeptide, then the animal is infected with *E. canis* and if an antibody does not specifically bind to the purified *E. canis* polypeptide, then the animal is either vaccinated or is not infected. The first purified *E. canis* polypeptide can comprise SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 15, 16, 17 or a combination thereof. The *E. canis* vaccine can comprise at least one *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, p153 polypeptide, or a combination thereof. The *E. canis* vaccine can comprise a vector encoding at least one *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, p153 polypeptide, or a combination thereof.

30 The method can further comprise detecting whether an antibody in the sample specifically binds to a second purified *E. canis* polypeptide that is an element of an *E. canis* vaccine, and determining that the animal has been vaccinated for *E. canis* by detecting that an antibody in the sample specifically binds to the second purified *E. canis*

polypeptide, or determining that the animal has not been vaccinated for *E. canis* and has not been infected by *E. canis* by detecting that no antibody in the sample specifically binds to the second purified *E. canis* polypeptide.

Another embodiment of the invention provides a method of distinguishing
5 between animals that have been infected with *E. canis* and animals that have not been infected or have been vaccinated with an *E. canis* vaccine. The method comprises contacting a biological sample from an animal with a first purified *E. canis* polypeptide that does not specifically bind to antibodies that are a component of the animal's immune response to an *E. canis* vaccine, detecting whether an antibody in the sample specifically
10 binds to the first purified *E. canis* polypeptide, and determining that the animal is infected by correlating a positive result in the detecting step to a natural infection and determining that the animal has been vaccinated or is not infected by correlating a negative result to a vaccination or no infection. The first purified *E. canis* polypeptide can comprise SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17 or combinations thereof. The method can further
15 comprise detecting whether an antibody in the sample specifically binds to a second purified *E. canis* polypeptide that specifically binds an antibody that is a component of the animal's immune response to the vaccine, thereby determining whether the animal has been vaccinated.

Still another embodiment of the invention provides a method of determining
20 whether an animal is either not infected or has been vaccinated against *E. canis* with an *E. canis* vaccine, or is infected with *E. canis* comprising determining the animal's immune response to a first purified polypeptide derived from *E. canis* that is not an element of an *E. canis* vaccine. The first *E. canis* polypeptide can comprise SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17 or combinations thereof. The method can further comprise
25 determining, in those animals that do not have an immune response to the first purified polypeptide, whether the animal has been vaccinated by determining the animal's immune response to a second purified polypeptide that is an element of the *E. canis* vaccine.

Even another embodiment of the invention provides a method for determining the
30 vaccination or infection status of an animal for *E. canis*. The method comprises contacting a biological sample from the animal with a reagent comprising a first purified *E. canis* polypeptide that is not an element of an *E. canis* vaccine and detecting whether the first purified *E. canis* polypeptide specifically binds to an antibody in the biological

sample. If the first purified *E. canis* polypeptide specifically binds to an antibody in the sample, then the animal is infected with *E. canis* and, if the first purified *E. canis* polypeptide does not specifically bind to an antibody in the sample, then the animal is either not infected with *E. canis* or has been vaccinated with a vaccine that does not
5 comprise the first purified *E. canis* polypeptide. The first purified *E. canis* polypeptide can comprise SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17 or combinations thereof. The method can further comprise, detecting whether an antibody in the sample specifically binds to a second purified *E. canis* polypeptide that specifically binds an antibody that is a component of the animal's immune response to the *E. canis* vaccine,
10 thereby determining whether the animal has been vaccinated.

Another embodiment of the invention provides a method of determining whether an animal is infected with *E. canis*, is vaccinated with an *E. canis* vaccine, or is not infected and not vaccinated. The method comprises contacting a biological sample from the animal with a first purified *E. canis* polypeptide that is not an element of the *E. canis*
15 vaccine, contacting the biological sample with a second purified *E. canis* polypeptide that is an element of the *E. canis* vaccine; and detecting whether antibodies in the sample specifically bind to the first and the second purified *E. canis* polypeptides. If antibodies in the sample specifically bind to both the first and second purified *E. canis* polypeptides, then the animal is infected with *E. canis*, and if an antibody in the sample specifically
20 binds to the second purified *E. canis* polypeptide but not the first purified *E. canis* polypeptide, then the animal has been vaccinated but is not infected and wherein, and if an antibody does not specifically bind to either polypeptide, then the animal is not infected and not vaccinated. The first purified *E. canis* polypeptide can comprise SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17 or combinations thereof.

25 Yet another embodiment of the invention provides a method of determining an animal's vaccination and infection status for *E. canis*. The method comprises contacting a biological sample from an animal with a first purified polypeptide that does not specifically bind to antibodies that are a component of the animal's immune response to an *E. canis* vaccine and a second polypeptide that specifically binds to an antibody that is
30 a component of the animal's immune response to an *E. canis* vaccine; detecting whether antibodies in the sample specifically bind to the first and second purified polypeptides; determining that the animal is infected by detecting the specific binding of antibodies in the sample to both the first and second purified polypeptides, determining that that the

animal is vaccinated and not infected by detecting the specific binding of an antibody to the second purified polypeptide but not the first purified polypeptide, and determining that the animal is not vaccinated and not infected by detecting the absence of specific binding to the first and second purified *E. canis* polypeptides. The first *E. canis* polypeptide can comprise SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17 or combinations thereof.

Even another embodiment of the invention provides a method for determining the presence or absence of an antibody or fragment thereof, in a test sample, wherein the antibody or fragment thereof specifically binds to a purified polypeptide comprising SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, or 17. The method comprises contacting the test sample with a purified polypeptide comprising SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, or 17 under conditions suitable for specific binding of the purified polypeptide to the antibody or fragment thereof, and detecting the presence or absence of specific binding. The presence of specific binding indicates the presence of the antibody or fragment thereof. The absence of specific binding indicates the absence the antibody or fragment thereof. The method can further comprise detecting the amount of specific binding. The test sample can be serum, blood, or saliva. The purified polypeptide can be immobilized to a solid support. The purified polypeptide can be labeled. The detection can be by radioimmunoassay, enzyme-linked immunosorbent assay, immunohistochemical, or immunoenzyme-assay.

Yet another embodiment of the invention provides a method for determining the presence or absence of a polypeptide comprising SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17 in a test sample. The method comprises contacting the test sample with an antibody or fragment thereof that specifically binds a purified polypeptide consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17 under conditions suitable for specific binding of the polypeptide to the antibody or fragment thereof, and detecting the presence or absence of specific binding. The presence of specific binding indicates the presence of the polypeptide, and the absence of specific binding indicates that the absence the polypeptide. The method can further comprise detecting the amount of specific binding. The test sample can be serum, blood, or saliva. The antibody or fragment thereof can be immobilized to a solid support. The antibody or fragment thereof can be labeled. The detection can be by radioimmunoassay, enzyme-linked immunosorbent assay, immunohistochemical assay or immunoenzyme-assay.

Another embodiment of the invention provides a composition comprising one or more purified polypeptides consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17 or combinations thereof and a polynucleotide encoding the one or more purified polypeptides.

The purified polypeptide can be in a multimeric form. The purified polypeptide can be linked to a heterologous protein (an amino acid sequence not normally associated with the purified polypeptide in nature) an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, or a combination thereof.

Even another embodiment of the invention provides a fusion protein comprising one or more polypeptides consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:15, SEQ ID NO:16, SEQ ID NO:17 or a combination thereof.

Another embodiment of the invention provides a method of generating an immune response in an animal comprising administering one or more purified polypeptides comprising SEQ ID NOs:2, 4, 6, 8, 10, 15, 16, 17, or a combination thereof to the animal.

Yet another embodiment of the invention provides a method for the prophylaxis, treatment, or amelioration of an *Ehrlichia canis* infection in an animal. The method comprises administering (1) one or more purified polypeptides comprising SEQ ID NOs:2, 4, 6, 8, 10, 15, 16, 17, or a combination thereof;

one or more nucleic acids encoding one or more purified polypeptides comprising SEQ ID NOs:2, 4, 6, 8, 10, 15, 16, 17, or a combination thereof

Therefore, the invention provides *Ehrlichia canis* antigens that can be used to differentiate *E. canis* naturally-infected animals from animals that have been challenged with *E. canis*, e.g., vaccinated against *E. canis*. The invention also provides compositions and methods for determining the presence of *E. canis* antigens and antibodies and for the treatment, amelioration, and prevention of *E. canis* infection.

Brief Description of the Drawings

Figure 1 shows SNAP® 3Dx® Assay evaluation of laboratory beagles. The SNAP® device used as described by manufacturer. "Pre" sample is from day 0. "Post"

sample is from day 42. The *E. canis* positive spot became positive in all 4 dogs for the day 42 sample. Similar results were observed for the day 70 sample.

Figure 2 shows a gel of *E. canis* proteins separated using 2D gel electrophoresis. Stained with BIOSAFE™ Coomassie Blue (Bio-Rad Inc.).

5 Figure 3 shows a Western blot of *E. canis* proteins using dog sera harvested at day 0. The plasma dilution is 1:100. These dogs were negative for reactivity with *E. canis* antigens.

Figure 4 shows a Western blot of *E. canis* proteins using dog sera from a pool of four challenged animals. The sera dilution is 1:100.

10 Figure 5 shows a Western blot of *E. canis* proteins using dog plasma from a pool of infected animals. The sera dilution is 1:1000.

Figure 6 shows a Western blot of six different *E. canis* DIVA antigens expressed in *E. coli* and probed with either dog sera from a pool of four infected animals (A) or dog sera pooled from four challenged animals (B). Sera dilutions were 1:100 for challenged
15 animals or 1:500 for the infected animals. The DIVA antigens represented include: (1) 200kDa antigen, (2) Ribosomal protein L1, (3a and 3b) "ATPase"- two different segments, (4) 120kDa antigen, (5) Heat shock proteins / p16 antigen.

Figure 7 demonstrates that cloned p16 antigen is recognized by sera from dogs infected with *E. canis* but not those challenged with the cultured organism. Lysates from
20 uninduced (U) or induced (I) bacteria transformed with a vector expressing the p16 antigen or the original genomic fragment (+C) were separated by SDS-PAGE and transferred to nitrocellulose for Western blot analysis.

Figure 8 shows the repeated sequence in SEQ ID NO: 15.

Figure 9A shows SEQ ID NO:16.

25 Figure 9B shows SEQ ID NO:17.

Detailed Description of the Invention

Ehrlichia canis antigens that can be used to differentiate *E. canis* naturally-infected animals from animals that have been challenged with *E. canis*, e.g., vaccinated against *E. canis*, are disclosed.

30 Before describing the present invention in detail, a number of terms will be defined. As used herein, the singular forms "a," "an", and "the" include plural referents unless the context clearly dictates otherwise.

As used herein, the term "polypeptide" refers to a compound of a single chain or a complex of two or more chains of amino acid residues linked by peptide bonds. The chain(s) may be of any length and can comprise a fusion protein. Although "protein" is often used in reference to relatively large polypeptides, and "peptide" is often used in reference to small polypeptides, usage of these terms in the art overlaps and varies. The term "polypeptide" as used herein thus refers interchangeably to peptides, polypeptides, proteins, or fusion proteins unless otherwise noted. The term "amino acid" refers to a monomeric unit of a peptide, polypeptide or protein.

As used herein, "antigen" as used herein refers to a molecule against which a subject can initiate a humoral and/or cellular immune response. Antigens can be any type of biologic molecule including, for example, simple intermediary metabolites, sugars, lipids, and hormones as well as macromolecules such as complex carbohydrates, phospholipids, nucleic acids and proteins. In the compositions and methods of the invention, it is preferred that the antigen is a polypeptide, *e.g.*, one comprising at least about six or more amino acids.

As used herein, a "derivative" of an *E. canis* antigen polypeptide, or an antigen or polypeptide that is "derived from" an *E. canis* antigen or polypeptide, refers to a antigen or polypeptide in which the native form has been purified, modified or altered. Such modifications include, but are not limited to: amino acid substitutions, modifications, additions or deletions; alterations in the pattern of lipidation, glycosylation or phosphorylation; reactions of free amino, carboxyl, or hydroxyl side groups of the amino acid residues present in the polypeptide with other organic and non-organic molecules; and other modifications, any of which may result in changes in primary, secondary or tertiary structure.

A "biological sample" is any sample from an animal that is expected to contain immunoglobulins. Generally, these samples are whole blood and blood components, but in some circumstances may include saliva, urine, tears, other bodily fluids, tissue extracts or cellular extracts.

An "infection," such as in an *E. canis* infection, means that an animal has been exposed to *E. canis*, regardless of whether the animal exhibits clinical symptoms of *E. canis*. A natural infection refers to an exposure that occurs as a result of one of the

natural transmission methods for *E. canis*, such as transmission by ticks. An infection does not include an exposure to *E. canis* through vaccination.

A “polypeptide or antigen that is not an element of an *E. canis* vaccine” is any *E. canis* polypeptide or antigen that is not present in, or is not an immunogenically active portion of, a particular *E. canis* vaccine or vaccines. Elements of the vaccine(s) can be portions of a subunit vaccine that includes less than the entire bacterium; these portions can be chemically synthesized or expressed recombinantly before becoming part of the vaccine, and these portions can be encoded by one or more vectors that express an immunogenic composition *in vivo*.

An “antibody that is a component of an animal’s immune response to an *E. canis* vaccine” refers to an antibody that is elicited as the result of a vaccination with an *E. canis* vaccine. These antibodies can be identical to or similar to antibodies elicited as the result of a natural *E. canis* infection. These antibodies will be maintained at a sufficient titer and so as to provide a protective and neutralizing effect against the bacteria. A successful vaccination produces a measurable level of the antibody (or antibodies) that is elicited by a component of the *E. canis* vaccine. Examples of *E. canis* antigens that elicit antibodies that can be a component of an animal’s immune response to an *E. canis* vaccine are p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9 (see U.S. Pat. Nos. 6660269; 6,458,942; 6,403,780; 6,392,023), proA, ProB, mmpA, cytochrome oxidase (see U.S. Pat. Publ. 20040170972), p43 (see U.S. Pat. No. 6,355,777), which is the N-terminal portion of p153, a glycoprotein (see U.S. Pat. Publ. 2004/0121433), and p153.

An immune response is the development in an organism of a cellular and/or antibody mediated immune response to an antigen such as a polypeptide. Usually such a response includes but is not limited to one or more of the following: production of antibodies, B cells, helper T cells, suppressor T cells, and/or cytotoxic T cells. An immune response can be detected using any of several assays known to those with skill in the art.

Polypeptides of the Invention

Biological samples from animals that have been vaccinated against *E. canis* have the potential for producing a positive result in a test for *E. canis* infection due to the presence of antibodies produced in response to the vaccine. In one aspect, the invention

provides a method of distinguishing between animals that have been infected with *E. canis*, animals that have not been infected with *E. canis*, and animals that have been vaccinated against *E. canis*. Methods include contacting a biological sample from the animal with an antigen derived from *E. canis* that does not specifically bind to an antibody that is a component of the animal's antibody response to a particular *E. canis* vaccine.

The development of *E. canis* antibodies in an animal against a vaccine is dependent upon the particular vaccine used to vaccinate the animal. The difference in the immune response between animals that are vaccinated against *E. canis* and animals that are naturally or experimentally infected with *E. canis* provides a means for determining whether an animal has been vaccinated or is naturally or experimentally infected. Therefore, using the methods of the invention, animals that have been infected with *E. canis* can be distinguished from animals that have not been infected with *E. canis* or have been vaccinated against *E. canis*. Antigens of the invention, their immunodominant regions, and epitopes can be used in the methods of the invention. These compositions can be referred to as *E. canis* DIVA antigens (**D**ifferentiate **I**nfected from **V**accinated **A**nimals). An *E. canis* DIVA antigen induces an immune response, e.g., the production of specific antibodies, in an animal that is different from the immune response induced in the animal by a particular *E. canis* vaccine.

Accordingly, the detection of the binding between an *E. canis* DIVA antigen and an antibody that is not a component of an animal's immune response to a particular vaccine can indicate a natural infection. The absence of such binding can indicate vaccination or no infection. In addition, a second, separate antigen, such as an *E. canis* antigen that specifically binds an antibody that is a component of animal's immune response to a particular *E. canis* vaccine, can be used to detect antibodies produced in response to vaccination. The detection of neither antibody indicates no infection and no vaccination. As such, various combinations of separate capture reagents can lead to a determination of the vaccination and/or infection status of the test subject.

In one aspect, a method of the invention includes contacting a biological sample from an animal with an antigen that is a part of the native *E. canis* bacteria, but is not an element of a particular *E. canis* vaccine. An animal is any mammal that is likely to be vaccinated against *E. canis* and, in particular, canines. In addition, humans may be vaccinated against *E. canis*. In another aspect, the invention includes a method of

determining whether an animal has not been infected by *E. canis* and has not been vaccinated against *E. canis*. A biological sample from an animal is analyzed to detect the presence or absence of antibodies specific for an *E. canis* DIVA antigen, and the presence or absence of antibodies specific for a particular *E. canis* vaccine. It is then determined
5 that the animal has not been infected and has not been or vaccinated by determining the absence of such antibodies.

In one aspect of the invention, a DIVA antigen is not an element of an *E. canis* vaccine. The vaccination or infection status of an animal can be determined by detecting whether antibodies in the sample bind to one or more antigens used in the vaccine. If
10 antibodies in the sample bind to one or more of the antigens, the animal is either vaccinated or infected. If no antibody binds the DIVA polypeptide, then it can be determined that the animal has been vaccinated. If no binding is detected for either antigen, then it can be determined that the animal is not infected and not vaccinated.

A polypeptide of the invention can be post-translationally modified. A purified
15 polypeptide is a polypeptide preparation that is substantially free of cellular material, other types of polypeptides, chemical precursors, chemicals used in synthesis of the polypeptide, or combinations thereof. A polypeptide preparation that is substantially free of cellular material, culture medium, chemical precursors, chemicals used in synthesis of the polypeptide has less than about 30%, 20%, 10%, 5%, 1% or more of other
20 polypeptides, culture medium, chemical precursors, and/or other chemicals used in synthesis. Therefore, a purified polypeptide is about 70%, 80%, 90%, 95%, 99% or more pure.

Purified polypeptides of the invention can either be full-length polypeptides or fragments of polypeptides. For example, fragments of polypeptides of the invention can
25 comprise about 6, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 250, 500, 750 contiguous amino acids or more of polypeptides of the invention. Examples of polypeptides of the invention include those shown in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, or 17. Variant polypeptides are at least about 80, or about 90, 96, 98, or 99% identical to the polypeptide sequences shown in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, or 17 and are also
30 polypeptides of the invention. Variant polypeptides have one or more conservative amino acid variations or other minor modifications and retain biological activity, *i.e.*, are

biologically functional equivalents. A biologically active equivalent has substantially equivalent function when compared to the corresponding wild-type polypeptide.

Percent sequence identity has an art recognized meaning and there are a number of methods to measure identity between two polypeptide or polynucleotide sequences. 5 *See, e.g.,* Lesk, Ed., *Computational Molecular Biology*, Oxford University Press, New York, (1988); Smith, Ed., *Biocomputing: Informatics And Genome Projects*, Academic Press, New York, (1993); Griffin & Griffin, Eds., *Computer Analysis Of Sequence Data, Part I*, Humana Press, New Jersey, (1994); von Heinje, *Sequence Analysis In Molecular Biology*, Academic Press, (1987); and Gribskov & Devereux, Eds., *Sequence Analysis* 10 *Primer*, M Stockton Press, New York, (1991). Methods for aligning polynucleotides or polypeptides are codified in computer programs, including the GCG program package (Devereux *et al.*, *Nuc. Acids Res.* 12:387 (1984)), BLASTP, BLASTN, FASTA (Atschul *et al.*, *J. Molec. Biol.* 215:403 (1990)), and Bestfit program (Wisconsin Sequence Analysis Package, Version 8 for Unix, Genetics Computer Group, University Research 15 Park, 575 Science Drive, Madison, WI 53711) which uses the local homology algorithm of Smith and Waterman (*Adv. App. Math.*, 2:482-489 (1981)). For example, the computer program ALIGN which employs the FASTA algorithm can be used, with an affine gap search with a gap open penalty of -12 and a gap extension penalty of -2.

When using any of the sequence alignment programs to determine whether a 20 particular sequence is, for instance, about 95% identical to a reference sequence, the parameters are set such that the percentage of identity is calculated over the full length of the reference polynucleotide and that gaps in identity of up to 5% of the total number of nucleotides in the reference polynucleotide are allowed.

Variants can generally be identified by modifying one of the polypeptide 25 sequences of the invention, and evaluating the properties of the modified polypeptide to determine if it is a biological equivalent. A variant is a biological equivalent if it reacts substantially the same as a polypeptide of the invention in an assay such as an immunohistochemical assay, an enzyme-linked immunosorbent Assay (ELISA), a radioimmunoassay (RIA), immunoenzyme assay or a western blot assay, e.g. has 90- 30 110% of the activity of the original polypeptide. In one embodiment, the assay is a competition assay wherein the biologically equivalent polypeptide is capable of reducing binding of the polypeptide of the invention to a corresponding reactive antigen or antibody by about 80, 95, 99, or 100%. An antibody that specifically binds a

corresponding wild-type polypeptide also specifically binds the variant polypeptide. Variant polypeptides of the invention can comprise about 1, 2, 3, 4, 5, or 6 conservative amino acid substitutions.

A conservative substitution is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydrophobic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

A polypeptide of the invention can further comprise a signal (or leader) sequence that co-translationally or post-translationally directs transfer of the protein. The polypeptide can also comprise a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide can be conjugated to an immunoglobulin Fc region or bovine serum albumin.

A polypeptide can be covalently or non-covalently linked to an amino acid sequence to which the polypeptide is not normally associated with in nature. Additionally, a polypeptide can be covalently or non-covalently linked to compounds or molecules other than amino acids. For example, a polypeptide can be linked to an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, or a combination thereof. In one embodiment of the invention a protein purification ligand can be one or more C amino acid residues at, for example, the amino terminus or carboxy terminus of a polypeptide of the invention. An amino acid spacer is a sequence of amino acids that are not usually associated with a polypeptide of the invention in nature. An amino acid spacer can comprise about 1, 5, 10, 20, 100, or 1,000 amino acids.

If desired, a polypeptide can be a fusion protein, which can also contain other amino acid sequences, such as amino acid linkers, amino acid spacers, signal sequences, TMR stop transfer sequences, transmembrane domains, as well as ligands useful in protein purification, such as glutathione-S-transferase, histidine tag, and staphylococcal protein A, or combinations thereof. More than one polypeptide of the invention can be present in a fusion protein. Fragments of polypeptides of the invention can be present in a fusion protein of the invention. A fusion protein of the invention can comprise one or

more polypeptides shown in SEQ ID NO: 2, 4, 6, 8, 10, 12, 14, 15, 16, or 17, fragments thereof, or combinations thereof.

Polypeptides of the invention can be in a multimeric form. That is, a polypeptide can comprise one or more copies of SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17 or a combination thereof. A multimeric polypeptide can be a multiple antigen peptide (MAP).
5 *See e.g.*, Tam, J. Immunol. Methods, 196:17-32 (1996).

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

In one embodiment of the invention, a DIVA antigen comprises an immunodominant epitope or region. That is, an epitope or region that more frequently
25 elicits and binds to antibodies in a population thereof when compared with other epitopes. An antigen can have one or more immunodominant epitopes. Immunodominant epitopes can be mapped on, for example, a polypeptide after the polypeptide has been administered to an animal or prior to such administration. *See e.g.*, U.S. Pat. Publ.
30 2004/0209324.

A polypeptide of the invention can be produced recombinantly. A polynucleotide encoding a polypeptide of the invention can be introduced into a recombinant expression vector, which can be expressed in a suitable expression host cell system using techniques

well known in the art. A variety of bacterial, yeast, plant, mammalian, and insect expression systems are available in the art and any such expression system can be used. Optionally, a polynucleotide encoding a polypeptide can be translated in a cell-free translation system. A polypeptide can also be chemically synthesized or obtained from *E. canis* cells.

An immunogenic polypeptide of the invention can comprise an amino acid sequence shown in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, or 17. An immunogenic polypeptide can elicit antibodies or other immune responses (e.g., T-cell responses of the immune system) that recognize epitopes of polypeptides having SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, or 17. An immunogenic polypeptide of the invention can also be a fragment of a polypeptide that has an amino acid sequence shown in SEQ ID NOs: 2, 4, 6, 8, 10, 12, 14, 15, 16, 17. An immunogenic polypeptide fragment of the invention can be about 6, 10, 20, 30, 40, 50, 60, 70, 80, 90, 100, 250, 500, 750 amino acids in length.

Antibodies specific for *E. canis* can be detected in biological fluids or tissues by any method known in the art. The simplest methods generally are immunoassay methods. One such method is a competition-based method wherein serum samples are preincubated with an *E. canis* antigen that is not an element of an *E. canis* vaccine (e.g., an *E. canis* DIVA antigen), and then added to a solid phase, such a microtiter plate, having an immobilized monoclonal antibody specific for the *E. canis* DIVA antigen. Antibodies specific for the *E. canis* DIVA antigen in the sample will prevent the *E. canis* DIVA antigen from binding to the immobilized antibody. Detection of any binding of the *E. canis* DIVA antigen to the immobilized antibody can be determined by adding a second binding partner for the *E. canis* antigen, either directly labeled or capable of becoming labeled through binding to another binding partner having a label. A positive sample, *i.e.* a sample having antibodies specific for an *E. canis* DIVA antigen, is associated with a decrease in signal from the label.

In one particular embodiment, antibodies to an *E. canis* DIVA antigen in a biological sample can be detected by contacting the sample with an *E. canis* DIVA antigen and adding the sample to microtiter plate coated with an anti-DIVA antigen monoclonal antibody. Binding of the DIVA antigen to the microtiter plate can be detected by adding a rabbit polyclonal antibody against the DIVA antigen and adding an HRP-conjugated donkey anti-rabbit polyclonal antibody. Antibodies in the sample will

prevent the binding of the DIVA antigen to the immobilized antibody, thereby causing a decrease in signal.

Another method for detecting antibodies specific for an *E. canis* DIVA antigen is a sandwich assay where a biological sample suspected of containing an antibody specific for an *E. canis* DIVA antigen is contacted with an immobilized *E. canis* DIVA antigen to form an immunological complex. The presence of an antibody specific for an *E. canis* DIVA antigen is determined by the detection of the binding of a labeled binding partner for the *E. canis* antibody, such as a second antibody.

In one aspect of the invention, *E. canis* DIVA antigens can be immobilized on a suitable solid support. A biological sample is brought into contact with the *E. canis* DIVA antigen, to which the anti-*E. canis* antibodies bind, if such antibodies are present in the sample. The binding can be detected by any suitable means, e.g., enzymes, radionuclides, particulates or fluorescent labels. In a suitable embodiment, the detection reagent can be associated with a protein that is the same or similar to that which is used to capture anti-*E. canis* antibodies (if present). In one particular embodiment, antibodies to *E. canis* can be detected by immobilizing an *E. canis* antigen on a solid support. Biological samples can be contacted with the solid support and, following the removal of unbound sample, binding of the *E. canis* antibodies to the antigen can be accomplished with, for example, a labeled IgG antibody.

DIVA antigens of the invention can also comprise mimitopes of DIVA antigens of the invention. A mimitope is a random peptide epitope that mimics a natural antigenic epitope during epitope presentation. Random peptide epitopes can be identified by generating or selecting a library of random peptide epitopes. The library is contacted with an antibody. Mimitopes are identified that are specifically immunoreactive with the antibody. Random peptide libraries can, for example, be displayed on phage or generated as combinatorial libraries.

E. canis DIVA antigens, e.g., polypeptides, can be natural, i.e., isolated from a natural source, or can be synthetic (i.e., chemically synthesized or recombinantly produced using genetic engineering techniques). Natural proteins can be isolated from the whole bacterium by conventional techniques, such as affinity chromatography. Polyclonal or monoclonal antibodies can be used to prepare a suitable affinity column by well-known techniques.

Proteins that are immunologically cross-reactive with a natural *E. canis* protein can be chemically synthesized. For example, polypeptides having fewer than about 100 amino acids, more usually fewer than about 80 amino acids, and typically fewer than about 50 amino acids, can be synthesized by the well-known Merrifield solid-phase synthesis method where amino acids are sequentially added to a growing chain. Merrifield, 1963, J. Am. Chem. Soc., 85:2149-2156). Recombinant proteins can also be used. These proteins can be produced by expression in cultured cells of recombinant DNA molecules encoding a desired portion of the *E. canis* genome. The portion of the *E. canis* genome can itself be natural or synthetic, with natural genes obtainable from the isolated bacterium by conventional techniques.

E. canis Polynucleotides

Polynucleotides of the invention contain less than an entire microbial genome and can be single- or double-stranded nucleic acids. A polynucleotide can be RNA, DNA, cDNA, genomic DNA, chemically synthesized RNA or DNA or combinations thereof. The polynucleotides can be purified free of other components, such as proteins, lipids and other polynucleotides. For example, the polynucleotide can be 50%, 75%, 90%, 95%, 96%, 97%, 98%, 99%, or 100% purified. The polynucleotides of the invention encode the polypeptides described above. In one embodiment of the invention the polynucleotides encode polypeptides shown in SEQ ID NOs:2, 4, 6, 8, 10, 12, 14, 15, 16, 17 or combinations thereof. Polynucleotides of the invention include those shown in SEQ ID NO:1, 3, 5, 7, 9, 11, 13, or combinations thereof. Polynucleotides of the invention can comprise other nucleotide sequences, such as sequences coding for linkers, signal sequences, TMR stop transfer sequences, transmembrane domains, or ligands useful in protein purification such as glutathione-S-transferase, histidine tag, and staphylococcal protein A.

Polynucleotides of the invention can be isolated. An isolated polynucleotide is a polynucleotide that is not immediately contiguous with one or both of the 5' and 3' flanking genomic sequences that it is naturally associated with. An isolated polynucleotide can be, for example, a recombinant DNA molecule of any length, provided that the nucleic acid sequences naturally found immediately flanking the recombinant DNA molecule in a naturally-occurring genome is removed or absent. Isolated polynucleotides also include non-naturally occurring nucleic acid molecules. A nucleic acid molecule existing among hundreds to millions of other nucleic acid

molecules within, for example, cDNA or genomic libraries, or gel slices containing a genomic DNA restriction digest are not to be considered an isolated polynucleotide. The complete nucleotide sequence for *E. canis* is available from, e.g., GenBank as accession number NCBI: NZ_AAEJ01000001.

5 Polynucleotides of the invention can also comprise fragments that encode immunogenic polypeptides. Polynucleotides of the invention can encode full-length polypeptides, polypeptide fragments, and variant or fusion polypeptides.

Degenerate nucleotide sequences encoding polypeptides of the invention, as well as homologous nucleotide sequences that are at least about 80, or about 90, 96, 98, or
10 99% identical to the polynucleotide sequences of the invention and the complements thereof are also polynucleotides of the invention. Percent sequence identity can be calculated as described in the "Polypeptides" section. Degenerate nucleotide sequences are polynucleotides that encode a polypeptide of the invention or fragments thereof, but differ in nucleic acid sequence from the wild-type polynucleotide sequence, due to the
15 degeneracy of the genetic code. Complementary DNA (cDNA) molecules, species homologs, and variants of *E. canis* polynucleotides that encode biologically functional *E. canis* polypeptides also are *E. canis* polynucleotides. Polynucleotides of the invention can be isolated from nucleic acid sequences present in, for example, a biological sample, such as blood, serum, saliva, or tissue from an infected individual. Polynucleotides can
20 also be synthesized in the laboratory, for example, using an automatic synthesizer. An amplification method such as PCR can be used to amplify polynucleotides from either genomic DNA or cDNA encoding the polypeptides.

Polynucleotides of the invention can comprise coding sequences for naturally occurring polypeptides or can encode altered sequences that do not occur in nature. If
25 desired, polynucleotides can be cloned into an expression vector comprising expression control elements, including for example, origins of replication, promoters, enhancers, or other regulatory elements that drive expression of the polynucleotides of the invention in host cells. An expression vector can be, for example, a plasmid, such as pBR322, pUC, or ColE1, or an adenovirus vector, such as an adenovirus Type 2 vector or Type 5 vector.
30 Optionally, other vectors can be used, including but not limited to Sindbis virus, simian virus 40, alphavirus vectors, poxvirus vectors, and cytomegalovirus and retroviral vectors, such as murine sarcoma virus, mouse mammary tumor virus, Moloney murine leukemia virus, and Rous sarcoma virus. Minichromosomes such as MC and MC1, bacteriophages,

phagemids, yeast artificial chromosomes, bacterial artificial chromosomes, virus particles, virus-like particles, cosmids (plasmids into which phage lambda *cos* sites have been inserted) and replicons (genetic elements that are capable of replication under their own control in a cell) can also be used.

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

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

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

a hybridized complex comprising the probe or primer and a complementary polynucleotide from the test sample indicates the presence of *E. canis* or an *E. canis* polynucleotide sequence in the sample.

Antibodies

5 Antibodies of the invention are antibody molecules that specifically and stably bind to an *E. canis* polypeptide of the invention or fragment thereof. An antibody of the invention can be a polyclonal antibody, a monoclonal antibody, a single chain antibody (scFv), or a fragment of an antibody. Fragments of antibodies are a portion of an intact antibody comprising the antigen binding site or variable region of an intact antibody,
10 wherein the portion is free of the constant heavy chain domains of the Fc region of the intact antibody. Examples of antibody fragments include Fab, Fab', Fab'-SH, F(ab')₂ and F_v fragments.

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

 "Specifically binds" or "specific for" means that an antigen, e.g., a polypeptide, recognizes and binds to an antibody of the invention with greater affinity than to other,
30 non-specific molecules. For example, an antibody raised against an antigen (e.g., a polypeptide) to which it binds more efficiently than to a non-specific protein can be described as specifically binding to the antigen. Binding specifically can be tested using,

for example, an enzyme-linked immunosorbant assay (ELISA), a radioimmunoassay (RIA), or a western blot assay using methodology well known in the art.

Additionally, monoclonal antibodies directed against epitopes present on a antigen, e.g., a polypeptide of the invention, can also be readily produced. For example, 5 normal B cells from a mammal, such as a mouse, which was immunized with a polypeptide of the invention can be fused with, for example, HAT-sensitive mouse myeloma cells to produce hybridomas. Hybridomas producing *E. canis*-specific antibodies can be identified using RIA or ELISA and isolated by cloning in semi-solid agar or by limiting dilution. Clones producing *E. canis*-specific antibodies are isolated by 10 another round of screening. Monoclonal antibodies can be screened for specificity using standard techniques, for example, by binding a polypeptide of the invention to a microtiter plate and measuring binding of the monoclonal antibody by an ELISA assay. Techniques for producing and processing monoclonal antibodies are known in the art. See e.g., Kohler & Milstein, *Nature*, 256:495 (1975). Particular isotypes of a monoclonal 15 antibody can be prepared directly, by selecting from the initial fusion, or prepared secondarily, from a parental hybridoma secreting a monoclonal antibody of a different isotype by using a sib selection technique to isolate class-switch variants. See Steplewski *et al.*, *P.N.A.S. U.S.A.* 82:8653 1985; Spria *et al.*, *J. Immunolog. Meth.* 74:307, 1984. Monoclonal antibodies of the invention can also be recombinant monoclonal antibodies. 20 See, e.g., U.S. Patent No. 4,474,893; U.S. Patent No. 4,816,567. Antibodies of the invention can also be chemically constructed. See, e.g., U.S. Patent No. 4,676,980.

Antibodies of the invention can be chimeric (see, e.g., U.S. Patent No. 5,482,856), humanized (see, e.g., Jones *et al.*, *Nature* 321:522 (1986); Reichmann *et al.*, *Nature* 332:323 (1988); Presta, *Curr. Op. Struct. Biol.* 2:593 (1992)), or human antibodies. 25 Human antibodies can be made by, for example, direct immortalization, phage display, transgenic mice, or a Trimer method, see e.g., Reisener *et al.*, *Trends Biotechnol.* 16:242-246 (1998).

Antibodies that specifically bind *E. canis* antigens (e.g., *E. canis* polypeptides shown in SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 15, 16, 17), are particularly useful for 30 detecting the presence of *E. canis* or *E. canis* antigens in a sample, such as a serum, blood, urine or saliva sample from an *E. canis*-infected animal such as a human or dog. An immunoassay for *E. canis* or an *E. canis* antigen can utilize one antibody or several antibodies. An immunoassay for *E. canis* or an *E. canis* antigen can use, for example, a

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

Antibodies of the invention or fragments thereof can be bound to a support and used to detect the presence of *E. canis* or an *E. canis* antigen, e.g., an *E. canis* DIVA antigen or *E. canis* non-DIVA antigen. Supports include, for example, glass, polystyrene, polypropylene, polyethylene, dextran, nylon, amylases, natural and modified celluloses,
15 polyacrylamides, agaroses and magletite.

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

Antibodies of the invention can also be used in immunolocalization studies to analyze the presence and distribution of a polypeptide of the invention during various cellular events or physiological conditions. Antibodies can also be used to identify molecules involved in passive immunization and to identify molecules involved in the biosynthesis of non-protein antigens. Identification of such molecules can be useful in
25 vaccine development. Antibodies of the invention, including, for example, monoclonal antibodies and single chain antibodies, can be used to monitor the course of amelioration of a disease caused by *E. canis*. By measuring the increase or decrease of *E. canis* antibodies to *E. canis* antigens in a test sample from an animal, it can be determined
30

whether a particular therapeutic regiment aimed at ameliorating the disorder is effective. Antibodies can be detected and/or quantified using for example, direct binding assays such as RIA, ELISA, or western blot assays.

Detection

5 Methods of the invention can be accomplished using, for example, immunoassay techniques well known to those of skill in the art, including, but not limited to, using microplates and lateral flow devices. In one embodiment, one or more *E. canis* DIVA antigens are immobilized on a solid support at a distinct location. Detection of antigen-antibody complexes on the solid support can be by any means known in the art. For
10 example, U.S. Patent No. 5,726,010, which is incorporated herein by reference in its entirety, describes an example of a lateral flow device useful in the present invention. The device of the invention can be used to detect one or more antibodies to *E. canis* antigens.

 Immobilization of one or more analyte capture reagents, *e.g.*, *E. canis*
15 polypeptides, onto a device or solid support is performed so that an analyte capture reagent will not be washed away by the sample, diluent and/or wash procedures. One or more analyte capture reagents can be attached to a surface by physical adsorption (*i.e.*, without the use of chemical linkers) or by chemical binding (*i.e.*, with the use of chemical linkers). Chemical binding can generate stronger attachment of capture reagents on a
20 surface and provide defined orientation and conformation of the surface-bound molecules.

 Another embodiment of the invention provides a device that is suitable for a lateral flow assay. For example, a test sample is added to a flow matrix at a first region (a sample application zone). The test sample is carried in a fluid flow path by capillary
25 action to a second region of the flow matrix where a label capable of binding and forming a first complex with an analyte in the test sample. The first complex is carried to a third region of the flow matrix where an *E. canis* polypeptide is immobilized at a distinct location. A second complex is formed between an immobilized polypeptide and the first complex including the antibody from the sample. For example, a first complex
30 comprising a gold sol particle and an *E. canis* polypeptide bound to an *E. canis* antibody will specifically bind and form a second complex with a second immobilized *E. canis*

polypeptide or with a second antibody directed to *E. canis* antibodies. The label that is part of the second complex can be directly visualized.

5 In another aspect, the invention includes one or more labeled specific binding reagents that can be mixed with a test sample prior to application to a device of the invention. In this case it is not necessary to have labeled specific binding reagents deposited and dried on a specific binding reagent pad in the device. A labeled specific binding reagent, whether added to a test sample or pre-deposited on the device, can be for example, a labeled antibody that specifically binds an antibody for *E. canis*.

10 Any or all of the above embodiments can be provided as a kit. In one particular example, such a kit would include a device complete with specific binding reagents (*e.g.*, a non-immobilized labeled specific binding reagent and an immobilized analyte capture reagent) and wash reagent, as well as detector reagent and positive and negative control reagents, if desired or appropriate. In addition, other additives can be included, such as stabilizers, buffers, and the like. The relative amounts of the various reagents can be
15 varied, to provide for concentrations in solution of the reagents that substantially optimize the sensitivity of the assay. Particularly, the reagents can be provided as dry powders, usually lyophilized, which on dissolution will provide for a reagent solution having the appropriate concentrations for combining with a sample.

An *E. canis* DIVA antigen, *e.g.*, a polypeptide, can be an immobilized analyte
20 capture reagent in a reaction zone (solid phase). A second analyte capture reagent, *e.g.* an anti-IgG or anti-IgM antibody, that has been conjugated to a label, can either be added to the sample before the sample is added to the device, or the second analyte capture reagent can be incorporated into the device. For example the labeled specific binding reagent can be deposited and dried on a fluid flow path that provides fluid communication between
25 the sample application zone and the solid phase. Contact of the labeled specific binding reagent with the fluid sample results in dissolution of the labeled specific binding reagent.

The device can also include a liquid reagent that transports unbound material (*e.g.*, unreacted fluid sample and unbound specific binding reagents) away from the reaction zone (solid phase). A liquid reagent can be a wash reagent and serve only to remove
30 unbound material from the reaction zone, or it can include a detector reagent and serve to both remove unbound material and facilitate analyte detection. For example, in the case of a specific binding reagent conjugated to an enzyme, the detector reagent includes a

substrate that produces a detectable signal upon reaction with the enzyme-antibody conjugate at the reactive zone. In the case of a labeled specific binding reagent conjugated to a radioactive, fluorescent, or light-absorbing molecule, the detector reagent acts merely as a wash solution facilitating detection of complex formation at the reactive zone by washing away unbound labeled reagent.

Two or more liquid reagents can be present in a device, for example, a device can comprise a liquid reagent that acts as a wash reagent and a liquid reagent that acts as a detector reagent and facilitates analyte detection.

A liquid reagent can further include a limited quantity of an "inhibitor", *i.e.*, a substance that blocks the development of the detectable end product. A limited quantity is an amount of inhibitor sufficient to block end product development until most or all excess, unbound material is transported away from the second region, at which time detectable end product is produced.

Methods of Treatment, Amelioration, or Prevention of a Disease Caused by *E. canis*

In one embodiment of the invention, a DIVA polypeptide, polynucleotide or antibody of the invention can be used to treat, ameliorate, or prevent a disease caused by *E. canis*. If, however, a DIVA polypeptide is used to treat, ameliorate, or prevent a disease caused by *E. canis*, it could not, thereafter, be used as a DIVA polypeptide for the detection and differentiation of infected, non-vaccinated, and vaccinated animals because a vaccinated animal's immune system would recognize the DIVA antigen used for vaccination. However, a DIVA polypeptide that does not cross-react with antibodies to the DIVA polypeptide used for treatment, amelioration or prevention of a disease caused by *E. canis* may still be used as an *E. canis* DIVA antigen.

For example, if SEQ ID NO:2 or a fragment thereof is used as a vaccine, then SEQ ID NOs:4, 6, 8, 10, 12, 14, 15, 16, 17 or combinations thereof can be used as a DIVA polypeptide, if they do not cross-react with antibodies specific for SEQ ID NO:2. Therefore, the DIVA polypeptides, polynucleotides, and antibodies can be used in two different ways: (1) as compositions for the prevention, treatment, or amelioration of a disease or infection caused by *E. canis*; and (2) as an *E. canis* DIVA antigen for the detection and differentiation of animals that are vaccinated; non-vaccinated; infected or not infected with *E. canis*.

Polypeptides, polynucleotides, and antibodies of the invention can be used to treat, ameliorate, or prevent a disease caused by *E. canis*. For example, an antibody, such as a monoclonal antibody of the invention or fragments thereof, can be administered to an animal, such as a human. In one embodiment of the invention an antibody or fragment thereof is administered to an animal in a pharmaceutical composition comprising a pharmaceutically acceptable carrier. A pharmaceutical composition comprises a therapeutically effective amount of an antibody or fragments thereof. A therapeutically effective amount is an amount effective in alleviating the symptoms of *E. canis* infection or in reducing the amount of *E. canis* organisms in a subject.

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

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

A polypeptide, polynucleotide, or antibody of the invention can be administered to a mammal, such as a mouse, rabbit, guinea pig, macaque, baboon, chimpanzee, human, cow, sheep, pig, horse, dog, cat, or to animals such as chickens or ducks, to elicit antibodies *in vivo*. Injection of a polynucleotide has the practical advantages of simplicity of construction and modification. Further, injection of a polynucleotide results in the synthesis of a polypeptide in the host. Thus, the polypeptide is presented to the host immune system with native post-translational modifications, structure, and conformation. A polynucleotide can be delivered to a subject as "naked DNA."

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

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

Pharmaceutically acceptable salts can also be used in compositions of the invention, for example, mineral salts such as hydrochlorides, hydrobromides, phosphates, or sulfates, as well as salts of organic acids such as acetates, propionates, malonates, or benzoates. Especially useful protein substrates are serum albumins, keyhole limpet hemocyanin, immunoglobulin molecules, thyroglobulin, ovalbumin, tetanus toxoid, and

other proteins well known to those of skill in the art. Compositions of the invention can also contain liquids or excipients, such as water, saline, phosphate buffered saline, Ringer's solution, Hank's solution, glucose, glycerol, dextrose, malodextrin, ethanol, or the like, singly or in combination, as well as substances such as wetting agents, emulsifying agents, tonicity adjusting agents, detergent, or pH buffering agents. Additional active agents, such as bacteriocidal agents can also be used.

If desired, co-stimulatory molecules, which improve immunogen presentation to lymphocytes, such as B7-1 or B7-2, or cytokines such as MIP1 α , GM-CSF, IL-2, and IL-12, can be included in a composition of the invention. Optionally, adjuvants can also be included in a composition. Adjuvants are substances that can be used to nonspecifically augment a specific immune response. Generally, an adjuvant and a polypeptide of the invention are mixed prior to presentation to the immune system, or presented separately, but are presented into the same site of the animal. Adjuvants can include, for example, oil adjuvants (*e.g.* Freund's complete and incomplete adjuvants) mineral salts (*e.g.* Alk(SO₄)₂; AlNa(SO₄)₂, AlNH₄(SO₄), Silica, Alum, Al(OH)₃, and Ca₃(PO₄)₂), polynucleotides (*i.e.* Polyic and Poly AU acids), and certain natural substances (*e.g.* wax D from *Mycobacterium tuberculosis*, as well as substances found in *Corynebacterium parvum*, *Bordetella pertussis* and members of the genus *Brucella*). Adjuvants which can be used include, but are not limited to MF59-0, aluminum hydroxide, N-acetyl-muramyl-L-threonyl-D-isoglutamine (thr-MDP), N-acetyl-nor-muramyl-L-alanyl-D-isoglutamine (CGP 11637), referred to as nor-MDP), N-acetylmuramyl-L-alanyl-D-isoglutaminyl-L-alanine-2-(1'-2'-dipalmitoyl-sn-glycero-3-hydroxyphosphoryloxy)-ethylamine (CGP 19835A, referred to as MTP-PE), and RIBI, which contains three components extracted from bacteria, monophosphoryl lipid A, trehalose dimycolate and cell wall skeleton (MPL+TDM+CWS) in a 2% squalene/TWEEN® 80 emulsion.

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

Administration of polypeptides, polynucleotides, or antibodies can elicit an immune response in the animal that lasts for at least 1 week, 1 month, 3 months, 6 months, 1 year, or longer. Optionally, an immune response can be maintained in an

animal by providing one or more booster injections of the polypeptide, polynucleotide, or antibodies at 1 month, 3 months, 6 months, 1 year, or more after the primary injection. If desired, co-stimulatory molecules or adjuvants can also be provided before, after, or together with the compositions.

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

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

All patents, patent applications, and other scientific or technical writings referred to anywhere herein are incorporated by reference in their entirety. The invention illustratively described herein suitably can be practiced in the absence of any element or elements, limitation or limitations that are not specifically disclosed herein. Thus, for
25 example, in each instance herein any of the terms "comprising", "consisting essentially of", and "consisting of" can be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it
30 is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such

modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.

EXAMPLES

Example 1

Preparation of formalin killed *E. canis* for immunization into dogs

E. canis was grown in canine cell culture using methods described in the literature. See e.g., Breitschwerdt, Antimicrobial Agents and Chemotherapy, 1998, Vol 42:362-368. Using light microscopy, 030 cells were estimated to be greater than 80% infected by *E. canis*. Two liters of *E. canis* infected cell culture were collected, centrifuged and the pellet retained yielding 7.31 gms of material (wet weight). It is presumed water made up 80% of the weight of the material, giving an estimated dry weight of 1.462 gms (20% of the weight of the material). The cell pellet was resuspended to 20 mg/ml in PBS (dry weight) for a total volume of 73 ml.

To this resuspended cell pellet, 0.73 ml of formalin solution was added (Sigma Catalog HT50-1-2 Formalin Solution 10%, neutral buffered) for a final formaldehyde concentration of 0.04%. The solution was stirred overnight at 4°C. The inactivated mixture was centrifuged and the cell pellet retained. The pellet was washed by resuspension into 250 mls of PBS. The material was collected by centrifugation and the wash was repeated one time.

The washed cell pellet was resuspended into 73 mls of PBS. The sample was aliquoted to 73 screw cap vials and frozen at -80°C. Each vial contains 20 mgs (dry weight) of formalin inactivated *E. canis* cell culture, suitable for combining with the appropriate adjuvant for immunization into animals.

Example 2

Preparation of formalin fixed *E. canis* with two different adjuvants, protocol for the immunization of beagles with *E. canis* antigen, and testing of sera from immunized beagles using SNAP® 3Dx®.

5 The preparation of antigen with aluminum hydroxide adjuvant is a technique well known to those skilled in the art. For example see "Antibodies, A Laboratory Manual", Cold Spring Harbor Press, 1988, pp 99.

 For immunization into dogs (laboratory beagles), two sets of doses were prepared with aluminum hydroxide adjuvant prepared as described above and two sets of doses
10 were prepared with Ribi adjuvant (Corixa Corp., Seattle WA) using the protocol described by the manufacturer. Each dose contained approximately 20 mg of formalin inactivated *E. canis* cell culture (dry weight).

 Kennel kept laboratory beagles were selected for immunization with the *E. canis* formalin inactivated antigen. Two groups of two dogs each; with each group using a
15 different adjuvant were dosed with the formalin fixed *E. canis* preparation (aluminum oxide or Ribi). On day 0 all 4 dogs were found to be sero-negative using both the SNAP® 3Dx® diagnostic as well as Western blot analysis using *E. canis* organism.

 The IACUC committee of Covance Research Products Inc. approved the protocol for immunization of laboratory beagles. Dogs were challenged on days 0, 28 and 56 with
20 weekly 1 ml bleeds being monitored using SNAP® 3Dx®. All dogs were dosed with the appropriate test article subcutaneously in the dorsoscapular area. All four animals seroconverted to a positive test on SNAP®3Dx® *E. canis* by day 42. Production bleeds were taken on days 42 and 70 (approximately 50 ml blood that yielded approximately 25 ml sera).

25 Figure 1 shows SNAP®3Dx® Assay evaluation of laboratory beagles. The SNAP® device was used as described by manufacturer. "Pre" sample is from day 0. "Post" sample is from day 42. The *E. canis* positive spot becomes positive in all 4 dogs for the day 42 sample. Similar results were observed for the day 70 sample.

 Experiments with a third vaccine comprising a third adjuvant, BCG, (Calbiochem
30 of EMD Biosciences, Inc. San Diego, CA) revealed similar results. Preparation of the third vaccine was identical to the preparations described for the Ribi adjuvante vaccine described above except: 1) formalin inactivation was for 24 hrs at 4 C, and 2) 1 mg of BCG was added. The vaccination schedule was day 0, day 14, with weekly bleeds assayed for reactivity with *E. canis* proteins.

Example 3**Enrichment of *E. canis* from cell culture using PERCOLL® gradients.**

5 For DNA isolation and Western blot analysis, *E. canis* was enriched from cell culture using PERCOLL® density gradients. The process of isolating intracellular pathogens from cell culture, such as *Ehrlichia*, is a technique well known to those skilled in the art. For example, see Akira *et al.* (1982) Purification of *Rickettsia tsutsugamushi* by PERCOLL® density gradient centrifugation, Microbiol. Immunol., 26:321-328.

10 A typical *E. canis* enrichment began with 1.5 liters of infected cell culture (see above). The cells were centrifuged 6,000 x g, the cell pellet retained and the supernatant discarded. The cell pellet was resuspended into 20 ml of PBS that was followed by a second centrifugation. The supernatant was discarded and supernatant retained. The pellet was then resuspended into 20 ml of PBS, sonicated for 5 seconds at 20 kHz, power
15 setting 1.5 using a Branson sonicator. The sample was then centrifuged at 500 x g for 5 minutes to pellet large debris.

PERCOLL® was added to the supernatant to a final concentration of 32% (4.5 ml of PERCOLL® with 10 ml of sample). The sample was loaded into Oak Ridge tubes compatible with a 70.1 Ti ultracentrifuge rotor, and centrifuged for 30 minutes at 63,000
20 x g. The opaque band was collected using a Pasteur pipette. The opaque band is highly enriched for *Ehrlichia* (confirmed using light microscopy of the collected sample). After a 1:4 dilution with PBS, the sample was aliquoted and centrifuged at 12,000 x g. The supernatant was discarded and the *Ehrlichia* pellet stored at -80°C.

Example 4**Testing of sera or plasma from challenged and infected dogs by Western blot.**

25 The use of 1-dimensional SDS-PAGE gel analysis and 2-dimensional gel analysis (1st dimension isoelectric focusing, 2nd dimension SDS-PAGE) is well known to those skilled in the art. For example see Current Protocols in Molecular Biology, eds. F.M. Ausubel *et al.*, John Wiley & Sons Inc., 1997, pages 10.2.2-10.3.11. The use of Western
30 blots to analyze proteins separated using these methods are well known to those skilled in

the art. For example see Current Protocols in Molecular Biology, eds. F.M. Ausubel et. al., John Wiley & Sons Inc., 1997, pages 10.8.1-10.8.116.

Initial work was performed using Western analysis of proteins separated with 1D gels (data not shown), followed by Western analysis of proteins separated using 2D gels. Proteins from whole *E. canis* harvested from cell culture were analyzed using 2D gel electrophoresis (materials and reagents used as described by the manufacturer; Bio-Rad Life Sciences Research, Hercules, CA 94547). The amount of sample to load per gel was determined empirically (see Figure 2). The proteins were blotted to nitrocellulose and probed using canine sera from laboratory beagles at day 0, dogs challenged with formalin fixed *E. canis* antigen (see above), or sera from animals infected with *E. canis* (see Figures 3, 4 & 5).

Positive canine sera and plasma was isolated from dogs infected with *E. canis*. *E. canis* infection was verified by Western analysis of lymphocytes harvested from whole blood from these dogs, and confirmed by use of the IDEXX SNAP®3Dx® assay with canine sera or plasma (commercially available from IDEXX Laboratories Inc., used as described by the manufacturer).

For Western blot analysis proteins were separated using 1D SDS-PAGE or 2D isoelectric focusing/SDS-PAGE gels followed by electro-blotting of the proteins from the gels to nitrocellulose. The nitrocellulose blots were incubated in a blocking solution of 2.5% non fat dry milk dissolved into Tris buffered saline (pH 7.5), 0.05% TWEEN® 20. Canine sera or plasma was diluted to the titer as described into buffer containing an *E. coli* lysate to block non-specific binding with 30% normal calf sera and incubated for 2 hrs at room temperature or over night at 4°C. After washing 3 times in TBS-TWEEN® (0.05%), the blots were transferred to a buffer containing 50% fetal calf sera, 50% TBS-TWEEN®-Kathon (0.05% & 0.5% respectively) to prevent nonspecific binding of a rabbit anti-canine Fc polyclonal antibody conjugated to horseradish peroxidase (Jackson Immuno Research, West Grove, PA 19390). The rabbit anti-canine Fc polyclonal antibody conjugate was diluted 1:5,000. The gels were washed 3 times with TBS-TWEEN® (0.05%), one time with TBS, and the presence of HRP detected using ECL Western Blotting Detection Reagents (Amersham Biosciences, Piscataway, NJ 08855-1327) used as described by manufacturer. Digital images of exposed X-ray film were captured using a GelDoc 2000 (Bio-Rad Inc.).

Example 5

Isolation of DNA from *E. canis* and construction of a lambda expression library and screening of the *E. canis* lambda expression library for clones having DIVA activity.

The preparation and screening of lambda expression libraries is a technique well known to those skilled in the art. For example, see Current Protocols in Molecular Biology, eds. F.M. Ausubel *et al.*, John Wiley & Sons Inc., 1997, pages 5.1 through 5.8.6. For the construction of the expression library, genomic DNA was purified from *E. canis* isolated from cell culture by PERCOLL® gradient centrifugation (see above). DNA was purified using a genomic DNA purification kit from Qiagen Sciences (Germantown, MD). A Lambda ZAP® II predigested EcoRI/CIAP Vector Kit (Stratagene Corp., La Jolla, CA 92037) was used as specified by the manufacturer for construction of the library. *E. canis* genomic DNA was partially digested with TSP509 and fragments ranging from 2-6 kb were isolated using agarose gel electrophoresis and ligated into the lambda vector. Phage were packaged and grown as specified by the manufacturer.

Approximately 120,000 individual lambda plaques were screened for binding to sera isolated from dogs identified as positive for infection with *E. canis*, but negative for reactivity with sera from animals challenged with an *E. canis* grown in cell culture (see above). From the initial screen 84 individual plaques were identified as having this activity.

Lambda plaques were subjected to two rounds of plaque purification and retested to verify positive reactivity with sera from *E. canis* infected animals, negative reactivity when screened with sera from challenged animals.

Isolated lambda plaques were screened for cross reactivity with sera from animals identified as being seropositive for *Anaplasma phagocytophilia*, *Borrelia burgdorferi* (causative agent of Lyme disease), *Rickettsia rickettsii* (causative agent of Rocky Mountain Spotted Fever), *Leptospira interrogans* and *Dirofilaria immitis* (causative agent of canine heartworm).

At the end of the screening process, 43 lambda plaques were found to react with sera from animals infected with *E. canis* that did not react with challenge sera or sera from dogs infected with other canine pathogens (see above).

Using the ZAP® feature of the cloning vector as per the manufacturers instructions, inserts into the lambda vector were converted to plasmids. The plasmids were transformed into the *E. coli* strain XL-1 blue for protein expression and analysis of

encoded proteins by Western blot. The ends of the *E. canis* DNA inserts were subjected to DNA sequence analysis using T7 and T3 sequencing primers.

Sequence information from both the T7 and T3 reactions for all 43 clones was submitted for BLAST analysis to the NCBI website. Results were tabulated in an excel format. Based on sequence identity between the clone and the available shotgun genome sequence for *E. canis* (NCBI: NZ_AAEJ01000001), segments of genomic DNA for each clone were identified. Individual clones sharing common genes were grouped for further analysis by Western blot using pools of infected and bacterial-challenged canine sera. Based on similar banding patterns, duplicate clones were eliminated. Any clones showing reactivity to both sets of sera were eliminated. As a result of this analysis, 23 clones were selected for further evaluation. The grouping of the clones and the common antigen per group is shown in Table 1.

Table 1.

Common Antigen	Clone Number(s)
120kDa Antigen	2, 10, 17, 33, 35, 79
Heat Shock Proteins	4, 9, 24, 66
ATPase	7, 84
Ribosomal Protein L1	21, 47, 65
200kDa Antigen	26, 55, 76
Hypothetical Protein	75
Pyruvate Dehydrogenase	5
Ribosomal Protein (50S)	6
Unknown	57
Transcriptional Regulator	82

15

Example 6

Western blot analysis using individual *E. canis* positive canine serum samples

All 23 clones were analyzed on individual SDS-PAGE gels. Each gel was transferred to nitrocellulose and subjected to Western blotting using individual samples of canine sera from dogs that were only positive for *E. canis* infections by ELISA/SNAP® testing. Canine serum was diluted 1:500 in the same diluent described in Example 4 containing *E. coli* lysate and reactivity was detected using standard colorimetric horseradish peroxidase techniques (Opti-4CN, Bio-Rad). A total of thirteen individual canine serum samples were evaluated. Blots were compared across samples to determine the number of dogs showing reactivity to a predominant band or set of bands per clone.

The results are summarized in Table 2 and Figure 6 (clones listed in bold are depicted in the figure).

Table 2.

Common Antigen	Clone Number(s)	Positive Reactors
120kDa Antigen	2, 10, 17, 33, 35	13/13
Heat Shock Proteins	9	12/13
ATPase	7, 84	12/13
Ribosomal Protein L1	21, 47, 65	12/13
200kDa Antigen	26, 55 , 76	12/13

5

All 23 clones were also analyzed by Western blot using pooled canine sera that had tested positive for other vector-borne infectious diseases. Samples testing positive by ELISA or SNAP® for the following single infections were evaluated: Heartworm, Lyme, *Anaplasma phagocytophilum*, or *E. ewingii*. None of the clones identified in the table above showed cross-reactivity with positive canine sera for these other vector-borne infections.

10

Example 7

Identification of relevant gene segments encoding *E. canis* DIVA antigens.

15

a. 120kDa Antigen

This antigen were previously described by Yu *et al.* (J Clin Microbiol. 2000 Jan;38(1):369-74) and shown to be useful in the diagnosis of *E. canis* infections in dogs. The accession number for this gene is AF112369 and the associated protein is AAD34330. Clones 2, 10, 17, and 33 contain full-length segments of the 120kDa antigen gene. Clone 35 may contain a truncation of this gene. (See SEQ ID NOs:1 and 2).

20

This gene was amplified from *E. canis* genomic DNA and subcloned into a pET expression system with a 6-His tag according to the manufacturer's instructions (Invitrogen). Sequencing results of this plasmid exactly matched the gene sequence encoding the protein shown in SEQ NO:ID 2, from amino acids 58 to 589. Protein lysates from BL21 bacteria induced to express this protein were analyzed by Western blotting with infected canine sera and compared to Western blots probed with sera from animals challenged with culture-adapted organisms. Consistent with previous findings, only sera from infected dogs recognized this protein of the expected molecular weight (data not shown).

25

30

P120 has a 36 amino acid motif that is repeated 14 times. See, Figure 8, SEQ ID NO:15. The repeated portion (underlined region in Figure_8) is a 60 kD peptide. Figure 9A shows the aligned 14 repeats (SEQ ID NO:16). Figure 9B shows the consensus sequence of the 14 repeats (SEQ ID NO:17).

5 One embodiment of the invention provides a polypeptide comprising:

KEEX₁TPEVX₂AEDLQPAVDX₃SX₄EHSSSEVGX₅KVSX₆TS (SEQ ID NO:17).

10 Where X₁ = S or N
X₂ = K or R
X₃ = G, D, or S
X₄ = V or I
X₅ = E or K
X₆ = E or K

15 Another embodiment of the invention provides a multimeric polypeptide where SEQ ID NO:17 is repeated two or more times. The multimeric polypeptide can also comprise one or more heterologous polypeptides.

b. 200kDa Antigen

20 This antigen was previously described by McBride *et al.* (J Clin Microbiol. 2001 Jan;39(1):315-22) and shown to be useful in the diagnosis of ehrlichiosis. The accession number for this gene is AF252298 and associated protein AAK01145. A portion of this protein sequence is associated with a published patent (SEQ ID NO:2 of U.S. Pat. No. 6,355,777, accession number AAE96254). We have identified a different region of this
25 protein that serves as diagnostic antigen for ehrlichiosis and a DIVA reagent. The portion of the gene spans from nucleotide 1081 of AF252298 through to the end, nucleotide 4266. (See SEQ ID NOs:3 and 4).

30 This gene was amplified from *E. canis* genomic DNA and subcloned into a pET expression system with a 6-His tag according to the manufacturer's instructions (Invitrogen). Sequencing results of this plasmid exactly matched the gene sequence encoding the protein shown in SEQ ID NO:4, from amino acids 1 to 1061. Protein lysates from BL21 bacteria induced to express this protein were analyzed by Western blotting with infected canine sera and compared to Western blots probed with sera from animals challenged with culture-adapted organisms. Consistent with previous findings,

only sera from infected dogs recognized this protein of the expected molecular weight (data not shown).

c. ATPase

5 This gene (Locus tag "Ecan02000699") has been predicted by automated computational analysis of the shotgun genome sequence of *E. canis*. It codes for a protein of more than 4000 amino acids (ZP_00210575). The *E. canis* DIVA screen identified two separate regions of this gene and its associated protein as potential immunodominant antigens and DIVA reagents. The segments of the protein identified in
10 clones 84 and 7 are amino acids 1984-2774 and 2980-3740, respectively, of accession number 46308382. (See SEQ ID NOs: 5, 6, 7, 8).

Both fragments of this gene was amplified from *E. canis* genomic DNA and subcloned separately into a pET expression system with a 6-His tag according to the manufacturer's instructions (Invitrogen). Sequencing results of this plasmid exactly
15 matched the gene sequences associated with the proteins shown SEQ ID NOs:6 and 8, from amino acids 1 to 782 and 1 to 746 respectively. Protein lysates from BL21 bacteria induced to express these proteins were analyzed by Western blotting with infected canine sera and compared to Western blots probed with sera from animals challenged with culture-adapted organisms. Consistent with previous findings, only sera from infected
20 dogs recognized these proteins of the expected molecular weight (data not shown).

d. Heat Shock Proteins

Although this clone contained a gene for the heat shock protein, GrpE, the gene sequence coding for the immunodominant antigen arises from a hypothetical protein
25 sequence predicted by the automated computational analysis of the genome. Based on the molecular weight and pI of the protein, the gene of interest in clone 9 is locus number "Ecan02000495" and the associated protein 46308954.

Because this protein is only predicted from the computer annotation of the genome and has not been previously identified from *E. canis* organisms as an
30 immunodominant protein, this is the first evidence that this gene is expressed in *E. canis* and stimulates an immune response in the infected canine host. The protein will be identified as the p16 antigen (see SEQ ID NO: 9 and 10).

This gene was amplified from the pBlueScript vector containing the genomic DNA of interest and subcloned into a pET expression system with a 6-His tag according to the manufacturer's instructions (Invitrogen). Sequencing results of this plasmid exactly matched the gene sequence associated with locus number "Ecan02000495".

5 Protein lysates from BL21 bacteria induced to express this protein were analyzed by Western blotting with infected canine sera and compared to Western blots probed with sera from animals challenged with culture-adapted organisms. Consistent with previous findings, only sera from infected dogs recognized this protein of the expected molecular weight (see Figure 7).

10 **e. Ribosomal Protein L1**

This gene is identified by the locus tag "Ecan02000476" from the *E. canis* genome. The associated protein has the accession number ZP_00211130 (see SEQ ID NOs:11 and 12). The identification of this protein has been predicted based on automated computational analysis of the genome. A BLAST analysis of this protein reveals that the
15 sequence is about 70% identical to a surface protein of *E. chaffeensis* (Accession number 4894576). Immunoreactivity to the *E. chaffeensis* protein has previously been reported by Yu *et al.*, (J Clin Microbiol. 1999 Aug;37(8):2568-75). The *E. chaffeensis* protein (Accession number 4894576) is referred to as the 106kDa protein precursor.

f. Possible Non-120kDa Antigens

20 Within the genomic fragment containing the gene for the 120kDa antigen, other genes are present that may also be immunodominant and DIVA reagents. For instance, clone 10 produces a different banding pattern on Western blots probed with infected sera, compared to clones containing the 120kDa antigen alone. Clone 10 contains genetic information for the VirD4 components of a Type IV secretory pathway and this gene
25 sequence is identified by the locus tag "Ecan02000624". This gene codes for a protein of 723 amino acids (ZP_00211244), but only a portion of this protein appears to be expressed by clone 10, as determined by the molecular weight of the protein identified on the gel (see SEQ ID NOs:13 and14) .

SEQ ID NO:1 120kDa Antigen Nucleotide Sequence

ORIGIN

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1 ATGGATATTG ATAACAATAA TGTGACTACA TCAAGTACGC AAGATAAAAG TGGGAATTTA
61 ATGGAAGTGA TTATGCGTAT ATTAATTTT GGTAAATAAT CAGATGAGAA AGTAAGCAAT
121 GAAGACACTA AAGTTCTTGT AGAGAGTTTA CAACCTGCTG TGAATGACAA TGTAGGAAAT
181 CCATCAAGTG AAGTTGGTAA AGAAGAAAAT GCTCCTGAAG TTAAAGCGGA AGATTTGCAA
241 CCTGCTGTAG ATGGTAGTGT AGAACATTCA TCAAGTGAAG TTGGGAAAAA AGTATCTGAA
301 ACTAGTAAAG AGGAAAGTAC TCCTGAAGTT AAAGCAGAAG ATTTGCAACC TGCTGTAGAT
361 GGTAGTATAG AACATTCATC AAGTGAAGTT GGAGAAAAAG TATCTAAAAC TAGTAAAGAG
421 GAAAGTACTC CTGAAGTTAA AGCAGAAGAT TTGCAACCTG CTGTAGATGA TAGTGTGGAA
481 CATTCATCAA GTGAAGTTGG AGAAAAAGTA TCTGAACTA GTAAAGAGGA AAATACTCCT
541 GAAGTAAAG CAGAAGATTT GCAACCTGCT GTAGATGGTA GTATAGAACA TTCATCAAGT
601 GAAGTTGGAG AAAAAGTATC TAAACTAGT AAAGAGGAAA GTACTCCTGA AGTTAAAGCA
661 GAAGATTTGC AACCTGCTGT AGATGATAGT GTGGAACATT CATCAAGTGA AGTTGGAGAA
721 AAAGTATCTG AAAGTATGTA AGAGGAAAAT ACTCCTGAAG TTAAAGCAGA AGATTTGCAA
781 CCTGCTGTAG ATGGTAGTGT GGAACATTCA TCAAGTGAAG TTGGAGAAAA AGTATCTAAA
841 ACTAGTAAAG AGGAAAGTAC TCCTGAAGTT AAAGCAGAAG ATTTGCAACC TGCTGTAGAT
901 GATAGTGTGG AACATTCATC AAGTGAAGTT GGAGAAAAAG TATCTGAAAC TAGTAAAGAG
961 GAAAATTTGC CTGAAGTTAG AGCAGAAGAT TTGCAACCTG CTGTAGATGG TAGTGTAGAA
1021 CATTCATCAA GTGAAGTTGG AGAAAAAGTA TCTGAACTA GTAAAGAGGA AAGTACTCCT
1081 GAAGTAAAG CAGAAGATTT GCAACCTGCT GTAGATAGTA GTATAGAACA TTCATCAAGT
1141 GAAGTTGGGA AAAAAGTATC TGAAGTATG AAAGAGGAAA GTACTCCTGA AGTTAAAGCA
1201 GAAGATTTGC AACCTGCTGT AGATGGTAGT GTAGAACATT CATCAAGTGA AGTTGGAGAA
1261 AAAGTATCTG AAAGTATGTA AGAGGAAAAT ACTCCTGAAG TTAAAGCAGA AGATTTGCAA
1321 CCTGCTGTAG ATGGTAGTGT AGAACATTCA TCAAGTGAAG TTGGAGAAAA AGTATCTGAA
1381 ACTAGTAAAG AGGAAATATC TCCTGAAGTT AAAGCGGAAG ATTTGCAACC TGCTGTAGAT
1441 GGTAGTGTAG AACATTCATC AAGTGAAGTT GGAGAAAAAG TATCTGAAAC TAGTAAAGAA
1501 GAAAGTACTC CTGAAGTTAA AGCAGAAGAT TTGCAACCTG CTGTAGATGA TAGTGTAGAA
1561 CATTCATCAA GTGAAGTTGG AGAAAAAGTA TCTGAACTA GTAAAGAAGA AAGTACTCCT
1621 GAAGTAAAG CGGAAGATTT GCAACCTGCT GTAGATGGTA GTGTGGAACA TTCATCAAGT
1681 GAAGTTGGAG AAAAAGTATC TGAGACTAGT AAAGAGGAAA GTACTCCTGA AGTTAAAGCG
1741 GAAGTACAGC CTGTTGCAGA TGTAATCCT GTTCCTTTAA ATCCTATGCC TCAATAGATG
1801 AATATTGATA CTAATATAAT ATTCCATTAC CATAAAGACT GTAAAAAAGG TTCAGCTGTA
1861 GGAACAGATG AAATGTGTTG TCCTGTATCA GAATTAATGG CTGGGGAACA TGTTTCATATG
1921 TATGGAATTT ATGTCTATAG AGTTCAATCA GTAAAGGATT TAAGTGGTGT ATTTAATATA
1981 GATCATTCTA CATGTGATTG TAATTTAGAT GTTTATTTTG TAGGATACAA TTCTTTTACT
2041 AACAAAGAAA CAGTTGATTT AATATAA

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SEQ ID NO:2 120kDa Antigen Protein Sequence

ORIGIN

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1 MDIDNNVTT SSTQDKSGNL MEVIMRILNF GNNSDEKVSND EDTKVLVESL QPAVNDNVGN
61 PSSEVGKEEN APEVKAEDLQ PAVDGSVEHS SSEVGKVKSE TSKEESTPEV KAEDLQPAVD
121 GSIEHSSSEV GEKVSKESTKE ESTPEVKAED LQPAVDDSV EHSSEVGKEV SETSKEENTP
181 EVKAEDLQPA VDGSIEHSSS EVGEKVSKE KEESTPEVKA EDLQPAVDDS VEHSSSEVGE
241 KVSETSKEEN TPEVKAEDLQ PAVDGSVEHS SSEVGKVKSE TSKEESTPEV KAEDLQPAVD
301 DSVEHSSSEV GEKVSETSKE ENTPEVRAED LQPAVDSVE HSSSEVGKEV SETSKEESTP
361 EVKAEDLQPA VDSSIEHSSS EVGKVKSETS KEESTPEVKA EDLQPAVDGS VEHSSSEVGE
421 KVSETSKEEN TPEVKAEDLQ PAVDGSVEHS SSEVGKVKSE TSKEENTPEV KAEDLQPAVD
481 GSVEHSSSEV GEKVSETSKE ESTPEVKAED LQPAVDDSV EHSSEVGKEV SETSKEESTP
541 EVKAEDLQPA VDGSVEHSSS EVGEKVSETS KEESTPEVKA EVQPVADGNP VPLNPMPSID
601 NIDTNIIIFY HKDCKKGS AV GTDEMCCPV ELMAGEHVHM YGIYVYRVQS VKDLSGVFNI
661 DHSTCDCLND VYFVGYSNFT NKETVDLI.

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SEQ ID NO 3 200kDa Antigen nucleotide sequence from 1081 to end

ORIGIN

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1 AATTTAGAT TTTGGACTTG TAGATGGAGA TGGTAAAAAT CCTTTACATC ATGCTGTGTA
61 ACATTTGCCA CCTGTTATAC TTAAGGGCGT AATGGACCAT GTAAAAATA GTAGTGAGTT
121 TCAAGATTTA GTAAATGATC CTGATTATTT TGGAAATACT ATAGCTCATT ATGCAGTTAA
181 GAATAAAAAA GCTGATTTAA CATGTGTTAA CATGCTGAAA GCTTCAGGAG CTGATTTAAA
241 TGTTAGGAAT GTAGTTGGTC GAGCTCCAAT ACATGTTGCT TCTTCTAATG GTAAGGCTAA
301 TGCAGTTTCT GGACTTGTAT CATGTGGTAT TGACGTTAAT TCTCAAGATG TGAATGGAGA
361 TACACCACTT CATATTGCTG TTGAAGGCGG TAGTATGGAG ACGGTATTAG CAGTGTTAAA
421 TCAGAGAGGT GCTGATGTTA GTGTCCAGAA TAACGATGGA GTTACACCTA TGCTTAGTGC

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481 TGCTAAATAT GGAGATATAG GTGTAATAAA AGCTTTAGGT TCAGCTAAAC CAAATATTAA
 541 AGGTGAAGAC ACTGTTGCTA AATCATTGCT GATGGAGGAT TACAAAGGTT TTACACCCTT
 601 GCATTTTGTA GCTGGTGGTG GTAGCAGAGA TACATTCCTG GTCGTAAGAA AAAATTTATGA
 661 AAAATGTCAT GACTTAGCTA CTATTAGGGC AGCTTTAATG CAAGATAGAA GTGGTGGTGA
 721 GCTTGTAAT TTAGGGGATT TTGAAAGTGA AAATATATTG GGTTCGCCAA ATGCAAAATT
 781 CTTGCAGCAT ATTCAATCAG CAAATTTTGG TTTTCTCTCA GCGCATTGTG CTATAGTATC
 841 GTCTAATCAC AATGTAATGA AAGATATCTT AAATTTTGT TGGGATTCGT TACACCTACC
 901 AAGTGAGCGT GGGTATAATG CAATGCAGGT TGCTGCTTTG TTTGGTGACA AAGAAGCAGT
 961 GAAAATGCTT GCTAAAAGTG CTAAGCCAAG TGATCTTAAT TTTAAGACTT CAGCAACTCC
 1021 TACTCCGTTA AATCTTGCAT GTCTTAGAGG TGATAATGAG GTAGTACGTG GGTTAGTAGG
 1081 TCAACATGGT ATTGACATTA ACCAACGTAT GGGAAAGTAT AAAAAGACTG TATTGCATTA
 1141 TGCAATCAGC AAAGGAGATA GTTTTCTTGT GCAAAAGATA TTAGCTCATA CTGGAGTTGA
 1201 TGTTAATTGT GAGAATAACC TAGGTCAAAC GCCTTTACAT TTAGCAGTTG AGGGAGGAGA
 1261 TCCTAAGATA GTATCTTCTC TTCTTAAAGC TGGTGACGTA GTTAATCGTC TGGATGATAA
 1321 TGGTAGATCT GTACTTTCTT CTGCGATAGT TCCAGGTAGA AAAGAAAAGG GAGTGCTGGG
 1381 TATAGTTAAT AAATTGCTGG ATAGAGGTGC AGATATTAAT TTAGATGGAG ACCACAATAT
 1441 ACTTTTTGAT CAGTGTCTAA GGGTGGGATA TAATAATGTA TTAGATAAGT TAATACAACA
 1501 AGGGGTTGAA GTTAATCGAA ATAGTGAAT ACCTCCAATG GTTTATGCTG CAATATCTGG
 1561 TAATAAGCAT GCTATCAAT CATTAGCTAA TGCTGGTGGG GATGTTAATG AAGTAGTAAA
 1621 TAATCCATCT AGTAGGCATT CAGGAAATCC TTTAATTATG GTTGCAGTAG CAGATGGTAA
 1681 TGCAGGTCTT CTTAAAACAT TAGTTTCTGA AGGATGTGAT GTTGGTAAAT CTGGAAAAGA
 1741 TGGAATAACA GCGTTACATT ATGCTGTTAG TCATTTCAGT AAAGAGTTTG GTAATAAAGC
 1801 TATAAAGATA TTAATTTTCA GTAATAGTGT TGGGACTAAT AGAGATATTC TTAAGTCAAA
 1861 GAATAACGCA GGTGATACAC CTTTACATGA AGCTCTTAAG TCAGGTAATA TTAATCTGT
 1921 ACAGAATATC TTAAGTGCTG TACATCCAAG ATACGCAAG GAGATATTA CAGCCAGAGA
 1981 CAAAGAAGGG TACACACCAA TGCAATATAC TGTGGAGTA AATAATGTTG ATGTTGGTAG
 2041 AAGTATTCTA GAGTCTATGC TCTCTAAAG TGTGAATAAT CTTGGAGAGA TTGTTGGAGC
 2101 ACAGGATAGT AATTTTCGAA CACCTCTGCA TGCTGCTATT AAAATATCTG ATTATCGTGC
 2161 TCGGACATG ATAATAGGTA GCTTATCGAA AACAGAATTG TCAAAGTTAT CGCAATTAAC
 2221 AGATATTAAAC GGGGATACAC CACTACATCT TTCTTGTCAG TCTGGTAAATG TCGAGATGAC
 2281 ACAATTCCTT CTTGGAGGTT TGGATAAACG TGAATTACCT AAGACATTAA AGATAGCAAA
 2341 TAAAAATGGA GATACTCCTT TACATGATGC TATAAGAAAT GATGATATTA AATCTGCAAA
 2401 AATGATGATT AGGAATTGTA ACAAAGAAGA ACTTGCTAAT GTATTAAAT GTAAAGATAG
 2461 TTTTGGTAAT ACAGTATTGC ATACTATTGC TGACCAAGTT ATTGCGAATC CAGAATCAAA
 2521 GAAAGACCTT GATGGTTTGA TGAATTTAGC AGTGAAGAG CTAAGAAATC AAGATCTGAA
 2581 AGATCTAGTT AATACGCGAA ATAACCTCTGA CGATACTGTT GCACATTGTG CTCTTTTATC
 2641 GGATATGAAA TATGCTCAA AGATACTTAA ATCATGTAAC CATGATACAT TAGTGAGAGG
 2701 AAATAGTAAT AATCAATCTT TATCAGAGTG TATTCGTGAT GATAGTAAAT ATAAAAAGG
 2761 TGAATTTT AGTAAGTCTT TATTTTCAAA ATTAAAGAAA CTTGAGGCAC GAGCTGCCAG
 2821 CGCTAGTTAT GAAGAATTAT CTAGTATCAG TAGTGGTAGT GATGTTTCTT CTGTATCAAC
 2881 AAATAGCACA GAAGTAAGTG CAGTACCTGA AGTGGCAAGA AGTAGTGGT CTGTGCTGTT
 2941 CAAACATGTG CAAGAAACAG GAGTTGACAC GTCTGGTCTT TCTGATATAG AAAGTTTAGA
 3001 GAGATTATCT GATACTAGTC TTGGGTCAA TGATTTTGAT CAGCGAATGG CAGATTTAGA
 3061 TCAAGAAATA GCAAAATATT TTAGTGGTTT ACCAGAAGTT ACCCAGGTAG CTGTAAGTCA
 3121 ACAACAAGCA GCATCTCCTA GTTCAGGTCA AGCTGCTGGT GTGCAACAAA AAGAGATGCA
 3181 GAGATAA

SEQ ID NO:4 200kDa Antigen Partial Protein Sequence
ORIGIN

1 NLDFGLVDGD GKNPLHHAVE HLPPVILKGV MDHVKNSSFE QDLVNDPDYF GNTIAHYAVK
 61 NKNADLTLEF MLKASGADLN VRNVGRAPV HVASSNGKAN AVSGLVSCGI DVNSQDVNGD
 121 TPLHIAVEGG SMETVLAVLN QRGADVSVQN NDGVTPLMSA AKYGDIGVIK ALGSAKPNIK
 181 GEDTVAKSL MEDYKGFPL HFVAGGSRD TFRVVRKNYE KCHDLATIRA ALMQDRSGGE
 241 LVNLGDFESE NILGSPNAKF LQHIQSANFG FSPAHCIAVS SNHNVMDIL NFGVDSLHLF
 301 SERGYNAMQV AALFGDKEAV KMLAKSAKPS DLNFKTSATP TPLNLACLRG DNEVVRGLVG
 361 QHGIDINQRM GSDKNTVLHY AISKGDSFLV QKILAHTGVD VNCENNLGQT PLHLAVEGGD
 421 PKIVSLLKA GAVVNRLDDN GRSVLSSAIV PGRKEKGVLG IVNKLDRGA DINLDGDHNI
 481 LFDQCLRGY NNVLDKLIQQ GVEVNRNSEI RPMVYAAIS NEHAIKSLAN AGGDVNEVVN
 541 NPSSRHSGNP LIMVAVADGN AGLLKTIVSE GCDVGKSGKD GNTALHYAVS HSDKEFGNKA
 601 IKILISRSNV GTNRDILTQK NNAGDTPLHE ALKSGNINSV QNILSAVHPR YAKEILTARD
 661 KEGYTPMHYT VGVNNVDVGR SILESMLSKG VNNLGEIVGA QDSNFRTPHL AAIKISDYRA
 721 ADMIIGSLSK TELSKLSQLT DINGDTPLHL SCQSGNVEMT QFFLGGLDKR ELPKTLKIAN
 781 KNGDTPLHDA IRNDDIKSAK MMIRNCNKEE LANVLKCKDS FGNTVLHTIA DQVIANPESK
 841 KDLDDLMLLA VKRLKNQDLK DLVNRNNSD DTVAHCALLS DMKYAQKILK SCNHDTLVRG
 901 NSNNQSLSEC IRDDSKYKKG GIFSKSLFSK LKKLEAARA ASYEELSSIS SGSDVSSVST
 961 NSTEVSAPVE VARSSGAVSF KHVQETGVD SGPDSIESLE RLSDTSLGSN DFDQRMADLD
 1021 QEIANIVSGL PEVTQVAVSQ QQAASPSGQ AAGVQQKEMQ R.

SEQ ID NO:5 ATPase - Clone 84 Fragment Nucleotide Sequence

ORIGIN

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1  AATTATGCTG  AAACACTCTT  ATCATTGTTG  GAATCTCGAG  CAGAAGGACG  TGAATCTCCA
61  TCAAGTGCAT  TTGTTCAAAC  TGGTCAATCA  GAAGTACCTC  GGAGTGAGGC  TGCAGAGCCA
121  TTAATTCAT  TTCCTCATGA  TGAAGAAAGT  ACTGCATTAG  GTTCTCAAGC  AACTATGACA
181  GGAGTGTCTA  CTCAGGCTAG  TCCGTGAGCA  GCATATCAGG  ATGATAGTGA  AATATCACGT
241  ATGAGGTCTA  TGGCAGGAAC  ATCTGCTCAA  GCTGATCAAT  CAGCAGTACA  TCGTCGGAGT
301  GGTACAGCAT  TAGAGCCATT  AATTGAATTG  CCTGATGAAG  AAGAAAATGC  TGCATTAGAT
361  TTTCAAACAG  CTATGACAGG  AGTGCCTACT  CAGGCTAGTC  CGTCAGCAGT  ACATCGGAGT
421  GGTGTTGCAT  CAGATCCTAC  GCTACCTGAT  GATGAAAGAA  TTGATGTTCC  ATCAGTTTCA
481  TCTCAAGTTG  TAAGACCTTT  TAGTGATGGT  GAAGATTATT  CAGTATATGA  TAAATCAGGT
541  GTAGTAAGTG  GTCATGAAAG  ACCTGTTTCT  TCTAGAGATT  CAAGACAATT  GGATGCATTT
601  GGTGATCCAT  CAGATGATTT  ATTGCCGGAG  AGTGAAATTA  TTGTTAGCAG  CAGTAAGAAA
661  GCAATATTAG  ATAGCCAAAA  TGAATAGAA  TCTCTTATTC  AGAGTGGAGA  TACTTCTAGA
721  TGTATTAGGG  CAATTAATAG  TGCTCCTAGT  GCGTCAGTGT  TTCAACTGAA  GACTTTATCG
781  AATGATATAT  CTATTGCTGG  ACGTGCTTTT  TTAAATGGTA  ATATTGATTT  AATAGAAGCT
841  TGTATGAATT  CTGGCAAGAA  ATTAAATCCA  AATATTACTG  ATAATGAAA  AAATACTCTA
901  TTACATCAAT  TTGTAGGATA  TTTTGAACGC  GATCCGAGAA  TGTTGCTTGA  TGCAGGAATG
961  CGTAATCTGT  TTTTGAGATT  ATGCATGGAT  TATGGTTTCG  ATATTAATCA  TAAAAATAGT
1021  AATGGTAATA  CAGTACTTGA  TAGATTAAT  GATTTAGTAG  AAGGGTTAAG  TAGTTCGCAA
1081  GTTGATCTTG  AAAGTAGTGG  TATTGATGAG  TTTATGATCT  CATTGTAGC  TCATTCTAGA
1141  ATGAGTGATC  AAGCAGTAAA  GAATATTGCT  ACTGCGCAAA  ATGAGTTTTT  TGCACGTGAT
1201  TCTGTTTATA  ATATTAGTCG  TTTAGTTGAT  ACTTCTATAG  TTTTGCAGAA  TAAATTCAGT
1261  GAAGTATTTT  ATGAAGCTCG  TGGACGTATT  TTATCTGAAG  AAGCTGGTAA  ACATAAGGGT
1321  GTTGCTGAAG  CAAATTATTC  AAGATTGAAT  AAAATATTAA  ATGATGAATG  TCGTAGAAG
1381  ACTTTAGCTA  ATACAGATGC  CGATGGAAAT  AATGTTTTAC  AGAGATTGTG  TCAAGATATT
1441  GCTTCTGGAA  AAATCAATGC  TCGTGATGAC  AGAGTATTAA  AACTTTTTGA  GACAATTATA
1501  TCTAATTTAA  AAGACAAAGA  TAAAGCATTA  CTAGAGGATT  TATTATTTAA  TAATAGAAAC
1561  TCAAGATTTG  AAAATTGCAT  TGAAGCTATA  CCACGTATTC  CTGGTGCCGA  TGCTCTATTT
1621  AAAAAACTAG  AAGAGTTATT  ATTAAAAAAG  AAAATAGCAG  AGTCTTGTGA  TTTTAATTCT
1681  ATGTTAGTGA  ATTGTGCTGA  GTCTGCTAAT  GATAATTTAT  ATAATTACCT  GCGCACTAAT
1741  TATGCAGTTA  TTGGTATAAA  TAACGTAGAT  ATAAATGGCA  ATTCATCCCT  ATGTAAAGCT
1801  GTTGTTACTG  GGTCAACAAG  TATTGTTAAA  GCAGTATTAT  CAACTGGAAC  TAATATTAAAT
1861  AGGAAAGATA  AAAATGGTAA  TACACCTTTA  CATGCATTGT  TAATTTTTAT  GATGCTAAC
1921  CCTGAACCTG  TCAAGGAGCA  ACATATTTCA  CTTGTGAAAT  TCTTAGCGTC  TCGTGGAGCT
1981  TTAATTAAATG  TAAAAAATA  TATGAATATT  TCTCCAATTA  TGCTTGCAGA  ATCTATTGAT
2041  AAGAAAGAGG  AACTTGCTAA  GAAATTTACA  AATCAAAAAG  TTAGTATTTT  AGAATCTTTA
2101  ATAGCTGGTA  GTGAAGAACA  TTTAGGGCTT  AAATCCAAAT  GTATATCTGA  GTTAAAGCCT
2161  TATATGAAT  TAGGAAAAG  CATGAAGTAC  GAAGATATAC  ATGCTGATGT  AATAGGTGGT
2221  GTATTATCTG  CTGATATGTG  TAATGCTAGA  TTGCAGATAG  GTAAATTATT  AAATGGTGAT
2281  TTTTGTAAG  AAAATGAATT  AAAGACAGTA  AAATTTAATT  TTTCTGATAC  AAATAAGGGT
2341  TATGTACAAA  ATGTTGGTAA  AAAAGAAAT  TAT

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SEQ ID NO:6 ATPase - Clone 84 Fragment Protein Sequence

ORIGIN

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1  NYAETTLSTFG  ESRAEGRESP  SSAFVQTGQS  EVPRSEAAEP  LIQFPHEDES  TALGSQATMT
61  GVSTQASPSA  AYQDDSEISR  MRSMAGTSAQ  ADQSAVHRRS  GTALEPLIEL  PDEEENALD
121  FQTAMTGVPT  QASPSAVHRS  GVASDPTLPD  DERIDVPSVS  SQVVRPFSDG  EDYSVYDKSG
181  VVSGHERPVS  SRDSRQLDAF  GDPSDDLPE  SEIIVSSSKK  AILDSQNEIE  SLIQSGDTSR
241  CIRAINSAPS  ASVFQLKTL  NDISIAGRAF  LNGNIDLIEA  CMNSGKKNP  NITDNEKNL
301  LHQFVG YFER  DPRMLLDAGM  RNLFLRLCMD  YGFDINHKN  NGNTVLDRLN  DLVEGLSSSQ
361  VDLESSGIDE  FMISLLAHSR  MSDQAVKNIA  TAQNEFFARD  SVYNISRLVD  TSIVLQNKFS
421  EVFYEVCGRI  LSEEAGKHK  VAEANYSR  KILNDECLRK  TLANTDADGN  NVLQRLCQDI
481  ASGKINARDD  RVLKLFETII  SNLKD KDKAL  LEDLLFN  SRFENCIEAI  PRIPGADALF
541  KKLEELLKK  KIAESCDFNS  MLVNCAESAN  DNLYNYLRTN  YAVIGINNVD  INGNSSLCKA
601  VVTGSQGIK  AVLSTGTNIN  RKDKNGNTPL  HALLIFMMSN  PELVKEQHIS  LVKFLASRGA
661  LLNVKNNMNI  SPIMLAESID  KKEELAKKFT  NQKVSILES  IAGSEEHLGL  KSKCISELKP
721  YIELGKGMKY  EDIHADVIG  VLSADMCNAR  LQIGKLLNGD  FCKENELKTV  KFNFSDTNKG
781  YVQNVGKKRN  Y

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SEQ ID NO:7 ATPase - Clone 7 Fragment Nucleotide Sequence

ORIGIN

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1  GTAAAAAAT  TAAGATTATT  ATTAAATTCA  ATAAGTGAGT  TACCGCAAGA  ATTTAAAGAT
61  CAAATTTTAA  GTACTAGAAG  TACTATAGAT  AAATTACGAA  ATAGAATTAA  TGCTGCATA
121  AAGTCTGACG  ATAGAGAAGG  TATTGCACAT  GCTGTAGAA  CTATGGCTAG  TTCTATTGT

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181 GAATTATTAG GACATTGTAG ATTAATTTTT AAGAAATTAT ATGATGAAAA TGCTGATAAA
241 AGTTTGCTAG AATTATGTAT TAAAGAATAT CAATCTGATT TAAACAAATT ATTGGAACAA
301 GGTATTGATA TATGTGCTTC AGAAGTCTCA TCAGAATGTA AGGATTTAGT TTGTAAAGTA
361 TGTGAAGATG AATTTGAGAA ATATGACTCT TTATCTAAAG TACAAAGATT CAGGGAATTA
421 TCTGGTGAAA TTGCTGATTT GGATGATAAA TTAACAAGAA GGGCTTCTTT TGTTGAGACT
481 TTTGGATTAT TTAGCAGTAG ATTAAGACAT TATAGGGAAA TTTTAGGAGA TGGTGATTTA
541 AAATTTGAG AGAGGATAGT TGA AAAAATAT CAAGAGGATT TAAAGGAATT ATTAGAATTA
601 TCTGTTGATC TTCATTTGTT AATAAATTTA CCAGCATTAG AAGATTTACG CGATCATAGA
661 AATTTAGTGC ATAGAGCATG TAATGCTGAA ATTGAAAAAT ATCTAACTTT ATTTGATGAT
721 CAACAATTAC GTACATTATC GCAAGAAGTG AATAATGCTC ATGGTGAATT GATACAGATG
781 TTTTCTAAGT TTAGTATATT TGTGATGGC GTTACTGGTA TTGAACAGAG CACATCTCAA
841 GTAGAGCACC CTCGTTCTGA TATTGCTAAA AGAGATACTA CAACACCAAA GCAACGTGTT
901 GTGCAAGGTA AAGATGATAT ACAATCTAGT GATAGTGATA GTGATAGTGA TAGTAAATAC
961 GGTGATGATG ATAGTAAAAA AGCATCAGTT AGTGCACCTG CTGTTGACCA AGTTGTACCT
1021 GTAGCTGATG TTCAACCTGA ACCTCAGCTA GGTGAAGGAT TGGAAACATT AGAGTCTAGT
1081 ATAGCTGAAG GACCTGAGTT GCCTGGTGAT GCATCTACTG CTAAGCAATC TATACCTTTT
1141 GCGATAACAC CATCAAGTCC TGAGACAGTT GATGAAAAAC TTGAAAGTTC TGGTGTTAGT
1201 CAAGATGGTA TTACAACACC AGGACAACGT GTTGTGCAAG GTAAAGATGA TATACAATCT
1261 AGTGATAGTG ATAGTGATAG TAAATACGGT GATGATGATA GTAAAAAGC ATCAGCTAGT
1321 GCACCTGCTG TTGACCAAGT TGTACCTGTA GCTGATGTTT AACCTGAACC TCAGCTAGGT
1381 GAAAAATTGG AAACATTAGA GTCTAGTATA ACTAAAGGAC CTGAGTTGCC TGGTGATGCA
1441 TCTACTGCTA AGCAATCTAT ACCTTTTTCG ATAACACCAT CAAGTCCTGA GACAGTTGAT
1501 GAAAAACTTG AAAGTTCTGG TGTAGTCAA GATGGTATTA CAACACCAGG ACAACGTGTT
1561 GTGCAAGGTA AAGATGATAT ACAATCTAGT GATAGTGATA GTGATAGTAA ATACGGTGAT
1621 GATGATAGTA AAAAAGCATC AGCTAGTGCA CCTGCTGTTG ACCAAGTTGT ACCTTCTGAC
1681 ACTCGTGCAG ATGGAGTATC AGAACCATTA GCATCTCATG TGGATCAAGG ATCTGATGTA
1741 CCTGGTGATG CATCTGTTGA TGGTGTTGAT TTAAGATTAG GACGGTTATC TACTGAGCAA
1801 AGTGGATTGT TGCCACGTCA TGAACAAAAT GTAAGAGCAT TTATTTTAGA ACAGAGTTTG
1861 TTAGATCAAT TATATATGGA CTATATAGAT TTACACCCTG ATCAGAAAAG TTGTGAAGCT
1921 TATAATTGAG CATGTCATGG ATATAATACA AGATTAGAGT TACAGAGGA ATATAACAGG
1981 ATTTTGAAT CACATGAATC AGCATCTCCA AATGAAATTA ATAGTTTTTC AAAAAATAT
2041 AGAGCAGCAT TAAGAGATGT TGCGCAGGAT ATTGTTAATC AGGGTCCAAT GTTTTATCTT
2101 TCTAGAGATG CAATGCTATT AAGGGCTAGA GTAGACACAT TGTGTGATAT GTGTCGTTCA
2161 ATACGTAATC TGTATATGGT TGAATTAGAT GCCATAGATA AAGAAGAAAA ATCGTTACAA
2221 TCTGATATGA AATCTGCAAG TTCTAGTGAT AAAAAGTTGA TACAAGAAAA AATAAAATTA
2281 CTT

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SEQ ID NO:8 ATPase - Clone 7 Fragment Protein Sequence
ORIGIN

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1 VKKLRLLLNS ISELPQELKD QILSTRSTID KLRNRINACI KSDDREGIAH AVESMASSYC
61 ELLGHCRILF KKLVDENADK SLLELCIKEY QSDLNKLLEQ GIDICASEVS SECKDLVCKV
121 CEDEFKLYDS LSKVQRFRLE SGEIADLDDK LTRRASFVET FGLFSSRLRH YREILGDGDL
181 KFRERIVEKY QEDLKELLEL SVDLHLLINL PALEDLRDHR NLVHRACNAE IEKYLTLFDD
241 QQLRTLSEV NNAHGELIQM FSKFSIFVDG VTGIEQSTSQ VEHPRSDIAK RDTTTPKQRV
301 VQKDDIQSS DSDSDSDSKY GDDSKKASV SAPAVDQVVP VADVQPEPQL GEGLETLESS
361 IAEGPPELPGD ASTAKQSIPF AITPSSPETV DEKLESSGV S QDGITTPGQR VVQKDDIQS
421 DSDSDSDSKY GDDSKKASAS APAVDQVVPV ADVQPEPQLG EKLETLESSI TKGPPELPGDA
481 STAKQSIPFA ITPSSPETVD EKLESSGV S QDGITTPGQR VQKDDIQSS DSDSDSKYGD
541 DSKKASASA PAVDQVVPSPD TRADVSEPL ASHVDQGS DV PGDASVDGVD LRLGRLSTEQ
601 SGLLPRHEQN VRAFILEQSL LDQLYMDYID LHPDQKSCEA YNSALHGYNT RLELQKEYNR
661 IFESHESASP NEINSFSQKY RAALRDVAQD IVNQGPMFYS SRDAMLLRAR VDTLCDMCRS
721 IRNLYMVELD AIDKEEKSLO SDMKSSASSD KKLIQEKIKL L

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SEQ ID NO:9: p16 Antigen Nucleotide Sequence
ORIGIN

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1 ATGTTACACG TTCAAATCA TGTTGATCAA CATACAAATC ATATAGAACA TGATGATTAC
61 CATTTTACTG GTCCTACTAG TTTTGAAGTT AATCTTTCTG AAGAAGAAAA AATGGAGTTA
121 CAAGAAGTAT CTTCTATTGA TAGTGTAGGA TGCGAAGATT GTGATCCAAA TTGTCGTTAT
181 CCTTTAGAAAT TAGTAGAATG TCAGCGTATT GAGGAAAGAC CAGTATGCAA TGCAGGTTTA
241 GAGAGCTTGA CTGTTGATGC ATATCAATTA GGATTGTTGT TAGGTGGTTT TTTAAGTGCT
301 ATGAATTACA TATCTTATAG CTATCCTTGT TATTATTATG ATGTTTGTGA TAGAAATTA
361 TACGACTGTT GTCATAAGAA TCGCTGTTAT TACAACTGTT GTGATTGTGC GTAA

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SEQ ID NO:10 p16 Antigen Protein Sequence
ORIGIN

1 MLHVQNHDVQ HTNHIEHDDY HFTGPTSFEV NLSEEEKMEL QEVSSIDSVG CEDCDPNCRY
 61 PLELVEQCRI EERPVCNAGL ESLTVDAYQL GLLLGGLSA MNYISYSYPC YYYDCCDRNY
 121 YDCCHKNACY YNCCDCA.

SEQ ID NO:11 Ribosomal Protein L1 Nucleotide Sequence
 ORIGIN

1 ATGACGATTT TCTTAGAAAG TGATGATGAT AAGAGTAACT TTAAGAAGAC ATTGGAGAAC
 61 GGTACTAAAG ACAAGACAAA TCTAGATAAT ACTTATTATG ACTATCATCA TGAAGATGAT
 121 ATGGGAAATA CTGAATATCA TTATGTGAGT TTGGATAGAG TGGATCATGT TAAGATGCCT
 181 GAAGAGCCTG TAGGTTATGG TGGAGATACT TTACCTATTG TTCCTACTAC AGCTGCTAGT
 241 GTATCTGGTA GTGATGCAGG CGTTGCTGTA GGTAAATGTTA AAGATTTTGA AGATAATGTT
 301 TTTTCATCATA CATCTACTAT AAGAAACGAT GAATTGAAGA TAGATTTACG AATACATACT
 361 TTAAAGGATT TATCTGATAA AAGATTACGT GAAATTGAAA AGGGATTTAA TGATACGGTA
 421 ACAAAATTTA AAAATAATTT TGGGTTAGAA CCAAATGATG GAGAACTAT TTTTGATTTA
 481 TACCTTTTTG ATGATAAGGA ACAATATAAT TATTATGGAA AGCTTTATAA CTAGGAATT
 541 AGTGGATCTG GAGGTATGAC TTTCTATGGA AATGCTAATG TTCCATATAA AATTTATGTA
 601 CATCAATATG GTGAAATATT GAATTTAAAA CATGAATTAA CTCATGCATT AGAAAGTTAT
 661 GCATCTGGAC ATAAATTGCA TGGTTCTGAC GTAAATAGCA GAATATTTAC GGAAGGATTA
 721 GCTGATTATA TCCAAGAAGA TAATAGTTTT ATTATGAGAG GATTAAAGGA TCGAGAGATC
 781 ACTTCAGATG TATTGAAAGA TTCTTCTGGT AATGTAGATC ATTTAAGTGG TGTTCAGTGG
 841 AATGAAAATC AGAGGTTAAG TTATAGTATA GGACATGCAT TTGTAAGCTT TTTACAAGAG
 901 AAATATCCTA AGTTAATTTT GGAATATTTA AACGCATTAA AAGAGGATAA TATTATTCGT
 961 GCTAAAGAAA TAATTAGTAT GGATAAGTAT CCAGATTTTG AGCCGTGGGT GAAGTCTAAA
 1021 GACATTAGTT TATATTTAGA AAATATGAAT GTATTAAAGT TAGGATTAGG TGAGAAAATG
 1081 TTTTCTGCTG AAAGTGCTAG CTATTTTGAA GATCAAGGTG TCAATAAAGA ATATTACCAT
 1141 GAAAATATTT ATGATATGAG TGGTAACTA GTAGGTGAAA TGTCACCTGT AGTGCATTAT
 1201 GCACAAAAAA ATGTGATTCG TATTTGGAAT ATTGCAAGTC CTGATATGAT AGAGGTGCCA
 1261 CCAGAATATA ACTTCTGAA ATTGGTAACT ACTCCATCTG GTAAGTCTGC ATATGTATAT
 1321 TGTGATAAGA ATGGGCATGA GTATTTTAAT ACTAAAGATT ACATAGATTC TCGTTTTAAT
 1381 ATATTGGCAA GATATGATGT TAAGCTTCGT GAAAGTAGTG ATGCTTTGGA TATTAGAGGT
 1441 CGTTACTCAG ATGCTGCTAA AGTGTTTAGT AAGCTGCCTA ATGCGGATTT GCTGTTGGAT
 1501 AAGTTTTTAG AAAAAATAGG TTATAGTAGT TATAAGCAGA TAATAATGAG TAATCCAGAA
 1561 CAGCTTAATT CTATTAAGGC TTATGTAGTA AAAGAAGTGT TTGAAAATTT TAGGGAATCT
 1621 GAGGTCAAAA AGGTGTTGAG TGGTGAGTCT CATCCGGAAG TAAGAAATGT ATTAATGGAT
 1681 CTTACCTATG TTGATTTAAA GAGTGTATA GGAGTAAATG GTGCAGATAT TGACAGTATT
 1741 ATTTCTAATC CAGATGTAAT GTTGCGTACT GCTGTGTTAG GTAAAGGAAA TGCAAGTGGG
 1801 ATATCTCTAT ATGTAGATGA TCAGAAAGTT GGTGAGCTGT CAACTGAAGC AGGTTATTGT
 1861 GTTAAAAATC TTGATACTGG TAAAGTGAT TTTATGTTC ATAATGTTGT TGGAATGATA
 1921 GCAAGTGGTT ATGAAGACAG AGCATATATG GTTGATTTAG AAAAAGATGG TAAGTTTACT
 1981 ACTGCTCTAG TTAATAATAT AAAAAAGCA GCAGATGGAA ATGTTGTATG GGATAATCAA
 2041 TTTAATCATC CGAATATTAA TAACTTGCAC TCAAATTATA AGGAGCTGTT GTTAAATGAT
 2101 GCTTCAGTTA AAGATTACTC TCATCTGCG GATGTGAAAT TTAATAAAGA TGATACAGTA
 2161 ATTGTTAAAG GTGAATTATT AGATGATAAA GGTACTGTAA GTGTAGATGA TGATGTACAT
 2221 CGTGCAAGTT TTAAGCATGA TGATCAATA CTACATCAGT TTAAGAGTAT GTCTTTTAC
 2281 ATTACTGAAC CATCAGCTGA TTCAGGTGAC AATTATGGAA GTGATTTTTT CATTTCTGAT
 2341 GAAGGAAAAA ATCTTAGATT TCAACTTCCT AAAGCTATTA CGCATTGAA ATTGGTTAAT
 2401 GTTAATGGAA ATAATAAGTT GGTACCATGT ACTAAAGATG GGAATGAACA TCCTGAAGGT
 2461 ATGCCATCTG ATTTAACGGA TGAATATAGA TATATAGATC CTATTTTTTG TCATACATTT
 2521 GAGAAACAAA GTTATTCTAA AAATAGTATT AGTGTGGGT TAGTGGACT CAGTAAATAT
 2581 AAAGAAGGAT CTATGTTTAA ATTACAGCAT TATTCTGATG ATTATCATAT TCATAAGGAT
 2641 GAACAAGGTA ATGTTATTAG GCCTAATAAC AGATCTTACG TTACAAAAGT GGATTTAGTA
 2701 TATGATGATA AAGTTATTGG GATGTTGTCT GATAGTATAA ATCAATTTCA GGGTGATATT
 2761 TTCATTTCTG CAAGCCTTAA TTATAGCCAC AATGATTTTC TTTTCATCTA GTACTTTTAC
 2821 AAAGTTAATA TTGAGGCGTT AGAAAATGGA ATATATAGTG GAAGATATGA TGTAGGAGAT
 2881 GGTGACCAAA TAGCAGGTCT TAATACTGAT ACAGGTTATA GTGATAAAGC TATTTTTTAC
 2941 TTTAAAAATG ATAGCGCATC TACTGATATG CCGGCTAGTG ATGTTACTAC TATTTTACCT
 3001 TATATAAATG AGCTTTAA

SEQ ID NO:12 Ribosomal Protein L1 Protein Sequence
 ORIGIN

1 MTIFLESDDD KSNFKKTLEN GTKDKTNLDN TYYDYHHEDD MGNTEYHYVS LDRVHDVHKMP
 61 EEPVGYGGDT LPIVPTTAA SSGSDAGVAV GNVKDFEDNV FHHTSTIRND ELKIDLRIHT
 121 LKDLSDKRLR EIEKGFNDTV TKFKNNFGLE PNDGETIFDL YLFDDKEQYN YYGKLYNLGI
 181 SSGSGMTFYG NANVPYKIYV HQYGEILNLK HELTHALESY ASGHKLHGS VNSRIFTFGL
 241 ADYIQEDNSF IMRGLKDREI TSDVLKDSSG NVDHLSGVAV NENQRLSYSI GHAFVSFLQE

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301 KYPKLISEYL NALKEDNIIR AKEIISMDKY PDFEPWVSKS DISLYLENMN VLKLGLEKEM
361 FSAESASYFE DQGVNKEYYH ENIYDMSGKL VGEMSPVVHY AQKNVIRIWN IASPDMEIVR
421 PEYNFLKLVT TPSGKSAYVY CDKNGHEYFN TKDYIDSAFN ILARYDVKLR ESSDALDIRG
481 RYSDAAKVFS KLPNADLLLD KFLEKIGYSS YKQIIMSNEP QLNSIKAYVY KEVFENFRES
541 EVKKVLSGES HPEVRNVLM D LTYVDLKSVI GVNADIDSI ISNPDVMLRT AVLKGKNASG
601 ISLYVDDQKV GELSTEAGYC VKNLDTGKVV FMFHNVVGM I ASGYEDRAYM VVLEKDGKFT
661 TALVNNIQKA ADGNVVWDNQ FNHPNINNLH SNYKELLND ASVKDYSHLA DVKFNKDDTV
721 IVKGELDDDK GTVSVDDDDVH RAVVKHDDQI LHQFKSMSFY ITEPSADSGD NYGSDFFISD
781 EGKNLRFQLP KAITHLKLVN VNGNKKLVPC TKDGNHPEG MPSDLTDEYR YIDPIFAHTF
841 EKQSYSKNSI SVGLVDFSKY KEGSMFKLQH YSDDYHIHKD EQGNVIRPNN RSYVTKVDLV
901 YDDKVI GMLS DSINQFQGDI FISASLNYSH NDFLSSKYFQ KVNIEALENG IYSGRYDVGD
961 GDQIAGLNTD TGYSDKAIFY FKNDASASTM PASDVTTILP YINEL.

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SEQ ID NO:13 Type IV Secretory Protein VirD4 Nucleotide Sequence
ORIGIN

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1 ATGGATAGTA TAAGTGCAAA TCACATACGC AATATTTTAT TCCTTGTTTT AGGCGCATTT
61 TTTGGACTGG AATTTTGCTT TTATTTATCA GGTGTATTAT TCATCTTAAT GGTCTGGGGA
121 CCAAATTACC TAGATTTTAA TGCTATAAAT CCCAGTTTGA GTGATTTTCC AGACAGAATT
181 TGGCCAACTA TTTTGTACTA TGTACAACAT TGGTGGAAGA ACCCTTCTGC ATACGATGCA
241 GTTTTATTAC TTAAGCTAAT AACGTCATTA TGTACACCAG TAGGTATTCT AAGCATAGTA
301 TTATGGAACC TTAGAAATAT ATTATTCGAT TGGAGGCCAT TTAAGAAGAA AGAATCACTG
361 CATGGAGATT CAAGATGGGC AACAGAAAAA GATATTCGCA AAATAGGATT ACGTAGTAGA
421 AAAGGAATAT TATTAGGGAA AGACAAGAGA GGATATCTCA TTGCAGATGG ATATCAACAT
481 GCATTGTTAT TTGCACCAAC TGGATCCGGA AAAGGTGTAG GTTTTGTAAAT ACCAAACTTA
541 TTATTCTGGG AAGATTCTGT AGTAGTACAC GATATAAAAT TAGAGAACTA TGATCTTACA
601 AGTGGGTGGA GAAAAAAAAG GGGACAAGAA GTTTTCGTGT GGAACCCAGC ACAACCTGAC
661 GGTATAAGTC ACTGTTACAA CCCATTAGAT TGGATAAGCT CTAAGCCTGG ACAATGGTA
721 GATGATGTAC AAAAAATTGC CAATCTAATA ATGCCTGAAC AAGATTTTGT GTATAACGAA
781 GCACGTAGTT TATTTGTAGG AGTAGTATTA TACTTACTAG CAGTACCAGA AAAAGTAAAA
841 TCCTTTGGAG AAGTTGTAAG AACAAATGCGC AGCGATGACG TAGTCTACAA CTTAGCAGTA
901 GTACTAGACA CAATAGGGAA AAAGATTAC CCAGTTGCAT ACATGAATAT AGCTGCATTT
961 TTACAAAAAG CAGACAAAGA ACGCTCAGGT GTTGATCAA CTATGAACTC ATCTTTAGAA
1021 TTATGGGCAA ACCCATTAAT AGATACAGCA ACAGCATCAA GTGATTTTAA TATCAAGAA
1081 TTTAAAAGGA AAAAAGTAAC AGTATATGTT GGATTAACAC CAGATAATTG AACTCGTCTT
1141 AGACCTTTAA TGCAGGTATT TTATCAACAA GCTACAGAAT TTTTATGTAG AACTTTACCA
1201 TCAGATGATG AACCATATGG TGTACTGTTC TTAATGGATG AGTTTCCAAC ATTAGGAAAA
1261 ATGGAGCAAT TTCAAACAGG TATCGCATAT TTCCGTGGAT ATAGAGTTAG ACTATTTTTG
1321 ATTATTCAAG ATACTGAACA GCTTAAGGGT ATATATGAAG AAGCAGGAAT GAACTCATTC
1381 TTATCAAACT CTACTTATAG AATAACTTTT GCTGCAAATA ATATAGAAAC TGCAAATTTA
1441 ATATCACAGT TAATAGGAAA TAAAACTGTT AACCAGAGT CTTTAAACAG ACCTAAATTT
1501 TTAGATTTGA ACCCTGCATC ACGTTCATTA CATATATCAG AAACACAAAG AGCTTTACTA
1561 TTACCTCAAG AAGTAATAAT GTTACCCAGA GATGAGCAAA TACTTTTAAAT AGAATCTACT
1621 TATCCTATAA AATCAAAGAA AATAAAATAC TATGAAGACA AAAATTTTAC AAAAAACTA
1681 TTAAAGAGTA CCTTTGTTCC AACTCAAGAG CCTTATGATC CCAACAAAAC AAAAAACGCA
1741 ACAAAAGAAA ACGAAGAACC TATGCCAAGT ATTGAAAGCG ATCTTCCTAA AAATACATCT
1801 GACAATACTG AAAACAATAT GGAAGATGGT GCAATGTACA GCAGCATAGA AGAAGATTAT
1861 GACGATGATG ATGATGATTT TAATTTTGAA GACTTAGATG AATATATGGA TGAAGAAGAA
1921 GATTATGATG ATGAAGAATA TGATGATATA GATTATGATG ATAATAACAA TAGTAATGAG
1981 GAGTATGAAG AAGATAATCC AGAAGAAGAT GACAATAGCA ATAATCTAGA CGATGAGGAA
2041 GAGGAAGAAG ATAATATTAT AGATTATGAA GATGAAGAAG AATATGATGA TAACATAGAC
2101 TACAAAGATG ATGACAATAA CTACAACAAA GATACCACTG ACGATCAAGA CTCAAAAAAA
2161 CATAATGAAT AG

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SEQ ID NO:14 Type IV Secretory Protein VirD4 Protein Sequence
ORIGIN

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1 MDSISANHIR NILFLVLGAF FGLEFCFYLS GVLFILMVWG PNYLDFNAIN PSLSDFFPDRI
61 WPTIFDYVQH WWKNPSAYDA VLLLKLITSL CTPVGILSIV LWNLRNIFD WRPFKKKESL
121 HGDSRWATEK DIRKIGLRSR KGILLGKDKR GYLIADGYQH ALLFAPTGS G KGVGFVIPNL
181 LFWEDEVVH DIKLENYDLT SGWRKKRGQE VFVWNPAQPD GISHCYNPLD WISSKPGQMV
241 DDVQKIANLI MPEQDFWYNE ARSLFVGVL YLLAVPEKVK SFGEVVRTMR SDDVVYNLAV
301 VLDTIGKKIH PVAYMNIAAF LQKADKERSG VVSTMNSSLE LWANPLIDTA TASSDFNIQE
361 FKRKKVTYVY GLTPDNLTRL RPLMQVFYQQ ATEFLCRTLP SDDEPYGVLF LMDEFPTLKG
421 MEQFQTGIAY FRGYRVRLFL IIQDTEQLKG IYEEAGMNSF LSNSTYRITF AANNIETANL
481 ISQLIGNKTV NQESLNRPKF LDLNPASRSL HISETQRALL LPQEVIMLPR DEQILLIEST
541 YPKSKKIKY YEDKNFTKKL LKSTFVPTQE PYDPNKTATA TKENEEMPMS IESDLPKNTS

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601 DNTENNMEDG AMYSSIEEDY DDDDDDFNFE DLDEYMDEEE DYDDEEYDDI DYDDNNNSNE
661 EYEEDNPED DNSNNLDDEE EEEDNIIDYE DEEEYDDNID YKDDDNYNK DTDDQDSKK
721 HNE.

CLAIMS:

We claim:

1. A method of distinguishing between animals that have been infected with *Ehrlichia canis* and animals that have not been infected with *E. canis* or have been vaccinated with an *E. canis* vaccine, the method comprising:

- (a) contacting a biological sample from an animal with a first purified *E. canis* polypeptide that does not specifically bind to antibodies that are a component of the animal's immune response to an *E. canis* vaccine;
- (b) detecting whether an antibody in the sample specifically binds to the first purified *E. canis* polypeptide; and

wherein if an antibody in the sample specifically binds to the first purified *E. canis* polypeptide, then the animal is infected with *E. canis* and if an antibody does not specifically bind to the purified *E. canis* polypeptide, then the animal is either vaccinated with an *E. canis* vaccine or is not infected with *E. canis*.

2. The method of claim 1, wherein the first purified *E. canis* polypeptide comprises SEQ ID NOs: 2, 4, 6, 8, 10, 15, 16, 17, or combinations thereof.

3. The method of claim 1, wherein the *E. canis* vaccine comprises at least one *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, p153 polypeptide, or a vector encoding at least one *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, p153 polypeptide, or a combination thereof.

4. The method of claim 1 further comprising detecting whether an antibody in the sample specifically binds to a second purified *E. canis* polypeptide that is an element of an *E. canis* vaccine, and determining that the animal has been vaccinated for *E. canis* by detecting that an antibody in the sample specifically binds to the second purified *E. canis* polypeptide, or determining that the animal has not been vaccinated for *E. canis* and has not been infected by *E. canis* by detecting that no antibody in the sample specifically binds to the second purified *E. canis* polypeptide.

5. A method of determining whether an animal is either not infected or has been vaccinated against *E. canis* with an *E. canis* vaccine, or is infected with *E. canis* comprising determining the animal's immune response to a first purified polypeptide derived from *E. canis* that is not an element of an *E. canis* vaccine and wherein the first purified polypeptide does not specifically bind to antibodies produced by the animal as a result of the vaccination with the *E. canis* vaccine.
6. The method of claim 5, wherein the first *E. canis* polypeptide comprises SEQ ID NOs: 2, 4, 6, 8, 10, 15, 16, 17, or combinations thereof.
7. The method of claim 5, wherein the *E. canis* vaccine comprises at least one polypeptide selected from the group consisting of *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, or p153 polypeptide or a vector encoding at least one polypeptide selected from the group consisting of *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, p153 polypeptide, or a combination thereof.
8. The method of claim 5, further comprising, in those animals that do not have an immune response to the first purified polypeptide, determining whether the animal has been vaccinated by determining the animal's immune response to a second purified polypeptide that is an element of the *E. canis* vaccine.
9. The method of claim 5, wherein the second polypeptide is an *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, or p153 polypeptide or a combination thereof.
10. A method of determining an animal's vaccination and infection status for *E. canis* comprising:
 - (a) contacting a biological sample from an animal with a first purified polypeptide that does not specifically bind to antibodies that are a component of the animal's immune response to an *E. canis* vaccine and a second polypeptide that specifically binds to an antibody that is a component of the animal's immune response to an *E. canis* vaccine;

- (b) detecting whether antibodies in the sample specifically bind to the first and second purified polypeptides;
- (c) determining that the animal is infected by detecting the specific binding of antibodies in the sample to both the first and second purified polypeptides, determining that the animal is vaccinated and not infected by detecting the specific binding of an antibody to the second purified polypeptide but not the first purified polypeptide, and determining that the animal is not vaccinated and not infected by detecting the absence of specific binding to the first and second purified *E. canis* polypeptides.

11. The method of claim 10, wherein the first *E. canis* polypeptide comprises SEQ ID NOs: 2, 4, 6, 8, 10, 15, 16, 17 or combinations thereof.

12. The method of claim 10, wherein the second *E. canis* polypeptide is *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, p153 polypeptide, or a vector encoding at least one polypeptide selected from the group consisting of *E. canis* p28-1, p28-2, p28-3, p28-4, p28-5, p28-6, p28-7, p28-8, p28-9, proA, ProB, mmpA, cytochrome oxidase, p43, or p153 polypeptide or a combination thereof.

13. A method for determining the presence or absence of an antibody or fragment thereof, in a test sample, wherein the antibody or fragment thereof specifically binds to a purified polypeptide consisting of SEQ ID NOs: 2, 4, 6, 8, 10, 15, 16, or 17, comprising:

- contacting the test sample with a purified polypeptide comprising SEQ ID NOs: 2, 4, 6, 8, 10, 15, 16, or 17 under conditions suitable for specific binding of the purified polypeptide to the antibody or fragment thereof; and
- detecting the presence or absence of specific binding;

wherein the presence of specific binding indicates the presence of the antibody or fragment thereof, and wherein the absence of specific binding indicates the absence the antibody or fragment thereof.

14. The method of claim 13, wherein the method further comprises detecting the amount of specific binding.

15. The method of claim 13, wherein the purified polypeptide is immobilized to a solid support.

16. A composition comprising one or more purified polypeptides consisting of SEQ ID NO:16, SEQ ID NO:17, or combinations thereof.

17. The composition of claim 16, wherein the purified polypeptide is in a multimeric form.

18. The composition of claim 16, wherein the one or more purified polypeptides are linked to a heterologous protein, an indicator reagent, an amino acid spacer, an amino acid linker, a signal sequence, a stop transfer sequence, a transmembrane domain, a protein purification ligand, or a combination thereof.

19. A method of generating an immune response in an animal comprising administering one or more purified polypeptides comprising SEQ ID NOs:2, 4, 6, 8, 10, 15, 16, 17, or a combination thereof to the animal.

20. A method for the prophylaxis, treatment, or amelioration of an *Ehrlichia canis* infection in an animal comprising administering

(a) one or more purified polypeptides comprising SEQ ID NOs:2, 4, 6, 8, 10, 15, 16, 17, or a combination thereof; or

(b) one or more nucleic acids encoding one or more purified polypeptides comprising SEQ ID NOs:2, 4, 6, 8, 10, 15, 16, 17, or a combination thereof

to the animal.

(c) one or more antibodies that specifically bind one or more purified polypeptides comprising SEQ ID NOs:2, 4, 6, 8, 10, 16, 17, 18, or a combination thereof to the animal;

whereby the *E. canis* infection is prevented, ameliorated, or treated.

FIG. 1

HTWM / LYME / EC: SNAP 3 DX

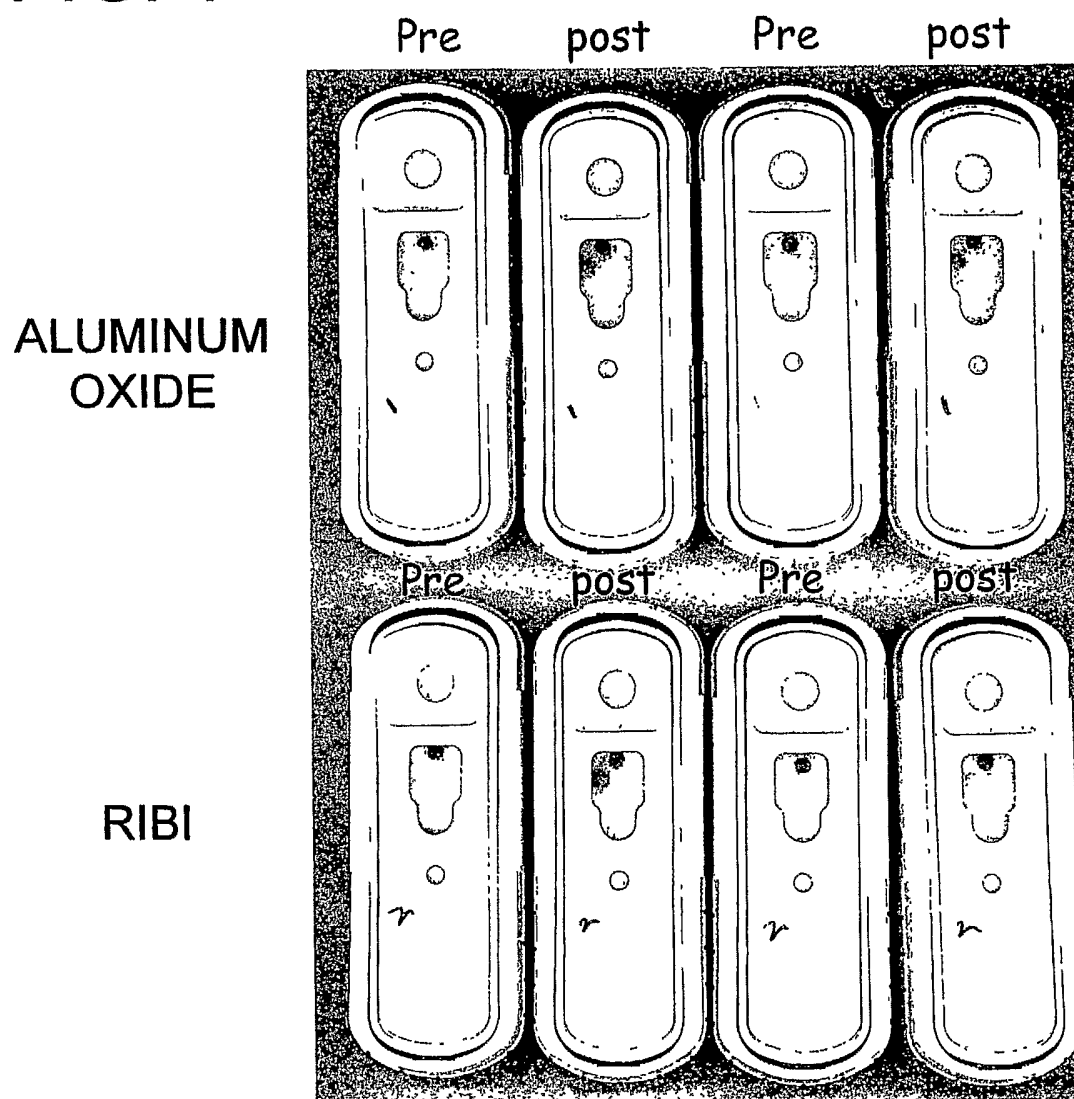


FIG. 2

2D GEL ANALYSIS OF
ISOLATED *E. canis* - STAINED WITH
BIOSAFE COOMASIE BLUE

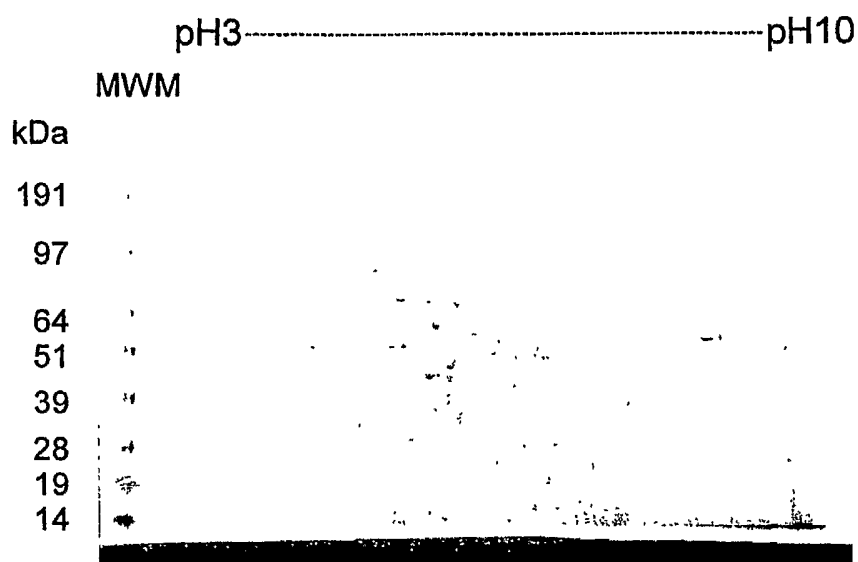


FIG. 3

WESTERN BLOT OF *E. Canis* PROTEINS RESOLVED USING 2D
GELS PROBED WITH NORMAL CANINE PLASMA.

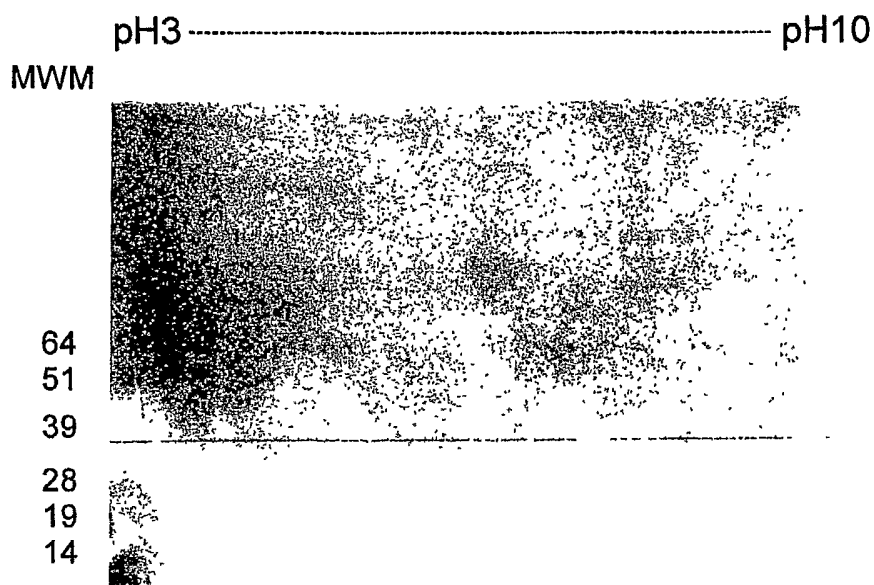


FIG. 4

WESTERN ANALYSIS WITH VACCINATED SERA
POOL OF 4 VACCINATED DOGS - 1:100

pH10 ----- pH3



FIG. 5

WESTERN ANALYSIS WITH INFECTED SERA
POOL OF 3 POSITIVE DOGS - 1:100

pH10 ----- pH3

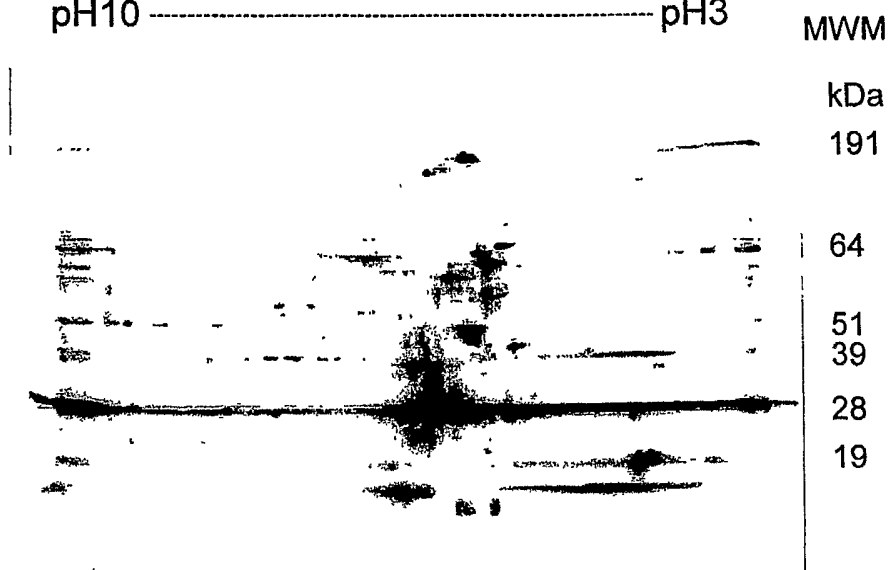
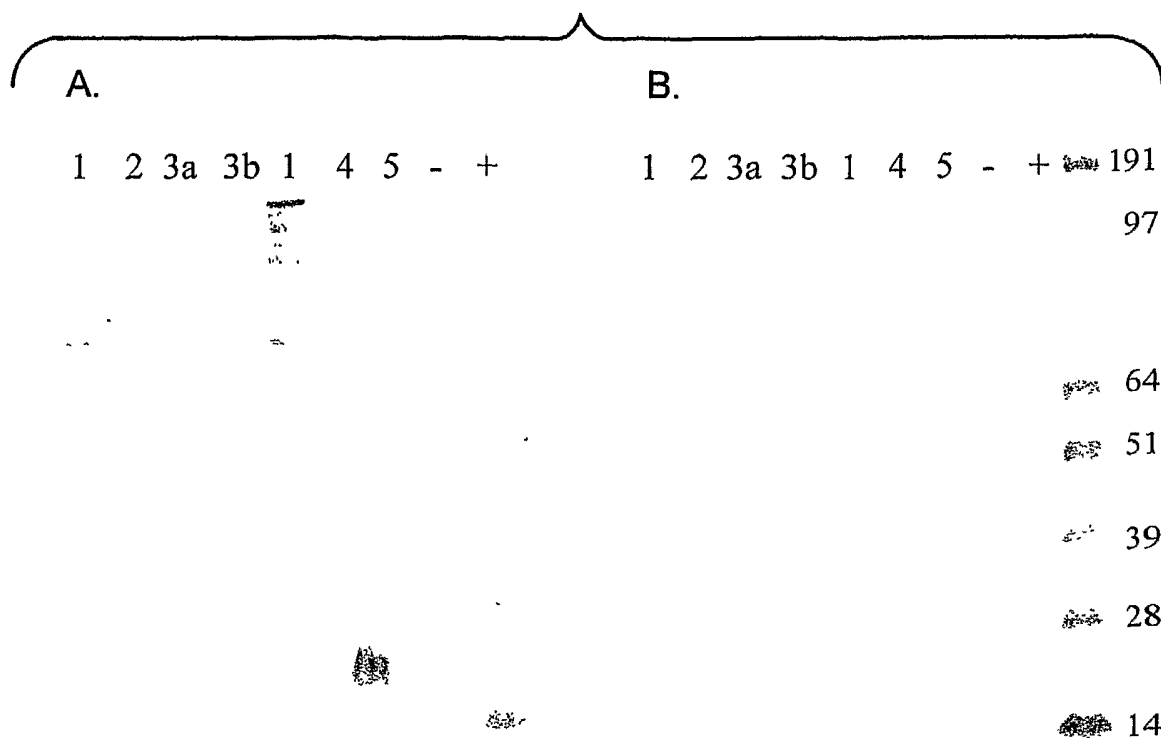
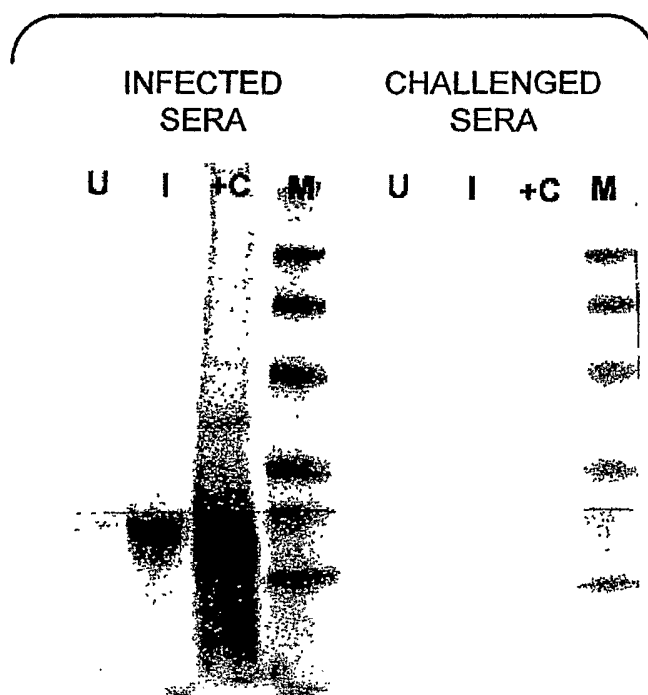


FIG. 6**FIG. 7**

5 / 5

SEQ ID NO: 15

FIG. 8

MDIDNNNVTTSSSTQDKSGNLMEVIMRI LNFGNNSD
 EKVSNE~~DTKVLVESLQPAVNDNVGNPSSEVGKEEN~~
 APEVKAEDLQPAVDGSVENSSSEVGKKV~~STTSKEE~~
 STPEVKAEDLQPAVDGSIENSSSEVGKVS~~TSKE~~
 ESTPEVKAEDLQPAVDDSVENSSSEVGKVS~~ETSK~~
 EENTPEVKAEDLQPAVDGSIENSSSEVGKVS~~TS~~
 KEESTPEVKAEDLQPAVDDSVENSSSEVGKVS~~ET~~
 SKEENTPEVKAEDLQPAVDGSVENSSSEVGKVS~~K~~
 TSKEESTPEVKAEDLQPAVDDSVENSSSEVGKVS
 ETSKEENTPEVKAEDLQPAVDGSVENSSSEVGKVS
 SETSKEESTPEVKAEDLQPAVDSSIENSSSEVGKK
 VSETSK~~EE~~STPEVKAEDLQPAVDGSVENSSSEVG
 KVSETSK~~EE~~NTPEVKAEDLQPAVDGSVENSSSEVG
 EKVSETSK~~EE~~NTPEVKAEDLQPAVDGSVENSSSEV
 GEKVSETSK~~EE~~STPEVKAEDLQPAVDDSVENSSSE
 VGEKVSETSK~~EE~~STPEVKAEDLQPAVDGSVENSSS
 EVGEKVSETSK~~EE~~STPEVKAEDLQPAVDGVPADGNPVPANP
 MP~~SI~~DNIDTNIIFHYHKDCKKGS~~AV~~GTDEMCCPVS
 ELMAGEHVHMYGIYVYRVQSVKDL~~SG~~VFNIDHSTC
 DCNLDVYFVGYN~~S~~FTNKETVDLI

FIG. 9A

KEENAPEVKAEDLQPAVDGSVEHSSSEVGKKVSETS
 KEESTPEVKAEDLQPAVDGSIEHSSSEVGKVSKTS
 KEESTPEVKAEDLQPAVDDSVEHSSSEVGKVSETS
 KEENTPEVKAEDLQPAVDGSIEHSSSEVGKVSKTS
 KEESTPEVKAEDLQPAVDDSVEHSSSEVGKVSETS
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 KEESTPEVKAEDLQPAVDSSIEHSSSEVGKKVSETS
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 KEESTPEVKAEDLQPAVDDSVEHSSSEVGKVSETS
 KEESTPEVKAEDLQPAVDGSVEHSSSEVGKVSETS
 KEESTPEVKAE SEQ ID NO:16

FIG. 9B

KEESTPEVKAEDLQPAVDGSVEHSSSEVGKVSETS CONSENSUS
 N R D I K K SEQ ID NO:17
 S