US 20040058316A1

(19) **United States**

(12) **Patent Application Publication**

Jensen et al.

(10) **Pub. No.: US 2004/0058316 A1**

(43) **Pub. Date: Mar. 25, 2004**

(54) USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE STATUS OF AN ANIMAL

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(21) Appl. No.: **10/670,695**

(22) Filed: **Sep. 25, 2003**

Related U.S. Application Data

(63) Continuation of application No. 09/521,738, filed on Mar. 9, 2000.

Publication Classification

(51) **Int. Cl.**^{7} **C12Q 1/70**; G01N 33/554; G01N 33/569

(52) **U.S. Cl.** **435/5**; 435/7.32

(57) ABSTRACT

The present invention includes a method to determine the immune status of an animal that includes the steps of (a) contacting a biological specimen of the animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent, under conditions suitable for formation of a complex between the recombinant antigen and the antibody and (b) detecting the presence or absence of the complex, wherein presence or absence of a complex is indicative of the immune status of the animal. Preferably such a method indicates whether the animal should be vaccinated. The present invention also includes an assay comprising (a) a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent; and (b) a means to detect an antibody that selectively binds to the recombinant antigen. Also included in the present invention are recombinant antigens and nucleic acid molecules encoding such antigens as well as methods to produce and use such nucleic acid molecule and recombinant antigens.

USE OF RECOMBINANT ANTIGENS TO DETERMINE THE IMMUNE STATUS OF AN ANIMAL

FIELD OF THE INVENTION

[0001] The present invention relates generally to materials and methods useful for the detection of antibodies in an animal. In particular, the invention relates to the use of recombinant antigens to determine the immune status of an animal in order to determine whether the animal has antibodies indicative of protection from infection by an infectious agent.

BACKGROUND OF THE INVENTION

[0002] The need for vaccinations against pathogens has long been recognized in humans and other animals. The long term efficacy of vaccines, especially vaccines against viruses, has become a topic of interest more recently. One recent study, for example, showed that neutralizing antibody titers against feline parvovirus (FPV), feline herpesvirus (FHV), and feline calicivirus (FCV) remain in cats for at least three years following vaccination; see Scott, et al., 1997*, Feline Practice* 25, 12-19. The antibody titers do decline over time, however, and the exact time that any given cat remains protected against disease cannot be predicted without testing. Current guidelines for vaccination recommend that cats be revaccinated every three years; see, for example, Elston, et al., 1998*, Feline Practice* 26, 14-16; Elston, et al., 1998, *J. Am. Vet. Med. Assoc.* 212, 227-241. For dogs, the current recommendation is to revaccinate against canine parvovirus and canine distemper virus yearly.

[0003] Vaccinations, however, are not risk-free. Anaphylaxis, post-vaccine canine distemper encephalitis, polyarthritis, glomerulonephritis, immune-mediated hemolytic anemia, autoimmune nonregenerative anemia and immune-mediated thrombocytopenia are all reported adverse reactions to vaccinations; see, for example, McCaw, et al., 1998*, J. Am. Vet. Med. Assoc.* 213, 72-75. A small proportion of cats have also been reported to develop fibrosarcomas after multiple vaccine injections; see, for example, Hershey et al., 2000*, J. Am. Vet. Med. Assoc.* 216, 58-61. The risks associated with vaccination, coupled with recent research demonstrating that at least some cats may not require certain vaccinations for more than seven years and that at least some dogs may not require revaccination for more than two years, are indicative of the desirability of measuring antibody titers to determine the immune status of animals prior to vaccination; see, Scott, et al., 1999*, Am. J. Vet. Res.* 60, 652-58 1999; McCaw, et al., ibid.

[0004] The duration of immunity experiments performed by Scott, et al., 1999, ibid., and McCaw, et al., ibid, however, utilized virus neutralization ("VN") tests to determine the amount of protective antibodies in test animals. Depending on the particular assay, VN tests typically require between three and four days to perform, and can require as long as six or seven days. Time is only one disadvantage of the VN test: the test also requires skilled laboratory personnel to perform, incurs significant cost, and involves the use of live virus, presenting a biohazard risk.

[0005] An enzyme-linked immunosorbent assay (ELISA) represents an alternative to VN tests. ELISAs usually require an overnight coating step, with the actual test being performed in less than one day. This test does require multiple steps and requires a relatively skilled technician for performance and analysis. Standard methods use whole virus or virus-infected cells as the antigen for the detection of protective antibodies, again posing a biohazard risk. See, for example, Hill, et al., 1995*, Am. J. Vet. Res.* 56, 1181-1187; Spencer, et al., 1991*, J. Wildl. Dis.* 27, 578-583; Fiscus, et al., 1985*, Am. J. Vet. Res.* 46, 859-63. Furthermore, whole virus preparations are contaminated with antigens from the cells used to grow the virus. The procedure for obtaining canine parvovirus (CPV) in Fiscus, et al., ibid., for example, is not sufficient to completely remove such cellular antigens from the preparation. When using a biological specimen such as blood or serum from a vaccinated animal as a test sample, cellular antigens in the virus preparation can react with antibodies previously produced by the animal in response to such cellular proteins being in the virus preparation with which the animal was previously vaccinated. The presence of such cellular antigens in an immunoassay frequently increases the level of the signal in the assay, thereby leading to false positive or ambiguous results.

[0006] Thus, the methods currently practiced to determine the immune status of an animal suffer from a number of disadvantages, which are multiplied with each antibody type that one wishes to detect. Accordingly, there remains a need for an improved assay for the detection of antibodies in a test sample that does not require the use of biohazardous material and does not utilize materials containing contaminants that lead to false positives. There also remains a need for an assay for the detection of antibodies to one or more infectious agents that can be performed in a relatively short time period, in a veterinarian's office, inexpensively, by unskilled personnel. There further remains a need for antigen reagents that not only are stable and economic to produce but also are consistent from batch to batch.

SUMMARY OF THE INVENTION

[0007] The present invention relates generally to materials and methods useful for the detection of the immune status of an animal. In particular, the invention relates to recombinant antigens and their use as reagents to determine the presence of antibodies indicative of protection against disease in an animal.

[0008] One embodiment of the present invention is a method to determine the immune status of an animal. Such a method includes the steps of: (a) contacting a biological specimen of the animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent, under conditions suitable for formation of a complex between the recombinant antigen and the antibody; and (b) detecting the presence or absence of the complex, wherein presence or absence of a complex is indicative of the immune status of the animal. For example, presence of a complex indicates that the animal is not susceptible to (i.e., is protected from) infection by the infectious agent.

[0009] Another embodiment of the present invention is a method to determine whether to vaccinate an animal. Such a method includes the steps of: (a) contacting a biological specimen of the animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent, under conditions suitable for formation of a complex between the recombinant antigen and the antibody; and (b) detecting the presence or absence of the complex. Presence of such a complex indicates that the animal need not be vaccinated, whereas absence of such a complex indicates that the animal should be vaccinated.

[**0010**] Yet another embodiment of the present invention is an assay to determine the immune status of an animal. Such an assay includes (a) a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent; and (b) a means to detect an antibody that selectively binds to the recombinant antigen.

[**0011**] The present invention also includes the following recombinant antigens: PFCVCP$_{671}$, PFCVCP$_{547}$, PFPVVP2$_{584}$, PFPVVP2C$_{243}$, PFPVpVP12620, PFPVpVP2$_{477}$, PFHVgB$_{943}$, PFHVgB$_{250}$, PFHVgC$_{534}$, PFHVgC$_{467}$, PFHVgC$_{467(opt)}$, PFHVgD$_{374}$, PFHVgD$_{300}$, PFeLVp27$_{253}$, PFeLVp27$_{619}$, PFeLVp27-gp70$_{611}$, PCDVH$_{604}$, and PCDVF$_{662}$. These recombinant antigens are represented, respectively by the following amino acid sequences: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34 and SEQ ID NO:36. Also included are nucleic acid molecules encoding such recombinant antigens as well as nucleic acid molecules fully complementary to such coding sequences. Also included are recombinant molecules and recombinant cells including such nucleic acid molecules as well as methods to produce such nucleic acid molecules, recombinant molecules, recombinant cells, and recombinant antigens.

DETAILED DESCRIPTION OF THE INVENTION

[**0012**] The present invention includes a method to determine the immune status of an animal. As used herein, the phrase to determine the immune status of an animal refers to a method to detect antibodies in that animal that are selective for a given infectious agent. Presence of such antibodies indicates that the animal is protected from infection by the infectious agent. Such an animal need not be vaccinated as it is not susceptible to infection by the infectious agent. A method of the present invention to determine the immune status of an animal includes the steps of: (a) contacting a biological specimen of the animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent, under conditions suitable for formation of a complex between the recombinant antigen and the antibody; and (b) detecting the presence or absence of the complex, wherein presence or absence of a complex is indicative of the immune status of the animal. In one embodiment, such a method is used to determine whether to vaccinate an animal. The present invention also includes an assay to determine the immune status of an animal as well as recombinant antigens that can be used in such a method or assay. Also included are nucleic acid molecules encoding such recombinant antigens, recombinant molecules and recombinant cells as well as methods to produce and use such molecules and cells.

[**0013**] It was surprising to the inventors that recombinant antigens are essential to a method to accurately determine the immune status of an animal. Use of whole virus in such a method was found to be unacceptable due to the potential for false positives caused by cellular antigens co-purifying with the virus preparation. The problem with cellular antigens was compounded when virus was isolated in a large-scale preparation. Although attempts were made to overcome these problems, using, for example, ultracentrifugation or cesium chloride purification techniques to purify virus, unacceptable levels of cellular antigens remained. As described in more detail in the Examples, not only did reagents containing feline calicivirus (FCV), feline herpesvirus (FHV), or feline parvovirus (FPV) purified from Crandell feline kidney (CRFK) cells in which the respective virus had grown (i.e., FCV or FHV purified by ultracentrifugation or FPV through cesium chloride) yield positive results in an ELISA to detect antibodies in cats previously administered the respective virus, but so did the respective "control" reagents purified from uninfected CRFK cells in the same manner. Data obtained from the "control" reagents represented unacceptable false positive results, leading the inventors to pursue alternative routes to develop an immune status assay. The inventors subsequently found that a recombinantly produced viral antigen yields unexpectedly good results, with acceptable background levels, in the determination of the immune status of an animal by immunoassay.

[**0014**] As such, the present invention includes a method to determine the immune status of an animal that includes the following steps: (a) contacting a biological specimen of the animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent, under conditions suitable for formation of a complex between the recombinant antigen and the antibody; and (b) detecting the presence or absence of the complex, wherein presence or absence of a complex is indicative of the immune status of the animal. It is to be noted that the term "a" entity or "an" entity refers to one or more of that entity; for example, a recombinant antigen refers to one or more antigens or at least one antigen. As such, the terms "a" (or "an"), "one or more" and "at least one" can be used interchangeably herein. It is also to be noted that the terms "comprising", "including", and "having" can be used interchangeably.

[**0015**] As used herein, a recombinant infectious agent antigen is an antigen of an infectious agent that is produced using recombinant nucleic acid technology. Such an antigen, also referred to herein as a recombinant antigen of the present invention or simply as a recombinant antigen, can be identified in a straight-forward manner by its ability to specifically detect an antibody selective for that infectious agent. As used herein, an antibody selective for an infectious agent, also referred to herein as an anti-infectious agent antibody, is an antibody that selectively binds to that infectious agent in that it preferentially binds to that infectious agent as opposed to binding to a different, unrelated, infectious agent. It is to be noted that, in accordance with the present invention, such an antibody exists in a biological specimen of an animal because a given infectious agent, upon infecting the animal, induces an immune response that includes the production of such an antibody selective for that infectious agent. A recombinant antigen of the present invention is also able to specifically detect the presence of such an antibody in that the recombinant antigen is sufficiently similar to the corresponding antigen on the infectious agent to enable such detection. The specificity of such detection enables one to ascertain that an animal has antibodies to a given infectious agent rather than to an unrelated infectious agent. Binding of an antigen and antibody can be measured using a variety of methods known to those skilled in the art, such as, but not limited to, those methods disclosed elsewhere herein. Preferably, a recombinant antigen of the present invention has a binding affinity of from about 10^8 liters per mole (M^{-1}) to about 10^{12} M^{-1} for an anti-infectious agent antibody of the present invention.

[**0016**] A recombinant infectious agent antigen of the present invention can correspond exactly to the antigen as found on the infectious agent or the recombinant antigen can be a homolog of such a native antigen. Examples of homologs include proteins in which amino acids have been deleted (e.g., a truncated version of the protein, such as a peptide), inserted, inverted, substituted and/or derivatized (e.g., by glycosylation, phosphorylation, acetylation, myristoylation, prenylation, palmitoylation, amidation and/or addition of glycerophosphatidyl inositol) such that the homolog includes at least one epitope capable of forming an immunocomplex, also referred to herein as a complex, with an anti-infectious agent antibody. As used herein, the term epitope refers to the smallest portion of a protein or other antigen capable of selectively binding to the antigen binding site of an antibody. It is well accepted by those skilled in the art that the minimal size of a protein epitope is about four amino acids. In one embodiment, a recombinant antigen of the present invention is modified to produce a more soluble antigen. Methods to produce more soluble antigens by modifying either a nucleic acid sequence or the protein itself are well known to those skilled in the art. One example of such a method, not intended to be limiting, is protein iodoacetimidation.

[**0017**] A recombinant antigen homolog can be the result of natural allelic variation or natural mutation. Homologs of the present invention can also be produced using techniques known in the art including, but not limited to, direct modifications to the protein or modifications to the nucleic acid molecule encoding the protein using, for example, classic or recombinant nucleic acid molecule techniques to effect random or targeted mutagenesis.

[**0018**] It is to be appreciated that recombinant antigens of the present invention include, but are not limited to, full-length proteins, proteins that are encoded by allelic variants of a given nucleic acid sequence, hybrid proteins, fusion proteins, multivalent proteins, and proteins that are truncated homologs of, or are proteolytic products of, at least a portion of a protein. As used herein, the term hybrid protein refers to a single protein produced from at least two different proteins; i.e., having domains from at least two different proteins.

[**0019**] Due to the method by which it is produced, a recombinant antigen of the present invention is removed from its natural milieu. As such, a recombinant antigen is isolated or biologically pure. Such terms do not reflect the extent to which a recombinant antigen is purified. A preferred recombinant antigen is purified from the recombinant cell which expresses the protein. Examples of methods to produce recombinant antigens of the present invention are disclosed elsewhere herein.

[**0020**] A recombinant infectious agent antigen of the present invention is any recombinant antigen that corresponds to (e.g., is derived from) an infectious agent. Preferred is an infectious agent for which one desires to determine if an animal is susceptible to infection by that agent. Suitable infectious agents include, but are not limited to, viruses, bacteria, fungi, endoparasites and ectoparasites. As such, suitable recombinant infectious agent antigens include, but are not limited to, recombinant viral, bacterial, fungal, endoparasite and ectoparasite antigens. Examples of viral infectious agents include, but are not limited to, adenoviruses, caliciviruses, coronaviruses, distemper viruses, hepatitis viruses, herpesviruses, immunodeficiency viruses, infectious peritonitis viruses, leukemia viruses, oncogenic viruses, papilloma viruses, parainfluenza viruses, parvoviruses, rabies viruses, and reoviruses, as well as other cancer-causing or cancer-related viruses. Examples of bacterial infectious agents include, but are not limited to, Actinomyces, Bacillus, Bacteroides, Bartonella, Bordetella, Borrelia, Brucella, Campylobacter, Capnocytophaga, Clostridium, Corynebacterium, Coxiella, Dermatophilus, Ehrlichia, Enterococcus, Escherichia, Francisella, Fusobacterium, Haemobartonella, Helicobacter, Klebsiella, L-form bacteria, Leptospira, Listeria, Mycobacteria, Mycoplasma, Neorickettsia, Nocardia, Pasteurella, Peptococcus, Peptostreptococcus, Proteus, Pseudomonas, Rickettsia, Rochalimaea, Salmonella, Shigella, Staphylococcus, Streptococcus, and Yersinia. Examples of fungal infectious agents include, but are not limited to, Absidia, Acremonium, Altemaria, Aspergillus, Basidiobolus, Bipolaris, Blastomyces, Candida, Chlamydia, Coccidioides, Conidiobolus, Cryptococcus, Curvalaria, Epidermophyton, Exophiala, Geotrichum, Histoplasma, Madurella, Malassezia, Microsporum, Moniliella, Mortierella, Mucor, Paecilomyces, Penicillium, Phialemonium, Phialophora, Pro to theca, Pseudallescheria, Pseudomicrodochium, Pythium, Rhinosporidium, Rhizopus, Scolecobasidium, Sporothrix, Stemphylium, Trichophyton, Trichosporon, and Xylohypha. Example of protozoan parasite infectious agents include, but are not limited to, Babesia, Balantidium, Besnoitia, Cryptosporidium, Eimeria, Encephalitozoon, Entamoeba, Giardia, Hammondia, Hepatozoon, Isospora, Leishmania, Microsporidia, Neospora, Nosema, Pentatrichomonas, Plasmodium, Pneumocystis, Sarcocystis, Schistosoma, Theileria, Toxoplasma, and Trypanosoma. Examples of helminth parasite infectious agents include, but are not limited to, Acanthocheilonema, Aelurostrongylus, Ancylostoma, Angiostrongylus, Ascaris, Brugia, Bunostomum, Capillaria, Chabertia, Cooperia, Crenosoma, Dictyocaulus, Dioctophyme, Dipetalonema, Diphyllobothrium, Diplydium, Dirofilaria, Dracunculus, Enterobius, Filaroides, Haemonchus, Lagochilascaris, Loa, Mansonella, Muellerius, Nanophyetus, Necator, Nematodirus, Oesophagostomum, Onchocerca, Opisthorchis, Ostertagia, Parafilaria, Paragonimus, Parascaris, Physaloptera, Protostrongylus, Setaria, Spirocerca, Spirometra, Stephanofilaria, Strongyloides, Strongylus, Thelazia, Toxascaris, Toxocara, Trichinella, Trichostrongylus, Trichuris. Uncinaria, and Wuchereria. Examples of ectoparasite infectious agents include, but are not limited to, fleas; ticks, including hard ticks and soft ticks; flies, such as midges, mosquitos, sand flies, black flies, horse flies, horn flies, deer flies, tsetse flies, stable flies, myiasis-causing flies and biting gnats; ants; spiders, lice; mites; and true bugs, such as bed bugs and kissing bugs.

[**0021**] Preferred recombinant antigens of the present invention include an adenovirus protein, a calicivirus protein, a coronavirus protein, a distemper virus protein, a herpesvirus protein, an immunodeficiency virus protein, an influenza virus protein, a leukemia virus protein, a parvovirus protein, a rabies virus protein, a Bartonella protein, an Ehrlichia protein, a Haemobartonella protein, a Leptospira protein, a Streptococcus protein, a protozoan myeloecephalitis protein, a Dirofilaria protein, and a Giardia protein. More preferred recombinant antigens include a feline calicivirus protein, a feline coronavirus protein, a feline herpesvirus protein, a feline leukemia virus protein, a feline parvovirus protein, a canine adenovirus protein, a canine coronavirus protein, a canine distemper virus protein, a canine parvovirus protein, a rabies virus protein, an equine herpesvirus I protein, an equine herpesvirus IV protein, an equine influenza virus protein, a *Streptococcus equii* protein, and an Ehrlichia protein. Even more preferred recombinant antigens of the present invention include a feline calicivirus capsid protein (a rFCVCP protein), a feline herpesvirus glycoprotein B (gB) protein (a rFHVgB protein), a feline herpesvirus glycoprotein C (gC) protein (a rFHVgC protein), a feline herpesvirus glycoprotein D (gD) protein (a rFHV gD protein), a feline parvovirus VP12 protein (a rFPVVP12 protein), a feline parvovirus VP2 protein (a rFPVVP2 protein), a feline leukemia virus p27 protein (a rFeLVp27 protein), a feline leukemia virus glycoprotein70 protein (a rFeLVgp70 protein), a p27/gp70 fusion protein (a rFeLVp27-gp70 protein), a canine distemper virus fusion protein (a rCDVF protein), and a canine distemper virus hemagglutinin protein (a rCDVH protein). Even more preferred recombinant antigens of the present invention include PFCVCP$_{67}$, PFCVCP$_{547}$, PFPVVP2$_{584}$, PFPVVP2C$_{243}$, PFPVpVP12620, PFPVpVP2$_{477}$, PFHVgB$_{943}$, PFHVgB$_{250}$, PFHVgC$_{534}$, PFHVgC$_{467}$, PFHVgC$_{467(opt)}$, PFHVgD$_{374}$, PFHVgD$_{300}$, PFeLVp27$_{253}$, PFeLVp27$_{619}$, PFeLVp27-gp70$_{611}$, PCDVH$_{604}$, and PCDVF$_{662}$, the characteristics and production of which are described in the Examples. Such recombinant proteins have the following respective amino acid sequences: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34 and SEQ ID NO:36.

[**0022**] Particularly preferred recombinant antigens of the present invention include proteins having at least one of the following amino acid sequences: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34 and SEQ ID NO:36. Also preferred are recombinant antigens that are fragments of any of such antigens having such cited amino acid sequences, the fragments being able to bind to antibodies selective for the corresponding infectious agent. Preferred recombinant antigens can be encoded by nucleic acid molecules that: (a) have at least one of the following nucleic acid sequences: SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, and SEQ ID NO:35; (b) are degenerates of the nucleic acid sequences of (a); (c) are allelic variants of the nucleic acid sequences of (a); or (d) are fragments of any of the nucleic acid molecules of (a), (b), or (c). The foregoing SEQ ID NOs represent nucleic acid and amino acid sequences deduced according to methods disclosed in the Examples. It should be noted that since nucleic acid sequencing technology is not entirely error-free, the foregoing SEQ ID NOs, at best, represent apparent nucleic acid and amino acid sequences of certain nucleic acid molecules and recombinant antigens, respectively, of the present invention. In addition, variation seen in the foregoing SEQ ID NOs can also be due, at least in part, to allelic variation, which can be caused by, among other factors, genetic drift.

[**0023**] Additional preferred recombinant antigens of the present invention share at least about 70%, preferably at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90%, more preferably at least about 95%, and more preferably about 100% identity at the amino acid level with a protein having at least one of the following amino acid sequences: SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ ID NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34 and SEQ ID NO:36. Also preferred are fragments of such antigens, and particularly fragments that are at least about 5, 10, 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, or 900 amino acids in length.

[**0024**] The present invention also includes a recombinant antigen nucleic acid molecule. Recombinant antigen nucleic acid molecules of the present invention include any recombinant nucleic acid molecule that encodes a recombinant antigen of the present invention as well as a nucleic acid molecule fully complementary to any such coding sequence. A nucleic acid molecule of the present invention can be single-stranded or double-stranded. In accordance with the present invention, an isolated nucleic acid molecule is a nucleic acid molecule that has been removed from its natural milieu, i.e., that has been subjected to human manipulation, and can include DNA, RNA, or derivatives of either DNA or RNA. It is to be noted that the term isolated does not reflect the extent to which the nucleic acid molecule has been purified. A recombinant antigen nucleic acid molecule of the present invention can be isolated from its natural source or produced using recombinant DNA technology, e.g., polymerase chain reaction (PCR) amplification or cloning, or chemical synthesis. Although the phrase, nucleic acid molecule, primarily refers to the physical nucleic acid molecule and the phrase, nucleic acid sequence, primarily refers to the sequence of nucleotides on the nucleic acid molecule, the two phrases can be used interchangeably.

[**0025**] A nucleic acid molecule of the present invention can be a natural isolate or a homolog thereof. Nucleic acid molecule homologs include natural allelic variants and nucleic acid molecules modified by one or more nucleotide insertions, deletions, substitutions, and/or inversions in a manner such that the modification(s) do not substantially interfere with the nucleic acid molecule's ability to encode a recombinant antigen of the present invention. A nucleic acid molecule homolog of the present invention can be produced using a number of methods known to those skilled in the art; see, for example, Sambrook et al., 1989, *Molecu-*

lar Cloning: A Laboratory Manual, Cold Spring Harbor Labs Press; Sambrook et al., ibid., is incorporated by reference herein in its entirety. For example, nucleic acid molecules can be modified using a variety of techniques including, but not limited to, classic mutagenesis and recombinant DNA techniques such as site-directed mutagenesis, chemical treatment, restriction enzyme cleavage, ligation of nucleic acid fragments, PCR amplification, synthesis of oligonucleotide mixtures and ligation of mixture groups to build a mixture of nucleic acid molecules, and combinations thereof. Nucleic acid molecule homologs can be selected by hybridization or by screening for the function of a protein encoded by the nucleic acid molecule, e.g., ability to detect antibodies selective for the corresponding infectious agent.

[**0026**] Suitable and preferred nucleic acid molecules of the present invention encode suitable and preferred recombinant antigens as disclosed herein. Particularly preferred nucleic acid molecules of the present invention include the following nucleic acid sequences: SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, and SEQ ID NO:35; as well as nucleic acid molecules having nucleic acid sequences fully complementary to such sequences. Particularly preferred double-stranded nucleic acid molecules include $nFCVCP_{2013}$, $nFCVCP_{1641}$, $nFPVVP2_{1752}$, $nFPVVP2C_{729}$, $nFPVpVP12_{1860}$, $nFPVpVP2_{1431}$, $nFHVgB_{2829}$, $nFHVgB_{750}$, $nFHVgC_{1602}$, $nFHVgC_{1401}$, $nFHVgC_{1401(opt)}$, $nFHVgD_{1122}$, $nFHVgD_{900}$, $nFeLVp27_{759}$, $nFeLVp27_{1857}$, $nFeLVp27\text{-}gp70_{1833}$, $nCDVH_{1812}$, and $nCDVF_{1986}$. Also preferred are nucleic acid molecules having degenerate sequences to any of the afore-mentioned nucleic acid molecules having cited nucleic acid sequences and nucleic acid molecules that are allelic variants thereof as well as fragments of any of the above-mentioned nucleic acid molecules. As used herein a nucleic acid molecule having a sequence that is degenerate as compared to a cited nucleic acid sequence is a nucleic acid molecule that encodes the same protein as the nucleic acid molecule having the cited sequence, but has a different nucleic acid sequence due to the degeneracy of the genetic code. As used herein, an allelic variant of a nucleic acid molecule having a cited nucleic acid sequence is a nucleic acid molecule that is a gene occurring at essentially the same locus (or loci) in the genome as the gene including the particular SEQ ID NO's cited herein, but which, due to natural variations caused by, for example, mutation or recombination, has a similar but not identical sequence. Also included in the term allelic variant are allelic variants of cDNAs derived from such genes. Because natural selection typically selects against alterations that affect function, allelic variants usually encode proteins having similar activity to that of the protein encoded by the gene to which they are being compared. Allelic variants of nucleic acid molecules can also comprise alterations in the 5' or 3' untranslated regions of the gene (e.g., in regulatory control regions), or can involve alternative splicing of a nascent transcript, thereby bringing alternative exons into juxtaposition. Allelic variants are well known to those skilled in the art and would be expected to be found within a given infectious agent.

[**0027**] Additional preferred recombinant antigen nucleic acid molecules of the present invention share at least about 70%, preferably at least about 75%, more preferably at least about 80%, more preferably at least about 85%, more preferably at least about 90%, more preferably at least about 95%, and more preferably about 100% identity at the nucleic acid level with a nucleic acid molecule having at least one of the following nucleic acid sequences: SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, and SEQ ID NO:35. Also preferred are fragments of such nucleic acid molecules, an particularly fragments that are at least about 15, 20, 25, 30, 40, 50, 60, 70, 80, 90, 100, 150, 200, 250, 300, 350, 400, 450, 500, 550, 600, 650, 700, 750, 800, 850, 900, 950, 1000, 1100, 1200, 1300, 1400, 1500, 1600, 1700, 1800, 1900, 2000, 2100, 2200, 2300, 2400, 2500, 2600, 2700, or 2800 nucleotides in length.

[**0028**] The minimal size of a recombinant antigen of the present invention is a size sufficient to be encoded by a nucleic acid molecule capable of forming a stable hybrid (i.e., hybridize under stringent hybridization conditions) with the complementary sequence of a nucleic acid molecule encoding the corresponding protein. The size of a nucleic acid molecule encoding such a protein is dependent on the nucleic acid composition and the percent homology between the nucleic acid molecule and the complementary nucleic acid sequence. It can easily be understood that the extent of homology required to form a stable hybrid under stringent conditions can vary depending on whether the homologous sequences are interspersed throughout a given nucleic acid molecule or are clustered (i.e., localized) in distinct regions on a given nucleic acid molecule.

[**0029**] The minimal size of a nucleic acid molecule capable of forming a stable hybrid with a nucleic acid molecule encoding a recombinant antigen is typically at least about 12 to about 15 nucleotides in length if the nucleic acid molecule is GC-rich and at least about 15 to about 17 nucleotides in length if it is AT-rich. The minimal size of a nucleic acid molecule used to encode a recombinant antigen homolog of the present invention is from about 12 to about 18 nucleotides in length. Thus, the minimal size of a recombinant antigen homolog of the present invention is from about 4 to about 6 amino acids in length. There is no limit, other than a practical limit, on the maximal size of a nucleic acid molecule encoding a recombinant antigen of the present invention because a nucleic acid molecule of the present invention can include a portion of a full-length coding region, a full-length coding region, or multiple coding regions (either partial or full-length). The preferred size of a protein encoded by a nucleic acid molecule of the present invention depends on whether a full-length, fusion, multivalent, or functional portion of such a protein is desired.

[**0030**] Stringent hybridization conditions are determined based on defined physical properties of the target nucleic acid molecule to which a nucleic acid molecule is being hybridized, and can be defined mathematically. Stringent hybridization conditions are those experimental parameters that allow an individual skilled in the art to identify significant similarities between heterologous nucleic acid molecules, i.e., those conditions that allow the identification of nucleic acid molecules that are at least about 70% identical, or that share less than about 30% mismatch. These conditions are well known to those skilled in the art. See, for example, Sambrook, et al., 1989, ibid., and Meinkoth, et al., 1984, *Anal. Biochem.* 138, 267-284; Meinkoth, et al., is incorporated by reference herein in its entirety.

[**0031**] Furthermore, it is known in the art that there are commercially available computer programs for determining the degree of similarity between two nucleic acid sequences or amino acid sequences. These computer programs include various known methods to determine the percentage identity and the number and length of gaps between nucleic acid molecules and proteins. It is further known that the various available sequence analysis programs produce substantially similar results when the two compared molecules encode amino acid sequences that have greater than 30% amino acid identity. See Johnson et al., 1993 *J. Mol. Biol.* 233, 716-738, 1993, and Feng et al., 1985, *J. Mol. Evol.* 21, 112-125, 1985, each of which is incorporated by reference herein in its entirety. Preferred methods to determine the percent identity among amino acid sequences and also among nucleic acid sequences include analysis using one or more of the commercially available computer programs designed to compare and analyze nucleic acid or amino acid sequences. These computer programs include, but are in no way limited to, GCG™ (available from Genetics Computer Group, Madison, Wis.), DNAsis™ (available from Hitachi Software, San Bruno, Calif.) and MacVector™ (available from the Eastman Kodak Company, New Haven, Conn.). A particularly preferred method to determine the percent identity among amino acid sequences and also among nucleic acid sequences is to perform the analysis using the DNAsis™ computer program, using default parameters.

[**0032**] The present invention also includes mimetopes of recombinant antigens of the present invention. In accordance with the present invention, a "mimetope" refers to any compound that is able to mimic the ability of a recombinant antigen of the present invention to bind to an antibody. A mimetope can be a peptide that has been modified to decrease its susceptibility to degradation but that still retains antibody-binding activity. Other examples of mimetopes include, but are not limited to, carbohydrate-based compounds, lipid-based compounds, nucleic acid-based compounds, natural organic compounds, synthetically derived organic compounds, anti-idiotypic antibodies and/or catalytic antibodies, or fragments thereof. A mimetope can be obtained by, for example, screening libraries of synthetic compounds for compounds capable of binding to anti-infectious agent antibodies. A mimetope can also be obtained by, for example, rational drug design. In a rational drug design procedure, the three-dimensional structure of a compound of the present invention can be analyzed by, for example, nuclear magnetic resonance (NMR) or x-ray crystallography. The three-dimensional structure can then be used to predict structures of potential mimetopes by, for example, computer modeling. The predicted mimetope structures can then be produced by, for example, chemical synthesis, recombinant DNA technology, or by isolation from a natural source.

[**0033**] One embodiment of the present invention includes a recombinant vector that includes at least one isolated nucleic acid molecule of the present invention, inserted into any vector capable of delivering the nucleic acid molecule into a host cell. Such a vector contains heterologous nucleic acid sequences, that is nucleic acid sequences that are not naturally found adjacent to nucleic acid molecules of the present invention and that preferably are derived from a species other than the species from which the nucleic acid molecule(s) are derived. The vector can be either RNA or DNA, either prokaryotic or eukaryotic, and typically is a virus or a plasmid. Recombinant vectors can be used in the cloning, sequencing, and/or otherwise manipulating of antigen nucleic acid molecules of the present invention.

[**0034**] One type of recombinant vector, referred to herein as a recombinant molecule, comprises a nucleic acid molecule of the present invention operatively linked to an expression vector. The phrase operatively linked refers to insertion of a nucleic acid molecule into an expression vector in a manner such that the molecule is able to be expressed when transformed into a host cell. As used herein, an expression vector is a DNA or RNA vector that is capable of transforming a host cell and of effecting expression of a specified nucleic acid molecule. Preferably, the expression vector is also capable of replicating within the host cell. Expression vectors can be either prokaryotic or eukaryotic, and are typically viruses or plasmids. Expression vectors of the present invention include any vectors that function (i.e., direct gene expression) in recombinant cells of the present invention, including in bacterial, fungal, parasite, insect, other animal, and plant cells. Preferred expression vectors of the present invention can direct gene expression in bacterial, yeast, insect and mammalian cells, and more preferably in bacteria.

[**0035**] In particular, expression vectors of the present invention contain regulatory sequences such as transcription control sequences, translation control sequences, origins of replication, and other regulatory sequences that are compatible with the recombinant cell and that control the expression of nucleic acid molecules of the present invention. In particular, recombinant molecules of the present invention include transcription control sequences. Transcription control sequences are sequences which control the initiation, elongation, and termination of transcription. Particularly important transcription control sequences are those which control transcription initiation, such as promoter, enhancer, operator and repressor sequences. Suitable transcription control sequences include any transcription control sequence that can function in at least one of the recombinant cells of the present invention. A variety of such transcription control sequences are known to those skilled in the art. Preferred transcription control sequences include those which function in bacterial, yeast, insect or mammalian cells. More preferred transcription control sequences include those that function in bacteria, such as, but not limited to, tac, lac, trp, trc, oxy-pro, omp/lpp, rrnB, bacteriophage lambda (such as lambda PL and lambda PR and fusions that include such promoters), bacteriophage T7, T71ac, bacteriophage T3, bacteriophage SP6, bacteriophage SP01, and antibiotic resistance gene transcription control sequences.

[**0036**] Suitable and preferred nucleic acid molecules to include in recombinant vectors of the present invention are as disclosed herein. Preferred nucleic acid molecules to include in recombinant vectors, and particularly in recombinant molecules, include $nFCVCP_{2013}$, $nFCVCP_{1641}$, $nFPVVP2_{1752}$, $nFPVVP2C_{729}$, $nFPVpVP12_{61860}$, $nFPVpVP2_{1431}$, $nFHVgB_{2829}$, $nFHVgB_{750}$, $nFHVgC_{1602}$, $nFHVgC_{1401}$, $nFHVgC_{1401(opt)}$, $nFHVgD_{1122}$, $nFHVgD_{900}$, nFeLVp27$_{759}$, nFeLVp27$_{1857}$, nFeLVp27-gp70$_{1833}$, nCDVH$_{812}$, and nCDVF$_{1986}$. Particularly preferred recombinant molecules of the present invention include pλP$_R$His-nFCVCP$_{2013}$, pλP$_R$-nFCVCP$_{1641}$, pλP$_R$His-nFPVVP2$_{1752}$, pλP$_R$His-nFPVVP2C$_{729}$, pλP$_R$-nFPVVP2C$_{729}$, pλP$_R$His-nFPVpVP12$_{1860}$, pλP$_R$His-nFPVpVP2$_{1431}$, pλP$_R$-nFPVpVP2$_{1431}$, pλP$_R$His-nFHVgB$_{2829}$, pλP$_R$His-nFHVgB$_{750}$, pλP$_R$His-nFHVgC$_{1602}$, pλP$_R$His-nFHVgC$_{1401}$, pλP$_R$-nFHVgC$_{1401(\mathrm{opt})}$, pλP$_R$His-nFHVgD$_{1122}$, pλP$_R$His-nFHVgD$_{900}$, pλP$_R$-nFeLVp27$_{759}$, pλP$_R$His-nFeLVp27$_{1857}$, pλP$_R$-nFeLVp27-gp70$_{1833}$, pλP$_R$His-nCDVH$_{1812}$, and pλP$_R$His-nCDVF$_{1986}$, the production of which are described in the Examples section.

[**0037**] Recombinant molecules of the present invention may also (a) contain secretory signals (i.e., signal segment nucleic acid sequences) to enable an expressed antigen of the present invention to be secreted from the cell that produces the protein and/or (b) contain fusion sequences which lead to the expression of nucleic acid molecules of the present invention as fusion proteins. Examples of suitable signal segments include any signal segment capable of directing the secretion of a protein of the present invention. Suitable fusion segments for use with the present invention include, but are not limited to, segments that can: enhance a protein's stability, enhance attachment of a protein to a substrate, and/or assist purification of a isolated antigen of the present invention (e.g., by affinity chromatography). A suitable fusion segment can be a domain of any size that has the desired function (e.g., imparts increased stability, enhances attachment to a substrate, and/or simplifies purification of a protein). Fusion segments can be joined to amino and/or carboxyl termini of the of the protein and can be susceptible to cleavage in order to enable straightforward recovery of a isolated antigen of the present invention. Fusion proteins are preferably produced by culturing a recombinant cell transformed with a fusion nucleic acid molecule that encodes a protein including the fusion segment attached to either the carboxyl and/or amino terminal end of a domain. Preferred fusion segments include a metal binding domain (e.g., a poly-histidine segment); an immunoglobulin binding domain (e.g., Protein A; Protein G; T cell; B cell; Fc receptor or complement protein antibody-binding domains); a sugar binding domain (e.g., a maltose binding domain); and/or a "tag" domain (e.g., at least a portion of O-galactosidase, a strep tag peptide, other domains that can be purified using compounds that bind to the domain, such as monoclonal antibodies). A more preferred fusion segment is a metal binding domain. Examples of particularly preferred fusion proteins of the present invention include PHis-PFCVCP$_{671}$, PHis-PFCVCP$_{547}$, PHis-PFPVVP2$_{584}$, PHis-PFPVVP2C$_{243}$, PHis-PFPVpVP12620, PHis-PFPVpVP2$_{477}$, PHis-PFHVgB$_{943}$, PHis-PFHVgB$_{250}$, PHis-PFHVgC$_{34}$, PHis-PFHVgC$_{467}$, PHis-PFHVgC$_{467(\mathrm{opt})}$, PHis-PFHVgD$_{374}$, PHis-PFHVgD$_{300}$, PHis-PFeLVp27$_{253}$, PHis-PFeLVp27$_{619}$, PHis-PFeLVp27-gp70$_{611}$, PHis-PCDVH$_{604}$, and PHis-PCDVF$_{662}$; methods to produce such fusion proteins are disclosed in the Examples. The present invention also includes post-translational modification of a recombinant antigen to introduce a ligand. Examples of ligands include biotin, biotin-like compounds, avidin, avidin-like compounds, metal binding compounds, sugar binding compounds, immunoglobulin binding domains, and other tag domains.

[**0038**] Another embodiment of the present invention includes a recombinant cell comprising a host cell transformed with one or more nucleic acid molecules or recombinant molecules of the present invention. Transformation of a nucleic acid molecule into a cell can be accomplished by any method by which a nucleic acid molecule can be inserted into the cell. Transformation techniques include, but are not limited to, transfection, electroporation, microinjection, lipofection, adsorption, and protoplast fusion. Transformed nucleic acid molecules of the present invention can remain extrachromosomal or can integrate into one or more sites within a chromosome of the transformed (i.e., recombinant) cell in such a manner that their ability to be expressed is retained. Suitable nucleic acid molecules with which to transform a cell include any nucleic acid molecules disclosed herein that encode a recombinant antigen. Particularly preferred nucleic acid molecules with which to transform a cell include nFCVCP$_{2013}$, nFCVCP$_{1641}$, nFPVVP2$_{1752}$, nFPVVP2C$_{729}$, nFPVpVP12$_{1860}$, nFPVpVP2$_{1431}$, nFHVgB$_{2829}$, nFHVgB$_{750}$, nFHVgC$_{1602}$, nFHVgC$_{1401}$, nFHVgC$_{1401(\mathrm{opt})}$, nFHVgD$_{1122}$, nFHVgD$_{900}$, nFeLVp27$_{759}$, nFeLVp27$_{857}$, nFeLVp27-gp70$_{1833}$, nCDVH$_{1812}$, and nCDVF$_{1986}$.

[**0039**] Suitable host cells to transform include any cell that can be transformed with a nucleic acid molecule of the present invention. Host cells can be either untransformed cells or cells that are already transformed with at least one nucleic acid molecule. Host cells of the present invention can be any cell capable of producing at least one protein of the present invention, and include bacterial, fungal (including yeast), parasite (including helminth, protozoa and ectoparasite), other insect, other animal and plant cells. Preferred host cells include bacterial, mycobacterial, yeast, insect and mammalian cells. More preferred host cells include Salmonella, Escherichia, Bacillus, Listeria, Saccharomyces, Pichia, Spodoptera, Mycobacteria, and Trichoplusia cells. Particularly preferred host cells are *Escherichia coli.*

[**0040**] A recombinant cell is preferably produced by transforming a host cell with a recombinant molecule encoding a recombinant antigen of the present invention operatively linked to an expression vector containing a transcription control sequence. Particularly preferred recombinant molecules include pλP$_R$His-nFCVCP$_{2013}$, pλP$_R$-nFCVCP$_{1641}$, pλP$_R$His-nFPVVP2$_{1752}$, pλP$_R$His-nFPVVP2C$_{729}$, pλP$_R$-nFPVVP^{2}C$_{729}$, pλP$_R$His-nFPVpVP12$_{1860}$, pλP$_R$His-nFPVpVP2$_{1431}$, pλP$_R$-nFPVpVP2$_{1431}$, pλP$_R$His-nFHVgB$_{2829}$, pλP$_R$His-nFHVgB$_{750}$, pλP$_R$His-nFHVgC$_{1602}$, pλP$_R$His-nFHVgC$_{1401}$, pλP$_R$-nFHVgC$_{1401(\mathrm{opt})}$, pλP$_R$His-nFHVgD$_{1122}$, pλP$_R$His-nFHVgD$_{900}$, pλP$_R$-nFeLVp27$_{759}$, pλP$_R$His-nFeLVp27$_{1857}$, pλP$_R$-nFeLVp27-gp70$_{1833}$, pλP$_R$His-nCDVH$_{1812}$, and pλP$_R$His-nCDVF$_{1986}$. Particularly preferred recombinant cells include *E. coli*:pλP$_R$His-nFCVCP$_{2013}$, *E. coli*:pλP$_R$-nFCVCP$_{1641}$, *E. coli*:pλP$_R$His-nFPVVP21$_{752}$, *E. coli*:pλP$_R$His-nFPVVP2C$_{729}$, *E. coli*:pλP$_R$-nFPVVP2C$_{729}$, *E. coli*:pλP$_R$His-nFPVpVP121860, *E. coli*:pλP$_R$His-nFPVpVP2$_{1431}$, *E. coli*:pλP$_R$-nFPVpVP2$_{1431}$, *E. coli*:pλP$_R$His-nFHVgB$_{2829}$, *E. coli*:pλP$_R$His-nFHVgB$_{750}$, *E. coli*:pλP$_R$His-nFHVgC$_{1602}$, *E. coli*:pλP$_R$His-nFHVgC$_{1401}$, *E. coli*:pλP$_R$-nFHVgC$_{1401(\mathrm{opt})}$, *E. coli*:pλP$_R$His-nFHVgD$_{1122}$, *E. coli*:pλP$_R$His-nFHVgD$_{900}$, *E. coli*:pλP$_R$-nFeLVp27$_{759}$, *E. coli*:pλP$_R$His-nFeLVp27$_{1857}$, *E. coli*:pλP$_R$-nFeLVp27-gp70$_{1833}$, *E. coli*:pλP$_R$His-nCDVH$_{1812}$, and *E.*

coli:pλP_RHis-nCDVF$_{1986}$. Details regarding the production of these recombinant cells are disclosed herein.

[0041] Recombinant DNA technologies can be used to improve expression of transformed nucleic acid molecules by manipulating, for example, the number of copies of the nucleic acid molecules within a host cell, the efficiency with which those nucleic acid molecules are transcribed, the efficiency with which the resultant transcripts are translated, and the efficiency of post-translational modifications. Recombinant techniques useful for increasing the expression of nucleic acid molecules of the present invention include, but are not limited to, operatively linking nucleic acid molecules to high-copy number plasmids, integration of the nucleic acid molecules into one or more host cell chromosomes, addition of vector stability sequences to plasmids, substitutions or modifications of transcription control signals (e.g., promoters, operators, enhancers), substitutions or modifications of translational control signals (e.g., ribosome binding sites, Shine-Dalgarno sequences), modification of nucleic acid molecules of the present invention to correspond to the codon usage of the host cell, deletion of sequences that destabilize transcripts, and use of control signals that temporally separate recombinant cell growth from recombinant enzyme production during fermentation. The activity of an expressed recombinant antigen of the present invention may be improved by fragmenting, modifying, or derivatizing a nucleic acid molecule encoding such an antigen.

[0042] Recombinant antigens of the present inventions can be produced in a variety of ways known to those skilled in the art. In one embodiment, a recombinant antigen of the present invention is produced by culturing a cell capable of expressing the antigen under conditions effective to produce the antigen, and recovering the antigen. A preferred cell to culture is a recombinant cell of the present invention. Effective culture conditions include, but are not limited to, effective media, bioreactor, temperature, pH and oxygen conditions that permit protein production. An effective, medium refers to any medium in which a cell is cultured to produce a recombinant antigen of the present invention. Such medium typically comprises an aqueous medium having assimilable carbon, nitrogen and phosphate sources, and appropriate salts, minerals, metals and other nutrients, such as vitamins. Recombinant cells of the present invention can be cultured in conventional fermentation bioreactors, shake flasks, test tubes, microtiter dishes, and petri plates. Culturing can be carried out at a temperature, pH and oxygen content appropriate for a recombinant cell. Such culturing conditions are within the expertise of one of ordinary skill in the art. Examples of suitable conditions are included in the Examples section.

[0043] Depending on the vector and host system used for production, the expressed recombinant antigens may either remain within the recombinant cell; be secreted into the fermentation medium; be secreted into a space between two cellular membranes, such as the periplasmic space in *E. coli*; or be retained on the outer surface of a cell or viral membrane.

[0044] The phrase "recovering the antigen", as well as similar phrases, refers to collecting the whole fermentation medium containing the recombinant product and need not imply additional steps of separation or purification. Proteins of the present invention can be purified using a variety of standard protein purification techniques, such as, but not limited to, affinity chromatography, ion exchange chromatography, filtration, electrophoresis, hydrophobic interaction chromatography, gel filtration chromatography, reverse phase chromatography, Concanavalin A chromatography, chromatofocusing and differential solubilization. Recombinant antigens of the present invention are preferably retrieved in "substantially pure" form. As used herein, "substantially pure" refers to a purity that allows for the effective use of the protein as a detection reagent. Preferably, such a recombinant antigen reagent does not cause false positive reactions. In a preferred embodiment, recombinant antigens of the present invention are at least about 60% pure, preferably at least about 65% pure, more preferably at least about 70% pure, more preferably at least about 75% pure, more preferably at least about 80% pure, more preferably at least about 85% pure, more preferably at least about 90% pure, and more preferably at least about 95% pure. In one embodiment, a recombinant antigen of the present invention is at least about 98% to 100% pure.

[0045] One embodiment of the present invention is a method to determine the immune status of an animal to a desired infectious agent by detecting antibodies in that animal that selectively bind to that infectious agent. The method includes the steps of: (a) contacting a biological specimen of the animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent, under conditions suitable for formation of a complex between the recombinant antigen and the antibody; and (b) detecting the presence or absence of the complex, wherein presence or absence of a complex is indicative of the immune status of the animal. Presence of a complex indicates that an animal is protected from, or is not susceptible to, infection by that infectious agent, and as such, that animal need not be vaccinated. Absence of a complex suggests that an animal may not be protected from, or may be susceptible to, infection by that infectious agent, and as such, it is desirable to vaccinate that animal.

[0046] Antibodies to be detected can be maternal antibodies transferred to the offspring or can be generated (i.e., produced) in response to a natural infection by an infectious agent or vaccination. Vaccination can be accomplished in a variety of ways known to those skilled in the art including, but not limited to, administering the infectious agent itself or any immunogenic form thereof, such as, but not limited to, a modified live infectious agent, an inactivated, disrupted, fractionated or attenuated infectious agent, a native or recombinant antigen, or a nucleic acid molecule that invokes an immune response against the infectious agent. Antibodies to be detected can be of any class, i.e., immunoglobulin A (IgA), immunoglobulin D (IgD), immunoglobulin E (IgE), immunoglobulin G (IgG), or immunoglobulin M (IgM) antibodies IgE, IgG, or IgM antibodies. Preferred antibodies to detect are IgA, IgG and IgM antibodies.

[0047] Any animal that possesses maternal antibodies or generates antibodies in response to an infectious agent or corresponding vaccine can be tested in accordance with the present invention. In one embodiment, a preferred animal to test is an animal that was vaccinated (i.e., administered a vaccine) at least about six months, one year, two years, or three years prior to testing. In another embodiment, a preferred animal to test is an animal for whom infection or vaccination status is unknown. Suitable animals for whom to determine an immune status include, but are not limited to, cats (i.e., felids), dogs (i.e., canids), horses (i.e., equids), humans and other primates, ferrets and other Mustelids, cattle, sheep, swine, and rodents, as well as other companion animals (i.e., pets), food animals, work animals, or zoo animals. Preferred animals to test include cats, dogs, horses and other companion animals, with cats, dogs and horses being even more preferred. As used herein, a cat refers to any member of the cat family (i.e., Felidae), including domestic cats, wild cats and zoo cats. Examples of cats include, but are not limited to, domestic cats, lions, tigers, leopards, panthers, cougars, bobcats, lynx, jaguars, cheetahs, and servals. A preferred cat to test is a domestic cat. As used herein, a dog refers to any member of the family Canidae, including, but not limited to, domestic dogs, wild dogs, foxes, wolves, jackals, and coyotes and other members of the family Canidae. As used herein, a horse refers to an equid. An equid is a hoofed mammal and includes, but is not limited to, domestic horses and wild horses, such as, horses, asses, donkeys, and zebras. Preferred horses to test include domestic horses, including race horses.

[0048] A biological specimen refers to any sample that can be collected (i.e. obtained) from an animal in which antibodies may be found. A suitable biological specimen includes, but is not limited to, a bodily fluid composition or a cellular composition. Examples of a bodily fluid include, but are not limited to, blood, serum, plasma, saliva, urine, tears, aqueous humor, cerebrospinal fluid, lymph, nasal secretion, tracheobronchial aspirate, milk, colostrum, intestinal secretion, and feces, with blood, serum, plasma, saliva, urine, tears, milk and colostrum being preferred and blood, serum or plasma being even more preferred.

[0049] As used herein, the term contacting refers to combining or mixing, in this case, a biological specimen and a recombinant antigen of the present invention. Formation of a complex, or immunocomplex, between a recombinant antigen and any antibody selective for an infectious agent (i.e., an anti-infectious agent antibody) present in the biological specimen refers to the ability of the recombinant antigen to selectively bind to the antibody in order to form a stable complex that can be detected. As used herein, the term selectively binds to an antibody or specific for an antibody refers to the ability of a recombinant antigen of the present invention to preferentially bind to an antibody that indicates that the animal is protected from disease, without being able to substantially bind to other, unrelated, antibodies. Binding between the recombinant antigen and anti-infectious agent antibody is effected under conditions suitable to form a complex; such conditions (e.g., appropriate concentrations, buffers, temperatures, reaction times) as well as methods to optimize such conditions are known to those skilled in the art, and examples are disclosed herein. Examples of complex formation conditions are also disclosed in, for example, in Sambrook et al., ibid., and Harlow, et al., 1988, *Antibodies, a Laboratory Manual*, Cold Spring Harbor Labs Press; Harlow et al., ibid., in incorporated herein by reference in its entirety.

[0050] As used herein, the phrase detecting the presence or absence of a complex refers to determining if any complex is formed, i.e., assaying for the presence (i.e., existence) or absence (i.e., non-existence) of a complex. If complexes are formed, the amount of complexes formed can, but need not be, determined. Complex formation, or selective binding, between a recombinant antigen and anti-infectious agent antibody can be measured (i.e., detected, determined) using a variety of methods standard in the art; see, for example, Sambrook, et al., ibid., Harlow, et al., ibid., and examples herein.

[0051] A complex can be measured in a variety of ways including, but not limited to, one of the following assays: an enzyme-linked immunoassay, a radioimmunoassay, a fluorescence immunoassay, a luminescence assay (such as a chemi-luminescent assay or a bio-luminescent assay), a phosphorescence assay, an immunoblot assay (e.g., a Western blot), an immunodot assay, an immunoprecipitation assay, a lateral flow assay, a flow-through assay, an agglutination assay, a particulate-based assay (e.g., using particulates such as, but not limited to, magnetic particles or plastic polymers, such as latex or polystyrene beads), and an electronic sensory assay (e.g., using an electronic chip). In one embodiment, it is preferred not to use a virus neutralization assay, a hemagglutination assay, or a complement fixation assay. Such assays are well known to those skilled in the art; see for, example, Harlow, et al., ibid. Assays can be used to give qualitative or quantitative results depending on how they are used.

[0052] Some assays, such as agglutination, particulate separation, and immunoprecipitation, can be observed visually (e.g., either by eye or by a machines, such as a densitometer or spectrophotometer) without the need for a detectable marker. In other assays, conjugation (i.e., attachment, joining) of a detectable marker to a recombinant antigen of the present invention or to an antibody-binding partner of the present invention that selectively binds to the antibody being detected aids in measuring complex formation. Conjugation is conducted in such a manner that the ability of a recombinant antigen or antibody-binding partner to selectively bind to anti-infectious agent antibodies is not compromised. Conjugation can be accomplished, for example, by joining a detectable marker to a recombinant antigen or antibody-binding partner or by constructing a genetic chimera that encodes a recombinant antigen fused to a detectable marker or an antibody-binding partner fused to a detectable marker.

[0053] Examples of detectable markers include, but are not limited to, an enzyme, a radioactive label, a fluorescent label, a luminescent label (e.g., bioluminescent label or a chemi-luminescent label), a chromophoric (e.g., calorimetric) label, a metal sol label, a metal-binding label, a physical label, an electronic label, or a ligand. A ligand refers to a molecule that binds selectively to another molecule. Preferred detectable markers include, but are not limited to, a phosphatase (e.g., alkaline phosphatase), a peroxidase (e.g., horseradish peroxidase), a beta-galactosidase, a luciferase, fluorescein, a radioisotope, a bead (e.g., a color bead, a magnetic bead), colloidal gold, biotin, avidin, and biotin-related compounds or avidin-related compounds (e.g., streptavidin or ImmunoPure® NeutrAvidin).

[0054] An antibody-binding partner of the present invention is any compound that can bind to an anti-infectious agent antibody of the present invention. Preferably an antibody-binding partner binds to the constant region of such an antibody, such as to the Fc region of an IgA, IgD, IgE, IgG, or IgM antibody. Examples of such antibody-binding partners include anti-isotype antibodies (e.g., anti-IgA antibodies, anti-IgD antibodies, anti-IgE antibodies, anti-IgG antibodies, and anti-IgM antibodies) that selectively bind to the constant region of antibodies of the animal being tested, antibody Fc receptors (e.g., IgA receptors, IgD receptors, IgE receptors, IgG receptors, IgM receptors), antibody-binding bacterial surface proteins (e.g., Protein A or Protein G, or recombinant forms of these proteins), antibody-binding cells (e.g., a B cell, T cell, or a macrophage), other antibody-binding eukaryotic cell surface proteins, and antibody-binding complement proteins, as well as any portion of these proteins that selectively bind to an anti-infectious agent antibody. Preferred antibody-binding partners include Protein A, Protein G, an anti-IgG antibody, an anti-IgM antibody, an anti-IgA antibody, an anti-IgE antibody, an Fc_γ receptor molecule, an Fc_ϵ receptor molecule, an Fc_μ receptor molecule, and an Fc receptor molecule as well as any portion of any of such proteins that selectively bind to the constant region of an anti-infectious agent antibody. It is within the scope of the present invention that a complex between an anti-infectious agent antibody and a recombinant antigen of the present invention can be determined using one or more layers and/or types of secondary antibodies or other binding compounds. For example, an unlabeled secondary antibody can be bound to an anti-infectious agent antibody and the unlabeled secondary antibody can then be bound by a labeled tertiary antibody.

[0055] In one embodiment of the present invention, the presence or absence of a complex is detected by applying a detection reagent that binds to the complex, if present, to obtain a test signal. The term applying refers to adding a detection reagent to the biological specimen after the recombinant antigen is combined with the specimen under conditions to form a complex with any anti-infectious agent antibody in the specimen. The detection reagent binds to any complex present and such binding results in a test signal, i.e., an event that can be detected. If anti-infectious agent antibody is present in the biological specimen, a test signal will ensue. If there is no anti-infectious agent antibody present, no test signal will occur. Preferably, the detection reagent comprises an antibody-binding partner of the present invention conjugated to a detectable marker of the present invention.

[0056] In one embodiment a complex can be formed and measured in solution. In another embodiment, a recombinant antigen of the present invention or an antibody-binding partner of the present invention can be immobilized on (e.g., coated onto) a substrate. Preferably, a recombinant antigen of the present invention is immobilized on a substrate. Immobilization techniques are known to those skilled in the art. Suitable substrates on which to immobilize a recombinant antigen or antibody-binding partner of the present invention or a composition include, but are not limited to, plastic, glass, gel, celluloid, paper, fabric, electronic chip, and particulate materials such as latex, polystyrene, nylon, nitrocellulose, agarose, cotton, PVDF (poly-vinylidene-fluoride), and magnetic resin. Suitable substrates include, but are not limited to, a well (e.g., microtiter dish well), a plate, a dipstick, a strip, a bead, a sponge, a lateral flow apparatus, a membrane, a filter, a tube, a dish, a celluloid-type matrix, a magnetic particle, an electronic sensory device (e.g., an electronic sensory chip), and other particulates. In one embodiment, a substrate, such as a particulate, can include a detectable marker.

[0057] In a preferred embodiment, a method to determine the immune status of an animal can be conducted within about one day, more preferably within about two hours, more preferably within about one hour, and even more preferably within a time period of between about one minute and about fifteen minutes.

[0058] A method of the present invention to detect immune status can be qualitative, quantitative, or semi-quantitative. In one embodiment, the method includes a step of comparing the intensity of a test signal of the present invention with a reference signal obtained by contacting a reference reagent with the detection reagent to determine the amount of anti-infectious agent antibody in the biological specimen. In one embodiment, the reference signal represents a threshold, such that if the test signal is more intense than the reference signal the animal from which the biological specimen is collected is deemed to be protected from infection by the infectious agent. In one embodiment the reference reagent is immobilized on a substrate, preferably on the same substrate as is a recombinant antigen. Suitable reference reagents include antibodies isolated from the same species of animal as is being tested. Preferred reference reagents to use in immune status assays for cats, dogs and horses, include feline antibodies, canine antibodies and equine antibodies, respectively.

[0059] One embodiment of a method of the present invention to determine the immune status of an animal is to determine the immune status with respect to more than one infectious agent. It is contemplated that any number of recombinant antigens can be used in such a determination. In one embodiment, a biological specimen from an animal is contacted with a recombinant calicivirus antigen, a recombinant herpesvirus antigen and a recombinant parvovirus antigen under conditions such that the immune status of the animal to calicivirus, herpesvirus and parvovirus infection is determined.

[0060] Another embodiment of the present invention includes the use of an immune status assay to determine whether a human should be treated for rabies virus infection. In such an embodiment, a biological specimen is collected from an animal suspected of having exposed the human to rabies virus infection and contacted with a recombinant rabies virus antigen in accordance with the present invention. Presence of a complex indicates that the human should be treated for rabies infection.

[0061] A preferred method to detect anti-infectious agent antibodies is an immunosorbent assay. In one embodiment, a recombinant antigen of the present invention is immobilized on a substrate, such as a microtiter dish well or a dipstick. A biological specimen collected from an animal is applied to the substrate and incubated under conditions sufficient to allow for complex formation. Excess fluid, if any, is removed and a detection reagent that can selectively bind to the anti-infectious agent antibody is added to the substrate and incubated to allow formation of a complex between the detection reagent and the recombinant antigen:anti-infectious agent antibody complex. Excess detection reagent is removed, a developing agent is added if required, and the substrate is submitted to a detection device for analysis. Alternatively, an antibody-binding partner as described above is immobilized on a substrate, and a biological specimen is incubated with the antibody-binding partner to form a complex. Complex detection can then be accomplished by applying a detectable marker-conjugated recombinant antigen of the present invention to the complex.

[0062] Another preferred method to determine the immune status of an animal is a lateral flow assay, examples of which are disclosed in U.S. Pat. No. 5,424,193, issued Jun. 13, 1995, by Pronovost et al.; U.S. Pat. No. 5,415,994, issued May 16, 1995, by Imrich et al; WO 94/29696, published Dec. 22, 1994, by Miller et al.; and WO 94/01775, published Jan. 20, 1994, by Pawlak et al.; each of these patent publications is incorporated by reference herein in its entirety. Another preferred method to determine the immune status of an animal is a flow-through assay, examples of which are disclosed in U.S. Pat. No. 4,632,901, issued Dec. 30, 1986 by Valkirs et al., and U.S. Pat. No. 4,727,019, issued Feb. 23, 1988, by Valkirs et al; U.S. Pat. No. 4,632,901, ibid., and U.S. Pat. No. 4,727,019, ibid., are both incorporated by reference herein in their entireties.

[0063] Another embodiment of the present invention is a method to determine whether to vaccinate an animal. Such a method includes the steps of: (a) contacting a biological specimen of the animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent, under conditions suitable for formation of a complex between the recombinant antigen and the antibody; and (b) detecting the presence or absence of the complex. Presence of such a complex indicates that the animal need not be vaccinated, whereas absence of such a complex indicates that the animal should be vaccinated. Detection of such a complex can be accomplished in a manner similar to that disclosed herein for determining the immune status of an animal.

[0064] Yet another embodiment of the present invention is an assay, or kit, to determine the immune status of an anima and/or to determine whether to vaccinate an animal. Such an assay includes (a) a recombinant infectious agent antigen that is specific for detecting an antibody selective for that infectious agent; and (b) a means to detect an antibody that selectively binds to the recombinant antigen. In one embodiment, the means includes a detection reagent of the present invention. An assay of the present invention can also, but need not, include (a) a solid support comprising a test area and a reference area; and (b) a reference reagent. Preferably the test area includes one or more recombinant antigens of the present invention and the reference area comprises one or more reference reagents of the present invention. An assay of the present invention can also, but need not, include a control area for assay validation. Preferably, a recombinant infectious agent antigen of the present invention is immobilized on a substrate such as those disclosed herein. Particularly preferred assays are ELISAs, lateral flow assays, and flow-through assays.

[0065] The following examples are provided for the purposes of illustration and are not intended to limit the scope of the present invention.

EXAMPLES

[0066] It is to be noted that the Examples include a number of molecular biology, microbiology, immunology and biochemistry techniques considered to be known to those skilled in the art. Disclosure of such techniques can be found, for example, in Sambrook et al., ibid., Harlow et al., ibid., and related references.

Example 1

[0067] This Example demonstrates that use of a whole virus preparation to determine the immune status of an animal leads to false positives and, as such, is an unacceptable reagent.

[0068] A. Purification of Feline Calicivirus and Feline Rhinotracheitis Virus

[0069] Feline rhinotracheitis virus (also known as feline herpesvirus, or FHV) and feline calicivirus (FCV) were cultured in Crandall Reese Feline Kidney (CRFK) cells in DMEM high glucose (available from Gibco BRL, Gaithersburg, Md.) with 2% fetal bovine serum (FBS) for FHV and no fetal bovine serum for FCV. Aliquots of titered ($TCID_{50}$) virus-containing tissue culture supernatant were collected and stored at −70° C. until use.

[0070] FCV- or FHV-containing supernatant aliquots were each thawed quickly in a 37° C. water bath and clarified by centrifugation at 1000×g for 10 min at 4° C. Five volumes of a 60% (w/v) Iodixanol solution (available from OptiPrepä, Nycomed, Oslo, Norway) were mixed with one volume of 0.8% NaCl, 60 mM HEPES, pH 7.4 to produce a 50% Iodixanol solution. Three ml of the lodixanol-containing supernatant aliquot were transferred to 16×102 mm Beckman Ultra Clear centrifuge tubes (available from Beckman, Fullerton, Calif.). Three ml of the 50% Iodixanol solution were underlayed under the supernatant aliquot. The virus was sedimented by centrifugation at 100,000×g for 1 hr at 4° C. using a Beckman SW28 fixed-angle rotor (available from Beckman). The virus formed a sharp band on top of the lodixanol cushion. Three ml of the supernatant were removed. The residual content of the tube was mixed to produce a concentrated virus suspension in approximately 25% lodixanol. The suspension was transferred to 16×76 mm Beckman Quickseal tubes (available from Beckman). The residual air space in the heat seal tubes was filled with the 0.8% NaCl, 60 mM HEPES buffer and the tubes heat sealed. The tubes were centrifuged at 350,000×g for 1 to 3 hr at 4° C. using a Beckman VTi-65.1 rotor (available from Beckman). The rotor was allowed to decelerate from 21×g (500 rpm) without the brake. The seals on the tubes were ruptured, and most of the supernatant was removed with a long Pasteur pipette. Approximately 1 ml of fluid was left in each tube. This material was transferred to a common tube and the original tube was rinsed with 0.5 ml of 0.8% NaCl/60 mM HEPES buffer and that material was added to the common tube. Total protein was determined by the BioRad Protein Assay (available from BioRad, Richmond, Calif.). Aliquots of virus were stored at −70° C. Preparation purity was determined by ELISA. FCV purified in this manner is referred to as an Optiprep-purified FCV preparation, or Optiprep-purified FCV. FHV purified in this manner is referred to as an Optiprep-purified FHV preparation, or Optiprep-purified FHV.

[0071] B. Purification of Feline Panleukopenia Virus

[0072] Feline panleukopenia virus (FPV) was cultured in Crandall Reese Feline Kidney (CRFK) cells in DMEM high glucose with 2% fetal bovine serum. Aliquots of titered ($TCID_{50}$) virus-containing tissue culture supernatant were collected and stored at −70° C. until use.

[0073] A FPV-containing supernatant aliquot was clarified by centrifugation at 7000×g for 15 min at 4° C. The pellet was discarded and virus was precipitated from the supernatant by the addition of solid polyethylene glycol (PEG) 3350 to 0.75 M PEG, and 0.2 M sodium chloride. The mixture was incubated 30 min on ice and then centrifuged at 7000×g for 30 min at 4° C. The pellet was resuspended in 0.2 M boric acid buffer (pH 7.4) with 0.5M NaCl. The material was centrifuged at 450×g for 5 min to remove insoluble matter. The virus was banded in an isopyknic cesium chloride (CsCl) gradient (1.40 g/ml) by equilibrium centrifugation at 150,000×g for 20 hr at 4° C. (40,000 rpm in Beckman SW65 Ti rotor). Total protein was determined by the BioRad Protein Assay. Aliquots of virus were stored at −70° C. Preparation purity was determined by ELISA. FPV purified in this manner is referred to as a CsCl-purified FPV preparation, or CsCl-purified FPV.

[0074] C. Testing of a Whole FCV Preparation as an Immune Status Reagent

[0075] A Optiprep-purified FCV preparation, produced as described in Example 1A, as well as a preparation prepared in the same manner but in which CRFK cells were not infected with FCV (i.e., an Optiprep-purified non-infected cell, or NIC, preparation) was each tested for its ability to react with serum from FCV-vaccinated (positive) cats or barrier control (negative) cats by ELISA.

[0076] The ELISA was conducted as follows. The Optiprep-purified FCV and NIC preparations were each diluted according to protein concentration as indicated in Table 1 into 50 mM carbonate/bicarbonate buffer (pH 9.6). After dilution, plates were coated with a 100-μL aliquot of each dilution in wells in a PolySorp strip (Nunc, available from VWR Scientific, West Chester, Pa.). Each strip was placed in a strip holder plate and incubated overnight at 4° C. The coated wells were washed four times with PBST (10 mM PBS, containing 8.5 g NaCl, 0.20 g KH_2PO_4, and 1.16 g Na_2HPO_4 in 1L water, at pH=7.2, 0.05% Tween-20 ($C_{58}H_{114}O_{26}$; FW=1227, available from Fisher Scientific, Pittsburgh, Pa.), using an automatic plate washer (available from Bio-tek Instruments, Inc., Winooski, Vt.). After washing, a 200-μL aliquot of StabilCoat (available from SurModics, Eden Prairie, Minn.) was added to each well and the strips were incubated for one hour at 22° C. The wells were then washed four times with PBST using an automatic plate washer. Vaccinated (positive) or barrier (negative) cat serum was diluted 1:50 prior to addition to the wells with diluent A (PBST, 4% FBS, 0.5% ProClin 300 (available from Supelco, Bellefonte, Pa.). A 100-μL aliquot of the appropriate diluted serum was then added to each of the appropriate wells, and the plate was incubated for two hours at 22° C., followed by four washes with PBST using an automatic plate washer. Goat anti-cat IgG (H & L)-HRP (available from Kirkegaard & Perry Laboratories, Gaithersburg, Md.) was diluted in diluent A to 500 ng/ml, and a 100-μL aliquot was then added to each well. The plates were incubated for one hour at 22° C., followed by four washes with PBST using an automatic plate washer. A 100-μL aliquot of two-component substrate (TMB Peroxidase Substrate System, available from Kirkegaard & Perry Laboratories) was added to each of wells, which were then incubated at 22° C. for 5 min. Reactions were stopped by adding 100 μL of 1 M H_3PO_4 to each of the wells, at which time an automatic plate reader was used to determine O.D at 450 nm (using, for example, Molecular Devices SpectraMax 250, available from Molecular Devices, Sunnyvale, Calif.). ELISA results are shown in Table 1.

TABLE 1

ELISA using Optiprep-purified FCV or NIC to test serum collected from FCV-vaccinated (positive) or barrier (negative) cats

protein (ng/ml)	positive (FCV)	negative (FCV)	positive (NIC)	negative (NIC)
20000	4.15	0.61		
10000	4.15	0.70	3.368	0.616
5000	4.15	0.88	3.231	0.506
2500	4.15	0.84	2.901	0.396
1250	4.15	0.86	2.485	0.362
625	4.15	0.74	2.035	0.303
313	4.04	0.66	1.586	0.264
156	4.00	0.62	1.204	0.244
78	3.72	0.52	0.782	0.216
39	3.22	0.45	0.721	0.165
20	2.68	0.36	0.629	0.134
10	2.34	0.36	0.598	0.124
5	2.16	0.31	0.653	0.13

[0077] These data indicate that although an Optiprep-purified FCV preparation can detect antibodies in FCV-vaccinated cats, so does an Optiprep-purified NIC preparation (i.e., a preparation produced from uninfected cells using a similar procedure). As such, whole FCV is an unacceptable reagent for the determination of the immune status of a cat due to the possibility of a high percentage of false positive reactions due to the presence of cellular proteins that react with serum from vaccinated cats.

[0078] D. Testing of a Whole FHV Preparation as an Immune Status Reagent

[0079] A Optiprep-purified FHV preparation, produced as described in Example 1A, as well as a preparation prepared in the same manner but in which CRFK cells were not infected with FHV (i.e., an Optiprep-purified non-infected cell, or NIC, preparation) was each tested for its ability to react with serum from FHV-vaccinated (positive) cats or barrier control (negative) cats by ELISA.

[0080] The ELISA was conducted as described in Example 1C except that an Optiprep-purified FHV preparation was used instead of an Optiprep-purified FCV preparation, serum from FHV-vaccinated cats was used, and preparation dilutions were conducted as indicated in Table 2. Results are shown in Table 2.

TABLE 2

ELISA using Optiprep-purified FHV or NIC to test serum collected from FHV-vaccinated (positive) or barrier (negative) cats

protein (ng/ml)	positive (FHV)	negative (FHV)	positive (NIC)	negative (NIC)
20000	4.13	0.02		
10000	4.13	0.02	3.368	0.616
5000	4.15	0.00	3.231	0.506
2500	4.14	0.01	2.901	0.396
1250	4.01	0.13	2.485	0.362
625	3.73	0.37	2.035	0.303
313	3.47	0.46	1.586	0.264
156	2.95	0.40	1.204	0.244
78	2.25	0.47	0.782	0.216
39	1.68	0.38	0.721	0.165
20	1.40	0.50	0.629	0.134
10	0.80	0.26	0.598	0.124
5	0.72	0.17	0.653	0.13

[0081] These data indicate that although an Optiprep-purified FHV preparation can detect antibodies in FHV-vaccinated cats, so does an Optiprep-purified NIC preparation (i.e., a preparation produced from uninfected cells using a similar procedure). As such, whole FHV is an unacceptable reagent for the determination of the immune status of a cat due to the possibility of a high percentage of false positive reactions due to the presence of cellular proteins that react with serum from vaccinated cats.

[0082] E. Testing of a Whole FPV Preparation as an Immune Status Reagent

[0083] A CsCl-purified FPV preparation, produced as described in Example 1B, as well as a preparation prepared in the same manner but in which CRFK cells were not infected with FPV (i.e., a CsCl-purified non-infected cell, or NIC, preparation) was each tested for its ability to react with serum from FPV-vaccinated (positive) cats or barrier control (negative) cats by ELISA.

[0084] The ELISA was conducted as described in Example 1C except that a CsCl-purified FPV preparation was used instead of an Optiprep-purified FCV preparation, serum from FPV-vaccinated cats was used, and preparation dilutions were conducted as indicated in Table 3. Results are shown in Table 3.

TABLE 3

ELISA using CsCl-purified FPV or NIC to test serum collected from FPV-vaccinated (positive) or barrier (negative) cats

protein (ng/ml)	positive (FPV)	negative (FPV)	positive (NIC)	negative (NIC)
10000	4.082	0.468	3.368	0.616
5000	4.031	0.474	3.231	0.506
2500	3.947	0.492	2.901	0.396
1250	3.799	0.5	2.485	0.362
625	3.233	0.481	2.035	0.303
313	2.58	0.393	1.586	0.264
156	1.929	0.287	1.204	0.244
78	1.115	0.21	0.782	0.216
39	0.836	0.16	0.721	0.165
20	0.655	0.134	0.629	0.134
10	0.752	0.111	0.598	0.124
5	0.527	0.103	0.653	0.13

[0085] These data indicate that although a CsCl-purified FPV preparation can detect antibodies in FPV-vaccinated cats, so does a CsCl-purified NIC preparation (i.e., a preparation produced from uninfected cells using a similar procedure). As such, whole FPV is an unacceptable reagent for the determination of the immune status of a cat due to the possibility of a high percentage of false positive reactions due to the presence of cellular proteins that react with serum from vaccinated cats.

Example 2

[0086] This Example describes the isolation and expression of nucleic acid molecules of the present invention that encode feline calicivirus coat proteins (FCVCPs) of the present invention. Also described is the purification of recombinant feline calicivirus coat proteins (rFCVCPs) of the present invention.

[0087] A. A nucleic acid molecule of 2016 nucleotides designated herein as nFCVCP$_{2013}$ with a coding strand represented by SEQ ID NO:1, encoding a full-length FCVCP, was produced by PCR amplification and TA cloning using standard techniques, such as those described in Sambrook et al., ibid. Nucleic acid molecule nFCVCP$_{2013}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B, described in PCT Publication No. WO 98/12563, published Mar. 26, 1998, by Grieve et al., in such a manner that the nucleotides of the recombinant vector encoding the N-terminal histidine (His) tag were ligated in frame with the nucleotides encoding the feline calicivirus coat protein. The resulting recombinant molecule, designated herein as pλP$_R$His-nFCVCP$_{2013}$, was transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFCVCP$_{2013}$ using standard techniques, such as those disclosed in Sambrook et al., ibid. Recombinant cell *E. coli*:pλP$_R$His-nFCVCP$_{2013}$ was cultured as described in WO 98/12563, ibid., to produce a 672-amino acid FCVCP protein, having SEQ ID NO:2, designated PFCVCP$_{671}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFCVCP$_{671}$, was purified from *E. coli* by standard protein purification techniques.

[0088] B. A nucleic acid molecule of 1644 nucleotides, designated herein as nFCVCP$_{1641}$ with a coding strand represented by SEQ ID NO:3, which spans nucleotides 373 to 2016 of SEQ ID NO:1, encoding a mature FCVCP, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFCVCP$_{1641}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B/Hisless, a modified version of recombinant vector λPR cro/T^2 ori/RSET-B (described in Example 2A) from which codons encoding the His tag had been removed. The resulting recombinant molecule, designated herein as pλP$_R$-nFCVCP$_{1641}$, was transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$-nFCVCP$_{1641}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$-nFCVCP$_{1641}$ was cultured as described in Example 2A WO 98/12563, ibid., to produce a 548-amino acid FCVCP protein, designated PFCVCP$_{547}$, the amino acid sequence of which is represented herein as SEQ ID NO:4. PFCVCP$_{547}$ was purified from *E. coli* by standard protein purification techniques.

Example 3

[0089] This Example describes the isolation and expression of nucleic acid molecules of the present invention that encode feline parvovirus capsid proteins (FPVVPs) of the present invention. Also described is the purification of recombinant feline parvovirus capsid proteins (rFPVVPs) of the present invention.

[0090] A. A nucleic acid molecule of 1755 nucleotides, designated herein as nFPVVP2$_{1752}$ with a coding strand represented by SEQ ID NO:5, encoding a full-length feline parvovirus VP2 capsid protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFPVVP2$_{1752}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFPVVP2$_{1752}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFPVVP2$_{1752}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFPVVP2$_{1752}$ was cultured as described in Example 2A to produce a 585-amino acid FPVVP2 protein, having SEQ ID NO:6, designated PFPVVP2$_5$84, fused to a

His tag. The fusion protein, referred to herein as PHis-PFPVVP2$_{584}$, was purified from *E. coli* by standard protein purification techniques.

[0091] B. A nucleic acid molecule of 729 nucleotides, designated herein as nFPVVP2C$_{729}$ with a coding strand represented by SEQ ID NO:7, which spans nucleotides 703 to 1431 of SEQ ID NO:5, encoding a truncated VP2 capsid protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFPVVP2C$_{729}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFPVVP2C$_{729}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFPVVP2C$_{729}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFPVVP2C$_{729}$ was cultured as described in Example 2A to produce a 243-amino acid FPVVP2 protein, having SEQ ID NO:8, designated PFPVVP2C$_{243}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFPVVP2C$_{243}$, was purified from *E. coli* by standard protein purification techniques.

[0092] Nucleic acid molecule nFPVVP2C$_{729}$ was also ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B/Hisless as described in Example 2B to produce recombinant molecule pλP$_R$-nFPVVP^{2}C$_{729}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$-nFPVVP2C$_{729}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$-nFPVVP2C$_{729}$ was cultured as described in Example 2A to produce a 243-amino acid FPVVP2 protein, designated herein as PFPVVP2C$_{243}$, the amino acid sequence of which is represented herein as SEQ ID NO:8. PFPVVP2C$_{243}$ was purified from *E. coli* by standard protein purification techniques.

[0093] C. A nucleic acid molecule of 1860 nucleotides, designated herein as nFPVpVP12$_{1860}$ with a coding strand represented by SEQ ID NO:9, encoding a truncated VP1-VP2 capsid protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFPVpVP12$_{1860}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFPVpVP12$_{1860}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFPVpVP121860 as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFPVpVP12$_{1860}$ was cultured as described in Example 2A to produce a 620-amino acid FPVVP12 protein, having SEQ ID NO:10, designated PFPVpVP12$_{620}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFPVpVP12$_{620}$, was purified from *E. coli* by standard protein purification techniques.

[0094] D. A nucleic acid molecule of 1431 nucleotides, designated herein as nFPVpVP2$_{1431}$ with a coding strand represented by SEQ ID NO:11, which spans nucleotides 1 to 1431 of SEQ ID NO:5, encoding a truncated VP2 capsid protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFPVpVP2$_{1431}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B/Hisless as described in Example 2B to produce recombinant molecule pλP$_R$-nFPVpVP2$_{1431}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$-nFPVpVP2$_{143}$, as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$-nFPVpVP2$_{1431}$, was cultured as described in Example 2A to produce a 477-amino acid truncated FPVVP2 protein, designated PFPVpVP2$_{477}$, the amino acid sequence of which is represented as SEQ ID NO:12. PFPVpVP2$_{477}$ was purified from *E. coli* by standard protein purification techniques.

[0095] Nucleic acid molecule nFPVpVP2$_{1431}$ was also ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFPVpVP2$_{1431}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFPVpVP2$_{1431}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFPVpVP2$_{1431}$ was cultured as described in Example 2A to produce a 477-amino acid truncated FPVVP2 protein, designated PFPVpVP2$_{477}$, with SEQ ID NO:12, fused to a His tag. The fusion protein, designated PHis-PFPVpVP2$_{477}$ was purified from *E. coli* by standard protein purification techniques.

Example 4

[0096] This Example describes the isolation and expression of nucleic acid molecules of the present invention that encode feline herpesvirus glycoproteins of the present invention. Also described is the purification of recombinant feline herpesvirus glycoproteins (rFHVgB, rFHVgC, and rFHV gD proteins) of the present invention.

[0097] A. A nucleic acid molecule of 2832 nucleotides, designated herein as nFHVgB$_{2829}$ with a coding strand represented by SEQ ID NO:13, encoding a full-length feline herpesvirus glycoprotein B protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFHVgB$_{2829}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFHVgB$_{2829}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFHVgB$_{2829}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFHVgB$_{2829}$ was cultured as described in Example 2A to produce a 944-amino acid FHVgB protein, having SEQ ID NO:14, designated PFHVgB$_{943}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFHVgB$_{943}$, was purified from *E. coli* by standard protein purification techniques.

[0098] B. A nucleic acid molecule of 750 nucleotides, designated herein as nFHVgB$_{750}$ with a coding strand represented by SEQ ID NO:15, spanning nucleotides 1 to 750 of SEQ ID NO:13, encoding a truncated feline herpesvirus glycoprotein B protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFHVgB$_{750}$ was ligated to recombinant vector λP^{R}cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFHVgB$_{750}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFHVgB$_{750}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFHVgB$_{750}$ was cultured as described in Example 2A to produce a 250-amino acid FHVgB protein, having SEQ ID NO:16, designated PFHVgB$_{250}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFHVgB$_{250}$, was purified from *E. coli* by standard protein purification techniques.

[0099] C. A nucleic acid molecule of 1605 nucleotides, designated herein as nFHVgC$_{1602}$ with a coding strand represented by SEQ ID NO:17, encoding a full-length feline herpesvirus glycoprotein C protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFHVgC$_{1602}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFHVgC$_{1602}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFHVgC$_{1602}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFHVgC$_{1602}$ was cultured as described in Example 2A to produce a 535-amino acid FHVgC protein, having SEQ ID NO:18, designated PFHVgC$_{534}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFHVgC$_{534}$, was purified from *E. coli* by standard protein purification techniques.

[0100] D. A nucleic acid molecule of 1401 nucleotides, designated herein as nFHVgC$_{140}$, with a coding strand represented by SEQ ID NO:19, spanning nucleotides 97 to 1497 of SEQ ID NO:17, encoding a truncated feline herpesvirus glycoprotein C protein was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFHVgC$_{1401}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFHVgC$_{1401}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFHVgC$_{1401}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFHVgC$_{1401}$, was cultured as described in Example 2A to produce a 467-amino acid FHVgC protein, having SEQ ID NO:20, designated PFHVgC$_{467}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFHVgC$_{467}$, was purified from *E. coli* by standard protein purification techniques.

[0101] E. A nucleic acid molecule of 1401 nucleotides, designated nFHVgC$_{1401(opt)}$, encoding feline herpesvirus protein PFHVgC$_{467}$ but in which a number of codons were optimized for expression in *E. coli* was produced as follows. A series of PCR mutagenesis steps was performed on nFHVgC$_{1401}$, the coding strand of which is represented by SEQ ID NO:19, using standard techniques, such as those described in Sambrook et al., ibid., to target the following codons: two arginine codons spanning nucleotides 119 to 124 of SEQ ID NO:19; three serine codons spanning nucleotides 133 to 141 of SEQ ID NO:19; a glycine codon spanning nucleotides 724 to 726 of SEQ ID NO:19; and a leucine codon spanning nucleotides 727 to 729 of SEQ ID NO:19. The resulting nucleic acid molecule, namely nFHVgC$_{1401(opt)}$, has a coding strand sequence as represented in SEQ ID NO:21. Nucleic acid molecule nFHVgC$_{1401(opt)}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B/Hisless as described in Example 2B to produce recombinant molecule pλP$_R$-nFHVgC$_{1401(opt)}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$-nFHVgC$_{1401(opt)}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$-nFHVgC$_{1401(opt)}$ was cultured as described in Example 2A to produce a 467-amino acid FHVgC protein, designated PFHVgC$_{467(opt)}$. PFHVgC$_{467(opt)}$, the amino acid sequence of which is represented as SEQ ID NO:22, which is identical to SEQ ID NO:20, was purified from *E. coli* by standard protein purification techniques.

[0102] F. A nucleic acid molecule of 1125 nucleotides, designated herein as nFHVgD$_{1122}$ with a coding strand represented by SEQ ID NO:23, encoding a full-length feline herpesvirus glycoprotein D protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFHVgD,^{122} was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pλP$_R$His-nFHVgD$_{1122}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFHVgD$_{122}$ as described in Example 2A. Recombinant cell *E. coli*:pX-PRHis-nFHVgD$_{1122}$ was cultured as described in Example 2A to produce a 375-amino acid FHVgD protein, having SEQ ID NO:24, designated PFHVgD$_{374}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFHVgD$_{374}$, was purified from *E. coli* by standard protein purification techniques.

[0103] G. A nucleic acid molecule of 900 nucleotides, designated herein as nFHVgD$_{900}$ with a coding strand represented by SEQ ID NO:25, spanning nucleotides 85 to 894 of SEQ ID NO:23, encoding a truncated feline herpesvirus glycoprotein D protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFHVgD$_{900}$ was ligated to recombinant vector λP^{R}cro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule pkPRHis-nFHVgD$_{900}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$His-nFHVgD$_{900}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$His-nFHVgD$_{900}$ was cultured as described in Example 2A to produce a 300-amino acid FHVgD protein, having SEQ ID NO:26, designated PFHVgD$_{300}$, fused to a His tag. The fusion protein, referred to herein as PHis-PFHVgD$_{300}$, was purified from *E. coli* by standard protein purification techniques.

Example 5

[0104] This Example describes the isolation and expression of nucleic acid molecules of the present invention that encode feline leukemia virus (FeLV) proteins of the present invention. Also described is the purification of recombinant feline herpesvirus proteins (rFeLVp27 and rFeLVgp70 proteins) of the present invention.

[0105] A. A nucleic acid molecule of 789 nucleotides, designated herein as nFeLVp27$_{759}$ with a coding strand represented by SEQ ID NO:27, encoding a mature FeLV p27 protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFeLVp27$_{759}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B/Hisless as described in Example 2B to produce recombinant molecule pXPR-nFeLVp27$_{759}$, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:pλP$_R$-nFeLVp27$_{759}$ as described in Example 2A. Recombinant cell *E. coli*:pλP$_R$-nFeLVp27$_{759}$ was cultured as described in Example 2A to produce a 263-amino acid FeLV p27 protein designated PFeLVp27$_{253}$, the amino acid sequence of which is represented as SEQ ID NO:28. PFeLVp27$_{253}$ was purified from *E. coli* by standard protein purification techniques.

[0106] B. A nucleic acid molecule of 1857 nucleotides, designated herein as nFeLVgp70$_{1830}$ with a coding strand represented by SEQ ID NO:29, encoding a mature FeLV envelope glycoprotein 70 (gp70) protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFeLVgp70$_{1830}$ was ligated to recombinant vector λP$_R$cro/T^2 ori/RSET-B as described in

Example 2A to produce recombinant molecule $p\lambda P_R$His-nFeLVp27_{1857}, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:$p\lambda P_R$His-nFeLVp27_{1857} as described in Example 2A. Recombinant cell *E. coli*:$p\lambda P_R$His-nFeLVp27_{1857} was cultured as described in Example 2A to produce a 619-amino acid FeLV gp70 protein designated PFeLVgp70_{610}, the amino acid sequence of which is represented as SEQ ID NO:30, fused to a His tag. The fusion protein, referred to herein as PHis-PFeLVgp70_{610}, was purified from *E. coli* by standard protein purification techniques.

[0107] C. A nucleic acid molecule of 1833 nucleotides, designated herein as nFeLVp27-gp70_{1833} with a coding strand represented by SEQ ID NO:31, encoding a fusion protein of the carboxy-terminus of FeLV Pr65-gag and gp70, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nFeLVp27-gp70_{1833} was ligated to recombinant vector λP^Rcro/T^2 ori/RSET-B/Hisless as described in Example 2B to produce recombinant molecule pλPR-nFeLVp27-gp70_{1833} which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:$p\lambda P_R$-nFeLVp27-gp70_{1833} as described in Example 2A. Recombinant cell *E. coli*:$p\lambda P_R$-nFeLVp27-gp70_{1833} was cultured as described in Example 2A to produce a 611-amino acid fusion protein, designated as PFeLVp27-gp70_{611}, the amino acid sequence of which is represented as SEQ ID NO:32. PFeLVp27-gp70_{611} was purified from *E. coli* by standard protein purification techniques.

[0108] Nucleic acid molecule nFeLVp27-gp70_{1833} was also ligated to recombinant vector λP_Rcro/T^2 ori/RSET-B as described in Example 2B to produce recombinant molecule $p\lambda P_R$His-nFeLVp27-gp70_{1833} which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:$p\lambda P_R$His-nFeLVp27-gp70_{1833} as described in Example 2A. Recombinant cell *E. coli*:$p\lambda P_R$His-nFeLVp27-gp70_{1833} was cultured as described in Example 2A to produce a 611-amino acid fusion protein, designated as PFeLVp27-gp70_{611}, the amino acid sequence of which is represented as SEQ ID NO:32, fused to a His tag. The fusion protein, designated PHis-PFeLVp27-gp70_{611}, was purified from *E. coli* by standard protein purification techniques.

Example 6

[0109] This Example describes the isolation and expression of nucleic acid molecules of the present invention that encode canine distemper virus (CDV) proteins of the present invention. Also described is the purification of recombinant CDV hemagglutinin (rCDVH) and fusion (rCDVF) proteins of the present invention.

[0110] A. A nucleic acid molecule of 1812 nucleotides, designated herein as nCDVH_{1812} with a coding strand represented by SEQ ID NO:33, encoding a CDV hemagglutinin protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nCDVH_{1812} was ligated to recombinant vector λP_Rcro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule $p\lambda P_R$His-nCDVH_{1812}, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:$p\lambda P_R$His-nCDVH_{1812} as described in Example 2A. Recombinant cell *E. coli*:$p\lambda P_R$His-nCDVH_{1812} was cultured as described in Example 2A to produce a 604-amino acid protein designated PCDVH_{604}, the amino acid sequence of which is represented as SEQ ID NO:34, fused to a His tag. The fusion protein, designated PHis-PCDVH_{604}, was purified from *E. coli* by standard protein purification techniques.

[0111] B. A nucleic acid molecule of 1986 nucleotides, designated herein as nCDVF_{1986} with a coding strand represented by SEQ ID NO:35, encoding a CDV fusion protein, was produced by PCR amplification and TA cloning as described in Example 2A. Nucleic acid molecule nCDVF_{1986} was ligated to recombinant vector λP_Rcro/T^2 ori/RSET-B as described in Example 2A to produce recombinant molecule $p\lambda P_R$His-nCDVF_{1986}, which was then transformed into *Escherichia coli* to produce recombinant cell *E. coli*:$p\lambda P_R$His-nCDVF_{1986} as described in Example 2A. Recombinant cell *E. coli*:$p\lambda P_R$His-nCDVF_{1986} was cultured as described in Example 2A to produce a 662-amino acid protein designated PCDVF_{662}, the amino acid sequence of which is represented as SEQ ID NO:36, fused to a His tag. The fusion protein, designated PHis-PCDVF_{662}, was purified from *E. coli* by standard protein purification techniques.

Example 7

[0112] This Example demonstrates an immune status assay of the present invention. In particular, this Example demonstrates a correlation between humoral immune responses in cats previously vaccinated with panleukopenia (FPV), herpesvirus 1 (FHV-1), and calicivirus (FCV) vaccines and protection of such cats from challenge infections.

[0113] Forty cats were treated in the following manner: 14 cats were vaccinated with FCV, FHV-1 and FPV vaccines once, 6 months prior to challenge; 12 cats were vaccinated with FCV, FHV-1 and FPV vaccines either once or twice, with the last vaccine given 30 to 36 months prior to challenge; and 14 cats were unvaccinated. Challenge was accomplished following USDA challenge protocols utilized for vaccine approval. An immune status ELISA was utilized to determine the amounts of anti-FCV antibodies, anti-FHV antibodies, and anti-FPV antibodies in the serum of each of the cats prior to challenge using, respectively, the following recombinant antigens of the present invention: recombinant FCV coat protein (rFCVCP) protein PFCVCP_{547}, the amino acid sequence of which is represented as SEQ ID NO:4, and the production of which is described in Example 2B; recombinant FHV glycoprotein C (rFHVgC) protein PHis-PFHVgC_{467}, a fusion protein of FHVgC_{467},the amino acid sequence of which is represented by SEQ ID NO:22, the production of which is described in Example 4D; and recombinant FPV VP2 capsid protein (rFPVVP2) protein PFPVpVP2_{477}, the amino acid sequence of which is represented as SEQ ID NO:12, and the production of which is described in Example 3D. Cutoff values were based on results from 30 unvaccinated cats. ELISAs were conducted in a similar manner to those described in Example 1C, with the following modifications: The specified recombinant antigens were used to coat plates (100 μL per well) at the following concentrations: rFCVCP protein PFCVCP_{547} (starting concentration of 3 mg/ml) was diluted to 20 ng/ml (1:150,000 dilution); rFHVgC protein PFHVgC_{467} (starting concentration of 2.24 mg/ml) was diluted to 50 ng/ml (1:44,800); and rFPVVP2 protein PFPVpVP2_{477} (starting concentration of 1.12 mg/ml) was diluted to 120 ng/ml (1:9333). For wells containing rFCVCP and rFHVgC antigens, cat serum being tested was diluted 1:800 in diluent A; for wells containing rFPVVP2 antigen, the cat serum being tested was diluted 1:100 with diluent A.

[0114] Antibody levels were compared to clinical scores (FCV, FHV-1) or development of neutropenia (FPV). Cats were considered protected against FCV or FHV-1 if the clinical score was ≦50% of the mean of the unvaccinated cat group clinical score. Correlations between anti-FCV, anti-FHV and anti-FPV antibody levels and respective clinical scores for FCV, clinical scores for FHV-1, and development of neutropenia (FPV) are shown, respectively in Tables 4, 5, and 6.

TABLE 4

Correlation between clinical scores after FCV challenge and anti-FCV antibody levels measured by ELISA using recombinant antigen PFCVCP$_{547}$

Sample	Group	OD Ave	OD SD	ELISA	Clin Score
79	vaccine I	4.200	0.000	+	0
80	vaccine I	4.200	0.000	+	1
93	vaccine I	4.200	0.000	+	5
100	vaccine I	4.200	0.000	+	3
116	vaccine I	4.200	0.000	+	0
118	vaccine I	4.200	0.000	+	4
119	vaccine I	4.200	0.000	+	1
122	vaccine I	4.200	0.000	+	0
123	vaccine I	4.200	0.000	+	1
130	vaccine I	4.200	0.000	+	8
148	vaccine I	4.200	0.000	+	0
155	vaccine I	4.200	0.000	+	2
156	vaccine I	4.200	0.000	+	0
7029	vaccine I	4.200	0.000	+	0
QVY3	vaccine II	4.200	0.000	+	2
AMI4	vaccine II	4.200	0.000	+	0
AMX1	vaccine II	4.200	0.000	+	0
G444	vaccine II	4.200	0.000	+	0
BWN3	vaccine II	4.200	0.000	+	0
QWM3	vaccine II	4.200	0.000	+	0
QVF3	vaccine II	4.200	0.000	+	0
G087	vaccine II	4.200	0.000	+	0
3592	vaccine II	4.200	0.000	+	0
1959	vaccine II	4.200	0.000	+	2
AME5	vaccine II	4.200	0.000	+	0
3513	vaccine II	4.200	0.000	+	0
7086	control I			–	7
7090	control I			–	17
7113	control I			–	19
7115	control I			–	23
7122	control I			–	12
7123	control I			–	27
7124	control I			–	24
7131	control I			–	21
7132	control I			–	34
7133	control I			–	25
ALV3	control II			–	44
ALT2	control II			–	35
ALV5	control II			–	38
ALZ1	control II			–	47
AIY2	negative	0.447	0.213	–	
AIW5	negative	0.383	0.098	–	
AIY3	negative	0.514	0.255	–	
AIU5	negative	0.479	0.206	–	
AIW7	negative	0.463	0.094	–	
AIY2	negative	0.345	0.090	–	
AIU4	negative	0.440	0.118	–	
AIW6	negative	0.389	0.071	–	
AIV1	negative	0.427	0.111	–	
AIW1	negative	0.307	0.098	–	
AIW3	negative	0.299	0.104	–	
AIU3	negative	0.389	0.041	–	
AIW4	negative	0.368	0.197	–	
AIW2	negative	0.429	0.181	–	
AIY1	negative	2.370	1.125	+	
	Neg. Ave	0.406			
	Neg. SD	0.064			
	Ave + 2SD	0.533			

[0115]

TABLE 5

Correlation between clinical scores after FHV-1 challenge and anti-FHV antibody levels measured by ELISA using recombinant antigen PFHVgC$_{467}$

Sample	Group	OD Ave	OD SD	ELISA	Clin Score
79	vaccine I	0.612	0.238	+/–	1
80	vaccine I	0.823	0.219	+	12
93	vaccine I	0.412	0.152	–	38
100	vaccine I	1.203	0.087	+	2
116	vaccine I	0.776	0.165	+	5
118	vaccine I	3.064	0.405	+	1
119	vaccine I	0.697	0.047	+	5
122	vaccine I	0.702	0.148	+	7
123	vaccine I	0.929	0.134	+	4
130	vaccine I	1.291	0.352	+	14
148	vaccine I	0.769	0.297	+	6
155	vaccine I	3.659	0.473	+	3
156	vaccine I	3.563	0.212	+	1
7029	vaccine I	0.460	0.080	–	42
3512	vaccine II	0.285	0.109	–	10
3514	vaccine II	1.764	0.596	+	8
3515	vaccine II	0.663	0.239	+	8
3519	vaccine II	1.349	0.389	+	14
3522	vaccine II	0.575	0.178	–	11
3528	vaccine II	0.660	0.257	+	11
3530	vaccine II	0.922	0.205	+	13
3531	vaccine II	0.404	0.101	–	11
3532	vaccine II	0.708	0.294	+	8
3535	vaccine II	1.574	0.584	+	16
3537	vaccine II	2.761	0.338	+	9
3542	vaccine II	0.407	0.173	–	17
7086	control I	0.271	0.036	–	24
7090	control I	0.207	0.015	–	19
7113	control I	0.296	0.070	–	19
7115	control I	0.327	0.209	–	15
7122	control I	0.259	0.055	–	22
7123	control I	0.258	0.039	–	16
7124	control I	0.215	0.016	–	18
7131	control I	0.807	0.118	+	16
7132	control I	0.290	0.102	–	27
7133	control I	0.259	0.042	–	14
2110	control II	0.377	0.287	–	26
2112	control II	0.396	0.125	–	33
2116	control II	0.185	0.076	–	37
2119	control II	0.295	0.116	–	42
AIY2	negative	0.208	0.036	–	
AIW5	negative	0.271	0.128	–	
AIY3	negative	0.402	0.031	–	
AIU5	negative	0.192	0.008	–	
AIY1	negative	0.222	0.024	–	
AIW7	negative	0.310	0.021	–	
AIY2	negative	0.240	0.038	–	
AIU4	negative	0.402	0.158	–	
AIW6	negative	0.199	0.049	–	
AIV1	negative	0.374	0.056	–	
AIW1	negative	0.233	0.045	–	
AIW3	negative	0.283	0.045	–	

TABLE 5-continued

Correlation between clinical scores after FHV-1 challenge and anti-FHV antibody levels measured by ELISA using recombinant antigen PFHVgC$_{467}$

Sample	Group	OD Ave	OD SD	ELISA	Clin Score
AIU3	negative	0.175	0.046	–	
AIW4	negative	0.164	0.057	–	
AIW2	negative	0.323	0.070	–	
	Neg. Ave	0.266			
	Neg. SD	0.040			
	Ave + 2SD	0.346			

[0116]

TABLE 6

Correlation between development of neutropenia after FPV challenge and anti-FPV antibodies measured by ELISA using recombinant antigen PFPVpVP2$_{477}$

Sample	Group	OD Ave.	OD SD	ELISA	Panleuk?
79	vaccine I	3.952	0.294	+	no
80	vaccine I	0.748	0.099	+	no
100	vaccine I	1.625	0.324	+	no
116	vaccine I	2.915	0.373	+	no
118	vaccine I	3.432	0.374	+	no
119	vaccine I	2.820	0.428	+	no
122	vaccine I	2.174	0.278	+	no
123	vaccine I	2.780	0.410	+	no
130	vaccine I	0.678	0.194	+	no
148	vaccine I	0.300	0.073	–	no
155	vaccine I	1.550	0.247	+	no
156	vaccine I	0.808	0.206	+	no
7029	vaccine I	1.041	0.136	+	no
3512	vaccine II	0.505	0.122	–	no
3514	vaccine II	0.450	0.074	–	no
3515	vaccine II	0.547	0.115	–	no
3519	vaccine II	1.675	0.214	+	no
3522	vaccine II	0.292	0.042	–	no
3528	vaccine II	0.395	0.091	–	no
3530	vaccine II	0.369	0.102	–	no
3531	vaccine II	0.534	0.155	–	no
3532	vaccine II	0.427	0.145	–	no
3535	vaccine II	0.345	0.078	–	no
3537	vaccine II	1.221	0.353	+	no
3542	vaccine II	0.377	0.061	–	no
7132	control I	1.115	0.297	+	yes
7086	control I	0.301	0.063	–	yes
7090	control I	0.262	0.012	–	yes
7113	control I	0.275	0.065	–	yes
7115	control I	0.596	0.157	–	yes
7122	control I	0.278	0.087	–	yes
7123	control I	0.378	0.213	–	yes
7124	control I	0.615	0.308	+/–	yes
7131	control I	0.377	0.083	–	yes
7133	control I	0.310	0.114	–	yes
2110	control II	0.299	0.071	–	yes
2112	control II	0.578	0.199	–	yes
2116	control II	0.324	0.125	–	yes
2119	control II	0.306	0.079	–	yes
AIY2	negative	0.236	0.042	–	
AIW5	negative	0.145	0.093	–	
AIY3	negative	0.240	0.071	–	
AIU5	negative	0.153	0.055	–	
AIY1	negative	0.266	0.081	–	
AIW7	negative	0.195	0.092	–	
AIY2	negative	0.214	0.138	–	
AIU4	negative	0.196	0.111	–	
AIW6	negative	0.162	0.043	–	
AIV1	negative	0.292	0.074	–	
AIW1	negative	0.228	0.068	–	
AIW3	negative	0.121	0.030	–	
AIU3	negative	0.122	0.037	–	
AIW4	negative	0.165	0.053	–	
AIW2	negative	0.209	0.066	–	
	Neg. Ave	0.196			
	Neg. SD	0.030			
	Ave + 2SD	0.256			

[0117] These data indicate the utility of an immune status of the present invention in predicting that a cat is protected from viral challenge. Specifically, the results in Table 4 indicate that all 26 vaccinated cats were protected from FCV challenge and that each of those cats had antibody levels predicting protection. The results in Table 5 indicate that 22 of 26 vaccinated cats were protected from FHV-1 challenge and that 18 of the 22 protected cats had antibody levels predicting protection. Of the four cats in this group that were not protected, 2 cats had antibody levels predicting lack of protection and 2 cats had antibody levels predicting protection. The results in Table 6 indicate that neutropenia was detected in all 14 unvaccinated cats but in none of the vaccinated cats, confirming panleukopenia in the unvaccinated cats. Of the vaccinated cats, 14 of the 25 cats available for study had FPV antibody levels predicting protection.

[0118] In conclusion, an immune status assay of the present invention shows high positive correlation with protection from challenge in healthy, vaccinated cats exposed to virulent FCV, FHV-1, or FPV.

[0119] While various embodiments of the present invention have been described in detail, it is apparent that modifications and adaptations of those embodiments will occur to those skilled in the art. It is to be expressly understood, however, that such modifications and adaptations are within the scope of the present invention, as set forth in the following claims.

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                              SEQUENCE LISTING


<160> NUMBER OF SEQ ID NOS: 36

<210> SEQ ID NO 1
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<211> LENGTH: 2013
<212> TYPE: DNA
<213> ORGANISM: Feline calicivirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2013)

<400> SEQUENCE: 1

atg tgc tca acc tgc gct aac gtg ctt aaa tat tat gat tgg gac ccc       48
Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp Pro
  1               5                  10                  15

cat ttc aaa ttg gta atc aac ccc aac aac ttc ctc tct gtt ggc ttt       96
His Phe Lys Leu Val Ile Asn Pro Asn Asn Phe Leu Ser Val Gly Phe
             20                  25                  30

tgt agt aac cct tta atg tgt tgc tac cca gaa ctc ctt ccg gaa ttt      144
Cys Ser Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu Pro Glu Phe
         35                  40                  45

gga act gtt tgg gat tgc gat cgg tca cca ctt gaa att tac cta gaa      192
Gly Thr Val Trp Asp Cys Asp Arg Ser Pro Leu Glu Ile Tyr Leu Glu
     50                  55                  60

tca ata ctt ggt gat gat gaa tgg gca tcc act ttt gac gct gtt gac      240
Ser Ile Leu Gly Asp Asp Glu Trp Ala Ser Thr Phe Asp Ala Val Asp
 65                  70                  75                  80

cca gtc gtt ccc cca atg cac tgg ggt gct gct gga aaa att ttc cag      288
Pro Val Val Pro Pro Met His Trp Gly Ala Ala Gly Lys Ile Phe Gln
                 85                  90                  95

cca cac ccc ggt gtt ctc atg cac cat ctc att ggt aag gtt gct gca      336
Pro His Pro Gly Val Leu Met His His Leu Ile Gly Lys Val Ala Ala
            100                 105                 110

ggt tgg gac ccc gat ctg cct cta att cga ctc gag gcg gat gac ggg      384
Gly Trp Asp Pro Asp Leu Pro Leu Ile Arg Leu Glu Ala Asp Asp Gly
        115                 120                 125

tca atc aca gca ccc gag caa gga aca atg gtt ggc ggc gtc atc gct      432
Ser Ile Thr Ala Pro Glu Gln Gly Thr Met Val Gly Gly Val Ile Ala
    130                 135                 140

gaa ccc agc gcc cag atg tca aca gct gct gat atg gcc acc ggg aaa      480
Glu Pro Ser Ala Gln Met Ser Thr Ala Ala Asp Met Ala Thr Gly Lys
145                 150                 155                 160

agc gtt gat tct gag tgg gag gca ttc ttc tcc ttt cac acc agc gtc      528
Ser Val Asp Ser Glu Trp Glu Ala Phe Phe Ser Phe His Thr Ser Val
                165                 170                 175

aat tgg agt aca tct gaa acc caa gga aag att ctc ttc aaa caa tcc      576
Asn Trp Ser Thr Ser Glu Thr Gln Gly Lys Ile Leu Phe Lys Gln Ser
            180                 185                 190

tta ggc cct ttg ctc aac cca tat cta gaa cac ctt gct aag cta tat      624
Leu Gly Pro Leu Leu Asn Pro Tyr Leu Glu His Leu Ala Lys Leu Tyr
        195                 200                 205

gtt gcg tgg tct ggg tcg att gag gtt agg ttc tct atc tct ggc tct      672
Val Ala Trp Ser Gly Ser Ile Glu Val Arg Phe Ser Ile Ser Gly Ser
    210                 215                 220

ggt gtc ttt ggt ggg aag ctc gca gct att gtt gta cct cct ggg gtt      720
Gly Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val Pro Pro Gly Val
225                 230                 235                 240

gat cca gtg cag agt act tcg atg cta caa tac ccc cat gtt ttg ttt      768
Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro His Val Leu Phe
                245                 250                 255

gat gct cgt cag gtg gaa cca gtt atc ttc tgt ctt cct gat cta aga      816
Asp Ala Arg Gln Val Glu Pro Val Ile Phe Cys Leu Pro Asp Leu Arg
            260                 265                 270
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agc acc ctg tac cac ctt atg tct gac act gac act aca tcc ttg gtc      864
Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr Thr Ser Leu Val
        275                 280                 285

att atg gtg tac aat gat ctc atc aat ccc tat gcc aat gat gcc aac      912
Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala Asn Asp Ala Asn
    290                 295                 300

tct tct ggg tgt att gtc act gtc gag aca aaa cct ggc cct gac ttc      960
Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys Pro Gly Pro Asp Phe
305                 310                 315                 320

aag ttt cac ctc ctt aag cca ccc gga tct atg cta acc cat ggc tct     1008
Lys Phe His Leu Leu Lys Pro Pro Gly Ser Met Leu Thr His Gly Ser
                325                 330                 335

atc cct tct gat tta att ccc aaa aca tct tcg ctc tgg atc ggt aac     1056
Ile Pro Ser Asp Leu Ile Pro Lys Thr Ser Ser Leu Trp Ile Gly Asn
            340                 345                 350

cgc tac tgg tca gac ata act gat ttt gtg att cgg ccg ttt gtc ttc     1104
Arg Tyr Trp Ser Asp Ile Thr Asp Phe Val Ile Arg Pro Phe Val Phe
        355                 360                 365

caa gca aat cgt cat ttt gac ttt aat caa gag acc gca ggg tgg agc     1152
Gln Ala Asn Arg His Phe Asp Phe Asn Gln Glu Thr Ala Gly Trp Ser
    370                 375                 380

aca cca cgg ttt cgg cct ata tct gtt acc att act gaa cag aac gga     1200
Thr Pro Arg Phe Arg Pro Ile Ser Val Thr Ile Thr Glu Gln Asn Gly
385                 390                 395                 400

gca aaa ttg ggc att ggg gtg gca aca gat tac ata gtg cct gga atc     1248
Ala Lys Leu Gly Ile Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile
                405                 410                 415

cct gat ggc tgg cct gac acc aca att cct ggg gag ttg ata cca gct     1296
Pro Asp Gly Trp Pro Asp Thr Thr Ile Pro Gly Glu Leu Ile Pro Ala
            420                 425                 430

ggt gat tac gca atc acc aat ggt act ggc aat gac atc acc acg gct     1344
Gly Asp Tyr Ala Ile Thr Asn Gly Thr Gly Asn Asp Ile Thr Thr Ala
        435                 440                 445

aca gga tat gac act gct gat ata att aag aac aat acc aac ttt agg     1392
Thr Gly Tyr Asp Thr Ala Asp Ile Ile Lys Asn Asn Thr Asn Phe Arg
    450                 455                 460

ggc atg tac ata tgt ggt tcg ctc cag cgt gcc tgg ggt gat aag aaa     1440
Gly Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys
465                 470                 475                 480

att tcc aac act gcc ttt atc acc act gcc acc cta gat ggt gac aac     1488
Ile Ser Asn Thr Ala Phe Ile Thr Thr Ala Thr Leu Asp Gly Asp Asn
                485                 490                 495

aac aac aag atc aat ccc tgt aat acc ata gac cag tca aag atc gtc     1536
Asn Asn Lys Ile Asn Pro Cys Asn Thr Ile Asp Gln Ser Lys Ile Val
            500                 505                 510

gtg ttt caa gac aac cat gtt gga aag aaa gcg caa acc tca gac gat     1584
Val Phe Gln Asp Asn His Val Gly Lys Lys Ala Gln Thr Ser Asp Asp
        515                 520                 525

aca ttg gcc ctg ctt ggt tac act ggc att ggt gag cag gcc atc ggg     1632
Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Gln Ala Ile Gly
    530                 535                 540

tct gat agg gac cgg gtt gtg cgc atc agc act ctc cct gaa act ggt     1680
Ser Asp Arg Asp Arg Val Val Arg Ile Ser Thr Leu Pro Glu Thr Gly
545                 550                 555                 560

gct cga ggc ggt aac cac cca att ttc tac aag aac tcc att aaa ttg     1728
Ala Arg Gly Gly Asn His Pro Ile Phe Tyr Lys Asn Ser Ile Lys Leu
                565                 570                 575
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gga tat gta att agg tct att gat gtc ttt aat tca caa atc ttg cac     1776
Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser Gln Ile Leu His
            580                 585                 590

act tcc aga cag tta tcg cta aat cat tac cta ctc cca cct gat tct     1824
Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu Leu Pro Pro Asp Ser
        595                 600                 605

ttt gcc gtc tat aga ata att gac tca aat ggc tcg tgg ttt gat att     1872
Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn Gly Ser Trp Phe Asp Ile
    610                 615                 620

gga att gat agt gat ggg ttc tct ttt gtt ggt gtt tct ggc ttt ggt     1920
Gly Ile Asp Ser Asp Gly Phe Ser Phe Val Gly Val Ser Gly Phe Gly
625                 630                 635                 640

aaa tta gaa ttt ccc ctt tct gcc tcc tac atg gga ata caa ttg gca     1968
Lys Leu Glu Phe Pro Leu Ser Ala Ser Tyr Met Gly Ile Gln Leu Ala
                645                 650                 655

aag atc cgg ctt gcc tct aac att agg agt ccc atg act aag tta         2013
Lys Ile Arg Leu Ala Ser Asn Ile Arg Ser Pro Met Thr Lys Leu
            660                 665                 670


<210> SEQ ID NO 2
<211> LENGTH: 671
<212> TYPE: PRT
<213> ORGANISM: Feline calicivirus

<400> SEQUENCE: 2

Met Cys Ser Thr Cys Ala Asn Val Leu Lys Tyr Tyr Asp Trp Asp Pro
  1               5                   10                  15

His Phe Lys Leu Val Ile Asn Pro Asn Asn Phe Leu Ser Val Gly Phe
             20                  25                  30

Cys Ser Asn Pro Leu Met Cys Cys Tyr Pro Glu Leu Leu Pro Glu Phe
         35                  40                  45

Gly Thr Val Trp Asp Cys Asp Arg Ser Pro Leu Glu Ile Tyr Leu Glu
     50                  55                  60

Ser Ile Leu Gly Asp Asp Glu Trp Ala Ser Thr Phe Asp Ala Val Asp
 65                  70                  75                  80

Pro Val Val Pro Pro Met His Trp Gly Ala Ala Gly Lys Ile Phe Gln
                 85                  90                  95

Pro His Pro Gly Val Leu Met His His Leu Ile Gly Lys Val Ala Ala
            100                 105                 110

Gly Trp Asp Pro Asp Leu Pro Leu Ile Arg Leu Glu Ala Asp Asp Gly
        115                 120                 125

Ser Ile Thr Ala Pro Glu Gln Gly Thr Met Val Gly Gly Val Ile Ala
    130                 135                 140

Glu Pro Ser Ala Gln Met Ser Thr Ala Ala Asp Met Ala Thr Gly Lys
145                 150                 155                 160

Ser Val Asp Ser Glu Trp Glu Ala Phe Phe Ser Phe His Thr Ser Val
                165                 170                 175

Asn Trp Ser Thr Ser Glu Thr Gln Gly Lys Ile Leu Phe Lys Gln Ser
            180                 185                 190

Leu Gly Pro Leu Leu Asn Pro Tyr Leu Glu His Leu Ala Lys Leu Tyr
        195                 200                 205

Val Ala Trp Ser Gly Ser Ile Glu Val Arg Phe Ser Ile Ser Gly Ser
    210                 215                 220

Gly Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val Pro Pro Gly Val
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225                 230                 235                 240

Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro His Val Leu Phe
                245                 250                 255

Asp Ala Arg Gln Val Glu Pro Val Ile Phe Cys Leu Pro Asp Leu Arg
            260                 265                 270

Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr Thr Ser Leu Val
        275                 280                 285

Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala Asn Asp Ala Asn
    290                 295                 300

Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys Pro Gly Pro Asp Phe
305                 310                 315                 320

Lys Phe His Leu Leu Lys Pro Pro Gly Ser Met Leu Thr His Gly Ser
                325                 330                 335

Ile Pro Ser Asp Leu Ile Pro Lys Thr Ser Ser Leu Trp Ile Gly Asn
            340                 345                 350

Arg Tyr Trp Ser Asp Ile Thr Asp Phe Val Ile Arg Pro Phe Val Phe
        355                 360                 365

Gln Ala Asn Arg His Phe Asp Phe Asn Gln Glu Thr Ala Gly Trp Ser
    370                 375                 380

Thr Pro Arg Phe Arg Pro Ile Ser Val Thr Ile Thr Glu Gln Asn Gly
385                 390                 395                 400

Ala Lys Leu Gly Ile Gly Val Ala Thr Asp Tyr Ile Val Pro Gly Ile
                405                 410                 415

Pro Asp Gly Trp Pro Asp Thr Thr Ile Pro Gly Glu Leu Ile Pro Ala
            420                 425                 430

Gly Asp Tyr Ala Ile Thr Asn Gly Thr Gly Asn Asp Ile Thr Thr Ala
        435                 440                 445

Thr Gly Tyr Asp Thr Ala Asp Ile Ile Lys Asn Asn Thr Asn Phe Arg
    450                 455                 460

Gly Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp Gly Asp Lys Lys
465                 470                 475                 480

Ile Ser Asn Thr Ala Phe Ile Thr Thr Ala Thr Leu Asp Gly Asp Asn
                485                 490                 495

Asn Asn Lys Ile Asn Pro Cys Asn Thr Ile Asp Gln Ser Lys Ile Val
            500                 505                 510

Val Phe Gln Asp Asn His Val Gly Lys Lys Ala Gln Thr Ser Asp Asp
        515                 520                 525

Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu Gln Ala Ile Gly
    530                 535                 540

Ser Asp Arg Asp Arg Val Val Arg Ile Ser Thr Leu Pro Glu Thr Gly
545                 550                 555                 560

Ala Arg Gly Gly Asn His Pro Ile Phe Tyr Lys Asn Ser Ile Lys Leu
                565                 570                 575

Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser Gln Ile Leu His
            580                 585                 590

Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu Leu Pro Pro Asp Ser
        595                 600                 605

Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn Gly Ser Trp Phe Asp Ile
    610                 615                 620

Gly Ile Asp Ser Asp Gly Phe Ser Phe Val Gly Val Ser Gly Phe Gly
625                 630                 635                 640
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Lys Leu Glu Phe Pro Leu Ser Ala Ser Tyr Met Gly Ile Gln Leu Ala
               645                650                655

Lys Ile Arg Leu Ala Ser Asn Ile Arg Ser Pro Met Thr Lys Leu
           660                665                670


<210> SEQ ID NO 3
<211> LENGTH: 1641
<212> TYPE: DNA
<213> ORGANISM: Feline calicivirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1641)

<400> SEQUENCE: 3

gcg gat gac ggg tca atc aca gca ccc gag caa gga aca atg gtt ggc       48
Ala Asp Asp Gly Ser Ile Thr Ala Pro Glu Gln Gly Thr Met Val Gly
  1              5                 10                 15

ggc gtc atc gct gaa ccc agc gcc cag atg tca aca gct gct gat atg       96
Gly Val Ile Ala Glu Pro Ser Ala Gln Met Ser Thr Ala Ala Asp Met
            20                 25                 30

gcc acc ggg aaa agc gtt gat tct gag tgg gag gca ttc ttc tcc ttt      144
Ala Thr Gly Lys Ser Val Asp Ser Glu Trp Glu Ala Phe Phe Ser Phe
         35                 40                 45

cac acc agc gtc aat tgg agt aca tct gaa acc caa gga aag att ctc      192
His Thr Ser Val Asn Trp Ser Thr Ser Glu Thr Gln Gly Lys Ile Leu
     50                 55                 60

ttc aaa caa tcc tta ggc cct ttg ctc aac cca tat cta gaa cac ctt      240
Phe Lys Gln Ser Leu Gly Pro Leu Leu Asn Pro Tyr Leu Glu His Leu
 65                 70                 75                80

gct aag cta tat gtt gcg tgg tct ggg tcg att gag gtt agg ttc tct      288
Ala Lys Leu Tyr Val Ala Trp Ser Gly Ser Ile Glu Val Arg Phe Ser
                85                 90                 95

atc tct ggc tct ggt gtc ttt ggt ggg aag ctc gca gct att gtt gta      336
Ile Ser Gly Ser Gly Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val
           100                105                110

cct cct ggg gtt gat cca gtg cag agt act tcg atg cta caa tac ccc      384
Pro Pro Gly Val Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro
        115                120                125

cat gtt ttg ttt gat gct cgt cag gtg gaa cca gtt atc ttc tgt ctt      432
His Val Leu Phe Asp Ala Arg Gln Val Glu Pro Val Ile Phe Cys Leu
    130                135                140

cct gat cta aga agc acc ctg tac cac ctt atg tct gac act gac act      480
Pro Asp Leu Arg Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr
145                150                155               160

aca tcc ttg gtc att atg gtg tac aat gat ctc atc aat ccc tat gcc      528
Thr Ser Leu Val Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala
               165                170                175

aat gat gcc aac tct tct ggg tgt att gtc act gtc gag aca aaa cct      576
Asn Asp Ala Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys Pro
           180                185                190

ggc cct gac ttc aag ttt cac ctc ctt aag cca ccc gga tct atg cta      624
Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser Met Leu
        195                200                205

acc cat ggc tct atc cct tct gat tta att ccc aaa aca tct tcg ctc      672
Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Thr Ser Ser Leu
    210                215                220

tgg atc ggt aac cgc tac tgg tca gac ata act gat ttt gtg att cgg      720
Trp Ile Gly Asn Arg Tyr Trp Ser Asp Ile Thr Asp Phe Val Ile Arg
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225                 230                 235                 240

ccg ttt gtc ttc caa gca aat cgt cat ttt gac ttt aat caa gag acc          768
Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp Phe Asn Gln Glu Thr
                245                 250                 255

gca ggg tgg agc aca cca cgg ttt cgg cct ata tct gtt acc att act          816
Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro Ile Ser Val Thr Ile Thr
            260                 265                 270

gaa cag aac gga gca aaa ttg ggc att ggg gtg gca aca gat tac ata          864
Glu Gln Asn Gly Ala Lys Leu Gly Ile Gly Val Ala Thr Asp Tyr Ile
        275                 280                 285

gtg cct gga atc cct gat ggc tgg cct gac acc aca att cct ggg gag          912
Val Pro Gly Ile Pro Asp Gly Trp Pro Asp Thr Thr Ile Pro Gly Glu
    290                 295                 300

ttg ata cca gct ggt gat tac gca atc acc aat ggt act ggc aat gac          960
Leu Ile Pro Ala Gly Asp Tyr Ala Ile Thr Asn Gly Thr Gly Asn Asp
305                 310                 315                 320

atc acc acg gct aca gga tat gac act gct gat ata att aag aac aat         1008
Ile Thr Thr Ala Thr Gly Tyr Asp Thr Ala Asp Ile Ile Lys Asn Asn
                325                 330                 335

acc aac ttt agg ggc atg tac ata tgt ggt tcg ctc cag cgt gcc tgg         1056
Thr Asn Phe Arg Gly Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp
            340                 345                 350

ggt gat aag aaa att tcc aac act gcc ttt atc acc act gcc acc cta         1104
Gly Asp Lys Lys Ile Ser Asn Thr Ala Phe Ile Thr Thr Ala Thr Leu
        355                 360                 365

gat ggt gac aac aac aac aag atc aat ccc tgt aat acc ata gac cag         1152
Asp Gly Asp Asn Asn Asn Lys Ile Asn Pro Cys Asn Thr Ile Asp Gln
    370                 375                 380

tca aag atc gtc gtg ttt caa gac aac cat gtt gga aag aaa gcg caa         1200
Ser Lys Ile Val Val Phe Gln Asp Asn His Val Gly Lys Lys Ala Gln
385                 390                 395                 400

acc tca gac gat aca ttg gcc ctg ctt ggt tac act ggc att ggt gag         1248
Thr Ser Asp Asp Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu
                405                 410                 415

cag gcc atc ggg tct gat agg gac cgg gtt gtg cgc atc agc act ctc         1296
Gln Ala Ile Gly Ser Asp Arg Asp Arg Val Val Arg Ile Ser Thr Leu
            420                 425                 430

cct gaa act ggt gct cga ggc ggt aac cac cca att ttc tac aag aac         1344
Pro Glu Thr Gly Ala Arg Gly Gly Asn His Pro Ile Phe Tyr Lys Asn
        435                 440                 445

tcc att aaa ttg gga tat gta att agg tct att gat gtc ttt aat tca         1392
Ser Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser
    450                 455                 460

caa atc ttg cac act tcc aga cag tta tcg cta aat cat tac cta ctc         1440
Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu Leu
465                 470                 475                 480

cca cct gat tct ttt gcc gtc tat aga ata att gac tca aat ggc tcg         1488
Pro Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn Gly Ser
                485                 490                 495

tgg ttt gat att gga att gat agt gat ggg ttc tct ttt gtt ggt gtt         1536
Trp Phe Asp Ile Gly Ile Asp Ser Asp Gly Phe Ser Phe Val Gly Val
            500                 505                 510

tct ggc ttt ggt aaa tta gaa ttt ccc ctt tct gcc tcc tac atg gga         1584
Ser Gly Phe Gly Lys Leu Glu Phe Pro Leu Ser Ala Ser Tyr Met Gly
        515                 520                 525

ata caa ttg gca aag atc cgg ctt gcc tct aac att agg agt ccc atg         1632
Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn Ile Arg Ser Pro Met
```

```
    530                 535                 540

act aag tta                                                         1641
Thr Lys Leu
545


<210> SEQ ID NO 4
<211> LENGTH: 547
<212> TYPE: PRT
<213> ORGANISM: Feline calicivirus

<400> SEQUENCE: 4

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

Gly Val Ile Ala Glu Pro Ser Ala Gln Met Ser Thr Ala Ala Asp Met
             20                  25                  30

Ala Thr Gly Lys Ser Val Asp Ser Glu Trp Glu Ala Phe Phe Ser Phe
         35                  40                  45

His Thr Ser Val Asn Trp Ser Thr Ser Glu Thr Gln Gly Lys Ile Leu
     50                  55                  60

Phe Lys Gln Ser Leu Gly Pro Leu Leu Asn Pro Tyr Leu Glu His Leu
 65                  70                  75                  80

Ala Lys Leu Tyr Val Ala Trp Ser Gly Ser Ile Glu Val Arg Phe Ser
                 85                  90                  95

Ile Ser Gly Ser Gly Val Phe Gly Gly Lys Leu Ala Ala Ile Val Val
            100                 105                 110

Pro Pro Gly Val Asp Pro Val Gln Ser Thr Ser Met Leu Gln Tyr Pro
        115                 120                 125

His Val Leu Phe Asp Ala Arg Gln Val Glu Pro Val Ile Phe Cys Leu
    130                 135                 140

Pro Asp Leu Arg Ser Thr Leu Tyr His Leu Met Ser Asp Thr Asp Thr
145                 150                 155                 160

Thr Ser Leu Val Ile Met Val Tyr Asn Asp Leu Ile Asn Pro Tyr Ala
                165                 170                 175

Asn Asp Ala Asn Ser Ser Gly Cys Ile Val Thr Val Glu Thr Lys Pro
            180                 185                 190

Gly Pro Asp Phe Lys Phe His Leu Leu Lys Pro Pro Gly Ser Met Leu
        195                 200                 205

Thr His Gly Ser Ile Pro Ser Asp Leu Ile Pro Lys Thr Ser Ser Leu
    210                 215                 220

Trp Ile Gly Asn Arg Tyr Trp Ser Asp Ile Thr Asp Phe Val Ile Arg
225                 230                 235                 240

Pro Phe Val Phe Gln Ala Asn Arg His Phe Asp Phe Asn Gln Glu Thr
                245                 250                 255

Ala Gly Trp Ser Thr Pro Arg Phe Arg Pro Ile Ser Val Thr Ile Thr
            260                 265                 270

Glu Gln Asn Gly Ala Lys Leu Gly Ile Gly Val Ala Thr Asp Tyr Ile
        275                 280                 285

Val Pro Gly Ile Pro Asp Gly Trp Pro Asp Thr Thr Ile Pro Gly Glu
    290                 295                 300

Leu Ile Pro Ala Gly Asp Tyr Ala Ile Thr Asn Gly Thr Gly Asn Asp
305                 310                 315                 320

Ile Thr Thr Ala Thr Gly Tyr Asp Thr Ala Asp Ile Ile Lys Asn Asn
                325                 330                 335
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Thr Asn Phe Arg Gly Met Tyr Ile Cys Gly Ser Leu Gln Arg Ala Trp
            340                 345                 350

Gly Asp Lys Lys Ile Ser Asn Thr Ala Phe Ile Thr Thr Ala Thr Leu
        355                 360                 365

Asp Gly Asp Asn Asn Asn Lys Ile Asn Pro Cys Asn Thr Ile Asp Gln
    370                 375                 380

Ser Lys Ile Val Val Phe Gln Asp Asn His Val Gly Lys Lys Ala Gln
385                 390                 395                 400

Thr Ser Asp Asp Thr Leu Ala Leu Leu Gly Tyr Thr Gly Ile Gly Glu
                405                 410                 415

Gln Ala Ile Gly Ser Asp Arg Asp Arg Val Val Arg Ile Ser Thr Leu
            420                 425                 430

Pro Glu Thr Gly Ala Arg Gly Gly Asn His Pro Ile Phe Tyr Lys Asn
        435                 440                 445

Ser Ile Lys Leu Gly Tyr Val Ile Arg Ser Ile Asp Val Phe Asn Ser
    450                 455                 460

Gln Ile Leu His Thr Ser Arg Gln Leu Ser Leu Asn His Tyr Leu Leu
465                 470                 475                 480

Pro Pro Asp Ser Phe Ala Val Tyr Arg Ile Ile Asp Ser Asn Gly Ser
                485                 490                 495

Trp Phe Asp Ile Gly Ile Asp Ser Asp Gly Phe Ser Phe Val Gly Val
            500                 505                 510

Ser Gly Phe Gly Lys Leu Glu Phe Pro Leu Ser Ala Ser Tyr Met Gly
        515                 520                 525

Ile Gln Leu Ala Lys Ile Arg Leu Ala Ser Asn Ile Arg Ser Pro Met
    530                 535                 540

Thr Lys Leu
545


<210> SEQ ID NO 5
<211> LENGTH: 1752
<212> TYPE: DNA
<213> ORGANISM: Feline parvovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1752)

<400> SEQUENCE: 5

atg agt gat gga gca gtt caa cca gac ggt ggt caa cct gct gtc aga       48
Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
  1               5                  10                  15

aat gaa aga gct aca gga tct ggg aac ggg tct gga ggc ggg ggt ggt       96
Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
             20                  25                  30

ggt ggt tct ggg ggt gtg ggg att tct acg ggt act ttc aat aat cag      144
Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
         35                  40                  45

acg gaa ttt aaa ttt ttg gaa aac ggg tgg gtg gaa atc aca gca aac      192
Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
     50                  55                  60

tca agc aga ctt gta cat tta aat atg cca gaa agt gaa aat tat aaa      240
Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
 65                  70                  75                  80

aga gta gtt gta aat aat atg gat aaa act gca gtt aaa gga aac atg      288
Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
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                 85                  90                  95

gct tta gat gat att cat gta caa att gta aca cct tgg tca ttg gtt          336
Ala Leu Asp Asp Ile His Val Gln Ile Val Thr Pro Trp Ser Leu Val
            100                 105                 110

gat gca aat gct tgg gga gtt tgg ttt aat cca gga gat tgg caa cta          384
Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
        115                 120                 125

att gtt aat act atg agt gag ttg cat tta gtt agt ttt gaa caa gaa          432
Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu
    130                 135                 140

att ttt aat gtt gtt tta aag act gtt tca gaa tct gct act cag cca          480
Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro
145                 150                 155                 160

cca act aaa gtt tat aat aat gat tta act gca tca ttg atg gtt gca          528
Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
                165                 170                 175

tta gat agt aat aat act atg cca ttt act cca gca gct atg aga tct          576
Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
            180                 185                 190

gag aca ttg ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg          624
Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
        195                 200                 205

aga tat tat ttt caa tgg gat aga aca tta ata cca tct cat act gga          672
Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
    210                 215                 220

act agt ggc aca cca aca aat gta tat cat ggt aca gat cca gat gat          720
Thr Ser Gly Thr Pro Thr Asn Val Tyr His Gly Thr Asp Pro Asp Asp
225                 230                 235                 240

gtt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta aga          768
Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg
                245                 250                 255

aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt aaa cca          816
Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro
            260                 265                 270

tgt aga tta aca cat aca tgg caa aca aat aga gca ttg ggc tta cca          864
Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro
        275                 280                 285

cca ttt tta aat tct ttg cct caa tct gaa gga gct act aac ttt ggt          912
Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly
    290                 295                 300

gat ata gga gtt caa caa gat aaa aga cgt ggt gta act caa atg gga          960
Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly
305                 310                 315                 320

aat aca gac tat att act gaa gct act att atg aga cca gct gag gtt         1008
Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val
                325                 330                 335

ggt tat agt gca cca tat tat tct ttt gaa gcg tct aca caa ggg cca         1056
Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro
            340                 345                 350

ttt aaa aca cct att gca gca gga cgg ggg gga gcg caa aca gat gaa         1104
Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu
        355                 360                 365

aat caa gca gca gat ggt gat cca aga tat gca ttt ggt aga caa cat         1152
Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His
    370                 375                 380

ggt caa aaa act act aca aca gga gaa aca cct gag aga ttt aca tat         1200
Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr
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385                 390                 395                 400

ata gca cat caa gat aca gga aga tat cca gaa gga gat tgg att caa     1248
Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln
                405                 410                 415

aat att aac ttt aac ctt cct gta aca aat gat aat gta ttg cta cca     1296
Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro
            420                 425                 430

aca gat cca att ggg ggt aaa aca gga att aac tat act aat ata ttt     1344
Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
        435                 440                 445

aat act tat ggt cct tta act gca tta aat aat gta cca cca gtt tat     1392
Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
    450                 455                 460

cca aat ggt caa att tgg gat aaa gaa ttt gat act gac tta aaa cca     1440
Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
465                 470                 475                 480

aga ctt cat gta aat gca cca ttt gtt tgt caa aat aat tgt cct ggt     1488
Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly
                485                 490                 495

caa tta ttt gta aaa gtt gcg cct aat tta acg aat gaa tat gat cct     1536
Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro
            500                 505                 510

gat gca tct gct aat atg tca aga att gta act tat tca gat ttt tgg     1584
Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp
        515                 520                 525

tgg aaa ggt aaa tta gta ttt aaa gct aaa cta aga gca tct cat act     1632
Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr
    530                 535                 540

tgg aat cca att caa caa atg agc att aat gta gat aac caa ttt aac     1680
Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn
545                 550                 555                 560

tat gta cca aat aat att gga gct atg aaa att gta tat gaa aaa tct     1728
Tyr Val Pro Asn Asn Ile Gly Ala Met Lys Ile Val Tyr Glu Lys Ser
                565                 570                 575

caa cta gca cct aga aaa tta tat                                     1752
Gln Leu Ala Pro Arg Lys Leu Tyr
            580


<210> SEQ ID NO 6
<211> LENGTH: 584
<212> TYPE: PRT
<213> ORGANISM: Feline parvovirus

<400> SEQUENCE: 6

Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
  1               5                  10                  15

Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
             20                  25                  30

Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
         35                  40                  45

Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
     50                  55                  60

Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
 65                  70                  75                  80

Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
                 85                  90                  95
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Ala Leu Asp Asp Ile His Val Gln Ile Val Thr Pro Trp Ser Leu Val
            100                 105                 110

Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
        115                 120                 125

Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu
    130                 135                 140

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

Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
                165                 170                 175

Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
            180                 185                 190

Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
        195                 200                 205

Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
    210                 215                 220

Thr Ser Gly Thr Pro Thr Asn Val Tyr His Gly Thr Asp Pro Asp Asp
225                 230                 235                 240

Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg
                245                 250                 255

Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro
            260                 265                 270

Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro
        275                 280                 285

Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly
    290                 295                 300

Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly
305                 310                 315                 320

Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val
                325                 330                 335

Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro
            340                 345                 350

Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu
        355                 360                 365

Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His
    370                 375                 380

Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr
385                 390                 395                 400

Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Glu Gly Asp Trp Ile Gln
                405                 410                 415

Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro
            420                 425                 430

Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
        435                 440                 445

Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
    450                 455                 460

Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp Leu Lys Pro
465                 470                 475                 480

Arg Leu His Val Asn Ala Pro Phe Val Cys Gln Asn Asn Cys Pro Gly
                485                 490                 495

Gln Leu Phe Val Lys Val Ala Pro Asn Leu Thr Asn Glu Tyr Asp Pro
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            500                 505                 510

Asp Ala Ser Ala Asn Met Ser Arg Ile Val Thr Tyr Ser Asp Phe Trp
        515                 520                 525

Trp Lys Gly Lys Leu Val Phe Lys Ala Lys Leu Arg Ala Ser His Thr
    530                 535                 540

Trp Asn Pro Ile Gln Gln Met Ser Ile Asn Val Asp Asn Gln Phe Asn
545                 550                 555                 560

Tyr Val Pro Asn Asn Ile Gly Ala Met Lys Ile Val Tyr Glu Lys Ser
                565                 570                 575

Gln Leu Ala Pro Arg Lys Leu Tyr
            580


<210> SEQ ID NO 7
<211> LENGTH: 729
<212> TYPE: DNA
<213> ORGANISM: Feline parvovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(729)

<400> SEQUENCE: 7

ggt aca gat cca gat gat gtt caa ttt tat act att gaa aat tct gtg       48
Gly Thr Asp Pro Asp Asp Val Gln Phe Tyr Thr Ile Glu Asn Ser Val
  1               5                  10                  15

cca gta cac tta cta aga aca ggt gat gaa ttt gct aca gga aca ttt       96
Pro Val His Leu Leu Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe
             20                  25                  30

ttt ttt gat tgt aaa cca tgt aga tta aca cat aca tgg caa aca aat      144
Phe Phe Asp Cys Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn
         35                  40                  45

aga gca ttg ggc tta cca cca ttt tta aat tct ttg cct caa tct gaa      192
Arg Ala Leu Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu
     50                  55                  60

gga gct act aac ttt ggt gat ata gga gtt caa caa gat aaa aga cgt      240
Gly Ala Thr Asn Phe Gly Asp Ile Gly Val Gln Gln Asp Lys Arg Arg
 65                  70                  75                  80

ggt gta act caa atg gga aat aca gac tat att act gaa gct act att      288
Gly Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile
                 85                  90                  95

atg aga cca gct gag gtt ggt tat agt gca cca tat tat tct ttt gaa      336
Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu
            100                 105                 110

gcg tct aca caa ggg cca ttt aaa aca cct att gca gca gga cgg ggg      384
Ala Ser Thr Gln Gly Pro Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly
        115                 120                 125

gga gcg caa aca gat gaa aat caa gca gca gat ggt gat cca aga tat      432
Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr
    130                 135                 140

gca ttt ggt aga caa cat ggt caa aaa act act aca aca gga gaa aca      480
Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr
145                 150                 155                 160

cct gag aga ttt aca tat ata gca cat caa gat aca gga aga tat cca      528
Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp Thr Gly Arg Tyr Pro
                165                 170                 175

gaa gga gat tgg att caa aat att aac ttt aac ctt cct gta aca aat      576
Glu Gly Asp Trp Ile Gln Asn Ile Asn Phe Asn Leu Pro Val Thr Asn
            180                 185                 190
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gat aat gta ttg cta cca aca gat cca att ggg ggt aaa aca gga att          624
Asp Asn Val Leu Leu Pro Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile
        195                 200                 205

aac tat act aat ata ttt aat act tat ggt cct tta act gca tta aat          672
Asn Tyr Thr Asn Ile Phe Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn
    210                 215                 220

aat gta cca cca gtt tat cca aat ggt caa att tgg gat aaa gaa ttt          720
Asn Val Pro Pro Val Tyr Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe
225                 230                 235                 240

gat act gac                                                              729
Asp Thr Asp


<210> SEQ ID NO 8
<211> LENGTH: 243
<212> TYPE: PRT
<213> ORGANISM: Feline parvovirus

<400> SEQUENCE: 8

Gly Thr Asp Pro Asp Asp Val Gln Phe Tyr Thr Ile Glu Asn Ser Val
  1               5                  10                  15

Pro Val His Leu Leu Arg Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe
             20                  25                  30

Phe Phe Asp Cys Lys Pro Cys Arg Leu Thr His Thr Trp Gln Thr Asn
          35                  40                  45

Arg Ala Leu Gly Leu Pro Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu
     50                  55                  60

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

Gly Val Thr Gln Met Gly Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile
                 85                  90                  95

Met Arg Pro Ala Glu Val Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu
            100                 105                 110

Ala Ser Thr Gln Gly Pro Phe Lys Thr Pro Ile Ala Ala Gly Arg Gly
        115                 120                 125

Gly Ala Gln Thr Asp Glu Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr
    130                 135                 140

Ala Phe Gly Arg Gln His Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr
145                 150                 155                 160

Pro Glu Arg Phe Thr Tyr Ile Ala His Gln Asp Thr Gly Arg Tyr Pro
                165                 170                 175

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

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

Asn Tyr Thr Asn Ile Phe Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn
    210                 215                 220

Asn Val Pro Pro Val Tyr Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe
225                 230                 235                 240

Asp Thr Asp


<210> SEQ ID NO 9
<211> LENGTH: 1860
<212> TYPE: DNA
<213> ORGANISM: Feline parvovirus
<220> FEATURE:
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<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1860)

<400> SEQUENCE: 9

atg gca cct ccg gca aag aga gcc agg aga gga ctt gtg cct cca ggt       48
Met Ala Pro Pro Ala Lys Arg Ala Arg Arg Gly Leu Val Pro Pro Gly
  1               5                  10                  15

tat aaa tat ctt ggg cct ggg aac agt ctt gac caa gga gaa cca act       96
Tyr Lys Tyr Leu Gly Pro Gly Asn Ser Leu Asp Gln Gly Glu Pro Thr
             20                  25                  30

aac cct tct gac gcc gct gca aaa gaa cac gac gaa gct tac gct gct      144
Asn Pro Ser Asp Ala Ala Ala Lys Glu His Asp Glu Ala Tyr Ala Ala
         35                  40                  45

tat ctt cgc tct ggt aaa aac cca tac tta tat ttc tcg cca gca gat      192
Tyr Leu Arg Ser Gly Lys Asn Pro Tyr Leu Tyr Phe Ser Pro Ala Asp
     50                  55                  60

caa cgc ttt ata gat caa act aag gac gct aca gat tgg ggg ggg aaa      240
Gln Arg Phe Ile Asp Gln Thr Lys Asp Ala Thr Asp Trp Gly Gly Lys
 65                  70                  75                  80

ata gga cat tat ttt ttt aga gct aaa aaa gca att gct cca gta tta      288
Ile Gly His Tyr Phe Phe Arg Ala Lys Lys Ala Ile Ala Pro Val Leu
                 85                  90                  95

act gat aca cca gat cat cca tca aca tca aga cca aca aaa cca act      336
Thr Asp Thr Pro Asp His Pro Ser Thr Ser Arg Pro Thr Lys Pro Thr
            100                 105                 110

aaa aga agt aaa cca cca cct cat att ttc atc aat ctt gca aaa aaa      384
Lys Arg Ser Lys Pro Pro Pro His Ile Phe Ile Asn Leu Ala Lys Lys
        115                 120                 125

aaa aaa gcc ggt gca gga caa gta aaa aga gac aat caa gca cca atg      432
Lys Lys Ala Gly Ala Gly Gln Val Lys Arg Asp Asn Gln Ala Pro Met
    130                 135                 140

agt gat gga gca gtt caa cca gac ggt ggt caa cct gct gtc aga aat      480
Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg Asn
145                 150                 155                 160

gaa aga gct aca gga tct ggg aac ggg tct gga ggc ggg ggt ggt ggt      528
Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly Gly
                165                 170                 175

ggt tct ggg ggt gtg ggg att tct acg ggt act ttc aat aat cag acg      576
Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln Thr
            180                 185                 190

gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa atc aca gca aac tca      624
Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn Ser
        195                 200                 205

agc aga ctt gta cat tta aat atg cca gaa agt gaa aat tat aaa aga      672
Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys Arg
    210                 215                 220

gta gtt gta aat aat atg gat aaa act gca gtt aaa gga aac atg gct      720
Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met Ala
225                 230                 235                 240

tta gat gac act cat gta caa att gta aca cct tgg tca ttg gtt gat      768
Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val Asp
                245                 250                 255

gca aat gct tgg gga gtt tgg ttt aat cca gga gat tgg caa cta att      816
Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu Ile
            260                 265                 270

gtt aat act atg agt gag ttg cat tta gtt agt ttt gaa caa gaa att      864
Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu Ile
        275                 280                 285
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ttt aat gtt gtt tta aag act gtt tca gaa tct gct act cag cca cca       912
Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro
    290                 295                 300

act aaa gtt tat aat aat gat tta act gca tca ttg atg gtt gca tta       960
Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu
305                 310                 315                 320

gat agt aat aat act atg cca ttt act cca gca gct atg aga tct gag      1008
Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu
                325                 330                 335

aca ttg ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg aga      1056
Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg
            340                 345                 350

tat tat ttt caa tgg gat aga aca tta ata cca tct cat act gga act      1104
Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr
        355                 360                 365

agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat gtt      1152
Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp Val
    370                 375                 380

caa ttt tat act att gaa aat tct gtg cca gta cac tta cta aga aca      1200
Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg Thr
385                 390                 395                 400

ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt aaa cca tgt      1248
Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro Cys
                405                 410                 415

aga cta aca cat aca tgg caa aca aac aga gca ttg ggc tta cca cca      1296
Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro Pro
            420                 425                 430

ttt cta aat tct ttg cct caa tct gaa gga gct act aac ttt ggt gat      1344
Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly Asp
        435                 440                 445

ata gga gtt caa caa gat aaa aga cgt ggt gta act caa atg gga aat      1392
Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly Asn
    450                 455                 460

aca gac tat att act gaa gct act att atg aga cca gct gag gtt ggt      1440
Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val Gly
465                 470                 475                 480

tat agt gca cca tat tat tct ttt gaa gcg tct aca caa ggg cca ttt      1488
Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro Phe
                485                 490                 495

aaa ata cct att gca gca gga cgg ggg gga gcg caa aca gat gaa aat      1536
Lys Ile Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu Asn
            500                 505                 510

caa gca gca gat ggt gat cca aga tat gca ttt ggt aga caa cat ggt      1584
Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His Gly
        515                 520                 525

caa aaa act act aca aca gga gaa aca cct gag aga ttt aca tat ata      1632
Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile
    530                 535                 540

gca cat caa gat aca gga aga tat cca gca gga gat tgg att caa aat      1680
Ala His Gln Asp Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln Asn
545                 550                 555                 560

att aac ttt aac ctt cct gta aca aat gat aat gta ttg cta cca aca      1728
Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr
                565                 570                 575

gat cca att gga ggt aaa aca gga atc aac tat act aat ata ttt aat      1776
Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn
            580                 585                 590
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act tat ggt cct tta act gca tta aat aat gta cca cca gtt tat cca          1824
Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro
        595                 600                 605

aat ggt caa att tgg gat aaa gaa ttt gat act gac                          1860
Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp
    610                 615                 620


<210> SEQ ID NO 10
<211> LENGTH: 620
<212> TYPE: PRT
<213> ORGANISM: Feline parvovirus

<400> SEQUENCE: 10

Met Ala Pro Pro Ala Lys Arg Ala Arg Arg Gly Leu Val Pro Pro Gly
  1               5                  10                  15

Tyr Lys Tyr Leu Gly Pro Gly Asn Ser Leu Asp Gln Gly Glu Pro Thr
             20                  25                  30

Asn Pro Ser Asp Ala Ala Ala Lys Glu His Asp Glu Ala Tyr Ala Ala
         35                  40                  45

Tyr Leu Arg Ser Gly Lys Asn Pro Tyr Leu Tyr Phe Ser Pro Ala Asp
     50                  55                  60

Gln Arg Phe Ile Asp Gln Thr Lys Asp Ala Thr Asp Trp Gly Gly Lys
 65                  70                  75                  80

Ile Gly His Tyr Phe Phe Arg Ala Lys Lys Ala Ile Ala Pro Val Leu
                 85                  90                  95

Thr Asp Thr Pro Asp His Pro Ser Thr Ser Arg Pro Thr Lys Pro Thr
            100                 105                 110

Lys Arg Ser Lys Pro Pro Pro His Ile Phe Ile Asn Leu Ala Lys Lys
        115                 120                 125

Lys Lys Ala Gly Ala Gly Gln Val Lys Arg Asp Asn Gln Ala Pro Met
    130                 135                 140

Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg Asn
145                 150                 155                 160

Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly Gly
                165                 170                 175

Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln Thr
            180                 185                 190

Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn Ser
        195                 200                 205

Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys Arg
    210                 215                 220

Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met Ala
225                 230                 235                 240

Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val Asp
                245                 250                 255

Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu Ile
            260                 265                 270

Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu Ile
        275                 280                 285

Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro Pro
    290                 295                 300

Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala Leu
305                 310                 315                 320
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Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser Glu
                325                 330                 335

Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp Arg
            340                 345                 350

Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly Thr
        355                 360                 365

Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp Val
    370                 375                 380

Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg Thr
385                 390                 395                 400

Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro Cys
                405                 410                 415

Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro Pro
            420                 425                 430

Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly Asp
        435                 440                 445

Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly Asn
    450                 455                 460

Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val Gly
465                 470                 475                 480

Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro Phe
                485                 490                 495

Lys Ile Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu Asn
            500                 505                 510

Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His Gly
        515                 520                 525

Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr Ile
    530                 535                 540

Ala His Gln Asp Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln Asn
545                 550                 555                 560

Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro Thr
                565                 570                 575

Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe Asn
            580                 585                 590

Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr Pro
        595                 600                 605

Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp
    610                 615                 620


<210> SEQ ID NO 11
<211> LENGTH: 1431
<212> TYPE: DNA
<213> ORGANISM: Feline parvovirus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1431)

<400> SEQUENCE: 11

atg agt gat gga gca gtt caa cca gac ggt ggt caa cct gct gtc aga       48
Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
  1               5                  10                  15

aat gaa aga gct aca gga tct ggg aac ggg tct gga ggc ggg ggt ggt       96
Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
             20                  25                  30
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ggt ggt tct ggg ggt gtg ggg att tct acg ggt act ttc aat aat cag      144
Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
         35                  40                  45

acg gaa ttt aaa ttt ttg gaa aac gga tgg gtg gaa atc aca gca aac      192
Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
     50                  55                  60

tca agc aga ctt gta cat tta aat atg cca gaa agt gaa aat tat aaa      240
Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
 65                  70                  75                  80

aga gta gtt gta aat aat atg gat aaa act gca gtt aaa gga aac atg      288
Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
                 85                  90                  95

gct tta gat gac act cat gta caa att gta aca cct tgg tca ttg gtt      336
Ala Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val
            100                 105                 110

gat gca aat gct tgg gga gtt tgg ttt aat cca gga gat tgg caa cta      384
Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
        115                 120                 125

att gtt aat act atg agt gag ttg cat tta gtt agt ttt gaa caa gaa      432
Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu
    130                 135                 140

att ttt aat gtt gtt tta aag act gtt tca gaa tct gct act cag cca      480
Ile Phe Asn Val Val Leu Lys Thr Val Ser Glu Ser Ala Thr Gln Pro
145                 150                 155                 160

cca act aaa gtt tat aat aat gat tta act gca tca ttg atg gtt gca      528
Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
                165                 170                 175

tta gat agt aat aat act atg cca ttt act cca gca gct atg aga tct      576
Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
            180                 185                 190

gag aca ttg ggt ttt tat cca tgg aaa cca acc ata cca act cca tgg      624
Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
        195                 200                 205

aga tat tat ttt caa tgg gat aga aca tta ata cca tct cat act gga      672
Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
    210                 215                 220

act agt ggc aca cca aca aat ata tat cat ggt aca gat cca gat gat      720
Thr Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp
225                 230                 235                 240

gtt caa ttt tat act att gaa aat tct gtg cca gta cac tta cta aga      768
Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg
                245                 250                 255

aca ggt gat gaa ttt gct aca gga aca ttt ttt ttt gat tgt aaa cca      816
Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro
            260                 265                 270

tgt aga cta aca cat aca tgg caa aca aac aga gca ttg ggc tta cca      864
Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro
        275                 280                 285

cca ttt cta aat tct ttg cct caa tct gaa gga gct act aac ttt ggt      912
Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly
    290                 295                 300

gat ata gga gtt caa caa gat aaa aga cgt ggt gta act caa atg gga      960
Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly
305                 310                 315                 320

aat aca gac tat att act gaa gct act att atg aga cca gct gag gtt     1008
Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val
                325                 330                 335
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ggt tat agt gca cca tat tat tct ttt gaa gcg tct aca caa ggg cca     1056
Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro
            340                 345                 350

ttt aaa ata cct att gca gca gga cgg ggg gga gcg caa aca gat gaa     1104
Phe Lys Ile Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu
        355                 360                 365

aat caa gca gca gat ggt gat cca aga tat gca ttt ggt aga caa cat     1152
Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His
    370                 375                 380

ggt caa aaa act act aca aca gga gaa aca cct gag aga ttt aca tat     1200
Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr
385                 390                 395                 400

ata gca cat caa gat aca gga aga tat cca gca gga gat tgg att caa     1248
Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln
                405                 410                 415

aat att aac ttt aac ctt cct gta aca aat gat aat gta ttg cta cca     1296
Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro
            420                 425                 430

aca gat cca att gga ggt aaa aca gga atc aac tat act aat ata ttt     1344
Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
        435                 440                 445

aat act tat ggt cct tta act gca tta aat aat gta cca cca gtt tat     1392
Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
    450                 455                 460

cca aat ggt caa att tgg gat aaa gaa ttt gat act gac                 1431
Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp
465                 470                 475


<210> SEQ ID NO 12
<211> LENGTH: 477
<212> TYPE: PRT
<213> ORGANISM: Feline parvovirus

<400> SEQUENCE: 12

Met Ser Asp Gly Ala Val Gln Pro Asp Gly Gly Gln Pro Ala Val Arg
  1               5                  10                  15

Asn Glu Arg Ala Thr Gly Ser Gly Asn Gly Ser Gly Gly Gly Gly Gly
             20                  25                  30

Gly Gly Ser Gly Gly Val Gly Ile Ser Thr Gly Thr Phe Asn Asn Gln
         35                  40                  45

Thr Glu Phe Lys Phe Leu Glu Asn Gly Trp Val Glu Ile Thr Ala Asn
     50                  55                  60

Ser Ser Arg Leu Val His Leu Asn Met Pro Glu Ser Glu Asn Tyr Lys
 65                  70                  75                  80

Arg Val Val Val Asn Asn Met Asp Lys Thr Ala Val Lys Gly Asn Met
                 85                  90                  95

Ala Leu Asp Asp Thr His Val Gln Ile Val Thr Pro Trp Ser Leu Val
            100                 105                 110

Asp Ala Asn Ala Trp Gly Val Trp Phe Asn Pro Gly Asp Trp Gln Leu
        115                 120                 125

Ile Val Asn Thr Met Ser Glu Leu His Leu Val Ser Phe Glu Gln Glu
    130                 135                 140

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

Pro Thr Lys Val Tyr Asn Asn Asp Leu Thr Ala Ser Leu Met Val Ala
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                165                 170                 175

Leu Asp Ser Asn Asn Thr Met Pro Phe Thr Pro Ala Ala Met Arg Ser
            180                 185                 190

Glu Thr Leu Gly Phe Tyr Pro Trp Lys Pro Thr Ile Pro Thr Pro Trp
        195                 200                 205

Arg Tyr Tyr Phe Gln Trp Asp Arg Thr Leu Ile Pro Ser His Thr Gly
    210                 215                 220

Thr Ser Gly Thr Pro Thr Asn Ile Tyr His Gly Thr Asp Pro Asp Asp
225                 230                 235                 240

Val Gln Phe Tyr Thr Ile Glu Asn Ser Val Pro Val His Leu Leu Arg
                245                 250                 255

Thr Gly Asp Glu Phe Ala Thr Gly Thr Phe Phe Phe Asp Cys Lys Pro
            260                 265                 270

Cys Arg Leu Thr His Thr Trp Gln Thr Asn Arg Ala Leu Gly Leu Pro
        275                 280                 285

Pro Phe Leu Asn Ser Leu Pro Gln Ser Glu Gly Ala Thr Asn Phe Gly
    290                 295                 300

Asp Ile Gly Val Gln Gln Asp Lys Arg Arg Gly Val Thr Gln Met Gly
305                 310                 315                 320

Asn Thr Asp Tyr Ile Thr Glu Ala Thr Ile Met Arg Pro Ala Glu Val
                325                 330                 335

Gly Tyr Ser Ala Pro Tyr Tyr Ser Phe Glu Ala Ser Thr Gln Gly Pro
            340                 345                 350

Phe Lys Ile Pro Ile Ala Ala Gly Arg Gly Gly Ala Gln Thr Asp Glu
        355                 360                 365

Asn Gln Ala Ala Asp Gly Asp Pro Arg Tyr Ala Phe Gly Arg Gln His
    370                 375                 380

Gly Gln Lys Thr Thr Thr Thr Gly Glu Thr Pro Glu Arg Phe Thr Tyr
385                 390                 395                 400

Ile Ala His Gln Asp Thr Gly Arg Tyr Pro Ala Gly Asp Trp Ile Gln
                405                 410                 415

Asn Ile Asn Phe Asn Leu Pro Val Thr Asn Asp Asn Val Leu Leu Pro
            420                 425                 430

Thr Asp Pro Ile Gly Gly Lys Thr Gly Ile Asn Tyr Thr Asn Ile Phe
        435                 440                 445

Asn Thr Tyr Gly Pro Leu Thr Ala Leu Asn Asn Val Pro Pro Val Tyr
    450                 455                 460

Pro Asn Gly Gln Ile Trp Asp Lys Glu Phe Asp Thr Asp
465                 470                 475


<210> SEQ ID NO 13
<211> LENGTH: 2829
<212> TYPE: DNA
<213> ORGANISM: Feline herpesvirus 1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(2829)

<400> SEQUENCE: 13

atg tcc act cgt ggc gat ctt ggg aag cgg cga cga ggg agt cgt tgg            48
Met Ser Thr Arg Gly Asp Leu Gly Lys Arg Arg Arg Gly Ser Arg Trp
  1               5                  10                  15

cag gga cac agt ggc tat ttt cga cag aga tgt ttt ttc cct tct cta            96
Gln Gly His Ser Gly Tyr Phe Arg Gln Arg Cys Phe Phe Pro Ser Leu
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            20                  25                  30

ctc ggt att gca gcg act ggc tcc aga cat ggt aac gga tcg tcg gga      144
Leu Gly Ile Ala Ala Thr Gly Ser Arg His Gly Asn Gly Ser Ser Gly
         35                  40                  45

tta acc aga cta gct aga tat gtt tca ttt atc tgg atc gta cta ttc      192
Leu Thr Arg Leu Ala Arg Tyr Val Ser Phe Ile Trp Ile Val Leu Phe
     50                  55                  60

tta gtc ggt ccc cgt cca gta gag ggt caa tct gga agc aca tcg gaa      240
Leu Val Gly Pro Arg Pro Val Glu Gly Gln Ser Gly Ser Thr Ser Glu
 65                  70                  75                  80

caa ccc cgg cgg act gta gct acc cct gag gta ggg gta cac cac caa      288
Gln Pro Arg Arg Thr Val Ala Thr Pro Glu Val Gly Val His His Gln
                 85                  90                  95

aac caa cta cag atc cca ccg ata tgt cga tat gag gaa gct ctc cgt      336
Asn Gln Leu Gln Ile Pro Pro Ile Cys Arg Tyr Glu Glu Ala Leu Arg
            100                 105                 110

gcg tcc caa ata gag gct aac gga cca tcg act ttt tat atg tgt cca      384
Ala Ser Gln Ile Glu Ala Asn Gly Pro Ser Thr Phe Tyr Met Cys Pro
        115                 120                 125

cca cct tca gga tct act gtc gtg cgt tta gag cca cca cgg gcc tgt      432
Pro Pro Ser Gly Ser Thr Val Val Arg Leu Glu Pro Pro Arg Ala Cys
    130                 135                 140

cca gat tat aaa cta ggg aaa aat ttt acc gag ggt ata gct gta ata      480
Pro Asp Tyr Lys Leu Gly Lys Asn Phe Thr Glu Gly Ile Ala Val Ile
145                 150                 155                 160

ttt aaa gaa aat ata gcg cca tat aaa ttc aag gca aat ata tac tat      528
Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Asn Ile Tyr Tyr
                165                 170                 175

aaa aac att att atg aca acg gta tgg tct ggg agt tcc tat gcc gtt      576
Lys Asn Ile Ile Met Thr Thr Val Trp Ser Gly Ser Ser Tyr Ala Val
            180                 185                 190

aca acc aac cga tat aca gac agg gtt ccc gtg aaa gtt caa gag att      624
Thr Thr Asn Arg Tyr Thr Asp Arg Val Pro Val Lys Val Gln Glu Ile
        195                 200                 205

aca gat ctc ata gat aga cgg ggt atg tgc ctc tcg aaa gct gat tac      672
Thr Asp Leu Ile Asp Arg Arg Gly Met Cys Leu Ser Lys Ala Asp Tyr
    210                 215                 220

gtt cgt aac aat tat caa ttt acg gcc ttt gat cga gac gag gat ccc      720
Val Arg Asn Asn Tyr Gln Phe Thr Ala Phe Asp Arg Asp Glu Asp Pro
225                 230                 235                 240

aga gaa ctg cct ctg aaa cct cca agt tca aca ctc tcc aga gtc cgt      768
Arg Glu Leu Pro Leu Lys Pro Pro Ser Ser Thr Leu Ser Arg Val Arg
                245                 250                 255

gga tgg cac acc aat gaa aca tac aca aag atc gtg ctg ctg gat ttc      816
Gly Trp His Thr Asn Glu Thr Tyr Thr Lys Ile Val Leu Leu Asp Phe
            260                 265                 270

cac cac tct ggg acc tct gta aat tgc atc gta gag gaa gtg gat gca      864
His His Ser Gly Thr Ser Val Asn Cys Ile Val Glu Glu Val Asp Ala
        275                 280                 285

aga tct gta tat cca tat gac tca ttt gct atc tcc act ggt gac gtg      912
Arg Ser Val Tyr Pro Tyr Asp Ser Phe Ala Ile Ser Thr Gly Asp Val
    290                 295                 300

att cac atg tct cca ttc ttt ggg ctg agg gat gga gcc cat gta gaa      960
Ile His Met Ser Pro Phe Phe Gly Leu Arg Asp Gly Ala His Val Glu
305                 310                 315                 320

cat act agt tat tct tca gac aga ttt caa caa atc gag gga tac tat     1008
His Thr Ser Tyr Ser Ser Asp Arg Phe Gln Gln Ile Glu Gly Tyr Tyr
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                325                 330                 335

cca ata gac ttg gat acc gat tac act ggg gca cca gtt tct cgc aat     1056
Pro Ile Asp Leu Asp Thr Asp Tyr Thr Gly Ala Pro Val Ser Arg Asn
            340                 345                 350

ttt ttg gaa act ccg cat gtg aca gtg gcc tgg aac tgg acc cca aag     1104
Phe Leu Glu Thr Pro His Val Thr Val Ala Trp Asn Trp Thr Pro Lys
        355                 360                 365

tct ggt cgg gta tgt acc tta gcc aaa tgg agg gaa ata gat gaa atg     1152
Ser Gly Arg Val Cys Thr Leu Ala Lys Trp Arg Glu Ile Asp Glu Met
    370                 375                 380

cta ccg atg aat ata ggc tcc tat aga ttt aca gcc aag acc ata tcc     1200
Leu Pro Met Asn Ile Gly Ser Tyr Arg Phe Thr Ala Lys Thr Ile Ser
385                 390                 395                 400

gct act ttc atc tcc aat act tca caa ttt gaa atc aat cgt atc cgt     1248
Ala Thr Phe Ile Ser Asn Thr Ser Gln Phe Glu Ile Asn Arg Ile Arg
                405                 410                 415

ttg ggg gac tgt gcc acc aag gag gca gcc gaa gcc ata gac cgg att     1296
Leu Gly Asp Cys Ala Thr Lys Glu Ala Ala Glu Ala Ile Asp Arg Ile
            420                 425                 430

tat aag agt aaa tat agt aaa act cat att cag act gga acc ctg gag     1344
Tyr Lys Ser Lys Tyr Ser Lys Thr His Ile Gln Thr Gly Thr Leu Glu
        435                 440                 445

acc tac cta gcc cgt ggg gga ttt cta ata gct ttc cgt ccc atg atc     1392
Thr Tyr Leu Ala Arg Gly Gly Phe Leu Ile Ala Phe Arg Pro Met Ile
    450                 455                 460

agc aac gaa cta gca aag tta tat atc aat gaa tta gca cgt tcc aat     1440
Ser Asn Glu Leu Ala Lys Leu Tyr Ile Asn Glu Leu Ala Arg Ser Asn
465                 470                 475                 480

cgc acg gta gtg gat ctc agt gca ctc ctc aat cca tct ggg gaa aca     1488
Arg Thr Val Val Asp Leu Ser Ala Leu Leu Asn Pro Ser Gly Glu Thr
                485                 490                 495

gta caa cga act aga aga tcg gtc cca tct aat caa cat cat agg tcg     1536
Val Gln Arg Thr Arg Arg Ser Val Pro Ser Asn Gln His His Arg Ser
            500                 505                 510

cgg cgc agc aca ata gag ggg ggt ata gaa acc gtg aac aat gca tca     1584
Arg Arg Ser Thr Ile Glu Gly Gly Ile Glu Thr Val Asn Asn Ala Ser
        515                 520                 525

ctc ctc aag acc acc tca tct gtg gaa ttc gca atg cta caa ttt gcc     1632
Leu Leu Lys Thr Thr Ser Ser Val Glu Phe Ala Met Leu Gln Phe Ala
    530                 535                 540

tat gac tac ata caa gcc cat gta aat gaa atg ttg agt cgg ata gcc     1680
Tyr Asp Tyr Ile Gln Ala His Val Asn Glu Met Leu Ser Arg Ile Ala
545                 550                 555                 560

act gcc tgg tgt aca ctt cag aac cgc gaa cat gtg ctg tgg aca gag     1728
Thr Ala Trp Cys Thr Leu Gln Asn Arg Glu His Val Leu Trp Thr Glu
                565                 570                 575

acc cta aaa ctc aat ccc ggt ggg gtg gtc tcg atg gcc cta gaa cgt     1776
Thr Leu Lys Leu Asn Pro Gly Gly Val Val Ser Met Ala Leu Glu Arg
            580                 585                 590

cgt gta tcc gcg cgc cta ctt gga gat gcc gtc gcc gta aca caa tgt     1824
Arg Val Ser Ala Arg Leu Leu Gly Asp Ala Val Ala Val Thr Gln Cys
        595                 600                 605

gtt aac att tct agc gga cat gtc tat atc caa aat tct atg cgg gtg     1872
Val Asn Ile Ser Ser Gly His Val Tyr Ile Gln Asn Ser Met Arg Val
    610                 615                 620

acg ggt tca tca acg aca tgt tac agc cgc cct ctt gtt tcc ttc cgt     1920
Thr Gly Ser Ser Thr Thr Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg
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625                 630                 635                 640

gcc ctc aat gac tcc gaa tac ata gaa gga caa cta ggg gaa aac aat     1968
Ala Leu Asn Asp Ser Glu Tyr Ile Glu Gly Gln Leu Gly Glu Asn Asn
                645                 650                 655

gaa ctt ctc gtg gaa cga aaa cta att gag cct tgc act gtc aat aat     2016
Glu Leu Leu Val Glu Arg Lys Leu Ile Glu Pro Cys Thr Val Asn Asn
            660                 665                 670

aag cgg tat ttt aag ttt ggg gca gat tat gta tat ttt gag gat tat     2064
Lys Arg Tyr Phe Lys Phe Gly Ala Asp Tyr Val Tyr Phe Glu Asp Tyr
        675                 680                 685

gcg tat gtc cgt aaa gtc ccg cta tcg gag ata gaa ctg ata agt gcg     2112
Ala Tyr Val Arg Lys Val Pro Leu Ser Glu Ile Glu Leu Ile Ser Ala
    690                 695                 700

tat gtg att aaa tct act ctc cta gag gat cgt gaa ttt ctc cac tca     2160
Tyr Val Ile Lys Ser Thr Leu Leu Glu Asp Arg Glu Phe Leu His Ser
705                 710                 715                 720

agt tat aca cga gct gag ctg gaa gat acc ggc cct ttt gac tac agc     2208
Ser Tyr Thr Arg Ala Glu Leu Glu Asp Thr Gly Pro Phe Asp Tyr Ser
                725                 730                 735

gag att caa cgc cgc aac caa ctc cac gcc tta aaa ttt tat gat ata     2256
Glu Ile Gln Arg Arg Asn Gln Leu His Ala Leu Lys Phe Tyr Asp Ile
            740                 745                 750

gac agc ata gtc aga gtg gat aat aat ctt gtc atc atg cgt ggt atg     2304
Asp Ser Ile Val Arg Val Asp Asn Asn Leu Val Ile Met Arg Gly Met
        755                 760                 765

gca aat ttt ttt cag gga ctc ggg gat gtg ggg gct ggt ttc ggc aag     2352
Ala Asn Phe Phe Gln Gly Leu Gly Asp Val Gly Ala Gly Phe Gly Lys
    770                 775                 780

gtg gtc tta ggg gct gcg agt gcg gta atc tca aca gta tca ggc gta     2400
Val Val Leu Gly Ala Ala Ser Ala Val Ile Ser Thr Val Ser Gly Val
785                 790                 795                 800

tca tca ttt cta aac aac cca ttt gga gca ttg gcc gtg gga ctg tta     2448
Ser Ser Phe Leu Asn Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu
                805                 810                 815

ata tta gct ggc atc gtc gca gca ttc ctg gca tat cgc tat ata tct     2496
Ile Leu Ala Gly Ile Val Ala Ala Phe Leu Ala Tyr Arg Tyr Ile Ser
            820                 825                 830

aga tta cgt gca aat cca atg aaa gcc tta tat cct gtg acg act agg     2544
Arg Leu Arg Ala Asn Pro Met Lys Ala Leu Tyr Pro Val Thr Thr Arg
        835                 840                 845

aat ttg aaa cag acg gct aag agc ccc gcc tca acg gct ggt ggg gat     2592
Asn Leu Lys Gln Thr Ala Lys Ser Pro Ala Ser Thr Ala Gly Gly Asp
    850                 855                 860

agc gac ccg gga gtc gat gac ttc gat gag gaa aag cta atg cag gca     2640
Ser Asp Pro Gly Val Asp Asp Phe Asp Glu Glu Lys Leu Met Gln Ala
865                 870                 875                 880

agg gag atg ata aaa tat atg tcc ctc gta tcg gct atg gag caa caa     2688
Arg Glu Met Ile Lys Tyr Met Ser Leu Val Ser Ala Met Glu Gln Gln
                885                 890                 895

gaa cat aag gcg atg aaa aag aat aag ggc cca gcg atc cta acg agt     2736
Glu His Lys Ala Met Lys Lys Asn Lys Gly Pro Ala Ile Leu Thr Ser
            900                 905                 910

cat ctc act aac atg gcc ctc cgt cgc cgt gga cct aaa tac caa cgc     2784
His Leu Thr Asn Met Ala Leu Arg Arg Arg Gly Pro Lys Tyr Gln Arg
        915                 920                 925

ctc aat aat ctt gat agc ggt gat gat act gaa aca aat ctt gtc         2829
Leu Asn Asn Leu Asp Ser Gly Asp Asp Thr Glu Thr Asn Leu Val
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    930                 935                 940

<210> SEQ ID NO 14
<211> LENGTH: 943
<212> TYPE: PRT
<213> ORGANISM: Feline herpesvirus 1

<400> SEQUENCE: 14

Met Ser Thr Arg Gly Asp Leu Gly Lys Arg Arg Arg Gly Ser Arg Trp
  1               5                  10                  15

Gln Gly His Ser Gly Tyr Phe Arg Gln Arg Cys Phe Phe Pro Ser Leu
             20                  25                  30

Leu Gly Ile Ala Ala Thr Gly Ser Arg His Gly Asn Gly Ser Ser Gly
         35                  40                  45

Leu Thr Arg Leu Ala Arg Tyr Val Ser Phe Ile Trp Ile Val Leu Phe
     50                  55                  60

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

Gln Pro Arg Arg Thr Val Ala Thr Pro Glu Val Gly Val His His Gln
                 85                  90                  95

Asn Gln Leu Gln Ile Pro Pro Ile Cys Arg Tyr Glu Glu Ala Leu Arg
            100                 105                 110

Ala Ser Gln Ile Glu Ala Asn Gly Pro Ser Thr Phe Tyr Met Cys Pro
        115                 120                 125

Pro Pro Ser Gly Ser Thr Val Val Arg Leu Glu Pro Pro Arg Ala Cys
    130                 135                 140

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

Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Asn Ile Tyr Tyr
                165                 170                 175

Lys Asn Ile Ile Met Thr Thr Val Trp Ser Gly Ser Ser Tyr Ala Val
            180                 185                 190

Thr Thr Asn Arg Tyr Thr Asp Arg Val Pro Val Lys Val Gln Glu Ile
        195                 200                 205

Thr Asp Leu Ile Asp Arg Arg Gly Met Cys Leu Ser Lys Ala Asp Tyr
    210                 215                 220

Val Arg Asn Asn Tyr Gln Phe Thr Ala Phe Asp Arg Asp Glu Asp Pro
225                 230                 235                 240

Arg Glu Leu Pro Leu Lys Pro Pro Ser Ser Thr Leu Ser Arg Val Arg
                245                 250                 255

Gly Trp His Thr Asn Glu Thr Tyr Thr Lys Ile Val Leu Leu Asp Phe
            260                 265                 270

His His Ser Gly Thr Ser Val Asn Cys Ile Val Glu Glu Val Asp Ala
        275                 280                 285

Arg Ser Val Tyr Pro Tyr Asp Ser Phe Ala Ile Ser Thr Gly Asp Val
    290                 295                 300

Ile His Met Ser Pro Phe Phe Gly Leu Arg Asp Gly Ala His Val Glu
305                 310                 315                 320

His Thr Ser Tyr Ser Ser Asp Arg Phe Gln Gln Ile Glu Gly Tyr Tyr
                325                 330                 335

Pro Ile Asp Leu Asp Thr Asp Tyr Thr Gly Ala Pro Val Ser Arg Asn
            340                 345                 350
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Phe Leu Glu Thr Pro His Val Thr Val Ala Trp Asn Trp Thr Pro Lys
        355                 360                 365

Ser Gly Arg Val Cys Thr Leu Ala Lys Trp Arg Glu Ile Asp Glu Met
    370                 375                 380

Leu Pro Met Asn Ile Gly Ser Tyr Arg Phe Thr Ala Lys Thr Ile Ser
385                 390                 395                 400

Ala Thr Phe Ile Ser Asn Thr Ser Gln Phe Glu Ile Asn Arg Ile Arg
                405                 410                 415

Leu Gly Asp Cys Ala Thr Lys Glu Ala Ala Glu Ala Ile Asp Arg Ile
            420                 425                 430

Tyr Lys Ser Lys Tyr Ser Lys Thr His Ile Gln Thr Gly Thr Leu Glu
        435                 440                 445

Thr Tyr Leu Ala Arg Gly Gly Phe Leu Ile Ala Phe Arg Pro Met Ile
    450                 455                 460

Ser Asn Glu Leu Ala Lys Leu Tyr Ile Asn Glu Leu Ala Arg Ser Asn
465                 470                 475                 480

Arg Thr Val Val Asp Leu Ser Ala Leu Leu Asn Pro Ser Gly Glu Thr
                485                 490                 495

Val Gln Arg Thr Arg Arg Ser Val Pro Ser Asn Gln His His Arg Ser
            500                 505                 510

Arg Arg Ser Thr Ile Glu Gly Gly Ile Glu Thr Val Asn Asn Ala Ser
        515                 520                 525

Leu Leu Lys Thr Thr Ser Ser Val Glu Phe Ala Met Leu Gln Phe Ala
    530                 535                 540

Tyr Asp Tyr Ile Gln Ala His Val Asn Glu Met Leu Ser Arg Ile Ala
545                 550                 555                 560

Thr Ala Trp Cys Thr Leu Gln Asn Arg Glu His Val Leu Trp Thr Glu
                565                 570                 575

Thr Leu Lys Leu Asn Pro Gly Gly Val Val Ser Met Ala Leu Glu Arg
            580                 585                 590

Arg Val Ser Ala Arg Leu Leu Gly Asp Ala Val Ala Val Thr Gln Cys
        595                 600                 605

Val Asn Ile Ser Ser Gly His Val Tyr Ile Gln Asn Ser Met Arg Val
    610                 615                 620

Thr Gly Ser Ser Thr Thr Cys Tyr Ser Arg Pro Leu Val Ser Phe Arg
625                 630                 635                 640

Ala Leu Asn Asp Ser Glu Tyr Ile Glu Gly Gln Leu Gly Glu Asn Asn
                645                 650                 655

Glu Leu Leu Val Glu Arg Lys Leu Ile Glu Pro Cys Thr Val Asn Asn
            660                 665                 670

Lys Arg Tyr Phe Lys Phe Gly Ala Asp Tyr Val Tyr Phe Glu Asp Tyr
        675                 680                 685

Ala Tyr Val Arg Lys Val Pro Leu Ser Glu Ile Glu Leu Ile Ser Ala
    690                 695                 700

Tyr Val Ile Lys Ser Thr Leu Leu Glu Asp Arg Glu Phe Leu His Ser
705                 710                 715                 720

Ser Tyr Thr Arg Ala Glu Leu Glu Asp Thr Gly Pro Phe Asp Tyr Ser
                725                 730                 735

Glu Ile Gln Arg Arg Asn Gln Leu His Ala Leu Lys Phe Tyr Asp Ile
            740                 745                 750

Asp Ser Ile Val Arg Val Asp Asn Asn Leu Val Ile Met Arg Gly Met
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        755                 760                 765

Ala Asn Phe Phe Gln Gly Leu Gly Asp Val Gly Ala Gly Phe Gly Lys
    770                 775                 780

Val Val Leu Gly Ala Ala Ser Ala Val Ile Ser Thr Val Ser Gly Val
785                 790                 795                 800

Ser Ser Phe Leu Asn Asn Pro Phe Gly Ala Leu Ala Val Gly Leu Leu
                805                 810                 815

Ile Leu Ala Gly Ile Val Ala Ala Phe Leu Ala Tyr Arg Tyr Ile Ser
            820                 825                 830

Arg Leu Arg Ala Asn Pro Met Lys Ala Leu Tyr Pro Val Thr Thr Arg
        835                 840                 845

Asn Leu Lys Gln Thr Ala Lys Ser Pro Ala Ser Thr Ala Gly Gly Asp
    850                 855                 860

Ser Asp Pro Gly Val Asp Asp Phe Asp Glu Glu Lys Leu Met Gln Ala
865                 870                 875                 880

Arg Glu Met Ile Lys Tyr Met Ser Leu Val Ser Ala Met Glu Gln Gln
                885                 890                 895

Glu His Lys Ala Met Lys Lys Asn Lys Gly Pro Ala Ile Leu Thr Ser
            900                 905                 910

His Leu Thr Asn Met Ala Leu Arg Arg Arg Gly Pro Lys Tyr Gln Arg
        915                 920                 925

Leu Asn Asn Leu Asp Ser Gly Asp Asp Thr Glu Thr Asn Leu Val
    930                 935                 940


<210> SEQ ID NO 15
<211> LENGTH: 750
<212> TYPE: DNA
<213> ORGANISM: Feline herpesvirus 1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(750)

<400> SEQUENCE: 15

atg tcc act cgt ggc gat ctt ggg aag cgg cga cga ggg agt cgt tgg           48
Met Ser Thr Arg Gly Asp Leu Gly Lys Arg Arg Arg Gly Ser Arg Trp
  1               5                  10                  15

cag gga cac agt ggc tat ttt cga cag aga tgt ttt ttc cct tct cta           96
Gln Gly His Ser Gly Tyr Phe Arg Gln Arg Cys Phe Phe Pro Ser Leu
             20                  25                  30

ctc ggt att gca gcg act ggc tcc aga cat ggt aac gga tcg tcg gga          144
Leu Gly Ile Ala Ala Thr Gly Ser Arg His Gly Asn Gly Ser Ser Gly
         35                  40                  45

tta acc aga cta gct aga tat gtt tca ttt atc tgg atc gta cta ttc          192
Leu Thr Arg Leu Ala Arg Tyr Val Ser Phe Ile Trp Ile Val Leu Phe
     50                  55                  60

tta gtc ggt ccc cgt cca gta gag ggt caa tct gga agc aca tcg gaa          240
Leu Val Gly Pro Arg Pro Val Glu Gly Gln Ser Gly Ser Thr Ser Glu
 65                  70                  75                  80

caa ccc cgg cgg act gta gct acc cct gag gta ggg gta cac cac caa          288
Gln Pro Arg Arg Thr Val Ala Thr Pro Glu Val Gly Val His His Gln
                 85                  90                  95

aac caa cta cag atc cca ccg ata tgt cga tat gag gaa gct ctc cgt          336
Asn Gln Leu Gln Ile Pro Pro Ile Cys Arg Tyr Glu Glu Ala Leu Arg
            100                 105                 110

gcg tcc caa ata gag gct aac gga cca tcg act ttt tat atg tgt cca          384
Ala Ser Gln Ile Glu Ala Asn Gly Pro Ser Thr Phe Tyr Met Cys Pro
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        115                 120                 125

cca cct tca gga tct act gtc gtg cgt tta gag cca cca cgg gcc tgt      432
Pro Pro Ser Gly Ser Thr Val Val Arg Leu Glu Pro Pro Arg Ala Cys
    130                 135                 140

cca gat tat aaa cta ggg aaa aat ttt acc gag ggt ata gct gta ata      480
Pro Asp Tyr Lys Leu Gly Lys Asn Phe Thr Glu Gly Ile Ala Val Ile
145                 150                 155                 160

ttt aaa gaa aat ata gcg cca tat aaa ttc aag gca aat ata tac tat      528
Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Asn Ile Tyr Tyr
                165                 170                 175

aaa aac att att atg aca acg gta tgg tct ggg agt tcc tat gcc gtt      576
Lys Asn Ile Ile Met Thr Thr Val Trp Ser Gly Ser Ser Tyr Ala Val
            180                 185                 190

aca acc aac cga tat aca gac agg gtt ccc gtg aaa gtt caa gag att      624
Thr Thr Asn Arg Tyr Thr Asp Arg Val Pro Val Lys Val Gln Glu Ile
        195                 200                 205

aca gat ctc ata gat aga cgg ggt atg tgc ctc tcg aaa gct gat tac      672
Thr Asp Leu Ile Asp Arg Arg Gly Met Cys Leu Ser Lys Ala Asp Tyr
    210                 215                 220

gtt cgt aac aat tat caa ttt acg gcc ttt gat cga gac gag gat ccc      720
Val Arg Asn Asn Tyr Gln Phe Thr Ala Phe Asp Arg Asp Glu Asp Pro
225                 230                 235                 240

aga gaa ctg cct ctg aaa cct cca agt tca                              750
Arg Glu Leu Pro Leu Lys Pro Pro Ser Ser
                245                 250


<210> SEQ ID NO 16
<211> LENGTH: 250
<212> TYPE: PRT
<213> ORGANISM: Feline herpesvirus 1

<400> SEQUENCE: 16

Met Ser Thr Arg Gly Asp Leu Gly Lys Arg Arg Arg Gly Ser Arg Trp
  1               5                  10                  15

Gln Gly His Ser Gly Tyr Phe Arg Gln Arg Cys Phe Phe Pro Ser Leu
             20                  25                  30

Leu Gly Ile Ala Ala Thr Gly Ser Arg His Gly Asn Gly Ser Ser Gly
         35                  40                  45

Leu Thr Arg Leu Ala Arg Tyr Val Ser Phe Ile Trp Ile Val Leu Phe
     50                  55                  60

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

Gln Pro Arg Arg Thr Val Ala Thr Pro Glu Val Gly Val His His Gln
                 85                  90                  95

Asn Gln Leu Gln Ile Pro Pro Ile Cys Arg Tyr Glu Glu Ala Leu Arg
            100                 105                 110

Ala Ser Gln Ile Glu Ala Asn Gly Pro Ser Thr Phe Tyr Met Cys Pro
        115                 120                 125

Pro Pro Ser Gly Ser Thr Val Val Arg Leu Glu Pro Pro Arg Ala Cys
    130                 135                 140

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

Phe Lys Glu Asn Ile Ala Pro Tyr Lys Phe Lys Ala Asn Ile Tyr Tyr
                165                 170                 175

Lys Asn Ile Ile Met Thr Thr Val Trp Ser Gly Ser Ser Tyr Ala Val
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            180                 185                 190

Thr Thr Asn Arg Tyr Thr Asp Arg Val Pro Val Lys Val Gln Glu Ile
        195                 200                 205

Thr Asp Leu Ile Asp Arg Arg Gly Met Cys Leu Ser Lys Ala Asp Tyr
    210                 215                 220

Val Arg Asn Asn Tyr Gln Phe Thr Ala Phe Asp Arg Asp Glu Asp Pro
225                 230                 235                 240

Arg Glu Leu Pro Leu Lys Pro Pro Ser Ser
                245                 250


<210> SEQ ID NO 17
<211> LENGTH: 1602
<212> TYPE: DNA
<213> ORGANISM: Feline herpesvirus 1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1602)

<400> SEQUENCE: 17

atg aga cga tat agg atg gga cgc gga atc tac ctt ctc tat atc tgt       48
Met Arg Arg Tyr Arg Met Gly Arg Gly Ile Tyr Leu Leu Tyr Ile Cys
  1             5                   10                   15

ctg tta tat aca tat ctc cag ttt ggt act tcg tcg aca acc gcg gtc       96
Leu Leu Tyr Thr Tyr Leu Gln Phe Gly Thr Ser Ser Thr Thr Ala Val
             20                  25                  30

agt att gaa aat agt gat aat agt act gcg gag atg tta tca tct acc      144
Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser Thr
         35                  40                  45

agc atg tcc gct acc acc ccg ata tcc cag cca aca tct cca ttc act      192
Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe Thr
     50                  55                  60

act cca act aga aga tct aca aat ata gct aca agt tcg agt acc acc      240
Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr Thr
 65                  70                  75                  80

cag gca tcc cag cca aca tct aca tta act act cta act aga agc tcg      288
Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser Ser
                 85                  90                  95

aca act ata gct aca agt ccg agt acc acc cag gca gcc aca ttc ata      336
Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe Ile
            100                 105                 110

gga tca tct acc gat tcc aat acc act tta ctc aaa aca aca aaa aaa      384
Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys Lys
        115                 120                 125

cca aag cgt aaa aag aat aag aat aac ggg gcc aga ttt aaa tta tat      432
Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu Tyr
    130                 135                 140

tgt gga tat aag ggg gtt atc tac aga ccg tat ttt agc cct ctt cag      480
Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu Gln
145                 150                 155                 160

cta aac tgt act cta ccc aca gaa cct cat att acc aac cct att gac      528
Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile Asp
                165                 170                 175

ttc gag atc tgg ttt aaa cca cgc acc aga ttt ggg gat ttt ctt ggg      576
Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu Gly
            180                 185                 190

gat aaa gaa gac ttc gta ggg aat cat acc cgc acc agc ata tta cta      624
Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu Leu
        195                 200                 205
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ttt agc agc cgt aat ggg agt gtt aat tcc atg gat ctt ggg gac gcg      672
Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp Ala
    210                 215                 220

aca ctc ggg atc cta caa tct agg ata cca gat tac aca tta tat aat      720
Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr Asn
225                 230                 235                 240

att ccc ata caa cat acc gaa gcg atg tca ttg gga atc aaa tct gtg      768
Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser Val
                245                 250                 255

gaa tct gcc acg tcc ggt gtt tat aca tgg cgg gtc tat ggt gga gat      816
Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly Asp
            260                 265                 270

gta cta aat aaa aca gtg cta gga cag gta aat gta tct gta gtg gca      864
Val Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val Ala
        275                 280                 285

tat cac ccc ccg agc gta aat ctt aca cca cgc gcc agt cta ttt aat      912
Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe Asn
    290                 295                 300

aag acc ttt gag gcg gta tgt gca gtg gcg aat tac ttc ccc ccg cga      960
Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro Arg
305                 310                 315                 320

tcc acg aaa cta aca tgg tat ctt gac ggg aag cca ata gaa agg caa     1008
Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg Gln
                325                 330                 335

tac att tca gat acg gca agt gta tgg ata gat gga ctc atc acc aga     1056
Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr Arg
            340                 345                 350

agt tct gtg ttg gct att ccg aca act gaa aca gat tcc gag aaa cca     1104
Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys Pro
        355                 360                 365

gat ata cga tgt gat ttg gaa tgg cat gaa agt cct gtg tcc tat aag     1152
Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr Lys
    370                 375                 380

aga ttc acg aaa agt gta gcc ccg gac gtc tat tac cca cct act gtg     1200
Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr Val
385                 390                 395                 400

tct gtt acc ttc gct gat aca cgg gct ata tgt gat gtt aaa tgt gta     1248
Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys Val
                405                 410                 415

cca cgg gac ggg ata tcc ttg atg tgg aaa att ggt aac tac cat cta     1296
Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His Leu
            420                 425                 430

cca aaa gca atg agt gct gat ata ctg atc aca ggt ccg tgt ata gaa     1344
Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile Glu
        435                 440                 445

cgt cca ggt ttg gtc aac att cag agt atg tgt gat ata tca gaa acg     1392
Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu Thr
    450                 455                 460

gat gga ccc gtg agt tat acc tgt cag acc atc gga tac cca cca att     1440
Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro Ile
465                 470                 475                 480

cta ccg gga ttt tac gac aca caa gtc tac gac gcg tcc cct gaa atc     1488
Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu Ile
                485                 490                 495

gtc agt gaa tca atg ttg gtt agt gtc gtt gct gta ata cta gga gct     1536
Val Ser Glu Ser Met Leu Val Ser Val Val Ala Val Ile Leu Gly Ala
            500                 505                 510
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gtt ctc atc aca gtc ttt atc ttt att acg gca tta tgt tta tat tat      1584
Val Leu Ile Thr Val Phe Ile Phe Ile Thr Ala Leu Cys Leu Tyr Tyr
        515                 520                 525

tct cat ccc cgg cga tta                                              1602
Ser His Pro Arg Arg Leu
    530


<210> SEQ ID NO 18
<211> LENGTH: 534
<212> TYPE: PRT
<213> ORGANISM: Feline herpesvirus 1

<400> SEQUENCE: 18

Met Arg Arg Tyr Arg Met Gly Arg Gly Ile Tyr Leu Leu Tyr Ile Cys
  1               5                  10                  15

Leu Leu Tyr Thr Tyr Leu Gln Phe Gly Thr Ser Ser Thr Thr Ala Val
             20                  25                  30

Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser Thr
         35                  40                  45

Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe Thr
     50                  55                  60

Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr Thr
 65                  70                  75                  80

Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser Ser
                 85                  90                  95

Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe Ile
            100                 105                 110

Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys Lys
        115                 120                 125

Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu Tyr
    130                 135                 140

Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu Gln
145                 150                 155                 160

Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile Asp
                165                 170                 175

Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu Gly
            180                 185                 190

Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu Leu
        195                 200                 205

Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp Ala
    210                 215                 220

Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr Asn
225                 230                 235                 240

Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser Val
                245                 250                 255

Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly Asp
            260                 265                 270

Val Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val Ala
        275                 280                 285

Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe Asn
    290                 295                 300

Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro Arg
305                 310                 315                 320
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Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg Gln
                325                 330                 335

Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr Arg
            340                 345                 350

Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys Pro
        355                 360                 365

Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr Lys
    370                 375                 380

Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr Val
385                 390                 395                 400

Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys Val
                405                 410                 415

Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His Leu
            420                 425                 430

Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile Glu
        435                 440                 445

Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu Thr
    450                 455                 460

Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro Ile
465                 470                 475                 480

Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu Ile
                485                 490                 495

Val Ser Glu Ser Met Leu Val Ser Val Val Ala Val Ile Leu Gly Ala
            500                 505                 510

Val Leu Ile Thr Val Phe Ile Phe Ile Thr Ala Leu Cys Leu Tyr Tyr
        515                 520                 525

Ser His Pro Arg Arg Leu
    530


<210> SEQ ID NO 19
<211> LENGTH: 1401
<212> TYPE: DNA
<213> ORGANISM: Feline herpesvirus 1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1401)

<400> SEQUENCE: 19

agt att gaa aat agt gat aat agt act gcg gag atg tta tca tct acc       48
Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser Thr
  1               5                  10                  15

agc atg tcc gct acc acc ccg ata tcc cag cca aca tct cca ttc act       96
Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe Thr
             20                  25                  30

act cca act aga aga tct aca aat ata gct aca agt tcg agt acc acc      144
Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr Thr
         35                  40                  45

cag gca tcc cag cca aca tct aca tta act act cta act aga agc tcg      192
Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser Ser
     50                  55                  60

aca act ata gct aca agt ccg agt acc acc cag gca gcc aca ttc ata      240
Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe Ile
 65                  70                  75                  80

gga tca tct acc gat tcc aat acc act tta ctc aaa aca aca aaa aaa      288
Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys Lys
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                 85                  90                  95

cca aag cgt aaa aag aat aag aat aac ggg gcc aga ttt aaa tta tat      336
Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu Tyr
            100                 105                 110

tgt gga tat aag ggg gtt atc tac aga ccg tat ttt agc cct ctt cag      384
Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu Gln
        115                 120                 125

cta aac tgt act cta ccc aca gaa cct cat att acc aac cct att gac      432
Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile Asp
    130                 135                 140

ttc gag atc tgg ttt aaa cca cgc acc aga ttt ggg gat ttt ctt ggg      480
Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu Gly
145                 150                 155                 160

gat aaa gaa gac ttc gta ggg aat cat acc cgc acc agc ata tta cta      528
Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu Leu
                165                 170                 175

ttt agc agc cgt aat ggg agt gtt aat tcc atg gat ctt ggg gac gcg      576
Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp Ala
            180                 185                 190

aca ctc ggg atc cta caa tct agg ata cca gat tac aca tta tat aat      624
Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr Asn
        195                 200                 205

att ccc ata caa cat acc gaa gcg atg tca ttg gga atc aaa tct gtg      672
Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser Val
    210                 215                 220

gaa tct gcc acg tcc ggt gtt tat aca tgg cgg gtc tat ggt gga gat      720
Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly Asp
225                 230                 235                 240

gta cta aat aaa aca gtg cta gga cag gta aat gta tct gta gtg gca      768
Val Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val Ala
                245                 250                 255

tat cac ccc ccg agc gta aat ctt aca cca cgc gcc agt cta ttt aat      816
Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe Asn
            260                 265                 270

aag acc ttt gag gcg gta tgt gca gtg gcg aat tac ttc ccc ccg cga      864
Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro Arg
        275                 280                 285

tcc acg aaa cta aca tgg tat ctt gac ggg aag cca ata gaa agg caa      912
Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg Gln
    290                 295                 300

tac att tca gat acg gca agt gta tgg ata gat gga ctc atc acc aga      960
Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr Arg
305                 310                 315                 320

agt tct gtg ttg gct att ccg aca act gaa aca gat tcc gag aaa cca     1008
Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys Pro
                325                 330                 335

gat ata cga tgt gat ttg gaa tgg cat gaa agt cct gtg tcc tat aag     1056
Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr Lys
            340                 345                 350

aga ttc acg aaa agt gta gcc ccg gac gtc tat tac cca cct act gtg     1104
Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr Val
        355                 360                 365

tct gtt acc ttc gct gat aca cgg gct ata tgt gat gtt aaa tgt gta     1152
Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys Val
    370                 375                 380

cca cgg gac ggg ata tcc ttg atg tgg aaa att ggt aac tac cat cta     1200
Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His Leu
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385                 390                 395                 400

cca aaa gca atg agt gct gat ata ctg atc aca ggt ccg tgt ata gaa     1248
Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile Glu
                405                 410                 415

cgt cca ggt ttg gtc aac att cag agt atg tgt gat ata tca gaa acg     1296
Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu Thr
            420                 425                 430

gat gga ccc gtg agt tat acc tgt cag acc atc gga tac cca cca att     1344
Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro Ile
        435                 440                 445

cta ccg gga ttt tac gac aca caa gtc tac gac gcg tcc cct gaa atc     1392
Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu Ile
    450                 455                 460

gtc agt gaa                                                         1401
Val Ser Glu
465


<210> SEQ ID NO 20
<211> LENGTH: 467
<212> TYPE: PRT
<213> ORGANISM: Feline herpesvirus 1

<400> SEQUENCE: 20

Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser Thr
  1               5                  10                  15

Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe Thr
             20                  25                  30

Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr Thr
         35                  40                  45

Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser Ser
     50                  55                  60

Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe Ile
 65                  70                  75                  80

Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys Lys
                 85                  90                  95

Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu Tyr
            100                 105                 110

Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu Gln
        115                 120                 125

Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile Asp
    130                 135                 140

Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu Gly
145                 150                 155                 160

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

Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp Ala
            180                 185                 190

Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr Asn
        195                 200                 205

Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser Val
    210                 215                 220

Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly Asp
225                 230                 235                 240

Val Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val Ala
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                245                 250                 255

Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe Asn
            260                 265                 270

Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro Arg
        275                 280                 285

Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg Gln
    290                 295                 300

Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr Arg
305                 310                 315                 320

Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys Pro
                325                 330                 335

Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr Lys
            340                 345                 350

Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr Val
        355                 360                 365

Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys Val
    370                 375                 380

Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His Leu
385                 390                 395                 400

Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile Glu
                405                 410                 415

Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu Thr
            420                 425                 430

Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro Ile
        435                 440                 445

Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu Ile
    450                 455                 460

Val Ser Glu
465


<210> SEQ ID NO 21
<211> LENGTH: 1401
<212> TYPE: DNA
<213> ORGANISM: Feline herpesvirus 1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1401)

<400> SEQUENCE: 21

atg tcc atc gaa aac agc gat aat agt act gcg gag atg tta tca tct           48
Met Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser
  1             5                    10                  15

acc agc atg tcc gct acc acc ccg ata tcc cag cca aca tct cca ttc           96
Thr Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe
             20                  25                  30

act act cca act cgt cgc tct aca aat ata gct aca tcc tct tcc acc          144
Thr Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr
         35                  40                  45

acc cag gca tcc cag cca aca tct aca tta act act cta act aga agc          192
Thr Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser
     50                  55                  60

tcg aca act ata gct aca agt ccg agt acc acc cag gca gcc aca ttc          240
Ser Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe
 65                  70                  75                  80

ata gga tca tct acc gat tcc aat acc act tta ctc aaa aca aca aaa          288
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Ile Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys
                85                  90                  95

aaa cca aag cgt aaa aag aat aag aat aac ggg gcc aga ttt aaa tta      336
Lys Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu
            100                 105                 110

gat tgt gga tat aag ggg gtt atc tac aga ccg tat ttt agc cct ctt      384
Asp Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu
        115                 120                 125

cag cta aac tgt act cta ccc aca gaa cct cat att acc aac cct att      432
Gln Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile
    130                 135                 140

gac ttc gag atc tgg ttt aaa cca cgc acc aga ttt ggg gat ttt ctt      480
Asp Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu
145                 150                 155                 160

ggg gat aaa gaa gac ttc gta ggg aat cat acc cgc acc agc ata tta      528
Gly Asp Lys Glu Asp Phe Val Gly Asn His Thr Arg Thr Ser Ile Leu
                165                 170                 175

cta ttt agc agc cgt aat ggg agt gtt aat tcc atg gat ctt ggg gac      576
Leu Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp
            180                 185                 190

gcg aca ctc ggg atc cta caa tct agg ata cca gat tac aca tta tat      624
Ala Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr
        195                 200                 205

aat att ccc ata caa cat acc gaa gcg atg tca ttg gga atc aaa tct      672
Asn Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser
    210                 215                 220

gtg gaa tct gcc act tct ggt gtt tat aca tgg cgt gtc tat ggt gga      720
Val Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly
225                 230                 235                 240

gat ggt ctg aac aaa aca gtg ctg ggt cag gta aat gta tct gta gtg      768
Asp Gly Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val
                245                 250                 255

gca tat cac ccc ccg agc gta aat ctt aca cca cgc gcc agt cta ttt      816
Ala Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe
            260                 265                 270

aat aag acc ttt gag gcg gta tgt gca gtg gcg aat tac ttc ccc ccg      864
Asn Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro
        275                 280                 285

cga tcc acg aaa cta aca tgg tat ctt gac ggg aag cca ata gaa agg      912
Arg Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg
    290                 295                 300

caa tac att tca gat acg gca agt gta tgg ata gat gga ctc atc acc      960
Gln Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr
305                 310                 315                 320

aga agt tct gtg ttg gct att ccg aca act gaa aca gat tcc gag aaa     1008
Arg Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys
                325                 330                 335

cca gat ata cga tgt gat ttg gaa tgg cat gaa agt cct gtg tcc tat     1056
Pro Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr
            340                 345                 350

aag aga ttc acg aaa agt gta gcc ccg gac gtc tat tac cca cct act     1104
Lys Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr
        355                 360                 365

gtg tct gtt acc ttc gct gat aca cgg gct ata tgt gat gtt aaa tgt     1152
Val Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys
    370                 375                 380

gta cca cgg gac ggg ata tcc ttg atg tgg aaa att ggt aac tac cat     1200
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Val Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His
385                 390                 395                 400

cta cca aaa gca atg agt gct gat ata ctg atc aca ggt ccg tgt ata     1248
Leu Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile
                405                 410                 415

gaa cgt cca ggt ttg gtc aac att cag agt atg tgt gat ata tca gaa     1296
Glu Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu
            420                 425                 430

acg gat gga ccc gtg agt tat acc tgt cag acc atc gga tac cca cca     1344
Thr Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro
        435                 440                 445

att cta ccg gga ttt tac gac aca caa gtc tac gac gcg tcc cct gaa     1392
Ile Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu
    450                 455                 460

atc gtc tcc                                                         1401
Ile Val Ser
465


<210> SEQ ID NO 22
<211> LENGTH: 467
<212> TYPE: PRT
<213> ORGANISM: Feline herpesvirus 1

<400> SEQUENCE: 22

Met Ser Ile Glu Asn Ser Asp Asn Ser Thr Ala Glu Met Leu Ser Ser
  1               5                  10                  15

Thr Ser Met Ser Ala Thr Thr Pro Ile Ser Gln Pro Thr Ser Pro Phe
             20                  25                  30

Thr Thr Pro Thr Arg Arg Ser Thr Asn Ile Ala Thr Ser Ser Ser Thr
         35                  40                  45

Thr Gln Ala Ser Gln Pro Thr Ser Thr Leu Thr Thr Leu Thr Arg Ser
     50                  55                  60

Ser Thr Thr Ile Ala Thr Ser Pro Ser Thr Thr Gln Ala Ala Thr Phe
 65                  70                  75                  80

Ile Gly Ser Ser Thr Asp Ser Asn Thr Thr Leu Leu Lys Thr Thr Lys
                 85                  90                  95

Lys Pro Lys Arg Lys Lys Asn Lys Asn Asn Gly Ala Arg Phe Lys Leu
            100                 105                 110

Asp Cys Gly Tyr Lys Gly Val Ile Tyr Arg Pro Tyr Phe Ser Pro Leu
        115                 120                 125

Gln Leu Asn Cys Thr Leu Pro Thr Glu Pro His Ile Thr Asn Pro Ile
    130                 135                 140

Asp Phe Glu Ile Trp Phe Lys Pro Arg Thr Arg Phe Gly Asp Phe Leu
145                 150                 155                 160

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

Leu Phe Ser Ser Arg Asn Gly Ser Val Asn Ser Met Asp Leu Gly Asp
            180                 185                 190

Ala Thr Leu Gly Ile Leu Gln Ser Arg Ile Pro Asp Tyr Thr Leu Tyr
        195                 200                 205

Asn Ile Pro Ile Gln His Thr Glu Ala Met Ser Leu Gly Ile Lys Ser
    210                 215                 220

Val Glu Ser Ala Thr Ser Gly Val Tyr Thr Trp Arg Val Tyr Gly Gly
225                 230                 235                 240
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Asp Gly Leu Asn Lys Thr Val Leu Gly Gln Val Asn Val Ser Val Val
                245                 250                 255

Ala Tyr His Pro Pro Ser Val Asn Leu Thr Pro Arg Ala Ser Leu Phe
            260                 265                 270

Asn Lys Thr Phe Glu Ala Val Cys Ala Val Ala Asn Tyr Phe Pro Pro
        275                 280                 285

Arg Ser Thr Lys Leu Thr Trp Tyr Leu Asp Gly Lys Pro Ile Glu Arg
    290                 295                 300

Gln Tyr Ile Ser Asp Thr Ala Ser Val Trp Ile Asp Gly Leu Ile Thr
305                 310                 315                 320

Arg Ser Ser Val Leu Ala Ile Pro Thr Thr Glu Thr Asp Ser Glu Lys
                325                 330                 335

Pro Asp Ile Arg Cys Asp Leu Glu Trp His Glu Ser Pro Val Ser Tyr
            340                 345                 350

Lys Arg Phe Thr Lys Ser Val Ala Pro Asp Val Tyr Tyr Pro Pro Thr
        355                 360                 365

Val Ser Val Thr Phe Ala Asp Thr Arg Ala Ile Cys Asp Val Lys Cys
    370                 375                 380

Val Pro Arg Asp Gly Ile Ser Leu Met Trp Lys Ile Gly Asn Tyr His
385                 390                 395                 400

Leu Pro Lys Ala Met Ser Ala Asp Ile Leu Ile Thr Gly Pro Cys Ile
                405                 410                 415

Glu Arg Pro Gly Leu Val Asn Ile Gln Ser Met Cys Asp Ile Ser Glu
            420                 425                 430

Thr Asp Gly Pro Val Ser Tyr Thr Cys Gln Thr Ile Gly Tyr Pro Pro
        435                 440                 445

Ile Leu Pro Gly Phe Tyr Asp Thr Gln Val Tyr Asp Ala Ser Pro Glu
    450                 455                 460

Ile Val Ser
465


<210> SEQ ID NO 23
<211> LENGTH: 1122
<212> TYPE: DNA
<213> ORGANISM: Feline herpesvirus 1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1122)

<400> SEQUENCE: 23

atg atg aca cgt cta cat ttt tgg tgg tgt gga atc ttt gcg gtc ctg       48
Met Met Thr Arg Leu His Phe Trp Trp Cys Gly Ile Phe Ala Val Leu
  1               5                  10                  15

aaa tat ctg gta tgt act tca agc ctt acg acc acg cca aaa aca act       96
Lys Tyr Leu Val Cys Thr Ser Ser Leu Thr Thr Thr Pro Lys Thr Thr
             20                  25                  30

acg gtt tat gtg aag gga ttt aat ata cct cca cta cgc tac aat tat      144
Thr Val Tyr Val Lys Gly Phe Asn Ile Pro Pro Leu Arg Tyr Asn Tyr
         35                  40                  45

act caa gcc aga atc gtg cca aaa att ccc cag gcg atg gat ccg aag      192
Thr Gln Ala Arg Ile Val Pro Lys Ile Pro Gln Ala Met Asp Pro Lys
     50                  55                  60

ata aca gct gaa gta cgt tat gta aca tca atg gat tca tgt ggg atg      240
Ile Thr Ala Glu Val Arg Tyr Val Thr Ser Met Asp Ser Cys Gly Met
 65                  70                  75                  80
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gtg gca ttg ata tca gag ccg gat ata gac gct act att cga acc ata      288
Val Ala Leu Ile Ser Glu Pro Asp Ile Asp Ala Thr Ile Arg Thr Ile
                 85                  90                  95

caa cta tct caa aaa aaa aca tat aac gcg act ata agt tgg ttt aag      336
Gln Leu Ser Gln Lys Lys Thr Tyr Asn Ala Thr Ile Ser Trp Phe Lys
            100                 105                 110

gta acc cag ggt tgt gaa tac cct atg ttt ctt atg gat atg aga ctt      384
Val Thr Gln Gly Cys Glu Tyr Pro Met Phe Leu Met Asp Met Arg Leu
        115                 120                 125

tgt gat cct aaa cgg gaa ttt gga ata tgt gct tta cgg tcg cct tca      432
Cys Asp Pro Lys Arg Glu Phe Gly Ile Cys Ala Leu Arg Ser Pro Ser
    130                 135                 140

tat tgg ttg gaa cct tta aca aag tat atg ttc cta aca gac gat gaa      480
Tyr Trp Leu Glu Pro Leu Thr Lys Tyr Met Phe Leu Thr Asp Asp Glu
145                 150                 155                 160

ctg ggt ttg att atg atg gcc ccg gcc caa ttt aat caa gga caa tat      528
Leu Gly Leu Ile Met Met Ala Pro Ala Gln Phe Asn Gln Gly Gln Tyr
                165                 170                 175

cga aga gtt ata acc atc gat ggt tcc atg ttt tat aca gat ttt atg      576
Arg Arg Val Ile Thr Ile Asp Gly Ser Met Phe Tyr Thr Asp Phe Met
            180                 185                 190

gta caa cta tct cca acg cca tgt tgg ttc gca aaa ccc gat aga tac      624
Val Gln Leu Ser Pro Thr Pro Cys Trp Phe Ala Lys Pro Asp Arg Tyr
        195                 200                 205

gaa gag att cta cat gaa tgg tgt cga aat gtt aaa act att ggc ctt      672
Glu Glu Ile Leu His Glu Trp Cys Arg Asn Val Lys Thr Ile Gly Leu
    210                 215                 220

gat gga gct cgt gat tac cac tat tat tgg gta ccc tat aac cca caa      720
Asp Gly Ala Arg Asp Tyr His Tyr Tyr Trp Val Pro Tyr Asn Pro Gln
225                 230                 235                 240

cct cac cat aaa gcc gta ctc tta tat tgg tat cgg act cat ggc cga      768
Pro His His Lys Ala Val Leu Leu Tyr Trp Tyr Arg Thr His Gly Arg
                245                 250                 255

gaa ccc cca gta aga ttc caa gag gcc att cga tat gat cgt ccc gcc      816
Glu Pro Pro Val Arg Phe Gln Glu Ala Ile Arg Tyr Asp Arg Pro Ala
            260                 265                 270

ata ccg tct ggg agt gag gat tcg aaa cgg tcc aac gac tct aga gga      864
Ile Pro Ser Gly Ser Glu Asp Ser Lys Arg Ser Asn Asp Ser Arg Gly
        275                 280                 285

gaa tcg agt gga ccc aat tgg ata gac att gaa aat tac act cct aaa      912
Glu Ser Ser Gly Pro Asn Trp Ile Asp Ile Glu Asn Tyr Thr Pro Lys
    290                 295                 300

aat aat gtg cct att ata ata tct gac gat gac gtt cct aca gcc cct      960
Asn Asn Val Pro Ile Ile Ile Ser Asp Asp Asp Val Pro Thr Ala Pro
305                 310                 315                 320

ccc aag ggc atg aat aat cag tca gta gtg ata ccc gca atc gta cta     1008
Pro Lys Gly Met Asn Asn Gln Ser Val Val Ile Pro Ala Ile Val Leu
                325                 330                 335

agt tgt ctt ata ata gca ctg att cta gga gtg ata tat tat att ttg     1056
Ser Cys Leu Ile Ile Ala Leu Ile Leu Gly Val Ile Tyr Tyr Ile Leu
            340                 345                 350

agg gta aag agg tct cga tca act gca tat caa caa ctt cct ata ata     1104
Arg Val Lys Arg Ser Arg Ser Thr Ala Tyr Gln Gln Leu Pro Ile Ile
        355                 360                 365

cat aca act cac cat cct                                             1122
His Thr Thr His His Pro
    370
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<210> SEQ ID NO 24
<211> LENGTH: 374
<212> TYPE: PRT
<213> ORGANISM: Feline herpesvirus 1

<400> SEQUENCE: 24

Met Met Thr Arg Leu His Phe Trp Trp Cys Gly Ile Phe Ala Val Leu
  1               5                  10                  15

Lys Tyr Leu Val Cys Thr Ser Ser Leu Thr Thr Thr Pro Lys Thr Thr
             20                  25                  30

Thr Val Tyr Val Lys Gly Phe Asn Ile Pro Pro Leu Arg Tyr Asn Tyr
         35                  40                  45

Thr Gln Ala Arg Ile Val Pro Lys Ile Pro Gln Ala Met Asp Pro Lys
     50                  55                  60

Ile Thr Ala Glu Val Arg Tyr Val Thr Ser Met Asp Ser Cys Gly Met
 65                  70                  75                  80

Val Ala Leu Ile Ser Glu Pro Asp Ile Asp Ala Thr Ile Arg Thr Ile
                 85                  90                  95

Gln Leu Ser Gln Lys Lys Thr Tyr Asn Ala Thr Ile Ser Trp Phe Lys
            100                 105                 110

Val Thr Gln Gly Cys Glu Tyr Pro Met Phe Leu Met Asp Met Arg Leu
        115                 120                 125

Cys Asp Pro Lys Arg Glu Phe Gly Ile Cys Ala Leu Arg Ser Pro Ser
    130                 135                 140

Tyr Trp Leu Glu Pro Leu Thr Lys Tyr Met Phe Leu Thr Asp Asp Glu
145                 150                 155                 160

Leu Gly Leu Ile Met Met Ala Pro Ala Gln Phe Asn Gln Gly Gln Tyr
                165                 170                 175

Arg Arg Val Ile Thr Ile Asp Gly Ser Met Phe Tyr Thr Asp Phe Met
            180                 185                 190

Val Gln Leu Ser Pro Thr Pro Cys Trp Phe Ala Lys Pro Asp Arg Tyr
        195                 200                 205

Glu Glu Ile Leu His Glu Trp Cys Arg Asn Val Lys Thr Ile Gly Leu
    210                 215                 220

Asp Gly Ala Arg Asp Tyr His Tyr Tyr Trp Val Pro Tyr Asn Pro Gln
225                 230                 235                 240

Pro His His Lys Ala Val Leu Leu Tyr Trp Tyr Arg Thr His Gly Arg
                245                 250                 255

Glu Pro Pro Val Arg Phe Gln Glu Ala Ile Arg Tyr Asp Arg Pro Ala
            260                 265                 270

Ile Pro Ser Gly Ser Glu Asp Ser Lys Arg Ser Asn Asp Ser Arg Gly
        275                 280                 285

Glu Ser Ser Gly Pro Asn Trp Ile Asp Ile Glu Asn Tyr Thr Pro Lys
    290                 295                 300

Asn Asn Val Pro Ile Ile Ile Ser Asp Asp Asp Val Pro Thr Ala Pro
305                 310                 315                 320

Pro Lys Gly Met Asn Asn Gln Ser Val Val Ile Pro Ala Ile Val Leu
                325                 330                 335

Ser Cys Leu Ile Ile Ala Leu Ile Leu Gly Val Ile Tyr Tyr Ile Leu
            340                 345                 350

Arg Val Lys Arg Ser Arg Ser Thr Ala Tyr Gln Gln Leu Pro Ile Ile
        355                 360                 365
```

-continued

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His Thr Thr His His Pro
    370


<210> SEQ ID NO 25
<211> LENGTH: 900
<212> TYPE: DNA
<213> ORGANISM: Feline herpesvirus 1
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(900)

<400> SEQUENCE: 25

cca aaa aca act acg gtt tat gtg aag gga ttt aat ata cct cca cta       48
Pro Lys Thr Thr Thr Val Tyr Val Lys Gly Phe Asn Ile Pro Pro Leu
  1               5                  10                  15

cgc tac aat tat act caa gcc aga atc gtg cca aaa att ccc cag gcg       96
Arg Tyr Asn Tyr Thr Gln Ala Arg Ile Val Pro Lys Ile Pro Gln Ala
             20                  25                  30

atg gat ccg aag ata aca gct gaa gta cgt tat gta aca tca atg gat      144
Met Asp Pro Lys Ile Thr Ala Glu Val Arg Tyr Val Thr Ser Met Asp
         35                  40                  45

tca tgt ggg atg gtg gca ttg ata tca gag ccg gat ata gac gct act      192
Ser Cys Gly Met Val Ala Leu Ile Ser Glu Pro Asp Ile Asp Ala Thr
     50                  55                  60

att cga acc ata caa cta tct caa aaa aaa aca tat aac gcg act ata      240
Ile Arg Thr Ile Gln Leu Ser Gln Lys Lys Thr Tyr Asn Ala Thr Ile
 65                  70                  75                  80

agt tgg ttt aag gta acc cag ggt tgt gaa tac cct atg ttt ctt atg      288
Ser Trp Phe Lys Val Thr Gln Gly Cys Glu Tyr Pro Met Phe Leu Met
                 85                  90                  95

gat atg aga ctt tgt gat cct aaa cgg gaa ttt gga ata tgt gct tta      336
Asp Met Arg Leu Cys Asp Pro Lys Arg Glu Phe Gly Ile Cys Ala Leu
            100                 105                 110

cgg tcg cct tca tat tgg ttg gaa cct tta aca aag tat atg ttc cta      384
Arg Ser Pro Ser Tyr Trp Leu Glu Pro Leu Thr Lys Tyr Met Phe Leu
        115                 120                 125

aca gac gat gaa ctg ggt ttg att atg atg gcc ccg gcc caa ttt aat      432
Thr Asp Asp Glu Leu Gly Leu Ile Met Met Ala Pro Ala Gln Phe Asn
    130                 135                 140

caa gga caa tat cga aga gtt ata acc atc gat ggt tcc atg ttt tat      480
Gln Gly Gln Tyr Arg Arg Val Ile Thr Ile Asp Gly Ser Met Phe Tyr
145                 150                 155                 160

aca gat ttt atg gta caa cta tct cca acg cca tgt tgg ttc gca aaa      528
Thr Asp Phe Met Val Gln Leu Ser Pro Thr Pro Cys Trp Phe Ala Lys
                165                 170                 175

ccc gat aga tac gaa gag att cta cat gaa tgg tgt cga aat gtt aaa      576
Pro Asp Arg Tyr Glu Glu Ile Leu His Glu Trp Cys Arg Asn Val Lys
            180                 185                 190

act att ggc ctt gat gga gct cgt gat tac cac tat tat tgg gta ccc      624
Thr Ile Gly Leu Asp Gly Ala Arg Asp Tyr His Tyr Tyr Trp Val Pro
        195                 200                 205

tat aac cca caa cct cac cat aaa gcc gta ctc tta tat tgg tat cgg      672
Tyr Asn Pro Gln Pro His His Lys Ala Val Leu Leu Tyr Trp Tyr Arg
    210                 215                 220

act cat ggc cga gaa ccc cca gta aga ttc caa gag gcc att cga tat      720
Thr His Gly Arg Glu Pro Pro Val Arg Phe Gln Glu Ala Ile Arg Tyr
225                 230                 235                 240

gat cgt ccc gcc ata ccg tct ggg agt gag gat tcg aaa cgg tcc aac      768
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Asp Arg Pro Ala Ile Pro Ser Gly Ser Glu Asp Ser Lys Arg Ser Asn
                245                 250                 255

gac tct aga gga gaa tcg agt gga ccc aat tgg ata gac att gaa aat      816
Asp Ser Arg Gly Glu Ser Ser Gly Pro Asn Trp Ile Asp Ile Glu Asn
            260                 265                 270

tac act cct aaa aat aat gtg cct att ata ata tct gac gat gac gtt      864
Tyr Thr Pro Lys Asn Asn Val Pro Ile Ile Ile Ser Asp Asp Asp Val
        275                 280                 285

cct aca gcc cct ccc aag ggc atg aat aat cag tca                      900
Pro Thr Ala Pro Pro Lys Gly Met Asn Asn Gln Ser
    290                 295                 300


<210> SEQ ID NO 26
<211> LENGTH: 300
<212> TYPE: PRT
<213> ORGANISM: Feline herpesvirus 1

<400> SEQUENCE: 26

Pro Lys Thr Thr Thr Val Tyr Val Lys Gly Phe Asn Ile Pro Pro Leu
  1               5                  10                  15

Arg Tyr Asn Tyr Thr Gln Ala Arg Ile Val Pro Lys Ile Pro Gln Ala
             20                  25                  30

Met Asp Pro Lys Ile Thr Ala Glu Val Arg Tyr Val Thr Ser Met Asp
         35                  40                  45

Ser Cys Gly Met Val Ala Leu Ile Ser Glu Pro Asp Ile Asp Ala Thr
     50                  55                  60

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

Ser Trp Phe Lys Val Thr Gln Gly Cys Glu Tyr Pro Met Phe Leu Met
                 85                  90                  95

Asp Met Arg Leu Cys Asp Pro Lys Arg Glu Phe Gly Ile Cys Ala Leu
            100                 105                 110

Arg Ser Pro Ser Tyr Trp Leu Glu Pro Leu Thr Lys Tyr Met Phe Leu
        115                 120                 125

Thr Asp Asp Glu Leu Gly Leu Ile Met Met Ala Pro Ala Gln Phe Asn
    130                 135                 140

Gln Gly Gln Tyr Arg Arg Val Ile Thr Ile Asp Gly Ser Met Phe Tyr
145                 150                 155                 160

Thr Asp Phe Met Val Gln Leu Ser Pro Thr Pro Cys Trp Phe Ala Lys
                165                 170                 175

Pro Asp Arg Tyr Glu Glu Ile Leu His Glu Trp Cys Arg Asn Val Lys
            180                 185                 190

Thr Ile Gly Leu Asp Gly Ala Arg Asp Tyr His Tyr Tyr Trp Val Pro
        195                 200                 205

Tyr Asn Pro Gln Pro His His Lys Ala Val Leu Leu Tyr Trp Tyr Arg
    210                 215                 220

Thr His Gly Arg Glu Pro Pro Val Arg Phe Gln Glu Ala Ile Arg Tyr
225                 230                 235                 240

Asp Arg Pro Ala Ile Pro Ser Gly Ser Glu Asp Ser Lys Arg Ser Asn
                245                 250                 255

Asp Ser Arg Gly Glu Ser Ser Gly Pro Asn Trp Ile Asp Ile Glu Asn
            260                 265                 270

Tyr Thr Pro Lys Asn Asn Val Pro Ile Ile Ile Ser Asp Asp Asp Val
        275                 280                 285
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Pro Thr Ala Pro Pro Lys Gly Met Asn Asn Gln Ser
    290                 295                 300


<210> SEQ ID NO 27
<211> LENGTH: 759
<212> TYPE: DNA
<213> ORGANISM: Feline leukemia virus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(759)

<400> SEQUENCE: 27

atg ccg ctg cgt gaa ggt ccg aac aac cgt ccc cag tat tgg cca ttc       48
Met Pro Leu Arg Glu Gly Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe
  1               5                  10                  15

tca gct tca gac ctg tat aac tgg aag tcg cat aac ccc cct ttc tcc       96
Ser Ala Ser Asp Leu Tyr Asn Trp Lys Ser His Asn Pro Pro Phe Ser
             20                  25                  30

caa gac ccc gtg gcc cta act aac cta att gag tcc att tta gtg acg      144
Gln Asp Pro Val Ala Leu Thr Asn Leu Ile Glu Ser Ile Leu Val Thr
         35                  40                  45

cat caa cca acc tgg gac gac tgc cag caa ctc ttg cag gca ctc ctg      192
His Gln Pro Thr Trp Asp Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu
     50                  55                  60

aca ggc gaa gaa agg caa agg gtc ctt ctt gag gcc cga aag cag gtt      240
Thr Gly Glu Glu Arg Gln Arg Val Leu Leu Glu Ala Arg Lys Gln Val
 65                  70                  75                  80

cca ggc gag gac gga cgg cca acc cag ctg ccc aat gtc att gac gaa      288
Pro Gly Glu Asp Gly Arg Pro Thr Gln Leu Pro Asn Val Ile Asp Glu
                 85                  90                  95

gct ttc ccc ttg acc cgt ccc aac tgg gat ttt gct acg ccg gca ggt      336
Ala Phe Pro Leu Thr Arg Pro Asn Trp Asp Phe Ala Thr Pro Ala Gly
            100                 105                 110

agg gag cac cta cgc ctt tat cgc cag ttg ctg tta gcg ggt ctc cgc      384
Arg Glu His Leu Arg Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg
        115                 120                 125

ggg gct gca aga cgc ccc act aat ttg gca cag gta aag caa gtt gta      432
Gly Ala Ala Arg Arg Pro Thr Asn Leu Ala Gln Val Lys Gln Val Val
    130                 135                 140

caa ggg aaa gag gaa acg cca gcc tca ttc tta gaa aga tta aaa gag      480
Gln Gly Lys Glu Glu Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu
145                 150                 155                 160

gct tac aga atg tat act ccc tat gac cct gag gac cca ggg cag gct      528
Ala Tyr Arg Met Tyr Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala
                165                 170                 175

gct agt gtt atc ctg tcc ttt atc tac cag tct agc ccg gac ata aga      576
Ala Ser Val Ile Leu Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg
            180                 185                 190

aat aag tta caa agg cta gaa ggc cta cag ggg ttc aca ctg tct gat      624
Asn Lys Leu Gln Arg Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp
        195                 200                 205

ttg cta aaa gag gca gaa aag ata tac aac aaa agg gag acc cca gag      672
Leu Leu Lys Glu Ala Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu
    210                 215                 220

gaa agg gaa gaa aga tta tgg cag cgg cag gaa gaa aga gat aaa aag      720
Glu Arg Glu Glu Arg Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys
225                 230                 235                 240

cgc cat aag gag atg act aag gtc tgt gag aat tct agc                  759
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Arg His Lys Glu Met Thr Lys Val Cys Glu Asn Ser Ser
                245                 250


<210> SEQ ID NO 28
<211> LENGTH: 253
<212> TYPE: PRT
<213> ORGANISM: Feline leukemia virus

<400> SEQUENCE: 28

Met Pro Leu Arg Glu Gly Pro Asn Asn Arg Pro Gln Tyr Trp Pro Phe
  1               5                   10                  15

Ser Ala Ser Asp Leu Tyr Asn Trp Lys Ser His Asn Pro Pro Phe Ser
             20                  25                  30

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

His Gln Pro Thr Trp Asp Asp Cys Gln Gln Leu Leu Gln Ala Leu Leu
     50                  55                  60

Thr Gly Glu Glu Arg Gln Arg Val Leu Leu Glu Ala Arg Lys Gln Val
 65                  70                  75                  80

Pro Gly Glu Asp Gly Arg Pro Thr Gln Leu Pro Asn Val Ile Asp Glu
                 85                  90                  95

Ala Phe Pro Leu Thr Arg Pro Asn Trp Asp Phe Ala Thr Pro Ala Gly
            100                 105                 110

Arg Glu His Leu Arg Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg
        115                 120                 125

Gly Ala Ala Arg Arg Pro Thr Asn Leu Ala Gln Val Lys Gln Val Val
    130                 135                 140

Gln Gly Lys Glu Glu Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu
145                 150                 155                 160

Ala Tyr Arg Met Tyr Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala
                165                 170                 175

Ala Ser Val Ile Leu Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg
            180                 185                 190

Asn Lys Leu Gln Arg Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp
        195                 200                 205

Leu Leu Lys Glu Ala Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu
    210                 215                 220

Glu Arg Glu Glu Arg Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys
225                 230                 235                 240

Arg His Lys Glu Met Thr Lys Val Cys Glu Asn Ser Ser
                245                 250


<210> SEQ ID NO 29
<211> LENGTH: 1830
<212> TYPE: DNA
<213> ORGANISM: Feline leukemia virus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1830)

<400> SEQUENCE: 29

atg gcc aat cct agt cca ccc caa atg tat aat gta act tgg gta ata       48
Met Ala Asn Pro Ser Pro Pro Gln Met Tyr Asn Val Thr Trp Val Ile
  1               5                   10                  15

acc aat gta caa acc aac acc caa gct aat gcc acc tct atg tta gga       96
Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly
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             20                  25                  30

acc tta acc gat gtc tac cct acc cta cat gtt gac tta tgt gac cta      144
Thr Leu Thr Asp Val Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu
         35                  40                  45

gtg gga gac acc tgg gaa cct atg gtc cta agc cca acc ggg tac cct      192
Val Gly Asp Thr Trp Glu Pro Met Val Leu Ser Pro Thr Gly Tyr Pro
     50                  55                  60

ccc tca aaa tat gga tgt aaa act aca gat aga aaa aaa cag caa cag      240
Pro Ser Lys Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln
 65                  70                  75                  80

aca tac ccc ttt tac gtc tgc ccc ggg cat cgc ccc tcg ctg ggg cca      288
Thr Tyr Pro Phe Tyr Val Cys Pro Gly His Arg Pro Ser Leu Gly Pro
                 85                  90                  95

aag gga aca cat tgt gga ggg gca caa gat ggg ttt tgt gcc gca tgg      336
Lys Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp
            100                 105                 110

gga tgt gaa acc acc gga gaa gct tgg tgg aag ccc tcc tcc tca tgg      384
Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp Lys Pro Ser Ser Ser Trp
        115                 120                 125

gac tat atc aca gta aaa aga ggg agt agt cag aac aat aac tgt gag      432
Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asn Asn Asn Cys Glu
    130                 135                 140

gga aaa tgc aac ccc ctg att ttg cag ttc acc cag aag ggg aaa caa      480
Gly Lys Cys Asn Pro Leu Ile Leu Gln Phe Thr Gln Lys Gly Lys Gln
145                 150                 155                 160

gcc tct tgg gac gga cct aag atg tgg gga ttg cgg cta tac cgt aca      528
Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg Leu Tyr Arg Thr
                165                 170                 175

gga tat gac cct atc gcc tta ttc acg gta tcc cgg cgg gtg tca acc      576
Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser Arg Arg Val Ser Thr
            180                 185                 190

att acg ccg cct cag gca atg gga cca gac cta gtc tta cct gat caa      624
Ile Thr Pro Pro Gln Ala Met Gly Pro Asp Leu Val Leu Pro Asp Gln
        195                 200                 205

aaa ccc cca tcc cga caa tct caa aca ggg tcc aaa gtg gcg acc cag      672
Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly Ser Lys Val Ala Thr Gln
    210                 215                 220

agg ccc caa acg aat gaa agc gcc cca agg tct gtt gcc ccc acc acc      720
Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg Ser Val Ala Pro Thr Thr
225                 230                 235                 240

gtg ggt ccc aaa cgg att ggg acc gga gat agg tta ata aat tta gta      768
Val Gly Pro Lys Arg Ile Gly Thr Gly Asp Arg Leu Ile Asn Leu Val
                245                 250                 255

caa ggg gca tac cta gcc tta aat gcc acc gac ccc aac aaa act aaa      816
Gln Gly Ala Tyr Leu Ala Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys
            260                 265                 270

gac tgt tgg ctc tgc ctg gtt tct cga cca ccc tat tac gaa ggg att      864
Asp Cys Trp Leu Cys Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile
        275                 280                 285

gca atc tta ggt aac tac agc aac caa aca aac cct ccc cca tcc tgc      912
Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys
    290                 295                 300

cta tct att ccg cca cac aag ctg acc ata tct aaa gta tca ggg caa      960
Leu Ser Ile Pro Pro His Lys Leu Thr Ile Ser Lys Val Ser Gly Gln
305                 310                 315                 320

gga ctg tgc ata ggg act gtt cct aag acc cac cag gct ttg tgc aat     1008
Gly Leu Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn
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                325                 330                 335

aag acg cac cag gga cat aca ggg gcg gac tat cga gcc gcc ccg cgg         1056
Lys Thr His Gln Gly His Thr Gly Ala Asp Tyr Arg Ala Ala Pro Arg
            340                 345                 350

tat cta gcc gcc ccc aat ggc acc tat tgg gcc tgt aac act gga ctc         1104
Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu
        355                 360                 365

acc cca tgc att tcc atg gcg gtg ctc aat ttg acc tct gat ttt tgt         1152
Thr Pro Cys Ile Ser Met Ala Val Leu Asn Leu Thr Ser Asp Phe Cys
    370                 375                 380

gtc tta atc gaa tta tgg ccc aga gtg act tac cat caa ccc gaa tat         1200
Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr
385                 390                 395                 400

gtg tac aca cat ttt gcc aaa gct ggc agg ttc cga aga gaa cca ata         1248
Val Tyr Thr His Phe Ala Lys Ala Gly Arg Phe Arg Arg Glu Pro Ile
                405                 410                 415

tca cta act gtt gcc ctc atg ttg gga gga ctc act gta ggg ggc ata         1296
Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile
            420                 425                 430

gcc gcg ggg gtc gga aca ggg act aaa gcc ctc ctt gaa aca gcc cag         1344
Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
        435                 440                 445

ttc aga caa cta caa atg gcc atg cac aca gac atc cag gcc cta gaa         1392
Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu
    450                 455                 460

gag tca att agt gcc tta gaa aag tcc ctg acc tcc ctt tct gaa gta         1440
Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser Glu Val
465                 470                 475                 480

gtc tta caa aac aga cgg ggc cta gat att cta ttc cta caa gag gga         1488
Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly
                485                 490                 495

ggg ctc tgt gcc gca tta aaa gaa gaa tgt tgc ttc tat gcg gat cac         1536
Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His
            500                 505                 510

acc gga ctc gtc cga gac aat atg gct aaa tta aga gaa aga cta aaa         1584
Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu Arg Glu Arg Leu Lys
        515                 520                 525

cag cgg caa caa ctg ttt gac tcc caa cag gga tgg ttt gaa gga tgg         1632
Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp
    530                 535                 540

ttc aac agg tcc ccc tgg ttt aca acc cta att tcc tcc att atg ggc         1680
Phe Asn Arg Ser Pro Trp Phe Thr Thr Leu Ile Ser Ser Ile Met Gly
545                 550                 555                 560

ccc tta cta atc cta ctc cta att ctc ctc ttc ggc cca tac atc ctt         1728
Pro Leu Leu Ile Leu Leu Leu Ile Leu Leu Phe Gly Pro Tyr Ile Leu
                565                 570                 575

aac aga tta gta caa ttc gta aaa gac aga ata tct gtg gta caa gcc         1776
Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala
            580                 585                 590

tta att tta acc caa cag tac caa cag ata aag caa tac gat ccg gac         1824
Leu Ile Leu Thr Gln Gln Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp
        595                 600                 605

cga cca                                                                 1830
Arg Pro
    610


<210> SEQ ID NO 30
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<211> LENGTH: 610
<212> TYPE: PRT
<213> ORGANISM: Feline leukemia virus

<400> SEQUENCE: 30

Met Ala Asn Pro Ser Pro Pro Gln Met Tyr Asn Val Thr Trp Val Ile
  1               5                  10                  15

Thr Asn Val Gln Thr Asn Thr Gln Ala Asn Ala Thr Ser Met Leu Gly
             20                  25                  30

Thr Leu Thr Asp Val Tyr Pro Thr Leu His Val Asp Leu Cys Asp Leu
         35                  40                  45

Val Gly Asp Thr Trp Glu Pro Met Val Leu Ser Pro Thr Gly Tyr Pro
     50                  55                  60

Pro Ser Lys Tyr Gly Cys Lys Thr Thr Asp Arg Lys Lys Gln Gln Gln
 65                  70                  75                  80

Thr Tyr Pro Phe Tyr Val Cys Pro Gly His Arg Pro Ser Leu Gly Pro
                 85                  90                  95

Lys Gly Thr His Cys Gly Gly Ala Gln Asp Gly Phe Cys Ala Ala Trp
            100                 105                 110

Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp Lys Pro Ser Ser Ser Trp
        115                 120                 125

Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser Gln Asn Asn Asn Cys Glu
    130                 135                 140

Gly Lys Cys Asn Pro Leu Ile Leu Gln Phe Thr Gln Lys Gly Lys Gln
145                 150                 155                 160

Ala Ser Trp Asp Gly Pro Lys Met Trp Gly Leu Arg Leu Tyr Arg Thr
                165                 170                 175

Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val Ser Arg Arg Val Ser Thr
            180                 185                 190

Ile Thr Pro Pro Gln Ala Met Gly Pro Asp Leu Val Leu Pro Asp Gln
        195                 200                 205

Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly Ser Lys Val Ala Thr Gln
    210                 215                 220

Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg Ser Val Ala Pro Thr Thr
225                 230                 235                 240

Val Gly Pro Lys Arg Ile Gly Thr Gly Asp Arg Leu Ile Asn Leu Val
                245                 250                 255

Gln Gly Ala Tyr Leu Ala Leu Asn Ala Thr Asp Pro Asn Lys Thr Lys
            260                 265                 270

Asp Cys Trp Leu Cys Leu Val Ser Arg Pro Pro Tyr Tyr Glu Gly Ile
        275                 280                 285

Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr Asn Pro Pro Pro Ser Cys
    290                 295                 300

Leu Ser Ile Pro Pro His Lys Leu Thr Ile Ser Lys Val Ser Gly Gln
305                 310                 315                 320

Gly Leu Cys Ile Gly Thr Val Pro Lys Thr His Gln Ala Leu Cys Asn
                325                 330                 335

Lys Thr His Gln Gly His Thr Gly Ala Asp Tyr Arg Ala Ala Pro Arg
            340                 345                 350

Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp Ala Cys Asn Thr Gly Leu
        355                 360                 365

Thr Pro Cys Ile Ser Met Ala Val Leu Asn Leu Thr Ser Asp Phe Cys
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    370                 375                 380

Val Leu Ile Glu Leu Trp Pro Arg Val Thr Tyr His Gln Pro Glu Tyr
385                 390                 395                 400

Val Tyr Thr His Phe Ala Lys Ala Gly Arg Phe Arg Arg Glu Pro Ile
                405                 410                 415

Ser Leu Thr Val Ala Leu Met Leu Gly Gly Leu Thr Val Gly Gly Ile
            420                 425                 430

Ala Ala Gly Val Gly Thr Gly Thr Lys Ala Leu Leu Glu Thr Ala Gln
        435                 440                 445

Phe Arg Gln Leu Gln Met Ala Met His Thr Asp Ile Gln Ala Leu Glu
    450                 455                 460

Glu Ser Ile Ser Ala Leu Glu Lys Ser Leu Thr Ser Leu Ser Glu Val
465                 470                 475                 480

Val Leu Gln Asn Arg Arg Gly Leu Asp Ile Leu Phe Leu Gln Glu Gly
                485                 490                 495

Gly Leu Cys Ala Ala Leu Lys Glu Glu Cys Cys Phe Tyr Ala Asp His
            500                 505                 510

Thr Gly Leu Val Arg Asp Asn Met Ala Lys Leu Arg Glu Arg Leu Lys
        515                 520                 525

Gln Arg Gln Gln Leu Phe Asp Ser Gln Gln Gly Trp Phe Glu Gly Trp
    530                 535                 540

Phe Asn Arg Ser Pro Trp Phe Thr Thr Leu Ile Ser Ser Ile Met Gly
545                 550                 555                 560

Pro Leu Leu Ile Leu Leu Leu Ile Leu Leu Phe Gly Pro Tyr Ile Leu
                565                 570                 575

Asn Arg Leu Val Gln Phe Val Lys Asp Arg Ile Ser Val Val Gln Ala
            580                 585                 590

Leu Ile Leu Thr Gln Gln Tyr Gln Gln Ile Lys Gln Tyr Asp Pro Asp
        595                 600                 605

Arg Pro
    610


<210> SEQ ID NO 31
<211> LENGTH: 1833
<212> TYPE: DNA
<213> ORGANISM: Feline leukemia virus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1833)

<400> SEQUENCE: 31

atg gag cac cta cgc ctt tat cgc cag ttg ctg tta gcg ggt ctc cgc       48
Met Glu His Leu Arg Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg
  1               5                  10                  15

ggg gct gca aga cac ccc act aat ttg gca cag gtt aag caa ttt tta       96
Gly Ala Ala Arg His Pro Thr Asn Leu Ala Gln Val Lys Gln Phe Leu
             20                  25                  30

caa ggg aaa gaa gaa acg cca gcc tca ttc tta gaa aga tta aaa gag      144
Gln Gly Lys Glu Glu Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu
         35                  40                  45

gct tac cga atg tat act ccc tat gac cct gag gac cca ggg cag gct      192
Ala Tyr Arg Met Tyr Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala
     50                  55                  60

gct agt gtt atc ctg tcc ttt atc tac cag tct agc ccg gac ata aga      240
Ala Ser Val Ile Leu Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg
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 65                  70                  75                  80

aat aag tta caa agg cta gaa ggc cta cag ggg ttc aca ctg tct gat      288
Asn Lys Leu Gln Arg Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp
                  85                  90                  95

ttg cta aaa gag gca gaa aag ata tac aac aaa agg gag acc cca gag      336
Leu Leu Lys Glu Ala Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu
             100                 105                 110

gaa agg gaa gaa aga tta tgg cag cgg cag gaa gaa aga gat aaa aag      384
Glu Arg Glu Glu Arg Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys
         115                 120                 125

cgc cat aag gag atg act aaa gtt ctg gcc aca gta gtt gct cag aat      432
Arg His Lys Glu Met Thr Lys Val Leu Ala Thr Val Val Ala Gln Asn
     130                 135                 140

aga gat aag gat aga gag gaa agt aaa ctg gga gat caa aga aaa ata      480
Arg Asp Lys Asp Arg Glu Glu Ser Lys Leu Gly Asp Gln Arg Lys Ile
145                 150                 155                 160

cct ctg ggg aaa gac cag tgt gcc tat tgc aag gaa aag gga cat tgg      528
Pro Leu Gly Lys Asp Gln Cys Ala Tyr Cys Lys Glu Lys Gly His Trp
                 165                 170                 175

gtt cgc gat tgc ccc aac cgg ccc cgg aag aaa ccc gcc aac tcc act      576
Val Arg Asp Cys Pro Asn Arg Pro Arg Lys Lys Pro Ala Asn Ser Thr
             180                 185                 190

ctc ctc aac tta gaa gat atg gcc aat cct agt cca ccc caa atg tat      624
Leu Leu Asn Leu Glu Asp Met Ala Asn Pro Ser Pro Pro Gln Met Tyr
         195                 200                 205

aat gta act tgg gta ata acc aat gta caa acc aac acc caa gct aat      672
Asn Val Thr Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn
     210                 215                 220

gcc acc tct atg tta gga acc tta acc gat gtc tac cct acc cta cat      720
Ala Thr Ser Met Leu Gly Thr Leu Thr Asp Val Tyr Pro Thr Leu His
225                 230                 235                 240

gtt gac tta tgt gac cta gtg gga gac acc tgg gaa cct atg gtc cta      768
Val Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Met Val Leu
                 245                 250                 255

agc cca acc ggg tac cct ccc tca aaa tat gga tgt aaa act aca gat      816
Ser Pro Thr Gly Tyr Pro Pro Ser Lys Tyr Gly Cys Lys Thr Thr Asp
             260                 265                 270

aga aaa aaa cag caa cag aca tac ccc ttt tac gtc tgc ccc ggg cat      864
Arg Lys Lys Gln Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His
         275                 280                 285

cgc ccc tcg ctg ggg cca aag gga aca cat tgt gga ggg gca caa gat      912
Arg Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Gly Ala Gln Asp
     290                 295                 300

ggg ttt tgt gcc gca tgg gga tgt gaa acc acc gga gaa gct tgg tgg      960
Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp
305                 310                 315                 320

aag ccc tcc tcc tca tgg gac tat atc aca gta aaa aga ggg agt agt     1008
Lys Pro Ser Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser
                 325                 330                 335

cag aac aat aac tgt gag gga aaa tgc aac ccc ctg att ttg cag ttc     1056
Gln Asn Asn Asn Cys Glu Gly Lys Cys Asn Pro Leu Ile Leu Gln Phe
             340                 345                 350

acc cag aag ggg aaa caa gcc tct tgg gac gga cct aag atg tgg gga     1104
Thr Gln Lys Gly Lys Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly
         355                 360                 365

ttg cgg cta tac cgt aca gga tat gac cct atc gcc tta ttc acg gta     1152
Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val
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    370                 375                 380

tcc cgg cgg gtg tca acc att acg ccg cct cag gca atg gga cca gac     1200
Ser Arg Arg Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asp
385                 390                 395                 400

cta gtc tta cct gat caa aaa ccc cca tcc cga caa tct caa aca ggg     1248
Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly
                405                 410                 415

tcc aaa gtg gcg acc cag agg ccc caa acg aat gaa agc gcc cca agg     1296
Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg
            420                 425                 430

tct gtt gcc ccc acc acc gtg ggt ccc aaa cgg att ggg acc gga gat     1344
Ser Val Ala Pro Thr Thr Val Gly Pro Lys Arg Ile Gly Thr Gly Asp
        435                 440                 445

agg tta ata aat tta gta caa ggg gca tac cta gcc tta aat gcc acc     1392
Arg Leu Ile Asn Leu Val Gln Gly Ala Tyr Leu Ala Leu Asn Ala Thr
    450                 455                 460

gac ccc aac aaa act aaa gac tgt tgg ctc tgc ctg gtt tct cga cca     1440
Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro
465                 470                 475                 480

ccc tat tac gaa ggg att gca atc tta ggt aac tac agc aac caa aca     1488
Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr
                485                 490                 495

aac cct ccc cca tcc tgc cta tct att ccg cca cac aag ctg acc ata     1536
Asn Pro Pro Pro Ser Cys Leu Ser Ile Pro Pro His Lys Leu Thr Ile
            500                 505                 510

tct aaa gta tca ggg caa gga ctg tgc ata ggg act gtt cct aag acc     1584
Ser Lys Val Ser Gly Gln Gly Leu Cys Ile Gly Thr Val Pro Lys Thr
        515                 520                 525

cac cag gct ttg tgc aat aag acg cac cag gga cat aca ggg gcg gac     1632
His Gln Ala Leu Cys Asn Lys Thr His Gln Gly His Thr Gly Ala Asp
    530                 535                 540

tat cga gcc gcc ccg cgg tat cta gcc gcc ccc aat ggc acc tat tgg     1680
Tyr Arg Ala Ala Pro Arg Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp
545                 550                 555                 560

gcc tgt aac act gga ctc acc cca tgc att tcc atg gcg gtg ctc aat     1728
Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser Met Ala Val Leu Asn
                565                 570                 575

ttg acc tct gat ttt tgt gtc tta atc gaa tta tgg ccc aga gtg act     1776
Leu Thr Ser Asp Phe Cys Val Leu Ile Glu Leu Trp Pro Arg Val Thr
            580                 585                 590

tac cat caa ccc gaa tat gtg tac aca cat ttt gcc aaa gct ggc agg     1824
Tyr His Gln Pro Glu Tyr Val Tyr Thr His Phe Ala Lys Ala Gly Arg
        595                 600                 605

ttc cga aga                                                         1833
Phe Arg Arg
    610


<210> SEQ ID NO 32
<211> LENGTH: 611
<212> TYPE: PRT
<213> ORGANISM: Feline leukemia virus

<400> SEQUENCE: 32

Met Glu His Leu Arg Leu Tyr Arg Gln Leu Leu Leu Ala Gly Leu Arg
  1               5                  10                  15

Gly Ala Ala Arg His Pro Thr Asn Leu Ala Gln Val Lys Gln Phe Leu
             20                  25                  30
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Gln Gly Lys Glu Glu Thr Pro Ala Ser Phe Leu Glu Arg Leu Lys Glu
         35                  40                  45

Ala Tyr Arg Met Tyr Thr Pro Tyr Asp Pro Glu Asp Pro Gly Gln Ala
     50                  55                  60

Ala Ser Val Ile Leu Ser Phe Ile Tyr Gln Ser Ser Pro Asp Ile Arg
 65                  70                  75                  80

Asn Lys Leu Gln Arg Leu Glu Gly Leu Gln Gly Phe Thr Leu Ser Asp
                 85                  90                  95

Leu Leu Lys Glu Ala Glu Lys Ile Tyr Asn Lys Arg Glu Thr Pro Glu
            100                 105                 110

Glu Arg Glu Glu Arg Leu Trp Gln Arg Gln Glu Glu Arg Asp Lys Lys
        115                 120                 125

Arg His Lys Glu Met Thr Lys Val Leu Ala Thr Val Val Ala Gln Asn
    130                 135                 140

Arg Asp Lys Asp Arg Glu Glu Ser Lys Leu Gly Asp Gln Arg Lys Ile
145                 150                 155                 160

Pro Leu Gly Lys Asp Gln Cys Ala Tyr Cys Lys Glu Lys Gly His Trp
                165                 170                 175

Val Arg Asp Cys Pro Asn Arg Pro Arg Lys Lys Pro Ala Asn Ser Thr
            180                 185                 190

Leu Leu Asn Leu Glu Asp Met Ala Asn Pro Ser Pro Pro Gln Met Tyr
        195                 200                 205

Asn Val Thr Trp Val Ile Thr Asn Val Gln Thr Asn Thr Gln Ala Asn
    210                 215                 220

Ala Thr Ser Met Leu Gly Thr Leu Thr Asp Val Tyr Pro Thr Leu His
225                 230                 235                 240

Val Asp Leu Cys Asp Leu Val Gly Asp Thr Trp Glu Pro Met Val Leu
                245                 250                 255

Ser Pro Thr Gly Tyr Pro Pro Ser Lys Tyr Gly Cys Lys Thr Thr Asp
            260                 265                 270

Arg Lys Lys Gln Gln Gln Thr Tyr Pro Phe Tyr Val Cys Pro Gly His
        275                 280                 285

Arg Pro Ser Leu Gly Pro Lys Gly Thr His Cys Gly Gly Ala Gln Asp
    290                 295                 300

Gly Phe Cys Ala Ala Trp Gly Cys Glu Thr Thr Gly Glu Ala Trp Trp
305                 310                 315                 320

Lys Pro Ser Ser Ser Trp Asp Tyr Ile Thr Val Lys Arg Gly Ser Ser
                325                 330                 335

Gln Asn Asn Asn Cys Glu Gly Lys Cys Asn Pro Leu Ile Leu Gln Phe
            340                 345                 350

Thr Gln Lys Gly Lys Gln Ala Ser Trp Asp Gly Pro Lys Met Trp Gly
        355                 360                 365

Leu Arg Leu Tyr Arg Thr Gly Tyr Asp Pro Ile Ala Leu Phe Thr Val
    370                 375                 380

Ser Arg Arg Val Ser Thr Ile Thr Pro Pro Gln Ala Met Gly Pro Asp
385                 390                 395                 400

Leu Val Leu Pro Asp Gln Lys Pro Pro Ser Arg Gln Ser Gln Thr Gly
                405                 410                 415

Ser Lys Val Ala Thr Gln Arg Pro Gln Thr Asn Glu Ser Ala Pro Arg
            420                 425                 430

Ser Val Ala Pro Thr Thr Val Gly Pro Lys Arg Ile Gly Thr Gly Asp
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        435                 440                 445

Arg Leu Ile Asn Leu Val Gln Gly Ala Tyr Leu Ala Leu Asn Ala Thr
    450                 455                 460

Asp Pro Asn Lys Thr Lys Asp Cys Trp Leu Cys Leu Val Ser Arg Pro
465                 470                 475                 480

Pro Tyr Tyr Glu Gly Ile Ala Ile Leu Gly Asn Tyr Ser Asn Gln Thr
                485                 490                 495

Asn Pro Pro Pro Ser Cys Leu Ser Ile Pro Pro His Lys Leu Thr Ile
            500                 505                 510

Ser Lys Val Ser Gly Gln Gly Leu Cys Ile Gly Thr Val Pro Lys Thr
        515                 520                 525

His Gln Ala Leu Cys Asn Lys Thr His Gln Gly His Thr Gly Ala Asp
    530                 535                 540

Tyr Arg Ala Ala Pro Arg Tyr Leu Ala Ala Pro Asn Gly Thr Tyr Trp
545                 550                 555                 560

Ala Cys Asn Thr Gly Leu Thr Pro Cys Ile Ser Met Ala Val Leu Asn
                565                 570                 575

Leu Thr Ser Asp Phe Cys Val Leu Ile Glu Leu Trp Pro Arg Val Thr
            580                 585                 590

Tyr His Gln Pro Glu Tyr Val Tyr Thr His Phe Ala Lys Ala Gly Arg
        595                 600                 605

Phe Arg Arg
    610


<210> SEQ ID NO 33
<211> LENGTH: 1812
<212> TYPE: DNA
<213> ORGANISM: canine distemper virus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1812)

<400> SEQUENCE: 33

atg ctc ccc tac caa gac aag gtg ggt gcc ttc tac aag gat aat gca       48
Met Leu Pro Tyr Gln Asp Lys Val Gly Ala Phe Tyr Lys Asp Asn Ala
  1               5                  10                  15

aga gcc aat tca acc aag ctg tcc tta gtg aca gaa gga cat ggg ggc       96
Arg Ala Asn Ser Thr Lys Leu Ser Leu Val Thr Glu Gly His Gly Gly
             20                  25                  30

agg aga cca cct tat ttg ttg ttt gtc ctt ctc atc tta ttg gtt ggt      144
Arg Arg Pro Pro Tyr Leu Leu Phe Val Leu Leu Ile Leu Leu Val Gly
         35                  40                  45

atc ctg gcc ttg ctt gct atc act gga gtt cga ttt cac caa gta tca      192
Ile Leu Ala Leu Leu Ala Ile Thr Gly Val Arg Phe His Gln Val Ser
     50                  55                  60

act agt aat atg gaa ttt agc aga ttg ctg aaa gag gat atg gag aaa      240
Thr Ser Asn Met Glu Phe Ser Arg Leu Leu Lys Glu Asp Met Glu Lys
 65                  70                  75                  80

tca gag gcc gta cat cac caa gtc ata gat gtc ttg aca ccg ctc ttc      288
Ser Glu Ala Val His His Gln Val Ile Asp Val Leu Thr Pro Leu Phe
                85                  90                  95

aag att att gga gat gag att ggg tta cgg ttg cca caa aag cta aac      336
Lys Ile Ile Gly Asp Glu Ile Gly Leu Arg Leu Pro Gln Lys Leu Asn
            100                 105                 110

gag atc aaa caa ttt atc ctt caa aag aca aat ttc ttc aat ccg aac      384
Glu Ile Lys Gln Phe Ile Leu Gln Lys Thr Asn Phe Phe Asn Pro Asn
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        115                 120                 125

aga gaa ttc gac ttc cgc gat ctc cac tgg tgc att aac ccg cct agt      432
Arg Glu Phe Asp Phe Arg Asp Leu His Trp Cys Ile Asn Pro Pro Ser
    130                 135                 140

acg gtc aag gtg aat ttt act aat tac tgt gag tca att ggg atc aga      480
Thr Val Lys Val Asn Phe Thr Asn Tyr Cys Glu Ser Ile Gly Ile Arg
145                 150                 155                 160

aaa gct att gca tcg gca gca aat cct atc ctt tta tca gcc cta tct      528
Lys Ala Ile Ala Ser Ala Ala Asn Pro Ile Leu Leu Ser Ala Leu Ser
                165                 170                 175

ggg ggc aga ggt gac ata ttc cca cca cac aga tgc agt gga gct act      576
Gly Gly Arg Gly Asp Ile Phe Pro Pro His Arg Cys Ser Gly Ala Thr
            180                 185                 190

act tca gta ggc aaa gtt ttc ccc cta tca gtc tca tta tcc atg tct      624
Thr Ser Val Gly Lys Val Phe Pro Leu Ser Val Ser Leu Ser Met Ser
        195                 200                 205

ttg atc tca aga acc tca gag gta atc aat atg ctg acc gct atc tca      672
Leu Ile Ser Arg Thr Ser Glu Val Ile Asn Met Leu Thr Ala Ile Ser
    210                 215                 220

gac ggc gtg tat ggc aaa act tac ttg cta gtg cct gat gat ata gaa      720
Asp Gly Val Tyr Gly Lys Thr Tyr Leu Leu Val Pro Asp Asp Ile Glu
225                 230                 235                 240

aga gag ttc gac act cga gag att cga gtc ttt gaa ata ggg ttc atc      768
Arg Glu Phe Asp Thr Arg Glu Ile Arg Val Phe Glu Ile Gly Phe Ile
                245                 250                 255

aaa agg tgg ctg aat gac atg cca tta ctc caa aca acc aac tat atg      816
Lys Arg Trp Leu Asn Asp Met Pro Leu Leu Gln Thr Thr Asn Tyr Met
            260                 265                 270

gta ctc ccg aag aat tcc aaa gcc aag gta tgt act ata gca gtg ggt      864
Val Leu Pro Lys Asn Ser Lys Ala Lys Val Cys Thr Ile Ala Val Gly
        275                 280                 285

gag ttg aca ctg gct tcc ttg tgt gta gaa gag agc act gta tta tta      912
Glu Leu Thr Leu Ala Ser Leu Cys Val Glu Glu Ser Thr Val Leu Leu
    290                 295                 300

tat cat gac agc agt ggt tca caa gat ggt att cta gta gtg aca ctg      960
Tyr His Asp Ser Ser Gly Ser Gln Asp Gly Ile Leu Val Val Thr Leu
305                 310                 315                 320

ggg ata ttt tgg gca aca cct atg gat cac att gag gaa gtg ata cct     1008
Gly Ile Phe Trp Ala Thr Pro Met Asp His Ile Glu Glu Val Ile Pro
                325                 330                 335

gtc gct cac cca tca atg aag aaa ata cat ata aca aac cac cgt ggt     1056
Val Ala His Pro Ser Met Lys Lys Ile His Ile Thr Asn His Arg Gly
            340                 345                 350

ttt ata aaa gat tca att gca acc tgg atg gtg cct gcc ctg gcc tct     1104
Phe Ile Lys Asp Ser Ile Ala Thr Trp Met Val Pro Ala Leu Ala Ser
        355                 360                 365

gag aaa caa gaa gaa caa aaa ggt tgt ctg gag tca gct tgt caa aga     1152
Glu Lys Gln Glu Glu Gln Lys Gly Cys Leu Glu Ser Ala Cys Gln Arg
    370                 375                 380

aaa acc tac ccc atg tgc aac caa gcg tca tgg gaa ccc ttc gga gga     1200
Lys Thr Tyr Pro Met Cys Asn Gln Ala Ser Trp Glu Pro Phe Gly Gly
385                 390                 395                 400

aga cag ttg cca tct tat ggg cgg ttg aca tta cct cta gat gca agt     1248
Arg Gln Leu Pro Ser Tyr Gly Arg Leu Thr Leu Pro Leu Asp Ala Ser
                405                 410                 415

gtt gac ctt caa ctt aac ata tcg ttc aca tac ggt ccg gtt ata ctg     1296
Val Asp Leu Gln Leu Asn Ile Ser Phe Thr Tyr Gly Pro Val Ile Leu
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            420                 425                 430

aat gga gat ggt atg gat tat tat gaa agc cca ctt ttg aac tcc gga     1344
Asn Gly Asp Gly Met Asp Tyr Tyr Glu Ser Pro Leu Leu Asn Ser Gly
        435                 440                 445

tgg ctt acc att ccc ccc aaa gac gga aca atc tct gga ttg ata aac     1392
Trp Leu Thr Ile Pro Pro Lys Asp Gly Thr Ile Ser Gly Leu Ile Asn
    450                 455                 460

aaa gca ggt aga gga gac cag ttc act gta ctc ccc cat gtg tta aca     1440
Lys Ala Gly Arg Gly Asp Gln Phe Thr Val Leu Pro His Val Leu Thr
465                 470                 475                 480

ttt gcg ccc agg gaa tca agt gga aat tgt tat tta cct att caa aca     1488
Phe Ala Pro Arg Glu Ser Ser Gly Asn Cys Tyr Leu Pro Ile Gln Thr
                485                 490                 495

tct caa att aga gat aga gat gtc ctc att gag tcc aat ata gtg gtg     1536
Ser Gln Ile Arg Asp Arg Asp Val Leu Ile Glu Ser Asn Ile Val Val
            500                 505                 510

ttg cct aca cag agt att aga tat gtc ata gca acg tat gac ata tca     1584
Leu Pro Thr Gln Ser Ile Arg Tyr Val Ile Ala Thr Tyr Asp Ile Ser
        515                 520                 525

cga agt gat cat gct att gtt tat tat gtt tat gac cca atc cgg acg     1632
Arg Ser Asp His Ala Ile Val Tyr Tyr Val Tyr Asp Pro Ile Arg Thr
    530                 535                 540

att tct tat acg cac cca ttt aga cta act acc aag ggt aga cct gat     1680
Ile Ser Tyr Thr His Pro Phe Arg Leu Thr Thr Lys Gly Arg Pro Asp
545                 550                 555                 560

ttc cta agg att gaa tgt ttt gtg tgg gat gac aat ttg tgg tgt cac     1728
Phe Leu Arg Ile Glu Cys Phe Val Trp Asp Asp Asn Leu Trp Cys His
                565                 570                 575

caa ttt tac aga ttc gag gct gac atc gcc aac tct aca acc agt gtt     1776
Gln Phe Tyr Arg Phe Glu Ala Asp Ile Ala Asn Ser Thr Thr Ser Val
            580                 585                 590

gag aat tta gtc cgt ata aga ttc tca tgt aac cgt                     1812
Glu Asn Leu Val Arg Ile Arg Phe Ser Cys Asn Arg
        595                 600


<210> SEQ ID NO 34
<211> LENGTH: 604
<212> TYPE: PRT
<213> ORGANISM: canine distemper virus

<400> SEQUENCE: 34

Met Leu Pro Tyr Gln Asp Lys Val Gly Ala Phe Tyr Lys Asp Asn Ala
  1               5                  10                  15

Arg Ala Asn Ser Thr Lys Leu Ser Leu Val Thr Glu Gly His Gly Gly
             20                  25                  30

Arg Arg Pro Pro Tyr Leu Leu Phe Val Leu Leu Ile Leu Leu Val Gly
         35                  40                  45

Ile Leu Ala Leu Leu Ala Ile Thr Gly Val Arg Phe His Gln Val Ser
     50                  55                  60

Thr Ser Asn Met Glu Phe Ser Arg Leu Leu Lys Glu Asp Met Glu Lys
 65                  70                  75                  80

Ser Glu Ala Val His His Gln Val Ile Asp Val Leu Thr Pro Leu Phe
                 85                  90                  95

Lys Ile Ile Gly Asp Glu Ile Gly Leu Arg Leu Pro Gln Lys Leu Asn
            100                 105                 110

Glu Ile Lys Gln Phe Ile Leu Gln Lys Thr Asn Phe Phe Asn Pro Asn
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        115                 120                 125

Arg Glu Phe Asp Phe Arg Asp Leu His Trp Cys Ile Asn Pro Pro Ser
    130                 135                 140

Thr Val Lys Val Asn Phe Thr Asn Tyr Cys Glu Ser Ile Gly Ile Arg
145                 150                 155                 160

Lys Ala Ile Ala Ser Ala Ala Asn Pro Ile Leu Leu Ser Ala Leu Ser
                165                 170                 175

Gly Gly Arg Gly Asp Ile Phe Pro Pro His Arg Cys Ser Gly Ala Thr
            180                 185                 190

Thr Ser Val Gly Lys Val Phe Pro Leu Ser Val Ser Leu Ser Met Ser
        195                 200                 205

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

Asp Gly Val Tyr Gly Lys Thr Tyr Leu Leu Val Pro Asp Asp Ile Glu
225                 230                 235                 240

Arg Glu Phe Asp Thr Arg Glu Ile Arg Val Phe Glu Ile Gly Phe Ile
                245                 250                 255

Lys Arg Trp Leu Asn Asp Met Pro Leu Leu Gln Thr Thr Asn Tyr Met
            260                 265                 270

Val Leu Pro Lys Asn Ser Lys Ala Lys Val Cys Thr Ile Ala Val Gly
        275                 280                 285

Glu Leu Thr Leu Ala Ser Leu Cys Val Glu Glu Ser Thr Val Leu Leu
    290                 295                 300

Tyr His Asp Ser Ser Gly Ser Gln Asp Gly Ile Leu Val Val Thr Leu
305                 310                 315                 320

Gly Ile Phe Trp Ala Thr Pro Met Asp His Ile Glu Glu Val Ile Pro
                325                 330                 335

Val Ala His Pro Ser Met Lys Lys Ile His Ile Thr Asn His Arg Gly
            340                 345                 350

Phe Ile Lys Asp Ser Ile Ala Thr Trp Met Val Pro Ala Leu Ala Ser
        355                 360                 365

Glu Lys Gln Glu Glu Gln Lys Gly Cys Leu Glu Ser Ala Cys Gln Arg
    370                 375                 380

Lys Thr Tyr Pro Met Cys Asn Gln Ala Ser Trp Glu Pro Phe Gly Gly
385                 390                 395                 400

Arg Gln Leu Pro Ser Tyr Gly Arg Leu Thr Leu Pro Leu Asp Ala Ser
                405                 410                 415

Val Asp Leu Gln Leu Asn Ile Ser Phe Thr Tyr Gly Pro Val Ile Leu
            420                 425                 430

Asn Gly Asp Gly Met Asp Tyr Tyr Glu Ser Pro Leu Leu Asn Ser Gly
        435                 440                 445

Trp Leu Thr Ile Pro Pro Lys Asp Gly Thr Ile Ser Gly Leu Ile Asn
    450                 455                 460

Lys Ala Gly Arg Gly Asp Gln Phe Thr Val Leu Pro His Val Leu Thr
465                 470                 475                 480

Phe Ala Pro Arg Glu Ser Ser Gly Asn Cys Tyr Leu Pro Ile Gln Thr
                485                 490                 495

Ser Gln Ile Arg Asp Arg Asp Val Leu Ile Glu Ser Asn Ile Val Val
            500                 505                 510

Leu Pro Thr Gln Ser Ile Arg Tyr Val Ile Ala Thr Tyr Asp Ile Ser
        515                 520                 525
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Arg Ser Asp His Ala Ile Val Tyr Tyr Val Tyr Asp Pro Ile Arg Thr
    530                 535                 540

Ile Ser Tyr Thr His Pro Phe Arg Leu Thr Thr Lys Gly Arg Pro Asp
545                 550                 555                 560

Phe Leu Arg Ile Glu Cys Phe Val Trp Asp Asp Asn Leu Trp Cys His
                565                 570                 575

Gln Phe Tyr Arg Phe Glu Ala Asp Ile Ala Asn Ser Thr Thr Ser Val
            580                 585                 590

Glu Asn Leu Val Arg Ile Arg Phe Ser Cys Asn Arg
        595                 600


<210> SEQ ID NO 35
<211> LENGTH: 1986
<212> TYPE: DNA
<213> ORGANISM: canine distemper virus
<220> FEATURE:
<221> NAME/KEY: CDS
<222> LOCATION: (1)..(1986)

<400> SEQUENCE: 35

atg cac agg gga atc ccc aaa agc tcc aaa acc caa aca cat acc caa       48
Met His Arg Gly Ile Pro Lys Ser Ser Lys Thr Gln Thr His Thr Gln
  1               5                  10                  15

caa gac cgc ccc cca caa ccc agc acc gaa ctc gaa gag acc agg acc       96
Gln Asp Arg Pro Pro Gln Pro Ser Thr Glu Leu Glu Glu Thr Arg Thr
             20                  25                  30

tcc cga gca cga cac agc aca aca tca gct cag cga tcc acg cac tac      144
Ser Arg Ala Arg His Ser Thr Thr Ser Ala Gln Arg Ser Thr His Tyr
         35                  40                  45

gat cct cga aca tcg gac aga ccc gtc tcc tac acc atg aac agg acc      192
Asp Pro Arg Thr Ser Asp Arg Pro Val Ser Tyr Thr Met Asn Arg Thr
     50                  55                  60

agg tcc cgc aag caa acc agc cac aga ttg aag aac atc cca gtt cac      240
Arg Ser Arg Lys Gln Thr Ser His Arg Leu Lys Asn Ile Pro Val His
 65                  70                  75                  80

gga aac cac gag gcc acc atc cag cac ata cca gag agt gtc tca aaa      288
Gly Asn His Glu Ala Thr Ile Gln His Ile Pro Glu Ser Val Ser Lys
                 85                  90                  95

gga gcg aga tcc cag atc gaa agg cgg caa ccc aat gca atc aac tca      336
Gly Ala Arg Ser Gln Ile Glu Arg Arg Gln Pro Asn Ala Ile Asn Ser
            100                 105                 110

ggc tct cat tgc acc tgg tta gtc ctg tgg tgc ctc gga atg gcc agt      384
Gly Ser His Cys Thr Trp Leu Val Leu Trp Cys Leu Gly Met Ala Ser
        115                 120                 125

ctc ttt ctt tgt tcc aag gct cag ata cat tgg gat aat ttg tca act      432
Leu Phe Leu Cys Ser Lys Ala Gln Ile His Trp Asp Asn Leu Ser Thr
    130                 135                 140

att ggg att atc ggg act gat aat gtc cat tac aag atc atg act agg      480
Ile Gly Ile Ile Gly Thr Asp Asn Val His Tyr Lys Ile Met Thr Arg
145                 150                 155                 160

ccc agt cac cag tac ttg gtc ata aaa ttg atc cct aat gct tca ctt      528
Pro Ser His Gln Tyr Leu Val Ile Lys Leu Ile Pro Asn Ala Ser Leu
                165                 170                 175

ata gag aat tgt acc aaa gca gaa tta ggt gag tat gag aaa tta ttg      576
Ile Glu Asn Cys Thr Lys Ala Glu Leu Gly Glu Tyr Glu Lys Leu Leu
            180                 185                 190

aat tca gtc ctc gaa cca atc aac caa gct ttg act cta atg acc aag      624
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Asn Ser Val Leu Glu Pro Ile Asn Gln Ala Leu Thr Leu Met Thr Lys
        195                 200                 205

aat gtg aag ccc ctg cag tca tta ggg tca ggt agg aga caa agg cgt      672
Asn Val Lys Pro Leu Gln Ser Leu Gly Ser Gly Arg Arg Gln Arg Arg
    210                 215                 220

ttt gca gga gtg gta ctt gca ggt gta gct tta gga gtg gct aca gct      720
Phe Ala Gly Val Val Leu Ala Gly Val Ala Leu Gly Val Ala Thr Ala
225                 230                 235                 240

gca caa atc act gca gga ata gct tta cat caa tcc aac ctc aat gct      768
Ala Gln Ile Thr Ala Gly Ile Ala Leu His Gln Ser Asn Leu Asn Ala
                245                 250                 255

caa gca atc caa tct ctt aga acc agc ctt gaa cag tct aac aaa gct      816
Gln Ala Ile Gln Ser Leu Arg Thr Ser Leu Glu Gln Ser Asn Lys Ala
            260                 265                 270

ata gaa gaa att agg gag gct acc caa gaa acc gtc att gcc gtt cag      864
Ile Glu Glu Ile Arg Glu Ala Thr Gln Glu Thr Val Ile Ala Val Gln
        275                 280                 285

gga gtc cag gac tac gtc aac aac gaa ctc gtc cct gcc atg caa cat      912
Gly Val Gln Asp Tyr Val Asn Asn Glu Leu Val Pro Ala Met Gln His
    290                 295                 300

atg tca tgt gaa tta gtt ggg cag aga tta ggg tta aga ctg ctt cgg      960
Met Ser Cys Glu Leu Val Gly Gln Arg Leu Gly Leu Arg Leu Leu Arg
305                 310                 315                 320

tat tat act gag ttg ttg tca ata ttt ggc ccg agt tta cgt gac cct     1008
Tyr Tyr Thr Glu Leu Leu Ser Ile Phe Gly Pro Ser Leu Arg Asp Pro
                325                 330                 335

att tca gcc gag ata tca att cag gca ctg att tat gct ctt gga gga     1056
Ile Ser Ala Glu Ile Ser Ile Gln Ala Leu Ile Tyr Ala Leu Gly Gly
            340                 345                 350

gaa att cat aag ata ctt gag aag ttg gga tat tct gga agt gat atg     1104
Glu Ile His Lys Ile Leu Glu Lys Leu Gly Tyr Ser Gly Ser Asp Met
        355                 360                 365

att gca atc ttg gag agt cgg ggg ata aaa aca aaa ata act cat gtt     1152
Ile Ala Ile Leu Glu Ser Arg Gly Ile Lys Thr Lys Ile Thr His Val
    370                 375                 380

gat ctt ccc ggg aaa ttc atc atc cta agt atc tca tac cca act tta     1200
Asp Leu Pro Gly Lys Phe Ile Ile Leu Ser Ile Ser Tyr Pro Thr Leu
385                 390                 395                 400

tca gaa gtc aag ggg gtt ata gtc cac aga ctg gaa gca gtt tct tac     1248
Ser Glu Val Lys Gly Val Ile Val His Arg Leu Glu Ala Val Ser Tyr
                405                 410                 415

aac ata gga tca caa gag tgg tac acc act gtc ccg agg tat att gca     1296
Asn Ile Gly Ser Gln Glu Trp Tyr Thr Thr Val Pro Arg Tyr Ile Ala
            420                 425                 430

act aat ggt tac tta ata tct aat ttt gat gag tca tct tgt gta ttc     1344
Thr Asn Gly Tyr Leu Ile Ser Asn Phe Asp Glu Ser Ser Cys Val Phe
        435                 440                 445

gtc tca gag tca gcc att tgt agc cag aac tcc ctg tat ccc atg agc     1392
Val Ser Glu Ser Ala Ile Cys Ser Gln Asn Ser Leu Tyr Pro Met Ser
    450                 455                 460

cca ctc tta caa caa tgt att agg ggc gac act tca tct tgt gct cgg     1440
Pro Leu Leu Gln Gln Cys Ile Arg Gly Asp Thr Ser Ser Cys Ala Arg
465                 470                 475                 480

acc ttg gta tct ggg act atg ggc aac aaa ttt att ctg tca aaa ggt     1488
Thr Leu Val Ser Gly Thr Met Gly Asn Lys Phe Ile Leu Ser Lys Gly
                485                 490                 495

aat atc gtc gca aat tgt gct tct ata cta tgt aag tgt tat agc aca     1536
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Asn Ile Val Ala Asn Cys Ala Ser Ile Leu Cys Lys Cys Tyr Ser Thr
            500                 505                 510

agc aca att att aat cag agt cct gat aag ttg ctg aca ttc att gcc     1584
Ser Thr Ile Ile Asn Gln Ser Pro Asp Lys Leu Leu Thr Phe Ile Ala
        515                 520                 525

tcc gat acc tgc cca ctg gtt gaa ata gat ggt gct act atc caa gtt     1632
Ser Asp Thr Cys Pro Leu Val Glu Ile Asp Gly Ala Thr Ile Gln Val
    530                 535                 540

gga ggc agg caa tac cct gat atg gta tac gaa ggc aaa gtt gcc tta     1680
Gly Gly Arg Gln Tyr Pro Asp Met Val Tyr Glu Gly Lys Val Ala Leu
545                 550                 555                 560

ggc cct gct ata tca ctt gat agg tta gat gta ggt aca aac tta ggg     1728
Gly Pro Ala Ile Ser Leu Asp Arg Leu Asp Val Gly Thr Asn Leu Gly
                565                 570                 575

aac gcc ctt aag aaa ctg gat gat gct aag gta ctg ata gac tcc tct     1776
Asn Ala Leu Lys Lys Leu Asp Asp Ala Lys Val Leu Ile Asp Ser Ser
            580                 585                 590

aac cag atc ctt gag acg gtt agg cgc tct tcc ttt aat ttt ggc agt     1824
Asn Gln Ile Leu Glu Thr Val Arg Arg Ser Ser Phe Asn Phe Gly Ser
        595                 600                 605

ctc ctc agc gtt cct ata tta agt tgt aca gcc ctg gct ttg ttg ttg     1872
Leu Leu Ser Val Pro Ile Leu Ser Cys Thr Ala Leu Ala Leu Leu Leu
    610                 615                 620

ctg att tac tgt tgt aaa aga cgc tac caa cag aca ctc aag cag cat     1920
Leu Ile Tyr Cys Cys Lys Arg Arg Tyr Gln Gln Thr Leu Lys Gln His
625                 630                 635                 640

act aag gtc gat ccg gca ttt aaa cct gat cta act gga act tcg aaa     1968
Thr Lys Val Asp Pro Ala Phe Lys Pro Asp Leu Thr Gly Thr Ser Lys
                645                 650                 655

tcc tat gtg aga tca ctc                                             1986
Ser Tyr Val Arg Ser Leu
            660


<210> SEQ ID NO 36
<211> LENGTH: 662
<212> TYPE: PRT
<213> ORGANISM: canine distemper virus

<400> SEQUENCE: 36

Met His Arg Gly Ile Pro Lys Ser Ser Lys Thr Gln Thr His Thr Gln
  1               5                  10                  15

Gln Asp Arg Pro Pro Gln Pro Ser Thr Glu Leu Glu Glu Thr Arg Thr
             20                  25                  30

Ser Arg Ala Arg His Ser Thr Thr Ser Ala Gln Arg Ser Thr His Tyr
         35                  40                  45

Asp Pro Arg Thr Ser Asp Arg Pro Val Ser Tyr Thr Met Asn Arg Thr
     50                  55                  60

Arg Ser Arg Lys Gln Thr Ser His Arg Leu Lys Asn Ile Pro Val His
 65                  70                  75                  80

Gly Asn His Glu Ala Thr Ile Gln His Ile Pro Glu Ser Val Ser Lys
                 85                  90                  95

Gly Ala Arg Ser Gln Ile Glu Arg Arg Gln Pro Asn Ala Ile Asn Ser
            100                 105                 110

Gly Ser His Cys Thr Trp Leu Val Leu Trp Cys Leu Gly Met Ala Ser
        115                 120                 125

Leu Phe Leu Cys Ser Lys Ala Gln Ile His Trp Asp Asn Leu Ser Thr
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    130                 135                 140

Ile Gly Ile Ile Gly Thr Asp Asn Val His Tyr Lys Ile Met Thr Arg
145                 150                 155                 160

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

Ile Glu Asn Cys Thr Lys Ala Glu Leu Gly Glu Tyr Glu Lys Leu Leu
            180                 185                 190

Asn Ser Val Leu Glu Pro Ile Asn Gln Ala Leu Thr Leu Met Thr Lys
        195                 200                 205

Asn Val Lys Pro Leu Gln Ser Leu Gly Ser Gly Arg Arg Gln Arg Arg
    210                 215                 220

Phe Ala Gly Val Val Leu Ala Gly Val Ala Leu Gly Val Ala Thr Ala
225                 230                 235                 240

Ala Gln Ile Thr Ala Gly Ile Ala Leu His Gln Ser Asn Leu Asn Ala
                245                 250                 255

Gln Ala Ile Gln Ser Leu Arg Thr Ser Leu Glu Gln Ser Asn Lys Ala
            260                 265                 270

Ile Glu Glu Ile Arg Glu Ala Thr Gln Glu Thr Val Ile Ala Val Gln
        275                 280                 285

Gly Val Gln Asp Tyr Val Asn Asn Glu Leu Val Pro Ala Met Gln His
    290                 295                 300

Met Ser Cys Glu Leu Val Gly Gln Arg Leu Gly Leu Arg Leu Leu Arg
305                 310                 315                 320

Tyr Tyr Thr Glu Leu Leu Ser Ile Phe Gly Pro Ser Leu Arg Asp Pro
                325                 330                 335

Ile Ser Ala Glu Ile Ser Ile Gln Ala Leu Ile Tyr Ala Leu Gly Gly
            340                 345                 350

Glu Ile His Lys Ile Leu Glu Lys Leu Gly Tyr Ser Gly Ser Asp Met
        355                 360                 365

Ile Ala Ile Leu Glu Ser Arg Gly Ile Lys Thr Lys Ile Thr His Val
    370                 375                 380

Asp Leu Pro Gly Lys Phe Ile Ile Leu Ser Ile Ser Tyr Pro Thr Leu
385                 390                 395                 400

Ser Glu Val Lys Gly Val Ile Val His Arg Leu Glu Ala Val Ser Tyr
                405                 410                 415

Asn Ile Gly Ser Gln Glu Trp Tyr Thr Thr Val Pro Arg Tyr Ile Ala
            420                 425                 430

Thr Asn Gly Tyr Leu Ile Ser Asn Phe Asp Glu Ser Ser Cys Val Phe
        435                 440                 445

Val Ser Glu Ser Ala Ile Cys Ser Gln Asn Ser Leu Tyr Pro Met Ser
    450                 455                 460

Pro Leu Leu Gln Gln Cys Ile Arg Gly Asp Thr Ser Ser Cys Ala Arg
465                 470                 475                 480

Thr Leu Val Ser Gly Thr Met Gly Asn Lys Phe Ile Leu Ser Lys Gly
                485                 490                 495

Asn Ile Val Ala Asn Cys Ala Ser Ile Leu Cys Lys Cys Tyr Ser Thr
            500                 505                 510

Ser Thr Ile Ile Asn Gln Ser Pro Asp Lys Leu Leu Thr Phe Ile Ala
        515                 520                 525

Ser Asp Thr Cys Pro Leu Val Glu Ile Asp Gly Ala Thr Ile Gln Val
    530                 535                 540
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Gly Gly Arg Gln Tyr Pro Asp Met Val Tyr Glu Gly Lys Val Ala Leu
545                 550                 555                 560

Gly Pro Ala Ile Ser Leu Asp Arg Leu Asp Val Gly Thr Asn Leu Gly
                565                 570                 575

Asn Ala Leu Lys Lys Leu Asp Asp Ala Lys Val Leu Ile Asp Ser Ser
            580                 585                 590

Asn Gln Ile Leu Glu Thr Val Arg Arg Ser Ser Phe Asn Phe Gly Ser
        595                 600                 605

Leu Leu Ser Val Pro Ile Leu Ser Cys Thr Ala Leu Ala Leu Leu Leu
    610                 615                 620

Leu Ile Tyr Cys Cys Lys Arg Arg Tyr Gln Gln Thr Leu Lys Gln His
625                 630                 635                 640

Thr Lys Val Asp Pro Ala Phe Lys Pro Asp Leu Thr Gly Thr Ser Lys
                645                 650                 655

Ser Tyr Val Arg Ser Leu
            660
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What is claimed is:

1. A method to determine the immune status of an animal, said method comprising the steps of:

(a) contacting a biological specimen of said animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for said infectious agent, under conditions suitable for formation of a complex between said recombinant antigen and said antibody; and

(b) detecting the presence or absence of said complex, wherein presence or absence of said complex is indicative of the immune status of said animal.

2. The method of claim 1, wherein presence of said complex is indicative of non-susceptibility to infection by said infectious agent.

3. The method of claim 1, wherein said antibody is selected from the group consisting of a maternally-derived antibody, an antibody generated in response to natural infection by said infectious agent and an antibody generated in response to vaccination against said infectious agent.

4. The method of claim 1, wherein said biological specimen is selected from the group consisting of blood, serum, plasma, saliva, urine, tears, aqueous humor, cerebrospinal fluid, lymph, nasal secretion, tracheobronchial aspirate, milk, colostrum, intestinal secretion, and feces.

5. The method of claim 1, wherein said animal is selected from the group consisting of a cat, dog, and horse.

6. The method of claim 1, wherein said recombinant antigen is immobilized on a substrate.

7. The method of claim 1, wherein said method comprises performing an assay selected from the group consisting of an enzyme-linked immunoassay, a radioimmunoassay, a fluorescence immunoassay, a luminescence assay, a phosphorescence assay, an immunoblot assay, an immunodot assay, an immunoprecipitation assay, a lateral flow assay, a flow-through assay, an agglutination assay, a particulate-based assay, and an electronic sensory assay.

8. The method of claim 1, wherein said step of detecting comprises applying a detection reagent that binds to said complex, if present, to obtain a test signal, wherein presence or absence of a test signal is indicative of the immune status of said animal.

9. The method of claim 8, wherein said detection reagent comprises an antibody-binding partner conjugated to a detectable marker.

10. The method of claim 9, wherein said antibody-binding partner is selected from the group consisting of an Fc-binding antibody, an Fc receptor, and an antibody-binding bacterial surface protein.

11. The method of claim 9, wherein said detectable marker is selected from the group consisting of an enzyme, a radioactive label, a fluorescent label, a luminescent label, a phosphorescent label, a chromophoric label, a metal sol label, a metal-binding label, a physical label, an electronic label, and a ligand.

12. The method of claim 1, wherein said recombinant antigen further comprises a detectable marker.

13. The method of claim 1, wherein said method is conducted within about one day.

14. The method of claim 1, wherein said method is conducted within about one hour.

15. The method of claim 1, wherein said method is conducted in a time period of between about one minute and about fifteen minutes.

16. The method of claim 1, wherein said recombinant antigen is selected from the group consisting of a recombinant viral antigen, a recombinant bacterial antigen, a recombinant fungal antigen, a recombinant endoparasite antigen, and a recombinant ectoparasite antigen.

17. The method of claim 1, wherein said recombinant antigen is a recombinant viral antigen.

18. The method of claim 1, wherein said recombinant antigen is selected from the group consisting of a calicivirus protein, a distemper virus protein, a herpesvirus protein, a leukemia virus protein, and a parvovirus protein.

19. The method of claim 1, wherein said recombinant antigen is selected from the group consisting of a feline calicivirus capsid protein, a feline herpesvirus glycoprotein B protein, a feline herpesvirus glycoprotein C protein, a feline herpesvirus glycoprotein D protein, a feline parvovirus VP12 protein, a feline parvovirus VP2 protein, a feline leukemia virus p27 protein, a feline leukemia virus gp70 protein, a feline leukemia virus p27-gp70 fusion protein, a canine distemper virus fusion protein, and a canine distemper virus hemagglutinin protein.

20. The method of claim 1, wherein said recombinant antigen is selected from the group consisting of PFCVCP$_{671}$, PFCVCP$_{547}$, PFPVVP2$_{584}$, PFPVVP2C$_{243}$, PFPVpVP2$_{1620}$, PFPVpVP2$_{477}$, PFHVgB$_{943}$, PFHVgB$_{250}$, PFHVgC$_{534}$, PFHVgC$_{467}$, PFHVgC$_{467(opt)}$, PFHVgD$_{374}$, PFHVgD$_{3}$00, PFeLVp27$_{253}$, PFeLVp27$_{6,9}$, PFeLVp27-gp70$_{6,1}$, PCDVH$_{604}$, PCDVF$_{662}$, PHis-PFCVCP$_{671}$, PHis-PFCVCP$_{547}$, PHis-PFPVVP2$_{584}$, PHis-PFPVVP2C$_{243}$, PHis-PFPVpVP12$_{620}$, PHis-PFPVpVP2$_{477}$, PHis-PFHVgB$_{943}$, PHis-PFHVgB$_{250}$, PHis-PFHVgC$_{534}$, PHis-PFHVgC$_{467}$, PHis-PFHVgC$_{467(opt)}$, PHis-PFHVgD$_{374}$, PHis-PFHVgD$_{300}$, PHis-PFeLVp27$_{253}$, PHis-PFeLVp27$_{619}$, PHis-PFeLVp27-gp70$_{611}$, PHis-PCDVH$_{604}$, and PHis-PCDVF$_{662}$.

21. The method of claim 1, wherein said recombinant antigen comprises an amino acid sequence selected from the group 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:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34 and SEQ ID NO:36.

22. The method of claim 1, wherein said recombinant antigen is encoded by a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, and SEQ ID NO:35.

23. The method of claim 1, wherein said biological specimen is contacted with a recombinant calicivirus antigen, a recombinant herpesvirus antigen and a recombinant parvovirus antigen under conditions such that the immune status of said animal to calicivirus, herpesvirus and parvovirus infection is determined.

24. A method to determine whether to vaccinate an animal, said method comprising the steps of:

(a) contacting a biological specimen of said animal with a recombinant infectious agent antigen that is specific for detecting an antibody selective for said infectious agent, under conditions suitable for formation of a complex between said recombinant antigen and said antibody; and

(b) detecting the presence or absence of said complex, wherein presence of said complex indicates that said animal need not be vaccinated and wherein absence of said complex indicates that said animal should be vaccinated.

25. The method of claim 24, wherein said step of detecting comprises applying a detection reagent that binds to said complex, if present, to obtain a test signal, wherein presence of said test signal indicates that said animal need not be vaccinated and wherein absence of said test signal indicates that said animal should be vaccinated.

26. A recombinant antigen comprising a recombinant protein having an amino acid sequence selected from the group 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:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34, SEQ ID NO:36, and an amino acid sequence encoded by an allelic variant of a nucleic acid sequence encoding any of said amino acid sequences.

27. The recombinant antigen of claim 26, wherein said recombinant antigen is encoded by a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, and SEQ ID NO:35, a nucleic acid molecule comprising an allelic variant of a nucleic acid molecule comprising any of said nucleic acid sequences, and a nucleic acid molecule comprising a degenerate of a nucleic acid molecule comprising any of said nucleic acid sequences.

28. A nucleic acid molecule selected from the group consisting of: (a) a nucleic acid molecule encoding a protein of claim 26; (b) a nucleic acid molecule encoding a protein comprising an amino acid sequence selected from the group consisting of SEQ ID NO:2, SEQ ID NO:4, SEQ ID NO:6, SEQ ID NO:8, SEQ ID NO:10, SEQ B NO:12, SEQ ID NO:14, SEQ ID NO:16, SEQ ID NO:18, SEQ ID NO:20, SEQ ID NO:22, SEQ ID NO:24, SEQ ID NO:26, SEQ ID NO:28, SEQ ID NO:30, SEQ ID NO:32, SEQ ID NO:34 and SEQ ID NO:36; (c) a nucleic acid molecule comprising a nucleic acid sequence selected from the group consisting of SEQ ID NO:1, SEQ ID NO:3, SEQ ID NO:5, SEQ ID NO:7, SEQ ID NO:9, SEQ ID NO:11, SEQ ID NO:13, SEQ ID NO:15, SEQ ID NO:17, SEQ ID NO:19, SEQ ID NO:21, SEQ ID NO:23, SEQ ID NO:25, SEQ ID NO:27, SEQ ID NO:29, SEQ ID NO:31, SEQ ID NO:33, and SEQ ID NO:35; (d) a nucleic acid molecule comprising an allelic variant of a nucleic acid molecule of (c); (e) a nucleic acid molecule comprising a degenerate of a nucleic acid molecule of (c); and (f) a nucleic acid molecule fully complementary to any of said nucleic acid molecules of (a), (b), (c), (d) or (e).

29. A recombinant molecule comprising a nucleic acid molecule of claim 28.

30. A recombinant cell comprising a nucleic acid molecule of claim 28.

31. A method to produce a recombinant antigen of claim 26, said method comprising culturing a recombinant cell of claim 30 and recovering said recombinant antigen.

32. The recombinant antigen of claim 26, wherein said recombinant antigen further comprises a component selected from the group consisting of a fusion segment and a ligand.

33. The recombinant antigen of claim 26, wherein said recombinant antigen further comprises a detectable marker.

34. An assay to determine the immune status of an animal, said assay comprising:

(a) a recombinant infectious agent antigen that is specific for detecting an antibody selective for said infectious agent, presence of said antibody being indicative of the immune status of said animal; and

(b) a means to detect an antibody that selectively binds to said recombinant antigen.

35. The assay of claim 34, wherein said means comprises a detection reagent.

36. The assay of claim 34, wherein said assay further comprises:

(a) a solid support comprising a test area and a reference area; and

(b) a reference reagent.

37. The assay of claim 34, wherein said test area comprises said recombinant antigen.

38. The assay of claim 34, wherein said assay further comprises a control area for assay validation.

39. The assay of claim 34, wherein said recombinant antigen comprises a recombinant protein selected from the group consisting of $PFCVCP_{671}$, $PFCVCP_{547}$, $PFPVVP2_{584}$, $PFPVVP2C_{243}$, PFPVpVP12620, $PFPVpVP2_{477}$, $PFHVgB_{943}$, $PFHVgB_{250}$, $PFHVgC_{534}$, $PFHVgC_{467}$, $PFHVgC_{467(opt)}$, $PFHVgD_{374}$, $PFHVgD_{300}$, $PFeLVp27_{253}$, $PFeLVp27_{619}$, $PFeLVp27\text{-}gp70_{611}$, $PCDVH_{604}$, and $PCDVF_{662}$.

* * * * *

专利名称(译)	使用重组抗原来确定动物的免疫状态		
公开(公告)号	US20040058316A1	公开(公告)日	2004-03-25
申请号	US10/670695	申请日	2003-09-25
[标]申请(专利权)人(译)	JENSEN韦恩 拉平迈克尔 - [R ROSEN David K制作 安德鲁斯JANET小号		
申请(专利权)人(译)	JENSEN WAYNE A. 拉平迈克尔布隆 ROSEN DAVID K. 安德鲁斯JANET S.		
当前申请(专利权)人(译)	JENSEN WAYNE A. 拉平迈克尔布隆 ROSEN DAVID K. 安德鲁斯JANET S.		
[标]发明人	JENSEN WAYNE A LAPPIN MICHAEL R ROSEN DAVID K ANDREWS JANET S		
发明人	JENSEN, WAYNE A. LAPPIN, MICHAEL R. ROSEN, DAVID K. ANDREWS, JANET S.		
IPC分类号	C07K14/005 C07K14/015 C07K14/03 C07K14/08 C07K14/13 C07K14/15 C12N1/15 C12N1/19 C12N1/21 C12N5/10 C12N15/09 C12P21/02 G01N33/53 G01N33/536 G01N33/569 C12Q1/70 G01N33/554		
CPC分类号	C07K14/005 C12N2710/16722 C12N2740/13022 G01N33/56983 C12N2750/14343 C12N2760/18422 C12N2750/14322		
外部链接	Espacenet USPTO		

摘要(译)

本发明包括一种确定动物免疫状态的方法，该方法包括以下步骤：（a）使动物的生物样本与重组感染因子抗原接触，所述重组感染因子抗原特异于检测对该感染因子具有选择性的抗体，条件是适合于在重组抗原和抗体之间形成复合物，和（b）检测复合物的存在或不存在，其中复合物的存在或不存在指示动物的免疫状态。优选地，这种方法表明动物是否应该接种疫苗。本发明还包括含有（a）重组感染因子抗原的试验，该抗原特异性地检测对该感染因子具有选择性的抗体。（b）检测选择性结合重组抗原的抗体的方法。本发明还包括重组抗原和编码这些抗原的核酸分子，以及产生和使用这种核酸分子和重组抗原的方法。

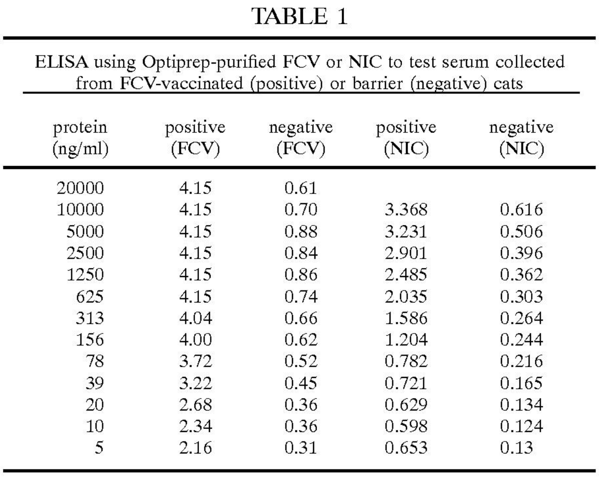

TABLE 1

ELISA using Optiprep-purified FCV or NIC to test serum collected from FCV-vaccinated (positive) or barrier (negative) cats

protein (ng/ml)	positive (FCV)	negative (FCV)	positive (NIC)	negative (NIC)
20000	4.15	0.61		
10000	4.15	0.70	3.368	0.616
5000	4.15	0.88	3.231	0.506
2500	4.15	0.84	2.901	0.396
1250	4.15	0.86	2.485	0.362
625	4.15	0.74	2.035	0.303
313	4.04	0.66	1.586	0.264
156	4.00	0.62	1.204	0.244
78	3.72	0.52	0.782	0.216
39	3.22	0.45	0.721	0.165
20	2.68	0.36	0.629	0.134
10	2.34	0.36	0.598	0.124
5	2.16	0.31	0.653	0.13