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(54) **RECOMBINANT AVIAN PARAMYXOVIRUS VACCINE AND METHOD FOR MAKING AND USING THEREOF**

REKOMBINANTER VOGELPARAMYXOVIRUS-IMPFSTOFF SOWIE VERFAHREN ZU SEINER HERSTELLUNG UND VERWENDUNG

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(56) References cited:
WO-A1-2007/104782 WO-A2-02/36617
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- **PEETERS B P H ET AL: "Generation of a recombinant chimeric Newcastle disease virus vaccine that allows serological differentiation between vaccinated and infected animals" VACCINE, ELSEVIER LTD, GB LNKD-DOI:10.1016/S0264-410X(00)00419-9, vol. 19, 1 January 2001 (2001-01-01), pages 1616-1627, XP003013376 ISSN: 0264-410X**
- **PALDURAI A ET AL: "Complete genome sequences of avian paramyxovirus type 8 strains goose/Delaware/1053/76 and pintail/Wakuya/20/78" VIRUS RESEARCH, AMSTERDAM, NL LNKD-DOI:10.1016/J.VIRUSRES.2009.02.003, vol. 142, no. 1-2, 1 June 2009 (2009-06-01), pages 144-153, XP026083824 ISSN: 0168-1702 [retrieved on 2009-02-13]**

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EP 2 467 158 B1

Description

FIELD OF THE INVENTION

[0001] The description relates to avian paramyxoviruses (APMV) and APMV sequences. The description relates to viral vectors for the insertion and expression of foreign genes for use as safe immunization vehicles to protect against a variety of pathogens. It relates to vector vaccine in a reverse genetics system for the production of live attenuated vaccines. It also relates to polynucleotides which can be used for the production of subunits in an *in vitro* expression vector or as sequences to be integrated into a viral or plasmid type *in vivo* expression vector.

[0002] The present description relates to unmodified and modified APMV virus, to methods of making and using the same, and to certain DNA and protein sequences. More in particular, the description relates to APMV virus in which the naturally occurring genome of the virus has been altered ("APMV mutants" or "recombinant APMV") and to methods of making and using such APMV mutants or recombinant APMV.

BACKGROUND OF THE INVENTION

[0003] Viral vector vaccines represent one of the most rapidly growing areas in vaccine development. Many vaccines in clinical development for major global infectious diseases, HIV, tuberculosis and malaria, are based on viral vectors. Viral vector vaccines for animals are already on the market, e.g. avipox vector vaccines for companion animals and poultry, avian herpesviruses vectored vaccines for poultry, and vaccinia virus vectored vaccines for wildlife. But other livestock vector vaccines are in development. The advantage of viral vector vaccines is that they can be administered safely due to the use of a vector backbone which is strongly attenuated and does not cause disease in the animal itself. The disadvantage of currently used viral vectors is the existence of maternally derived or antibodies acquired due to a past infection. These antibodies will neutralize the vector virus and thus diminish the success of the vector vaccine. One major impetus for the development of vector vaccines was the occurrence of highly pathogenic influenza virus H5N1 occurring first in Asia and later in Europe and Africa. Several vector vaccine candidates have been developed including fowl poxvirus (Taylor et al, 1988), vaccinia virus (Chambers et al., 1988), Rous sarcoma virus (Hunt et al, 1988), adenoviruses (Tang et al., 2002 , Gao et al, 2006), Venezuelan equine encephalitis virus (Schultz-Cherry et al, 2000), Newcastle disease virus (US6,719,979, Veits et al., 2006, Swayne et al, 2002, Park et al, 2006), herpesvirus of infectious laryngotracheitis (Veits et al. 2003), herpesvirus of turkey (Darteil et al., 1995), and adenovirus based vector vaccines (Hoelscher et al, 2008, Toro et al, 2007). The efficacy of these vector vaccines have been tested in naive birds, but so far no reports have been published on the efficacy of these vector vaccines in birds with a preexisting immunity to the viral vector and/or to the protein coded by the insert.

[0004] The virus family *Paramyxoviridae* includes both human (measles, mumps, parainfluenza and respiratory syncytial virus) and animal pathogens (Newcastle disease virus and rinderpest virus) that cause significant impact on public health as well as the global economy (Lamb et al., 2007). Members of this virus family are defined by having a monopartite, negative sense, single-stranded RNA genome. The *Paramyxoviridae* family consists of two subfamilies namely *Paramyxovirinae* and *Pneumovirinae*. Owing to recent reclassification, the subfamily *Paramyxovirinae* includes five genera, i.e *Morbillivirus, Henipavirus, Rubulavirus, Respirovirus* and *Avulavirus* while *Pneumovirinae* includes *Pneumovirus* and *Metapneumovirus* (Mayo, 2002). Avian paramyxoviruses (APMV) are classified in the genus *Avulavirus* and comprise nine antigenically distinct serotypes that have been defined using hemagglutination inhibition (HI) tests (Alexander, 1988). Of the nine serotypes, isolates belonging to the APMV-1 subtype can cause a devastating disease in commercial poultry and are classified as velogenic Newcastle disease virus (NDV). Milder forms of NDV are designated as mesogenic and lentogenic isolates, wherein the latter form is mostly asymptomatic in domestic poultry. Isolates belonging to the APMV-2, 3, 6 and 7 have also been associated with disease in domestic poultry. Specifically, infections by isolates of APMV-2 and 3 can cause mild respiratory disease and problems in egg quality and quantity (Bankowski et al., 1981; Redmann et al., 1991; Tumova et al., 1979; Zhang et al., 2007). Isolates of APMV-6 and 7 have been known to infect turkeys, ducks and migratory birds and can induce respiratory disease that may be complicated by secondary infection (Saif et al., 1997; Shortridge et al., 1980). On the other hand, isolates of APMV-4, 5, 8 and 9 have been isolated from ducks, waterfowl and other wild birds but the birds rarely show clinical signs after viral infection (Alexander et al., 1983; Capua et al., 2004; Gough et al., 1984; Maldonado et al., 1995; Shortridge et al., 1980).

[0005] The complete genomic sequences of several NDV isolates have been established and used to elucidate the various determinants of NDV virulence (de Leeuw et al., 1999; (Krishnamurthy et al., 1998; Zou et al., 2005). In the recent two years several APMV sequences other than APMV1 have been published, such as GenBank accession number EU338414 for APMV-2, EU403085 for APMV-3, FJ177514 for APMV-4, EU622637 for APMV-6, FJ231524 for APMV-7, FJ215863, FJ215864 and FJ619036 for APMV-8, EU910942 for APMV-9. Besides the sequence information, not much is known about virulence factors. Isolates of APMV 2-9 have been mostly isolated from migratory birds. Interestingly, there are very few reports of experimental infection of chickens with such isolates (Saif et al., 1997). Since these APMV

circulate widely in wild birds and in certain cases have been isolated from commercial flocks (Zhang et al., 2007) that sometimes cause disease in them (Saif et al., 1997; Shihmanter et al., 1998; Shihmanter et al., 1998), knowledge about their virulence in poultry is needed.

[0006] Most of the APMV isolates cause a relatively mild disease that may be exacerbated in the presence of concomitant bacterial or viral infections which might lead to economic impact. In particular, APMV-2 was first isolated as a secondary pathogen in 1956 from chickens affected by acute laryngotracheitis in Southern California (Bankowski et al., 1960). Since then numerous strains of this serotype have been isolated from several avian species signifying that APMV-2 is widely disseminated worldwide (Andral et al., 1984; Bradshaw et al., 1979; Fleury et al., 1979; Goodman et al., 1988; Lang et al., 1975; Lipkind et al., 1982; Lipkind et al., 1979; Zhang et al., 2006). Bankowski *et. al.* reported that natural as well as artificial exposure of laying turkey hens to APMV-2 caused a pronounced decline in hatchability and poultry yield (Bankowski ct al., 1981). Initial examples of APMV-4 isolation were from hunter-killed feral ducks on the Mississippi flyway in the United States (Webster et al., 1976) and from chickens, ducks and geese in Hong Kong during influenza surveillance programs of poultry (Alexander et al., 1979). Apart from an isolate from a ringed teal suffering from hemorrhagic enteritis (Gough et al., 1984), all other isolates were seemingly non-pathogenic in poultry and found to have wide distribution among waterfowl throughout the world (Stanislawek et al., 2002; Tumova et al., 1989; Yamane et al., 1982). Gough et al. reported that no clinical signs and very low HI titers (1:8 or less) were obtained after the intranasal inoculation of one-week old ducklings and two-week old chickens with the isolate from a ringed teal (Gough et al., 1984). Similarly, the first isolates of APMV-6 were also from domestic poultry in Hong Kong as a result of an influenza surveillance program and were reported to be non-pathogenic in chickens based on low HI titers from experimentally infected chickens (Shortridge et al., 1980). However, there have been reports of APMV-6 infection of turkeys leading to mild respiratory disease and egg production problems (Alexander, 2003).

[0007] APMV-8 (Goose/Delaware/1053/76) was first isolated in the USA from a hunter-killed Canada goose (*Branta canadensis*) (Rosenberger et al., 1974). A serological survey (from 1990 to 1992) of wildfowl in southern Spain showed a notable prevalence of APMV-8 antibodies in up to 43% of the tested sera (Maldonado et al., 1995). Another serological study to determine the status of live, healthy mallard ducks in New Zealand for APMV infection revealed the presence of APMV-8 antibodies in 56% of the tested sera (Stanislawek et al., 2002). Warke et al (2008) described that between 16% to 31% of investigated chicken sera might have had APMV-8 antibodies. But due to existing high titers against APMV1 the probability of a false positive HI test is possible since the sera do not react very specifically in the HI assay. With the exception of a few waterfowl isolates of APMV-8 isolated while the populations were being surveyed for avian influenza viruses (Stallknecht et al., 1991), there has been a dearth of information about the prevalence and pathogenicity of this virus.

[0008] The development of reverse genetics systems for the negative stranded RNA genome of NDV has made it possible to insert foreign gene sequences into the genome, thus making it possible to create recombinant NDV vectors for vaccination and gene therapy (Krishnamurthy et al., 2000; Peeters et al., 1999; Roemer-Oberdoerfer et al., 1999). Recombinant NDV vectors expressing foreign viral proteins such as the HA protein of the H1 subtype of influenza A virus (Nakaya et al., 2001), VP2 protein of infectious bursal disease virus (IBDV) (Huang et al., 2004), avian influenza virus hemagglutinin of subtype H5 (Veits et al., 2006; Ge et al., 2007) and subtype H7 (Park et al., 2006) have been reported. However the efficacy of most of such vaccines has been demonstrated only in SPF birds. NDV causes a devastating disease in poultry leading to serious economic losses in the poultry industry. Commercial chickens therefore are routinely vaccinated against NDV in most countries of the world. Due to this, chickens from immunized parent flocks have a high level of maternally derived antibodies. Conventional live NDV vaccines provide protection even in the presence of these antibodies. However recombinant NDV vaccines (with foreign gene insertions) are generally more attenuated as compared to live NDV vaccines and their efficacy may be impaired in presence of NDV maternal antibodies. Therefore, there is a need for a vector vaccine platform which can provide the basis for safe vaccines for the expression of heterologous antigens. Ideally, the recombinant vaccine can induce a strong humoral immune response, can be applicable by mass administration, and is inexpensive.

[0009] WO02/36617 discloses an NDV mutant that is suited as a marker strain. Peeters et al (2001, Vaccine 19: 1616-1627) disclose the generation of a recombinant Newcastle disease virus (NDV) vaccine in which the gene encoding the hemagglutinin-neuraminidase (HN) has been replaced by a hybrid HN gene consisting of the cytoplasmic domain, transmembrane region, and stalk region of HN of NDV, and the immunogenic globular domain of HN of avian paramyxovirus type 4 (APMV4). WO2007/104782 discloses a method to produce a recombinant Mononegavirales virus vector harbouring an additional transcription unit comprising a foreign gene operatively linked with an upstream Mononegavirales virus gene start (GS) sequence and a downstream Mononegavirales virus gene end (GE) sequence, characterized in that the foreign gene sequence encodes a protein, which protein contains a stretch of at least three basic amino acids and the nucleotide sequence of the codons encoding these amino acids does not contain a sequence that can be recognized by the viral polymerase of the Mononegavirales virus as a gene end (GE) sequence. Pauldurai et al (2009, Virus Research 142: 144-153) disclose the consensus genome sequences for avian paramyxovirus type 8 (APMV-8) strains goose/Delaware/1053/76 (prototype strain) and pintail/Wakuya/20/78. WO2009/101149 discloses paramyxovirus

from the group APMV3, APMV4, APMV5, APMV6, APMV7, APMV8, APMV9, Mapueravirus and Fer-de-Lance virus, which can be used for the production of a medicament for the treatment of tumours.

SUMMARY OF THE INVENTION

[0010] The present invention provides a vaccine comprising (i) a recombinant APMV viral vector and (ii) a pharmaceutically or veterinarily acceptable carrier, wherein the APMV viral vector is APMV-8 and wherein the APMV viral vector comprises a polynucleotide having at least 90% sequence identity to a polynucleotide having the sequence as set forth in SEQ ID NO:1 or a polynucleotide complementary to a polynucleotide having at least 90% sequence identity to a polynucleotide having the sequence as set forth in SEQ ID NO:1; wherein the APMV viral vector further comprises an isolated polynucleotide encoding an antigen of a pathogen, wherein the pathogen is avian, feline, canine, equine, bovine, ovine, caprine or porcine pathogen, wherein the polynucleotide is inserted in a nonessential region of the APMV genome, and further wherein the nonessential region is selected from the regions consisting of the untranslated region located upstream of the NP open reading frame, the intergenic regions between two open reading frames of the APMV genome, and the untranslated region located downstream of the L open reading frame.

[0011] In another aspect, the present invention provides a pharmaceutical composition or vaccine comprising a recombinant APMV viral vector, wherein the recombinant APMV viral vector comprises a heterologous polynucleotide that encodes and expresses an antigen of a pathogen for an animal, for use in inducing an immunological response in an animal to said antigen, wherein the use comprises inoculating the animal with the pharmaceutical composition or vaccine, wherein the APMV viral vector is APMV-8 and wherein the APMV viral vector comprises a polynucleotide having at least 90% sequence identity to a polynucleotide having the sequence as set forth in SEQ ID NO:1 or a polynucleotide complementary to a polynucleotide having at least 90% sequence identity to a polynucleotide having the sequence as set forth in SEQ ID NO:1,
wherein the pathogen is avian, feline, canine, equine, bovine, ovine, caprine or porcine, and further wherein the heterologous polynucleotide is inserted into a nonessential region of the APMV genome selected from regions consisting of the untranslated region located upstream of the NP open reading frame, the intergenic regions between two open reading frames of the APMV genome, and the untranslated region located downstream of the L open reading frame.

[0012] The present description relates to a vaccine or composition comprising (i) a recombinant APMV and (ii) a pharmaceutically or veterinarily acceptable carrier. The present description encompasses methods for modifying the genome of APMV to produce recombinant APMV virus or APMV rival vector; modified APMV prepared by such methods; DNA and protein sequences; and methods for infecting cells and host animals with such recombinant APMV to provoke the amplification of exogenous DNA and proteins encoded by the exogenous DNA, including antigenic proteins, by said cells and host animals.

[0013] One aspect of the description relates to APMV virus, DNA and protein sequences involved in making modified or recombinant virus. One embodiment of the description relates to the genomic and protein sequence of APMV-2, 4, 6, or 8.

[0014] Another aspect of the description relates to a modified recombinant APMV virus, which viruses have enhanced safety, strong humoral immune response, and a method of making such recombinant viruses.

[0015] Another aspect of the description relates to a recombinant APMV virus vaccine or composition having an increased level of safety compared to known APMV or other recombinant vaccines.

[0016] In another aspect, the present description provides unmodified and modified APMV viral vector for expressing a gene product in a host.

[0017] Another aspect of the description is directed to a recombinant APMV virus modified by the insertion therein of DNA from any source into the intergenic region or the nonessential region of the APMV genome. Synthetically modified APMV virus recombinants carrying heterologous genes coding for and expressing an antigen, are used according to the description to create novel compositions or vaccines.

[0018] Another aspect of the description relates to an APMV viral vector which provides a reverse genetics system, wherein the vector can be used as a backbone for recombinant vaccines or compositions in different host animals.

[0019] In one aspect, the present description relates to a pharmaceutical composition or vaccine for inducing an immunological response in a host animal inoculated with the composition or vaccine, the composition or vaccine including a pharmaceutical acceptable carrier and a modified APMV recombinant virus or viral vector. In yet another aspect of the description, the recombinant APMV virus or viral vector includes, within a non-essential region of the virus genome, a heterologous DNA which encodes an antigenic protein derived from a pathogen wherein the composition or vaccine when administered to a host, is capable of inducing an immunological response specific to the protein encoded by the pathogen.

[0020] Another aspect of the description relates to a method for inducing an immunological response in an animal to an antigen, which method comprises inoculating the animal with a vaccine or a pharmaceutical composition containing modified recombinant APMV virus or viral vector which comprises and expresses the antigenic determinant of a pathogen

for said animal. Yet another aspect of the description relates to a method for inducing an immunological response in an animal to an antigen in a prime-boost regime.

[0021] Another aspect of the description relates to a method of expressing a gene product in a cell culture in vitro by introducing into the cell a modified recombinant APMV virus, wherein the gene may be an antigenic protein derived from a pathogen.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] The following detailed description, given by way of example, and which is not intended to limit the invention to specific embodiments described, may be understood in conjunction with the accompanying figures, in which:

Figure 1 is a table showing virus isolation from several organs of chickens after experimental infection with APMV-2, 4, 6 in embryonated chicken eggs.

Figure 2 is a table showing the histology results of several organs of chickens after experimental infection with APMV-2, 4, 6.

Figure 3 depicts HI antibody titers in SPF chickens experimentally inoculated with APMV-2, 4 or 6. Chicken sera samples collected at day 2, 4, 7, 14 and 28 post infection were subject to the HI test to analyze the presence of HI antibodies.

Figure 4 shows HI antibody titers in SPF chickens and ducks experimentally infected with APMV-8. Chickens and ducks were oro-nasal infected with a dose of 10^6 EID_{50} of APMV-8. Sera samples were collected at day 2,4, 7, 14, and 28 p.i. and analyzed by the HI test with the APMV-8 antigen. The HI serum titers (in log_2) are shown on the left axis

Figure 5 shows the development of HI antibody titers in SPF chickens during a prime/boost vaccination scheme with APMV-8. One-day old SPF chickens were infected at day 1 (prime) and day 14 (boost) with a dose of 10^6 EID_{50} of APMV-8. Serum samples were obtained at day 7 and 14 p.i. after the first infection and day 7 and 14 p.i. after the second infection. The sera were subjected to the HI test. The HI serum titers (in log2) are shown on the left axis.

Figure 6 shows the analysis of RT-PCR products by agarose gel electrophoresis. Tracheal tissues were taken at day 2 p.i. from non-infected ducks (C1-C5) and APMV-8 infected ducks (I1-I5). The tissues were homogenized and RNA was prepared for RT-PCR, A water control (W) was prepared in parallel. The reaction products were separated on a 1.5 % agarose gel. The size of the fragment was controlled by using the 100 bp ladder (New England Biolabs). The sizes of the DNA fragments are shown at the right.

Figure 7 is a table showing virus isolation from chicken and ducks experimentally infected with APMV-8. The virus isolation from chicken tissue was performed in embryonated chicken eggs and the detection of viral RNA from duck tissue by RT-PCR.

Figure 8 is a table showing the results of the histological examination of several organs after infection of chicken and Pekin ducks with APMV-8.

Figure 9 shows the development of HI antibody titers in SPF chickens after infection with different doses of APMV-8. One-day old SPF chickens were infected at day 1 with different infectious doses (ID) of APMV-8 or mock-infected with virus transport medium (VTM). Blood was taken at day 7 and 14 p.i. and the obtained serum samples were analyzed by the HI test. The HI serum titers (in log2) are shown on the left axis. The geometric mean titer (GMT) of the serum samples are shown in the lowest row.

Figure 10 shows the development of HI antibody titers in Pekin ducks after infection with different doses of APMV-8. One-day old SPF Pekin ducks were infected at day 1 with different infectious doses (ID) of APMV-8 or mock-infected with virus transport medium (VTM). Blood was taken at day 7 and 14 p.i. and the obtained serum samples were analyzed by the HI test. The HI serum titers (in log2) are shown on the left axis. The geometric mean titer (GMT) of the serum samples are shown in the lowest row.

Figure 11 is a table showing the SEQ ID NOs of the corresponding DNA and protein sequences.

Figure 12 depicts the full length genome sequence of APMV-8 strain (APMV-8: SCWDS ID: MA-7, isolated from a mallard) and a genetic map of the full length APMV-8 genome.

Figure 12 depicts the DNA sequence (SEQ ID NO:2) encoding APMV-8 Nucleoprotein (NP) and the NP protein sequence (SEQ ID NO:3).

Figure 13 depicts the DNA sequence (SEQ ID NO:4) encoding APMV-8 Phospho Protein (P) and the P protein sequence (SEQ ID NO:5).

Figure 14 depicts the DNA sequence (SEQ ID NO:6) encoding APMV-8 Matrixprotein (M) and the M protein sequence (SEQ ID NO:7).

Figure 15 depicts the DNA sequence (SEQ ID NO:8) encoding APMV-8 Fusionprotein (F) and the F protein sequence (SEQ ID NO:9).

Figure 16 depicts the DNA sequence (SEQ ID NO:10) encoding APMV-8 Hemagglutinin/ neuraminidase (HN) and the HN protein sequence (SEQ ID NO:11).

Figure 17 depicts the DNA sequence (SEQ ID NO:12) encoding APMV-8 Polymerase (L) and the L protein sequence (SEQ ID NO:13). This APMV-8 L(1) protein is translated from the ATG codon located at positions 8273-8275 of SEQ ID NO:1.

Figure 18 depicts the protein sequence (2) of APMV-8 Polymerase (L) (SEQ ID NO:14). This APMV-8 L(2) protein is translated from the ATG codon located at positions 8297-8299 of SEQ ID NO:1, SEQ ID NO:14 does not contain the first 8 amino acids of SEQ ID NO:13.

Figure 19A is a flow diagram of the APMV-8 reverse genetics system. Figure 19B depicts the result of replication of APMV-8 virus in MDCK cells.

Figure 20 depicts the HI test result of commercial broiler chickens 2 weeks after APMV-8 vaccination.

Figure 21 depicts the HI test result of commercial broiler chickens 4 weeks after APMV-8 vaccination.

Figure 22 shows the HI test results after the *in ovo* vaccination at day 18 (study 1).

Figure 23 depicts the HI test results after the *in ovo* vaccination at day 19 (study 2).

Figure 24 shows the HI test results after the *in ovo* vaccination at day 18 (study 3).

Figure 25 depicts 5'-full length genome (5'-FLG) and 3'-full length genome (3'-FLG) sequences, including the franking sequences.

Figure 26 depicts plasmid maps of pcNDA-NP, pcNDA-P, pcDNA-L, and pcDNA3-T7.

Figure 27 depicts plasmid maps of pUC18-MG-APMV-8 and pCITE4A-EGFP.

Figure 28 depicts plasmid map of pUC57-FL-APMV-8.

Figure 29 depicts minigenome APMV-8 sequence.

Figure 30 shows the NP protein sequence alignment and the sequence identity at the DNA and protein levels.

Figure 31 shows the P protein sequence alignment and the sequence identity at the DNA and protein levels.

Figure 32 shows the M protein sequence alignment and the sequence identity at the DNA and protein levels.

Figure 33 shows the F protein sequence alignment and the sequence identity at the DNA and protein levels.

Figure 34 shows the HN protein sequence alignment and the sequence identity at the DNA and protein levels.

Figure 35 shows the L protein sequence alignment and the sequence identity at the DNA and protein levels.

DETAILED DESCRIPTION OF THE INVENTION

[0023] It is noted that in this disclosure and particularly in the claims, terms such as "comprises", "comprised", "comprising" and the like can have the meaning attributed to it in U.S. Patent law; e.g., they can mean "includes", "included", "including", and the like; and that terms such as "consisting essentially of" and "consists essentially of' have the meaning ascribed to them in U.S. Patent law, e.g., they allow for elements not explicitly recited, but exclude elements that are found in the prior art or that affect a basic or novel characteristic of the invention.

[0024] Unless otherwise noted, technical terms are used according to conventional usage. Definitions of common terms in molecular biology may be found in Benjamin Lewin, Genes V. published by Oxford University Press, 1994 (ISBN 0-19-854287-9); Kendrew et al. (eds.), The Encyclopedia of Molecular Biology, published by Blackwell Science Ltd., 1994 (ISBN 0-632-02182-9); and Robert A. Meyers (ed.), Molecular Biology and Biotechnology: a Comprehensive Desk Reference, published by VCH Publishers, Inc., 1995 (ISBN 1-56081-569-8).

[0025] The singular terms "a", "an", and "the" include plural referents unless context clearly indicates otherwise. Similarly, the word "or" is intended to include "and" unless the context clearly indicate otherwise. The word "or" means any one member of a particular list and also includes any combination of members of that list.

[0026] It is noted in this disclosure and the appended claims and/or paragraphs, the term "Avian Paramyxoviruses" or "APMV" is used interchangeably, and refers to and includes APMV-1, APMV-2, APMV-3, APMV-4, APMV-5, APMV-6, APMV-7, APMV-8, and APMV-9.

[0027] The term "animal" is used herein to include all mammals, birds and fish. The animal as used herein may be selected from the group consisting of equine (e.g., horse), canine (e.g., dogs, wolves, foxes, coyotes, jackals), feline (e.g., lions, tigers, domestic cats, wild cats, other big cats, and other felines including cheetahs and lynx), bovine (e.g., cattle), porcine (e.g., pig), ovine (e.g., sheep, goats, lamas, bisons), avian (e.g., chicken, duck, goose, turkey, quail, pheasant, parrot, finches, hawk, crow, ostrich, emu and cassowary), primate (e.g., prosimian, tarsier, monkey, gibbon, ape), humans, and fish. The term "animal" also includes an individual animal in all stages of development, including embryonic and fetal stages.

[0028] The terms "polypeptide" and "protein" are used interchangeably herein to refer to a polymer of consecutive amino acid residues.

[0029] The terms "nucleic acid", "nucleotide", and "polynucleotide" are used interchangeably and refer to RNA, DNA, cDNA (complementary DNA), or cRNA (complementary RNA) and derivatives thereof, such as those containing modified backbones. It should be appreciated that the description provides polynucleotides comprising sequences complementary to those described herein. The "polynucleotide" contemplated in the present description includes both the forward strand (5' to 3') and reverse complementary strand (3' to 5'). Polynucleotides according to the description can be prepared in

different ways (e.g. by chemical synthesis, by gene cloning etc.) and can take various forms (e.g. linear or branched, single or double stranded, or a hybrid thereof, primers, probes etc.).

[0030] The term "genomic DNA" or "genome" is used interchangeably and refers to the heritable genetic information of a host organism. The genomic DNA comprises the DNA of the nucleus (also referred to as chromosomal DNA) but also the DNA of the plastids (e.g., chloroplasts) and other cellular organelles (e.g., mitochondria). The genomic DNA or genome contemplated in the present description also refers to the RNA of a virus. The RNA may be a positive strand or a negative strand RNA. The term "genomic DNA" contemplated in the present description includes the genomic DNA containing sequences complementary to those described herein. The term "genomic DNA" also refers to messenger RNA (mRNA), complementary DNA (cDNA), and complementary RNA (cRNA). The term "genomic RA (nucleic acid)" as used herein includes RNA, mRNA, cRNA, DNA and cDNA.

[0031] The term "gene" is used broadly to refer to any segment of polynucleotide associated with a biological function. Thus, genes or polynucleotides include introns and exons as in genomic sequence, or just the coding sequences as in cDNAs, such as an open reading frame (ORF), starting from the start codon (methionine codon) and ending with a termination signal (stop codon). Genes and polynucleotides can also include regions that regulate their expression, such as transcription initiation, translation and transcription termination. Thus, also included are promoters and ribosome binding regions (in general these regulatory elements lie approximately between 60 and 250 nucleotides upstream of the start codon of the coding sequence or gene; Doree S M *et al.*; Pandher K *et al.*; Chung J Y *et al.*), transcription terminators (in general the terminator is located within approximately 50 nucleotides downstream of the stop codon of the coding sequence or gene; Ward C K *et al.*). Gene or polynucleotide also refers to a nucleic acid fragment that expresses mRNA or functional RNA, or encodes a specific protein, and which includes regulatory sequences.

[0032] The term "heterologous DNA" as used herein refers to the DNA derived from a different organism, such as a different cell type or a different species from the recipient. The term also refers a DNA or fragment thereof on the same genome of the host DNA wherein the heterologous DNA is inserted into a region of the genome which is different from its original location.

[0033] As used herein, the term "antigen" or "immunogen" means a substance that induces a specific immune response in a host animal. The antigen may comprise a whole organism, killed, attenuated or live; a subunit or portion of an organism; a recombinant vector containing an insert with immunogenic properties; a piece or fragment of DNA capable of inducing an immune response upon presentation to a host animal; a polypeptide, an epitope, a hapten, or any combination thereof. Alternately, the immunogen or antigen may comprise a toxin or antitoxin.

[0034] The term "immunogenic protein or peptide" as used herein includes polypeptides that are immunologically active in the sense that once administered to the host, it is able to evoke an immune response of the humoral and/or cellular type directed against the protein. Preferably the protein fragment is such that it has substantially the same immunological activity as the total protein. Thus, a protein fragment according to the description comprises or consists essentially of or consists of at least one epitope or antigenic determinant. An "immunogenic" protein or polypeptide, as used herein, includes the full-length sequence of the protein, analogs thereof, or immunogenic fragments thereof. By "immunogenic fragment" is meant a fragment of a protein which includes one or more epitopes and thus elicits the immunological response described above. Such fragments can be identified using any number of epitope mapping techniques well known in the art. See, e.g., Epitope Mapping Protocols in Methods in Molecular Biology, Vol. 66 (Glenn E. Morris, Ed., 1996). For example, linear epitopes may be determined by e.g., concurrently synthesizing large numbers of peptides on solid supports, the peptides corresponding to portions of the protein molecule, and reacting the peptides with antibodies while the peptides are still attached to the supports. Such techniques are known in the art and described in, e.g., U.S. Pat. No. 4,708,871; Geysen et al., 1984; Geysen et al., 1986. Similarly, conformational epitopes are readily identified by determining spatial conformation of amino acids such as by, e.g., x-ray crystallography and 2-dimensional nuclear magnetic resonance. See, e.g., Epitope Mapping Protocols, supra.

[0035] The term "immunogenic protein or peptide" further contemplates deletions, additions and substitutions to the sequence, so long as the polypeptide functions to produce an immunological response as defined herein. The term "conservative variation" denotes the replacement of an amino acid residue by another biologically similar residue, or the replacement of a nucleotide in a nucleic acid sequence such that the encoded amino acid residue does not change or is another biologically similar residue. In this regard, particularly preferred substitutions will generally be conservative in nature, i.e., those substitutions that take place within a family of amino acids. For example, amino acids are generally divided into four families: (1) acidic--aspartate and glutamate; (2) basiclysine, arginine, histidine; (3) non-polar--alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan; and (4) uncharged polar--glycine, asparagine, glutamine, cystine, serine, threonine, tyrosine. Phenylalanine, tryptophan, and tyrosine are sometimes classified as aromatic amino acids. Examples of conservative variations include the substitution of one hydrophobic residue such as isoleucine, valine, leucine or methionine for another hydrophobic residue, or the substitution of one polar residue for another polar residue, such as the substitution of arginine for lysine, glutamic acid for aspartic acid, or glutamine for asparagine, and the like; or a similar conservative replacement of an amino acid with a structurally related amino acid that will not have a major effect on the biological activity. Proteins having substantially the same amino acid sequence

as the reference molecule but possessing minor amino acid substitutions that do not substantially affect the immunogenicity of the protein are, therefore, within the definition of the reference polypeptide. All of the polypeptides produced by these modifications are included herein. The term "conservative variation" also includes the use of a substituted amino acid in place of an unsubstituted parent amino acid provided that antibodies raised to the substituted polypeptide also immunoreact with the unsubstituted polypeptide.

[0036] A "host cell" denotes a prokaryotic or eukaryotic cell that has been genetically altered, or is capable of being genetically altered by administration of an exogenous polynucleotide, such as a recombinant plasmid or vector. When referring to genetically altered cells, the term refers both to the originally altered cell and to the progeny thereof. Polynucleotides comprising a desired sequence can be inserted into a suitable cloning or expression vector, and the vector in turn can be introduced into a suitable host cell for replication and amplification. Polynucleotides can be introduced into host cells by any means known in the art. The vectors containing the polynucleotides of interest can be introduced into the host cell by any of a number of appropriate means, including direct uptake, endocytosis, transfection, f-mating, electroporation, transfection employing calcium chloride, rubidium chloride, calcium phosphate, DEAE-dextran, or other substances; microprojectile bombardment; lipofection; and infection (where the vector is infectious, for instance, a retroviral vector). The choice of introducing vectors or polynucleotides will often depend on features of the host cell.

[0037] An "immunological response" to a composition or vaccine is the development in the host of a cellular and/or antibody-mediated immune response to a composition or vaccine of interest. Usually, an "immunological response" includes but is not limited to one or more of the following effects: the production of antibodies, B cells, helper T cells, and/or cytotoxic T cells, directed specifically to an antigen or antigens included in the composition or vaccine of interest. Preferably, the host will display either a therapeutic or protective immunological response such that resistance to new infection will be enhanced and/or the clinical severity of the disease reduced. Such protection will be demonstrated by either a reduction or lack of symptoms normally displayed by an infected host, a quicker recovery time and/or a lowered viral titer in the infected host.

[0038] One embodiment of the description provides the genomic DNA sequence and encoded protein sequences of APMV-8. The complementary genomic DNA(cDNA) sequence of APMV-8 strain of the present description has a polynucleotide sequence as set forth in SEQ ID NO:1. The APMV-8 genomic cDNA sequence (SEQ ID NO:1) has 48% sequence identity to APMV-1 genomic DNA (SEQ ID NO:15), 61% sequence identity to APMV-2 genomic DNA (SEQ ID NO:16), 47.2% sequence identity to APMV-3 genomic DNA (SEQ ID NO:17), 47.6 % sequence identity to APMV-4 genomic DNA (SEQ ID NO:18), 52% sequence identity to APMV-6 genomic DNA (SEQ ID NO:19), 53% sequence identity to APMV-7 genomic DNA (SEQ ID NO:20), 99.1% sequence identity to APMV-8 genomic DNA (SEQ ID NO:37), 96.5% sequence identity to APMV-8 genomic DNA (SEQ ID NO:38), 96.4% sequence identity to APMV-8 genomic DNA (SEQ ID NO:39), 48% sequence identity to APMV-9 genomic DNA (SEQ ID NO:40). In another embodiment, the description provides a polynucleotide having a sequence as set forth in SEQ ID NO:1, 2, 4, 6, 8, 10 or 12, and variant or fragment thereof. The description further comprises a complementary strand to a polynucleotide described herein. In yet another embodiment, the description provides a polypeptide having a sequence as set forth in SEQ ID NO:3, 5, 7, 9, 11, 13 or 14, and variant or fragment thereof.

[0039] Moreover, homologs of polynucleotides or polypeptides from APMV, for example APMV-8, APMV-2, APMV-4, APMV-6 strains are intended to be within the scope of the present description. As used herein, the term "homologs" includes orthologs, analogs and paralogs. The term "analogs" refers to two polynucleotides or polypeptides that have the same or similar function, but that have evolved separately in unrelated organisms. The term "orthologs" refers to two polynucleotides or polypeptides from different species, but that have evolved from a common ancestral gene by speciation. Normally, orthologs encode polypeptides having the same or similar functions. The term "paralogs" refers to two polynucleotides or polypeptides that are related by duplication within a genome. Paralogs usually have different functions, but these functions may be related. Analogs, orthologs, and paralogs of a wild-type APMV polypeptide can differ from the wild-type APMV polypeptide by post-translational modifications, by amino acid sequence differences, or by both. In particular, homologs of the description will generally exhibit at least 80-85%, 85-90%, 90-95%, or 95%, 96%, 97%, 98%, 99% sequence identity with all or part of the polynucleotide or polypeptide sequences of APMV-8, and will exhibit a similar function.

[0040] In another aspect, the present description provides a genomic cDNA of APMV-8 having the sequence as set forth in SEQ ID NO:1. In yet another embodiment, the polynucleotide is a reverse complementary strand of the polynucleotide having the sequence as set forth in SEQ ID NO:1. In yet another embodiment, the polynucleotide or a reverse complementary strand of a polynucleotide of the present description has at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, 96%, 97%, 98% or 99% sequence identity to a polypeptide having a sequence as set forth in SEQ ID NO:1.

[0041] In one embodiment, the present description provides a fragment of polynucleotide encoding an AMPV-8 polypeptide, such as a polynucleotide encoding a polypeptide having a sequence as set forth in SEQ ID NO: 3, 5, 7, 9, 11, 13 or 14. In yet another aspect, the present description provides a polynucleotide encoding a polypeptide having at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, 96%, 97%, 98% or 99% sequence identity to

a polypeptide having a sequence as set forth in SEQ ID NO: 3, 5, 7, 9, 11, 13 or 14, or a conservative variant, an allelic variant, a homolog or an immunogenic fragment comprising at least eight or at east ten consecutive amino acids of one of these polypeptides, or a combination of these polypeptides.

[0042] In another aspect, the present description provides a polynucleotide having a nucleotide sequence as set forth in SEQ ID NO:1, 2, 4, 6, 8, 10, or 12, or a variant thereof. In yet another embodiment, the polynucleotide is a reverse complementary strand of the polynucleotide having the sequence as set forth in SEQ ID NO:1. In yet another aspect, the present description provides a polynucleotide or a reverse complementary strand of a polynucleotide having at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, 96%, 97%, 98% or 99% sequence identity to one of a polynucleotide having a sequence as set forth in SEQ ID NO:1, 2, 4, 6, 8, 10, or 12, or a variant thereof.

[0043] In another aspect, the present description provides a polypeptide having at least 70%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, 96%, 97%, 98% or 99% sequence identity to a polypeptide having a sequence as set forth in SEQ ID NO:3, 5, 7, 9, 11, 13 or 14. In yet another aspect, the present description provides fragments and variants of the APMV polypeptides identified above (SEQ ID NO: 3, 5, 7, 9, 11, 13 or 14) which may readily be prepared by one of skill in the art using well-known molecular biology techniques.

[0044] Variants are homologous polypeptides having an amino acid sequence at least 75%, 80%, 85%, 90%, 95%, 96%, 97%, 98%, or 99% identity to the amino acid sequence as set forth in SEQ ID NO: 3, 5, 7, 9, 11, 13 or 14.

[0045] Variants include allelic variants. The term "allelic variant" refers to a polynucleotide or a polypeptide containing polymorphisms that lead to changes in the amino acid sequences of a protein and that exist within a natural population (e.g., a virus species or variety). Such natural allelic variations can typically result in 1- 5% variance in a polynucleotide or a polypeptide. Allelic variants can be identified by sequencing the nucleic acid sequence of interest in a number of different species, which can be readily carried out by using hybridization probes to identify the same genetic locus in those species. Any and all such nucleic acid variations and resulting amino acid polymorphisms or variations that are the result of natural allelic variation and that do not alter the functional activity of gene of interest, are intended to be within the scope of the description.

[0046] The term "identity" with respect to sequences can refer to, for example, the number of positions with identical nucleotides or amino acids divided by the number of nucleotides or amino acids in the shorter of the two sequences wherein alignment of the two sequences can be determined in accordance with the Wilbur and Lipman algorithm (Wilbur and Lipman). The sequence identity or sequence similarity of two amino acid sequences, or the sequence identity between two nucleotide sequences can be determined using Vector NTI software package (Invitrogen, 1600 Faraday Ave., Carlsbad, CA). When RNA sequences are said to be similar, or have a degree of sequence identity or homology with DNA sequences, thymidine (T) in the DNA sequence is considered equal to uracil (U) in the RNA sequence. Thus, RNA sequences are within the scope of the description and can be derived from DNA sequences, by thymidine (T) in the DNA sequence being considered equal to uracil (U) in RNA sequences.

[0047] In one aspect, the present description relates to a pharmaceutical composition or vaccine for inducing an immunological response in a host animal inoculated with the vaccine or composition, the vaccine or composition including a pharmaceutical acceptable carrier and a modified APMV recombinant virus or viral vector. In yet another aspect of the description, the recombinant APMV virus or viral vector includes, within a non-essential region of the virus genome, a heterologous DNA sequence which encodes an antigenic protein derived from a pathogen wherein the composition or vaccine when administered to a host, is capable of inducing an immunological response specific to the protein encoded by the pathogen.

[0048] A "vector" refers to a recombinant DNA or RNA plasmid, bacteriophage, or virus that comprises a heterologous polynucleotide to be delivered to a target cell, either *in vitro* or *in vivo.* The heterologous polynucleotide may comprise a sequence of interest for purposes of prevention or therapy, and may optionally be in the form of an expression cassette. As used herein, a vector needs not be capable of replication in the ultimate target cell or subject. The term includes vectors for cloning as well as viral vectors.

[0049] The term "engineered" or "recombinant" means a polynucleotide of semisynthetic, or synthetic origin that either does not occur in nature or is linked to another polynucleotide in an arrangement not found in nature.

[0050] The term "nonessential region" refers to a region of a virus genome which is not essential for replication and propagation of the virus in tissue culture and whose deletion or inactivation may reduce virulence in a variety of animal systems. Any nonessential region or portion thereof can be deleted from the APMV genome or a foreign sequence can be inserted in it, and the viability and stability of the recombinant APMV resulting from the deletion or insertion can be used to ascertain whether a deleted region or portion thereof is indeed nonessential. In one embodiment, the nonessential region of the APMV genome is any region on the APMV-2, 4, 6, or 8 genome that does not encode Polymerase (L). In yet another embodiment, the nonessential region comprises an open reading frame encoding a nonessential protein. In this aspect, the open reading frame is selected from the group consisting of nucleoprotein (NP), phosphoprotein (P), matrixprotein (M), fusionprotein (F), and hemagglutinin/neuraminidase (HN). In one embodiment, the nonessential region is located upstream of the NP gene. In another embodiment, the nonessential region is located downstream of the L gene. In yet another embodiment, the nonessential region is a non-coding or intergenic region. In this aspect, the non-

coding or intergenic region may be a region between NP and P genes, between P and M genes, between M and F genes, or between F and HN genes on the APMV-2, 4, 6, or 8 genome. In yet another embodiment, the nonessential region may be in the region of nucleotide positions 1 - 140, 1526 - 1692, 2910 - 3085, 4195 - 4498, 6130 - 6382, 8116 - 8272, 8116 - 8289, or 15013 - 15342 of SEQ ID NO:1.

[0051] In another aspect, the description includes APMV chimeras in which one part or the full gene or several parts or full genes of the APMV vector are replaced by similar genes from other viruses, in particular those belonging to the paramyxoviridae family.

[0052] In one embodiment of the description, the vaccine or pharmaceutical composition comprises an antigen selected from the group of avian pathogens including, but not limited to, *Salmonella typhimurium, Salmonella enteritidis,* Infectious Bronchitis virus (IBV), Newcastle Disease virus (NDV), egg drop syndrome virus (EDS), or Infectious Bursal Disease virus (IBDV), Infectious Laryngotracheitis virus (ILTV), avian adenoviruses, Marek's disease virus (MDV), fowlpox virus, duck enteritis virus (DEV), duck parvoviruses, avian influenza virus, APMV, such as APMV-1, and the like, and combinations thereof.

[0053] In another embodiment, the vaccine or pharmaceutical composition comprises an antigen selected from a feline pathogen such as, but not limited to, feline herpesvirus (FHV), feline calicivirus (FCV), feline leukemia virus (FeLV), feline immunodeficiency virus (FIV), feline parvovirus (FPV), feline infectious peritonitis virus (FIPV), rabies virus, and the like, and combinations thereof.

[0054] In yet another embodiment, the vaccine or pharmaceutical composition of the present description comprises an antigen selected from a canine pathogen including, but not limited to, rabies virus, canine herpesvirus (CHV), canine parvovirus (CPV), canine distemper virus (CDV), canine parainfluenza 2 (CPI2), canine coronavirus, *Leptospira canicola, Leptospira icterohaemorragiae, Leptospira grippotyphosa, Borrelia burgdorferi, Bordetella bronchiseptica* and the like, and combinations thereof.

[0055] In yet another embodiment, the vaccine or pharmaceutical composition comprises an antigen selected from an equine pathogen, such as equine herpesvirus (type 1 or type 4), equine influenza virus, tetanus, west nile virus, equine arterivirus and the like or combinations thereof.

[0056] In yet another embodiment, the vaccine or pharmaceutical composition comprises an antigen selected from a bovine, ovine or caprine pathogen, such as rabies virus, bovine rotavirus, bovine parainfluenza virus type 3 (bPIV-3), bovine coronavirus, bovine viral diarrhea virus (BVDV), foot and mouth disease virus (FMDV), Rinderpest virus (RPV), Peste des Petits Ruminants virus (PPRV), malignant catarrhal fever viruses, bovine respiratory syncytial virus (BRSV), Infectious Bovine Rhinotracheitis virus (IBR), *Escherichia coli, Pasteurella multocida, Pasteurella haemolytica* and the like, and combinations thereof.

[0057] In still another embodiment, the vaccine or pharmaceutical composition comprises an antigen selected from a porcine pathogen such as, but not limited to, swine influenza virus (SIV), porcine circovirus type 2 (PCV-2), porcine reproductive respiratory syndrome virus (PRRS), pseudorabies virus (PRV), porcine parvovirus (PPV), FMDV, *Mycoplasma hyopneumoniae*, *Erysipelothrix rhusiopathiae, Pasteurella multocida*, *Bordetella bronchiseptica, Escherichia coli* and the like, and combinations thereof.

[0058] Construction of recombinant virus is well known in the art as described in, e.g., US patent Nos. 4,769,330, 4,722,848, 4,603, 112, 5,174, 993, and 5,756,103, 6,719,979. Specifically, a recombinant APMV virus may be constructed in two steps. First, the gene of interest to be inserted into the virus, such as an open reading frame of an antigen from an APMV-1 (NDV) or avian influenza virus or other organism, is placed into an *E.coli* plasmid construct into which the cDNA homologous to a section of cDNA of the APMV is inserted. Separately, the cDNA gene sequence to be inserted is preceded by a promoter region (gene start region) and followed by a gene end region which is specific for the APMV vector. The gene start/foreign antigen/gene end DNA fragment is flanked by cDNA fragment homologous of APMV-8 cDNA containing unique restriction enzyme cleavage sites. The resulting plasmid construct is then amplified by growing in *E.coli* bacteria and isolated. Next the recombinant plasmid is used in a restriction enzyme digest to cut out the gene start/foreign antigen/gene end DNA fragment that is flanked by cDNA homologous of APMV-8 cDNA and this fragment is ligated into the appropriately cleaved full length construct of APMV-8.

[0059] The full length construct containing the gene of interest is transfected into cells along with plasmids containing polynucleotides for expression of the APMV nucleoprotein (NP), the APMV phosphoprotein (P) and the APMV RNA polymerase (L) as well as the T7 RNA polymerase. All APMV cDNA constructs are under the control of the T7 polymerase promoter. The rescue of infectious virus is performed as described in Römer-Oberdörfer et al., 1999 and as shown in Figure 19A. The expression of the T7 RNA polymerase in transfected cells can be obtained by different means including transfection of plasmid DNA containing an expression cassette of the T7 RNA polymerase, recombinant virus (such as fowlpox or canarypox virus) expressing the T7 RNA polymerase or in cells that express the T7 RNA polymerase. In another aspect, the polynucleotides for expression of the APMV nucleoprotein (NP), the APMV phosphoprotein (P) and the APMV RNA polymerase (L) and the full length viral cRNA are under the control of the immediate early promoter of the human cytomegalovirus. The rescue of the virus is performed as described in Inoue K, et al., 2003.

[0060] Successful expression of the inserted cDNA of interest (foreign cDNA or heterologous cDNA) by the modified

infectious virus requires two conditions. First, the insertion must be introduced into a region of the genome of the virus in order that the modified virus remains viable. The second condition for expression of inserted cDNA is the presence of a regulatory sequences allowing expression of the gene in the viral background (for instance: gene start, gene stop, promoter, enhancer, polyadenylation signals, intergenic and untranslated regions).

[0061] In general, it is advantageous to employ a strong promoter functional in eukaryotic cells. In one embodiment, the promoter used for the transcription of viral mRNA by the viral RNA polymerase is the "gene start sequence". The "gene start sequence" is the binding site for the L protein to bind and to transcribe the downstream located viral RNA into viral mRNA.

[0062] In one embodiment, the description provides for the administration of a therapeutically effective amount of an APMV vaccine for the delivery and expression of an antigen, epitope or immunogen in a target cell. Determination of the therapeutically effective amount is routine experimentation for one of ordinary skill in the art. In one embodiment, the APMV vaccine formulation comprises an expression vector comprising a polynucleotide that encodes an antigen, epitope or immunogen and a pharmaceutically or veterinarily acceptable carrier, vehicle or excipient. In another embodiment, the pharmaceutically or veterinarily acceptable carrier, vehicle or excipient facilitates transfection and/or improves preservation of the vector or protein.

[0063] The pharmaceutically or veterinarily acceptable carriers or vehicles or excipients are well known to the one skilled in the art. For example, a pharmaceutically or veterinarily acceptable carrier or vehicle or excipient can be a 0.9% NaCl (e.g., saline) solution or a phosphate buffer. Other pharmaceutically or veterinarily acceptable carrier or vehicle or excipients that can be used for methods of this description include, but are not limited to, poly-(L-glutamate) or polyvinylpyrrolidone. The pharmaceutically or veterinarily acceptable carrier or vehicle or excipients may be any compound or combination of compounds facilitating the administration of the vector (or protein expressed from a vector *in vitro*), or facilitating transfection and/or improve preservation of the vector (or protein). Doses and dose volumes are herein discussed in the general description and can also be determined by the skilled artisan from this disclosure read in conjunction with the knowledge in the art, without any undue experimentation.

[0064] In another embodiment, pharmaceutically or veterinarily acceptable carrier, excipient, or vehicle may be a water-in-oil emulsion. Examples of suitable water-in-oil emulsions include oil-based water-in-oil vaccinal emulsions which are stable and fluid at 4°C containing: from 6 to 50 v/v % of an antigen-containing aqueous phase, from 12 to 25 v/v %, from 50 to 94 v/v % of an oil phase containing in total or in part a non-metabolizable oil (e.g., mineral oil such as paraffin oil) and/or metabolizable oil (e.g., vegetable oil, or fatty acid, polyol or alcohol esters), from 0.2 to 20 p/v % of surfactants, from 3 to 8 p/v %, the latter being in total or in part, or in a mixture either polyglycerol esters, said polyglycerol esters being polyglycerol (poly)ricinoleates, or polyoxyethylene ricin oils or else hydrogenated polyoxyethylene ricin oils. Examples of surfactants that may be used in a water-in-oil emulsion include ethoxylated sorbitan esters (e.g., polyoxyethylene (20) sorbitan monooleate (TWEEN 80®), available from AppliChem, Inc., Cheshire, CT) and sorbitan esters (e.g., sorbitan monooleate (SPAN 80®), available from Sigma Aldrich, St. Louis, MO). In addition, with respect to a water-in-oil emulsion, see also US Patent No. 6,919,084. In some embodiments, the antigen-containing aqueous phase comprises a saline solution comprising one or more buffering agents. An example of a suitable buffering solution is phosphate buffered saline. In one embodiment, the water-in-oil emulsion may be a water/oil/water (W/O/W) triple emulsion (see, e.g., U.S. Patent No. 6,358,500). Examples of other suitable emulsions are described in U.S. Patent No. 7,371,395.

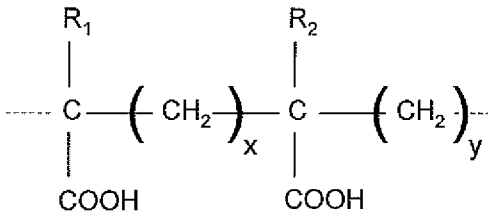
[0065] The pharmaceutical compositions and vaccines according to the description may comprise or consist essentially of one or more adjuvants. Suitable adjuvants for use in the practice of the present invention are (1) polymers of acrylic or methacrylic acid, maleic anhydride and alkenyl derivative polymers, (2) immunostimulating sequences (ISS), such as oligodeoxyribonucleotide sequences having one or more non-methylated CpG units (Klinman et al., 1996; WO98/16247), (3) an oil in water emulsion, such as the SPT emulsion described on p 147 of "Vaccine Design, The Subunit and Adjuvant Approach" published by M. Powell, M. Newman, Plenum Press 1995, and the emulsion MF59 described on p 183 of the same work, (4) cation lipids containing a quaternary ammonium salt, e.g., DDA (5) cytokines, (6) aluminum hydroxide or aluminum phosphate, (7) saponin or (8) other adjuvants discussed in any document cited herein, or (9) any combinations or mixtures thereof.

[0066] The oil in water emulsion (3), which is especially appropriate for viral vectors, can be based on: light liquid paraffin oil (European pharmacopoeia type), isoprenoid oil such as squalane, squalene, oil resulting from the oligomerization of alkenes, e.g. isobutene or decene, esters of acids or alcohols having a straight-chain alkyl group, such as vegetable oils, ethyl oleate, propylene glycol, di(caprylate/caprate), glycerol tri(caprylate/caprate) and propylene glycol dioleate, or esters of branched, fatty alcohols or acids, especially isostearic acid esters. The oil is used in combination with emulsifiers to form an emulsion. The emulsifiers may be nonionic surfactants, such as: esters of on the one hand sorbitan, mannide (e.g. anhydromannitol oleate), glycerol, polyglycerol or propylene glycol and on the other hand oleic, isostearic, ricinoleic or hydroxystearic acids, said esters being optionally ethoxylated, or polyoxypropylene-polyoxyethylene copolymer blocks, such as Pluronic, e.g., L121. Among the type (1) adjuvant polymers, preference is given to polymers of crosslinked acrylic or methacrylic acid, especially crosslinked by polyalkenyl ethers of sugars or polyalcohols. These compounds are known under the name carbomer (Pharmeuropa, vol. 8, no. 2, June 1996). One skilled in the art

can also refer to U.S. Patent No. 2,909,462, which provides such acrylic polymers crosslinked by a polyhydroxyl compound having at least three hydroxyl groups, preferably no more than eight such groups, the hydrogen atoms of at least three hydroxyl groups being replaced by unsaturated, aliphatic radicals having at least two carbon atoms. The preferred radicals are those containing 2 to 4 carbon atoms, e.g. vinyls, allyls and other ethylenically unsaturated groups. The unsaturated radicals can also contain other substituents, such as methyl. Products sold under the name Carbopol (BF Goodrich, Ohio, USA) are especially suitable. They are crosslinked by allyl saccharose or by allyl pentaerythritol. Among them, reference is made to Carbopol 974P, 934P and 971 P.

[0067] As to the maleic anhydride-alkenyl derivative copolymers, preference is given to EMA (Monsanto), which are straight-chain or crosslinked ethylene-maleic anhydride copolymers and they are, for example, crosslinked by divinyl ether. Reference is also made to J. Fields et al., 1960.

[0068] With regard to structure, the acrylic or methacrylic acid polymers and EMA are preferably formed by basic units having the following formula:



in which:

-R1 and R2, which can be the same or different, represent H or CH3
-x = 0 or 1, preferably x = 1
-y = 1 or 2, with x + y = 2.
For EMA, x = 0 and y = 2 and for carbomers x = y = 1.

[0069] These polymers are soluble in water or physiological salt solution (20 g/l NaCl) and the pH can be adjusted to 7.3 to 7.4, e.g., by soda (NaOH), to provide the adjuvant solution in which the expression vector(s) can be incorporated. The polymer concentration in the final immunological or vaccine composition can range between 0.01 and 1.5% w/v, between 0.05 and 1% w/v, and between 0.1 and 0.4% w/v.

[0070] Another aspect of the description relates to a method for inducing an immunological response in an animal to an antigen, which method comprises inoculating the animal with a vaccine or a pharmaceutical composition including modified recombinant APMV virus which comprises and encodes the antigen of a pathogen for said animal. Yet another aspect of the description relates to a method for inducing an immunological response in an animal to an antigen in a prime-boost administration regimen, which is comprised of at least one primary administration and at least one booster administration using at least one common polypeptide, antigen, epitope or immunogen. The immunological composition or vaccine used in primary administration may be same, may be different in nature from those used as a booster. In one aspect of the prime-boost protocol of the description, a composition or vaccine comprising the recombinant APMV virus (viral vector) of the present description is administered followed by the administration of an inactivated viral vaccine or composition comprising an antigen, or a vaccine or composition comprising a subunit (protein, antigen), or a DNA plasmid vaccine or composition that contains or expresses an antigen. Likewise, a prime-boost protocol may comprise the administration of an inactivated viral vaccine or composition comprising an antigen, or a vaccine or composition comprising a subunit (protein, antigen), or a DNA plasmid vaccine or composition that contains or expresses an antigen, followed by the administration of a composition or vaccine comprising the recombinant APMV virus (viral vector) of the present description. It is further noted that both the primary and the secondary administrations may comprise the composition or vaccine comprising the recombinant APMV virus (viral vector) of the present description.

[0071] The primary administration may comprise one or more administrations of the same viral vector-based immunological compositions of vaccines. Similarly, the booster administration may comprise one or more administrations of the same viral vector-based or immunological composition of vaccine. The administration route of the prime and the boost may be the same or different. Similarly, the origin of the protective gene present in the prime and the boost may be the same or different (e.g. different strain).

[0072] The various administrations are preferably carried out 1 to 6 weeks apart, and more particularly about 3 weeks apart. According to a preferred mode, an annual booster, preferably using the viral vector-based immunological composition of vaccine, is also envisaged. The animals are preferably at least one day old at the time of the first administration.

[0073] A variety of administration routes may be used such as subcutaneously or intramuscularly, intradermally, transdermally, spray, drinking water, eye drop, intranasal, oral, oral baits, *in ovo* or a combination (e.g. oculonasal,

oronasal).

[0074] The invention will now be further described by way of the following nonlimiting examples.

EXAMPLES

Example 1 APMV-2, APMV-4, and APMV-6

A. Viruses and Birds

[0075] One-day-old SPF (specific pathogen free) chickens (Merial, Gainesville, GA) were housed in positive pressure Horsfall-Baur isolation units. Feed and water were provided *ad libitum* and the birds were examined twice daily. The viruses (APMV-2, 4, and 6) used for experimental studies were isolated from wild birds and classified by the National Veterinary Service Laboratory (NVSL, Ames Iowa, USA). Viruses were propagated in 9-day-old embryonated SPF chicken eggs (SunRise Farms, Catskill, NY, USA) by inoculation via the allantoic route. The allantoic fluid was harvested at day 3 after inoculation, aliquoted, and stored at -80°C. The APMV subtype was confirmed by the HI test using standard sera (NVSL, Ames, Iowa, USA). The 50% egg infectious dose (EID_{50}) for each isolate was determined by inoculating 10-fold serial dilutions of allantoic fluid in embryonated SPF eggs. The titer was calculated following the method as described by Reed and Muench (Reed, LJ et al., 1938, Am. J. Epidemiol. 27:493-497). B. Experimental infection

[0076] Twenty-five one-day-old SPF chickens per group were infected with 10^6 EID_{50} per chicken by the ocular-nasal route. Chickens of the control group were mock inoculated with PBS (phosphate buffered saline). At days 2, 4, 7, 14, and 28 p. i. (post infection) five birds from each group were bled via the wing vein to collect serum samples, euthanized with CO_2, and necropsied. Tissue specimens of the trachea, lung, pancreas and gut were collected. For each organ, a fresh pair of sterile scissors and forceps was used. Half of the tissue sample was placed in a Lysing Matrix D tube (MP Biomedicals, Solon, OH) containing viral transport medium (1X minimal essential medium, 7.5% sodium bicarbonate, 15 mM HEPES, 1% fetal bovine serum, 4,000 U/ml penicillin, 400 μg/ml gentamycin, 8 μg/ml amphotericin B, 4,000 μg/ml streptomycin, 1000 μg/ml kanamycin sulfate). The second half of the tissue sample was fixed in 10% buffered formalin and embedded in paraffin wax. Sections of the paraffin-embedded tissues were stained with Mayer's hematoxylin and eosin (H&E).

[0077] The results showed that mild diarrhea was observed at day four and seven p. i. in birds infected with APMV-2 or APMV 4. During necropsy, birds infected with APMV-2 showed slightly enlarged pancreas at day two and four after infection. No other gross lesions were observed in any group.

C. Serology

[0078] The hemagglutination (HA) and hemagglutination-inhibition (HI) tests were used to detect virus in allantoic fluid and analyze the presence of HI antibodies in collected serum samples, respectively. The tests were conducted by standard procedures using 0.8% chicken red blood cells resuspended in PBS. The HI test was performed by the diluted-serum constant-antigen method. Eight HA units of viral antigen was used for each serum dilution.

[0079] The HI antibody titers were investigated at day 2, 4, 7, 14, and 28 p.i. Positive HI titers ($\geq$ 1:16) were observed in serum samples of APMV-2 infected birds at day 7 (1/5), day 14 (5/5), and day 28 p.i. (5/5). Interestingly, only one chicken infected with APMV-4 developed an HI titer which has been considered as positive during the course of the experiment at day 14 p.i. Similarly for APMV-6, two chickens out of five developed a HI titer of 1:16, only on day 28 p.i.. Mock inoculated birds remained negative for HI antibodies to all three APMV used in this experiment. In addition, to exclude cross contamination all sera were tested for HI antibodies against the other two antigens and remained negative.

D. Virus Isolation

[0080] The tissue samples collected in the Lysing Matrix D tubes (MP Biomedicals, Solon, OH, USA) were homogenized twice using the Fastprep®-24 (MP Biomedicals, Solon, OH) at a setting of 4.0 M/S for 20 seconds. Following incubation for 15 min at room temperature, the homogenized samples were centrifuged for 20 min at 2000 g at 4°C. Sterility was tested after inoculation of 50 μl of the obtained supernatant in 2 ml tryptose phosphate broth (TPB) (DIFCO, Becton Dickenson, Sparks, MD, USA) supplemented with 10% hydrolactalbumin by incubation at 37°C in an orbital shaker overnight. Non-sterile samples were filtered with 0.45 μm syringe filters (Whatman Inc., Florham Park, NJ, USA). Samples were stored at -80°C. Virus isolation was performed by inoculation of 0.1 ml into the allantoic cavity of 9-day-old embryonated SPF chicken eggs. After incubation for three days at 37.5°C, the allantoic fluid was harvested and tested for the presence of haemagglutinating activity by HA.

[0081] To analyze sites of virus replication, several organs (trachea, lung, gut, pancreas) were analyzed for infectious virus by virus isolation in embryonated eggs (Figure 1). Overall, replicating virus was only detected in a few chickens.

Briefly, APMV-4 was recovered on day 2 from trachea, lung and pancreas while APMV-6 was isolated from lung and pancreas. At day 4, APMV-2 was isolated from trachea and lung while APMV-6 was isolated from all tested organs except the gut. At day 7, APMV-2 was isolated from a single gut sample, APMV-4 was isolated from the pancreas while APMV-6 was isolated from lung and pancreas samples. Surprisingly, at day 14 p.i. no virus was isolated whereas at day 28 p.i. APMV-2, 4 and 6 could be isolated from the pancreas. No virus was isolated from mock inoculated birds. The identity of the back isolated virus was confirmed by HI test using standard sera as provided by NVSL.

[0082] To evaluate the pathological potential of the investigated viruses, microscopical lesions in the obtained organs were analyzed (Figure 2). At day 2 p.i., a catarrhal tracheitis in addition to ciliary loss on the respiratory epithelium and mild enteritis was observed in all infected chickens. At day 4 p.i., APMV-2 infected chickens showed an increased number of hypertrophic mucous glands in the trachea and focal ulcerations of the respiratory epithelium. APMV-4 infected birds showed changes highly suggestive of a respiratory infection such as mild tracheitis, mild to moderate multifocal lymphocytic pancreatitis and also a focal BALT (Bronchus-Associated Lymphoid Tissue) hyperplasia at day 4 p.i. The investigation on organs of APMV-6 infected chickens revealed tracheal changes such as catarrhal and ulcerative tracheitis and a focal pancreatitis that are consistent with a viral stimulation. At day 7 p.i., APMV-2 infected chickens showed focal tracheal attenuation or replacement of respiratory epithelium as indicative of healing. Birds infected with APMV-4 showed mild BALT hyperplasia while APMV-6 infected birds showed cystic enteropathy, focal enteritis and lymphocytic infiltrates in the pancreas. In addition to mild lymphocytic enteritis and mild GALT hyperplasia, APMV-2 infected birds also showed healing changes such as tracheal attenuation at day 14 p.i. Organ samples from chicken infected with APMV-4 or 6 showed changes suggestive of viral infection such as mild interstitial pneumonia, catarrhal tracheitis and BALT or GALT hyperplasia at day 14 p.i. All investigated samples obtained from infected chicken showed lesions such as GALT hyperplasia, lymphocytic pancreatitis and lymphocytic bronchitis at day 28 p.i. At day 2, birds of the control group showed a mild catarrhal tracheitis which could be attributed to environmental factors.

[0083] Figure 3 shows low HI titers (up to 1:32 at day 14) from SPF chickens infected with APMV-4 or APMV-6 indicating that only APMV-2 infection elicited an HI response that could be characterized as seropositive. Nevertheless, all three viruses were recovered from the infected birds' trachea, lungs, gut and pancreas up to day 7 p.i. and from the pancreas up to day 28 p.i.. Infection with APMV-2, 4, or 6 showed characteristic histopathological lesions (summarized in figure 2) in all the infected birds, indicative of stimulation with a viral antigen. The viral isolation and histological profiles of the infected birds clearly depicted the tropism of the viruses in the infected birds (trachea and lungs from day 2 to day 7 and gut, lung and pancreas from day 7 onwards). All isolates were detected in the pancreas up to 28 days p.i. but virus isolation was not possible at day 14 p.i.. This indicated that the investigated APMV can probably persist and later become reactivated. Thus virus carriers can be present in infected flocks. Only APMV-2 induced HI antibodies while HI antibodies of chickens infected with APMV-4 and 6 were not detected.

Example 2 APMV-8

A. Viruses and Birds

[0084] One-day-old SPF chickens (Merial, Gainesville, GA, USA) and Pekin ducks (Metzer Farms, Gonzales, CA, USA) were housed in positive pressure Horsfall Baur isolation units. Feed and water were provided *ad libitum*, and the birds were examined twice daily. The APMV-8 virus (APMV-8: SCWDS ID: MA-7) used for experimental studies was isolated from a mallard and classified by the National Veterinary Service Laboratory (NVSL, Ames Iowa, USA). The virus was propagated in 9-day-old embryonated SPF chicken eggs by inoculation via the allantoic route. Allantoic fluids were harvested at day 3 after inoculation, pooled, aliquoted and stored at -80 °C. The APMV-8 subtype was confirmed by HI testing using standard sera as provided by the National Veterinary Service Laboratory (Ames, IA, USA). The EID_{50} was determined by inoculating 10-fold serial dilutions of allantoic fluid in embryonated SPF eggs. The titer was calculated following the method as described by Reed and Muench (Reed & Muench, 1938).

B. Experimental infection

[0085] Twenty five one-day-old SPF chickens or Pekin ducks per group were infected via the oculonasal route with 10^6 EID_{50} per bird diluted in PBS. Birds of the control chicken or duck group were mock inoculated with PBS. Five birds from each group were bled via the brachial vein to collect serum samples, humanely euthanized with CO_2, and necropsy was performed at two, four, seven, fourteen and twenty eight days post infection (d p.i). Tissue specimens of the trachea, lung, pancreas, and gut (duodenum) were collected. For each organ, a fresh pair of sterile scissors and forceps was used. Half of the tissue sample was placed in a Lysing Matrix D tube (MP Biomedicals, Solon, OH, USA) containing viral transport medium (VTM, 1X minimal essential medium, 7.5% sodium bicarbonate, 15 mM HEPES, 1% fetal bovine serum, 4,000 U/ml penicillin, 400 μg/ml gentamycin, 8 μg/ml amphotericin B, 4,000 μg/ml streptomycin, 1000 μg/ml kanamycin sulfate). The second half of the tissue sample was fixed in 10% buffered formalin and routinely processed,

embedded, sectioned and stained with hematoxylin and eosin (H&E).

C. Virus Isolation

[0086] The tissue samples collected in the Lysing Matrix D tubes were homogenized twice using the FastPrep-24 (MP Biomedicals) at a setting of 4.0 M/S for 20 seconds. The homogenized samples were incubated for 15 min at room temperature and then centrifuged for 20 min at 2000xg at 4°C. 50 μl of the obtained supernatant was inoculated in 2 ml sterile TFB supplemented with 10% hydrolactalbumin followed by incubation at 37°C in an orbital shaker overnight to test for sterility. Non-sterile samples were filtered with 0.45 μm syringe filters (Whatman Inc.). Samples were stored at -80°C. Virus isolation was performed by inoculation of 0.1 ml into the allantoic cavity of 9-day-old embryonated SPF chicken eggs. After incubation for three days at 37.5°C, the allantoic fluid was harvested and tested for the presence of hemagluttinating activity by HA.

D. Serology

[0087] The hemagglutination (HA) and hemagglutination-inhibition (HI) tests were used to detect virus in allantoic fluid and to analyze the presence of HI antibodies in collected serum samples, respectively. The tests were conducted by standard procedures using 0.8% chicken red blood cells resuspended in PBS. The HI test was performed by the diluted-serum constant-antigen method. Eight HA units of viral antigen were used for each serum dilution. The geometric mean titer was determined as described previously (Brugh,1978).

[0088] Figure 4 shows HI antibody titers in SPF chickens and ducks infected with APMV-8. Chickens and ducks were oro-nasal infected with a dose of 10^6 EID_{50} of APMV-8. Sera samples were collected at day 2, 4, 7, 14, and 28 p.i. and analyzed by the HI test with the APMV-8 antigen. The HI serum titers (in $\log_2$) are shown on the left axis.

E. Pathogenicity indices of APMV-8 in chicken

[0089] To assess the virulence of APMV-8, the intracerebral pathogenicity index (ICPI) was determined following the World Organization for Animal Health (OIE, 2008) procedures for Newcastle disease virus. The mean dead time (MDT) in chicken embryos was determined as described previously (Swayne et al., 1998) using a serial dilution of APMV-8 from 10^{-1} through 10^{-8}.

[0090] The determination of the mean dead time (MDT) in embryonated eggs as well as the assessment of the intracerebral pathogenicity index (ICPI) is an important measurement for the pathogencity of the virus. With respect to the MDT in embryonated eggs, none of the embryos of the inoculated eggs died after the 7 day period and thus the APMV-8 isolate can be classified as lentogenic. The presence of virus was confirmed by HA test using the allantoic fluid of eggs inoculated with the 10^{-6} dilution. All the chickens intracerebrally inoculated showed no clinical signs over the observation time resulting in an ICPI value of zero which results in a lentogenic phenotype.

F. APMV-8 booster vaccination

[0091] Ten one-day-old SPF chickens per group were infected via the oculo-nasal route with 10^6 EID_{50} per bird. Birds of the control chicken group were mock inoculated with PBS. The birds were infected again with the same dose 14 days after the first infection. The presence of infectious virus was monitored at day 2, 4, 7 and 14 after the first infection and day 2 and 4 after the second infection by virus isolation from tracheal swabs using 9-day-old embryonated SPF eggs. Antibody response was monitored by HI titer of serum samples collected at 0, 7, and 14 days after each vaccination.

[0092] In order to investigate if a second immunization would allow developing a more sustainable HI titer, a prime/boost scheme experiment was performed (Figure 5). On day 7 after the first infection, all ten birds showed an HI ranging from 64 to 1024 (GMT 207). The titer declined at 14 d p.i. after the first infection (GMT 84) but increased after the boost infection at day 14 after the initial infection. On day 7 after the boost vaccination, the GMT increased to 137 and decreased again to a GMT of 73 at day 14 after the second infection. Infectious virus could be isolated from tracheal swabs at day 2 (5/10 birds) and day 4 (4/10) birds after the first infection. After the second infection no virus was isolated from the swabs taken at day 2 and 4 p.i..

G. Detection of viral RNA by RT-PCR

[0093] The detection of viral RNA from tissue samples was performed after homogenization of tissue samples followed by isolation of RNA by using the High Pure RNA isolation kit (Roche, Mannheim, Germany). A primer pair (8NPf1, 8NPr, see table 1) was used in an RT-PCR using the Supercript III One Step RT-PCR kit with Platinum Taq (Invitrogen, Carlsbad, CA, USA) following the instructions of the manufacturer. The obtained reaction products were analyzed on a

1% agarose gel (Figure 6). Tracheal tissues were taken at day 2 p.i. from non-infected ducks (C1-C5) and APMV-8 infected ducks (I1-I5). The tissues were homogenized and RNA was prepared for RT-PCR. A water control (W) was prepared in parallel. The reaction products were separated on a 1.5% agarose gel. The size of the fragment was controlled by using the 100 bp ladder (New England Biolabs, Boston, MA, USA). The sizes of the DNA fragments are shown at the right.

Table 1 Oligonucleotides used for RT-PCR for the detection of viral RNA in tissue samples

Name	Sequence	orientation	Location[A]	SEQ ID NO
APMV-PolyT	TTTTTTTTTTTTTTTTTTTACCAAACAR RGAA	sense	1-14	21
8NPf1	CAGGAGACCTGATGTTGCCTCAAC	sense	200-223	22
8NPr	GCAGGCGATCTATAGTCTCTGATAG	antisense	618-642	23

H. Determination of the minimal infectious dose in chicken and ducks

[0094] In order to determine which viral titer would be sufficient in chickens to detect a seroconversion, one-day-old SPF chickens were infected with different doses of APMV-8. The birds were housed as described above. Ten chickens per group were infected each with 10^1, 10^2, 10^3, 10^4, 10^5, or 10^6 EID_{50}. The virus was diluted in VTM. One group was inoculated with VTM and served as control. The birds were bled at day 7 and 14 after infection via the brachial vein. Based on the results obtained during the chicken experiment three-day-old Pekin ducks were infected with different amount of virus. The infection dose was chosen 10^3, 10^4, 10^5, or 10^6 EID_{50} per duck. One group was mock-infected with VTM. The birds were bled at day 7 and 14 after infection via the leg vein. The serum sample was analyzed for the presence of virus specific antibodies by HI as described above.

I. Determination of the pathogenicity in ducks and chickens

[0095] During the experiments, no clinical signs were observed in chickens and ducks. During necropsy, three infected chickens showed slightly enlarged pancreas and inflamed duodenum at day two and four p.i.. No other gross lesions were observed in any group.

[0096] The serological response was examined at 2,4, 7, 14, and 28 d p.i. by investigation of the HI titers in the serum (Figure 4). Serum samples of APMV-8 infected chickens showed positive HI titers (≥ 16) starting with 7 d p.i. (5/5, GMT: 111), 14 d p.i. (5/5, GMT: 48), and 28 d p.i. (5/5, GMT: 48). Serum samples of APMV-8 infected ducks also showed positive HI titers (≥ 16) at 7 (5/5, GMT 21), 14 (5/5, GMT 28), and 28 (4/5, GMT 14) d.p.i. The HI titers ranged from 32 to 256 for chickens, while for ducks the range was from 16 to 64. Sham inoculated birds remained negative for HI antibodies to APMV-8 at all time points investigated in both species.

[0097] To determine the sites of virus replication in chickens and ducks, several organs (trachea, lung, duodenum, and pancreas) were analyzed for infectious virus by virus isolation in embryonated eggs (Figure 7). In chickens, APMV-8 was recovered at 2 d p.i. from trachea, lung, and duodenum. At 4 d p.i., APMV-8 was isolated from all the analyzed organs; while at 7 d p.i., APMV-8 was isolated only from the pancreas. At 14 and 28 d p.i. no virus was isolated from any organ. No virus was isolated from sham inoculated birds. The identity of the back isolated virus was confirmed by HI test using standard sera as provided by NVSL. No virus was isolated from any of the collected duck tissues at any time point even after two subpassages in 9-day-old embryonated SPF chicken eggs. Therefore, RT-PCR primers were designed based on the APMV-8 sequence information available to detect the presence of viral RNA in the collected tissue samples (Figure 7). At 2 d p.i viral RNA was detected in the trachea (Figure 6), gut and pancreas while at 4 d p.i viral RNA was detected in all the organs analyzed. At 7, 14, and 28 d p.i, viral RNA was detected only in the trachea and lung. RT-PCR using RNA obtained from organs of mock inoculated birds did not result in the amplification of an RT-PCR fragment which indicates the absence of APMV-8 in these birds.

[0098] To evaluate the pathological potential of the investigated virus, the organs were analyzed for the presence of microscopic lesions (Figure 8). At 2 d p.i., a mild multifocal proliferative tracheitis was observed in all infected chickens. The remaining organs showed no difference to the control group. APMV-8 infected chickens showed focal attenuation or regeneration of respiratory epithelium in the trachea at 4 d p.i. as indicative of healing. Additionally, the birds also showed mild multifocal lymphocytic pancreatitis which indicated a viral infection. Infected chicken showed changes in the lung at 7 d p.i. such as moderate to severe BALT, tracheal changes such as catarrhal tracheitis and multifocal lymphocytic pancreatitis. These findings are consistent with an antigenic stimulation. At 14 d p.i, tracheal changes consistent with healing and pancreatic changes such as lymphocytic pancreatitis suggestive of viral infection were observed in infected chickens. At 28 d p.i., only a mild catarrhal tracheitis and mild enteritis were observed in some of the infected chickens. In infected ducks, multifocal mild lymphocytic tracheitis, lung changes (interstitial pneumonia) and

intestinal changes (lymphocytic enteritis) were observed at 2 d p.i while tracheal changes consistent with respiratory infection were seen at 4 d.p.i.. At 7 d p.i., infected ducks showed lymphocytic tracheitis and pancreatitis consistent with viral infection whereas the observed catarrhal tracheitis was a suggestive of healing at 14 d p.i.. In addition, infected ducks showed a lymphocytic pancreatitis at 14 d p.i.. Later, at 28 d p.i., in the lung of infected ducks a BALT hyperplasia and also mild multifocal heterophilic tracheitis were noticed. Both pathological microscopic lesions were indicative of a viral infection. In the non infected controls no changes in the examined organs were observed.

J. Determination of the minimal dose needed for induction of an immune response

[0099] In order to examine the minimal infectious dose which is necessary to induce a seroconversion in chicken, tenfold dilutions of APMV-8 were used to infect ten one-day-old SPF chickens (Figure 9). For the HI test, 4 HA units were used which results in a threshold of 16 to be considered as positive. The serum samples taken at day 14 p.i. showed that an EID_{50} of 10^3 was sufficient to induce an immune response in 4/10 chickens which was considered as positive (GMT 11). At day 14 after infection with an EID_{50} of 10^4 nine of ten birds showed a titer ≥16 (GMT 34). The infection with an EID_{50} of 10^5 and 10^6 induced an HI titer of ≥16 at day 14 p.i. in all birds with a GMT of 73 and 137, respectively.

[0100] Based on this result, 8 ducks each were infected with APMV-8 starting with a dose EID_{50} of 10^3 per bird up to a dose of EID_{50} of 10^6 per bird (Figure 10). Six out of eight ducks developed significant titers (≥16) 14 days after infection with a GMT of 14 after infection with an EID_{50} of 10^4/bird. At day 14 p.i. 6/8 ducks infected with an EID_{50} of 10^5/bird and 7/8 ducks infected with an EID_{50} of 10^6/birds developed significant titers (≥16) with a GMT of 17 and 23, respectively.

Example 3 Determination of the full length sequence of APMV-8

[0101] For the determination of the full length sequence of APMV-8, viral RNA sequence information is initially needed. To this end, the 3'-end of the viral genome was cloned by using a primer (APMV-polyT, see table 1) which contained a degenerated sequence based on available 3'- sequences of APMV1 (Genbank accession No. AF077761), APMV-2 (Genbank accession No. EU338414), and APMV-6 (Genbank accession No. EF569970). Viral RNA was purified from allantoic fluid using the High Pure RNA isolation kit (Roche, Mannheim, Germany). The sequence was amplified using the 5' RACE System for Rapid Amplification of cDNA Ends Version 2.0 (Invitrogen) following the manufacturer's instructions. Several fragments were obtained, gel eluted and cloned into the Topo TA cloning vector (Invitrogen) and positive selected clones were sequenced. The obtained nucleotide sequences were analyzed in an nblast search against the NCBI database which resulted in no similarities. A tblastx search against the NCBI database showed similarities to the nucleoprotein of 83% similarity of an Avian paramyxovirus 2 (APMV-2/Chicken/California/Yucaipa/56, Genbank accession No. EU338414) and of 56% similarity of an Avian paramyxovirus 6 strain (APMV-6/Goose/FarEast/4440/2003, Genbank accession No. EF569970). Using this primer, the primer walking method was employed using the 5' RACE System for Rapid Amplification of cDNA Ends Version 2.0 (Invitrogen). The 5'-RACE produced an approximately 800 bp fragment. Using this technique, new sequence information was obtained based on sequence information from the previous sequence which has been used for the delineation of new oligonucleotides. The 5'-end of the viral genome was also determined by the 5'-RACE method. The 3'-end of the viral genome was obtained after ligation of the RNA with T4 RNA ligase1 (New England Biolabs). The ligation reaction was purified again with High Pure RNA isolation kit (Roche) and an RT-PCR was performed using Superscript III One Step RT-PCR kit with Platinum Taq (Invitrogen). The obtained cDNA fragment was cloned into the pCR2.1 vector (Invitrogen) and sequenced. Three plasmids from each cloned fragment were sequenced in both directions, thus resulting in sequence 6x-coverage of per nucleotide.

[0102] The full length genome sequence of the analyzed APMV-8 strain is 15342 nucleotides, this is in accordance to the rule of six (Calain, P. & Roux, L., 1993) for *Paramyxovirinae.* Six open reading frames (ORF) have been detected and are encoding for proteins. The order of the proteins was determined as 3'-NP-P-M-F-HN-L-5' (the genome sequence SEQ ID NO:1 is in the 5' to 3' orientation antigenomic) using similarities of the protein sequence to proteins of other avian paramyxoviruses. The putative start and stop codons of the ORF's and the theoretical molecular weight (Swiss Institute of Bioinformatics ExPASy website) of the proteins are shown in table 2.

Table 2 Parameter of the proteins encoded by the APMV-8 sequence

Protein	Start codon	Stop codon	Theoretical MW (kD)
Nucleoprotein (NP)	141-143	1524-1526	51.2
Phospho protein (P)	1693-1695	2908-2910	43.5
Matrixprotein (M)	3076-3078	4193-4195	40.6
Fusioprotein (F)	4499-4501	6128-6130	58.5

(continued)

Protein	Start codon	Stop codon	Theoretical MW (kD)
Hemagglutinin/neuraminidase (HN)	6383-6385	8114-8116	63.5
Polymerase (L)	8273-8275 or 8297-8299	15011-15013	254.6 253.6

[0103] The putative genomic leader and trailer sequences were determined by determination of the putative gene start sequence of the NP gene (leader) and putative gene end sequence of the L protein (trailer). The leader sequence is located from nucleotide 1 to nucleotide 55. The putative gene start sequence (nt 56-63) of the NP gene ends the leader sequence. The trailer sequence is localized behind the last gene end sequence in the viral genome. Due to the presence of two putative gene end sequences for the RNA polymerase gene (nt 15161-15171 or 15288 -15297) two putative trailer sequences have been identified (nt 15172-15342 or nt 15289-15342). The location of the putative gene start sequence (poly G containing sequences) and gene end sequences (signal sequence for a polyadenylation) and the intergenic sequences were summarized in table 3.

Table 3 Sequence and location of putative gene start, intergenic, and gene end sequence of APMV-8

Gene	Gene start	Gene end	intergenic
Nucleoprotein	56-63	1615-1625	1626-1627
Phosphoprotein	1628-1635	2991-3001	3002-3031
Matrixprotein	3032-3039	4404-4416	4417-4441
Fusionprotein	4442-4449	6260-6271	6272-6278
Hemagglutinin/neuraminidase	6279-6287	8261-8273	8274-8275
RNA polymerase	8275-8283	15161-15171 or 15288-15297	

Table 4 SEQ ID NO v. DNA and protein sequences.

SEQ ID NO	Gene name	Type
1	APMV-8 genome sequence	DNA or RNA
2	APMV-8 Nucleoprotien (NP)	DNA or RNA
3	APMV-8 Nucleoprotien (NP)	Protein
4	APMV-8 phospho protein (P)	DNA or RNA
5	APMV-8 phospho protein (P)	Protein
6	APMV-8 Matrixprotein (M)	DNA or RNA
7	APMV-8 Matrixprotein (M)	Protein
8	APMV-8 Fusioprotein (F)	DNAorRNA
9	APMV-8 Fusioprotein (F)	Protein
10	APMV-8 Hemagglutinin/neuraminidase (HN)	DNA or RNA
11	APMV-8 Hemagglutinin/neuraminidase (HN)	Protein
12	APMV-8 Polymerase (L) DNA	DNA or RNA
13	APMV-8 Polymerase (L) protein 1	Protein
14	APMV-8 Polymerase (L) protein 2	Protein

[0104] The putative gene start sequences for APMV-8 were conserved containing a poly $(C)_5$ sequence followed by a 3'-GCU-5' sequence. The only exception is the putative gene start sequence for the viral RNA polymerase (3'-CUC-CCGCU-5'). The putative gene end sequences were also conserved and contain a poly $(U)_6$ sequence at the genomic

viral 5' sequence (Table 5).

Table 5 Gene Start and Gene End sequences of APMV-8

	Gene Name	Sequences (5-3' antigenomic orientation)	SEQ ID NO
Gene start	NP gene	**CCCCCGCU**UCUGUCA	24
	P gene	**CCCCCGCU**GGAGUUA	25
	M gene	**CCCCCGCU**UCUGUGC	26
	F gene	**CCCCCGCU**UUAGAAC	27
	HN gene	**CCCCCGCU**GGGUAAA	28
	L	**C**U**CCCGCU**GGAGAUG	29
Gene end	NP gene	AACUAA**AUUCUUUUUU**	30
	P gene	UAACUA**AUU**C**UUUUUU**	31
	M gene	AGGAUU**A**A**U**A**UUUUUU**	32
	F gene	CUAUAA**AUU**A**UUUUUU**	33
	HN gene	UACUUA**AUU**C**UUUUUU**	34
	L gene (1)	ACUAAA**AUU**C**UUUUUU**	35
	L gene (2)	UUAUUG**AUU**U**UUUUUU**	36

[0105] These sequences were predicted based on sequences which were described for other paramyxoviruses of the genus *Avulavirus* (Chang et al., 2001, Nayak et al, 2008, Jeon et al., 2008). There are two possible start codons for the ORF of the RNA polymerase. The first start codon (nt 8273-8275) is localized in the gene end -intergenic region- gene start region between the HN ORF and the viral RNA polymerase ORF. This makes this start codon unlikely but not impossible. The second start codon (8297 -8299) is down stream of the gene end -intergenic region- gene start region and may act as initiation codon for the start of the translation of the RNA polymerase of APMV-8.

[0106] The genome of APMV-8 is 15342 nt long. This is larger than APMV-1 (SQ ID NO:15, 15186 nt, de Leeuw & Peeters, 1999), APMV-2 (SEQ ID NO:16, 14,904 nt, Subbiah et al., 2008), and APMV-4 (SEQ ID NO:18, 15054 nt, Nayak et al., 2008), and smaller than APMV-3 (SEQ ID NO:17, 16,272 nt, Kumar et al., 2008) and APMV-9 (SEQ ID NO:20, 15,438 nt, Samuel et al., 2009). The length of 55 nt of the leader sequence seemed to be conserved between all APMV (Krishnamurthy & Samal, 1998, de Leeuw & Peeters, 1999, Subbiah et al., 2008, Nayak et al., 2008, Kumar et al., 2008, Samuel et al., 2009) whereas the trailer sequence seemed to be variable in length. The gene start and gene end sequences of the viral genes were also highly conserved for APMV-8 (as shown in Table 5). This has been also described for sequences of APMV-2 (Subbiah et al, 2008), APMV-3 (Kumar et al, 2008), APMV-4 (Jeon et al., 2008, Nayak et al, 2008), APMV-6 (Chang et al, 2001), and recently for APMV-9 (Samuel et al., 2009). The number of the nucleotides of the full length sequence is a multiple of six which is agreement with the role of six for the genomes of paramyxoviruses (Kolakofsky et al., 1998).

[0107] The sequence identity between APMV-1, 2, 3, 4, 6, 8, and 9 genome sequences are shown in Table 6.

Table 6 sequence identity percentage between the genome of APMV-1, 2, 3, 4, 6, 7, 8, and 9

APMV		1	2	3	4	6	7	8	8	8	8	9
	SEQ ID NO	15	16	17	18	19	20	1	37	38	39	40
8	1	48	61	47.2	47.6	52	53	100	99.1	96.5	96.4	48

[0108] The percent sequence identity between two nucleic acid or polypeptide sequences is determined using Vector NTI 11.0 (PC) software package (Invitrogen, 1600 Faraday Ave., Carlsbad, CA). A gap opening penalty of 15 and a gap extension penalty of 6.66 are used for determining the percent identity of two nucleic acids. A gap opening penalty of 10 and a gap extension penalty of 0.1 are used for determining the percent identity of two polypeptides. The percent identity was calculated based on the shorter sequence.

Example 4 Vaccination of one-day-old broiler chickens with APMV-8 strain

[0109] Twenty one-day-old broiler chickens were separated into two groups according to table 7 shown below.

[0110] At day 1, the one-day-old chickens were bled to determine the antibody status directed against Newcastle disease virus (NDV) and APMV-8 using the hemagglutination inhibition assay (HI test). The test was performed using allantoic fluid from either NDV strain Lasota or APMV-8 infected SPF eggs. Four HA units of NDV strain Lasota or APMV-8 and 1% chicken red blood cells were used for the HI test. The resulting HI titers show that the serum of the chickens contained HI antibodies directed against NDV but no detectable antibodies against APMV-8 virus.

Table 7. Infection/vaccination of one-day-old broiler chickens

Treatment	Group 1 (ten one-day-old chickens)	Group 2 (control) (ten one-day-old chickens)
Day 1: vaccination with APMV-8 strain	Yes	No
Day 14: HI test	Yes	Yes
Day 14: second vaccination with APMV-8 strain (boost)	5 chickens (group 1-1): 2nd vaccination/ 1st vaccination. 5 chickens (group 1-2): no 2nd vaccination/1st vaccination	5 chickens (group 2-1): 2nd vaccination 5 chickens (group 2-2): not vaccinated
Day 28: HI test	Yes	Yes

[0111] At day 1, group 1 of 10 chickens were infected with via the nasal route with 10^6 EID_{50} of APMV-8 strain, group 2 of 10 chickens were not infected serving as control.

[0112] Fourteen days after infection (day 14), the chickens were bled and the obtained serum samples were analyzed again for the presence of HI antibodies directed against NDV and APMV-8 (Figure 20). The result showed that the APMV-8 vaccinated chickens showed HI titers using APMV-8 as antigen. The APMV-8 specific HI titers were between 128 and 2048. The HI titers against NDV declined to a HI titer below 16, thus they are not considered as NDV positive. The result showed that chickens maternal derived antibodies directed against NDV did not omit the infection with APMV-8, thus interference of such antibodies with APMV-8 vaccination is unlikely.

[0113] Fourteen days after infection (day 14), the chickens in group 1 and group 2 were split. Five chickens in each of group 1 (group 1-1) and group 2 (group 2-1) were again infected with 10^6 EID_{50} of APMV-8 strain (table 7), the remaining five chickens in each group (group 1-2 and group 2-2) were not infected. This experiment is designed to investigate where a later infection of chickens would have an effect on the infection and whether a second infection (boost vaccination) would increase the antibody titer. Fourteen days later (day 28), all chickens were bled again and the serum was investigated for the presence of APMV-8 and NDV antibodies. The serum titers (Figure 21) showed that a first vaccination at day 14 (group 2-1) did induce APMV-8 specific antibody titers ranging from 32 to 512. In chickens vaccinated only at day 1 (group 1-2), the antibody titers declined to titers in a range from 128 to 512. In chickens which have been vaccinated at day 1 and day 14 (group 1-1), the APMV-8 specific antibody titer did not increase, sugesting that the virus used for the second infection was neutralized by APMV-8 specific antibodies induced by the first infection. The serum of the non-vaccinated controls (group 2-2) did not contain APMV-8 specific HI antibodies. At day 28, the NDV antibodies declined further, only 11 chickens out of the 20 chickens showed any HI titers with the NDV antigen whereas at day 14 fourteen chickens showed low antibody titers against NDV.

Example 5 *In ovo* vaccination of embryonated SPF eggs

[0114] This study was performed to test if an *in ovo* vaccination with APMV-8 would result in an antibody response in chickens and if *in ovo* vaccination would interfere with hatchability and livability.

[0115] In study 1,108 SPF eggs were *in ovo* vaccinated with APMV-8 virus strain using the INOVOJECT (Pfizer Animal Health, NY, USA) at day 18 of incubation. The virus was diluted in 0.9% sterile NaCl saline. The back titration of the diluted virus revealed a titer of $10^{5.5}$ EID_{50} /100µl. As control, 108 eggs were inoculated with 0.9% sterile NaCl saline. The volume for the inoculation was 100µl per egg. Eighty chickens hatched from the control group and forty-five chickens hatched from the APMV-8 vaccinated group. Ten chickens from each group were transferred to one Horsefall-Bauer unit. In addition, the chickens of the APMV-8 vaccinated group and five chickens of the control group were co-mingled in a Horsefall-Bauer unit to test transmission of APMV-8 after vaccination. Water and feed were provided *ad libitum.* Fourteen and twenty-eight days after hatch, blood samples were taken and tested for the presence of HI antibodies directed against APMV-8 using 4 HA units and 1% of chicken red blood cells. The results (Figure 22) showed that *in*

ovo vaccination at day 18 of incubation resulted in an immune response as indicated by the presence of HI titers in the tested serum samples. Fourteen days after hatch, an HI titer from 256 to 4048 was observed in the *in ovo* vaccinated group. In the serum of the contact chickens, an HI titer from 256 to 2048 was observed 14 days after contact with chickens from the vaccinated group, indicating shedding of the vitus used for vaccination. The control group did not show any HI titer specific for APMV-8. Fourteen days later, the chickens were bled again and showed titers from 256 to 4096 in the APMV-8 vaccinated group and 256 to 1024 in the APMV-8 contact group. The control group showed no presence of APMV-8 HI antibodies.

[0116] In study 2, 88 SPF (specific pathogen free) eggs were *in ovo* vaccinated using the INOVOJECT at day 19 of incubation. The APMV-8 virus strain was diluted in 0.9% sterile NaCl saline. The titer of the virus was $10^{5.75}$ EID_{50}/100µl as observed after back titration of the diluted virus. As control, 88 SPF eggs were inoculated with 0.9% sterile NaCl saline. The volume for the inoculation was 100µl per egg. Seventy-four chickens hatched from the control group (NaCl) and seventy-six chickens hatched from the APMV-8 vaccinated group. Ten chickens from each group were transferred to one Horsefall-Bauer unit. Water and feed were provided *ad libitum.* Fourteen days after hatch, blood samples were taken and tested for the presence of HI antibodies directed against APMV-8 using 4 HA units and 1% of chicken red blood cells. The results (Figure 23) showed that *in ovo* vaccination at day 19 of incubation resulted in an immune response with HI titers specific for APMV-8. Fourteen days after hatch, an HI titer from 256 to 4048 was observed in the APMV-8 *in ovo* vaccinated group. The control group did not show any HI titer specific for APMV-8. The chickens were bled again at day 28 after hatch. The HI titers for the APMV-8 vaccinated group ranged from 512 to 4096 (Figure 23) whereas the sera of the control chickens were still APMV-8 negative.

[0117] In a third study, 108 SPF eggs in group 1 and group 2 were *in ovo* vaccinated using the INOVOJECT at day 18 of incubation with $10^{3.5}$ EID_{50} and $10^{4.5}$ EID_{50}, respectively. The APMV-8 virus strain was diluted in 0.9% sterile NaCl saline. In a third group 108 SPF eggs were inoculated with 0.9% sterile NaCl saline as control. Eighty-three chickens hatched from group 1, seventy-nine chickens hatched from group 2, and eighty-eight chickens hatched from group 3 (see table 8). After hatch, ten chickens from each group were transferred to one Horsefall-Bauer unit. Water and feed were provided *ad libitum.* After hatch, ten chickens from group 3 were vaccinated subcutaneously in the neck region with a volume of 100 µl 10^6 EID_{50} APMV-8 virus. Fourteen days after hatch, blood samples were taken and tested for the presence of HI antibodies directed against APMV-8 using 4 HA units and 1% of chicken red blood cells (CRBS). The results (Figure 24) showed that *in ovo* vaccination at day 18 of incubation resulted in an immune response with HI titers specific for APMV-8. Fourteen days after hatch, an HI titer from 4096 to 16384 was observed in the APMV-8 *in ovo* vaccinated groups. The control group did not show any HI titer specific for APMV-8. The group subcutaneously vaccinated with APMV-8 showed a seroconversion with a titer ranging from 64 to 4096. The chickens were bled again at day 28 after hatch and tested for the presence of APMV-8 specific HI antibodies. The HI titer at four weeks after hatch decreased and ranged between 512 and 4096. The control group did not show any HI titer specific for APMV-8. The HI titer in the group which was subcutaneously vaccinated showed HI titers ranging between 32 and 256.

Table 8

	Group 1	Group 2	Group 3 (control)
SPF eggs	108	108	108
Hatched chicken	83	79	88
Vaccination with APMV-8 at day 18 of incubation	$10^{3.5}$ EID_{50} 100µl per egg	$10^{4.5}$ EID_{50} 100µl per egg	0.9% sterile NaCl saline

Example 6 Development of reverse genetics of the APMV-8 strain and generation of APMV-8 mutants expressing heterologous genes

Construction of the expression Plasmids containing the NP, P, and L genes of APMV-8

[0118] For the establishment of a reverse genetics system for paramyxoviruses, the establishment of plasmids expressing the proteins involved in viral RNA replication is essential. The open reading frames (ORF) of three APMV-8 proteins (nucleoprotein NP, phosphoprotein P, RNA dependent RNA polymerase protein or protein L) were cloned into the eukaryotic expressions vector pcDNA3 (Invitrogen, California, USA). To this end, the RNA of allantoic fluid containing APMV-8 was purified using the High Pure RNA Isolation Kit (Roche, Basel, Switzerland). The purified RNA was used for reverse transcription polymerase chain reaction (RT-PCR) using the Titan One Tube RT-PCR Kit (Roche). The ORFs of the proteins were amplified using the appropriate primer pairs: [NP (NP-FP, NP-RP), P (P-FP, P-RP), L (L-FP, L-RP), see table 9]. The reactions products were separated on a 0.7% agarose gel and eluted from the gel using the QIAquick

Gel Extraction Kit (Qiagen, Hilden, Germany) following the protocol provided by the manufacturer. The RT-PCR fragments were incubated with the appropriate restriction enzymes (NP and P with Eco RI/NotI; L with Kpn I/NotI), gel eluted again and ligated into the eukaryotic expression vector pcDNA3 cleaved with the appropriate restriction enzymes. The ligation reactions were transformed into Top10F cells (Invitrogen) and plasmid DNA harvested from the Top10F cells was digested with the appropriate restriction enzymes (see above). Plasmids containing DNA fragments (pcDNA-NP, pcDNA-P, pcDNA-L) with the appropriate size were sequenced.

Table 9. Primer for amplification of the genes for the proteins of the RNP complexes

Primer name	Primer sequence[a]	Orientation[b]	Position[c]	SEQ ID NO:
NP-FP-pc3	Eco RI ccGAATTC*ATG*TCATCTGTGTTCAATGAGTATCAGG	sense	141-168	41
NP-RP-pc3	Not I ccGCGGCCGC*TTA*CCATTCTAGCCCGTTCTCGTATG	antisense	1501-1526	42
P-FP-pc3	Eco RI ccGAATTC*ATG*GATTTCGCCAATGATGAAG	sense	1693-1714	43
P-RP-pc3	Not I ccGCGGCCGC*TTA*CGCATTATATATTGCCTGCTTGACTCG	antisense	2881-2910	44
L-FP-pc3	Kpn I ccGGTACC*ATG*GATATAAAACAAGTTGACCTG	sense	8292-8320	45
L-RP-pc3	Not I ccGCGGCCGC*TTA*TTTCAACTTGATGATTGCACCG	antisense	14989-15013	46

[a] The primer sequence contains the restriction enzyme cleavage sites used for cloning. The restriction sites are bold and identified. The start and stop codons are highlighted by italics. Virus specific sequences are underlined.
[b] The orientation of the primer sequence in accordance with the viral messenger RNA.
[c] The position are the virus specific sequences in the full length genome as shown.

Construction of a plasmid containing the full length genome of APMV-8

[0119] For the generation of a plasmid containing the full length APMV-8 genome, the cDNA genome of the virus was synthesized (Genscript, New York, USA) based on the generated consensus sequence in two different parts (5'-FLG, 3'-FLG, see Figure 25). The 5'-part (5'-FLG, SEQ ID NO:47) of the viral sequence was synthesized from nucleotide 1-5564. Preceding the APMV-8 sequence is a sequence cassette consisting of the CMV-IE promoter, followed by a restriction enzyme cleavage sequence for XmaI (for possible subsequent cloning procedures) and the hammerhead ribozyme sequence. At the 5'-end and the 3'-end of the sequence, restriction enzyme cleavage sites for Not I and SacII were added, respectively. The synthesized 3'-part (3'-FLG, SEQ ID NO:48) of the sequence (nucleotide 5503-15342) is followed by the hepatitis delta ribozyme sequence and poly-A signal sequence of the bovine growth hormone. For cloning purpose, the sequence for the Not I restriction enzyme was added at the 5'- end of 3'-FLG and the sequence for the Sac II restriction enzyme was added at the 3'-end of the sequence. Within the overlapping parts of 5'-FLG and 3'-FLG (nucleotide 5503-5564), the sequence for a unique restriction enzyme (Bmt I) was located which cleaves at nucleotide 5541 of the full length sequence. Both parts of the DNA (5'-FLG, 3'-FLG) were ligated separately into the plasmid pUC57 (Genscript) resulting in the plasmids pUC57/5'-FLG and pUC57/3'-FLG. To clone both fragments together, pUC57/5'-FLG was cleaved with BmtI and Sac II and the 5'-FLG-containing plasmid was gel eluted. In parallel, pUC57/3'-FLG was cleaved with the same enzymes and the fragment 3'-FLG was eluted. The 3'-FLG was subsequently ligated into 5'-FLG-containing plasmid to obtain a plasmid which contains the full length cDNA sequence of the APMV-8 genome under the control of the CMV-IE promoter (pUC57-FL-APMV-8).

Construction of the plasmid containing the minigenome of APMV-8

[0120] The plasmid containing all functional elements of a minigenome for APMV-8 (pMG-APMV-8) was constructed using the method described by Conzelmann, et al. (J Virol. 68:713-719, 1994). Plasmid pMG-APMV-8 contains the trailer and leader region of the APMV-8 genome which is flanked by the T7 promoter and the antigenome hepatitis delta virus ribozyme sequence (Collins, et al., PNAS USA 88:9663-9667, 1991).The antigenome hepatitis delta virus ribozyme sequence is followed by a T7 transcription terminator sequence. Between the trailer and leader region the coding sequence of the enhanced green fluorescent protein in antisense orientation is located. Preceding the trailer sequence and immediate after the T7 promoter three additional G residues are located. The insert is flanked by the restriction enzyme cleavage sites Eco RI and Not I and was cloned blunt end into the plasmid pUC57. This construct was subcloned into the plasmid pUC18. To this end, plasmid pMG-APMV-8 then was cleaved with Eco RI and Hind III and the appropriate fragment was gel eluted and ligated into the appropriately cleaved plasmid pUC18 to obtained puC18-MG-APMV-8. The presence of the insert was confirmed by sequencing.

Generation of an expression plasmid allowing the expression of the T7 polymerase

[0121] For the generation of a plasmid encoding the T7 DNA dependent RNA polymerase (T7 polymerase) the coding sequence (GenBank accession number AY264778) was synthesized by Genscript. The T7 polymerase sequence (SEQ ID NO:49) was modified for optimization of the codon usage for expression in a eukaryotic system and to remove possible splice donor/acceptor sites in the sequence. The T7 polymerase encoding sequence was flanked by an EcoRI (5') and NotI (3') site. The synthesized fragment was cloned blunt end into the vector pUC57 (pCU57-T7). This plasmid was cleaved with EcoRI/NotI and the T7 polymerase-encoding fragment was gel eluted. The fragment was then cloned into the eukaryotic expressions vector pcDNA3 (Invitrogen) to obtain pcDNA3-T7. The presence of the fragment in the vector pcDNA3-T7 was verified by sequencing.

Generation of a plasmid for the expression of the enhanced green fluorescent protein with the use of an internal ribosomal entry site under the control of a T7 promoter.

[0122] To test the functionality of the T7 polymerase, the open reading frame of the enhanced green fluorescent protein (EGFP) was amplified by PCR using the plasmid pEGFP-N1 (Clontech, California, USA) and the primer pair:

EGFP-FP (CCGGATCCATGGTGAGCAAGGGCGAGGAGCTG) SEQ ID NO:50 and
EGFP-RP (CCGCGGCCGCTTACTTGTACAGCTCGTCCATGCCG) SEQ ID NO:51

[0123] The obtained PCR fragment was gel eluted and incubated with the restriction enzymes BamHI and NatI. The reaction product was gel eluted and ligated into the appropriately cleaved vector pCITE 4A (Novagen). The obtained plasmid (pCITE4A-EGFP) was used for subsequent experiments. Plasmids pCITE4A-EGFP and pcDNA3-T7 were transfected alone or in combination into the chicken cell line DF1 grown in 24-well-plates using Lipofectin 2000 (Invitro-

gen). Twenty four hours after transfection, the medium was removed and sterile phosphate buffered saline (PBS) was added. The cells were evaluated using the inverted fluorescence microscope Axiovert 40 CFL (Zeiss, Jena, Germany). Green fluorescence was only observed in wells of the tissue culture plate which was co-transfected with both plasmids. This result indicates that both plasmids, pCITE4A-EGFP andpcDNA3-T7, were functional.

Validation of the functionality of the expressed viral proteins NP, P, and L using the minigenome plasmid

[0124] DF1 cells were co-transfected with pcDNA3-T7, pUC18-MG-APMV-8, pcDNA-NP, pcDNA-P, and pcDNA-L to validate the functionality of the expressed NP, P and L proteins. Twenty four hours after transfection, the medium was removed and sterile phosphate buffered saline (PBS) was added. The cells were evaluated using the inverted fluorescence microscope Axiovert 40 CFL (Zeiss, Jena, Germany). Green fluorescence was only observed in wells of the tissue culture plate which was co-transfected with the 5 plasmids. This result indicates that the expressed viral proteins NP, P and L were functional to transcribe the APMV-8 minigenome into mRNA and express the EGFP protein encoded by pUC18-MG-APMV-8.

Rescue of AMPV8 virus from plasmid containing the full length sequence of APMV-8

[0125] DF1 cells were co-transfected with pUC57-FL-APMV-8, pcDNA-NP, pcDNA-P, and pcDNA-L. After 48 to 96 hours, the supernatants of the DF1 cells were inoculated in 10-day-old embryonated eggs to propagate the virus. After 3 to 5 days, the allantoic fluid was harvested and tested for hemagglutination activity (HA) using 1% chicken red blood cells. Allantoic fluid tested positive for HA activity was used for three procedures. 1) DF1 cells were infected with the allantoic fluid and tested 36 hours after infection with an APMV-8 specific antiserum for the presence of APMV-8 protein expression in an indirect immunofluorescence assay. 2) The allantoic fluid was tested for APMV-8 specificity using an APMV-8 specific chicken serum (provided by the National Central Veterinary Laboratory, Ames, Iowa, USA) by an hemagglutination inhibition assay. 3) The rescue virus was identified by RT-PCR using APMV-8 specific oligonucleotides. The absence of viral cDNA was verified by omitting the RT step during the reaction. Samples tested positive in all three assays were further propagated in embryonated SPF chicken eggs.

Propagation of APMV-8 in cells other than chicken origin

[0126] Cells from different species [hamster (Baby hamster kidney cells, BHKL-21 cells), monkey (Vero cells, cell line with the origin of the kidney of an African green monkey), and canine (Madin-Darby canine kidney cells, MDCK), and quail (Quail muscle cell line QM7)] were grown in 24 well tissue culture plates and infected with a multiplicity of infection of 0.01. The cells were fixed with ice cold ethanol 24 hours after infection and analyzed for the presence of APMV-8 specific proteins by indirect immunofluorescence using an APMV-8 specific antiserum from an APMV-8 infected SPF chicken. The binding of the antibodies was visualized by using a goat anti-chicken IgY specific FITC conjugate. Non-infected cells were used as negative control. Only in the APMV-8 infected cells was green fluorescence observed. This indicated that APMV-8 was able to infect cells from species other than chicken.

[0127] The replication of APMV-8 was increased in presence of trypsin. MDCK cells were infected with APMV-8 as described above. After infection the cells were rinsed with serum-free medium and either overlaid with trypzin-containing serum-free medium in a concentration of lug/ml or with serum-free medium only. Twenty four, forty eight, and ninety six hours after infection the cell supernatants were removed and the TCID50 was determined on DF1 cells using indirect immunofluorescence as described above. The obtained data indicated that in presence of trypsin APMV-8 replicated to a higher titer than in absence of this enzyme (Figure 19B).

[0128] The results of this example showed that, like AMPV-1, APMV-8 is able to penetrate into cells of different species and to initiate its replication cycle. It is therefore a suitable vector for multiple species.

Production of recombinant APMV-8 virus expressing foreign genes using the reverse genetics system

[0129] For the generation of a recombinant APMV-8 virus (viral vector) expressing the hemagglutinin (HA) gene of a highly pathogenic avian influenza (HPAI), the coding sequence for the HA gene of HPAI of the H5 or H7 subtype virus is inserted in the non-essential regions, for example, between the M and F genes or between the P and M genes of the APMV-8 genome in the plasmid containing the full length APMV-8 genome. To this end the coding sequence of the hemagglutinin open reading frame is flanked by all the necessary regulatory sequences of the F gene which includes the gene start sequence, the 5' non-coding sequence, the 3' non-coding sequence and the gene stop sequence. The construct is synthesized in a way that the restriction enzyme cleavage sites Bsu 36I and Nhe I are used for the ligation of the appropriate fragment into the existing plasmid containing full length APMV-8 genome due to their uniqueness in the plasmid construct. The resulting plasmid is designated transcription plasmid which contains the hemagglutinin gene

in the nonessential region of the full length APMV-8 genome. Using this approach the coding sequences of a variety of viral and bacterial antigen can be cloned into the backbone of the APMV-8 sequence. Other possible antigens which could be inserted into the APMV-8 genome are the fusion protein of the Newcastle disease virus, the S protein of avian bronchitis virus, other hemagglutinin genes from non-H5 and non-H7 avian influenza virus, the chicken anemia virus structural protein gene VP1, glycoprotein genes from infectious laryngotracheitis virus.

Example 7 Vaccination of animals

[0130] The animals are vaccinated with one, two administrations or a prime-boost regime of the composition or vaccine containing the recombinant APMV-8 virus (viral vector) as described in example 6. For chickens/avian, various administrations are performed, for example, *in ovo* administration at D18 or D19, subcutaneous (SC) at one-day-old, or mucosal administration (spray, drinking water, eye drop) at different ages. The dose is between 3 and 7 log10 (preferably 4-6 log10 EID50). For mammals, mucosal route (intra-nasal, intra-ocular, oral) or parenteral (IM, SC, needle-free, transdermal or intra-dermal) is used. The dose ranges from 5 to 9 log (preferably 6-8 log). Two administrations are usually performed at 3-4 weeks interval. Heterologous prime-boost (for instance, boost with proteins) would be also advantageous.

[0131] The protective efficacy induced by the composition or vaccine is evaluated against the specific pathogen challenge in the animals. The protective effect is evaluated by clinical observations and/or viral load of the specific pathogen in tissues, blood or mucosal swabs. The blood samples from the vaccinated animals are taken at various stages and tested for serology. The results show that the composition or vaccine of the present invention is immunogenic and provides protection in the vaccinated animals.

[0132] All documents cited or referenced herein ("herein cited documents"), and all documents cited or referenced in herein cited documents, together with any manufacturer's instructions, descriptions, product specifications, and product sheets for any products mentioned herein may be employed in the practice of the invention.

References:

[0133]

1. Alexander, 1988. Newcastle disease, p. x, 378 p. In D. J. Alexander (ed.), Developments in veterinary virology. Kluwer Academic, Boston.

2. Alexander, Characterization of viruses which represent further distinct serotypes (PMV-8 and PMV-9) of avian paramyxoviruses. Arch Virol 78:29-36.

3. Alexander, et al., 1979. Properties of a newly isolated, serologically distinct avian paramyxovirus. Arch Virol 60:105-13.

4. Alexander, 2003. Newcastle Disease, other Paramyxoviruses, and Pneumovirus Avian Paramyxoviruses 2-9, p. 63-99. In Y. M. Saif (ed.), Diseases of poultry, 11th ed. Iowa State Press, Ames, Iowa.

5. Andral, et al., 1984. Isolation of avian paramyxovirus 2 and 3 from turkeys in Brittany. Vet Rec 114:570-1.

6. Bankowski, et al., 1981, Effect of paramyxovirus yucaipa on fertility, hatchability, and poult yield of turkeys. Avian Dis 25:517-20.

7. Bankowski, et al., 1960. Isolation of an Unidentified Agent from the Respiratory Tract of Chickens. Science 132:292-293.

8. Bradshaw, et al., 1979. The Epidemiology of Yucaipa Virus in Relationship to the Acute Respiratory Disease Syndrome in Turkeys. Avian Diseases 23:539-542.

9. Capua, et al., 2004. Isolation of an avian paramyxovirus type 9 from migratory waterfowl in Italy. Vet Rec 155:156.

10. Chambers, et al., 1988. Protection of chickens from lethal influenza infection by vaccineexpressed hemagglutinin. Virology 167:414-421.

11. Collins, P. L., et al., 1991. Rescue of synthetic analogs of respiratory syncytial virus genomic RNA and effect of truncations and mutations on the expression of a foreign reporter gene. Proc. Natl. Acad. Sci. USA 88:9663-9667

12. Conzelmann KK, and Schnell M., 1994. Rescue of synthetic genomic RNA analogs of rabies virus by plasmid-encoded proteins. J Virol. 68:713-719

13. Darteil, R., M. Bublot, E. Laplace, J.F. Bouquet, J.C. Audonnet and M. Riviere (1995). Herpesvirus of turkey recombinant viruses expressing infectious bursal disease virus (IBDV) VP2 immunogen induce protection against an IBDV virulent challenge in chickens. Virology, 211, 481-490.

14. de Leeuw, et al., 1999. Complete nucleotide sequence of Newcastle disease virus: evidence for the existence of a new genus within the subfamily Paramyxovirinae. J Gen Virol 80:131-136.

15. Fleury, et al., 1979. Isolation of twenty-three Yucaipa-like viruses from 616 wild birds in Senegal, West Africa. Avian Dis 23:742-4.

16. Gao, et al., (2006). Protection of mice and poultry from lethal H5N1 avian influenza virus through adenovirus-based immunization. J Virol 80:1959-1964.
17. Ge, et al., (2007) Newcastle disease virus-based live attenuated vaccine completely protects chickens and mice from lethal challenge of homologous and heterologous H5N1 avian influenza viruses. Journal of Virology, 81(1), 150-158.
18. Goodman, et al., 1988. Isolation of avian paramyxovirus-2 from domestic and wild birds in Costa Rica. Avian Dis 32:713-7.
19. Gough, et al., 1984. Avian paramyxovirus type 4 isolated from a ringed teal (Calonetta leucophrys). Vet Rec 115:653.
20. Hoelscher, et al., (2008). A broadly protective vaccine against globally dispersed clade 1 and clade 2 H5N1 influenza viruses. J Infect Dis. 197:1185-1188.
21. Huang, et al., (2004) A recombinant Newcastle Disease Virus (NDV) expressing VP2 protein of Infectious Bursal Disease Virus (IBDV) protects against NDV and IBDV. Journal of Virology, 78, 10054-10063.
22. Hunt, et al., (1988). Retrovirus-expressed hemagglutinin protects against lethal influenza virus infections. J Virol 62:3014-3019.
23. Inoue K, Shoji Y, Kurane I, Iijima T, Sakai T, Morimoto K. (2003). An improved method for recovering rabies virus from cloned cDNA. J Virol Methods. 107:229-236.
24. Krishnamurthy, et al., 1998. Nucleotide sequences of the trailer, nucleocapsid protein gene and intergenic regions of Newcastle disease virus strain Beaudette C and completion of the entire genome sequence. J Gen Virol 79:2419-2424.
25. Krishnamurthy, S., Huang, Z. & Samal, S. K. (2000) Recovery of a virulent strain of Newcastle disease virus from cloned cDNA: expression of a foreign gene results in growth retardation and attenuation. Virology, 278, 168-182.
26. Lamb, et al., 2007. Paramyxoviridae: The viruses and Their Replication, p. 1449-1496. *In* B. N. Fields, D. M. Knipe, and P. M. Howley (ed.), Fields' virology 5th ed. Wolters Kluwer Health/Lippincott Williams & Wilkins, Philadelphia.
27. Lang, G., A. Gagnon, and J. Howell. 1975. The occurrence of Paramyxovirus yucaipa in Canadian poultry. Can Vet J 16:233-7.
28. Lipkind, et al., 1982. Isolation of yucaipa-like avian paramyxovirus from a wild mallard duck (Anas platyrhinchos) wintering in Israel. Vet Rec 110:15-6.
29. Lipkind, et al., 1979. The isolation of yucaipa-like paramyxoviruses from epizootics of a respiratory disease in turkey poultry farms in Israel. Vet Rec 105:577-8.
30. Maldonado, et al., (1995) Serological survey for avian paramyxoviruses from wildfowl in aquatic habitats in Andalusia. Journal of Wildlife Diseases, 31(1), 66-69.
31. Mayo, et al., 2002. A summary of taxonomic changes recently approved by ICTV. Arch Virol 147:1655-63.
32. Nayak B, et al., (2008). Molecular characterization and complete genome sequence of avian paramyxovirus type 4 prototype strain duck/Hong Kong/D3/75. Virol J. 20;5:124.
33. Park, et al., (2006) Engineered viral vaccine constructs with dual specificity: Avian influenza and Newcastle disease. Proceedings of the National Academy of Sciences, 103(21), 8203-8208.
34. Peeters, et al., (1999) Rescue of Newcastle disease virus from cloned cDNA: evidence that cleavability of the fusion protein is a major determinant for virulence. Journal of Virology, 73(6), 5001-5009.
35. Redmann, et al., 1991. [Isolation of a paramyxovirus-3 from turkeys with respiratory tract disease in Germany]. Dtsch Tierarztl Wochenschr 98:138-41.
36. Reed, et al., 1938. A SIMPLE METHOD OF ESTIMATING FIFTY PER CENT ENDPOINTS. Am. J. Epidemiol. 27:493-497.
37. Römer-Oberdörfer, et al., (1999) Generation of recombinant lentogenic Newcastle disease virus from cDNA. Journal of General Virology, 80,2987-2995.
38. Rosenberger, et al., (1974) Isolation of Newcastle disease and type-A influenza viruses from migratory waterfowl in the Atlantic flyway. Avian Diseases, 18(4), 610-613.
39. Saif, et al., 1997. Natural and Experimental Infection of Turkeys with Avian Paramyxovirus-7. Avian Diseases 41:326-329.
40. Shihmanter, et al., 1998. Isolation of avian serotype 3 paramyxoviruses from imported caged birds in Israel. Avian Dis 42:829-31.
41. Shihmanter, et al., 1998. Avian paramyxoviruses serotype 3 isolated from captive birds in Israel: clinical signs, pathology, and antigenic characterization. Avian Dis 42:418-22.
42. Shortridge, et al., 1980. Isolation and properties of viruses from poultry in Hong Kong which represent a new (sixth) distinct group of avian paramyxoviruses. J Gen Virol 49:255-262.
43. Schultz-Cherry, et al., (2000). Influenza virus (A/HK/156/97) hemagglutinin expressed by an alphavirus replicon system protects chickens against lethal infection with Hong Kong-origin H5N1 viruses. Virology 278:55-59.

44. Stallknecht, et al., (1991) Avian paramyxoviruses from migrating and resident ducks in coastal Louisiana. Journal af Wildlive Diseases. 27:123-128.
45. Stanislawek, et al., (2002) Avian paramyxoviruses and influenza viruses isolated from mallard ducks (Anas platyrhynchos) in New Zealand. Archives of Virology, V147, 1287-1302.
46. Tang M, et al., 2002. Recombinant adenovirus encoding the HA gene from swine H3N2 influenza virus partially protects mice from challenge with heterologous virus: A/HK/I/68 (H3N2). Arch Virol 147:2125-2141.
47. Taylor, et al., (1998). Protective immunity against avian influenza induced by a fowlpox virus recombinant. Vaccine 6:504-508.
48. Toro, et al., (2007). Protective avian influenza in ovo vaccination with non-replicating human adenovirus vector. Vaccine 25:2886-2891.
49. Tumova, et al., 1979. A hitherto unreported paramyxovirus of turkeys. Res Vet Sci 27:135-40.
50. Tumova, et al., 1989. Further evidence of the circulation of PMV-4 and influenza viruses with N2-1957 enzyme in the migratory waterfowls. Acta Virol 33:573-6.
51. Veits, et al., (2003). Deletion of the non-essential UL0 gene of infectious laryngotracheitis (ILT) virus leads to attenuation in chickens, and UL0 mutants expressing influenza virus haemagglutinin (H7) protect against ILT and fowl plague. J Gen Virol 84:3343-3352.
52. Veits, et al., (2006) Newcastle disease virus expressing H5 hemagglutinin gene protects chickens against Newcastle disease and avian influenza. Proceedings of the National Academy of Sciences, 103(21), 8197-8202.
53. Webster, et al., 1976. Ortho- and paramyxoviruses from migrating feral ducks: characterization of a new group of influenza A viruses. J Gen Virol 32:217-25.
54. Yamane, et al., 1982. Characterization of avian paramyxoviruses isolated from feral ducks in northern Japan: the presence of three distinct viruses in nature. Microbiol Immunol 26:557-68.
55. Zhang, et al., 2007. Serological survey on prevalence of antibodies to avian paramyxovirus serotype 2 in China. Avian Dis 51:137-9.
56. Zhang, et al., 2006. Isolation, identification, and comparison of four isolates of avian paramyxovirus serotype 2 in China. Avian Dis 50:386-90.
57. Zou, et al., 2005. Complete Genome Sequence and Biological Characterizations of A Novel Goose Paramyxovirus-SF02 Isolated in China. Virus Genes 30:13-21.

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[0134]

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Ala Glu Ile Pro Val Cys Val Thr Leu Ser Gln Asp Pro Gly Glu Arg
        35                  40                  45

Trp Ser Leu Ala Cys Leu Asn Ile Arg Trp Leu Ala Ser Asp Ser Ser
    50                  55                  60

Thr Thr Pro Met Lys Gln Gly Ala Ile Leu Ser Leu Leu Ser Leu His
65                  70                  75                  80

Ser Asp Asn Met Arg Ala His Ala Thr Leu Ala Ala Arg Ser Ala Asp
                85                  90                  95

Ala Ser Leu Thr Ile Leu Glu Val Asp Glu Val Asp Ile Ser Asn Ser
            100                 105                 110

Leu Ile Lys Phe Asn Ala Arg Ser Gly Val Ser Asp Lys Arg Ser Asn
        115                 120                 125

Gln Leu Leu Ala Ile Ala Asp Asp Ile Pro Lys Ser Cys Ser Asn Gly
    130                 135                 140

His Pro Phe Leu Asp Thr Asp Ile Glu Thr Arg Asp Pro Leu Asp Leu
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Ser Glu Thr Ile Asp Arg Leu Gln Gly Ile Ala Ala Gln Ile Trp Val
                165                 170                 175

Ser Ala Ile Lys Ser Met Thr Ala Pro Asp Thr Ala Ser Glu Ser Glu
            180                 185                 190

Ser Lys Arg Leu Ala Lys Tyr Gln Gln Gln Gly Arg Leu Val Lys Gln
        195                 200                 205

Val Leu Leu His Ser Val Val Arg Thr Glu Phe Met Arg Val Ile Arg
    210                 215                 220

Gly Ser Leu Val Leu Arg Gln Phe Met Val Ser Glu Cys Lys Arg Ala
225                 230                 235                 240

Ser Ala Met Gly Gly Asp Thr Ser Arg Tyr Tyr Ala Met Val Gly Asp
                245                 250                 255

Ile Ser Leu Tyr Ile Lys Asn Ala Gly Leu Thr Ala Phe Phe Leu Thr
            260                 265                 270

Leu Lys Phe Gly Val Gly Thr Gln Tyr Pro Thr Leu Ala Met Ser Val
        275                 280                 285

Phe Ser Ser Asp Leu Lys Arg Leu Ala Ala Leu Ile Arg Leu Tyr Lys
    290                 295                 300

Thr Lys Gly Asp Asn Ala Pro Tyr Met Ala Phe Leu Glu Asp Ser Asp
305                 310                 315                 320

Met Gly Asn Phe Ala Pro Ala Asn Tyr Ser Thr Met Tyr Ser Tyr Ala
                325                 330                 335

Met Gly Ile Gly Thr Ile Leu Glu Ala Ser Val Ser Arg Tyr Gln Tyr
            340                 345                 350

Ala Arg Asp Phe Thr Ser Glu Asn Tyr Phe Arg Leu Gly Val Glu Thr
        355                 360                 365

Ala Gln Ser Gln Gln Gly Ala Phe Asp Glu Arg Thr Ala Arg Glu Met
    370                 375                 380

Gly Leu Thr Glu Glu Ser Lys Gln Gln Val Arg Ser Leu Leu Met Ser
385                 390                 395                 400

Val Asp Met Gly Pro Ser Ser Ile His Glu Pro Ser Arg Pro Ala Phe
                405                 410                 415
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Ile Ser Gln Glu Glu Asn Arg Gln Pro Ala Gln Asn Leu Ser Asp Thr
            420                 425                 430

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

Thr Thr Gly Arg Pro Pro Val Ser Gln Gly Asn Thr Arg Asn Leu Thr
        35                  40                  45

Asp Leu Trp Glu Lys Glu Thr Ala Ser Gln Thr Lys Thr Pro Ala Gln
    50                  55                  60

Ser Thr Gln Thr Thr Gln Val Gln Ser Asp Glu Asn Glu Glu Gly Glu
65                  70                  75                  80

Ile Lys Ser Glu Ser Thr Asp Gly His Ile Arg Gly Thr Val Asn Gln
                85                  90                  95

Ser Glu Gln Val Pro Glu Gln Asn Gln Ser Arg Ser Ser Pro Gly Asp
            100                 105                 110

Asp Leu Asp Arg Ala Leu Asn Lys Leu Glu Gly Arg Ile Asn Leu Ile
        115                 120                 125

Ser Ser Met Asp Lys Glu Ile Lys Lys Gly Pro Arg Ile Gln Asn Leu
    130                 135                 140

Pro Gly Ser Gln Ala Ala Thr Gln Gln Ala Thr His Pro Leu Ala Gly
145                 150                 155                 160

Asp Thr Pro Asn Met Gln Ala Gln Thr Lys Ala Leu Ala Lys Pro His
                165                 170                 175

Gln Glu Ala Ile Asn Pro Gly Asn Gln Asp Thr Gly Glu Ser Ile His
            180                 185                 190

Leu Pro Pro Ser Met Ala Pro Pro Glu Ser Leu Val Gly Ala Ile Arg
        195                 200                 205

Asn Ala Pro Gln Phe Val Pro Asp Gln Ser Met Thr Asn Val Asp Ala
    210                 215                 220
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```
Gly Ser Val Gln Leu His Ala Ser Cys Ala Glu Met Ile Ser Arg Met
225                 230                 235                 240

Phe Val Glu Val Ile Ser Lys Leu Asp Lys Leu Glu Ser Arg Leu Asn
                245                 250                 255

Asp Ile Ala Lys Val Val Asn Thr Thr Pro Leu Ile Arg Asn Asp Ile
            260                 265                 270

Asn Gln Leu Lys Ala Thr Thr Ala Leu Met Ser Asn Gln Ile Ala Ser
        275                 280                 285

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

Met Lys Ser Val Thr Lys Lys Ala Ala Val Val Ile Ala Gly Phe Gly
305                 310                 315                 320

Asp Asp Pro Thr Gln Ile Ile Glu Glu Gly Ile Met Ala Lys Asp Ala
                325                 330                 335

Leu Gly Lys Pro Val Pro Pro Thr Ser Val Ile Ser Ala Lys Ala Gln
            340                 345                 350

Thr Ser Ser Gly Val Ser Lys Gly Glu Ile Glu Gly Leu Ile Ala Leu
        355                 360                 365

Val Glu Thr Leu Val Asp Asn Asp Lys Lys Ala Ala Lys Leu Ile Lys
    370                 375                 380

Met Ile Asp Gln Val Lys Ser His Ala Asp Tyr Ala Arg Val Lys Gln
385                 390                 395                 400

Ala Ile Tyr Asn Ala
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<223> APMV8 M gene

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<220>
<223> APMV8 M protein

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

Gln Asn Ala Lys Glu Ser Ser Ile Phe Val Thr Leu Tyr Gly Phe Ile
    50                  55                  60

Gln Ala Ile Lys Glu Ser Ser Asp Arg Ser Lys Phe Phe His Pro Lys
65                  70                  75                  80

Asp Asp Phe Lys Pro Glu Thr Val Thr Ala Gly Leu Val Val Val Gly
                85                  90                  95
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Ala Ile Arg Met Met Ala Asp Val Asn Thr Ile Ser Asn Asp Ala Leu
            100                 105                 110

Ala Leu Glu Ile Thr Val Lys Lys Ser Ala Thr Ser Gln Glu Lys Met
        115                 120                 125

Thr Val Met Phe His Asn Ser Pro Pro Ser Leu Arg Thr Ala Ile Thr
    130                 135                 140

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

Ala Ser Lys Leu Thr Ala Gly Val Gln Tyr Ile Phe Arg Pro Met Phe
                165                 170                 175

Val Ser Ile Thr Lys Leu His Asn Gly Lys Leu Tyr Arg Val Pro Lys
            180                 185                 190

Ser Ile His Ser Ile Ser Ser Thr Leu Leu Tyr Ser Val Met Leu Glu
        195                 200                 205

Val Gly Phe Lys Val Asp Ile Gly Lys Asp His Pro Gln Ala Lys Met
    210                 215                 220

Leu Lys Lys Val Thr Ile Gly Asp Ala Asp Thr Tyr Trp Gly Phe Ala
225                 230                 235                 240

Trp Phe His Leu Cys Asn Phe Lys Lys Thr Ser Ser Lys Gly Lys Pro
                245                 250                 255

Arg Thr Leu Asp Glu Leu Lys Thr Lys Val Lys Asn Met Gly Leu Lys
            260                 265                 270

Leu Glu Leu His Asp Leu Trp Gly Pro Thr Ile Val Val Gln Ile Thr
        275                 280                 285

Gly Lys Ser Ser Lys Tyr Ala Gln Gly Phe Phe Ser Ser Asn Gly Thr
    290                 295                 300

Cys Cys Leu Pro Ile Ser Arg Ser Ala Pro Glu Leu Gly Lys Leu Leu
305                 310                 315                 320

Trp Ser Cys Ser Ala Thr Ile Gly Asp Ala Thr Val Val Ile Gln Ser
                325                 330                 335

Ser Glu Lys Gly Glu Leu Leu Arg Ser Asp Asp Leu Glu Ile Arg Gly
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Ala Val Ala Ser Lys Lys Gly Arg Leu Gly Ser Phe His Pro Phe Lys
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<212> DNA
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<220>
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Val Ala Ser Ala Asn Glu Trp Gln Leu Ala Ala Tyr Thr Thr Ser Leu
        35                  40                  45

Ser Gly Thr Ile Ala Val Arg Phe Leu Pro Val Leu Pro Asp Asn Met
    50                  55                  60

Thr Thr Cys Leu Lys Glu Thr Ile Thr Thr Tyr Asn Asn Thr Val Asn
65                  70                  75                  80

Asn Ile Leu Gly Pro Leu Lys Ser Asn Leu Asp Ala Leu Leu Ser Ser
                85                  90                  95

Glu Thr Tyr Pro Gln Thr Arg Leu Ile Gly Ala Val Ile Gly Ser Ile
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Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu
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Lys Gln Ala Gln Asp Asn Ala Arg Asn Ile Leu Ala Leu Lys Glu Ala
    130                 135                 140

Leu Ser Lys Thr Asn Glu Ala Val Lys Glu Leu Ser Ser Gly Leu Gln
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Gln Thr Ala Ile Ala Leu Gly Lys Ile Gln Ser Phe Val Asn Glu Glu
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Gly Ile Lys Gln Gln Asp Val Asn Ser Leu Tyr Glu Ala Gly Leu Ile
                245                 250                 255

Thr Gly Gln Val Ile Gly Tyr Asp Ser His Tyr Gln Leu Leu Val Ile
            260                 265                 270

Gln Val Asn Tyr Pro Ser Ile Ser Glu Val Thr Gly Val Arg Ala Thr
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Glu Leu Val Thr Val Ser Val Thr Thr Asp Lys Gly Glu Gly Lys Ala
    290                 295                 300

Ile Val Pro Gln Phe Val Ala Glu Ser Arg Val Thr Ile Glu Glu Leu
305                 310                 315                 320

Asp Val Ala Ser Cys Lys Phe Ser Ser Thr Thr Leu Tyr Cys Arg Gln
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Val Asn Thr Arg Ala Leu Pro Pro Leu Val Ala Ser Cys Leu Arg Gly
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Asn Tyr Asp Asp Cys Gln Tyr Thr Thr Glu Ile Gly Ala Leu Ser Ser
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Arg Tyr Ile Thr Leu Asp Gly Gly Val Leu Val Asn Cys Lys Ser Ile
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Val Cys Arg Cys Leu Asn Pro Ser Lys Ile Ile Ser Gln Asn Thr Asn
385                 390                 395                 400

Ala Ala Val Thr Tyr Val Asp Ala Thr Ile Cys Lys Thr Ile Gln Leu
                405                 410                 415

Asp Asp Ile Gln Leu Gln Leu Glu Gly Ser Leu Ser Ser Val Tyr Ala
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Arg Asn Ile Ser Ile Glu Ile Ser Gln Val Thr Thr Ser Gly Ser Leu
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Asp Ile Ser Ser Glu Ile Gly Asn Ile Asn Asn Thr Val Asn Arg Val
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Glu Asp Leu Ile His Gln Ser Glu Glu Trp Leu Ala Lys Val Asn Pro
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His Ile Val Asn Asn Thr Thr Leu Ile Val Leu Cys Val Leu Ser Ala
                485                 490                 495

Leu Ala Val Ile Trp Leu Ala Val Leu Thr Ala Ile Ile Ile Tyr Leu
            500                 505                 510

Arg Thr Lys Leu Lys Thr Ile Ser Ala Leu Ala Val Thr Asn Thr Ile
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Thr Thr Gly Cys Leu Ala Leu Ser Ile Val Ser Ile Val Gln Ile Gly
        35                  40                  45

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

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

Ile Asn Asp Ile Phe Arg Ile Val Ala Leu Asp Ile Pro Leu Gln Val
                85                  90                  95

Thr Ser Ile Gln Lys Asp Leu Ala Ser Gln Phe Asn Met Leu Ile Asp
            100                 105                 110
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Ser Leu Asn Ala Ile Lys Leu Gly Asn Gly Thr Asn Leu Ile Ile Pro
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Thr Ser Asp Lys Glu Tyr Ala Gly Gly Ile Gly Asn Pro Val Phe Thr
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Val Asp Ala Gly Gly Ser Ile Gly Phe Lys Gln Phe Ser Leu Ile Glu
145                 150                 155                 160

His Pro Ser Phe Ile Ala Gly Pro Thr Thr Thr Arg Gly Cys Thr Arg
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Ile Pro Thr Phe His Met Ser Glu Ser His Trp Cys Tyr Ser His Asn
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Ile Ile Ala Ala Gly Cys Gln Asp Ala Ser Ala Ser Ser Met Tyr Ile
        195                 200                 205

Ser Met Gly Val Leu His Val Ser Ser Ser Gly Thr Pro Ile Phe Leu
    210                 215                 220

Thr Thr Ala Ser Glu Leu Ile Asp Asp Gly Val Asn Arg Lys Ser Cys
225                 230                 235                 240

Ser Ile Val Ala Thr Gln Phe Gly Cys Asp Ile Leu Cys Ser Ile Val
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Thr Glu Lys Glu Gly Asp Asp Tyr Trp Ser Asp Thr Pro Thr Pro Met
            260                 265                 270

Arg His Gly Arg Phe Ser Phe Asn Gly Ser Phe Val Glu Ala Glu Leu
        275                 280                 285

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

Gly Ile Lys Gln Thr Ser Pro Glu Phe Thr Glu Leu Val Lys Tyr Gly
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Leu Phe Val Ser Thr Pro Thr Thr Val Cys Gln Ser Ser Trp Thr Tyr
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Asp Gln Val Lys Ala Ala Tyr Arg Pro Asp Tyr Ile Ser Gly Arg Phe
        355                 360                 365
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Ser Cys Ile Val Lys Ile Met Asn Ser Ser Thr Val Met Met Ala Ala
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Glu Gly Arg Ile Met Lys Ile Gly Ile Asp Tyr Phe Tyr Tyr Gln Arg
                405                 410                 415

Ser Ser Ser Trp Trp Pro Leu Ala Phe Val Thr Lys Leu Asp Pro Gln
            420                 425                 430

Glu Leu Ala Asp Thr Asn Ser Ile Trp Leu Thr Asn Ser Ile Pro Ile
        435                 440                 445

Pro Gln Ser Lys Phe Pro Arg Pro Ser Tyr Ser Glu Asn Tyr Cys Thr
    450                 455                 460

Lys Pro Ala Val Cys Pro Ala Thr Cys Val Thr Gly Val Tyr Ser Asp
465                 470                 475                 480

Ile Trp Pro Leu Thr Ser Ser Ser Ser Leu Pro Ser Ile Ile Trp Ile
                485                 490                 495

Gly Gln Tyr Leu Asp Ala Pro Val Gly Arg Thr Tyr Pro Arg Phe Gly
            500                 505                 510

Ile Ala Asn Gln Ser His Trp Tyr Leu Gln Glu Asp Ile Leu Pro Thr
        515                 520                 525

Ser Thr Ala Ser Ala Tyr Ser Thr Thr Thr Cys Phe Lys Asn Thr Ala
    530                 535                 540

Arg Asn Arg Val Phe Cys Val Thr Ile Ala Glu Phe Ala Asp Gly Leu
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gaaagctcaa gtattgtttt gactcgggct gaagttaaag tctgtataaa gttcctcggt 6720

gcaatcatca agttgaaata a 6741

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1               5                  10                  15

Ile Ile Gln Pro Glu Val His Leu Asp Ser Pro Ile Ile Leu Asn Lys
            20                  25                  30

Leu Ala Leu Leu Trp Arg Leu Ser Gly Leu Pro Met Pro Ala Asp Leu
        35                  40                  45

Arg Gln Lys Ser Val Val Met His Ile Pro Asp His Ile Leu Glu Lys
    50                  55                  60

Ser Glu Tyr Arg Ile Lys His Arg Leu Gly Lys Ile Lys Ser Asp Ile
65                  70                  75                  80

Thr His Tyr Cys Gln Tyr Phe Asn Ile Asn Leu Ala Asn Ile Asp Pro
                85                  90                  95
```

```
Ile Thr His Pro Lys Ser Leu Tyr Trp Leu Ser Arg Leu Thr Ile Ala
            100                 105                 110

Ser Ala Gly Thr Phe Arg His Met Lys Asp Arg Ile Leu Cys Thr Val
        115                 120                 125

Gly Ser Glu Phe Gly His Lys Ile Gln Asp Leu Phe Ser Leu Leu Ser
    130                 135                 140

His Lys Leu Val Gly Asn Gly Asp Leu Phe Asn Gln Ser Leu Ser Gly
145                 150                 155                 160

Thr Arg Leu Thr Ala Ser Pro Leu Ser Pro Leu Cys Asn Gln Phe Val
                165                 170                 175

Ser Asp Ile Lys Ser Ala Val Thr Thr Pro Trp Ser Glu Ala Arg Trp
            180                 185                 190

Ser Trp Leu His Ile Lys Gln Thr Met Arg Tyr Leu Ile Lys Gln Ser
        195                 200                 205

Arg Thr Thr Asn Ser Ala His Leu Thr Glu Ile Ile Lys Glu Glu Trp
    210                 215                 220

Gly Leu Val Gly Ile Thr Pro Asp Leu Val Ile Leu Phe Asp Arg Val
225                 230                 235                 240

Asn Asn Ser Leu Thr Ala Leu Thr Phe Glu Met Val Leu Met Tyr Ser
                245                 250                 255

Asp Val Leu Glu Ser Arg Asp Asn Ile Val Leu Val Gly Arg Leu Ser
            260                 265                 270

Thr Phe Leu Gln Pro Val Val Ser Arg Leu Glu Val Leu Phe Asp Leu
        275                 280                 285

Val Asp Ser Leu Ala Lys Ile Leu Gly Asp Thr Ile Tyr Glu Ile Ile
    290                 295                 300

Ala Val Leu Glu Ser Leu Ser Tyr Gly Ser Val Gln Leu His Asp Ala
305                 310                 315                 320

Ser His Ser His Ala Gly Ser Phe Phe Ser Phe Asn Met Asn Glu Leu
                325                 330                 335

Asp Asn Thr Leu Ser Lys Arg Val Asp Pro Lys His Lys Asn Thr Ile
            340                 345                 350
```

```
Met Ser Ile Ile Arg Gln Cys Phe Ser Asn Leu Asp Val Asp Gln Ala
        355                 360                 365

Ala Glu Met Leu Cys Leu Met Arg Leu Phe Gly His Pro Met Leu Thr
    370                 375                 380

Ala Pro Asp Ala Ala Ala Lys Val Arg Lys Ala Met Cys Ala Pro Lys
385                 390                 395                 400

Leu Val Glu His Asp Thr Ile Leu Gln Thr Leu Ser Phe Phe Lys Gly
                405                 410                 415

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

Val Glu Pro Ser Ser Ile Tyr Asp Asp Asp Leu Arg Gln Leu Tyr Leu
        435                 440                 445

Glu Ser Ala Glu Ile Ser His His Phe Met Leu Lys Asn Tyr Lys Ser
    450                 455                 460

Leu Ser Met Ile Glu Phe Lys Lys Ser Ile Asp Tyr Asp Leu His Asp
465                 470                 475                 480

Asp Leu Ser Thr Phe Leu Lys Asp Arg Ala Ile Cys Arg Pro Lys Ser
                485                 490                 495

Gln Trp Asp Val Ile Phe Arg Lys Ser Leu Arg Arg Ser His Thr Gln
            500                 505                 510

Ser Gln Tyr Leu Asp Glu Ile Lys Ser Asn Arg Leu Leu Ile Asp Phe
        515                 520                 525

Leu Asp Ser Ala Glu Phe Asp Pro Gly Lys Glu Phe Ala Tyr Val Thr
    530                 535                 540

Thr Met Asp Tyr Leu His Asp Asn Glu Phe Cys Ala Ser Tyr Ser Leu
545                 550                 555                 560

Lys Glu Lys Glu Ile Lys Thr Thr Gly Arg Ile Phe Ala Lys Met Thr
                565                 570                 575

Arg Asn Met Arg Ser Cys Gln Val Ile Leu Glu Ser Leu Leu Ser Lys
            580                 585                 590

His Ile Cys Lys Phe Phe Lys Glu Asn Gly Val Ser Met Glu Gln Leu
        595                 600                 605

Ser Leu Thr Lys Ser Leu Leu Ala Met Ser Gln Leu Ser Pro Lys Val
```

610 615 620

Ser Thr Leu Gln Asp Thr Ala Ser Arg His Val Gly Asn Ser Lys Ser
625 630 635 640

Gln Ile Ala Thr Ser Asn Pro Ser Arg His His Ser Thr Pro Asn Gln
645 650 655

Met Ser Leu Ser Asn Arg Lys Thr Val Val Ala Thr Phe Leu Thr Thr
660 665 670

Asp Leu Glu Lys Tyr Cys Leu Gln Trp Arg Tyr Ser Thr Ile Lys Leu
675 680 685

Phe Ala Gln Ala Leu Asn Gln Leu Phe Gly Ile Asp His Gly Phe Glu
690 695 700

Trp Ile His Leu Arg Leu Met Asn Ser Thr Leu Phe Val Gly Asp Pro
705 710 715 720

Tyr Ser Pro Pro Glu Asp Pro Thr Leu Glu Asp Ile Asp Lys Ala Pro
725 730 735

Asn Asp Asp Ile Phe Ile Val Ser Pro Arg Gly Gly Ile Glu Gly Leu
740 745 750

Cys Gln Lys Met Trp Thr Met Ile Ser Ile Ser Ala Ile His Cys Val
755 760 765

Ala Glu Lys Ile Gly Ala Arg Val Ala Ala Met Val Gln Gly Asp Asn
770 775 780

Gln Val Ile Ala Ile Thr Lys Glu Leu Phe Arg Gly Glu Lys Ala Cys
785 790 795 800

Asp Val Arg Asp Glu Leu Asp Glu Leu Gly Gln Val Phe Phe Asp Glu
805 810 815

Phe Lys Arg His Asn Tyr Ala Ile Gly His Asn Leu Lys Leu Asn Glu
820 825 830

Thr Ile Gln Ser Gln Ser Phe Phe Val Tyr Ser Lys Arg Ile Phe Phe
835 840 845

Glu Gly Arg Leu Leu Ser Gln Val Leu Lys Asn Ala Ala Lys Leu Cys
850 855 860

Met Val Ala Asp His Leu Gly Glu Asn Thr Val Ser Ser Cys Ser Asn
865 870 875 880

```
Leu Ser Ser Thr Ile Ala Arg Leu Val Glu Asn Gly Phe Glu Lys Asp
                885                 890                 895

Thr Ala Phe Val Leu Asn Leu Val Tyr Ile Met Thr Gln Ile Leu Phe
            900                 905                 910

Asp Glu His Tyr Ser Ile Val Cys Asp His His Ser Val Lys Ser Leu
        915                 920                 925

Ile Gly Ser Lys Asn His Arg Asn Leu Leu Tyr Ser Ser Leu Ile Pro
    930                 935                 940

Gly Gln Leu Gly Gly Phe Asn Phe Leu Asn Ile Ser Arg Leu Phe Thr
945                 950                 955                 960

Arg Asn Ile Gly Asp Pro Val Thr Cys Ser Leu Ser Asp Leu Lys Cys
                965                 970                 975

Phe Ile Ala Ala Gly Leu Leu Pro Pro Tyr Val Leu Lys Asn Val Val
            980                 985                 990

Leu Arg Glu Pro Gly Pro Gly Thr  Trp Leu Thr Leu Cys  Ser Asp Pro
        995                 1000                1005

Tyr Thr  Leu Asn Ile Pro Tyr  Thr Gln Leu Pro Thr  Thr Tyr Leu
    1010                1015                1020

Lys Lys  His Thr Gln Arg Ser  Leu Leu Ser Arg Ala  Val Asn Pro
    1025                1030                1035

Leu Leu  Ala Gly Val Gln Val  Pro Asn Gln His Glu  Glu Glu Glu
    1040                1045                1050

Met Leu  Ala Arg Phe Leu Leu  Asp Arg Glu Tyr Val  Met Pro Arg
    1055                1060                1065

Val Ala  His Val Ile Leu Glu  Ser Ser Val Leu Gly  Lys Arg Lys
    1070                1075                1080

Gln Ile  Gln Gly Leu Ile Asp  Thr Thr Pro Thr Ile  Ile Arg Thr
    1085                1090                1095

Ser Leu  Val Asn Leu Pro Val  Ser Arg Lys Lys Cys  Glu Lys Ile
    1100                1105                1110

Ile Asn  Tyr Ser Leu Asn Tyr  Ile Ala Glu Cys His  Asp Ser Leu
    1115                1120                1125
```

```
Leu Ser  Gln Val Cys Phe Ser  Asp Asn Lys Glu Tyr  Leu Trp Ser
    1130                 1135                 1140

Thr Ser  Leu Ile Ser Val Glu  Thr Cys Ser Val Thr  Ile Ala Asp
    1145                 1150                 1155

Tyr Leu  Arg Ala Val Ser Trp  Ser Asn Ile Leu Gly  Gly Arg Asn
    1160                 1165                 1170

Ile Ser  Gly Val Thr Thr Pro  Asp Thr Ile Glu Leu  Ile Gln Gly
    1175                 1180                 1185

Cys Leu  Ile Gly Glu Asn Ser  Ser Cys Thr Leu Cys  Glu Ser His
    1190                 1195                 1200

Asp Asp  Ala Phe Thr Trp Met  His Leu Pro Gly Pro  Leu Tyr Ile
    1205                 1210                 1215

Pro Glu  Pro Ser Val Thr Asn  Ser Lys Met Arg Val  Pro Tyr Leu
    1220                 1225                 1230

Gly Ser  Lys Thr Glu Glu Arg  Lys Thr Ala Ser Met  Ala Ala Ile
    1235                 1240                 1245

Lys Gly  Met Ser His His Leu  Arg Ala Val Leu Arg  Gly Thr Ser
    1250                 1255                 1260

Val Phe  Ile Trp Ala Phe Gly  Asp Thr Asp Ile Asn  Trp Asp Asn
    1265                 1270                 1275

Ala Leu  Gln Ile Ala Gln Ser  Arg Cys Asn Ile Thr  Leu Asp Gln
    1280                 1285                 1290

Met Arg  Leu Leu Thr Pro Ile  Pro Ser Ser Ser Asn  Ile Gln His
    1295                 1300                 1305

Arg Leu  Asp Asp Gly Ile Ser  Thr Gln Lys Phe Thr  Pro Ala Ser
    1310                 1315                 1320

Leu Ala  Arg Ile Thr Ser Phe  Val His Ile Cys Asn  Asp Ser Gln
    1325                 1330                 1335

Arg Leu  Glu Lys Asp Gly Ser  Ser Val Asp Ser Asn  Leu Ile Tyr
    1340                 1345                 1350

Gln Gln  Ile Met Leu Leu Gly  Leu Ser Ile Phe Glu  Thr Met Tyr
    1355                 1360                 1365
```

```
Ser Met  Asp Gln Lys Trp Val  Phe Asn Asn His Thr  Leu His Leu
    1370                1375                1380

His Thr  Gly His Ser Cys Cys  Pro Arg Glu Leu Asp  Ile Ser Leu
    1385                1390                1395

Val Asn  Pro Pro Arg His Gln  Thr Pro Glu Leu Thr  Ser Thr Thr
    1400                1405                1410

Thr Asn  Pro Phe Leu Tyr Asp  Gln Leu Pro Leu Asn  Gln Glu Asn
    1415                1420                1425

Leu Thr  Thr Leu Glu Ile Lys  Thr Phe Lys Phe Asn  Glu Leu Asn
    1430                1435                1440

Ile Asp  Gly Leu Asp Phe Gly  Glu Gly Ile Gln Leu  Leu Ser Arg
    1445                1450                1455

Cys Thr  Ala Arg Leu Met Ala  Glu Cys Ile Leu Glu  Glu Gly Ile
    1460                1465                1470

Gly Ser  Ser Val Lys Asn Glu  Ala Ile Val Asn Phe  Asp Asn Ser
    1475                1480                1485

Val Asn  Trp Ile Ser Glu Cys  Leu Met Cys Asp Ile  Arg Ser Leu
    1490                1495                1500

Cys Val  Asn Leu Gly Gln Glu  Ile Leu Cys Ser Leu  Ala Tyr Gln
    1505                1510                1515

Met Tyr  Tyr Leu Arg Ile Arg  Gly Arg Arg Ala Ile  Leu Asn Tyr
    1520                1525                1530

Leu Asp  Thr Thr Leu Gln Arg  Ile Pro Val Ile Gln  Leu Ala Asn
    1535                1540                1545

Ile Ala  Leu Thr Ile Ser His  Pro Glu Ile Phe Arg  Arg Ile Val
    1550                1555                1560

Asn Thr  Gly Ile His Asn Gln  Ile Lys Gly Pro Tyr  Val Ala Thr
    1565                1570                1575

Thr Asp  Phe Ile Ala Ala Ser  Arg Asp Ile Ile Leu  Ser Gly Ala
    1580                1585                1590

Arg Glu  Tyr Leu Ser Tyr Leu  Ser Ser Gly Gln Glu  Asp Cys Tyr
    1595                1600                1605

Thr Phe  Phe Asn Cys Gln Asp  Gly Asp Leu Thr Pro  Lys Met Glu
```

```
    1610                1615                1620

Gln Tyr  Leu Ala Arg Arg Ala  Cys Leu Leu Thr Leu  Leu Tyr Asn
    1625                1630                1635

Thr Gly  His Gln Ile Pro Val  Ile Arg Ser Leu Thr  Pro Ile Glu
    1640                1645                1650

Lys Cys  Lys Val Leu Thr Glu  Tyr Asn Gln Gln Ile  Glu Tyr Ala
    1655                1660                1665

Asp Gln  Glu Phe Ser Ser Val  Leu Lys Val Val Asn  Ala Leu Leu
    1670                1675                1680

Gln Asn  Pro Lys Ile Asp Ala  Leu Val Ser Asn Leu  Tyr Phe Thr
    1685                1690                1695

Thr Arg  Arg Val Leu Ser Asn  Leu Arg Ser Cys Asp  Lys Ala Arg
    1700                1705                1710

Ser Tyr  Ile Glu Tyr Leu Tyr  Thr Glu Asp Phe Gly  Glu Lys Glu
    1715                1720                1725

Asp Thr  Val Gln Tyr Asp Ile  Met Thr Thr Asn Asp  Ile Ile Leu
    1730                1735                1740

Thr His  Gly Leu Phe Thr Gln  Ile Glu Ile Ser Tyr  Gln Gly Asn
    1745                1750                1755

Ser Leu  His Lys Phe Leu Thr  Pro Asp Asn Ala Pro  Gly Ser Leu
    1760                1765                1770

Ile Pro  Phe Ser Ile Ser Pro  Asn Ser Leu Ala Cys  Asp Pro Leu
    1775                1780                1785

His His  Leu Leu Lys Ser Val  Gly Thr Ser Ser Thr  Ser Trp Tyr
    1790                1795                1800

Lys Tyr  Ala Ile Ala Tyr Ala  Val Ser Glu Lys Arg  Ser Ala Arg
    1805                1810                1815

Leu Gly  Gly Ser Leu Tyr Ile  Gly Glu Gly Ser Gly  Ser Val Met
    1820                1825                1830

Thr Leu  Leu Glu Tyr Leu Glu  Pro Ser Val Asp Ile  Phe Tyr Asn
    1835                1840                1845

Ser Leu  Phe Ser Asn Gly Met  Asn Pro Pro Gln Arg  Asn Tyr Gly
    1850                1855                1860
```

```
Leu Met  Pro Leu Gln Phe Val  Asn Ser Val Val Tyr  Lys Asn Leu
    1865                1870                1875

Thr Ala  Lys Ser Glu Cys Lys  Leu Gly Phe Val Gln  Gln Phe Lys
    1880                1885                1890

Pro Leu  Trp Arg Asp Ile Asp  Ile Glu Thr Asn Val  Thr Asp Pro
    1895                1900                1905

Ser Phe  Ile Asn Phe Ala Leu  Asn Glu Ile Pro Met  Gln Ser Leu
    1910                1915                1920

Lys Arg  Val Asn Cys Asp Val  Glu Phe Asp Arg Gly  Met Pro Ile
    1925                1930                1935

Glu Arg  Val Ile Gln Gly Tyr  Thr His Ile Leu Leu  Val Ala Thr
    1940                1945                1950

Tyr Gly  Leu Gln Gln Asp Ser  Ile Leu Trp Val Lys  Val Tyr Arg
    1955                1960                1965

Thr Ser  Glu Lys Val Phe Gln  Phe Leu Leu Ser Ala  Met Ile Met
    1970                1975                1980

Ile Phe  Gly Tyr Val Lys Ile  His Arg Asn Gly Tyr  Met Ser Thr
    1985                1990                1995

Lys Asp  Glu Glu Tyr Ile Leu  Met Ser Asp Cys Lys  Glu Pro Val
    2000                2005                2010

Asn Tyr  Thr Ala Val Pro Asn  Ile Leu Thr Arg Val  Ser Asp Leu
    2015                2020                2025

Val Ser  Lys Asn Leu Ser Leu  Ile His Pro Glu Asp  Leu Arg Lys
    2030                2035                2040

Val Arg  Cys Glu Thr Asp Ser  Leu Asn Leu Lys Cys  Asn His Ile
    2045                2050                2055

Tyr Glu  Lys Ile Ile Ala Arg  Lys Ile Pro Leu Gln  Val Ser Ser
    2060                2065                2070

Thr Asp  Ser Leu Leu Leu Gln  Leu Gly Gly Val Ile  Asn Ser Val
    2075                2080                2085

Gly Ser  Thr Asp Pro Arg Glu  Val Ala Thr Leu Ser  Ser Ile Glu
    2090                2095                2100
```

```
Cys Met  Asp Tyr Val Val Ser  Ser Ile Asp Leu Ala  Ile Leu Glu
    2105                2110                2115

Ala Asn  Ile Val Ile Ser Glu  Ser Ala Gly Leu Asp  Leu Ala Leu
    2120                2125                2130

Met Leu  Gly Pro Phe Asn Leu  Asn Lys Leu Lys Lys  Ile Asp Thr
    2135                2140                2145

Ile Leu  Lys Ser Ser Thr Tyr  Gln Leu Ile Pro Tyr  Trp Leu Arg
    2150                2155                2160

Tyr Glu  Tyr Ser Ile Asn Pro  Arg Ser Leu Ser Phe  Leu Ile Thr
    2165                2170                2175

Lys Leu  Gln Gln Cys Arg Ile  Ser Trp Ser Asp Met  Ile Thr Ile
    2180                2185                2190

Ser Glu  Phe Arg Lys Lys Ser  Lys Arg Pro Ile Phe  Ile Lys Arg
    2195                2200                2205

Val Ile  Gly Asn Gln Gln Leu  Lys Ser Phe Phe Asn  Glu Ser Ser
    2210                2215                2220

Ser Ile  Val Leu Thr Arg Ala  Glu Val Lys Val Cys  Ile Lys Phe
    2225                2230                2235

Leu Gly  Ala Ile Ile Lys Leu  Lys
    2240                2245
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1               5                  10                  15

Asp Ser Pro Ile Ile Leu Asn Lys Leu Ala Leu Leu Trp Arg Leu Ser
            20                  25                  30

Gly Leu Pro Met Pro Ala Asp Leu Arg Gln Lys Ser Val Val Met His
        35                  40                  45

Ile Pro Asp His Ile Leu Glu Lys Ser Glu Tyr Arg Ile Lys His Arg
    50                  55                  60
```

```
Leu Gly Lys Ile Lys Ser Asp Ile Thr His Tyr Cys Gln Tyr Phe Asn
65                  70                  75                  80

Ile Asn Leu Ala Asn Ile Asp Pro Ile Thr His Pro Lys Ser Leu Tyr
                85                  90                  95

Trp Leu Ser Arg Leu Thr Ile Ala Ser Ala Gly Thr Phe Arg His Met
            100                 105                 110

Lys Asp Arg Ile Leu Cys Thr Val Gly Ser Glu Phe Gly His Lys Ile
        115                 120                 125

Gln Asp Leu Phe Ser Leu Leu Ser His Lys Leu Val Gly Asn Gly Asp
    130                 135                 140

Leu Phe Asn Gln Ser Leu Ser Gly Thr Arg Leu Thr Ala Ser Pro Leu
145                 150                 155                 160

Ser Pro Leu Cys Asn Gln Phe Val Ser Asp Ile Lys Ser Ala Val Thr
                165                 170                 175

Thr Pro Trp Ser Glu Ala Arg Trp Ser Trp Leu His Ile Lys Gln Thr
            180                 185                 190

Met Arg Tyr Leu Ile Lys Gln Ser Arg Thr Thr Asn Ser Ala His Leu
        195                 200                 205

Thr Glu Ile Ile Lys Glu Glu Trp Gly Leu Val Gly Ile Thr Pro Asp
    210                 215                 220

Leu Val Ile Leu Phe Asp Arg Val Asn Asn Ser Leu Thr Ala Leu Thr
225                 230                 235                 240

Phe Glu Met Val Leu Met Tyr Ser Asp Val Leu Glu Ser Arg Asp Asn
                245                 250                 255

Ile Val Leu Val Gly Arg Leu Ser Thr Phe Leu Gln Pro Val Val Ser
            260                 265                 270

Arg Leu Glu Val Leu Phe Asp Leu Val Asp Ser Leu Ala Lys Ile Leu
        275                 280                 285

Gly Asp Thr Ile Tyr Glu Ile Ile Ala Val Leu Glu Ser Leu Ser Tyr
    290                 295                 300

Gly Ser Val Gln Leu His Asp Ala Ser His Ser His Ala Gly Ser Phe
305                 310                 315                 320
```

```
Phe Ser Phe Asn Met Asn Glu Leu Asp Asn Thr Leu Ser Lys Arg Val
                325                 330                 335

Asp Pro Lys His Lys Asn Thr Ile Met Ser Ile Ile Arg Gln Cys Phe
            340                 345                 350

Ser Asn Leu Asp Val Asp Gln Ala Ala Glu Met Leu Cys Leu Met Arg
        355                 360                 365

Leu Phe Gly His Pro Met Leu Thr Ala Pro Asp Ala Ala Ala Lys Val
    370                 375                 380

Arg Lys Ala Met Cys Ala Pro Lys Leu Val Glu His Asp Thr Ile Leu
385                 390                 395                 400

Gln Thr Leu Ser Phe Phe Lys Gly Ile Ile Ile Asn Gly Tyr Arg Arg
                405                 410                 415

Ser His Ser Gly Leu Trp Pro Asn Val Glu Pro Ser Ser Ile Tyr Asp
            420                 425                 430

Asp Asp Leu Arg Gln Leu Tyr Leu Glu Ser Ala Glu Ile Ser His His
        435                 440                 445

Phe Met Leu Lys Asn Tyr Lys Ser Leu Ser Met Ile Glu Phe Lys Lys
    450                 455                 460

Ser Ile Asp Tyr Asp Leu His Asp Asp Leu Ser Thr Phe Leu Lys Asp
465                 470                 475                 480

Arg Ala Ile Cys Arg Pro Lys Ser Gln Trp Asp Val Ile Phe Arg Lys
                485                 490                 495

Ser Leu Arg Arg Ser His Thr Gln Ser Gln Tyr Leu Asp Glu Ile Lys
            500                 505                 510

Ser Asn Arg Leu Leu Ile Asp Phe Leu Asp Ser Ala Glu Phe Asp Pro
        515                 520                 525

Gly Lys Glu Phe Ala Tyr Val Thr Thr Met Asp Tyr Leu His Asp Asn
    530                 535                 540

Glu Phe Cys Ala Ser Tyr Ser Leu Lys Glu Lys Glu Ile Lys Thr Thr
545                 550                 555                 560

Gly Arg Ile Phe Ala Lys Met Thr Arg Asn Met Arg Ser Cys Gln Val
                565                 570                 575
```

```
Ile Leu Glu Ser Leu Leu Ser Lys His Ile Cys Lys Phe Phe Lys Glu
            580                 585                 590

Asn Gly Val Ser Met Glu Gln Leu Ser Leu Thr Lys Ser Leu Leu Ala
        595                 600                 605

Met Ser Gln Leu Ser Pro Lys Val Ser Thr Leu Gln Asp Thr Ala Ser
    610                 615                 620

Arg His Val Gly Asn Ser Lys Ser Gln Ile Ala Thr Ser Asn Pro Ser
625                 630                 635                 640

Arg His His Ser Thr Pro Asn Gln Met Ser Leu Ser Asn Arg Lys Thr
                645                 650                 655

Val Val Ala Thr Phe Leu Thr Thr Asp Leu Glu Lys Tyr Cys Leu Gln
            660                 665                 670

Trp Arg Tyr Ser Thr Ile Lys Leu Phe Ala Gln Ala Leu Asn Gln Leu
        675                 680                 685

Phe Gly Ile Asp His Gly Phe Glu Trp Ile His Leu Arg Leu Met Asn
    690                 695                 700

Ser Thr Leu Phe Val Gly Asp Pro Tyr Ser Pro Pro Glu Asp Pro Thr
705                 710                 715                 720

Leu Glu Asp Ile Asp Lys Ala Pro Asn Asp Asp Ile Phe Ile Val Ser
                725                 730                 735

Pro Arg Gly Gly Ile Glu Gly Leu Cys Gln Lys Met Trp Thr Met Ile
            740                 745                 750

Ser Ile Ser Ala Ile His Cys Val Ala Glu Lys Ile Gly Ala Arg Val
        755                 760                 765

Ala Ala Met Val Gln Gly Asp Asn Gln Val Ile Ala Ile Thr Lys Glu
    770                 775                 780

Leu Phe Arg Gly Glu Lys Ala Cys Asp Val Arg Asp Glu Leu Asp Glu
785                 790                 795                 800

Leu Gly Gln Val Phe Phe Asp Glu Phe Lys Arg His Asn Tyr Ala Ile
                805                 810                 815

Gly His Asn Leu Lys Leu Asn Glu Thr Ile Gln Ser Gln Ser Phe Phe
            820                 825                 830

Val Tyr Ser Lys Arg Ile Phe Phe Glu Gly Arg Leu Leu Ser Gln Val
```

```
        835                 840                 845

Leu Lys Asn Ala Ala Lys Leu Cys Met Val Ala Asp His Leu Gly Glu
    850                 855                 860

Asn Thr Val Ser Ser Cys Ser Asn Leu Ser Ser Thr Ile Ala Arg Leu
865                 870                 875                 880

Val Glu Asn Gly Phe Glu Lys Asp Thr Ala Phe Val Leu Asn Leu Val
                885                 890                 895

Tyr Ile Met Thr Gln Ile Leu Phe Asp Glu His Tyr Ser Ile Val Cys
            900                 905                 910

Asp His His Ser Val Lys Ser Leu Ile Gly Ser Lys Asn His Arg Asn
        915                 920                 925

Leu Leu Tyr Ser Ser Leu Ile Pro Gly Gln Leu Gly Gly Phe Asn Phe
    930                 935                 940

Leu Asn Ile Ser Arg Leu Phe Thr Arg Asn Ile Gly Asp Pro Val Thr
945                 950                 955                 960

Cys Ser Leu Ser Asp Leu Lys Cys Phe Ile Ala Ala Gly Leu Leu Pro
                965                 970                 975

Pro Tyr Val Leu Lys Asn Val Val Leu Arg Glu Pro Gly Pro Gly Thr
            980                 985                 990

Trp Leu Thr Leu Cys Ser Asp Pro  Tyr Thr Leu Asn Ile  Pro Tyr Thr
        995                 1000                1005

Gln Leu  Pro Thr Thr Tyr Leu  Lys Lys His Thr Gln  Arg Ser Leu
    1010                1015                1020

Leu Ser  Arg Ala Val Asn Pro  Leu Leu Ala Gly Val  Gln Val Pro
    1025                1030                1035

Asn Gln  His Glu Glu Glu Glu  Met Leu Ala Arg Phe  Leu Leu Asp
    1040                1045                1050

Arg Glu  Tyr Val Met Pro Arg  Val Ala His Val Ile  Leu Glu Ser
    1055                1060                1065

Ser Val  Leu Gly Lys Arg Lys  Gln Ile Gln Gly Leu  Ile Asp Thr
    1070                1075                1080

Thr Pro  Thr Ile Ile Arg Thr  Ser Leu Val Asn Leu  Pro Val Ser
    1085                1090                1095
```

```
Arg Lys  Lys Cys Glu Lys Ile  Ile Asn Tyr Ser Leu  Asn Tyr Ile
    1100                 1105                 1110

Ala Glu  Cys His Asp Ser Leu  Leu Ser Gln Val Cys  Phe Ser Asp
    1115                 1120                 1125

Asn Lys  Glu Tyr Leu Trp Ser  Thr Ser Leu Ile Ser  Val Glu Thr
    1130                 1135                 1140

Cys Ser  Val Thr Ile Ala Asp  Tyr Leu Arg Ala Val  Ser Trp Ser
    1145                 1150                 1155

Asn Ile  Leu Gly Gly Arg Asn  Ile Ser Gly Val Thr  Thr Pro Asp
    1160                 1165                 1170

Thr Ile  Glu Leu Ile Gln Gly  Cys Leu Ile Gly Glu  Asn Ser Ser
    1175                 1180                 1185

Cys Thr  Leu Cys Glu Ser His  Asp Asp Ala Phe Thr  Trp Met His
    1190                 1195                 1200

Leu Pro  Gly Pro Leu Tyr Ile  Pro Glu Pro Ser Val  Thr Asn Ser
    1205                 1210                 1215

Lys Met  Arg Val Pro Tyr Leu  Gly Ser Lys Thr Glu  Glu Arg Lys
    1220                 1225                 1230

Thr Ala  Ser Met Ala Ala Ile  Lys Gly Met Ser His  His Leu Arg
    1235                 1240                 1245

Ala Val  Leu Arg Gly Thr Ser  Val Phe Ile Trp Ala  Phe Gly Asp
    1250                 1255                 1260

Thr Asp  Ile Asn Trp Asp Asn  Ala Leu Gln Ile Ala  Gln Ser Arg
    1265                 1270                 1275

Cys Asn  Ile Thr Leu Asp Gln  Met Arg Leu Leu Thr  Pro Ile Pro
    1280                 1285                 1290

Ser Ser  Ser Asn Ile Gln His  Arg Leu Asp Asp Gly  Ile Ser Thr
    1295                 1300                 1305

Gln Lys  Phe Thr Pro Ala Ser  Leu Ala Arg Ile Thr  Ser Phe Val
    1310                 1315                 1320

His Ile  Cys Asn Asp Ser Gln  Arg Leu Glu Lys Asp  Gly Ser Ser
    1325                 1330                 1335
```

```
Val Asp  Ser Asn Leu Ile Tyr  Gln Gln Ile Met Leu  Leu Gly Leu
    1340                 1345                 1350

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Arg Glu  Leu Asp Ile Ser Leu  Val Asn Pro Pro Arg  His Gln Thr
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His Ile  Leu Leu Val Ala Thr  Tyr Gly Leu Gln Gln  Asp Ser Ile
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Leu Thr  Arg Val Ser Asp Leu  Val Ser Lys Asn Leu  Ser Leu Ile
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ttcatcgagg aaaaccacga aaacatcatt gcctgcgcca agagcccccc ggaaaacaca 1500

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attctgcagg ccgatgccat taacggaaca gacaacgagg tggtgaccgt gaccgatgaa 1800

aatacaggcg agatttccga gaaagtgaag ctgggcacca aggccctggc cggacagtgg 1860

ctggcctata gcgtgacccg gtccgtgacc aagcgctctg tgatgacact ggcctacggg 1920

tctaaggaat ttggatttcg gcagcaggtg ctggaagaca ccattcagcc cgccatcgac 1980

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aagccaattc agacaaggct gaacctgatg ttcctggggc agtttcgcct gcagccaaca 2280

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gtgctggccg acttttacga ccagttcgcc gatcagctgc acgaaagcca gctggataag 2580

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gccttcgcct ga 2652

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<223> EGFP-FP primer

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<212> DNA
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<220>
<223> EGFP-RP primer

<400> 51
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<210> 52
<211> 1419
<212> DNA
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<220>
<223> APMV8 minigenome

<400> 52

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ttttaagtta ggctagacac ttcacaatca tttggcaaga agaatattac aggcaccaat 180

tttctttgag tgtcggattt tttcttaaaa tcatttttat tatgtatata tttgttatac 240

tctaggaata tagattcaga ggttagagaa attatcctat cccctagcga atgattacaa 300

gctatattac ttcaagtgca aattagaaca ttacacccct ttaaaatcgc agaaattaca 360

agctatatta cttcaagtgc aaattagaac attacacccc tttaaaatcg cagaaattac 420

ttgtacagct cgtccatgcc gagagtgatc ccggcggcgg tcacgaactc cagcaggacc 480

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tccgaaggag gacgcacgtc cactcggatg gctaagggag ggcgtagcat aacccccttgg 1380

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<211> 1386
<212> DNA
<213> artificial sequence

<220>
<223> NP gene of FJ215863

<400> 53

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ttatctcaag accccggtga gagatggagc cttgcttgct tgaatatcag atggcttgtg 180

agtgattcat caaccacacc aatgaagcaa ggagcaatat tgtcactgct gagtctacat 240

tcagacaata tgcgagctca cgcaacatta gcagcaaggt ctgcagatgc ttcactcacc 300

atacttgagg tagatgaagt agatattggc aactcactaa tcaaattcaa cgccagaagt 360

ggtgtatctg ataaacgctc aaatcaattg cttgcaattg cggatgacat ccccaaaagt 420

tgcagtaatg ggcatccatt tcttgacaca gacattgaga ccagagaccc gctcgatcta 480

tcagagacta tagaccgcct gcagggtatt gcagctcaga tatgggtgtc agccataaag 540

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caacaaggcc gactggttaa gcaagtactc ttgcattctg tagtcaggac agaatttatg 660

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aggctataca aaaccaaggg agacaatgca ccatacatgg cattcctgga ggactccgat 960

atgggaaatt ttgctccagc aaattatagc acaatgtact cttatgccat gggcattggg 1020

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tatttccgtc ttggagttga gacagcccaa agccagcagg gagcatttga cgagagaaca 1140

gcccgagaaa tgggcttgac tgaggaatca aaacagcagg ttagatcact gctaatgtca 1200

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tggtaa 1386

<210> 54
<211> 461
<212> PRT
<213> artificial sequence

<220>
<223> NP protein ACO48297

<400> 54

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Ala Glu Ile Pro Val Cys Val Thr Leu Ser Gln Asp Pro Gly Glu Arg
        35                  40                  45

Trp Ser Leu Ala Cys Leu Asn Ile Arg Trp Leu Val Ser Asp Ser Ser
    50                  55                  60

Thr Thr Pro Met Lys Gln Gly Ala Ile Leu Ser Leu Leu Ser Leu His
65                  70                  75                  80

Ser Asp Asn Met Arg Ala His Ala Thr Leu Ala Ala Arg Ser Ala Asp
                85                  90                  95

Ala Ser Leu Thr Ile Leu Glu Val Asp Glu Val Asp Ile Gly Asn Ser
            100                 105                 110

Leu Ile Lys Phe Asn Ala Arg Ser Gly Val Ser Asp Lys Arg Ser Asn
        115                 120                 125

Gln Leu Leu Ala Ile Ala Asp Asp Ile Pro Lys Ser Cys Ser Asn Gly
    130                 135                 140

His Pro Phe Leu Asp Thr Asp Ile Glu Thr Arg Asp Pro Leu Asp Leu
145                 150                 155                 160

Ser Glu Thr Ile Asp Arg Leu Gln Gly Ile Ala Ala Gln Ile Trp Val
                165                 170                 175

Ser Ala Ile Lys Ser Met Thr Ala Pro Asp Thr Ala Ser Glu Ser Glu
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                180                 185                 190

Ser Lys Arg Leu Ala Lys Tyr Gln Gln Gly Arg Leu Val Lys Gln
        195                 200                 205

Val Leu Leu His Ser Val Val Arg Thr Glu Phe Met Arg Val Ile Arg
    210                 215                 220

Gly Ser Leu Val Leu Arg Gln Phe Met Val Ser Glu Cys Lys Arg Ala
225                 230                 235                 240

Ser Ala Met Gly Gly Asp Thr Ser Arg Tyr Tyr Ala Met Val Gly Asp
                245                 250                 255

Ile Ser Leu Tyr Ile Lys Asn Ala Gly Leu Thr Ala Phe Phe Leu Thr
            260                 265                 270

Leu Lys Phe Gly Val Gly Thr Gln Tyr Pro Thr Leu Ala Met Ser Val
        275                 280                 285

Phe Ser Ser Asp Leu Lys Arg Leu Ala Ala Leu Ile Arg Leu Tyr Lys
    290                 295                 300

Thr Lys Gly Asp Asn Ala Pro Tyr Met Ala Phe Leu Glu Asp Ser Asp
305                 310                 315                 320

Met Gly Asn Phe Ala Pro Ala Asn Tyr Ser Thr Met Tyr Ser Tyr Ala
                325                 330                 335

Met Gly Ile Gly Thr Ile Leu Glu Ala Ser Val Ser Arg Tyr Gln Tyr
            340                 345                 350

Ala Arg Asp Phe Thr Ser Glu Asn Tyr Phe Arg Leu Gly Val Glu Thr
        355                 360                 365

Ala Gln Ser Gln Gln Gly Ala Phe Asp Glu Arg Thr Ala Arg Glu Met
    370                 375                 380

Gly Leu Thr Glu Glu Ser Lys Gln Gln Val Arg Ser Leu Leu Met Ser
385                 390                 395                 400

Val Asp Met Gly Pro Ser Ser Val His Glu Pro Ser Arg Pro Ala Phe
                405                 410                 415

Ile Ser Gln Glu Glu Asn Arg Gln Pro Ala Gln Asn Ser Ser Asp Thr
            420                 425                 430

Gln Gly Gln Thr Lys Pro Val Pro Lys Gln Pro Ala Pro Arg Ala Asp
        435                 440                 445
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Ser Asp Asp Ile Asp Pro Tyr Glu Asn Gly Leu Glu Trp
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<212> DNA
<213> artificial sequence

<220>
<223> P gene of FJ215863

<400> 55

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caagggaaca caagaaatct aactgatcta tgggaaaaag agactgcaag tcagaccaag 180

acaccggccc aatctccaca aaccacacaa gttcagtctg atgaaaatga ggagggagaa 240

atcaagtccg agtcaattga tggccacatc agaggaactg ttaatcaatc agagcaagtc 300

ccagaacaaa accagagcag atcttcacca ggtgatgatc tcgacagagc tctcaacaag 360

cttgaaggga gaatcaattc aatcagctca atggacaaag aaattaaaaa gggccctcgc 420

atccagaatc tccctgggtc ccaggcggca actcaacagg cgacccaccc attggcaggg 480

gacaccccga acatgcaagc acagacaaaa gccctggcga agccacatca agaggcaatc 540

aatcctggca accaggacac aggagagagt attcatttac caccttccat ggcaccacca 600

gagtcattag ttggtgcaat ccgcaatgca ccccaattcg tgccagacca atctatgacg 660

aatgtagatg cggggagtgt ccaactacat gcatcatgtg cagagatgat aagtagaatg 720

tttgtagaag ttatatccaa gcttgataaa ctcgagtcga gactgaatga tatagcaaaa 780

gttgtgaaca ccacccccct tattaggaat gatattaacc aacttaaggc cacaaccgca 840

ctgatgtcca accaaattgc ttccatacaa attcttgacc cagggaatgc aggggtgagg 900

tccctctctg aaatgaaatc tgtgacgaag aaagctgctg ttgtaattgc agggtttgga 960

gacgacccaa ctcaaattat tgaagaaggc attatggcca aagatgctct tggaaaacct 1020

gtgcctccaa catctgttat ctcagctaaa gctcagactt cttccggtgt gagtaagggt 1080

gaaatagaag gattgattgc attggtggaa acattagttg acaatgacaa gaaggcagca 1140

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<210> 56
<211> 405
<212> PRT
<213> artificial sequence

<220>
<223> P protein ACO48298

<400> 56

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

Thr Thr Gly Arg Pro Pro Val Ser Gln Gly Asn Thr Arg Asn Leu Thr
        35                  40                  45

Asp Leu Trp Glu Lys Glu Thr Ala Ser Gln Thr Lys Thr Pro Ala Gln
    50                  55                  60

Ser Pro Gln Thr Thr Gln Val Gln Ser Asp Glu Asn Glu Glu Gly Glu
65                  70                  75                  80

Ile Lys Ser Glu Ser Ile Asp Gly His Ile Arg Gly Thr Val Asn Gln
                85                  90                  95

Ser Glu Gln Val Pro Glu Gln Asn Gln Ser Arg Ser Ser Pro Gly Asp
            100                 105                 110

Asp Leu Asp Arg Ala Leu Asn Lys Leu Glu Gly Arg Ile Asn Ser Ile
        115                 120                 125

Ser Ser Met Asp Lys Glu Ile Lys Lys Gly Pro Arg Ile Gln Asn Leu
    130                 135                 140

Pro Gly Ser Gln Ala Ala Thr Gln Gln Ala Thr His Pro Leu Ala Gly
145                 150                 155                 160

Asp Thr Pro Asn Met Gln Ala Gln Thr Lys Ala Leu Ala Lys Pro His
                165                 170                 175

Gln Glu Ala Ile Asn Pro Gly Asn Gln Asp Thr Gly Glu Ser Ile His
            180                 185                 190

Leu Pro Pro Ser Met Ala Pro Pro Glu Ser Leu Val Gly Ala Ile Arg
        195                 200                 205

Asn Ala Pro Gln Phe Val Pro Asp Gln Ser Met Thr Asn Val Asp Ala
    210                 215                 220

Gly Ser Val Gln Leu His Ala Ser Cys Ala Glu Met Ile Ser Arg Met
225                 230                 235                 240

Phe Val Glu Val Ile Ser Lys Leu Asp Lys Leu Glu Ser Arg Leu Asn
                245                 250                 255
```

```
Asp Ile Ala Lys Val Val Asn Thr Thr Pro Leu Ile Arg Asn Asp Ile
            260                 265                 270

Asn Gln Leu Lys Ala Thr Thr Ala Leu Met Ser Asn Gln Ile Ala Ser
        275                 280                 285

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

Met Lys Ser Val Thr Lys Lys Ala Ala Val Val Ile Ala Gly Phe Gly
305                 310                 315                 320

Asp Asp Pro Thr Gln Ile Ile Glu Glu Gly Ile Met Ala Lys Asp Ala
                325                 330                 335

Leu Gly Lys Pro Val Pro Pro Thr Ser Val Ile Ser Ala Lys Ala Gln
            340                 345                 350

Thr Ser Ser Gly Val Ser Lys Gly Glu Ile Glu Gly Leu Ile Ala Leu
        355                 360                 365

Val Glu Thr Leu Val Asp Asn Asp Lys Lys Ala Ala Lys Leu Ile Lys
    370                 375                 380

Met Ile Asp Gln Val Lys Ser His Ala Asp Tyr Ala Arg Val Lys Gln
385                 390                 395                 400

Ala Ile Tyr Asn Ala
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<210> 57
<211> 1110
<212> DNA
<213> artificial sequence

<220>
<223> M gene of FJ215863

<400> 57

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agggtagatt caattggcga tgtgcagaac gccaaagagt cctcgatatt cgtgactcta 180

tatggtttca tccaagcaat taaggagagt acagatcgat cgaaattctt ccatccaaaa 240

gatgacttca aacctgagac agtcactgca ggactggtag tggtaggtgc gatccgaatg 300

atggctgatg ttaataccat ctctaatgac gcactagcgc tggagatcac tgttaagaaa 360

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actgcaataa ctatccgagc aggaggtttc atctcgaatg cagacgagaa tataaaatgt 480

gccagcaagt tgactgcagg agtgcagtac atattccgcc caatgtttgt ttcaatcact 540

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caggcaaaga tgctgaagaa ggtcacaatc ggcgatgcag acacatactg ggggtttgca 720

tggttccacc tgtgcaattt caaaaagaca tcctctaagg gaaagccaag aacgctagac 780

gaactaaaga caaaagtcaa aaacatgggg ttgaaattgg agttacatga cttgtggggt 840

ccgactattg tggtccaaat cactggcaag agcagcaaat atgctcaagg atttttttcc 900

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tggtcctgtt cagcaactat cggtgacgca acagttgtta tccagtcaag cgagaaaggg 1020

gaactcctaa ggtctgatga cctcgagata cgaggtgctg tggcctccaa gaaaggtaga 1080

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<210> 58
<211> 369
<212> PRT
<213> artificial sequence

<220>
<223> M protein of ACO48299

<400> 58

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

Gln Asn Ala Lys Glu Ser Ser Ile Phe Val Thr Leu Tyr Gly Phe Ile
    50                  55                  60

Gln Ala Ile Lys Glu Ser Thr Asp Arg Ser Lys Phe Phe His Pro Lys
65                  70                  75                  80

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

Ala Ile Arg Met Met Ala Asp Val Asn Thr Ile Ser Asn Asp Ala Leu
            100                 105                 110

Ala Leu Glu Ile Thr Val Lys Lys Ser Ala Thr Ser Gln Glu Lys Met
        115                 120                 125
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Thr Val Met Phe His Asn Ser Pro Pro Ser Leu Arg Thr Ala Ile Thr
    130                 135                 140

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

Ala Ser Lys Leu Thr Ala Gly Val Gln Tyr Ile Phe Arg Pro Met Phe
                165                 170                 175

Val Ser Ile Thr Lys Leu His Asn Gly Lys Leu Tyr Arg Val Pro Lys
            180                 185                 190

Ser Ile His Ser Ile Ser Ser Thr Leu Leu Tyr Ser Val Met Leu Glu
        195                 200                 205

Val Gly Phe Lys Val Asp Ile Gly Lys Asp His Pro Gln Ala Lys Met
    210                 215                 220

Leu Lys Lys Val Thr Ile Gly Asp Ala Asp Thr Tyr Trp Gly Phe Ala
225                 230                 235                 240

Trp Phe His Leu Cys Asn Phe Lys Lys Thr Ser Ser Lys Gly Lys Pro
                245                 250                 255

Arg Thr Leu Asp Glu Leu Lys Thr Lys Val Lys Asn Met Gly Leu Lys
            260                 265                 270

Leu Glu Leu His Asp Leu Trp Gly Pro Thr Ile Val Val Gln Ile Thr
        275                 280                 285

Gly Lys Ser Ser Lys Tyr Ala Gln Gly Phe Phe Ser Ser Asn Gly Thr
    290                 295                 300

Cys Cys Leu Pro Ile Ser Arg Ser Ala Pro Gly Leu Gly Lys Leu Leu
305                 310                 315                 320

Trp Ser Cys Ser Ala Thr Ile Gly Asp Ala Thr Val Val Ile Gln Ser
                325                 330                 335

Ser Glu Lys Gly Glu Leu Leu Arg Ser Asp Asp Leu Glu Ile Arg Gly
            340                 345                 350

Ala Val Ala Ser Lys Lys Gly Arg Leu Ser Ser Phe His Pro Phe Lys
        355                 360                 365

Lys
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<210> 59
<211> 1632
<212> DNA
<213> artificial sequence

<220>
<223> F gene of FJ215863

<400> 59

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aacatcttag gcccactcaa atccaatctg gatgcactgc tctcatctga gacttatccc 300

cagacaagat taattggggc agttataggt tcaattgctc tcggtgttgc aacatcggct 360

caaatcactg ctgcagttgc tctcaagcaa gcgcaagaca atgcaaggaa catactagca 420

ctcaaagaag cactgtccaa aaccaatgag gcggtcaagg agcttagtag tgggttacaa 480

caaacagcta ttgcacttgg taagatacag agttttgtga atgaggaaat tctgccatct 540

atcaaccaac tgagctgcga ggtgacagcc aataaacttg gggtgtattt atctctgtat 600

ctcacagaac tgaccaccat attcggtgca cagctgacta accctgcatt gacttcatta 660

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ggaattaaac aacaagacgt taattcgcta tatgaagccg gactaatcac aggacaagtc 780

attggttatg actctcagta ccagctgctg gtcatccagg tcaattatcc aagcatttct 840

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gaagggaaag caattgtacc ccaatttgta gctgaaagtc gggtgactat tgaagagctt 960

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gctgcagtaa catatgttga tgccacaatc tgcaaaacaa ttcaattgga tgatatacaa 1260

ctccagctgg aagggtcact atcatcagtt tatgcaagaa acatctcaat tgagatcagt 1320

caggtgacca cctccgggtc tttagatatc agcagtgaga taggaaacat caataatacg 1380

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cacattgtta ataatacaac actaatcgta ctctgtgtgt taagtgcgct tgctgtgatc 1500

tggctggcag tattaacggc tattataata tacttgagaa caaagttgaa gactatatcg 1560

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tctaagtttt ga 1632

<210> 60
<211> 543
<212> PRT
<213> artificial sequence

<220>
<223> F protein of ACO48300

<400> 60

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            20                  25                  30

Val Ala Ser Ala Asn Glu Trp Gln Leu Ala Ala Tyr Thr Thr Ser Leu
        35                  40                  45

Ser Gly Thr Ile Ala Val Arg Phe Leu Pro Val Leu Pro Asp Asn Met
    50                  55                  60

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

Asn Ile Leu Gly Pro Leu Lys Ser Asn Leu Asp Ala Leu Leu Ser Ser
                85                  90                  95

Glu Thr Tyr Pro Gln Thr Arg Leu Ile Gly Ala Val Ile Gly Ser Ile
            100                 105                 110

Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu
        115                 120                 125

Lys Gln Ala Gln Asp Asn Ala Arg Asn Ile Leu Ala Leu Lys Glu Ala
    130                 135                 140

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

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

Ile Leu Pro Ser Ile Asn Gln Leu Ser Cys Glu Val Thr Ala Asn Lys
            180                 185                 190

Leu Gly Val Tyr Leu Ser Leu Tyr Leu Thr Glu Leu Thr Thr Ile Phe
        195                 200                 205

Gly Ala Gln Leu Thr Asn Pro Ala Leu Thr Ser Leu Ser Tyr Gln Ala
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Leu Tyr Asn Leu Cys Gly Gly Asn Met Ala Met Leu Thr Gln Lys Ile
225                 230                 235                 240

Gly Ile Lys Gln Gln Asp Val Asn Ser Leu Tyr Glu Ala Gly Leu Ile
                245                 250                 255

Thr Gly Gln Val Ile Gly Tyr Asp Ser Gln Tyr Gln Leu Leu Val Ile
            260                 265                 270

Gln Val Asn Tyr Pro Ser Ile Ser Glu Val Thr Gly Val Arg Ala Thr
        275                 280                 285

Glu Leu Val Thr Val Ser Val Thr Thr Asp Lys Gly Glu Gly Lys Ala
    290                 295                 300

Ile Val Pro Gln Phe Val Ala Glu Ser Arg Val Thr Ile Glu Glu Leu
305                 310                 315                 320

Asp Val Ala Ser Cys Lys Phe Ser Ser Thr Thr Leu Tyr Cys Arg Gln
                325                 330                 335

Val Asn Thr Arg Ala Leu Pro Pro Leu Val Ala Ser Cys Leu Arg Gly
            340                 345                 350

Asn Tyr Asp Asp Cys Gln Tyr Thr Thr Glu Ile Gly Ala Leu Ser Ser
        355                 360                 365

Arg Tyr Ile Thr Leu Asp Gly Gly Val Leu Val Asn Cys Lys Ser Ile
    370                 375                 380

Val Cys Arg Cys Leu Asn Pro Ser Lys Ile Ile Ser Gln Asn Thr Asn
385                 390                 395                 400

Ala Ala Val Thr Tyr Val Asp Ala Thr Ile Cys Lys Thr Ile Gln Leu
                405                 410                 415

Asp Asp Ile Gln Leu Gln Leu Glu Gly Ser Leu Ser Ser Val Tyr Ala
            420                 425                 430

Arg Asn Ile Ser Ile Glu Ile Ser Gln Val Thr Thr Ser Gly Ser Leu
        435                 440                 445

Asp Ile Ser Ser Glu Ile Gly Asn Ile Asn Asn Thr Val Asn Arg Val
    450                 455                 460

Glu Asp Leu Ile His Gln Ser Glu Glu Trp Leu Ala Lys Val Asn Pro
465                 470                 475                 480
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His Ile Val Asn Asn Thr Thr Leu Ile Val Leu Cys Val Leu Ser Ala
485                 490                 495

Leu Ala Val Ile Trp Leu Ala Val Leu Thr Ala Ile Ile Ile Tyr Leu
500                 505                 510

Arg Thr Lys Leu Lys Thr Ile Ser Ala Leu Ala Val Thr Asn Thr Ile
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Gln Ser Asn Pro Tyr Val Asn Gln Thr Lys Arg Glu Ser Lys Phe
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aacgggacca accttatcat acctacatca gacaaggagt atgcaggagg aattggaaac 420

cctgtattta ctgtcgatgc tggaggttct ataggattca aacagtttag cttaatagaa 480

catccgagct ttattgctgg acctacaacg acccgaggct gtacaagaat acccactttt 540

cacatgtcag aaagtcattg gtgctactca cacaacatca tcgctgctgg ctgtcaagat 600

gccagtgcat ccagtatgta tatctcaatg ggagttctcc atgtgtcctc atctggcact 660

cccatttttc ttactactgc aagtgagctg atagacgatg gagttaaccg taagtcatgc 720

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gatgctcctg ttagaaggac ttatcccaga tttggaattg caaatcagtc acactggtac 1560

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<213> artificial sequence

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<223> HN protein of ACO48301

<400> 62

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            20                  25                  30

Thr Thr Gly Cys Leu Ala Leu Ser Ile Ile Ser Ile Val Gln Ile Gly
        35                  40                  45

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

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

Ile Asn Asp Ile Phe Arg Ile Val Ala Leu Asp Ile Pro Leu Gln Val
                85                  90                  95

Thr Asn Ile Gln Lys Asp Leu Ala Ser Gln Phe Asn Met Leu Ile Asp
            100                 105                 110

Ser Leu Asn Ala Ile Lys Leu Gly Asn Gly Thr Asn Leu Ile Ile Pro
        115                 120                 125

Thr Ser Asp Lys Glu Tyr Ala Gly Gly Ile Gly Asn Pro Val Phe Thr
    130                 135                 140
```

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

His Pro Ser Phe Ile Ala Gly Pro Thr Thr Thr Arg Gly Cys Thr Arg
                165                 170                 175

Ile Pro Thr Phe His Met Ser Glu Ser His Trp Cys Tyr Ser His Asn
            180                 185                 190

Ile Ile Ala Ala Gly Cys Gln Asp Ala Ser Ala Ser Ser Met Tyr Ile
        195                 200                 205

Ser Met Gly Val Leu His Val Ser Ser Ser Gly Thr Pro Ile Phe Leu
    210                 215                 220

Thr Thr Ala Ser Glu Leu Ile Asp Asp Gly Val Asn Arg Lys Ser Cys
225                 230                 235                 240

Ser Ile Val Ala Thr Arg Phe Gly Cys Asp Ile Leu Cys Ser Ile Val
                245                 250                 255

Thr Glu Lys Glu Gly Asp Asp Tyr Trp Ser Asp Thr Pro Thr Pro Met
            260                 265                 270

Arg His Gly Arg Phe Ser Phe Asn Gly Ser Phe Val Glu Ala Glu Leu
        275                 280                 285

Pro Val Ser Ser Met Phe Ser Ser Phe Ser Ala Asn Tyr Pro Ala Val
    290                 295                 300

Gly Ser Gly Glu Ile Val Lys Asp Arg Ile Leu Phe Pro Ile Tyr Gly
305                 310                 315                 320

Gly Ile Lys Gln Thr Ser Pro Glu Phe Thr Glu Leu Val Lys Tyr Gly
                325                 330                 335

Leu Phe Val Ser Thr Pro Thr Thr Val Cys Gln Ser Ser Trp Thr Tyr
            340                 345                 350

Asp Gln Val Lys Ala Ala Tyr Arg Pro Asp Tyr Ile Ser Gly Arg Phe
        355                 360                 365

Trp Ala Gln Val Ile Leu Ser Cys Ala Leu Asp Ala Val Asp Leu Ser
    370                 375                 380

Ser Cys Ile Val Lys Ile Met Asn Ser Ser Thr Val Met Met Ala Ala
385                 390                 395                 400
```

Glu Gly Arg Ile Met Lys Ile Gly Ile Asp Tyr Phe Tyr Tyr Gln Arg
405 410 415

Ser Ser Ser Trp Trp Pro Leu Ala Phe Val Thr Lys Leu Asp Pro Gln
420 425 430

Glu Leu Ala Asp Thr Asn Ser Ile Trp Leu Thr Asn Ser Ile Pro Ile
435 440 445

Pro Gln Ser Lys Phe Pro Arg Pro Ser Tyr Ser Glu Asn Tyr Cys Thr
450 455 460

Lys Pro Ala Val Cys Pro Ala Thr Cys Val Thr Gly Val Tyr Ser Asp
465 470 475 480

Ile Trp Pro Leu Thr Ser Ser Ser Ser Leu Pro Ser Ile Ile Trp Ile
485 490 495

Gly Gln Tyr Leu Asp Ala Pro Val Arg Arg Thr Tyr Pro Arg Phe Gly
500 505 510

Ile Ala Asn Gln Ser His Trp Tyr Leu Gln Glu Asp Ile Leu Pro Thr
515 520 525

Ser Thr Ala Ser Ala Tyr Ser Thr Thr Thr Cys Phe Lys Asn Thr Ala
530 535 540

Arg Asn Arg Val Phe Cys Val Thr Ile Ala Glu Phe Ala Asp Gly Leu
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Phe Gly Glu Tyr Arg Ile Thr Pro Gln Leu Tyr Glu Leu Val Arg Asn
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Asn

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<211> 6717
<212> DNA
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<220>
<223> L gene of FJ215863

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attaatttgg caaatcttga tccgataacc caccccaaaa gtttgtattg gttatccaga 300

ctaacaatag ctagtgctgg aacctttaga catatgaaag atagaatctt gtgtacagtt 360

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ggtaacggtg atttatttaa tcaaagtctc tcaggtacac gtttgactgc gagtccgtta 480

tccccttttat gcgatcaatt tgtctctgac atcaagtctg cagtcacgac accctggtca 540

gaagctcgtt ggtcttggct tcatatcaaa caaacaatga gatatctaat aaaacaatca 600

tgcactacaa attcggctca tttaacagaa atcataaaag aggaatgggg tttagtaggt 660

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            20                  25                  30

Gly Leu Pro Met Pro Ala Asp Leu Arg Gln Lys Ser Val Val Met His
        35                  40                  45

Ile Pro Asp His Ile Leu Glu Lys Ser Glu Tyr Arg Ile Lys His Arg
    50                  55                  60

Leu Gly Lys Ile Lys Ser Asp Ile Thr His Tyr Cys Gln Tyr Phe Asn
65                  70                  75                  80

Ile Asn Leu Ala Asn Leu Asp Pro Ile Thr His Pro Lys Ser Leu Tyr
                85                  90                  95

Trp Leu Ser Arg Leu Thr Ile Ala Ser Ala Gly Thr Phe Arg His Met
            100                 105                 110

Lys Asp Arg Ile Leu Cys Thr Val Gly Ser Glu Phe Gly His Lys Ile
        115                 120                 125
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Gln Asp Leu Phe Ser Leu Leu Ser His Lys Leu Val Gly Asn Gly Asp
    130                 135                 140

Leu Phe Asn Gln Ser Leu Ser Gly Thr Arg Leu Thr Ala Ser Pro Leu
145                 150                 155                 160

Ser Pro Leu Cys Asp Gln Phe Val Ser Asp Ile Lys Ser Ala Val Thr
                165                 170                 175

Thr Pro Trp Ser Glu Ala Arg Trp Ser Trp Leu His Ile Lys Gln Thr
            180                 185                 190

Met Arg Tyr Leu Ile Lys Gln Ser Cys Thr Thr Asn Ser Ala His Leu
        195                 200                 205

Thr Glu Ile Ile Lys Glu Glu Trp Gly Leu Val Gly Ile Thr Pro Asp
    210                 215                 220

Leu Val Ile Leu Phe Asp Arg Val Asn Asn Ser Leu Thr Ala Leu Thr
225                 230                 235                 240

Phe Glu Met Val Leu Met Tyr Ser Asp Val Leu Glu Ser Arg Asp Asn
                245                 250                 255

Ile Val Leu Val Gly Arg Leu Ser Thr Phe Leu Gln Pro Val Val Ser
            260                 265                 270

Arg Leu Glu Val Leu Phe Asp Leu Val Asp Ser Leu Ala Lys Ile Leu
        275                 280                 285

Gly Asp Thr Ile Tyr Glu Ile Ile Ala Val Leu Glu Ser Leu Ser Tyr
    290                 295                 300

Gly Ser Val Gln Leu His Asp Ala Ser His Ser His Ala Gly Ser Phe
305                 310                 315                 320

Phe Ser Phe Asn Met Asn Glu Leu Asp Asn Thr Leu Ser Lys Arg Val
                325                 330                 335

Asp Pro Lys His Lys Asn Thr Ile Met Ser Ile Ile Arg Gln Cys Phe
            340                 345                 350

Ser Asn Leu Asp Val Asp Gln Ala Ala Glu Met Leu Cys Leu Met Arg
        355                 360                 365

Leu Phe Gly His Pro Met Leu Thr Ala Pro Asp Ala Ala Ala Lys Val
    370                 375                 380

Arg Lys Ala Met Cys Ala Pro Lys Leu Val Glu His Asp Thr Ile Leu
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385 390 395 400

Gln Thr Leu Ser Phe Phe Lys Gly Ile Ile Ile Asn Gly Tyr Arg Arg
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Ser His Ser Gly Leu Trp Pro Asn Val Glu Pro Ser Ser Ile Tyr Asp
420 425 430

Asp Asp Leu Arg Gln Leu Tyr Leu Glu Ser Ala Glu Ile Ser His His
435 440 445

Phe Met Leu Lys Asn Tyr Lys Ser Leu Ser Met Ile Glu Phe Lys Lys
450 455 460

Ser Ile Asp Tyr Asp Leu His Asp Asp Leu Ser Thr Phe Leu Lys Asp
465 470 475 480

Arg Ala Ile Cys Arg Pro Lys Ser Gln Trp Asp Val Ile Phe Arg Lys
485 490 495

Ser Leu Arg Arg Ser His Thr Gln Ser Gln Tyr Leu Asp Glu Ile Lys
500 505 510

Ser Asn Arg Leu Leu Ile Asp Phe Leu Asp Ser Ala Glu Phe Asp Pro
515 520 525

Glu Lys Glu Phe Ala Tyr Val Thr Thr Met Asp Tyr Leu His Asp Asn
530 535 540

Glu Phe Cys Ala Ser Tyr Ser Leu Lys Glu Lys Glu Ile Lys Thr Thr
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Gly Arg Ile Phe Ala Lys Met Thr Arg Asn Met Arg Ser Cys Gln Val
565 570 575

Ile Leu Glu Ser Leu Leu Ser Lys His Ile Cys Lys Phe Phe Lys Glu
580 585 590

Asn Gly Val Ser Met Glu Gln Leu Ser Leu Thr Lys Ser Leu Leu Ala
595 600 605

Met Ser Gln Leu Ser Pro Lys Val Ser Thr Leu Gln Asp Thr Ala Ser
610 615 620

Arg His Val Gly Asn Ser Lys Ser Gln Ile Ala Thr Ser Asn Pro Ser
625 630 635 640

Arg His His Ser Thr Ala Asn Gln Met Ser Leu Ser Asn Arg Lys Thr
645 650 655

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Val Val Ala Thr Phe Leu Thr Thr Asp Leu Glu Lys Tyr Cys Leu Gln
            660                 665                 670

Trp Arg Tyr Ser Thr Ile Lys Leu Phe Ala Gln Ala Leu Asn Gln Leu
        675                 680                 685

Phe Gly Ile Asp His Gly Phe Glu Trp Ile His Leu Arg Leu Met Asn
    690                 695                 700

Ser Thr Leu Phe Val Gly Asp Pro Tyr Ser Pro Pro Glu Asp Pro Thr
705                 710                 715                 720

Leu Glu Asp Ile Asp Lys Ala Pro Asn Asp Asp Ile Phe Ile Val Ser
                725                 730                 735

Pro Arg Gly Gly Ile Glu Gly Leu Cys Gln Lys Met Trp Thr Met Ile
            740                 745                 750

Ser Ile Ser Ala Ile His Cys Val Ala Glu Lys Ile Gly Ala Arg Val
        755                 760                 765

Ala Ala Met Val Gln Gly Asp Asn Gln Val Ile Ala Ile Thr Lys Glu
    770                 775                 780

Leu Phe Arg Gly Glu Lys Ala Cys Asp Val Arg Asp Glu Leu Asp Glu
785                 790                 795                 800

Leu Gly Gln Val Phe Phe Asp Glu Phe Lys Arg His Asn Tyr Ala Ile
                805                 810                 815

Gly His Asn Leu Lys Leu Asn Glu Thr Ile Gln Ser Gln Ser Phe Phe
            820                 825                 830

Val Tyr Ser Lys Arg Ile Phe Phe Glu Gly Arg Leu Leu Ser Gln Val
        835                 840                 845

Leu Lys Asn Ala Ala Lys Leu Cys Met Val Ala Asp His Leu Gly Glu
    850                 855                 860

Asn Thr Val Ser Ser Cys Ser Asn Leu Ser Ser Thr Ile Ala Arg Leu
865                 870                 875                 880

Val Glu Asn Gly Phe Glu Lys Asp Thr Ala Phe Val Leu Asn Leu Val
                885                 890                 895

Tyr Ile Met Thr Gln Ile Leu Phe Asp Glu His Tyr Ser Ile Val Cys
            900                 905                 910
```

```
Asp His His Ser Val Lys Ser Leu Ile Gly Ser Lys Asn His Arg Asn
        915                 920                 925

Leu Leu Tyr Ser Ser Leu Ile Pro Gly Gln Leu Gly Gly Phe Asn Phe
    930                 935                 940

Leu Asn Ile Ser Arg Leu Phe Thr Arg Asn Ile Gly Asp Pro Val Thr
945                 950                 955                 960

Cys Ser Leu Ser Asp Leu Lys Cys Phe Ile Ala Ala Gly Leu Leu Pro
                965                 970                 975

Pro Tyr Val Leu Lys Asn Val Val Leu Arg Glu Pro Gly Pro Gly Thr
            980                 985                 990

Trp Leu Thr Leu Cys Ser Asp Pro  Tyr Thr Leu Asn Ile  Pro Tyr Thr
        995                 1000                1005

Gln Leu  Pro Thr Thr Tyr Leu  Lys Lys His Thr Gln  Arg Ser Leu
    1010                1015                1020

Leu Ser  Arg Ala Val Asn Pro  Leu Leu Ala Gly Val  Gln Val Pro
    1025                1030                1035

Asn Gln  His Glu Glu Glu Glu  Val Leu Ala Arg Phe  Leu Leu Asp
    1040                1045                1050

Arg Glu  Tyr Val Met Pro Arg  Val Ala His Val Ile  Leu Glu Thr
    1055                1060                1065

Ser Val  Leu Gly Lys Arg Lys  Gln Ile Gln Gly Leu  Ile Asp Thr
    1070                1075                1080

Thr Pro  Thr Ile Ile Arg Thr  Ser Leu Val Asn Leu  Pro Val Ser
    1085                1090                1095

Arg Lys  Lys Cys Glu Lys Ile  Ile Asn Tyr Ser Leu  Asn Tyr Ile
    1100                1105                1110

Ala Glu  Cys His Asp Ser Leu  Leu Ser Gln Val Cys  Phe Ser Asp
    1115                1120                1125

Asn Lys  Glu Tyr Leu Trp Ser  Thr Ser Leu Ile Ser  Val Glu Thr
    1130                1135                1140

Cys Ser  Val Thr Ile Ala Asp  Tyr Leu Arg Ala Val  Ser Trp Ser
    1145                1150                1155
```

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Asn Ile  Leu Gly Gly Arg Asn  Ile Ser Gly Val Thr  Thr Pro Asp
    1160                 1165                 1170

Thr Ile  Glu Leu Ile Gln Gly  Cys Leu Ile Gly Glu  Asn Ser Ser
    1175                 1180                 1185

Cys Thr  Leu Cys Glu Ser His  Asp Asp Ala Phe Thr  Trp Met His
    1190                 1195                 1200

Leu Pro  Gly Pro Leu Tyr Ile  Pro Glu Pro Ser Val  Thr Asn Ser
    1205                 1210                 1215

Lys Met  Arg Val Pro Tyr Leu  Gly Ser Lys Thr Glu  Glu Arg Lys
    1220                 1225                 1230

Thr Ala  Ser Met Ala Ala Ile  Lys Gly Met Ser His  His Leu Arg
    1235                 1240                 1245

Ala Val  Leu Arg Gly Thr Ser  Val Phe Ile Trp Ala  Phe Gly Asp
    1250                 1255                 1260

Thr Asp  Ile Asn Trp Asp Asn  Ala Leu Gln Ile Ala  Gln Ser Arg
    1265                 1270                 1275

Cys Asn  Ile Thr Leu Asp Gln  Met Arg Leu Leu Thr  Pro Ile Pro
    1280                 1285                 1290

Ser Ser  Ser Asn Ile Gln His  Arg Leu Asp Asp Gly  Ile Ser Thr
    1295                 1300                 1305

Gln Lys  Phe Thr Pro Ala Ser  Leu Ala Arg Ile Thr  Ser Phe Val
    1310                 1315                 1320

His Ile  Cys Asn Asp Ser Gln  Arg Leu Glu Lys Asp  Gly Ser Ser
    1325                 1330                 1335

Val Asp  Ser Asn Leu Ile Tyr  Gln Gln Ile Met Leu  Leu Gly Leu
    1340                 1345                 1350

Ser Ile  Phe Glu Thr Met Tyr  Ser Met Asp Gln Lys  Trp Val Phe
    1355                 1360                 1365

Asn Asn  His Thr Leu His Leu  His Thr Gly His Ser  Cys Cys Pro
    1370                 1375                 1380

Arg Glu  Leu Asp Ile Ser Leu  Val Asn Pro Pro Arg  His Gln Thr
    1385                 1390                 1395

Pro Glu  Leu Thr Ser Thr Thr  Thr Asn Pro Phe Leu  Tyr Asp Gln
```

```
    1400                1405                1410

Leu Pro  Leu Asn Gln Glu Asn  Leu Thr Thr Leu Glu  Ile Lys Thr
    1415                1420                1425

Phe Lys  Phe Asn Glu Leu Asn  Ile Asp Gly Leu Asp  Phe Gly Glu
    1430                1435                1440

Gly Ile  Gln Leu Leu Ser Arg  Cys Thr Ala Arg Leu  Met Ala Glu
    1445                1450                1455

Cys Ile  Leu Glu Glu Gly Ile  Gly Ser Ser Val Lys  Asn Glu Ala
    1460                1465                1470

Ile Val  Asn Phe Asp Asn Ser  Val Asn Trp Ile Ser  Glu Cys Leu
    1475                1480                1485

Met Cys  Asp Ile Arg Ser Leu  Cys Val Asn Leu Gly  Gln Glu Ile
    1490                1495                1500

Leu Cys  Ser Leu Ala Tyr Gln  Met Tyr Tyr Leu Arg  Ile Arg Gly
    1505                1510                1515

Arg Arg  Ala Ile Leu Asn Tyr  Leu Asp Thr Thr Leu  Gln Arg Ile
    1520                1525                1530

Pro Val  Ile Gln Leu Ala Asn  Ile Ala Leu Thr Ile  Ser His Pro
    1535                1540                1545

Glu Ile  Phe Arg Arg Ile Val  Asn Thr Gly Ile His  Asn Gln Ile
    1550                1555                1560

Lys Gly  Pro Tyr Val Ala Thr  Thr Asp Phe Ile Ala  Ala Ser Arg
    1565                1570                1575

Asp Ile  Ile Leu Ser Gly Ala  Arg Glu Tyr Leu Ser  Tyr Leu Ser
    1580                1585                1590

Ser Gly  Gln Glu Asp Cys Tyr  Thr Phe Phe Asn Cys  Gln Asp Gly
    1595                1600                1605

Asp Leu  Thr Pro Lys Met Glu  Gln Tyr Leu Ala Arg  Arg Ala Cys
    1610                1615                1620

Leu Leu  Thr Leu Leu Tyr Asn  Thr Gly His Gln Ile  Pro Val Ile
    1625                1630                1635

Arg Ser  Leu Thr Pro Ile Glu  Lys Cys Lys Val Leu  Thr Glu Tyr
    1640                1645                1650
```

```
Asn Gln  Gln Ile Glu Tyr Ala  Asp Gln Glu Phe Ser  Ser Val Leu
    1655                 1660                 1665

Lys Val  Val Asn Ala Leu Leu  Gln Asn Pro Lys Ile  Asp Ala Leu
    1670                 1675                 1680

Val Ser  Asn Leu Tyr Phe Thr  Thr Arg Arg Val Leu  Ser Asn Leu
    1685                 1690                 1695

Arg Ser  Cys Asp Lys Ala Arg  Ser Tyr Ile Glu Tyr  Leu Tyr Thr
    1700                 1705                 1710

Glu Asp  Phe Gly Glu Lys Glu  Asp Thr Val Gln Tyr  Asp Ile Met
    1715                 1720                 1725

Thr Thr  Asn Asp Ile Ile Leu  Thr His Gly Leu Phe  Thr Gln Ile
    1730                 1735                 1740

Glu Ile  Ser Tyr Gln Gly Asn  Ser Leu His Lys Phe  Leu Thr Pro
    1745                 1750                 1755

Asp Asn  Ala Pro Gly Ser Leu  Ile Pro Phe Ser Ile  Ser Pro Asn
    1760                 1765                 1770

Ser Leu  Ala Cys Asp Pro Leu  His His Leu Leu Lys  Ser Val Gly
    1775                 1780                 1785

Thr Ser  Ser Thr Ser Trp Tyr  Lys Tyr Ala Ile Ala  Tyr Ala Val
    1790                 1795                 1800

Ser Glu  Lys Arg Ser Ala Arg  Leu Gly Gly Ser Leu  Tyr Ile Gly
    1805                 1810                 1815

Glu Gly  Ser Gly Ser Val Met  Thr Leu Leu Glu Tyr  Leu Glu Pro
    1820                 1825                 1830

Ser Val  Asp Ile Phe Tyr Asn  Ser Leu Phe Ser Asn  Gly Met Asn
    1835                 1840                 1845

Pro Pro  Gln Arg Asn Tyr Gly  Leu Met Pro Leu Gln  Phe Val Asn
    1850                 1855                 1860

Ser Val  Val Tyr Lys Asn Leu  Thr Ala Lys Ser Glu  Cys Lys Leu
    1865                 1870                 1875

Gly Phe  Val Gln Gln Phe Lys  Pro Leu Trp Arg Asp  Ile Asp Ile
    1880                 1885                 1890
```

```
Glu Thr  Asn Val Thr Asp Pro  Ser Phe Val Asn Phe  Ala Leu Asn
    1895                1900                1905

Glu Ile  Pro Met Gln Ser Leu  Lys Arg Val Asn Cys  Asp Val Glu
    1910                1915                1920

Phe Asp  Arg Gly Met Pro Ile  Glu Arg Val Ile Gln  Gly Tyr Thr
    1925                1930                1935

His Ile  Leu Leu Val Ala Thr  Tyr Gly Leu Gln Gln  Asp Ser Ile
    1940                1945                1950

Leu Trp  Val Lys Val Tyr Arg  Thr Ser Glu Lys Val  Phe Gln Phe
    1955                1960                1965

Leu Leu  Ser Ala Met Ile Met  Ile Phe Gly Tyr Val  Lys Ile His
    1970                1975                1980

Arg Asn  Gly Tyr Met Ser Thr  Lys Asp Glu Glu Tyr  Ile Leu Met
    1985                1990                1995

Ser Asp  Cys Lys Glu Pro Val  Asn Tyr Thr Ala Val  Pro Asn Ile
    2000                2005                2010

Leu Thr  Arg Val Ser Asp Leu  Val Ser Lys Asn Leu  Ser Leu Ile
    2015                2020                2025

His Pro  Glu Asp Leu Arg Lys  Val Arg Cys Glu Thr  Asp Ser Leu
    2030                2035                2040

Asn Leu  Lys Cys Asn His Ile  Tyr Glu Lys Ile Ile  Ala Arg Lys
    2045                2050                2055

Ile Pro  Leu Gln Val Ser Ser  Thr Asp Ser Leu Leu  Leu Gln Leu
    2060                2065                2070

Gly Gly  Val Ile Asn Ser Val  Gly Ser Thr Asp Pro  Arg Glu Val
    2075                2080                2085

Ala Thr  Leu Ser Ser Ile Glu  Cys Met Asp Tyr Val  Val Ser Ser
    2090                2095                2100

Ile Asp  Leu Ala Ile Leu Glu  Ala Asn Ile Val Ile  Ser Glu Ser
    2105                2110                2115

Ala Gly  Leu Asp Leu Ala Leu  Met Leu Gly Pro Phe  Asn Leu Asn
    2120                2125                2130
```

```
Lys Leu  Lys Lys Ile Asp Thr  Ile Leu Lys Ser Ser  Thr Tyr Gln
    2135                 2140                 2145

Leu Ile  Pro Tyr Trp Leu Arg  Tyr Glu Tyr Ser Ile  Asn Pro Arg
    2150                 2155                 2160

Ser Leu  Ser Phe Leu Ile Thr  Lys Leu Gln Gln Cys  Arg Ile Ser
    2165                 2170                 2175

Trp Ser  Asp Met Ile Thr Ile  Ser Glu Phe Arg Lys  Lys Ser Lys
    2180                 2185                 2190

Arg Pro  Ile Phe Ile Lys Arg  Val Ile Gly Asn Gln  Gln Leu Lys
    2195                 2200                 2205

Ser Phe  Phe Asn Glu Ser Ser  Ser Ile Val Leu Thr  Arg Ala Glu
    2210                 2215                 2220

Val Lys  Val Cys Ile Lys Phe  Leu Gly Ala Ile Ile  Lys Leu Lys
    2225                 2230                 2235
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<211> 1386
<212> DNA
<213> artificial sequence

<220>
<223> NP gene of FJ215864

<400> 65

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aggagacctg atgttgcctc aacaggttta ctcagggcgg aaatacctgt ctgtgttaca 120

ttgtctcaag accccggtga gagatggagc cttgcttgcc ttaatatccg atggcttgtg 180

agtgattcat caaccacacc aatgaagcag ggagcaatat tgtcactgct gagtctacat 240

tcagacaata tgcgagctca cgcaacatta gcagcaaggt ctgcagatgc ttcactcacc 300

atacttgagg tagatgaagt agatattggc aactccctaa tcaaattcaa cgctagaagt 360

ggtgtatctg ataaacgatc aaatcaattg cttgcaattg cggatgacat ccccaaaagt 420

tgcagtaatg ggcatccatt tcttgacaca gacattgaga ccagagaccc gctcgatcta 480

tcagagacca tagaccgcct gcagggtatt gcagctcaga tatgggtgtc agccataaag 540

agcatgacag cgcctgacac cgcatcagag tcagaaagta agaggctggc caaataccaa 600

caacaaggcc gactggttaa gcaagtactt ttgcattctg tagtcaggac agaatttatg 660

agagttattc ggggcagctt ggtactgcgc cagtttatgg ttagcgagtg caagagggct 720

tcagccatgg gcggagacac atctaggtac tatgctatgg tgggtgacat cagtctgtac 780

atcaagaatg caggattgac tgcatttttc ctcaccctga agttcggggt tggtacccag 840

tatccaacct tagcaatgag tgttttctcc agtgacctta aaagacttgc tgcactcatc 900

aggctgtaca aaaccaaggg agacaatgca ccatacatgg cattcctgga ggactccgat 960

atgggaaatt ttgctccagc aaattatagc acaatgtact cttatgccat gggcattggg 1020

acgattctgg aagcatctgt atctcgatac cagtatgcta gagactttac cagtgagaat 1080

tatttccgtc ttggagttga gacagcccaa agccagcagg gagcgtttga cgagagaaca 1140

gcccgagaga tgggcttgac tgaggaatcc aaacagcagg ttagatcact gctaatgtca 1200

gtagacatgg gtcccagttc agttcgcgag ccatcccgcc ctgcattcat cagtcaagaa 1260

gaaaataggc agcctgccca gaattcttca gatactcagg gtcagaccaa gccagtcccg 1320

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tggtaa 1386

<210> 66
<211> 461
<212> PRT
<213> artificial sequence

<220>
<223> NP protein of ACO48303

<400> 66

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Met Ser Ser Val Phe Asn Glu Tyr Gln Ala Leu Gln Glu Gln Leu Val
1               5                  10                  15

Lys Pro Ala Val Arg Arg Pro Asp Val Ala Ser Thr Gly Leu Leu Arg
            20                  25                  30

Ala Glu Ile Pro Val Cys Val Thr Leu Ser Gln Asp Pro Gly Glu Arg
        35                  40                  45

Trp Ser Leu Ala Cys Leu Asn Ile Arg Trp Leu Val Ser Asp Ser Ser
    50                  55                  60

Thr Thr Pro Met Lys Gln Gly Ala Ile Leu Ser Leu Leu Ser Leu His
65                  70                  75                  80

Ser Asp Asn Met Arg Ala His Ala Thr Leu Ala Ala Arg Ser Ala Asp
                85                  90                  95

Ala Ser Leu Thr Ile Leu Glu Val Asp Glu Val Asp Ile Gly Asn Ser
            100                 105                 110

Leu Ile Lys Phe Asn Ala Arg Ser Gly Val Ser Asp Lys Arg Ser Asn
        115                 120                 125

Gln Leu Leu Ala Ile Ala Asp Asp Ile Pro Lys Ser Cys Ser Asn Gly
    130                 135                 140
```

```
His Pro Phe Leu Asp Thr Asp Ile Glu Thr Arg Asp Pro Leu Asp Leu
145                 150                 155                 160

Ser Glu Thr Ile Asp Arg Leu Gln Gly Ile Ala Ala Gln Ile Trp Val
                165                 170                 175

Ser Ala Ile Lys Ser Met Thr Ala Pro Asp Thr Ala Ser Glu Ser Glu
            180                 185                 190

Ser Lys Arg Leu Ala Lys Tyr Gln Gln Gln Gly Arg Leu Val Lys Gln
        195                 200                 205

Val Leu Leu His Ser Val Val Arg Thr Glu Phe Met Arg Val Ile Arg
    210                 215                 220

Gly Ser Leu Val Leu Arg Gln Phe Met Val Ser Glu Cys Lys Arg Ala
225                 230                 235                 240

Ser Ala Met Gly Gly Asp Thr Ser Arg Tyr Tyr Ala Met Val Gly Asp
                245                 250                 255

Ile Ser Leu Tyr Ile Lys Asn Ala Gly Leu Thr Ala Phe Phe Leu Thr
            260                 265                 270

Leu Lys Phe Gly Val Gly Thr Gln Tyr Pro Thr Leu Ala Met Ser Val
        275                 280                 285

Phe Ser Ser Asp Leu Lys Arg Leu Ala Ala Leu Ile Arg Leu Tyr Lys
    290                 295                 300

Thr Lys Gly Asp Asn Ala Pro Tyr Met Ala Phe Leu Glu Asp Ser Asp
305                 310                 315                 320

Met Gly Asn Phe Ala Pro Ala Asn Tyr Ser Thr Met Tyr Ser Tyr Ala
                325                 330                 335

Met Gly Ile Gly Thr Ile Leu Glu Ala Ser Val Ser Arg Tyr Gln Tyr
            340                 345                 350

Ala Arg Asp Phe Thr Ser Glu Asn Tyr Phe Arg Leu Gly Val Glu Thr
        355                 360                 365

Ala Gln Ser Gln Gln Gly Ala Phe Asp Glu Arg Thr Ala Arg Glu Met
    370                 375                 380

Gly Leu Thr Glu Glu Ser Lys Gln Gln Val Arg Ser Leu Leu Met Ser
385                 390                 395                 400
```

Val Asp Met Gly Pro Ser Ser Val Arg Glu Pro Ser Arg Pro Ala Phe
405 410 415

Ile Ser Gln Glu Glu Asn Arg Gln Pro Ala Gln Asn Ser Ser Asp Thr
420 425 430

Gln Gly Gln Thr Lys Pro Val Pro Asn Gln Pro Ala Pro Arg Ala Asp
435 440 445

Pro Asp Asp Ile Asp Pro Tyr Glu Asn Gly Leu Glu Trp
450 455 460

<210> 67
<211> 1218
<212> DNA
<213> artificial sequence

<220>
<223> P gene of FJ215864

<400> 67

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caagggaaca caagaaatct aactgatcta tgggaaaagg agactgcaag tcagaacaag 180

acatcggctc aatctccaca aaccacacaa gttcagtctg atggaaatga ggaggaagaa 240

atcaaatcag agtcaattga tggccacatc agtggaactg ttaatcaatt agagcaagtc 300

ccagaacaaa accagagcag atcttcacca ggtgatgatc tcgacagagc tctcaacaag 360

cttgaaggga gaatcaactc aatcagctca atggataaag aaattaaaaa gggccctcgc 420

atccagaatc tccctgggtc ccaagcagca actcaacagg cgacccaccc attggcaggg 480

gacaccccga acatgcaagc acggacaaaa cccctgacca agccacatca agaggcaatc 540

aatcctggca accaggacac aggagagaat attcatttac caccttccat ggcaccacca 600

gagtcattag ttggtgcaat ccgcaatgta ccccaattcg tgccagacca atctatgacg 660

aatgtagatg cggggagtgt ccaactacat gcatcatgtg cagagatgat aagtagaatg 720

tttgtagaag ttatatctaa gcttgataaa ctcgagtcga gactgaatga tatagcaaaa 780

gttgtaaaca ccacccccct tatcaggaat gatattaacc aacttaaggc cacaactgca 840

ctgatgtcca accaaattgc ttccatacaa attcttgacc cagggaatgc aggggtgagg 900

tccctctctg aaatgagatc tgtgacgaag aaagctgctg ttgtaattgc aggatttgga 960

gacgacccaa ctcaaattat tgaagaaggt atcatggcca aagatgctct tggaaaacct 1020

gtgcctccaa catctgttat cgcagccaaa gctcagactt cttccggtgt gagtaagggt 1080

gaaatagaag gattgattgc attggtggaa acattagttg acaatgacaa gaaggcagcg 1140

aaactgatta aaatgattga tcaagttaaa tcccacgccg attacgcccg agtcaagcag 1200

gcaatatata atgcataa 1218

<210> 68
<211> 405
<212> PRT
<213> artificial sequence

<220>
<223> P protein of ACO48304

<400> 68

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

Thr Thr Val Ile Lys Glu Ile Gln Lys Ser Glu Leu Lys Pro Pro Gln
            20                  25                  30

Thr Thr Gly Arg Pro Pro Val Ser Gln Gly Asn Thr Arg Asn Leu Thr
        35                  40                  45

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

Ser Pro Gln Thr Thr Gln Val Gln Ser Asp Gly Asn Glu Glu Glu Glu
65                  70                  75                  80

Ile Lys Ser Glu Ser Ile Asp Gly His Ile Ser Gly Thr Val Asn Gln
                85                  90                  95

Leu Glu Gln Val Pro Glu Gln Asn Gln Ser Arg Ser Ser Pro Gly Asp
            100                 105                 110

Asp Leu Asp Arg Ala Leu Asn Lys Leu Glu Gly Arg Ile Asn Ser Ile
        115                 120                 125

Ser Ser Met Asp Lys Glu Ile Lys Lys Gly Pro Arg Ile Gln Asn Leu
    130                 135                 140

Pro Gly Ser Gln Ala Ala Thr Gln Gln Ala Thr His Pro Leu Ala Gly
145                 150                 155                 160

Asp Thr Pro Asn Met Gln Ala Arg Thr Lys Pro Leu Thr Lys Pro His
                165                 170                 175

Gln Glu Ala Ile Asn Pro Gly Asn Gln Asp Thr Gly Glu Asn Ile His
            180                 185                 190

Leu Pro Pro Ser Met Ala Pro Pro Glu Ser Leu Val Gly Ala Ile Arg
        195                 200                 205
```

```
Asn Val Pro Gln Phe Val Pro Asp Gln Ser Met Thr Asn Val Asp Ala
    210                 215                 220

Gly Ser Val Gln Leu His Ala Ser Cys Ala Glu Met Ile Ser Arg Met
225                 230                 235                 240

Phe Val Glu Val Ile Ser Lys Leu Asp Lys Leu Glu Ser Arg Leu Asn
                245                 250                 255

Asp Ile Ala Lys Val Val Asn Thr Thr Pro Leu Ile Arg Asn Asp Ile
            260                 265                 270

Asn Gln Leu Lys Ala Thr Thr Ala Leu Met Ser Asn Gln Ile Ala Ser
        275                 280                 285

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

Met Arg Ser Val Thr Lys Lys Ala Ala Val Val Ile Ala Gly Phe Gly
305                 310                 315                 320

Asp Asp Pro Thr Gln Ile Ile Glu Glu Gly Ile Met Ala Lys Asp Ala
                325                 330                 335

Leu Gly Lys Pro Val Pro Pro Thr Ser Val Ile Ala Ala Lys Ala Gln
            340                 345                 350

Thr Ser Ser Gly Val Ser Lys Gly Glu Ile Glu Gly Leu Ile Ala Leu
        355                 360                 365

Val Glu Thr Leu Val Asp Asn Asp Lys Lys Ala Ala Lys Leu Ile Lys
    370                 375                 380

Met Ile Asp Gln Val Lys Ser His Ala Asp Tyr Ala Arg Val Lys Gln
385                 390                 395                 400

Ala Ile Tyr Asn Ala
                405
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<210> 69
<211> 1110
<212> DNA
<213> artificial sequence

<220>
<223> M gene of FJ215864

<400> 69

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agggtagatt caattggcga tgtgcagaat gccaaagagt cctcgatatt cgtgactcta 180

tatggtttca tccaagcaat taaggagaat tcagatcgat cgaaattctt ccatccaaaa 240

gatgacttca aacctgagac agtcactgca ggactggtag tagtgggtgc aatccgaatg 300

atggctgatg tcaataccat ctctaatgat gcactagcgc tggagatcac tgttaagaaa 360

tctgcaactt ctcaagagaa aatgacggtg atgttccaca atagcccccc ttcattgaga 420

actgcaataa ctatccgagc aggaggtttc atctcgaatg cagacgaaaa tataaaatgt 480

gccagcaagt tgactgcagg agtgcagtac atattccgtc caatgtttgt ttcaatcact 540

aaattacaca atggcaaact atatagggtg cccaaaagta tccacagcat ctcgtctacc 600

ctactgtata gtgtgatgtt ggaggtagga ttcaaagtgg acatcgggaa ggatcatccc 660

caggcaaaaa tgctgaagag ggtcacaatt ggcgatgcag acacatactg gggatttgca 720

tggttccacc tgtgcaattt caaaaagaca tcctctaagg gaaagccgag aacgctagac 780

gaactgaaga caaaagtcaa aaatatgggg ttgaaattgg agttacatga cctatggggt 840

ccgactattg tggtccaaat cactggcaag agcagcaaat atgctcaagg atttttttct 900

tccaatggta cttgttgcct cccaatcagc agatctgcac cagagcttgg gaagcttctg 960

tggtcctgct cagcaactat tggtgacgca acagttgtta tccaatcaag cgagaagggg 1020

gaactcctaa ggtctgatga tctcgagata cgaggtgctg tggcctccaa gaaaggtaga 1080

ctgagctcat ttcacccctt caaaaaatga 1110

<210> 70
<211> 369
<212> PRT
<213> artificial sequence

<220>
<223> M protein of ACO48305

<400> 70

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Met Ala Tyr Thr Thr Leu Lys Leu Trp Val Asp Glu Gly Asp Met Ser
1               5                  10                  15

Ser Ser Leu Leu Ser Phe Pro Leu Val Leu Lys Glu Thr Asp Arg Gly
            20                  25                  30

Thr Lys Lys Leu Gln Pro Gln Val Arg Val Asp Ser Ile Gly Asp Val
        35                  40                  45

Gln Asn Ala Lys Glu Ser Ser Ile Phe Val Thr Leu Tyr Gly Phe Ile
    50                  55                  60

Gln Ala Ile Lys Glu Asn Ser Asp Arg Ser Lys Phe Phe His Pro Lys
65                  70                  75                  80
```

```
Asp Asp Phe Lys Pro Glu Thr Val Thr Ala Gly Leu Val Val Val Gly
                85                  90                  95

Ala Ile Arg Met Met Ala Asp Val Asn Thr Ile Ser Asn Asp Ala Leu
            100                 105                 110

Ala Leu Glu Ile Thr Val Lys Lys Ser Ala Thr Ser Gln Glu Lys Met
        115                 120                 125

Thr Val Met Phe His Asn Ser Pro Pro Ser Leu Arg Thr Ala Ile Thr
    130                 135                 140

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

Ala Ser Lys Leu Thr Ala Gly Val Gln Tyr Ile Phe Arg Pro Met Phe
                165                 170                 175

Val Ser Ile Thr Lys Leu His Asn Gly Lys Leu Tyr Arg Val Pro Lys
            180                 185                 190

Ser Ile His Ser Ile Ser Ser Thr Leu Leu Tyr Ser Val Met Leu Glu
        195                 200                 205

Val Gly Phe Lys Val Asp Ile Gly Lys Asp His Pro Gln Ala Lys Met
    210                 215                 220

Leu Lys Arg Val Thr Ile Gly Asp Ala Asp Thr Tyr Trp Gly Phe Ala
225                 230                 235                 240

Trp Phe His Leu Cys Asn Phe Lys Lys Thr Ser Ser Lys Gly Lys Pro
                245                 250                 255

Arg Thr Leu Asp Glu Leu Lys Thr Lys Val Lys Asn Met Gly Leu Lys
            260                 265                 270

Leu Glu Leu His Asp Leu Trp Gly Pro Thr Ile Val Val Gln Ile Thr
        275                 280                 285

Gly Lys Ser Ser Lys Tyr Ala Gln Gly Phe Phe Ser Ser Asn Gly Thr
    290                 295                 300

Cys Cys Leu Pro Ile Ser Arg Ser Ala Pro Glu Leu Gly Lys Leu Leu
305                 310                 315                 320

Trp Ser Cys Ser Ala Thr Ile Gly Asp Ala Thr Val Val Ile Gln Ser
                325                 330                 335
```

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

Lys

<210> 71
<211> 1632
<212> DNA
<213> artificial sequence

<220>
<223> F gene of FJ215864

<400> 71

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ccggataata tgactacctg tcttagagaa acaataacta catataataa tactgtcaac 240

aacatcttag gcccactcaa atccaatctg gatgcactgc tctcatctga gacttatccc 300

cagacaagat taattggggc agttataggt tcaattgctc ttggtgttgc aacatcggct 360

caaatcactg ctgcagtcgc tctcaagcaa gcacaagata atgcaagaaa catactggca 420

ctcaaagagg cactgtccaa aactaatgag gcggtcaagg agcttagcag tggattgcaa 480

caaacagcta ttgcacttgg taagatacag agctttgtga atgaggaaat tctgccatct 540

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cacattgtta ataatactac actaattgta ctctgtgtgt taagtgcgct tgctgtgatc 1500

tggctggcag tattaacggc tattataata tacttgagaa caaagttgaa gactatatcg 1560

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<211> 543
<212> PRT
<213> artificial sequence

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<223> F protein of ACO48306

<400> 72

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            20                  25                  30

Val Ala Ser Ala Asn Glu Trp Gln Leu Ala Ala Tyr Thr Thr Ser Leu
        35                  40                  45

Ser Gly Thr Ile Ala Val Arg Phe Leu Pro Val Leu Pro Asp Asn Met
    50                  55                  60

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

Asn Ile Leu Gly Pro Leu Lys Ser Asn Leu Asp Ala Leu Leu Ser Ser
                85                  90                  95

Glu Thr Tyr Pro Gln Thr Arg Leu Ile Gly Ala Val Ile Gly Ser Ile
            100                 105                 110

Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu
        115                 120                 125

Lys Gln Ala Gln Asp Asn Ala Arg Asn Ile Leu Ala Leu Lys Glu Ala
    130                 135                 140

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

Gln Thr Ala Ile Ala Leu Gly Lys Ile Gln Ser Phe Val Asn Glu Glu
                165                 170                 175
```

```
Ile Leu Pro Ser Ile Asn Gln Leu Ser Cys Glu Val Thr Ala Asn Lys
            180                 185                 190

Leu Gly Val Tyr Leu Ser Leu Tyr Leu Thr Glu Leu Thr Thr Ile Phe
        195                 200                 205

Gly Ala Gln Leu Thr Asn Pro Ala Leu Thr Ser Leu Ser Tyr Gln Ala
    210                 215                 220

Leu Tyr Asn Leu Cys Gly Gly Asn Met Ala Met Leu Thr Gln Lys Ile
225                 230                 235                 240

Gly Ile Lys Gln Gln Asp Val Asn Ser Leu Tyr Glu Ala Gly Leu Ile
                245                 250                 255

Thr Gly Gln Val Ile Gly Tyr Asp Ser Gln Tyr Gln Leu Leu Val Ile
            260                 265                 270

Gln Val Asn Tyr Pro Ser Ile Ser Glu Val Thr Gly Val Arg Ala Thr
        275                 280                 285

Glu Leu Val Thr Val Ser Val Thr Thr Asp Lys Gly Glu Gly Lys Ala
    290                 295                 300

Ile Val Pro Gln Phe Val Ala Glu Ser Arg Val Thr Ile Glu Glu Leu
305                 310                 315                 320

Asp Val Ala Ser Cys Lys Phe Ser Ser Thr Thr Leu Tyr Cys Arg Gln
                325                 330                 335

Val Asn Thr Arg Ala Leu Pro Pro Leu Val Ala Ser Cys Leu Arg Gly
            340                 345                 350

Asn Tyr Asp Asp Cys Gln Tyr Thr Thr Glu Ile Gly Ala Leu Ser Ser
        355                 360                 365

Arg Tyr Ile Thr Leu Asp Gly Gly Val Leu Val Asn Cys Lys Ser Ile
    370                 375                 380

Val Cys Arg Cys Leu Asn Pro Ser Lys Ile Ile Ser Gln Asn Thr Asn
385                 390                 395                 400

Ala Ala Val Thr Tyr Val Asp Ala Thr Ile Cys Lys Thr Ile Gln Leu
                405                 410                 415

Asp Asp Ile Gln Leu Gln Leu Glu Gly Ser Leu Ser Ser Val Tyr Ala
            420                 425                 430
```

```
Arg Asn Ile Ser Ile Glu Ile Ser Gln Val Thr Thr Ser Gly Ser Leu
        435                 440                 445

Asp Ile Ser Ser Glu Ile Gly Asn Ile Asn Asn Thr Val Asn Arg Val
    450                 455                 460

Glu Asp Leu Ile His Gln Ser Glu Glu Trp Leu Ala Lys Val Asn Pro
465                 470                 475                 480

His Ile Val Asn Asn Thr Thr Leu Ile Val Leu Cys Val Leu Ser Ala
                485                 490                 495

Leu Ala Val Ile Trp Leu Ala Val Leu Thr Ala Ile Ile Ile Tyr Leu
            500                 505                 510

Arg Thr Lys Leu Lys Thr Ile Ser Ala Leu Ala Val Thr Asn Thr Ile
        515                 520                 525

Gln Ser Asn Pro Tyr Val Asn Gln Thr Lys Arg Glu Ser Lys Phe
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<211> 1734
<212> DNA
<213> artificial sequence

<220>
<223> HN gene of FJ215864

<400> 73

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gaggtggtaa caccttttgaa aaccactctg tctgatacac tcaggaatcc aattaaccag 240

ataaatgaca tattcaggat tgttgccctt gatattccat tgcaagtaac tagtatccaa 300

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aacgggacca accttatcat acctacatca gataaggagt atgcaggagg aattggaaac 420

cctgtattta ctgtcgatgc tggaggttct ataggattca agcaatttag cttaatagaa 480

catccgagct ttattgctgg acctacaacg acccgaggct gtacaagaat acccactttt 540

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gccagtgcat ctagtatgta tatctcaatg ggggttctcc atgtgtcttc atctggcact 660

cctatctttc ttactactgc aagtgaactg atagacgatg gagttaatcg taagtcatgc 720

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<210> 74
<211> 577

<212> PRT
<213> artificial sequence

<220>
<223> HN protein of ACO48307

<400> 74

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            20                  25                  30

Thr Thr Gly Cys Leu Ala Leu Ser Ile Val Ser Ile Val Gln Ile Gly
        35                  40                  45

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

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

Ile Asn Asp Ile Phe Arg Ile Val Ala Leu Asp Ile Pro Leu Gln Val
                85                  90                  95
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```
Thr Ser Ile Gln Lys Asp Leu Ala Ser Gln Phe Ser Met Leu Ile Asp
            100                 105                 110

Ser Leu Asn Ala Ile Lys Leu Gly Asn Gly Thr Asn Leu Ile Ile Pro
        115                 120                 125

Thr Ser Asp Lys Glu Tyr Ala Gly Gly Ile Gly Asn Pro Val Phe Thr
    130                 135                 140

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

His Pro Ser Phe Ile Ala Gly Pro Thr Thr Thr Arg Gly Cys Thr Arg
                165                 170                 175

Ile Pro Thr Phe His Met Ser Glu Ser His Trp Cys Tyr Ser His Asn
            180                 185                 190

Ile Ile Ala Ala Gly Cys Gln Asp Ala Ser Ala Ser Ser Met Tyr Ile
        195                 200                 205

Ser Met Gly Val Leu His Val Ser Ser Ser Gly Thr Pro Ile Phe Leu
    210                 215                 220

Thr Thr Ala Ser Glu Leu Ile Asp Asp Gly Val Asn Arg Lys Ser Cys
225                 230                 235                 240

Ser Ile Val Ala Thr Gln Phe Gly Cys Asp Ile Leu Cys Ser Ile Val
                245                 250                 255

Ile Glu Lys Glu Gly Asp Asp Tyr Trp Ser Asp Thr Pro Thr Pro Met
            260                 265                 270

Arg His Gly Arg Phe Ser Phe Asn Gly Ser Phe Val Glu Thr Glu Leu
        275                 280                 285

Pro Val Ser Ser Met Phe Ser Ser Phe Ser Ala Asn Tyr Pro Ala Val
    290                 295                 300

Gly Ser Gly Glu Ile Val Lys Asp Arg Ile Leu Phe Pro Ile Tyr Gly
305                 310                 315                 320

Gly Ile Lys Gln Thr Ser Pro Glu Phe Thr Glu Leu Val Lys Tyr Gly
                325                 330                 335

Leu Phe Val Ser Thr Pro Thr Thr Val Cys Gln Ser Ser Trp Thr Tyr
            340                 345                 350
```

```
Asp Gln Val Lys Ala Ala Tyr Arg Pro Asp Tyr Ile Ser Gly Arg Phe
        355                 360                 365

Trp Ala Gln Val Ile Leu Ser Cys Ala Leu Asp Ala Val Asp Leu Ser
    370                 375                 380

Ser Cys Ile Val Lys Ile Met Asn Ser Ser Thr Val Met Met Ala Ala
385                 390                 395                 400

Glu Gly Arg Ile Ile Lys Ile Gly Ile Asp Tyr Phe Tyr Tyr Gln Arg
                405                 410                 415

Ser Ser Ser Trp Trp Pro Leu Ala Phe Val Thr Lys Leu Asp Pro Gln
            420                 425                 430

Glu Leu Ala Asp Thr Asn Ser Ile Trp Leu Thr Asn Ser Ile Pro Ile
        435                 440                 445

Pro Gln Ser Lys Phe Pro Arg Pro Ser Tyr Ser Glu Asn Tyr Cys Thr
    450                 455                 460

Lys Pro Ala Val Cys Pro Ala Thr Cys Val Thr Gly Val Tyr Ser Asp
465                 470                 475                 480

Ile Trp Pro Leu Thr Ser Ser Ser Ser Leu Pro Ser Ile Ile Trp Ile
                485                 490                 495

Gly Gln Tyr Leu Asp Ala Pro Val Gly Arg Thr Tyr Pro Arg Phe Gly
            500                 505                 510

Ile Ala Asn Gln Ser His Trp Tyr Leu Gln Glu Asp Ile Leu Pro Thr
        515                 520                 525

Ser Thr Ala Ser Ala Tyr Ser Thr Thr Thr Cys Phe Lys Asn Thr Ala
    530                 535                 540

Arg Asn Arg Val Phe Cys Val Thr Ile Ala Glu Phe Ala Asp Gly Leu
545                 550                 555                 560

Phe Gly Glu Tyr Arg Ile Thr Pro Gln Leu Tyr Glu Leu Val Arg Asn
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Asn
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<213> artificial sequence

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<400> 75

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gtccagcaat ttaaaccgtt gtggagagac atagacattg agactaatgt tacagatcca 5700

tcatttgtca attttgcatt gaatgaaatc ccaatgcaat cattaaaacg agtaaattgt 5760

gatgtggaat ttgaccgtgg tatgccgatt gaacgggtta ttcagggtta cactcatatc 5820

ttacttgttg ctacttacgg attgcagcaa gattcaatac tgtgggtgaa agtatatagg 5880

acatctgaaa aagtatttca gttcttactg agtgccatga tcatgatctt tggttatgtc 5940

aaaatccaca ggaatggtta tatgtcggca aaggatgagg agtacatatt gatgtctgac 6000

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gattccctga atttgaagtg caatcatatt tatgagaaaa taattgctag aaaaattcca 6180

ttacaggtat catcaactga ttctttgctc ctccagttag gcggtgtcat caactcggtg 6240

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gtctcatcaa ttgatttggc tatattagag gcaaatattg tgatctcaga gagtgctggt 6360

cttgacctcg ctttaatgtt aggcccattc aacttgaata agcttaagaa aattgacaca 6420

atccttaagt caagcaccta tcagctaatc ccgtattggt tgcgctatga gtactctatt 6480

aatccgagat ctttgtcatt tctaatcact aaattacaac aatgccgaat ttcatggtca 6540

gatatgataa caatctctga attttgcaag aaatccaagc ggcctatatt tattaaacga 6600

gtaataggga atcaacagct gaaatcattc tttaatgaaa gctcaagtat tgttttgacc 6660

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<213> artificial sequence

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<400> 76

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            20                  25                  30

Gly Leu Pro Met Pro Ala Asp Leu Arg Gln Lys Ser Val Val Met His
        35                  40                  45

Ile Pro Asp His Ile Leu Glu Lys Ser Glu Tyr Arg Ile Lys His Arg
    50                  55                  60

Leu Gly Lys Ile Lys Ser Asp Ile Ala His Tyr Cys Gln Tyr Phe Asn
65                  70                  75                  80

Ile Asn Leu Ala Asn Leu Asp Pro Ile Thr His Pro Lys Ser Leu Tyr
```

85 90 95

Trp Leu Ser Arg Leu Thr Ile Ala Ser Ala Gly Thr Phe Arg His Met
100 105 110

Lys Asp Arg Ile Leu Cys Thr Val Gly Ser Glu Phe Gly His Lys Ile
115 120 125

Gln Asp Leu Phe Ser Leu Leu Ser His Lys Leu Val Gly Asn Gly Asp
130 135 140

Leu Phe Asn Gln Ser Leu Ser Gly Thr Arg Leu Thr Ala Ser Pro Leu
145 150 155 160

Ser Pro Leu Cys Asn Gln Phe Val Ser Asp Ile Lys Ser Ala Val Thr
165 170 175

Thr Pro Trp Ser Glu Ala Arg Trp Ser Trp Leu His Ile Lys Gln Thr
180 185 190

Met Arg Tyr Leu Ile Lys Gln Ser Arg Thr Thr Asn Ser Ala His Leu
195 200 205

Thr Glu Ile Ile Lys Glu Glu Trp Gly Leu Val Gly Ile Thr Pro Asp
210 215 220

Leu Val Ile Leu Phe Asp Arg Val Asn Asn Ser Leu Thr Ala Leu Thr
225 230 235 240

Phe Glu Met Val Leu Met Tyr Ser Asp Val Leu Glu Ser Arg Asp Asn
245 250 255

Ile Val Leu Val Gly Arg Leu Ser Thr Phe Leu Gln Pro Val Val Ser
260 265 270

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

Gly Asp Thr Ile Tyr Glu Ile Ile Ala Val Leu Glu Ser Leu Ser Tyr
290 295 300

Gly Ser Val Gln Leu His Asp Ala Ser His Ser His Ala Gly Ser Phe
305 310 315 320

Phe Ser Phe Asn Met Asn Glu Leu Asp Asn Thr Leu Ser Lys Arg Val
325 330 335

Asp Pro Lys His Lys Asn Thr Ile Met Ser Ile Ile Arg Gln Cys Phe
340 345 350

```
Ser Asn Leu Asp Val Asp Gln Ala Ala Glu Met Leu Cys Leu Met Arg
        355                 360                 365

Leu Phe Gly His Pro Met Leu Thr Ala Pro Asp Ala Ala Ala Lys Val
    370                 375                 380

Arg Lys Ala Met Cys Ala Pro Lys Leu Val Glu His Asp Thr Ile Leu
385                 390                 395                 400

Gln Thr Leu Ser Phe Phe Lys Gly Ile Ile Ile Asn Gly Tyr Arg Arg
                405                 410                 415

Ser His Ser Gly Leu Trp Pro Asn Val Glu Pro Ser Ser Ile Tyr Asp
            420                 425                 430

Asp Asp Leu Arg Gln Leu Tyr Leu Glu Ser Ala Glu Ile Ser His His
        435                 440                 445

Phe Met Leu Lys Asn Tyr Lys Ser Leu Ser Met Ile Glu Phe Lys Lys
    450                 455                 460

Ser Ile Asp Tyr Asp Leu His Asp Asp Leu Ser Thr Phe Leu Lys Asp
465                 470                 475                 480

Arg Ala Ile Cys Arg Pro Lys Ser Gln Trp Asp Val Ile Phe Arg Lys
                485                 490                 495

Ser Leu Arg Arg Ser His Thr Arg Ser Gln Tyr Met Asp Glu Ile Lys
            500                 505                 510

Ser Asn Arg Leu Leu Ile Asp Phe Leu Asp Ser Ala Asp Phe Asp Pro
        515                 520                 525

Glu Lys Glu Phe Ala Tyr Val Thr Thr Met Asp Tyr Leu His Asp Asn
    530                 535                 540

Glu Phe Cys Ala Ser Tyr Ser Leu Lys Glu Lys Glu Ile Lys Thr Thr
545                 550                 555                 560

Gly Arg Ile Phe Ala Lys Met Thr Arg Asn Met Arg Ser Cys Gln Val
                565                 570                 575

Ile Leu Glu Ser Leu Leu Ser Lys His Ile Cys Lys Phe Phe Lys Glu
            580                 585                 590

Asn Gly Val Ser Met Glu Gln Leu Ser Leu Thr Lys Ser Leu Leu Ala
        595                 600                 605
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Met Ser Gln Leu Ser Pro Lys Val Ser Thr Leu Gln Asp Thr Ala Ser
    610                 615                 620

Arg His Val Gly Asn Ser Lys Ser Gln Ile Ala Thr Ser Asn Pro Ser
625                 630                 635                 640

Arg His His Ser Thr Thr Asn Gln Met Ser Leu Ser Asn Arg Lys Thr
                645                 650                 655

Val Val Ala Thr Phe Leu Thr Thr Asp Leu Glu Lys Tyr Cys Leu Gln
            660                 665                 670

Trp Arg Tyr Ser Thr Ile Lys Leu Phe Ala Gln Ala Leu Asn Gln Leu
        675                 680                 685

Phe Gly Ile Asp His Gly Phe Glu Trp Ile His Leu Arg Leu Met Asn
    690                 695                 700

Ser Thr Leu Phe Val Gly Asp Pro Tyr Ser Pro Pro Glu Asp Pro Thr
705                 710                 715                 720

Leu Glu Asp Ile Asp Lys Ala Pro Asn Asp Asp Ile Phe Ile Val Ser
                725                 730                 735

Pro Arg Gly Gly Ile Glu Gly Leu Cys Gln Lys Met Trp Thr Met Ile
            740                 745                 750

Ser Ile Ser Ala Ile His Cys Val Ala Glu Lys Ile Gly Ala Arg Val
        755                 760                 765

Ala Ala Met Val Gln Gly Asp Asn Gln Val Ile Ala Ile Thr Lys Glu
    770                 775                 780

Leu Phe Arg Gly Glu Lys Ala Cys Asp Val Arg Asp Glu Leu Asp Glu
785                 790                 795                 800

Leu Gly Gln Val Phe Phe Asp Glu Phe Lys Arg His Asn Tyr Ala Ile
                805                 810                 815

Gly His Asn Leu Lys Leu Asn Glu Thr Ile Gln Ser Gln Ser Phe Phe
            820                 825                 830

Val Tyr Ser Lys Arg Ile Phe Phe Glu Gly Arg Leu Leu Ser Gln Val
        835                 840                 845

Leu Lys Asn Ala Ala Lys Leu Cys Met Val Ala Asp His Leu Gly Glu
    850                 855                 860
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```
Asn Thr Val Ser Ser Cys Ser Asn Leu Ser Ser Thr Ile Ala Arg Leu
865                 870                 875                 880

Val Glu Asn Gly Phe Glu Lys Asp Thr Ala Phe Val Leu Asn Leu Val
                885                 890                 895

Tyr Ile Met Thr Gln Ile Leu Phe Asp Glu His Tyr Ser Ile Val Cys
            900                 905                 910

Asp His Asn Ser Val Lys Ser Leu Ile Gly Ser Lys Asn Tyr Arg Asn
        915                 920                 925

Leu Leu Tyr Ser Ser Leu Ile Pro Gly Gln Leu Gly Gly Phe Asn Phe
    930                 935                 940

Leu Asn Ile Ser Arg Leu Phe Thr Arg Asn Ile Gly Asp Pro Val Thr
945                 950                 955                 960

Cys Ser Leu Ser Asp Leu Lys Cys Phe Ile Ala Ala Gly Leu Leu Pro
                965                 970                 975

Pro Tyr Val Leu Lys Asn Val Val Leu Arg Glu Pro Gly Pro Gly Thr
            980                 985                 990

Trp Leu Thr Leu Cys Ser Asp Pro  Tyr Thr Leu Asn Ile  Pro Tyr Thr
        995                 1000                1005

Gln Leu  Pro Thr Thr Tyr Leu  Lys Lys His Thr Gln  Arg Ser Leu
    1010                1015                1020

Leu Ser  Arg Ala Val Asn Pro  Leu Leu Ala Gly Val  Gln Val Pro
    1025                1030                1035

Asn Gln  His Glu Glu Glu Glu  Met Leu Ala Arg Phe  Leu Leu Asp
    1040                1045                1050

Arg Glu  Tyr Val Met Pro Arg  Val Ala His Val Ile  Leu Glu Thr
    1055                1060                1065

Ser Val  Leu Gly Lys Arg Lys  Gln Ile Gln Gly Leu  Ile Asp Thr
    1070                1075                1080

Thr Pro  Thr Ile Ile Arg Thr  Ser Leu Val Asn Leu  Pro Val Ser
    1085                1090                1095

Arg Lys  Lys Cys Glu Lys Ile  Ile Asn Tyr Ser Leu  Asn Tyr Ile
    1100                1105                1110

Ala Glu  Cys His Asp Ser Leu  Leu Ser Gln Ile Cys  Phe Ser Asp
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1115 1120 1125

Asn Lys Glu Tyr Leu Trp Ser Thr Ser Leu Ile Ser Val Glu Thr
1130 1135 1140

Cys Ser Val Thr Ile Ala Asp Tyr Leu Arg Ala Val Ser Trp Ser
1145 1150 1155

Asn Ile Leu Gly Gly Arg Asn Ile Ser Gly Val Thr Thr Pro Asp
1160 1165 1170

Thr Ile Glu Leu Ile Gln Gly Cys Leu Ile Gly Glu Asn Ser Ser
1175 1180 1185

Cys Thr Leu Cys Glu Ser His Asp Asp Ala Phe Thr Trp Met His
1190 1195 1200

Leu Pro Gly Pro Leu Tyr Ile Pro Glu Pro Ser Val Thr Asn Ser
1205 1210 1215

Lys Met Arg Val Pro Tyr Leu Gly Ser Lys Thr Glu Glu Arg Lys
1220 1225 1230

Thr Ala Ser Met Ala Ala Ile Lys Gly Met Ser His His Leu Arg
1235 1240 1245

Ala Val Leu Arg Gly Thr Ser Val Phe Ile Trp Ala Phe Gly Asp
1250 1255 1260

Thr Asp Ile Asn Trp Asp Asn Ala Leu Gln Ile Ala Gln Ser Arg
1265 1270 1275

Cys Asn Ile Thr Leu Asp Gln Met Arg Leu Leu Thr Pro Ile Pro
1280 1285 1290

Ser Ser Ser Asn Ile Gln His Arg Leu Asp Asp Gly Ile Ser Thr
1295 1300 1305

Gln Lys Phe Thr Pro Ala Ser Leu Ala Arg Ile Thr Ser Phe Val
1310 1315 1320

His Ile Cys Asn Asp Ser Gln Arg Leu Glu Lys Asp Gly Ser Ser
1325 1330 1335

Val Asp Ser Asn Leu Ile Tyr Gln Gln Ile Met Leu Leu Gly Leu
1340 1345 1350

Ser Ile Phe Glu Thr Met Tyr Ser Met Asp Gln Lys Trp Val Phe
1355 1360 1365

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Asn Asn  His Thr Leu His Leu  His Thr Gly His Ser  Cys Cys Pro
    1370                 1375                 1380

Arg Glu  Leu Asp Ile Ser Leu  Val Asn Pro Pro Arg  His Gln Thr
    1385                 1390                 1395

Pro Glu  Leu Thr Ser Thr Thr  Thr Asn Pro Phe Leu  Tyr Asp Gln
    1400                 1405                 1410

Leu Pro  Leu Asn Gln Asp Asn  Leu Thr Thr Leu Glu  Ile Lys Thr
    1415                 1420                 1425

Phe Lys  Phe Asn Glu Leu Asn  Ile Asp Gly Leu Asp  Phe Gly Glu
    1430                 1435                 1440

Gly Ile  Gln Leu Leu Ser Arg  Cys Thr Ala Arg Leu  Met Ala Glu
    1445                 1450                 1455

Cys Ile  Leu Glu Glu Gly Ile  Gly Ser Ser Val Lys  Asn Glu Ala
    1460                 1465                 1470

Ile Val  Asn Phe Asp Asn Ser  Val Asn Trp Ile Ser  Glu Cys Leu
    1475                 1480                 1485

Met Cys  Asp Ile Arg Ser Leu  Cys Val Asn Leu Gly  Gln Glu Ile
    1490                 1495                 1500

Leu Cys  Ser Leu Ala Tyr Gln  Met Tyr Tyr Leu Arg  Ile Arg Gly
    1505                 1510                 1515

Arg Arg  Ala Ile Leu Asn Tyr  Leu Asp Thr Thr Leu  Gln Arg Ile
    1520                 1525                 1530

Pro Val  Ile Gln Leu Ala Asn  Ile Ala Leu Thr Ile  Ser His Pro
    1535                 1540                 1545

Glu Ile  Phe Arg Arg Ile Val  Asn Thr Gly Ile His  Asn Gln Ile
    1550                 1555                 1560

Lys Gly  Pro Tyr Val Ala Thr  Thr Asp Phe Ile Ala  Ala Ser Arg
    1565                 1570                 1575

Asp Ile  Ile Leu Ser Gly Ala  Arg Glu Tyr Leu Ser  Tyr Leu Ser
    1580                 1585                 1590

Ser Gly  Gln Glu Asp Cys Tyr  Thr Phe Phe Asn Cys  Gln Asp Gly
    1595                 1600                 1605
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Asp Leu  Thr Pro Lys Met Glu  Gln Tyr Leu Ala Arg  Arg Ala Cys
    1610                 1615                 1620

Leu Leu  Thr Leu Leu Tyr Asn  Thr Gly His Gln Ile  Pro Ile Ile
    1625                 1630                 1635

Arg Ser  Leu Thr Pro Ile Glu  Lys Cys Lys Val Leu  Thr Glu Tyr
    1640                 1645                 1650

Asn Gln  Gln Ile Glu Tyr Ala  Asp Gln Glu Phe Ser  Ser Val Leu
    1655                 1660                 1665

Lys Val  Val Asn Ala Leu Leu  Gln Asn Pro Asn Ile  Asp Ala Leu
    1670                 1675                 1680

Val Ser  Asn Leu Tyr Phe Thr  Thr Arg Arg Val Leu  Ser Asn Leu
    1685                 1690                 1695

Arg Ser  Cys Asp Lys Ala Ile  Ser Tyr Ile Glu Tyr  Leu Tyr Thr
    1700                 1705                 1710

Glu Asp  Phe Gly Glu Lys Glu  Asp Thr Val Gln Tyr  Asp Ile Met
    1715                 1720                 1725

Thr Thr  Asn Asp Ile Ile Leu  Thr His Gly Leu Phe  Thr Gln Ile
    1730                 1735                 1740

Glu Ile  Ser Tyr Gln Gly Ser  Ser Leu His Lys Phe  Leu Thr Pro
    1745                 1750                 1755

Asp Asn  Ala Pro Gly Ser Leu  Ile Pro Phe Ser Ile  Ser Pro Asn
    1760                 1765                 1770

Ser Leu  Ala Cys Asp Pro Leu  His His Leu Leu Lys  Ser Val Gly
    1775                 1780                 1785

Thr Ser  Ser Thr Ser Trp Tyr  Lys Tyr Ala Ile Ala  Tyr Ala Val
    1790                 1795                 1800

Ser Glu  Lys Arg Ser Ala Arg  Leu Gly Gly Ser Leu  Tyr Ile Gly
    1805                 1810                 1815

Glu Gly  Ser Gly Ser Val Met  Thr Leu Leu Glu Tyr  Leu Glu Pro
    1820                 1825                 1830

Ser Val  Asp Ile Phe Tyr Asn  Ser Leu Phe Ser Asn  Gly Met Asn
    1835                 1840                 1845
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Pro Pro  Gln Arg Asn Tyr Gly  Leu Met Pro Leu Gln  Phe Val Asn
    1850                1855                1860

Ser Val  Val Tyr Lys Asn Leu  Thr Ala Lys Ser Glu  Cys Lys Leu
    1865                1870                1875

Gly Phe  Val Gln Gln Phe Lys  Pro Leu Trp Arg Asp  Ile Asp Ile
    1880                1885                1890

Glu Thr  Asn Val Thr Asp Pro  Ser Phe Val Asn Phe  Ala Leu Asn
    1895                1900                1905

Glu Ile  Pro Met Gln Ser Leu  Lys Arg Val Asn Cys  Asp Val Glu
    1910                1915                1920

Phe Asp  Arg Gly Met Pro Ile  Glu Arg Val Ile Gln  Gly Tyr Thr
    1925                1930                1935

His Ile  Leu Leu Val Ala Thr  Tyr Gly Leu Gln Gln  Asp Ser Ile
    1940                1945                1950

Leu Trp  Val Lys Val Tyr Arg  Thr Ser Glu Lys Val  Phe Gln Phe
    1955                1960                1965

Leu Leu  Ser Ala Met Ile Met  Ile Phe Gly Tyr Val  Lys Ile His
    1970                1975                1980

Arg Asn  Gly Tyr Met Ser Ala  Lys Asp Glu Glu Tyr  Ile Leu Met
    1985                1990                1995

Ser Asp  Cys Lys Glu Pro Val  Asn Tyr Thr Ala Val  Pro Asn Ile
    2000                2005                2010

Leu Thr  Arg Val Ser Asp Leu  Val Ser Lys Asn Leu  Ser Leu Ile
    2015                2020                2025

His Pro  Glu Asp Leu Arg Lys  Val Arg Cys Glu Thr  Asp Ser Leu
    2030                2035                2040

Asn Leu  Lys Cys Asn His Ile  Tyr Glu Lys Ile Ile  Ala Arg Lys
    2045                2050                2055

Ile Pro  Leu Gln Val Ser Ser  Thr Asp Ser Leu Leu  Leu Gln Leu
    2060                2065                2070

Gly Gly  Val Ile Asn Ser Val  Gly Ser Thr Asp Pro  Arg Glu Val
    2075                2080                2085

Ala Thr  Leu Ser Ser Ile Glu  Cys Met Asp Tyr Val  Val Ser Ser
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2090 2095 2100

Ile Asp Leu Ala Ile Leu Glu Ala Asn Ile Val Ile Ser Glu Ser
2105 2110 2115

Ala Gly Leu Asp Leu Ala Leu Met Leu Gly Pro Phe Asn Leu Asn
2120 2125 2130

Lys Leu Lys Lys Ile Asp Thr Ile Leu Lys Ser Ser Thr Tyr Gln
2135 2140 2145

Leu Ile Pro Tyr Trp Leu Arg Tyr Glu Tyr Ser Ile Asn Pro Arg
2150 2155 2160

Ser Leu Ser Phe Leu Ile Thr Lys Leu Gln Gln Cys Arg Ile Ser
2165 2170 2175

Trp Ser Asp Met Ile Thr Ile Ser Glu Phe Cys Lys Lys Ser Lys
2180 2185 2190

Arg Pro Ile Phe Ile Lys Arg Val Ile Gly Asn Gln Gln Leu Lys
2195 2200 2205

Ser Phe Phe Asn Glu Ser Ser Ser Ile Val Leu Thr Arg Ala Glu
2210 2215 2220

Val Lys Val Cys Ile Lys Phe Leu Gly Ala Ile Ile Lys Leu Lys
2225 2230 2235

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<400> 77

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agaacaactt gtaaagccgg ctgtcaggag acctgatgtt gcctcaacag gtttactcag 180

ggcggaaata cctgtctgtg ttacattgtc tcaagacccc ggtgagagat ggagccttgc 240

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aatattgtca ctgctgagtc tacattcaga caatatgcga gctcacgcaa cattagcagc 360

aaggtctgca gatgcttcac tcaccatact tgaggtagat gaagtagata ttggcaactc 420

cctaatcaaa ttcaacgcta gaagtggtgt atctgataaa cgatcaaatc aattgcttgc 480

aattgcggat gacatcccca aaagttgcag taatgggcat ccatttcttg acacagacat 540

tgagaccaga gacccgctcg atctatcaga gaccatagac cgcctgcagg gtattgcagc 600

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cctgaagttc ggggttggta cccagtatcc aaccttagca atgagtgttt tctccagtga 960

ccttaaaaga cttgctgcac tcatcaggct gtacaaaacc aagggagaca atgcaccata 1020

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tgctagagac tttaccagtg agaattattt ccgtcttgga gttgagacag cccaaagcca 1200

gcagggagcg tttgacgaga gaacagcccg agagatgggc ttgactgagg aatccaaaca 1260

gcaggttaga tcactgctaa tgtcagtaga catgggtccc agttcagttc gcgagccatc 1320

ccgccctgca ttcatcagtc aagaagaaaa taggcagcct gcccagaatt cttcagatac 1380

tcagggtcag accaagccag tcccgaatca acccgcacca agggccgacc cagatgacat 1440

tgatccatac gagaacgggc tagaatggta attcaatcac ctcgacacat ccacctatac 1500

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<400> 78

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Lys Pro Ala Val Arg Arg Pro Asp Val Ala Ser Thr Gly Leu Leu Arg
            20                  25                  30

Ala Glu Ile Pro Val Cys Val Thr Leu Ser Gln Asp Pro Gly Glu Arg
        35                  40                  45

Trp Ser Leu Ala Cys Leu Asn Ile Arg Trp Leu Val Ser Asp Ser Ser
    50                  55                  60

Thr Thr Pro Met Lys Gln Gly Ala Ile Leu Ser Leu Leu Ser Leu His
```

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65                  70                  75                  80

Ser Asp Asn Met Arg Ala His Ala Thr Leu Ala Ala Arg Ser Ala Asp
                85                  90                  95

Ala Ser Leu Thr Ile Leu Glu Val Asp Glu Val Asp Ile Gly Asn Ser
            100                 105                 110

Leu Ile Lys Phe Asn Ala Arg Ser Gly Val Ser Asp Lys Arg Ser Asn
        115                 120                 125

Gln Leu Leu Ala Ile Ala Asp Asp Ile Pro Lys Ser Cys Ser Asn Gly
    130                 135                 140

His Pro Phe Leu Asp Thr Asp Ile Glu Thr Arg Asp Pro Leu Asp Leu
145                 150                 155                 160

Ser Glu Thr Ile Asp Arg Leu Gln Gly Ile Ala Ala Gln Ile Trp Val
                165                 170                 175

Ser Ala Ile Lys Ser Met Thr Ala Pro Asp Thr Ala Ser Glu Ser Glu
            180                 185                 190

Ser Lys Arg Leu Ala Lys Tyr Gln Gln Gln Gly Arg Leu Val Lys Gln
        195                 200                 205

Val Leu Leu His Ser Val Val Arg Thr Glu Phe Met Arg Val Ile Arg
    210                 215                 220

Gly Ser Leu Val Leu Arg Gln Phe Met Val Ser Glu Cys Lys Arg Ala
225                 230                 235                 240

Ser Ala Met Gly Gly Asp Thr Ser Arg Tyr Tyr Ala Met Val Gly Asp
                245                 250                 255

Ile Ser Leu Tyr Ile Lys Asn Ala Gly Leu Thr Ala Phe Phe Leu Thr
            260                 265                 270

Leu Lys Phe Gly Val Gly Thr Gln Tyr Pro Thr Leu Ala Met Ser Val
        275                 280                 285

Phe Ser Ser Asp Leu Lys Arg Leu Ala Ala Leu Ile Arg Leu Tyr Lys
    290                 295                 300

Thr Lys Gly Asp Asn Ala Pro Tyr Met Ala Phe Leu Glu Asp Ser Asp
305                 310                 315                 320

Met Gly Asn Phe Ala Pro Ala Asn Tyr Ser Thr Met Tyr Ser Tyr Ala
                325                 330                 335
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Met Gly Ile Gly Thr Ile Leu Glu Ala Ser Val Ser Arg Tyr Gln Tyr
            340                 345                 350

Ala Arg Asp Phe Thr Ser Glu Asn Tyr Phe Arg Leu Gly Val Glu Thr
        355                 360                 365

Ala Gln Ser Gln Gln Gly Ala Phe Asp Glu Arg Thr Ala Arg Glu Met
    370                 375                 380

Gly Leu Thr Glu Glu Ser Lys Gln Gln Val Arg Ser Leu Leu Met Ser
385                 390                 395                 400

Val Asp Met Gly Pro Ser Ser Val Arg Glu Pro Ser Arg Pro Ala Phe
                405                 410                 415

Ile Ser Gln Glu Glu Asn Arg Gln Pro Ala Gln Asn Ser Ser Asp Thr
            420                 425                 430

Gln Gly Gln Thr Lys Pro Val Pro Asn Gln Pro Ala Pro Arg Ala Asp
        435                 440                 445

Pro Asp Asp Ile Asp Pro Tyr Glu Asn Gly Leu Glu Trp
    450                 455                 460
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<212> DNA
<213> artificial sequence

<220>
<223> P gene of FJ619036

<400> 79

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tcagtcaagg gaacacaaga aatctaactg atctatggga aaaggagact gcaagtcaga     240
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aagaaatcaa atcagagtca attgatggcc acatcagtgg aactgttaat caattagagc     360
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caatcaatcc tggcaaccag gacacaggag agaatattca tttaccacct tccatggcac     660

caccagagtc attagttggt gcaatccgca atgtacccca attcgtgcca gaccaatcta     720
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caaaagttgt aaacaccacc ccccttatca ggaatgatat taaccaactt aaggccacaa     900
ctgcactgat gtccaaccaa attgcttcca tacaaattct tgacccaggg aatgcagggg     960
tgaggtccct ctctgaaatg agatctgtga cgaagaaagc tgctgttgta attgcaggat    1020
ttggagacga cccaactcaa attattgaag aaggtatcat ggccaaagat gctcttggaa    1080
aacctgtgcc tccaacatct gttatcgcag ccaaagctca gacttcttcc ggtgtgagta    1140
agggtgaaat agaaggattg attgcattgg tggaaacatt agttgacaat gacaagaagg    1200
cagcgaaact gattaaaatg attgatcaag ttaaatccca cgccgattac gcccgagtca    1260
agcaggcaat atataatgca taatattgta attatacaaa caatcaatac tgctgtcggt    1320
tgcacccacc ttagcaaatc aataatcttt taaaattgat tgattaagaa aaaa          1374
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<210> 80
<211> 405
<212> PRT
<213> artificial sequence

<220>
<223> P protein of ACN88140

<400> 80

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Thr Thr Val Ile Lys Glu Ile Gln Lys Ser Glu Leu Lys Pro Pro Gln
            20                  25                  30

Thr Thr Gly Arg Pro Pro Val Ser Gln Gly Asn Thr Arg Asn Leu Thr
        35                  40                  45

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

Ser Pro Gln Thr Thr Gln Val Gln Ser Asp Gly Asn Glu Glu Glu Glu
65                  70                  75                  80

Ile Lys Ser Glu Ser Ile Asp Gly His Ile Ser Gly Thr Val Asn Gln
                85                  90                  95

Leu Glu Gln Val Pro Glu Gln Asn Gln Ser Arg Ser Ser Pro Gly Asp
            100                 105                 110

Asp Leu Asp Arg Ala Leu Asn Lys Leu Glu Gly Arg Ile Asn Ser Ile
        115                 120                 125
```

```
Ser Ser Met Asp Lys Glu Ile Lys Lys Gly Pro Arg Ile Gln Asn Leu
    130                 135                 140

Pro Gly Ser Gln Ala Ala Thr Gln Gln Ala Thr His Pro Leu Ala Gly
145                 150                 155                 160

Asp Thr Pro Asn Met Gln Ala Arg Thr Lys Pro Leu Thr Lys Pro His
                165                 170                 175

Gln Glu Ala Ile Asn Pro Gly Asn Gln Asp Thr Gly Glu Asn Ile His
            180                 185                 190

Leu Pro Pro Ser Met Ala Pro Pro Glu Ser Leu Val Gly Ala Ile Arg
        195                 200                 205

Asn Val Pro Gln Phe Val Pro Asp Gln Ser Met Thr Asn Val Asp Ala
    210                 215                 220

Gly Ser Val Gln Leu His Ala Ser Cys Ala Glu Met Ile Ser Arg Met
225                 230                 235                 240

Leu Val Glu Val Ile Ser Lys Leu Asp Lys Leu Glu Ser Arg Leu Asn
                245                 250                 255

Asp Ile Ala Lys Val Val Asn Thr Thr Pro Leu Ile Arg Asn Asp Ile
            260                 265                 270

Asn Gln Leu Lys Ala Thr Thr Ala Leu Met Ser Asn Gln Ile Ala Ser
        275                 280                 285

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

Met Arg Ser Val Thr Lys Lys Ala Ala Val Val Ile Ala Gly Phe Gly
305                 310                 315                 320

Asp Asp Pro Thr Gln Ile Ile Glu Glu Gly Ile Met Ala Lys Asp Ala
                325                 330                 335

Leu Gly Lys Pro Val Pro Pro Thr Ser Val Ile Ala Ala Lys Ala Gln
            340                 345                 350

Thr Ser Ser Gly Val Ser Lys Gly Glu Ile Glu Gly Leu Ile Ala Leu
        355                 360                 365

Val Glu Thr Leu Val Asp Asn Asp Lys Lys Ala Ala Lys Leu Ile Lys
    370                 375                 380
```

Met Ile Asp Gln Val Lys Ser His Ala Asp Tyr Ala Arg Val Lys Gln
385 390 395 400

Ala Ile Tyr Asn Ala
405

<210> 81
<211> 1110
<212> DNA
<213> artificial sequence

<220>
<223> M gene of FJ619036

<400> 81

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agggtagatt caattggcga tgtgcagaat gccaaagagt cctcgatatt cgtgactcta 180

tatggtttca tccaagcaat taaggagaat tcagatcgat cgaaattctt ccatccaaaa 240

gatgacttca aacctgagac agtcactgca ggactggtag tagtgggtgc aatccgaatg 300

atggctgatg tcaataccat ctctaatgat gcactagcgc tggagatcac tgttaagaaa 360

tctgcaactt ctcaagagaa aatgacggtg atgttccaca atagcccccc ttcattgaga 420

actgcaataa ctatccgagc aggaggtttc atctcgaatg cagacgaaaa tataaaatgt 480

gccagcaagt tgactgcagg agtgcagtac atattccgtc caatgtttgt ttcaatcact 540

aaattacaca atggcaaact atatagggtg cccaaaagta tccacagcat ctcgtctacc 600

ctactgtata gtgtgatgtt ggaggtagga ttcaaagtgg acatcgggaa ggatcatccc 660

caggcaaaaa tgctgaagag ggtcacaatt ggcgatgcag acacatactg gggatttgca 720

tggttccacc tgtgcaattt caaaaagaca tcctctaagg gaaagccgag aacgctagac 780

gaactgagga caaaagtcaa aaatatgggg ttgaaattgg agttacatga cctatggggt 840

ccgactattg tggtccaaat cactggcaag agcagcaaat atgctcaagg atttttttct 900

tccaatggta cttgttgcct cccaatcagc agatctgcac cagagcttgg gaagcttctg 960

tggtcctgct cagcaactat tggtgacgca acagttgtta tccaatcaag cgagaagggg 1020

gaactcctaa ggtctgatga tctcgagata cgaggtgctg tggcctccaa gaaaggtaga 1080

ctgagctcat ttcacccctt caaaaaatga 1110

<210> 82
<211> 369
<212> PRT
<213> artificial sequence

<220>
<223> M protein of ACN88143

<400> 82

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Met Ala Tyr Thr Thr Leu Lys Leu Trp Val Asp Glu Gly Asp Met Ser
1               5                  10                  15

Ser Ser Leu Leu Ser Phe Pro Leu Val Leu Lys Glu Thr Asp Arg Gly
            20                  25                  30

Thr Lys Lys Leu Gln Pro Gln Val Arg Val Asp Ser Ile Gly Asp Val
        35                  40                  45

Gln Asn Ala Lys Glu Ser Ser Ile Phe Val Thr Leu Tyr Gly Phe Ile
    50                  55                  60

Gln Ala Ile Lys Glu Asn Ser Asp Arg Ser Lys Phe Phe His Pro Lys
65                  70                  75                  80

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

Ala Ile Arg Met Met Ala Asp Val Asn Thr Ile Ser Asn Asp Ala Leu
            100                 105                 110

Ala Leu Glu Ile Thr Val Lys Lys Ser Ala Thr Ser Gln Glu Lys Met
        115                 120                 125

Thr Val Met Phe His Asn Ser Pro Pro Ser Leu Arg Thr Ala Ile Thr
    130                 135                 140

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

Ala Ser Lys Leu Thr Ala Gly Val Gln Tyr Ile Phe Arg Pro Met Phe
                165                 170                 175

Val Ser Ile Thr Lys Leu His Asn Gly Lys Leu Tyr Arg Val Pro Lys
            180                 185                 190

Ser Ile His Ser Ile Ser Ser Thr Leu Leu Tyr Ser Val Met Leu Glu
        195                 200                 205

Val Gly Phe Lys Val Asp Ile Gly Lys Asp His Pro Gln Ala Lys Met
    210                 215                 220

Leu Lys Arg Val Thr Ile Gly Asp Ala Asp Thr Tyr Trp Gly Phe Ala
225                 230                 235                 240

Trp Phe His Leu Cys Asn Phe Lys Lys Thr Ser Ser Lys Gly Lys Pro
                245                 250                 255
```

```
Arg Thr Leu Asp Glu Leu Arg Thr Lys Val Lys Asn Met Gly Leu Lys
            260                 265                 270

Leu Glu Leu His Asp Leu Trp Gly Pro Thr Ile Val Val Gln Ile Thr
        275                 280                 285

Gly Lys Ser Ser Lys Tyr Ala Gln Gly Phe Phe Ser Ser Asn Gly Thr
    290                 295                 300

Cys Cys Leu Pro Ile Ser Arg Ser Ala Pro Glu Leu Gly Lys Leu Leu
305                 310                 315                 320

Trp Ser Cys Ser Ala Thr Ile Gly Asp Ala Thr Val Val Ile Gln Ser
                325                 330                 335

Ser Glu Lys Gly Glu Leu Leu Arg Ser Asp Asp Leu Glu Ile Arg Gly
            340                 345                 350

Ala Val Ala Ser Lys Lys Gly Arg Leu Ser Ser Phe His Pro Phe Lys
        355                 360                 365

Lys
```

<210> 83
<211> 1632
<212> DNA
<213> artificial sequence

<220>
<223> F gene of FJ619036

<400> 83

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cttgctgcat atacaacatc actttcaggg acaattgccg tgcgattcct acctgtgctc 180

ccggataata tgactacctg tcttagagaa acaataacta catataataa tactgtcaac 240

aacatcttag gcccactcaa atccaatctg gatgcactgc tctcatctga gacttatccc 300

cagacaagat taattggggc agttataggt tcaattgctc ttggtgttgc aacatcggct 360

caaatcactg ctgcagtcgc tctcaagcaa gcacaagata atgcaagaaa catactggca 420

ctcaaagagg cactgtccaa aactaatgag gcggtcaagg agcttagcag tggattgcaa 480

caaacagcta ttgcacttgg taagatacag agctttgtga atgaggaaat tctgccatct 540

atcaaccaac tgagctgcga ggtgacagcc aataaacttg gggtgtattt atctctgtat 600

ctcacagaac tgaccactat attcggtgca cagttgacta accctgcatt gacttcatta 660

tcatatcaag cgctgtacaa cctgtgtggt ggcaacatgg caatgcttac tcagaagatt 720

ggaattaaac agcaagacgt taattcgcta tatgaagccg gactaatcac aggacaagtc 780

attggttatg actctcagta ccagctgctg gtcatccagg tcaattatcc aagcatttct 840

gaggtaactg gtgtgcgtgc gacagaatta gtcactgtta gtgtaacaac agacaagggt 900

gaagggaaag caattgtacc ccaatttgta gctgaaagtc gggtgactat tgaggagctt 960

gatgtagcat cttgtaaatt cagcagcaca accctatact gcaggcaggt caacacaagg 1020

gcacttcccc cgctagtggc tagctgtctc cgaggtaact atgatgattg tcaatatacc 1080

acagagattg gagcattatc atcccggtat ataacactag atggaggggt cttagtcaat 1140

tgtaagtcaa ttgtttgtag gtgccttaat ccaagtaaga tcatctctca aaatacaaat 1200

gctgcagtaa catatgttga tgctacaata tgcaaaacaa ttcaattgga tgacatacaa 1260

ctccagttgg aagggtcact atcatcagtt tatgcaagga acatctcaat tgagatcagt 1320

caggtgacta cctccggttc tttggatatc agcagtgaga tagggaacat caataatacg 1380

gtgaatcgtg tggaggattt aatccaccaa tcggaggaat ggctggcaaa agttaaccca 1440

cacattgtta ataatactac actaattgta ctctgtgtgt taagtgcgct tgctgtgatc 1500

tggctggcag tattaacggc tattataata tacttgagaa caaagttgaa gactatatcg 1560

gcattggctg taaccaatac aatacagtct aatccctatg ttaaccaaac gaaacgtgaa 1620

tctaagtttt ga 1632

<210> 84
<211> 543
<212> PRT
<213> artificial sequence

<220>
<223> F protein of ACN88144

<400> 84

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Met Gly Lys Ile Ser Ile Tyr Leu Ile Asn Ser Val Leu Leu Leu Leu
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Val Tyr Pro Val Asn Ser Ile Asp Asn Thr Leu Val Ala Pro Ile Gly
            20                  25                  30

Val Ala Ser Ala Asn Glu Trp Gln Leu Ala Ala Tyr Thr Thr Ser Leu
        35                  40                  45

Ser Gly Thr Ile Ala Val Arg Phe Leu Pro Val Leu Pro Asp Asn Met
    50                  55                  60

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

Asn Ile Leu Gly Pro Leu Lys Ser Asn Leu Asp Ala Leu Leu Ser Ser
```

```
                85                  90                  95

Glu Thr Tyr Pro Gln Thr Arg Leu Ile Gly Ala Val Ile Gly Ser Ile
            100                 105                 110

Ala Leu Gly Val Ala Thr Ser Ala Gln Ile Thr Ala Ala Val Ala Leu
        115                 120                 125

Lys Gln Ala Gln Asp Asn Ala Arg Asn Ile Leu Ala Leu Lys Glu Ala
    130                 135                 140

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

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

Ile Leu Pro Ser Ile Asn Gln Leu Ser Cys Glu Val Thr Ala Asn Lys
            180                 185                 190

Leu Gly Val Tyr Leu Ser Leu Tyr Leu Thr Glu Leu Thr Thr Ile Phe
        195                 200                 205

Gly Ala Gln Leu Thr Asn Pro Ala Leu Thr Ser Leu Ser Tyr Gln Ala
    210                 215                 220

Leu Tyr Asn Leu Cys Gly Gly Asn Met Ala Met Leu Thr Gln Lys Ile
225                 230                 235                 240

Gly Ile Lys Gln Gln Asp Val Asn Ser Leu Tyr Glu Ala Gly Leu Ile
                245                 250                 255

Thr Gly Gln Val Ile Gly Tyr Asp Ser Gln Tyr Gln Leu Leu Val Ile
            260                 265                 270

Gln Val Asn Tyr Pro Ser Ile Ser Glu Val Thr Gly Val Arg Ala Thr
        275                 280                 285

Glu Leu Val Thr Val Ser Val Thr Thr Asp Lys Gly Glu Gly Lys Ala
    290                 295                 300

Ile Val Pro Gln Phe Val Ala Glu Ser Arg Val Thr Ile Glu Glu Leu
305                 310                 315                 320

Asp Val Ala Ser Cys Lys Phe Ser Ser Thr Thr Leu Tyr Cys Arg Gln
                325                 330                 335

Val Asn Thr Arg Ala Leu Pro Pro Leu Val Ala Ser Cys Leu Arg Gly
            340                 345                 350
```

```
Asn Tyr Asp Asp Cys Gln Tyr Thr Thr Glu Ile Gly Ala Leu Ser Ser
        355                 360                 365

Arg Tyr Ile Thr Leu Asp Gly Gly Val Leu Val Asn Cys Lys Ser Ile
    370                 375                 380

Val Cys Arg Cys Leu Asn Pro Ser Lys Ile Ile Ser Gln Asn Thr Asn
385                 390                 395                 400

Ala Ala Val Thr Tyr Val Asp Ala Thr Ile Cys Lys Thr Ile Gln Leu
                405                 410                 415

Asp Asp Ile Gln Leu Gln Leu Glu Gly Ser Leu Ser Ser Val Tyr Ala
            420                 425                 430

Arg Asn Ile Ser Ile Glu Ile Ser Gln Val Thr Thr Ser Gly Ser Leu
        435                 440                 445

Asp Ile Ser Ser Glu Ile Gly Asn Ile Asn Asn Thr Val Asn Arg Val
    450                 455                 460

Glu Asp Leu Ile His Gln Ser Glu Glu Trp Leu Ala Lys Val Asn Pro
465                 470                 475                 480

His Ile Val Asn Asn Thr Thr Leu Ile Val Leu Cys Val Leu Ser Ala
                485                 490                 495

Leu Ala Val Ile Trp Leu Ala Val Leu Thr Ala Ile Ile Ile Tyr Leu
            500                 505                 510

Arg Thr Lys Leu Lys Thr Ile Ser Ala Leu Ala Val Thr Asn Thr Ile
        515                 520                 525

Gln Ser Asn Pro Tyr Val Asn Gln Thr Lys Arg Glu Ser Lys Phe
    530                 535                 540
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<210> 85
<211> 1734
<212> DNA
<213> artificial sequence

<220>
<223> HN gene of FJ619036

<400> 85

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attgttagca tagttcaaat tgggaatttg aaaattcctt ctgtagggga tctggcggac 180

gaggtggtaa caccttttgaa aaccactctg tctgatacac tcaggaatcc aattaaccag 240

ataaatgaca tattcaggat tgttgccctt gatattccat tgcaagtaac tagtatccaa 300

aaagacctcg caagtcaatt tagcatgttg atagatagtt taaatgctat caaattgggc 360

aacgggacca accttatcat acctacatca gataaggagt atgcaggagg aattggaaac 420

cctgtcttta ctgtcgatgc tggaggttct ataggattca agcaatttag cttaatagaa 480

catccgagct ttattgctgg acctacaacg acccgaggct gtacaagaat acccactttt 540

cacatgtcag aaagtcattg gtgctactca cacaacatca tcgctgctgg ctgtcaagat 600

gccagtgcat ctagtatgta tatctcaatg ggggttctcc atgtgtcttc atctggcact 660

cctatctttc ttactactgc aagtgaactg atagacgatg gagttaatcg taagtcatgc 720

agtattgtag caacccaatt cggctgtgac attttgtgca gtattgtcat agagaaggag 780

ggagatgatt attggtctga tactccgact ccaatgcgcc acggccgttt ttcattcaat 840

gggagttttg tagaaaccga actacccgtg tccagtatgt tctcgtcatt ctctgccaac 900

taccctgctg tgggatcagg cgaaattgta aaagatagaa tattattccc aatttacgga 960

ggtataaagc agacttcacc agagtttacc gaattagtga aatatggact ctttgtgtca 1020

acacctacaa ctgtatgtca gagtagctgg acttatgacc aggtaaaagc agcgtatagg 1080

ccagattaca tatcaggccg gttctgggca caagtgatac tcagctgcgc tcttgatgca 1140

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tggccattgg catttgttac aaaactagac ccgcaagagt tagcagacac aaactcgata 1320

tggctgacca attccatacc aatcccacaa tcaaagttcc ctcggccttc atattcagaa 1380

aattattgca caaagccagc agtttgccct gctacttgtg tcactggtgt atactctgat 1440

atttggccct tgacctcatc ttcatcactc ccgagcataa tttggatcgg ccagtacctt 1500

gatgcccctg ttggaaggac ttatcccaga tttggaattg caaatcaatc acactggtac 1560

cttcaagaag atattctacc cacctccact gcaagtgcgt attcaaccac tacatgtttt 1620

aagaatactg ccaggaatag agtgttctgc gtcaccattg ctgaatttgc agatgggttg 1680

tttggagagt acaggataac acctcagttg tatgaattag tgagaaataa ttga 1734

<210> 86
<211> 577
<212> PRT

<213> artificial sequence

<220>
<223> HN protein of ACN88145

<400> 86

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Arg Lys Thr Thr Trp Arg Ala Ile Phe Arg Trp Ser Val Leu Leu Ile
            20                  25                  30

Thr Thr Gly Cys Leu Ala Leu Ser Ile Val Ser Ile Val Gln Ile Gly
        35                  40                  45

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

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

Ile Asn Asp Ile Phe Arg Ile Val Ala Leu Asp Ile Pro Leu Gln Val
                85                  90                  95

Thr Ser Ile Gln Lys Asp Leu Ala Ser Gln Phe Ser Met Leu Ile Asp
            100                 105                 110

Ser Leu Asn Ala Ile Lys Leu Gly Asn Gly Thr Asn Leu Ile Ile Pro
        115                 120                 125

Thr Ser Asp Lys Glu Tyr Ala Gly Gly Ile Gly Asn Pro Val Phe Thr
    130                 135                 140

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

His Pro Ser Phe Ile Ala Gly Pro Thr Thr Thr Arg Gly Cys Thr Arg
                165                 170                 175

Ile Pro Thr Phe His Met Ser Glu Ser His Trp Cys Tyr Ser His Asn
            180                 185                 190

Ile Ile Ala Ala Gly Cys Gln Asp Ala Ser Ala Ser Ser Met Tyr Ile
        195                 200                 205

Ser Met Gly Val Leu His Val Ser Ser Ser Gly Thr Pro Ile Phe Leu
    210                 215                 220

Thr Thr Ala Ser Glu Leu Ile Asp Asp Gly Val Asn Arg Lys Ser Cys
225                 230                 235                 240

Ser Ile Val Ala Thr Gln Phe Gly Cys Asp Ile Leu Cys Ser Ile Val
                245                 250                 255

Ile Glu Lys Glu Gly Asp Asp Tyr Trp Ser Asp Thr Pro Thr Pro Met
            260                 265                 270
```

```
Arg His Gly Arg Phe Ser Phe Asn Gly Ser Phe Val Glu Thr Glu Leu
        275                 280                 285

Pro Val Ser Ser Met Phe Ser Ser Phe Ser Ala Asn Tyr Pro Ala Val
    290                 295                 300

Gly Ser Gly Glu Ile Val Lys Asp Arg Ile Leu Phe Pro Ile Tyr Gly
305                 310                 315                 320

Gly Ile Lys Gln Thr Ser Pro Glu Phe Thr Glu Leu Val Lys Tyr Gly
                325                 330                 335

Leu Phe Val Ser Thr Pro Thr Thr Val Cys Gln Ser Ser Trp Thr Tyr
            340                 345                 350

Asp Gln Val Lys Ala Ala Tyr Arg Pro Asp Tyr Ile Ser Gly Arg Phe
        355                 360                 365

Trp Ala Gln Val Ile Leu Ser Cys Ala Leu Asp Ala Val Asp Leu Ser
    370                 375                 380

Ser Cys Ile Val Lys Ile Met Asn Ser Ser Thr Val Met Met Ala Ala
385                 390                 395                 400

Glu Gly Arg Ile Ile Lys Ile Gly Ile Asp Tyr Phe Tyr Tyr Gln Arg
                405                 410                 415

Ser Ser Ser Trp Trp Pro Leu Ala Phe Val Thr Lys Leu Asp Pro Gln
            420                 425                 430

Glu Leu Ala Asp Thr Asn Ser Ile Trp Leu Thr Asn Ser Ile Pro Ile
        435                 440                 445

Pro Gln Ser Lys Phe Pro Arg Pro Ser Tyr Ser Glu Asn Tyr Cys Thr
    450                 455                 460

Lys Pro Ala Val Cys Pro Ala Thr Cys Val Thr Gly Val Tyr Ser Asp
465                 470                 475                 480

Ile Trp Pro Leu Thr Ser Ser Ser Ser Leu Pro Ser Ile Ile Trp Ile
                485                 490                 495

Gly Gln Tyr Leu Asp Ala Pro Val Gly Arg Thr Tyr Pro Arg Phe Gly
            500                 505                 510

Ile Ala Asn Gln Ser His Trp Tyr Leu Gln Glu Asp Ile Leu Pro Thr
        515                 520                 525
```

Ser Thr Ala Ser Ala Tyr Ser Thr Thr Thr Cys Phe Lys Asn Thr Ala
530 535 540

Arg Asn Arg Val Phe Cys Val Thr Ile Ala Glu Phe Ala Asp Gly Leu
545 550 555 560

Phe Gly Glu Tyr Arg Ile Thr Pro Gln Leu Tyr Glu Leu Val Arg Asn
565 570 575

Asn

<210> 87
<211> 6717
<212> DNA
<213> artificial sequence

<220>
<223> L gene of FJ619036

<400> 87

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cgacaaaaat ccgtagtgat gcacatccca gaccacatct tagaaaaatc agaatatcgg 180

atcaagcacc gtctagggaa aatcaagagt gacatagcac attactgtca gtattttaat 240

attaatttgg caaatcttga tccgataacc caccccaaaa gtttgtattg gttatccaga 300

ctaacaatag ctagtgctgg aacctttaga catatgaaag atagaatctt atgtacagtt 360

ggctccgaat tcggacacaa aattcaagat ttattttcac tgctgagcca taaattagta 420

ggtaacggtg atttatttaa tcaaagtctc tcaggtacac gtttgactgc gagtccgtta 480

tccccttttat gcaatcaatt tgtctctgac atcaagtctg cagtcacgac accctggtca 540

gaagctcgtt ggtcttggct tcatatcaaa caaacaatga gatacctgat aaaacaatca 600

cgcactacaa attcagctca tttaacagaa attataaaag aggaatgggg tttagtaggt 660

attactccag atcttgtcat tctttttgac agagtcaata atagtctaac tgcattaaca 720

tttgagatgg ttctaatgta ttcagatgta ttagaatccc gtgacaatat tgtgctagtg 780

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gcagagatgc tatgcctgat gagattattt ggacacccaa tgttaactgc accggatgca 1140

gcagccaaag taaggaaagc aatgtgtgct ccaaaacttg ttgaacatga caccatcttg 1200

cagacattat ccttcttcaa gggaataatt ataaatgggt acagaagatc acactctggc 1260

ctgtggccca atgtagagcc gtcttcaatc tatgatgatg atctcagaca gctgtactta 1320

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tcccacacgc ggtcccagta tatggacgaa attaagagca accgattgct aattgatttt 1560

cttgattctg ctgattttga ccctgaaaag gaatttgcat atgtaaccac aatggattat 1620

ttgcacgata atgaattttg tgcttcatat tctctaaagg aaaaggagat caaaactacc 1680

gggaggatat ttgcaaaaat gacacgcaat atgagaagtt gccaagtgat acttgaatct 1740

ctgttatcaa aacatatatg caagttcttc aaagagaacg gcgtttcgat ggagcaattg 1800

tcattgacca agagtctact tgcaatgtct caactctcac caaaagtctc gactctgcag 1860

gacactgcat cacgtcatgt aggcaactca aaatctcaga tcgcaaccag caacccatct 1920

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            20                  25                  30

Gly Leu Pro Met Pro Ala Asp Leu Arg Gln Lys Ser Val Val Met His
        35                  40                  45

Ile Pro Asp His Ile Leu Glu Lys Ser Glu Tyr Arg Ile Lys His Arg
    50                  55                  60

Leu Gly Lys Ile Lys Ser Asp Ile Ala His Tyr Cys Gln Tyr Phe Asn
65                  70                  75                  80

Ile Asn Leu Ala Asn Leu Asp Pro Ile Thr His Pro Lys Ser Leu Tyr
                85                  90                  95

Trp Leu Ser Arg Leu Thr Ile Ala Ser Ala Gly Thr Phe Arg His Met
            100                 105                 110

Lys Asp Arg Ile Leu Cys Thr Val Gly Ser Glu Phe Gly His Lys Ile
        115                 120                 125

Gln Asp Leu Phe Ser Leu Leu Ser His Lys Leu Val Gly Asn Gly Asp
    130                 135                 140

Leu Phe Asn Gln Ser Leu Ser Gly Thr Arg Leu Thr Ala Ser Pro Leu
145                 150                 155                 160

Ser Pro Leu Cys Asn Gln Phe Val Ser Asp Ile Lys Ser Ala Val Thr
                165                 170                 175

Thr Pro Trp Ser Glu Ala Arg Trp Ser Trp Leu His Ile Lys Gln Thr
            180                 185                 190

Met Arg Tyr Leu Ile Lys Gln Ser Arg Thr Thr Asn Ser Ala His Leu
        195                 200                 205

Thr Glu Ile Ile Lys Glu Glu Trp Gly Leu Val Gly Ile Thr Pro Asp
    210                 215                 220

Leu Val Ile Leu Phe Asp Arg Val Asn Asn Ser Leu Thr Ala Leu Thr
225                 230                 235                 240

Phe Glu Met Val Leu Met Tyr Ser Asp Val Leu Glu Ser Arg Asp Asn
                245                 250                 255

Ile Val Leu Val Gly Arg Leu Ser Thr Phe Leu Gln Pro Val Val Ser
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Arg Leu Glu Val Leu Phe Asp Leu Val Asp Ser Leu Ala Lys Thr Leu
275 280 285

Gly Asp Thr Ile Tyr Glu Ile Ile Ala Val Leu Glu Ser Leu Ser Tyr
290 295 300

Gly Ser Val Gln Leu His Asp Ala Ser His Ser His Ala Gly Ser Phe
305 310 315 320

Phe Ser Phe Asn Met Asn Glu Leu Asp Asn Thr Leu Ser Lys Arg Val
325 330 335

Asp Pro Lys His Lys Asn Thr Ile Met Ser Ile Ile Arg Gln Cys Phe
340 345 350

Ser Asn Leu Asp Val Asp Gln Ala Ala Glu Met Leu Cys Leu Met Arg
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Leu Phe Gly His Pro Met Leu Thr Ala Pro Asp Ala Ala Ala Lys Val
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Arg Lys Ala Met Cys Ala Pro Lys Leu Val Glu His Asp Thr Ile Leu
385 390 395 400

Gln Thr Leu Ser Phe Phe Lys Gly Ile Ile Ile Asn Gly Tyr Arg Arg
405 410 415

Ser His Ser Gly Leu Trp Pro Asn Val Glu Pro Ser Ser Ile Tyr Asp
420 425 430

Asp Asp Leu Arg Gln Leu Tyr Leu Glu Ser Ala Glu Ile Ser His His
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Phe Met Leu Lys Asn Tyr Lys Ser Leu Ser Met Ile Glu Phe Lys Lys
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Ser Ile Asp Tyr Asp Leu His Asp Asp Leu Ser Thr Phe Leu Lys Asp
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Arg Ala Ile Cys Arg Pro Lys Ser Gln Trp Asp Val Ile Phe Arg Lys
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Ser Leu Arg Arg Ser His Thr Arg Ser Gln Tyr Met Asp Glu Ile Lys
500 505 510

Ser Asn Arg Leu Leu Ile Asp Phe Leu Asp Ser Ala Asp Phe Asp Pro
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Glu Lys Glu Phe Ala Tyr Val Thr Thr Met Asp Tyr Leu His Asp Asn
    530                 535                 540

Glu Phe Cys Ala Ser Tyr Ser Leu Lys Glu Lys Glu Ile Lys Thr Thr
545                 550                 555                 560

Gly Arg Ile Phe Ala Lys Met Thr Arg Asn Met Arg Ser Cys Gln Val
                565                 570                 575

Ile Leu Glu Ser Leu Leu Ser Lys His Ile Cys Lys Phe Phe Lys Glu
            580                 585                 590

Asn Gly Val Ser Met Glu Gln Leu Ser Leu Thr Lys Ser Leu Leu Ala
        595                 600                 605

Met Ser Gln Leu Ser Pro Lys Val Ser Thr Leu Gln Asp Thr Ala Ser
    610                 615                 620

Arg His Val Gly Asn Ser Lys Ser Gln Ile Ala Thr Ser Asn Pro Ser
625                 630                 635                 640

Arg His His Ser Thr Thr Asn Gln Met Ser Leu Ser Asn Arg Lys Thr
                645                 650                 655

Val Val Ala Thr Phe Leu Thr Thr Asp Leu Glu Lys Tyr Cys Leu Gln
            660                 665                 670

Trp Arg Tyr Ser Thr Ile Lys Leu Phe Ala Gln Ala Leu Asn Gln Leu
        675                 680                 685

Phe Gly Ile Asp His Gly Phe Glu Trp Ile His Leu Arg Leu Met Asn
    690                 695                 700

Ser Thr Leu Phe Val Gly Asp Pro Tyr Ser Pro Pro Glu Asp Pro Thr
705                 710                 715                 720

Leu Glu Asp Ile Asp Lys Ala Pro Asn Asp Asp Ile Phe Ile Val Ser
                725                 730                 735

Pro Arg Gly Gly Ile Glu Gly Leu Cys Gln Lys Met Trp Thr Met Ile
            740                 745                 750

Ser Ile Ser Ala Ile His Cys Val Ala Glu Lys Ile Gly Ala Arg Val
        755                 760                 765

Ala Ala Met Val Gln Gly Asp Asn Gln Val Ile Ala Ile Thr Lys Glu
    770                 775                 780
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Leu Phe Arg Gly Glu Lys Ala Cys Asp Val Arg Asp Glu Leu Asp Glu
785                 790                 795                 800

Leu Gly Gln Val Phe Phe Asp Glu Phe Lys Arg His Asn Tyr Ala Ile
                805                 810                 815

Gly His Asn Leu Lys Leu Asn Glu Thr Ile Gln Ser Gln Ser Phe Phe
            820                 825                 830

Val Tyr Ser Lys Arg Ile Phe Phe Glu Gly Arg Leu Leu Ser Gln Val
        835                 840                 845

Leu Lys Asn Ala Ala Lys Leu Cys Met Val Ala Asp His Leu Gly Glu
    850                 855                 860

Asn Thr Val Ser Ser Cys Ser Asn Leu Ser Ser Thr Ile Ala Arg Leu
865                 870                 875                 880

Val Glu Asn Gly Phe Glu Lys Asp Thr Ala Phe Val Leu Asn Leu Val
                885                 890                 895

Tyr Ile Met Thr Gln Ile Leu Phe Asp Glu His Tyr Ser Ile Val Cys
            900                 905                 910

Asp His Asn Ser Val Lys Ser Leu Ile Gly Ser Lys Asn Tyr Arg Asn
        915                 920                 925

Leu Leu Tyr Ser Ser Leu Ile Pro Gly Gln Leu Gly Gly Phe Asn Phe
    930                 935                 940

Leu Asn Ile Ser Arg Leu Phe Thr Arg Asn Ile Gly Asp Pro Val Thr
945                 950                 955                 960

Cys Ser Leu Ser Asp Leu Lys Cys Phe Ile Ala Ala Gly Leu Leu Pro
                965                 970                 975

Pro Tyr Val Leu Lys Asn Val Val Leu Arg Glu Pro Gly Pro Gly Thr
            980                 985                 990

Trp Leu Thr Leu Cys Ser Asp Pro  Tyr Thr Leu Asn Ile  Pro Tyr Thr
        995                 1000                1005

Gln Leu  Pro Thr Thr Tyr Leu  Lys Lys His Thr Gln  Arg Ser Leu
    1010                1015                1020

Leu Ser  Arg Ala Val Asn Pro  Leu Leu Ala Gly Val  Gln Val Pro
    1025                1030                1035
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Asn Gln  His Glu Glu Glu Glu  Met Leu Ala Arg Phe  Leu Leu Asp
    1040                 1045                 1050

Arg Glu  Tyr Val Met Pro Arg  Val Ala His Val Thr  Leu Glu Thr
    1055                 1060                 1065

Ser Val  Leu Gly Lys Arg Lys  Gln Ile Gln Gly Leu  Ile Asp Thr
    1070                 1075                 1080

Thr Pro  Thr Ile Ile Arg Thr  Ser Leu Val Asn Leu  Pro Val Ser
    1085                 1090                 1095

Arg Lys  Lys Cys Glu Lys Ile  Ile Asn Tyr Ser Leu  Asn Tyr Ile
    1100                 1105                 1110

Ala Glu  Cys His Asp Ser Leu  Leu Ser Gln Ile Cys  Phe Ser Asp
    1115                 1120                 1125

Asn Lys  Glu Tyr Leu Trp Ser  Thr Ser Leu Ile Ser  Val Glu Thr
    1130                 1135                 1140

Cys Ser  Val Thr Ile Ala Asp  Tyr Leu Arg Ala Val  Ser Trp Ser
    1145                 1150                 1155

Asn Ile  Leu Gly Gly Arg Ser  Ile Ser Gly Val Thr  Thr Pro Asp
    1160                 1165                 1170

Thr Ile  Glu Leu Ile Gln Gly  Cys Leu Ile Gly Glu  Asn Ser Ser
    1175                 1180                 1185

Cys Thr  Leu Cys Glu Ser His  Asp Asp Ala Phe Thr  Trp Met His
    1190                 1195                 1200

Leu Pro  Gly Pro Leu Tyr Ile  Pro Glu Pro Ser Val  Thr Asn Ser
    1205                 1210                 1215

Lys Met  Arg Val Pro Tyr Leu  Gly Ser Lys Thr Glu  Glu Arg Lys
    1220                 1225                 1230

Thr Ala  Ser Met Ala Ala Ile  Lys Gly Met Ser His  His Leu Arg
    1235                 1240                 1245

Ala Val  Leu Arg Gly Thr Ser  Val Phe Ile Trp Ala  Ser Gly Asp
    1250                 1255                 1260

Thr Asp  Ile Asn Trp Asp Asn  Ala Leu Gln Ile Ala  Gln Ser Arg
    1265                 1270                 1275

Cys Asn  Ile Thr Leu Asp Gln  Met Arg Leu Leu Thr  Pro Ile Pro
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    1280                1285                1290

Ser Ser  Ser Asn Ile Gln Arg  Arg Leu Asp Asp Gly  Ile Ser Thr
    1295                1300                1305

Gln Lys  Phe Thr Pro Ala Ser  Leu Ala Arg Ile Thr  Ser Ser Val
    1310                1315                1320

His Ile  Cys Asn Asp Ser Gln  Arg Leu Glu Lys Asp  Gly Ser Ser
    1325                1330                1335

Val Asp  Ser Asn Leu Ile Tyr  Gln Gln Ile Met Leu  Leu Gly Leu
    1340                1345                1350

Ser Ile  Phe Glu Thr Met Tyr  Ser Met Asp Gln Lys  Trp Val Phe
    1355                1360                1365

Asn Asn  His Thr Leu His Leu  His Thr Gly His Ser  Cys Cys Pro
    1370                1375                1380

Arg Glu  Leu Asp Ile Ser Leu  Val Asn Pro Pro Arg  His Gln Thr
    1385                1390                1395

Pro Glu  Leu Thr Ser Thr Thr  Thr Asn Pro Phe Leu  Tyr Asp Gln
    1400                1405                1410

Leu Pro  Leu Asn Gln Asp Asn  Leu Thr Thr Leu Glu  Ile Lys Thr
    1415                1420                1425

Phe Lys  Phe Asn Glu Leu Asn  Ile Asp Gly Leu Asp  Phe Gly Glu
    1430                1435                1440

Gly Ile  Gln Leu Leu Ser Arg  Cys Thr Ala Arg Leu  Met Ala Glu
    1445                1450                1455

Cys Ile  Leu Glu Glu Gly Ile  Gly Ser Ser Val Lys  Asn Glu Ala
    1460                1465                1470

Ile Val  Asn Phe Asp Asn Ser  Val Asn Trp Ile Ser  Glu Cys Leu
    1475                1480                1485

Met Cys  Asp Ile Arg Ser Leu  Cys Val Asn Leu Gly  Gln Glu Ile
    1490                1495                1500

Leu Cys  Ser Leu Ala Tyr Gln  Met Tyr Tyr Leu Arg  Ile Arg Gly
    1505                1510                1515

Arg Arg  Ala Ile Leu Asn Tyr  Leu Asp Thr Thr Leu  Gln Arg Ile
    1520                1525                1530
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Pro Val  Ile Gln Leu Ala Asn  Ile Ala Leu Thr Ile  Ser His Pro
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Glu Ile  Phe Arg Arg Ile Val  Asn Thr Gly Ile His  Asn Gln Ile
    1550                 1555                 1560

Lys Gly  Pro Tyr Val Ala Thr  Thr Asp Phe Ile Ala  Ala Ser Arg
    1565                 1570                 1575

Asp Ile  Ile Leu Ser Gly Ala  Arg Glu Tyr Leu Ser  Tyr Leu Ser
    1580                 1585                 1590

Ser Gly  Gln Glu Asp Cys Tyr  Thr Phe Phe Asn Cys  Gln Asp Gly
    1595                 1600                 1605

Asp Leu  Thr Pro Lys Met Glu  Gln Tyr Leu Ala Arg  Arg Ala Cys
    1610                 1615                 1620

Leu Leu  Thr Leu Leu Tyr Asn  Thr Gly His Gln Ile  Pro Ile Ile
    1625                 1630                 1635

Arg Ser  Leu Thr Pro Ile Glu  Lys Cys Lys Val Leu  Thr Glu Tyr
    1640                 1645                 1650

Asn Gln  Gln Ile Glu Tyr Ala  Asp Gln Glu Phe Ser  Ser Val Leu
    1655                 1660                 1665

Lys Val  Val Asn Ala Leu Leu  Gln Asn Pro Asn Ile  Asp Ala Leu
    1670                 1675                 1680

Val Ser  Asn Leu Tyr Phe Thr  Thr Arg Arg Val Leu  Ser Asn Leu
    1685                 1690                 1695

Arg Ser  Cys Asp Lys Ala Ile  Ser Tyr Ile Glu Tyr  Leu Tyr Thr
    1700                 1705                 1710

Glu Asp  Phe Gly Glu Lys Glu  Asp Thr Val Gln Tyr  Asp Ile Met
    1715                 1720                 1725

Thr Thr  Asn Asp Ile Ile Leu  Thr His Gly Leu Phe  Thr Gln Ile
    1730                 1735                 1740

Glu Ile  Ser Tyr Gln Gly Ser  Ser Leu His Lys Phe  Leu Thr Pro
    1745                 1750                 1755

Asp Asn  Ala Pro Gly Ser Leu  Ile Pro Phe Ser Ile  Ser Pro Asn
    1760                 1765                 1770
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Ser Leu  Ala Cys Asp Pro Leu  His His Leu Leu Lys  Ser Val Gly
    1775                 1780                 1785

Thr Ser  Ser Thr Ser Trp Tyr  Lys Tyr Ala Ile Ala  Tyr Ala Val
    1790                 1795                 1800

Ser Glu  Lys Arg Ser Ala Arg  Leu Gly Gly Ser Leu  Tyr Ile Gly
    1805                 1810                 1815

Glu Gly  Ser Gly Ser Val Met  Thr Leu Leu Glu Tyr  Leu Glu Pro
    1820                 1825                 1830

Ser Val  Asp Ile Phe Tyr Asn  Ser Leu Phe Ser Asn  Gly Met Asn
    1835                 1840                 1845

Pro Pro  Gln Arg Asn Tyr Gly  Leu Met Pro Leu Gln  Phe Val Asn
    1850                 1855                 1860

Ser Val  Val Tyr Lys Asn Leu  Thr Ala Lys Ser Glu  Cys Lys Leu
    1865                 1870                 1875

Gly Phe  Val Gln Gln Phe Lys  Pro Leu Trp Arg Asp  Ile Asp Ile
    1880                 1885                 1890

Glu Thr  Asn Val Thr Asp Pro  Ser Phe Val Asn Phe  Ala Leu Asn
    1895                 1900                 1905

Glu Ile  Pro Met Gln Ser Leu  Lys Arg Val Asn Cys  Asp Val Glu
    1910                 1915                 1920

Phe Asp  Arg Gly Met Pro Ile  Glu Arg Val Ile Gln  Gly Tyr Thr
    1925                 1930                 1935

His Ile  Leu Leu Val Ala Thr  Tyr Gly Leu Gln Gln  Asp Ser Ile
    1940                 1945                 1950

Leu Trp  Val Lys Val Tyr Arg  Thr Ser Glu Lys Val  Phe Gln Phe
    1955                 1960                 1965

Leu Leu  Ser Ala Met Ile Met  Ile Phe Gly Tyr Val  Lys Ile His
    1970                 1975                 1980

Arg Asn  Gly Tyr Met Ser Ala  Lys Asp Glu Glu Tyr  Ile Leu Met
    1985                 1990                 1995

Ser Asp  Cys Lys Glu Pro Val  Asn Tyr Thr Ala Val  Pro Asn Ile
    2000                 2005                 2010
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Leu Thr  Arg Val Ser Asp Leu  Val Ser Lys Asn Leu  Ser Leu Ile
    2015                 2020                 2025

His Pro  Glu Asp Leu Arg Lys  Val Arg Cys Glu Thr  Asp Ser Leu
    2030                 2035                 2040

Asn Leu  Lys Cys Asn His Ile  Tyr Glu Lys Ile Ile  Ala Arg Lys
    2045                 2050                 2055

Ile Pro  Leu Gln Val Ser Ser  Thr Asp Ser Leu Leu  Leu Gln Leu
    2060                 2065                 2070

Gly Gly  Val Ile Asn Ser Val  Gly Ser Thr Asp Pro  Arg Glu Val
    2075                 2080                 2085

Ala Thr  Leu Ser Ser Ile Glu  Cys Met Asp Tyr Val  Val Ser Ser
    2090                 2095                 2100

Ile Asp  Leu Ala Ile Leu Glu  Ala Asn Ile Val Ile  Ser Glu Ser
    2105                 2110                 2115

Ala Asp  Leu Asp Leu Ala Leu  Met Leu Gly Pro Phe  Asn Leu Asn
    2120                 2125                 2130

Lys Leu  Lys Lys Ile Asp Thr  Ile Leu Lys Ser Ser  Thr Tyr Gln
    2135                 2140                 2145

Leu Ile  Pro Tyr Trp Leu Arg  Tyr Glu Tyr Ser Ile  Asn Pro Arg
    2150                 2155                 2160

Ser Leu  Ser Phe Leu Ile Thr  Lys Leu Gln Gln Cys  Arg Ile Ser
    2165                 2170                 2175

Trp Ser  Asp Met Ile Thr Ile  Ser Glu Phe Cys Lys  Lys Ser Lys
    2180                 2185                 2190

Arg Pro  Ile Phe Ile Lys Arg  Val Ile Gly Asn Gln  Arg Leu Lys
    2195                 2200                 2205

Ser Phe  Phe Asn Glu Ser Ser  Ser Ile Val Leu Thr  Arg Ala Glu
    2210                 2215                 2220

Val Lys  Val Cys Ile Lys Phe  Leu Gly Ala Ile Ile  Lys Leu Lys
    2225                 2230                 2235
```

Claims

1. A vaccine comprising (i) a recombinant APMV viral vector and (ii) a pharmaceutically or veterinarily acceptable carrier, wherein the APMV viral vector is APMV-8 and wherein the APMV viral vector comprises a polynucleotide having at least 90% sequence identity to a polynucleotide having the sequence as set forth in SEQ ID NO:1 or a polynucleotide complementary to a polynucleotide having at least 90% sequence identity to a polynucleotide having the sequence as set forth in SEQ ID NO:1; wherein the APMV viral vector further comprises an isolated polynucleotide encoding an antigen of a pathogen, wherein the pathogen is avian, feline, canine, equine, bovine, ovine, caprine or porcine pathogen, wherein the polynucleotide is inserted in a nonessential region of the APMV genome, and further wherein the nonessential region is selected from the regions consisting of the untranslated region located upstream of the NP open reading frame, the intergenic regions between two open reading frames of the APMV genome, and the untranslated region located downstream of the L open reading frame.

2. A pharmaceutical composition or vaccine comprising a recombinant APMV viral vector, wherein the recombinant APMV viral vector comprises a heterologous polynucleotide that encodes and expresses an antigen of a pathogen for an animal, for use in inducing an immunological response in an animal to said antigen, wherein the use comprises inoculating the animal with the pharmaceutical composition or vaccine,
wherein the APMV viral vector is APMV-8 and wherein the APMV viral vector comprises a polynucleotide having at least 90% sequence identity to a polynucleotide having the sequence as set forth in SEQ ID NO:1 or a polynucleotide complementary to a polynucleotide having at least 90% sequence identity to a polynucleotide having the sequence as set forth in SEQ ID NO:1,
wherein the pathogen is avian, feline, canine, equine, bovine, ovine, caprine or porcine, and further wherein the heterologous polynucleotide is inserted into a nonessential region of the APMV genome selected from regions consisting of the untranslated region located upstream of the NP open reading frame, the intergenic regions between two open reading frames of the APMV genome, and the untranslated region located downstream of the L open reading frame.

3. A pharmaceutical composition or vaccine for the use according to claim 2, wherein the immunological response in an animal to the antigen is induced in a prime-boost regime.

4. A pharmaceutical composition or vaccine for the use according to claim 2 or 3, wherein said animal is avian, equine, canine, feline, porcine, bovine, or ovine.

Patentansprüche

1. Impfstoff umfassend (i) einen rekombinanten viralen APMV-Vektor und (ii) einen pharmazeutisch oder veterinärmedizinisch verträglichen Träger, wobei der virale APMV-Vektor APMV-8 ist und wobei der virale AMPV-Vektor ein Polynucleotid, das mindestens 90% Sequenzidentität mit einem Polynucleotid hat, das die wie in SEQ ID NO:1 gezeigte Sequenz aufweist, oder ein Polynucleotid umfasst, das zu einem Polynucleotid komplementär ist, das mindestens 90% Sequenzidentität mit einem Polynucleotid hat, das die wie in SEQ ID NO:1 gezeigte Sequenz aufweist; wobei der virale APMV-Vektor des Weiteren ein isoliertes Polynucleotid umfasst, das ein Antigen eines Pathogens codiert, wobei der Pathogen ein Vogel-, Katzen-, Hunde-, Pferde-, Rinder-, Schafs-, Ziegen- oder Schweine-Pathogen ist, wobei das Polynucleotid in eine nicht-essentielle Region des APMV-Genoms inseriert ist und wobei des Weiteren die nicht-essentielle Region ausgewählt ist aus den Regionen bestehend aus der nicht-translatierten Region, die stromaufwärts des NP-offenen Leserasters lokalisiert ist, den intergenischen Regionen zwischen zwei offenen Leserastern des APMV-Genoms und der nichttranslatierten Region, die stromabwärts des L-offenen Leserasters lokalisiert ist.

2. Arzneimittel oder Impfstoff, das/der einen rekombinanten viralen APMV-Vektor umfasst, wobei der rekombinante virale APMV-Vektor ein heterologes Polynucleotid umfasst, das ein Antigen eines Pathogens für ein Tier codiert und exprimiert, zur Verwendung zum Induzieren einer Immunantwort in einem Tier auf das Antigen, wobei die Verwendung das Beimpfen des Tiers mit dem Arzneimittel oder dem Impfstoff umfasst,
wobei der virale APMV-Vektor APMV-8 ist und wobei der virale APMV-Vektor ein Polynucleotid, das mindestens 90% Sequenzidentität mit einem Polynucleotid hat, das die wie in SEQ ID NO:1 gezeigte Sequenz aufweist oder ein Polynucleotid umfasst, das zu einem Polynucleotid komplementär ist, das mindestens 90% Sequenzidentität mit einem Polynucleotid hat, das die in SEQ ID NO:1 gezeigte Sequenz aufweist,
wobei der Pathogen ein Vogel-, Katzen-, Hunde-, Pferde-, Rinder-, Schaf-, Ziegen- oder Schweine-Pathogen ist

und wobei des Weiteren das heterologe Polynucleotid in eine nicht-essentielle Region des APMV-Genoms inseriert wird, die ausgewählt ist aus den Regionen bestehend aus der nichttranslatierten Region, die stromaufwärts des NP-offenen Leserasters lokalisiert ist, den intergenischen Regionen zwischen zwei offenen Leserastern des APMV-Genoms und der nicht-translatierten Region, die stromabwärts des L-offenen Leserasters lokalisiert ist.

3. Arzneimittel oder Impfstoff zur Verwendung nach Anspruch 2, wobei die Immunantwort auf das Antigen in einem Tier in einem Prime-Boost-Schema induziert wird.

4. Arzneimittel oder Impfstoff zur Verwendung nach Anspruch 2 oder 3, wobei das Tier vogelartig, pferdeartig, hundeartig, katzenartig, schweineartig, rinderartig oder schafartig ist.

Revendications

1. Vaccin comprenant (i) un vecteur viral APMV recombinant et (ii) un support acceptable d'un point de vue pharmaceutique ou vétérinaire, le vecteur viral APMV étant l'APMV-8 et dans lequel le vecteur viral APMV comprend un polynucléotide présentant au moins 90 % d'identité de séquence avec un polynucléotide ayant la séquence telle que représentée par SEQ ID NO : 1 ou un polynucléotide complémentaire d'un polynucléotide présentant au moins 90 % d'identité de séquence avec un polynucléotide ayant la séquence telle que représentée par SEQ ID NO : 1 ; dans lequel le vecteur viral APMV comprend en outre un polynucléotide isolé codant pour un antigène d'un agent pathogène, dans lequel l'agent pathogène est un agent pathogène aviaire, félin, canin, équin, bovin, ovin, caprin ou porcin, dans lequel le polynucléotide est inséré dans une région non essentielle du génome de l'APMV, et dans lequel en outre la région non essentielle est choisie parmi les régions constituées de la région non traduite localisée en amont du cadre de lecture ouvert de NP, les régions intergéniques entre deux cadres de lecture ouverts du génome de l'APMV, et la région non traduite localisée en aval du cadre de lecture ouvert de L.

2. Composition pharmaceutique ou vaccin comprenant un vecteur viral APMV recombinant, dans lequel le vecteur viral APMV recombinant comprend un polynucléotide hétérologue qui code pour et exprime un antigène d'un agent pathogène pour un animal, pour une utilisation dans l'induction d'une réponse immunologique chez un animal contre ledit antigène, dans lequel l'utilisation comprend l'inoculation de l'animal avec la composition pharmaceutique ou le vaccin, dans lequel le vecteur viral APMV est l'APMV-8 et dans lequel le vecteur viral APMV comprend un polynucléotide présentant au moins 90 % d'identité de séquence avec un polynucléotide ayant la séquence telle que représentée par SEQ ID NO : 1 ou un polynucléotide complémentaire d'un polynucléotide présentant au moins 90 % d'identité de séquence avec un polynucléotide ayant la séquence telle que représentée par SEQ ID NO : 1, dans lequel l'agent pathogène est aviaire, félin, canin, équin, bovin, ovin, caprin ou porcin, et en outre dans lequel le polynucléotide hétérologue est inséré dans une région non essentielle du génome de APMV choisie parmi des régions constituées de la région non traduite en amont du cadre de lecture ouvert de NP, les régions intergéniques entre deux cadres de lecture ouverts du génome de l'APMV, et la région non traduite localisée en aval du cadre de lecture de L.

3. Composition pharmaceutique ou vaccin pour l'utilisation selon la revendication 2, dans lequel la réponse immunologique chez un animal contre l'antigène est induite dans un régime de sensibilisation-rappel.

4. Composition pharmaceutique ou vaccin pour l'utilisation selon la revendication 2 ou 3, dans lequel ledit animal est aviaire, équin, canin, félin, porcin, bovin, ou ovin.

Figure 1

Day of Necropsy	Organ	Control	APMV-2	APMV-4	APMV-6
2	Trachea	0/5	0/5	2/5	0/5
	Lung	0/5	0/5	1/5	2/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	0/5	1/5	2/5
4	Trachea	0/5	2/5	0/5	1/5
	Lung	0/5	2/5	0/5	1/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	0/5	0/5	1/5
7	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	2/5
	Gut	0/5	1/5	0/5	0/5
	Pancreas	0/5	0/5	0/5	1/5
14	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	0/5	0/5	0/5
28	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	2/5	1/5	1/5

Figure 2

Day of Necropsy	Organ	Control	APMV serotype		
			2	4	6
2	Trachea – catarrhal Tracheitis	+	+	+	+
	Gut – mild enteritis	-	+	+	+
4	Trachea – focal ulceration of the respiratory epithelium, mild tracheitis	-	+	+	+
	Lung – focal BALT hyperplasia	-	-	+	-
	Pancreas – multifocal lymphocytic pancreatitis	-	-	+	+
7	Trachea – focal tracheal attenuation	-	+	-	-
	Lung – mild BALT hyperplasia	-	-	+	+
	Gut – cystic enteropathy, focal enteritis	-	-	-	+
	Pancreas – lymphocytic infiltrates in the pancreas	-	-	-	+
14	Trachea – tracheal attenuation, catarrhal tracheitis	-	+	+	+
	Lung – mild interstitial pneumonia, BALT hyperplasia	-	-	+	+
	Gut – GALT hyperplasia	-	-	+	+
28	Lung – lymphocytic bronchitis	-	+	+	+
	Gut – GALT hyperplasia	-	+	+	+
	Pancreas – lymphocytic pancreatitis	-	+	+	+

Figure 3

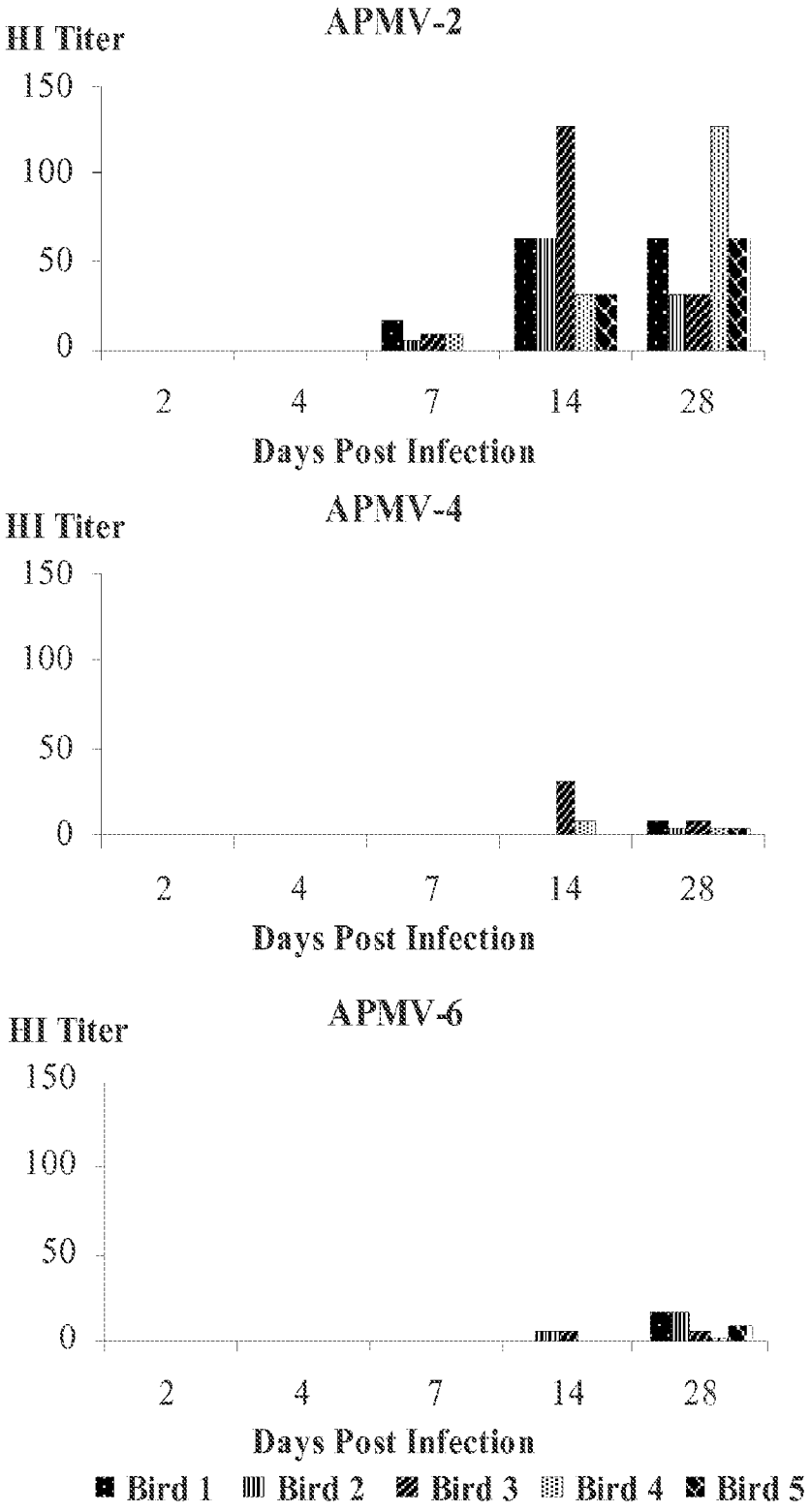
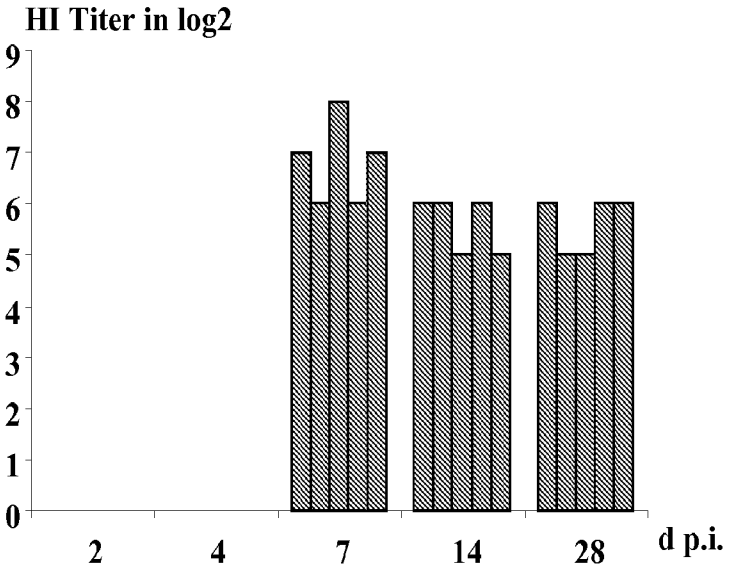
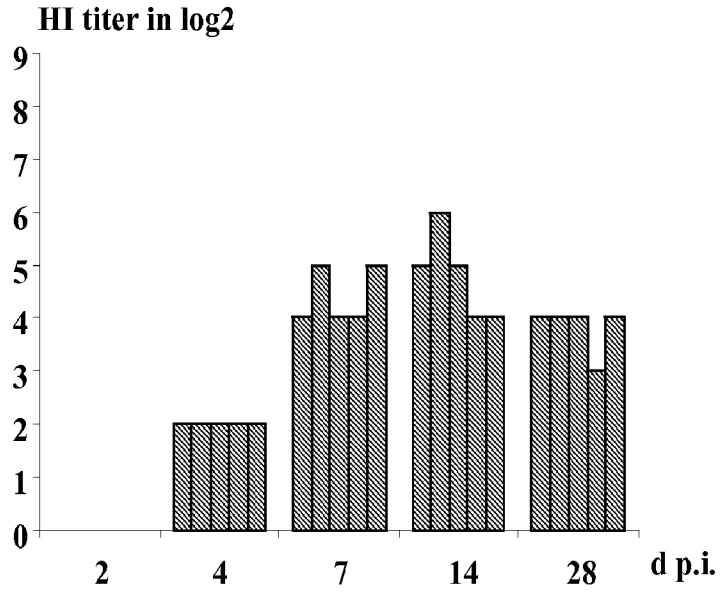

APMV-2
HI Titer
150
100
50
0
2
4
7
14
28
Days Post Infection
APMV-4
HI Titer
150
100
50
0
2
4
7
14
28
Days Post Infection
APMV-6
HI Titer
150
100
50
0
2
4
7
14
28
Days Post Infection
Bird 1
Bird 2
Bird 3
Bird 4
Bird 5

Figure 4



APMV-8 in chickens



APMV-8 in ducks

Figure 5

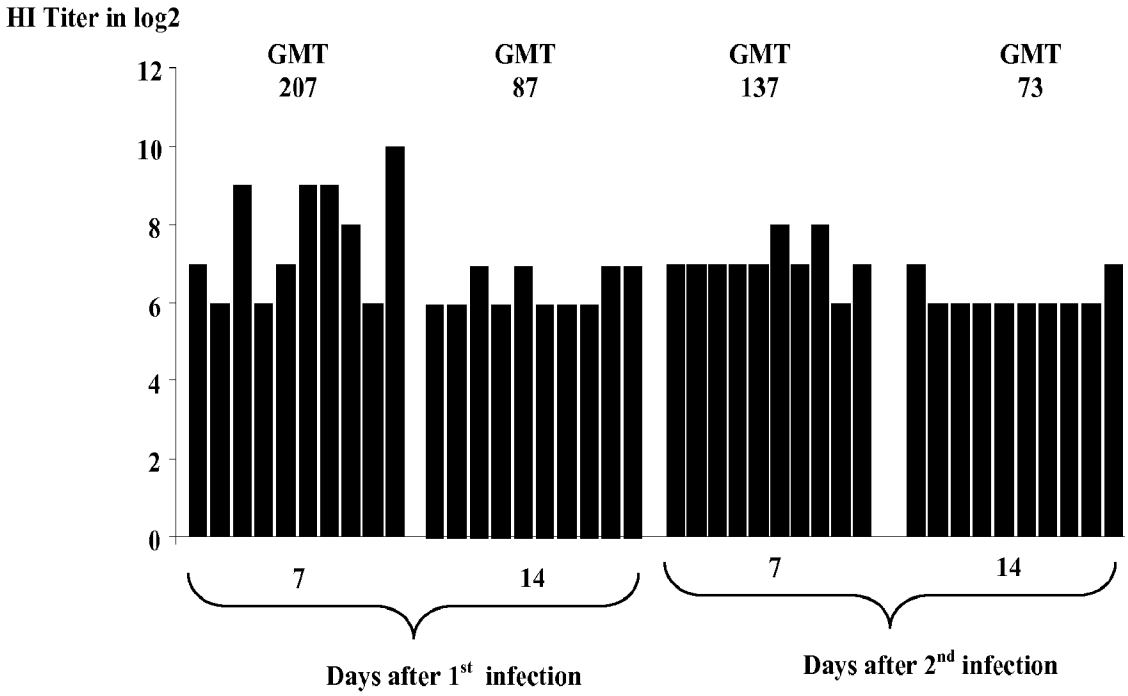

HI Titer in log2
GMT
207
GMT
87
GMT
137
GMT
73
12
10
8
6
4
2
0
7
14
7
14
Days after 1st infection
Days after 2nd infection

Figure 6

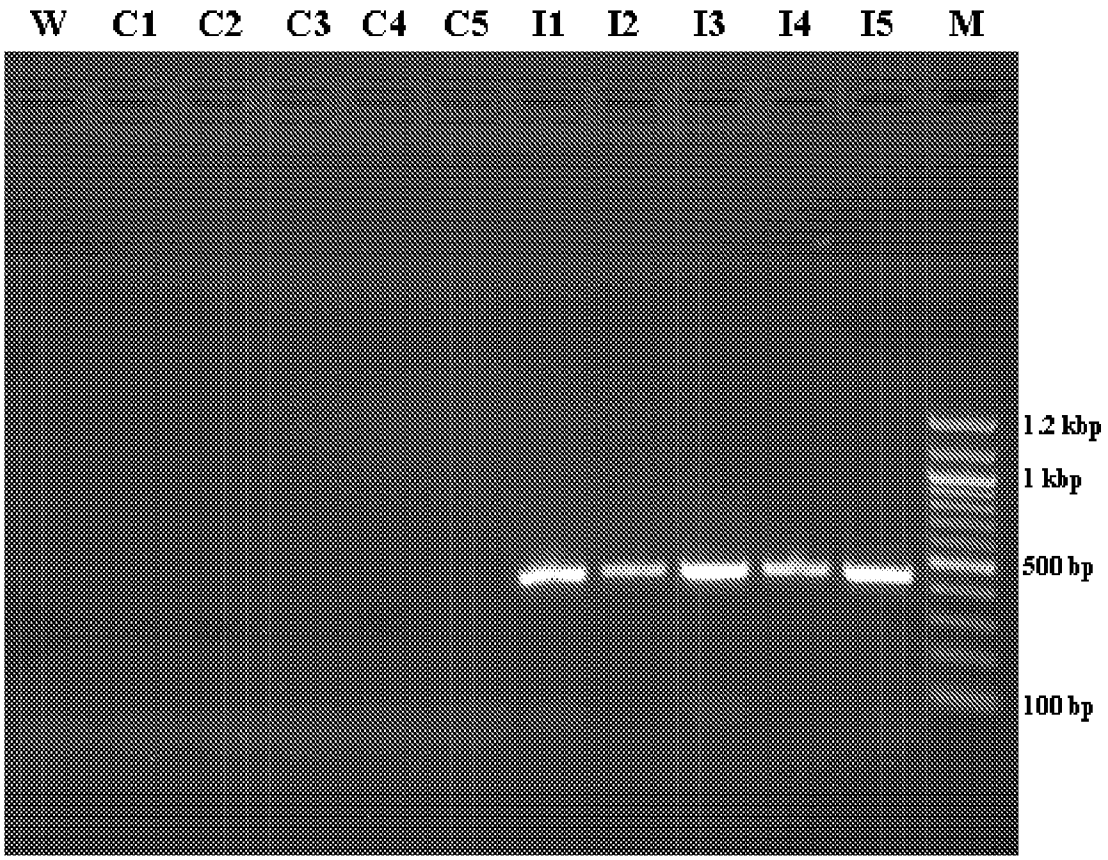


Figure 7

Day p.i.	Organ	Chicken		Ducks	
		Control	APMV-8	Control	APMV-8
		Virus isolation [a]		RT-PCR	
2	Trachea	0/5[b]	5/5	0/5	5/5
	Lung	0/5	3/5	0/5	3/5
	Gut	0/5	2/5	0/5	2/5
	Pancreas	0/5	0/5	0/5	0/5
4	Trachea	0/5	5/5	0/5	5/5
	Lung	0/5	1/5	0/5	1/5
	Gut	0/5	1/5	0/5	1/5
	Pancreas	0/5	1/5	0/5	1/5
7	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	2/5	0/5	2/5
14	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	0/5	0/5	0/5
	Pancreas	0/5	0/5	0/5	0/5
28	Trachea	0/5	0/5	0/5	0/5
	Lung	0/5	0/5	0/5	0/5
	Gut	0/5	1/5	0/5	1/5
	Pancreas	0/5	0/5	0/5	0/5

[a] Method used for the detection of virus

[b] Number of tissue samples tested positive/total number tested

Figure 8

Day p.i.	Organ	Chicken		Duck	
		Control	APMV-8	Control	APMV-8
2	Trachea – catarrhal tracheitis	0/5 [a]	5/5	0/5	3/5
	Lung- interstitial pneumonia	0/5	0/5	0/5	1/5
	Gut – mild enteritis	0/5	0/5	0/5	1/5
4	Trachea - regeneration of respiratory epithelium, minimal tracheitis	0/5	1/5	0/5	5/5
	Pancreas - mild multifocal lymphocytic pancreatitis	0/5	1/5	0/5	0/5
7	Trachea – catarrhal tracheitis	0/5	5/5	0/5	2/5
	Lung - moderate to severe BALT	0/5	4/5	0/5	0/5
	Pancreas – multifocal lymphocytic pancreatitis	0/5	3/5	0/5	1/5
14	Trachea - catarrhal tracheitis	0/5	5/5	0/5	4/5
	Pancreas – lymphocytic pancreatitis	0/5	2/5	0/5	1/5
28	Trachea – catarrhal tracheitis	0/5	5/5	0/5	4/5
	Lung – BALT hyperplasia	0/5	2/5	0/5	2/5
	Gut – mild enteritis	0/5	3/5	0/5	0/5

[a] number of tissues showing the histopathological changes/total number analyzed

Figure 9

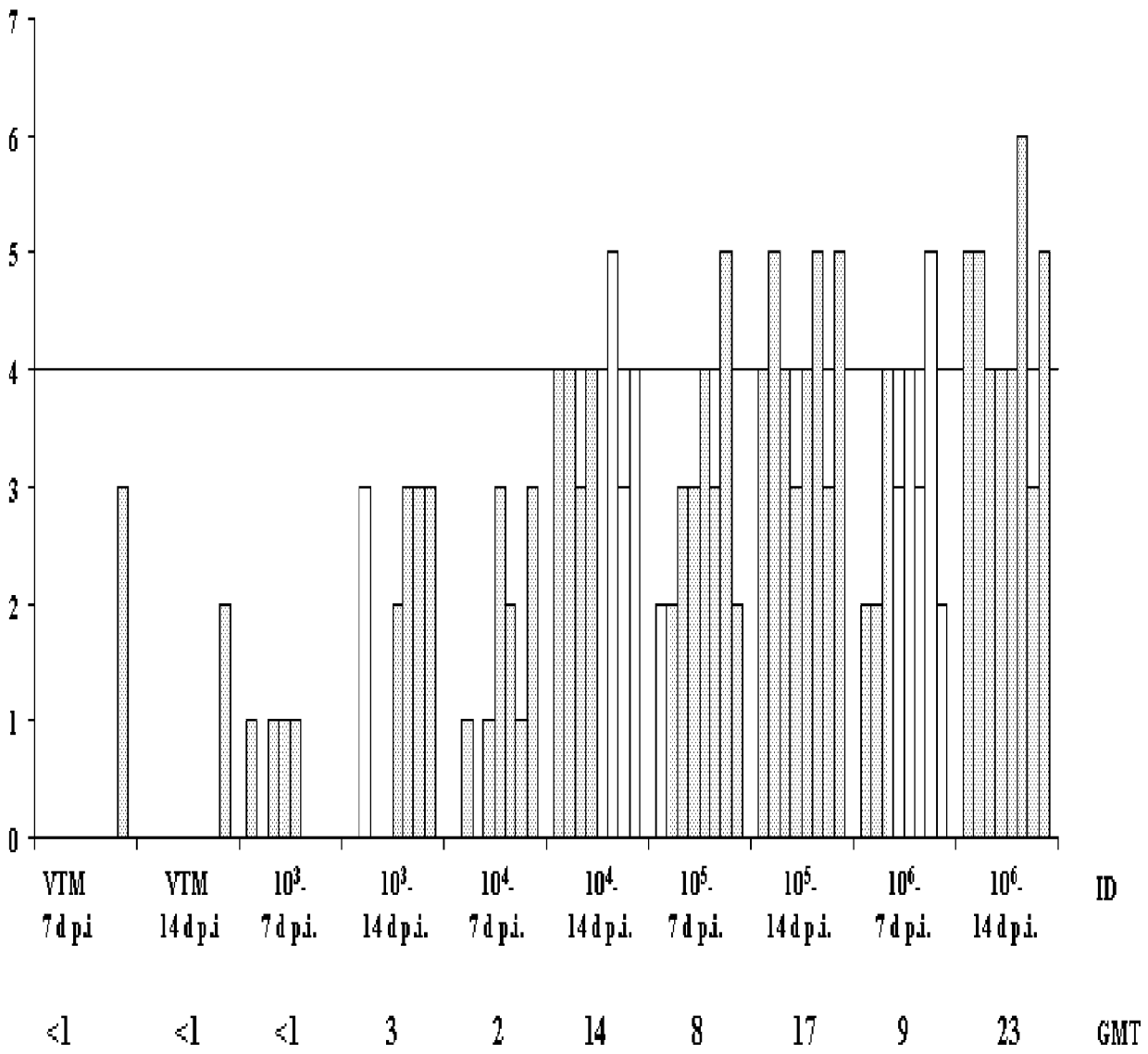

HI Titer in log2
7
6
5
4
3
2
1
0
VTM 7 d p.i
VTM 14 d p.i
10³- 7 d p.i.
10³- 14 d p.i.
10⁴- 7 d p.i.
10⁴- 14 d p.i.
10⁵- 7 d p.i.
10⁵- 14 d p.i.
10⁶- 7 d p.i.
10⁶- 14 d p.i.
ID
<1
<1
<1
3
2
14
8
17
9
23
GMT

Figure 10

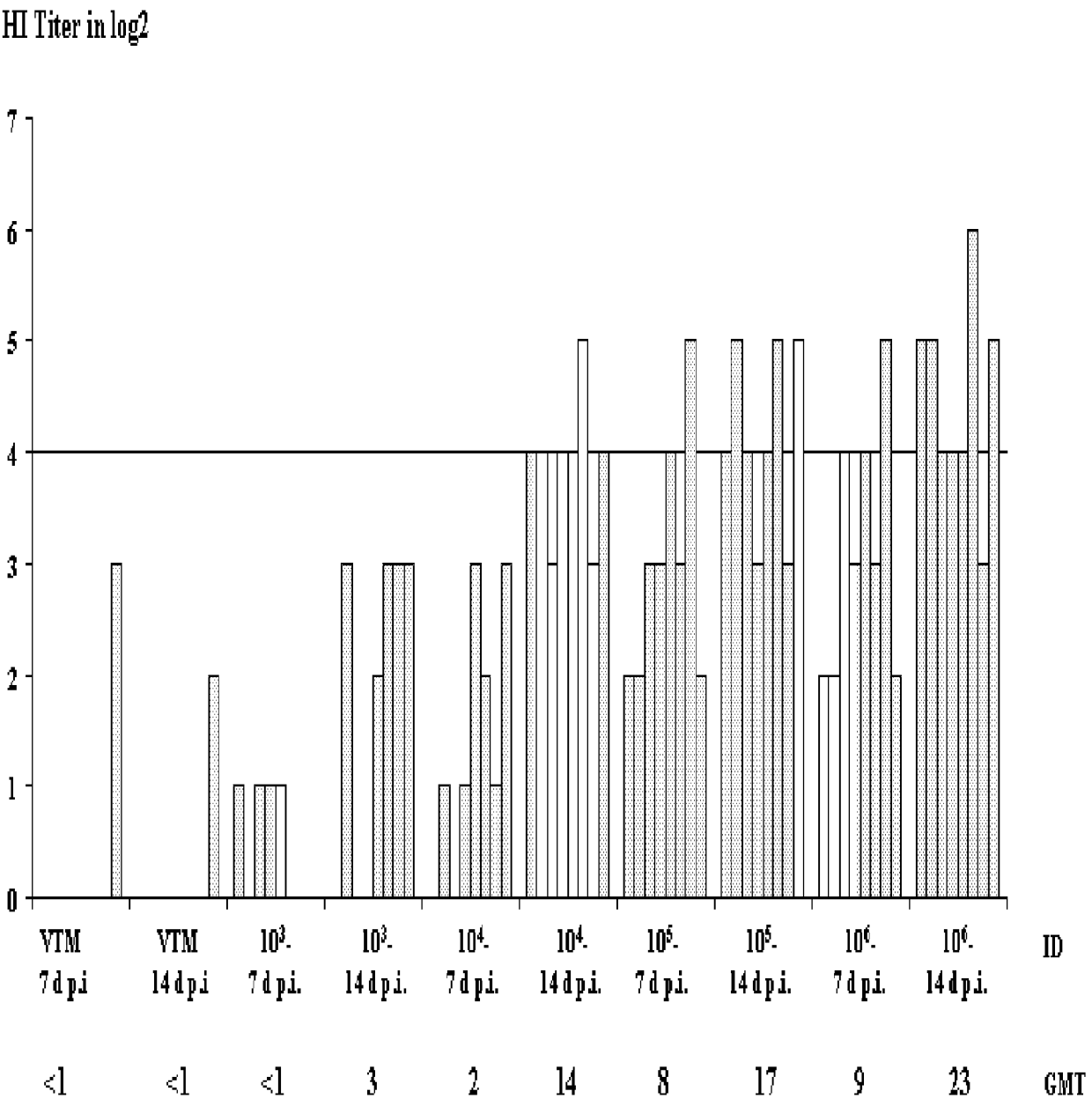

HI Titer in log2
7
6
5
4
3
2
1
0
VTM 7 d p.i
VTM 14 d p.i
10³- 7 d p.i.
10³- 14 d p.i.
10⁴- 7 d p.i.
10⁴- 14 d p.i.
10⁵- 7 d p.i.
10⁵- 14 d p.i.
10⁶- 7 d p.i.
10⁶- 14 d p.i.
ID
<1
<1
<1
3
2
14
8
17
9
23
GMT

Figure 11 (1/3)

SEQ ID NO:	type	Gene name
1	DNA	APMV-8 genomic DNA
2	DNA	APMV-8 Nucleoprotein (NP) DNA
3	Protein	APMV-8 Nucleoprotein (NP) protein
4	DNA	APMV-8 phosphoprotein (P) DNA
5	Protein	APMV-8 phosphoprotein (P) protein
6	DNA	APMV-8 Matrixprotein (M) DNA
7	Protein	APMV-8 Matrixprotein (M) protein
8	DNA	APMV-8 Fusionprotein (F) DNA
9	Protein	APMV-8 Fusionprotein (F) protein
10	DNA	APMV-8 Hemagglutinin/neuraminidase (HN) DNA
11	Protein	APMV-8 Hemagglutinin/neuraminidase (HN) protein
12	DNA	APMV-8 Polymerase (L) DNA
13	Protein	APMV-8 Polymerase (L) protein 1
14	Protein	APMV-8 Polymerase (L) protein 2
15	DNA	APMV-1 genomic DNA (AF077761)
16	DNA	APMV-2 genomic DNA (EU338414)
17	DNA	APMV-3 genomic DNA (EU403085)
18	DNA	APMV-4 genomic DNA (FJ177514)
19	DNA	APMV-6 genomic DNA (EU622637)
20	DNA	APMV-7 genomic DNA Genbank No. FJ231524
21	oligo	APMV-PolyT (sense)
22	Oligo	8NPf1 (sense)
23	oligo	8NPr (antisense)
24	oligo	NP gene start sequence
25	oligo	P gene start sequence
26	oligo	M gene start sequence
27	oligo	F gene start sequence
28	oligo	HN gene start sequence
29	oligo	L gene start sequence
30	oligo	NP gene end sequence
31	oligo	P gene end sequence
32	oligo	M gene end sequence
33	oligo	F gene end sequence
34	oligo	HN gene end sequence
35	oligo	L gene (1) end sequence
36	oligo	L gene (2) end sequence
37	DNA	APMV-8 genomic DNA Genbank No. FJ215863.1
38	DNA	APMV-8 genomic DNA Genbank No. FJ215864.1
39	DNA	APMV-8 genomic DNA Genbank No. FJ619036
40	DNA	APMV-9 genomic DNA Genbank No. EU910942
41	Oligo	NP-FP-pc3 primer

Figure 11 (2/3)		
42	Oligo	NP-RP-pc3 primer
43	Oligo	P-FP-pc3 primer
44	Oligo	P-RP-pc3 primer
45	Oligo	L-FP-pc3 primer
46	Oligo	L-RP-pc3 primer
47	DNA	5'-FLG of APMV-8 genome
48	DNA	3'-FLG of APMV-8 genome
49	DNA	Codon-optimized T7 polymerase (no EcoRI or NotI site)
50	oligo	EGFP-FP primer
51	oligo	EGFP-RP primer
52	DNA	APMV8 minigenome
53	DNA	NP gene of APMV-8 (FJ215863.1) Genbank FJ215863
54	Protein	NP protein of APMV-8 (FJ215863.1) Genbank ACO48297
55	DNA	P gene of APMV-8 (FJ215863.1) Genbank FJ215863
56	Protein	P protein of APMV-8 (FJ215863.1) Genbank ACO48298
57	DNA	M gene of APMV-8 (FJ215863.1) Genbank FJ215863
58	Protein	M protein of APMV-8 (FJ215863.1) Genbank ACO48299
59	DNA	F gene of APMV-8 (FJ215863.1) Genbank FJ215863
60	Protein	F protein of APMV-8 (FJ215863.1) Genbank ACO48300
61	DNA	HN gene of APMV-8 (FJ215863.1) Genbank FJ215863
62	Protein	HN protein of APMV-8 (FJ215863.1) Genbank ACO48301
63	DNA	L gene of APMV-8 (FJ215863.1) Genbank FJ215863
64	Protein	L protein of APMV-8 (FJ215863.1) Genbank ACO48302
65	DNA	NP gene of APMV-8 (FJ215864.1) Genbank FJ215864
66	Protein	NP protein of APMV-8 (FJ215864.1) Genbank ACO48303
67	DNA	P gene of APMV-8 (FJ215864.1) Genbank FJ215864
68	Protein	P protein of APMV-8 (FJ215864.1) Genbank ACO48304
69	DNA	M gene of APMV-8 (FJ215864.1) Genbank FJ215864
70	Protein	M protein of APMV-8 (FJ215864.1) Genbank ACO48305
71	DNA	F gene of APMV-8 (FJ215864.1) Genbank FJ215864
72	Protein	F protein of APMV-8 (FJ215864.1) Genbank ACO48306
73	DNA	HN gene of APMV-8 (FJ215864.1) Genbank FJ215864
74	Protein	HN protein of APMV-8 (FJ215864.1) Genbank ACO48307
75	DNA	L gene of APMV-8 (FJ215864.1) Genbank FJ215864
76	Protein	L protein of APMV-8 (FJ215864.1) Genbank ACO48308
77	DNA	NP gene of APMV-8 (FJ619036) Genbank FJ619036
78	Protein	NP protein of APMV-8 (FJ619036) Genbank ACN88139
79	DNA	P gene of APMV-8 (FJ619036) Genbank FJ619036
80	Protein	P protein of APMV-8 (FJ619036) Genbank ACN88140
81	DNA	M gene of APMV-8 (FJ619036) Genbank FJ619036
82	Protein	M protein of APMV-8 (FJ619036) Genbank ACN88143
83	DNA	F gene of APMV-8 (FJ619036) Genbank FJ619036
84	Protein	F protein of APMV-8 (FJ619036) Genbank ACN88144

Figure 11 (3/3)		
85	DNA	HN gene of APMV-8 (FJ619036) Genbank FJ619036
86	Protein	HN protein of APMV-8 (FJ619036) Genbank ACN88145
87	DNA	L gene of APMV-8 (FJ619036) Genbank FJ619036
88	Protein	L protein of APMV-8 (FJ619036) Genbank ACN88146

Figure 12 (1/5)

SEQ ID NO:1 full length genome sequence of APMV-8

15342 BP DNA (antigenome, 5′ to 3′)
BASE COUNT 4850 A 3168 C 3159 G 4165 T
ORIGIN

```
       1 ACCAAACAAG GAATGCAAGA CCAACGGGAA CTTTAAATAA AACAATCGAA TTATTGGGGG
      61 CGAAGCAAGT GGATCTCGAG CTCGAGGCCG AAACCCTGAA TTTCACTGGA GGTTTTGAAT
     121 AGGTCGCTAT AGGACTCAAT ATGTCATCTG TGTTCAATGA GTATCAGGCG CTTCAAGAAC
     181 AACTTGTGAA GCCGGCTGTC AGGAGACCTG ATGTTGCCTC AACGGGTTTA CTCAGAGCGG
     241 AAATACCTGT CTGTGTTACA TTATCTCAAG ACCCCGGTGA GAGATGGAGC CTTGCTTGCT
     301 TGAATATTAG ATGGCTTGCG AGTGATTCAT CAACCACACC AATGAAGCAA GGAGCAATAT
     361 TGTCACTGCT GAGTCTACAT TCAGACAATA TGCGAGCTCA CGCAACATTA GCAGCAAGGT
     421 CTGCAGATGC TTCACTCACC ATACTTGAGG TAGATGAAGT AGATATTAGC AACTCACTAA
     481 TCAAATTCAA CGCCAGAAGT GGTGTATCTG ACAAACGCTC AAATCAATTG CTTGCAATTG
     541 CGGATGACAT CCCCAAAAGT TGCAGTAATG GGCATCCATT TCTTGACACA GACATTGAGA
     601 CCAGAGACCC GCTCGATCTA TCAGAGACTA TAGATCGCCT GCAGGGTATT GCAGCTCAGA
     661 TATGGGTGTC AGCCATAAAG AGCATGACAG CGCCTGACAC CGCATCAGAG TCAGAAAGTA
     721 AGAGGCTGGC CAAATATCAA CAACAAGGCC GACTGGTTAA GCAAGTACTC TTGCATTCTG
     781 TAGTCAGGAC AGAATTTATG AGAGTTATTC GGGGCAGCTT GGTACTGCGC CAGTTTATGG
     841 TTAGCGAGTG CAAGAGGGCT TCAGCCATGG GCGGAGACAC ATCTAGGTAC TATGCTATGG
     901 TGGGTGACAT CAGTCTTTAC ATCAAGAATG CAGGATTGAC TGCATTTTTC CTCACCCTGA
     961 AGTTCGGAGT TGGTACCCAG TATCCAACCT TAGCAATGAG TGTTTTCTCC AGTGACCTTA
    1021 AAAGGCTTGC TGCACTCATC AGGCTATACA AAACCAAGGG AGACAATGCA CCATACATGG
    1081 CATTCCTGGA GGACTCCGAT ATGGGAAATT TTGCTCCAGC AAATTATAGC ACAATGTACT
    1141 CTTATGCCAT GGGCATTGGG ACAATTCTGG AAGCATCTGT ATCTCGATAC CAGTATGCCA
    1201 GAGACTTTAC CAGTGAGAAT TATTTCCGTC TTGGAGTTGA GACAGCCCAA AGCCAGCAGG
    1261 GAGCATTTGA CGAGAGAACA GCCCGAGAAA TGGGCTTGAC TGAGGAATCA AAACAGCAGG
    1321 TTAGATCACT GCTAATGTCA GTAGACATGG GTCCCAGTTC AATTCATGAG CCATCTCGCC
    1381 CTGCATTTAT CAGTCAAGAA GAAAATAGGC AGCCTGCCCA GAACTTGTCA GATACTCAGG
    1441 GTCAGACCAA GCCAGTCCCG AAGCAGCCCG CACCAAGGGC CGACTCAGAT GACATTGATC
    1501 CATACGAGAA CGGGCTAGAA TGGTAATTCA ACCACCCCGA CACATCCACC TATACACCAA
    1561 TTCCGTGACA TATTAACCCA ATCAAACATT TCATAAACTA TAGTAGTCAT TGATTTAAGA
    1621 AAAAATTGGG GGCGACCTCA ATTGTGAAAC ATACCAGATC CGTCCACAAC ACCACTCAAC
    1681 AACCCACACA CAATGGATTT CGCCAATGAT GAAGAAATTG CAGAACTTTT GAATCTCAGC
    1741 ACCAATGTAA TCAAGGAGAT TCAGAAATCC GAACTCAAGC CTCCCCAAAC CACCGGACGA
    1801 CCACCTGTCA GTCAAGGGAA CACAAGAAAT CTAACTGATC TATGGGAAAA GGAGACTGCA
    1861 AGTCAGACCA AGACACCGGC CCAATCTACA CAAACCACAC AAGTTCAGTC TGATGAAAAT
    1921 GAGGAGGGAG AAATCAAGTC CGAGTCAACT GATGGCCACA TCAGAGGAAC TGTTAATCAA
    1981 TCAGAGCAAG TCCCAGAACA AAACCAGAGC AGATCTTCAC CAGGTGATGA TCTCGACAGA
    2041 GCTCTCAACA AGCTTGAAGG GAGAATCAAT TTAATCAGCT CAATGGACAA AGAAATTAAA
    2101 AAGGGCCCTC GCATCCAGAA TCTCCCTGGG TCCCAGGCGG CAACTCAACA GGCGACCCAC
    2161 CCATTGGCAG GGGACACCCC GAACATGCAA GCACAGACAA AAGCCCTGGC GAAGCCACAT
    2221 CAAGAGGCAA TCAATCCTGG CAACCAGGAC ACAGGAGAGA GTATTCATTT ACCACCTTCC
    2281 ATGGCACCAC CAGAGTCATT AGTTGGTGCA ATCCGCAATG CACCCCAATT CGTGCCAGAC
    2341 CAATCTATGA CGAATGTAGA TGCGGGGAGT GTCCAACTAC ATGCATCATG TGCAGAGATG
    2401 ATAAGTAGAA TGTTTGTAGA AGTTATATCC AAGCTTGATA AACTCGAGTC GAGACTGAAT
    2461 GATATAGCAA AAGTTGTGAA CACTACCCCC CTTATTAGGA ATGATATTAA CCAACTTAAG
    2521 GCCACAACCG CACTGATGTC TAACCAAATT GCCTCCATAC AAATTCTTGA CCCAGGGAAT
    2581 GCAGGGGTGA GGTCCCTCTC TGAAATGAAA TCTGTGACGA AGAAAGCTGC TGTTGTAATT
    2641 GCAGGGTTTG GAGACGACCC AACTCAAATT ATTGAAGAAG GCATTATGGC CAAAGATGCT
    2701 CTTGGAAAAC CTGTGCCTCC AACATCTGTT ATCTCAGCCA AAGCTCAGAC TTCTTCCGGT
    2761 GTGAGTAAGG GTGAAATAGA AGGATTGATT GCATTGGTGG AAACATTAGT TGACAATGAC
    2821 AAGAAGGCAG CAAAACTGAT TAAAATGATT GATCAAGTTA AATCCCATGC CGATTACGCC
    2881 CGAGTCAAGC AGGCAATATA TAATGCGTAA TACTGTAACT ACACAAACAA TCAATACTGC
    2941 TGTCGGTTGC ACCCACCTCA GCAAATCAAT AATCTTTTAG AATTTATTGA TTAAGAAAAA
    3001 ATTGACTACT ATAAGAAAAG AACACCAAGT TGGGGGCGAA GACACGATTG ACCACAGTCG
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Figure 12 (2/5)

3061 CTATCTGTAA GGCTCCTCAC CAAAAATGGC ATATACAACA TTGAAACTGT GGGTGGATGA
3121 GGGTGACATG TCGTCTTCGC TCCTATCATT CCCGTTGGTA CTAAAAGAGA CAGACAGAGG
3181 CACAAAGGAG CTTCAACCAC AGGTAAGGGT AGATTCAATT GGCGATGTGC AGAACGCCAA
3241 AGAGTCCTCG ATATTCGTGA CTCTATATGG TTTCATCCAA GCAATTAAGG AGAGTTCAGA
3301 TCGATCGAAA TTCTTCCATC CAAAAGATGA CTTCAAACCT GAGACAGTCA CTGCAGGACT
3361 GGTAGTGGTA GGTGCGATCC GAATGATGGC TGATGTTAAT ACCATCTCTA ATGACGCACT
3421 AGCGCTGGAG ATCACTGTTA AGAAATCTGC AACTTCTCAA GAGAAAATGA CGGTGATGTT
3481 CCACAATAGC CCCCCTTCAT TGAGAACTGC AATAACTATC CGAGCAGGAG GTTTCATCTC
3541 GAATGCAGAC GAGAATATAA AATGTGCCAG CAAATTGACT GCAGGAGTGC AGTACATATT
3601 CCGCCCAATG TTTGTTTCAA TCACTAAATT ACACAATGGC AAACTATATA GGGTGCCCAA
3661 AAGCATCCAC AGCATCTCAT CCACTCTACT GTATAGTGTG ATGTTGGAGG TAGGATTCAA
3721 AGTGGATATT GGGAAGGATC ATCCCCAGGC AAAGATGCTG AAGAAGGTCA CAATCGGCGA
3781 TGCAGACACA TACTGGGGGT TTGCATGGTT CCACCTGTGC AATTTCAAAA AGACATCCTC
3841 TAAGGGAAAG CCAAGAACGC TAGACGAACT AAAGACAAAA GTCAAAAATA TGGGGTTGAA
3901 ATTGGAGTTA CATGACCTGT GGGGTCCGAC TATTGTGGTC CAAATCACTG GCAAGAGCAG
3961 CAAATATGCT CAAGGATTTT TTTCCTCCAA TGGTACTTGT TGTCTCCCAA TCAGCAGATC
4021 TGCACCAGAG CTTGGGAAGC TTCTGTGGTC TTGTTCAGCA ACTATAGGTG ACGCAACAGT
4081 TGTTATCCAA TCAAGCGAGA AAGGGGAACT CCTAAGGTCT GATGACCTCG AGATACGAGG
4141 TGCTGTGGCC TCCAAGAAAG GTAGACTGGG CTCATTTCAC CCCTTCAAAA AATGATGCAG
4201 GACATAGTAC AGAGAATTAG AGAGCCATTA GATGTGCGCA AAAAACATAA TCTGCGATGA
4261 ACTGCCCAGA CTCCACTTTA ATCTAGGTTG CAGGGAAATA GTACACGACA TGCGAAATAC
4321 TATCACGGTC ACCAGCAATC AATAAAGCTG ATCAATCACT ATATTAGGAA TCAAATAGGA
4381 TAACAATTAT TAATCCAATT TCCTAATTAT AAAAAATTGC TTTAAAGGTT ATTGACGAGT
4441 CGGGGGCGAA ATCTTGCCAC TTAGTCTGCA GTCAATCTTA GAATCTACAT ATTGAACTAT
4501 GGGTCAAATA TCAGTATATC TAATTAATAG CGTGCTATTA TTGCTGGTAT ATCCTGTGAA
4561 TTCGATTGAC AATACACTCA TTGCCCCAAT CGGAGTTGCC AGCGCAAATG AATGGCAGCT
4621 TGCTGCATAT ACAACATCAC TTTCAGGGAC AATTGCCGTG CGATTCCTAC CTGTGCTCCC
4681 GGATAATATG ACTACCTGTC TTAAAGAAAC AATCACTACA TACAATAATA CTGTCAACAA
4741 CATCTTAGGC CCACTCAAAT CCAATCTGGA TGCACTGCTC TCATCTGAGA CTTATCCCCA
4801 GACAAGATTA ATTGGGGCAG TTATAGGTTC AATTGCTCTC GGTGTTGCAA CATCGGCTCA
4861 AATCACTGCT GCAGTTGCTC TCAAGCAAGC GCAAGACAAT GCAAGGAACA TACTAGCACT
4921 CAAAGAAGCA CTGTCCAAAA CCAATGAGGC GGTCAAGGAG CTTAGTAGTG GGTTACAACA
4981 AACAGCTATT GCACTTGGTA AGATACAGAG TTTTGTGAAT GAGGAAATTC TGCCATCTAT
5041 CAACCAACTG AGCTGCGAGG TGACAGCCAA TAAACTTGGG GTGTATTTAT CTCTGTATCT
5101 CACAGAACTG ACCACCATAT TCGGTGCACA GCTGACCAAC CCTGCATTGA CTTCATTATC
5161 ATATCAAGCA CTGTACAACC TGTGTGGTGG CAACATGGCA ATGCTTACTC AGAAGATTGG
5221 AATTAAACAG CAAGACGTTA ATTCGCTATA TGAAGCCGGA CTAATCACAG GACAAGTCAT
5281 TGGTTATGAC TCTCATTACC AGCTGCTGGT CATCCAGGTC AATTATCCAA GCATTTCTGA
5341 GGTCACTGGT GTACGTGCGA CAGAATTAGT CACTGTTAGT GTAACAACAG ACAAGGGTGA
5401 AGGGAAAGCA ATTGTACCCC AATTTGTAGC TGAAAGTCGG GTGACTATTG AAGAGCTTGA
5461 TGTCGCATCT TGTAAATTCA GCAGCACGAC CCTATATTGC AGGCAGGTCA ACACAAGGGC
5521 ACTTCCCCCG CTAGTAGCTA GCTGTCTTCG AGGTAACTAT GATGATTGTC AATATACCAC
5581 AGAGATTGGA GCATTATCAT CCCGGTATAT AACACTAGAT GGGGGGGTCT TAGTTAATTG
5641 CAAGTCAATT GTTTGTAGGT GCCTTAATCC AAGTAAGATC ATCTCTCAAA ATACAAACGC
5701 TGCAGTAACA TATGTTGATG CCACAATCTG CAAAACAATT CAATTGGATG ATATACAACT
5761 CCAGCTGGAA GGGTCACTAT CATCAGTTTA TGCAAGAAAC ATCTCAATTG AGATCAGTCA
5821 GGTGACCACA TCCGGGTCTT TAGATATCAG CAGTGAGATA GGAAACATCA ATAATACGGT
5881 GAATCGTGTG GAGGATTTAA TTCACCAATC AGAGGAATGG CTGGCAAAGG TTAACCCACA
5941 CATTGTTAAT AATACAACAC TAATTGTACT CTGTGTGTTA AGTGCGCTTG CTGTGATCTG
6001 GCTGGCAGTA TTAACGGCTA TTATAATATA CTTGAGAACA AAGTTGAAGA CTATATCGGC
6061 ATTAGCTGTA ACCAATACAA TACAGTCTAA CCCCTATGTT AACCAAACGA AACATGAATC
6121 TAAGTTTTGA TCATTCAAGC CAAAACAGAG GATCTAGGCT CAGGTTAATA ATAGTTCAAT
6181 CAATATTTGA TTTATTAGGT TTTTTTCACT AATTATTAAT ATACTCGTGA TTAGATGATA
6241 ACGTTAAAAG TCTTAGATAT TTAATAAAAA ATGTAACCTG GGGGCGACCC ATTTATAGGT
6301 GAGTATATAT TAGGAAGTCC TTATATTGCA CTGTGATTTC AAACAATTAT ATTACCTCAT
6361 ATCTACCTTG TCTAAAGACA TCATGAGTAA CATTGCATCC AGTTTAGAAA ACATTGTAGA
6421 GCAGGATAGT CGAAAAACAA CTTGGAGGGC CATCTTTAGA TGGTCCGTTC TTCTTATTAC
6481 AACAGGATGC TTAGCCTTAT CCATTGTTAG CATAGTTCAA ATTGGAAATT TGAAAATTCC

Figure 12 (3/5)

6541 TTCTGTAGGG GATCTGGCTG ATGAAGTGGT GACACCCTTG AAAACCACTC TGTCAGATAC
6601 ACTCAGGAAT CCAATTAACC AGATAAATGA TATATTTAGG ATTGTTGCCC TTGATATTCC
6661 ATTGCAAGTG ACCAGTATCC AAAAAGACCT TGCAAGTCAA TTTAACATGT TGATAGATAG
6721 TTTAAATGCT ATCAAATTAG GCAACGGGAC CAACCTTATC ATACCTACAT CAGACAAGGA
6781 GTATGCAGGA GGAATTGGAA ACCCTGTATT TACTGTCGAT GCTGGAGGTT CTATAGGATT
6841 CAAACAGTTT AGCTTAATAG AACATCCGAG CTTTATTGCT GGACCTACAA CGACCCGAGG
6901 CTGTACAAGA ATACCCACTT TTCACATGTC AGAAAGTCAT TGGTGCTACT CACACAACAT
6961 CATCGCTGCT GGCTGTCAAG ATGCCAGTGC ATCCAGTATG TATATCTCAA TGGGAGTTCT
7021 CCATGTGTCC TCATCTGGCA CTCCCATTTT TCTTACTACT GCAAGTGAGC TGATAGACGA
7081 TGGAGTTAAC CGTAAGTCAT GCAGCATTGT AGCAACCCAA TTTGGCTGTG ACATTTTGTG
7141 CAGTATTGTC ACAGAGAAGG AGGGAGATGA TTACTGGTCT GATACTCCGA CTCCAATGCG
7201 CCACGGCCGT TTTTCATTCA ATGGTAGTTT TGTAGAAGCC GAACTACCAG TGTCCAGTAT
7261 GTTCTCATCA TTCTCTGCCA ACTACCCTGC TGTGGGATCA GGCGAAATTG TAAAAGATAG
7321 AATATTATTC CCAATTTACG GAGGTATAAA GCAGACTTCA CCAGAGTTTA CCGAATTAGT
7381 GAAATACGGA CTCTTTGTAT CAACACCTAC AACTGTGTGC CAGAGTAGCT GGACTTATGA
7441 CCAGGTAAAA GCTGCGTATA GGCCAGATTA CATATCAGGC CGGTTCTGGG CACAAGTGAT
7501 ACTCAGCTGC GCTCTTGATG CAGTCGACTT ATCAAGTTGT ATTGTAAAGA TTATGAATAG
7561 CAGCACAGTG ATGATGGCAG CGGAAGGAAG GATAATGAAG ATAGGGATTG ATTACTTTTA
7621 CTATCAGCGG TCATCTTCTT GGTGGCCATT GGCATTTGTC ACAAAACTAG ACCCGCAAGA
7681 GTTGGCAGAC ACAAACTCAA TATGGCTGAC CAATTCCATA CCAATCCCGC AATCAAAGTT
7741 CCCTCGGCCT TCATATTCAG AAAATTATTG CACAAAGCCA GCAGTTTGCC CTGCTACTTG
7801 TGTCACTGGT GTGTACTCTG ATATTTGGCC CCTGACCTCA TCTTCATCAC TCCCGAGCAT
7861 AATTTGGATC GGCCAGTACC TTGATGCTCC TGTTGGAAGG ACTTATCCTA GATTTGGAAT
7921 TGCAAATCAG TCACACTGGT ACCTCCAAGA AGATATTCTA CCCACTTCCA CCGCAAGTGC
7981 GTATTCAACC ACTACATGTT TTAAGAATAC TGCCAGGAAT AGAGTGTTCT GCGTCACCAT
8041 TGCCGAATTT GCAGATGGGT TGTTTGGAGA GTACAGGATA ACACCTCAGT TGTACGAATT
8101 AGTGAGAAAT AATTGAATAA CAATAATTTT GGGACTCATT TTGTCGCAAA GTGAAATTGT
8161 CATCTTTAAA AATAATCAAT TCGATGATTT TTATTGAACA TGATTAAGCA ATCATGTGGG
8221 AAATTTATTA TCTCATAAAT TCTAATAGTT GTAAATGATG AATTAAGAAA AAATGGAGGG
8281 CGACCTCTAC ACAAACATGG ATATAAAACA AGTTGACCTG ATAATACAAC CCGAGGTTCA
8341 TCTCGATTCA CCCATCATAT TGAATAAACT GGCACTATTA TGGCGCTTGA GTGGTTTACC
8401 CATGCCTGCA GACCTACGAC AAAAATCCGT AGTGATGCAC ATCCCGGACC ACATCTTAGA
8461 AAAATCAGAA TATCGGATCA AGCACCGTCT AGGGAAAATC AAGAGTGACA TAACACATTA
8521 CTGTCAGTAT TTTAATATTA ATTTGGCAAA TATTGATCCG ATAACCCACC CCAAAAGTTT
8581 GTATTGGTTA TCCAGACTAA CAATAGCTAG TGCTGGAACT TTTAGGCATA TGAAAGATAG
8641 AATCTTGTGT ACAGTTGGCT CTGAATTTGG ACACAAAATT CAAGATTTAT TTTCACTGCT
8701 GAGCCATAAA CTAGTAGGTA ACGGGGATTT ATTTAATCAA AGTCTCTCAG GTACACGTTT
8761 GACTGCAAGT CCGTTATCCC CTTTATGCAA TCAATTTGTC TCTGACATCA AGTCTGCAGT
8821 CACGACACCC TGGTCAGAAG CTCGTTGGTC TTGGCTTCAT ATCAAACAAA CAATGAGATA
8881 TCTGATAAAA CAATCACGCA CTACAAATTC GGCTCATTTA ACAGAAATCA TAAAAGAAGA
8941 ATGGGGTTTA GTAGGTATTA CTCCAGATCT TGTCATTCTT TTTGACAGAG TCAATAATAG
9001 TCTGACTGCA TTAACATTTG AGATGGTTCT AATGTATTCA GATGTATTAG AATCCCGTGA
9061 CAATATTGTG TTAGTGGGGC GACTATCTAC CTTTCTACAG CCAGTAGTTA GTAGACTGGA
9121 GGTGTTGTTT GATCTAGTAG ATTCATTGGC AAAAATCTTA GGTGACACAA TATATGAGAT
9181 TATTGCAGTG TTAGAGAGCT TGTCTTATGG GTCAGTTCAA CTACATGATG CAAGTCACTC
9241 TCATGCAGGG TCTTTTTTTT CATTTAACAT GAATGAACTT GATAACACAC TATCAAAGAG
9301 GGTAGATCCG AAACACAAGA ACACTATAAT GAGCATTATA AGACAATGCT TTTCTAATCT
9361 AGATGTTGAT CAAGCTGCAG AGATGCTATG CCTGATGAGA TTATTCGGAC ACCCAATGTT
9421 AACTGCACCG GATGCAGCAG CCAAAGTGAG GAAAGCAATG TGTGCTCCAA AACTTGTTGA
9481 ACACGACACC ATCTTGCAGA CATTATCTTT CTTCAAGGGG ATAATTATAA ATGGGTACAG
9541 AAGATCACAC TCTGGCCTGT GGCCCAATGT AGAGCCGTCT TCAATTTATG ATGATGATCT
9601 CAGACAGCTG TACTTAGAGT CAGCAGAGAT TTCCCATCAT TTTATGCTTA AAAACTACAA
9661 GAGTTTAAGC ATGATAGAAT TCAAGAAGAG CATAGACTAC GATCTTCATG ATGACCTAAG
9721 TACTTTCTTA AAGGATAGAG CAATTTGCCG GCCGAAATCC CAGTGGGATG TCATATTTCG
9781 TAAGTCTTTA CGCAGATCTC ATACGCAGTC CCAGTATCTG GACGAAATTA AGAGCAACCG
9841 ATTGCTAATT GATTTTCTTG ATTCTGCTGA ATTTGACCCT GGAAAAGAAT TTGCATATGT
9901 AACCACAATG GATTATTTGC ACGATAATGA ATTTTGTGCT TCATATTCTC TAAAGGAAAA
9961 GGAGATCAAA ACTACTGGGA GGATATTTGC AAAAATGACA CGCAATATGA GAAGTTGCCA

Figure 12 (4/5)

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10021 AGTAATACTT GAATCTTTGT TATCAAAGCA TATATGCAAG TTCTTCAAAG AGAATGGCGT
10081 TTCGATGGAG CAATTGTCAT TGACCAAGAG TCTACTTGCA ATGTCTCAAC TCTCACCAAA
10141 AGTCTCGACT TTGCAGGACA CTGCATCACG TCATGTAGGT AACTCAAAAT CTCAGATTGC
10201 AACCAGCAAC CCATCTCGGC ATCACTCGAC ACCCAATCAG ATGTCACTCT CAAATCGAAA
10261 AACGGTTGTA GCAACTTTCT TAACAACTGA CTTGGAAAAA TACTGCCTGC AGTGGCGATA
10321 TTCAACTATT AAATTGTTTG CACAAGCTCT AAATCAACTC TTTGGGATTG ATCACGGATT
10381 TGAATGGATA CATTTAAGAC TTATGAACAG CACCTTATTT GTTGGCGATC CTTACTCGCC
10441 TCCTGAAGAT CCAACACTAG AAGATATAGA TAAAGCACCA AATGATGATA TCTTCATAGT
10501 TTCTCCAAGG GGAGGCATAG AGGGTTTATG TCAGAAAATG TGGACCATGA TATCAATTAG
10561 TGCTATACAC TGTGTAGCAG AGAAAATTGG TGCACGAGTG GCAGCAATGG TGCAGGGTGA
10621 TAATCAAGTA ATAGCTATCA CCAAAGAATT ATTCAGAGGA GAGAAAGCTT GTGATGTCAG
10681 AGATGAGTTA GACGAGCTTG GTCAAGTGTT TTTTGATGAG TTCAAGAGAC ACAATTATGC
10741 AATTGGACAC AATCTTAAGC TAAATGAGAC AATACAAAGC CAATCCTTTT TTGTATATTC
10801 CAAACGAATA TTCTTTGAAG GGCGATTGCT TAGTCAAGTC CTCAAAAATG CTGCCAAGTT
10861 ATGTATGGTT GCTGACCATC TAGGTGAAAA CACTGTATCT TCCTGTAGCA ACCTGAGCTC
10921 GACAATTGCC CGCTTAGTGG AAAATGGGTT TGAGAAGGAC ACTGCTTTTG TGTTGAACCT
10981 AGTCTACATC ATGACTCAGA TTCTTTTTGA TGAGCATTAC TCGATTGTAT GCGATCACCA
11041 TAGTGTCAAA AGCTTGATTG GATCAAAAAA CCATCGGAAT TTATTGTATT CATCTCTAAT
11101 ACCAGGTCAG CTCGGCGGTT TCAACTTCCT CAATATAAGT CGGTTGTTCA CTAGGAATAT
11161 AGGTGACCCA GTAACATGTA GTCTGTCTGA TCTCAAATGC TTCATAGCCG CAGGTCTCCT
11221 TCCACCCTAT GTCCTAAAAA ATGTGGTTCT GCGTGAGCCT GGTCCTGGGA CATGGTTGAC
11281 GTTGTGCTCT GATCCTTACA CCCTTAACAT ACCATACACA CAGCTTCCAA CCACATATCT
11341 CAAAAAGCAC ACCCAGCGAT CATTGCTTTC ACGTGCAGTA AATCCTTTAT TAGCCGGTGT
11401 ACAAGTGCCA AATCAGCATG AGGAAGAAGA GATGTTGGCT CGCTTTCTCC TTGATCGTGA
11461 ATATGTGATG CCCCGCGTTG CTCATGTAAT ACTAGAATCA TCAGTCCTTG GCAAACGGAA
11521 ACAAATCCAA GGCTTAATTG ATACAACTCC AACCATCATT AGAACATCTC TAGTTAATCT
11581 GCCAGTGTCT AGAAAGAAAT GCGAAAAAAT AATCAATTAC TCTCTCAATT ATATTGCTGA
11641 GTGTCATGAC TCCTTACTTA GCCAGGTCTG CTTCAGTGAT AATAAGGAAT ACTTGTGGTC
11701 AACCTCCTTA ATATCAGTTG AGACCTGTAG TGTGACAATT GCGGACTATC TGAGAGCTGT
11761 CAGCTGGTCT AATATATTAG GGGGAAGAAA CATATCCGGG GTGACTACAC CTGATACTAT
11821 TGAATTAATT CAAGGTTGTT TAATAGGTGA AAATTCTAGT TGTACTCTTT GTGAATCGCA
11881 TGATGACGCA TTCACGTGGA TGCACTTGCC TGGCCCACTT TACATCCCTG AACCATCAGT
11941 TACTAACTCT AAAATGCGTG TGCCATATCT GGGTTCAAAA ACAGAGGAGC GGAAAACAGC
12001 CTCAATGGCA GCAATAAAAG GAATGTCACA TCACCTGCGT GCAGTCTTAA GAGGCACATC
12061 CGTATTTATT TGGGCATTTG GGGATACAGA TATCAATTGG GATAATGCAT TGCAGATTGC
12121 CCAATCACGG TGTAACATCA CATTGGATCA AATGAGATTA CTTACACCAA TTCCTAGCAG
12181 TTCAAATATT CAACATAGAC TCGATGACGG AATCAGCACG CAGAAATTTA CTCCTGCAAG
12241 CCTTGCTCGA ATCACATCCT TCGTTCACAT CTGTAATGAC AGCCAGAGGT TAGAGAAGGA
12301 TGGCTCATCT GTCGACTCAA ACTTGATTTA CCAGCAAATT ATGTTACTTG GACTCAGCAT
12361 CTTTGAAACA ATGTACTCAA TGGACCAAAA GTGGGTATTC AATAACCATA CCTTGCATTT
12421 GCACACTGGA CACTCCTGTT GTCCAAGGGA ACTAGACATA AGTTTGGTGA ACCCGCCGAG
12481 ACATCAGACC CCGGAGCTGA CTAGCACAAC AACCAACCCG TTCCTATATG ATCAGCTCCC
12541 ATTAAATCAA GAAAACTTGA CAACACTTGA GATTAAGACA TTTAAATTCA ATGAGCTCAA
12601 CATTGATGGT TTAGATTTTG GTGAAGGAAT ACAATTATTG AGTCGTTGTA CTGCAAGATT
12661 AATGGCAGAA TGTATTCTAG AGGAGGGAAT AGGCTCGTCA GTTAAAAATG AAGCAATTGT
12721 CAATTTTGAT AATTCAGTCA ATTGGATTTC AGAGTGCCTA ATGTGTGATA TTCGCTCACT
12781 TTGTGTTAAT TTAGGTCAAG AGATACTATG TAGCCTGGCA TACCAAATGT ATTACTTGCG
12841 AATCAGGGGT AGACGGGCCA TTCTTAATTA CTTGGACACA ACTTTGCAAA GGATCCCTGT
12901 GATACAATTA GCCAACATTG CACTCACCAT TTCGCACCCT GAGATATTTC GCAGAATTGT
12961 CAACACCGGG ATCCATAACC AGATTAAGGG CCCATATGTG GCAACAACGG ATTTCATAGC
13021 TGCAAGTAGA GATATCATAT TATCAGGTGC AAGGGAGTAT CTATCTTATT TAAGCAGTGG
13081 GCAGGAAGAC TGTTACACAT TCTTCAACTG TCAAGATGGG GATCTTACTC CAAAAATGGA
13141 ACAGTATCTT GCAAGGAGGG CATGCCTTTT AACATTATTG TATAATACTG GGCACCAGAT
13201 CCCCGTTATC CGATCACTGA CGCCAATAGA GAAGTGCAAG GTGCTCACAG AATACAATCA
13261 ACAAATTGAG TACGCAGATC AAGAGTTTAG CTCTGTACTA AAAGTGGTCA ATGCACTACT
13321 ACAAAATCCT AAGATAGATG CATTAGTTTC AAATCTCTAC TTCACCACCA GACGTGTTCT
13381 ATCAAACCTC AGATCATGTG ATAAGGCTAG ATCATATATT GAATATTTGT ACACTGAGGA
13441 CTTCGGAGAG AAAGAGGATA CAGTACAATA TGACATCATG ACAACAAACG ATATCATACT
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Figure 12 (5/5)

13501 TACTCATGGT CTATTCACAC AGATCGAAAT ATCTTATCAA GGGAATAGTC TCCATAAGTT
13561 CCTTACTCCG GATAACGCGC CTGGATCTTT GATCCCATTC TCTATTTCAC CAAATTCACT
13621 TGCATGTGAC CCTCTTCATC ACTTGCTCAA GTCGGTCGGT ACATCAAGCA CAAGTTGGTA
13681 CAAGTATGCA ATCGCCTATG CAGTGTCTGA AAAGAGGTCA GCTCGATTAG GAGGGAGCTT
13741 GTACATTGGT GAAGGGAGCG GAAGTGTGAT GACTTTACTC GAGTATCTTG AGCCATCTGT
13801 TGACATATTT TACAATTCAC TCTTCTCAAA TGGTATGAAC CCACCACAAC GAAATTATGG
13861 GCTTATGCCA CTACAATTTG TGAATTCGGT GGTTTATAAG AACTTAACGG CTAAATCAGA
13921 ATGTAAGCTA GGGTTTGTCC AGCAATTTAA ACCGTTGTGG AGAGACATAG ACATTGAGAC
13981 TAATGTTACA GATCCATCAT TTATCAATTT TGCATTGAAT GAAATCCCAA TGCAATCATT
14041 AAAACGAGTA AATTGTGATG TGGAATTTGA CCGTGGTATG CCGATTGAAC GGGTTATTCA
14101 GGGTTACACC CATATCTTAC TTGTTGCCAC TTACGGATTA CAGCAAGATT CAATACTGTG
14161 GGTGAAGGTA TATAGGACAT CTGAAAAAGT ATTTCAATTC TTACTGAGTG CCATGATCAT
14221 GATCTTTGGT TATGTAAAAA TCCACAGGAA TGGTTATATG TCGACAAAGG ATGAAGAGTA
14281 CATATTGATG TCTGACTGCA AGGAACCTGT AAACTATACA GCTGTCCCTA ACATTCTTAC
14341 ACGTGTAAGT GATTTAGTGT CGAAGAATCT GAGTCTTATC CATCCAGAAG ACCTCAGAAA
14401 AGTAAGGTGT GAAACAGATT CCCTGAATTT GAAGTGCAAT CATATTTATG AGAAAATAAT
14461 TGCCAGAAAA ATTCCATTAC AGGTATCATC AACTGACTCT TTGCTCCTCC AATTAGGCGG
14521 TGTTATCAAC TCGGTGGGCT CAACTGATCC TAGAGAGGTT GCAACATTAT CTTCTATTGA
14581 GTGTATGGAC TATGTTGTCT CATCAATTGA TTTGGCTATA TTGGAGGCAA ATATTGTAAT
14641 CTCAGAGAGT GCTGGTCTTG ACCTCGCTTT AATGTTAGGC CCATTCAACT TAAATAAGCT
14701 TAAGAAAATT GACACAATCC TTAAGTCAAG CACCTATCAG CTAATCCCGT ACTGGTTGCG
14761 CTATGAGTAC TCTATTAATC CGAGATCTTT GTCATTTCTA ATCACTAAAT TACAACAATG
14821 CCGAATTTCA TGGTCAGATA TGATCACGAT TTCTGAATTT CGTAAGAAAT CCAAGCGGCC
14881 TATATTTATC AAACGAGTAA TAGGGAATCA ACAGCTAAAA TCATTCTTTA ATGAAAGCTC
14941 AAGTATTGTT TTGACTCGGG CTGAAGTTAA AGTCTGTATA AAGTTCCTCG GTGCAATCAT
15001 CAAGTTGAAA TAATTTCTGC GATTTTAAAG GGGTGTAATG TTCTAATTTG CACTTGAAGT
15061 AATATAGCTT GTAATCATTC GCTAGGGGAT AGGATAATTT CTCTAACCTC TGAATCTATA
15121 TTCCTAGAGT ATAACAAATA TATACATAAT AAAAATGATT TTAAGAAAAA ATCCGACACT
15181 CAAAGAAAAT TGGTGCCTGT AATATTCTTC TTGCCAAATG ATTGTGAAGT GTCTAGCCTA
15241 ACTTAAAACA ATCGTATTCG ATAGGGAAGA ATGATATATA AAATAACTAA TAAAAAATTG
15301 TATTAGTAAA AATTACCGTA TTTCCTGTAT TCCATTTCTG GT

Figure 12

SEQ ID NO:2 DNA sequence encoding APMV-8 Nucleoprotein (NP)

```
   1  ATG TCA TCT GTG TTC AAT GAG TAT CAG GCG CTT CAA GAA CAA CTT GTG    48
  49  AAG CCG GCT GTC AGG AGA CCT GAT GTT GCC TCA ACG GGT TTA CTC AGA    96
  97  GCG GAA ATA CCT GTC TGT GTT ACA TTA TCT CAA GAC CCC GGT GAG AGA   144
 145  TGG AGC CTT GCT TGC TTG AAT ATT AGA TGG CTT GCG AGT GAT TCA TCA   192
 193  ACC ACA CCA ATG AAG CAA GGA GCA ATA TTG TCA CTG CTG AGT CTA CAT   240
 241  TCA GAC AAT ATG CGA GCT CAC GCA ACA TTA GCA GCA AGG TCT GCA GAT   288
 289  GCT TCA CTC ACC ATA CTT GAG GTA GAT GAA GTA GAT ATT AGC AAC TCA   336
 337  CTA ATC AAA TTC AAC GCC AGA AGT GGT GTA TCT GAC AAA CGC TCA AAT   384
 385  CAA TTG CTT GCA ATT GCG GAT GAC ATC CCC AAA AGT TGC AGT AAT GGG   432
 433  CAT CCA TTT CTT GAC ACA GAC ATT GAG ACC AGA GAC CCG CTC GAT CTA   480
 481  TCA GAG ACT ATA GAT CGC CTG CAG GGT ATT GCA GCT CAG ATA TGG GTG   528
 529  TCA GCC ATA AAG AGC ATG ACA GCG CCT GAC ACC GCA TCA GAG TCA GAA   576
 577  AGT AAG AGG CTG GCC AAA TAT CAA CAA CAA GGC CGA CTG GTT AAG CAA   624
 625  GTA CTC TTG CAT TCT GTA GTC AGG ACA GAA TTT ATG AGA GTT ATT CGG   672
 673  GGC AGC TTG GTA CTG CGC CAG TTT ATG GTT AGC GAG TGC AAG AGG GCT   720
 721  TCA GCC ATG GGC GGA GAC ACA TCT AGG TAC TAT GCT ATG GTG GGT GAC   768
 769  ATC AGT CTT TAC ATC AAG AAT GCA GGA TTG ACT GCA TTT TTC CTC ACC   816
 817  CTG AAG TTC GGA GTT GGT ACC CAG TAT CCA ACC TTA GCA ATG AGT GTT   864
 865  TTC TCC AGT GAC CTT AAA AGG CTT GCT GCA CTC ATC AGG CTA TAC AAA   912
 913  ACC AAG GGA GAC AAT GCA CCA TAC ATG GCA TTC CTG GAG GAC TCC GAT   960
 961  ATG GGA AAT TTT GCT CCA GCA AAT TAT AGC ACA ATG TAC TCT TAT GCC  1008
1009  ATG GGC ATT GGG ACA ATT CTG GAA GCA TCT GTA TCT CGA TAC CAG TAT  1056
1057  GCC AGA GAC TTT ACC AGT GAG AAT TAT TTC CGT CTT GGA GTT GAG ACA  1104
1105  GCC CAA AGC CAG CAG GGA GCA TTT GAC GAG AGA ACA GCC CGA GAA ATG  1152
1153  GGC TTG ACT GAG GAA TCA AAA CAG CAG GTT AGA TCA CTG CTA ATG TCA  1200
1201  GTA GAC ATG GGT CCC AGT TCA ATT CAT GAG CCA TCT CGC CCT GCA TTT  1248
1249  ATC AGT CAA GAA GAA AAT AGG CAG CCT GCC CAG AAC TTG TCA GAT ACT  1296
1297  CAG GGT CAG ACC AAG CCA GTC CCG AAG CAG CCC GCA CCA AGG GCC GAC  1344
1345  TCA GAT GAC ATT GAT CCA TAC GAG AAC GGG CTA GAA TGG TAA          1386
```

SEQ ID NO:3 Protein sequence of APMV-8 Nucleoprotein (NP)

```
1     MSSVFNEYQALQEQLVKPAVRRPDVASTGLLRAEIPVCVTLSQDPGER     48
49    WSLACLNIRWLASDSSTTPMKQGAILSLLSLHSDNMRAHATLAARSAD     96
97    ASLTILEVDEVDISNSLIKFNARSGVSDKRSNQLLAIADDIPKSCSNG    144
145   HPFLDTDIETRDPLDLSETIDRLQGIAAQIWVSAIKSMTAPDTASESE    192
193   SKRLAKYQQQGRLVKQVLLHSVVRTEFMRVIRGSLVLRQFMVSECKRA    240
241   SAMGGDTSRYYAMVGDISLYIKNAGLTAFFLTLKFGVGTQYPTLAMSV    288
289   FSSDLKRLAALIRLYKTKGDNAPYMAFLEDSDMGNFAPANYSTMYSYA    336
337   MGIGTILEASVSRYQYARDFTSENYFRLGVETAQSQQGAFDERTAREM    384
385   GLTEESKQQVRSLLMSVDMGPSSIHEPSRPAFISQEENRQPAQNLSDT    432
433   QGQTKPVPKQPAPRADSDDIDPYENGLEW*                      462
```

Figure 13

SEQ ID NO:4 DNA sequence encoding APMV-8 Phosphoprotein (P)

```
   1  ATG GAT TTC GCC AAT GAT GAA GAA ATT GCA GAA CTT TTG AAT CTC AGC      48
  49  ACC AAT GTA ATC AAG GAG ATT CAG AAA TCC GAA CTC AAG CCT CCC CAA      96
  97  ACC ACC GGA CGA CCA CCT GTC AGT CAA GGG AAC ACA AGA AAT CTA ACT     144
 145  GAT CTA TGG GAA AAG GAG ACT GCA AGT CAG ACC AAG ACA CCG GCC CAA     192
 193  TCT ACA CAA ACC ACA CAA GTT CAG TCT GAT GAA AAT GAG GAG GGA GAA     240
 241  ATC AAG TCC GAG TCA ACT GAT GGC CAC ATC AGA GGA ACT GTT AAT CAA     288
 289  TCA GAG CAA GTC CCA GAA CAA AAC CAG AGC AGA TCT TCA CCA GGT GAT     336
 337  GAT CTC GAC AGA GCT CTC AAC AAG CTT GAA GGG AGA ATC AAT TTA ATC     384
 385  AGC TCA ATG GAC AAA GAA ATT AAA AAG GGC CCT CGC ATC CAG AAT CTC     432
 433  CCT GGG TCC CAG GCG GCA ACT CAA CAG GCG ACC CAC CCA TTG GCA GGG     480
 481  GAC ACC CCG AAC ATG CAA GCA CAG ACA AAA GCC CTG GCG AAG CCA CAT     528
 529  CAA GAG GCA ATC AAT CCT GGC AAC CAG GAC ACA GGA GAG AGT ATT CAT     576
 577  TTA CCA CCT TCC ATG GCA CCA CCA GAG TCA TTA GTT GGT GCA ATC CGC     624
 625  AAT GCA CCC CAA TTC GTG CCA GAC CAA TCT ATG ACG AAT GTA GAT GCG     672
 673  GGG AGT GTC CAA CTA CAT GCA TCA TGT GCA GAG ATG ATA AGT AGA ATG     720
 721  TTT GTA GAA GTT ATA TCC AAG CTT GAT AAA CTC GAG TCG AGA CTG AAT     768
 769  GAT ATA GCA AAA GTT GTG AAC ACT ACC CCC CTT ATT AGG AAT GAT ATT     816
 817  AAC CAA CTT AAG GCC ACA ACC GCA CTG ATG TCT AAC CAA ATT GCC TCC     864
 865  ATA CAA ATT CTT GAC CCA GGG AAT GCA GGG GTG AGG TCC CTC TCT GAA     912
 913  ATG AAA TCT GTG ACG AAG AAA GCT GCT GTT GTA ATT GCA GGG TTT GGA     960
 961  GAC GAC CCA ACT CAA ATT ATT GAA GAA GGC ATT ATG GCC AAA GAT GCT    1008
1009  CTT GGA AAA CCT GTG CCT CCA ACA TCT GTT ATC TCA GCC AAA GCT CAG    1056
1057  ACT TCT TCC GGT GTG AGT AAG GGT GAA ATA GAA GGA TTG ATT GCA TTG    1104
1105  GTG GAA ACA TTA GTT GAC AAT GAC AAG AAG GCA GCA AAA CTG ATT AAA    1152
1153  ATG ATT GAT CAA GTT AAA TCC CAT GCC GAT TAC GCC CGA GTC AAG CAG    1200
1201  GCA ATA TAT AAT GCG TAA                                          1218
```

SEQ ID NO:5 Protein sequence of APMV-8 PhosphoProtein (P)

```
1     MDFANDEEIAELLNLSTNVIKEIQKSELKPPQTTGRPPVSQGNTRNLT      48
49    DLWEKETASQTKTPAQSTQTTQVQSDENEEGEIKSESTDGHIRGTVNQ      96
97    SEQVPEQNQSRSSPGDDLDRALNKLEGRINLISSMDKEIKKGPRIQNL     144
145   PGSQAATQQATHPLAGDTPNMQAQTKALAKPHQEAINPGNQDTGESIH     192
193   LPPSMAPPESLVGAIRNAPQFVPDQSMTNVDAGSVQLHASCAEMISRM     240
241   FVEVISKLDKLESRLNDIAKVVNTTPLIRNDINQLKATTALMSNQIAS     288
289   IQILDPGNAGVRSLSEMKSVTKKAAVVIAGFGDDPTQIIEEGIMAKDA     336
337   LGKPVPPTSVISAKAQTSSGVSKGEIEGLIALVETLVDNDKKAAKLIK     384
385   MIDQVKSHADYARVKQAIYNA*                               406
```

Figure 14

SEQ ID NO:6 DNA sequence encoding APMV-8 Matrixprotein (M)

```
   1  ATG GCA TAT ACA ACA TTG AAA CTG TGG GTG GAT GAG GGT GAC ATG TCG    48
  49  TCT TCG CTC CTA TCA TTC CCG TTG GTA CTA AAA GAG ACA GAC AGA GGC    96
  97  ACA AAG GAG CTT CAA CCA CAG GTA AGG GTA GAT TCA ATT GGC GAT GTG   144
 145  CAG AAC GCC AAA GAG TCC TCG ATA TTC GTG ACT CTA TAT GGT TTC ATC   192
 193  CAA GCA ATT AAG GAG AGT TCA GAT CGA TCG AAA TTC TTC CAT CCA AAA   240
 241  GAT GAC TTC AAA CCT GAG ACA GTC ACT GCA GGA CTG GTA GTG GTA GGT   288
 289  GCG ATC CGA ATG ATG GCT GAT GTT AAT ACC ATC TCT AAT GAC GCA CTA   336
 337  GCG CTG GAG ATC ACT GTT AAG AAA TCT GCA ACT TCT CAA GAG AAA ATG   384
 385  ACG GTG ATG TTC CAC AAT AGC CCC CCT TCA TTG AGA ACT GCA ATA ACT   432
 433  ATC CGA GCA GGA GGT TTC ATC TCG AAT GCA GAC GAG AAT ATA AAA TGT   480
 481  GCC AGC AAA TTG ACT GCA GGA GTG CAG TAC ATA TTC CGC CCA ATG TTT   528
 529  GTT TCA ATC ACT AAA TTA CAC AAT GGC AAA CTA TAT AGG GTG CCC AAA   576
 577  AGC ATC CAC AGC ATC TCA TCC ACT CTA CTG TAT AGT GTG ATG TTG GAG   624
 625  GTA GGA TTC AAA GTG GAT ATT GGG AAG GAT CAT CCC CAG GCA AAG ATG   672
 673  CTG AAG AAG GTC ACA ATC GGC GAT GCA GAC ACA TAC TGG GGG TTT GCA   720
 721  TGG TTC CAC CTG TGC AAT TTC AAA AAG ACA TCC TCT AAG GGA AAG CCA   768
 769  AGA ACG CTA GAC GAA CTA AAG ACA AAA GTC AAA AAT ATG GGG TTG AAA   816
 817  TTG GAG TTA CAT GAC CTG TGG GGT CCG ACT ATT GTG GTC CAA ATC ACT   864
 865  GGC AAG AGC AGC AAA TAT GCT CAA GGA TTT TTT TCC TCC AAT GGT ACT   912
 913  TGT TGT CTC CCA ATC AGC AGA TCT GCA CCA GAG CTT GGG AAG CTT CTG   960
 961  TGG TCT TGT TCA GCA ACT ATA GGT GAC GCA ACA GTT GTT ATC CAA TCA  1008
1009  AGC GAG AAA GGG GAA CTC CTA AGG TCT GAT GAC CTC GAG ATA CGA GGT  1056
1057  GCT GTG GCC TCC AAG AAA GGT AGA CTG GGC TCA TTT CAC CCC TTC AAA  1104
1105  AAA TGA                                                        1110
```

SEQ ID NO:7 Protein sequence of APMV-8 Matrixprotein (M)

```
1     MAYTTLKLWVDEGDMSSSLLSFPLVLKETDRGTKELQPQVRVDSIGDV      48
49    QNAKESSIFVTLYGFIQAIKESSDRSKFFHPKDDFKPETVTAGLVVVG      96
97    AIRMMADVNTISNDALALEITVKKSATSQEKMTVMFHNSPPSLRTAIT     144
145   IRAGGFISNADENIKCASKLTAGVQYIFRPMFVSITKLHNGKLYRVPK     192
193   SIHSISSTLLYSVMLEVGFKVDIGKDHPQAKMLKKVTIGDADTYWGFA     240
241   WFHLCNFKKTSSKGKPRTLDELKTKVKNMGLKLELHDLWGPTIVVQIT     288
289   GKSSKYAQGFFSSNGTCCLPISRSAPELGKLLWSCSATIGDATVVIQS     336
337   SEKGELLRSDDLEIRGAVASKKGRLGSFHPFKK*                   370
```

Figure 15

SEQ ID NO:8 DNA sequence encoding APMV-8 Fusionprotein (F)

```
   1  ATG GGT CAA ATA TCA GTA TAT CTA ATT AAT AGC GTG CTA TTA TTG CTG      48
  49  GTA TAT CCT GTG AAT TCG ATT GAC AAT ACA CTC ATT GCC CCA ATC GGA      96
  97  GTT GCC AGC GCA AAT GAA TGG CAG CTT GCT GCA TAT ACA ACA TCA CTT     144
 145  TCA GGG ACA ATT GCC GTG CGA TTC CTA CCT GTG CTC CCG GAT AAT ATG     192
 193  ACT ACC TGT CTT AAA GAA ACA ATC ACT ACA TAC AAT AAT ACT GTC AAC     240
 241  AAC ATC TTA GGC CCA CTC AAA TCC AAT CTG GAT GCA CTG CTC TCA TCT     288
 289  GAG ACT TAT CCC CAG ACA AGA TTA ATT GGG GCA GTT ATA GGT TCA ATT     336
 337  GCT CTC GGT GTT GCA ACA TCG GCT CAA ATC ACT GCT GCA GTT GCT CTC     384
 385  AAG CAA GCG CAA GAC AAT GCA AGG AAC ATA CTA GCA CTC AAA GAA GCA     432
 433  CTG TCC AAA ACC AAT GAG GCG GTC AAG GAG CTT AGT AGT GGG TTA CAA     480
 481  CAA ACA GCT ATT GCA CTT GGT AAG ATA CAG AGT TTT GTG AAT GAG GAA     528
 529  ATT CTG CCA TCT ATC AAC CAA CTG AGC TGC GAG GTG ACA GCC AAT AAA     576
 577  CTT GGG GTG TAT TTA TCT CTG TAT CTC ACA GAA CTG ACC ACC ATA TTC     624
 625  GGT GCA CAG CTG ACC AAC CCT GCA TTG ACT TCA TTA TCA TAT CAA GCA     672
 673  CTG TAC AAC CTG TGT GGT GGC AAC ATG GCA ATG CTT ACT CAG AAG ATT     720
 721  GGA ATT AAA CAG CAA GAC GTT AAT TCG CTA TAT GAA GCC GGA CTA ATC     768
 769  ACA GGA CAA GTC ATT GGT TAT GAC TCT CAT TAC CAG CTG CTG GTC ATC     816
 817  CAG GTC AAT TAT CCA AGC ATT TCT GAG GTC ACT GGT GTA CGT GCG ACA     864
 865  GAA TTA GTC ACT GTT AGT GTA ACA ACA GAC AAG GGT GAA GGG AAA GCA     912
 913  ATT GTA CCC CAA TTT GTA GCT GAA AGT CGG GTG ACT ATT GAA GAG CTT     960
 961  GAT GTC GCA TCT TGT AAA TTC AGC AGC ACG ACC CTA TAT TGC AGG CAG    1008
1009  GTC AAC ACA AGG GCA CTT CCC CCG CTA GTA GCT AGC TGT CTT CGA GGT    1056
1057  AAC TAT GAT GAT TGT CAA TAT ACC ACA GAG ATT GGA GCA TTA TCA TCC    1104
1105  CGG TAT ATA ACA CTA GAT GGG GGG GTC TTA GTT AAT TGC AAG TCA ATT    1152
1153  GTT TGT AGG TGC CTT AAT CCA AGT AAG ATC ATC TCT CAA AAT ACA AAC    1200
1201  GCT GCA GTA ACA TAT GTT GAT GCC ACA ATC TGC AAA ACA ATT CAA TTG    1248
1249  GAT GAT ATA CAA CTC CAG CTG GAA GGG TCA CTA TCA TCA GTT TAT GCA    1296
1297  AGA AAC ATC TCA ATT GAG ATC AGT CAG GTG ACC ACA TCC GGG TCT TTA    1344
1345  GAT ATC AGC AGT GAG ATA GGA AAC ATC AAT AAT ACG GTG AAT CGT GTG    1392
1393  GAG GAT TTA ATT CAC CAA TCA GAG GAA TGG CTG GCA AAG GTT AAC CCA    1440
1441  CAC ATT GTT AAT AAT ACA ACA CTA ATT GTA CTC TGT GTG TTA AGT GCG    1488
1489  CTT GCT GTG ATC TGG CTG GCA GTA TTA ACG GCT ATT ATA ATA TAC TTG    1536
1537  AGA ACA AAG TTG AAG ACT ATA TCG GCA TTA GCT GTA ACC AAT ACA ATA    1584
1585  CAG TCT AAC CCC TAT GTT AAC CAA ACG AAA CAT GAA TCT AAG TTT TGA    1632
```

SEQ ID NO:9 Protein sequence of APMV-8 Fusionprotein (F)

```
1     MGQISVYLINSVLLLLVYPVNSIDNTLIAPIGVASANEWQLAAYTTSL      48
49    SGTIAVRFLPVLPDNMTTCLKETITTYNNTVNNILGPLKSNLDALLSS      96
97    ETYPQTRLIGAVIGSIALGVATSAQITAAVALKQAQDNARNILALKEA     144
145   LSKTNEAVKELSSGLQQTAIALGKIQSFVNEEILPSINQLSCEVTANK     192
193   LGVYLSLYLTELTTIFGAQLTNPALTSLSYQALYNLCGGNMAMLTQKI     240
241   GIKQQDVNSLYEAGLITGQVIGYDSHYQLLVIQVNYPSISEVTGVRAT     288
289   ELVTVSVTTDKGEGKAIVPQFVAESRVTIEELDVASCKFSSTTLYCRQ     336
337   VNTRALPPLVASCLRGNYDDCQYTTEIGALSSRYITLDGGVLVNCKSI     384
385   VCRCLNPSKIISQNTNAAVTYVDATICKTIQLDDIQLQLEGSLSSVYA     432
433   RNISIEISQVTTSGSLDISSEIGNINNTVNRVEDLIHQSEEWLAKVNP     480
481   HIVNNTTLIVLCVLSALAVIWLAVLTAIIIYLRTKLKTISALAVTNTI     528
529   QSNPYVNQTKHESKF*                                    544
```

Figure 16

SEQ ID NO:10 DNA sequence encoding APMV-8 Hemagglutinin/neuraminidase (HN)

```
   1  ATG AGT AAC ATT GCA TCC AGT TTA GAA AAC ATT GTA GAG CAG GAT AGT      48
  49  CGA AAA ACA ACT TGG AGG GCC ATC TTT AGA TGG TCC GTT CTT CTT ATT      96
  97  ACA ACA GGA TGC TTA GCC TTA TCC ATT GTT AGC ATA GTT CAA ATT GGA     144
 145  AAT TTG AAA ATT CCT TCT GTA GGG GAT CTG GCT GAT GAA GTG GTG ACA     192
 193  CCC TTG AAA ACC ACT CTG TCA GAT ACA CTC AGG AAT CCA ATT AAC CAG     240
 241  ATA AAT GAT ATA TTT AGG ATT GTT GCC CTT GAT ATT CCA TTG CAA GTG     288
 289  ACC AGT ATC CAA AAA GAC CTT GCA AGT CAA TTT AAC ATG TTG ATA GAT     336
 337  AGT TTA AAT GCT ATC AAA TTA GGC AAC GGG ACC AAC CTT ATC ATA CCT     384
 385  ACA TCA GAC AAG GAG TAT GCA GGA GGA ATT GGA AAC CCT GTA TTT ACT     432
 433  GTC GAT GCT GGA GGT TCT ATA GGA TTC AAA CAG TTT AGC TTA ATA GAA     480
 481  CAT CCG AGC TTT ATT GCT GGA CCT ACA ACG ACC CGA GGC TGT ACA AGA     528
 529  ATA CCC ACT TTT CAC ATG TCA GAA AGT CAT TGG TGC TAC TCA CAC AAC     576
 577  ATC ATC GCT GCT GGC TGT CAA GAT GCC AGT GCA TCC AGT ATG TAT ATC     624
 625  TCA ATG GGA GTT CTC CAT GTG TCC TCA TCT GGC ACT CCC ATT TTT CTT     672
 673  ACT ACT GCA AGT GAG CTG ATA GAC GAT GGA GTT AAC CGT AAG TCA TGC     720
 721  AGC ATT GTA GCA ACC CAA TTT GGC TGT GAC ATT TTG TGC AGT ATT GTC     768
 769  ACA GAG AAG GAG GGA GAT GAT TAC TGG TCT GAT ACT CCG ACT CCA ATG     816
 817  CGC CAC GGC CGT TTT TCA TTC AAT GGT AGT TTT GTA GAA GCC GAA CTA     864
 865  CCA GTG TCC AGT ATG TTC TCA TCA TTC TCT GCC AAC TAC CCT GCT GTG     912
 913  GGA TCA GGC GAA ATT GTA AAA GAT AGA ATA TTA TTC CCA ATT TAC GGA     960
 961  GGT ATA AAG CAG ACT TCA CCA GAG TTT ACC GAA TTA GTG AAA TAC GGA    1008
1009  CTC TTT GTA TCA ACA CCT ACA ACT GTG TGC CAG AGT AGC TGG ACT TAT    1056
1057  GAC CAG GTA AAA GCT GCG TAT AGG CCA GAT TAC ATA TCA GGC CGG TTC    1104
1105  TGG GCA CAA GTG ATA CTC AGC TGC GCT CTT GAT GCA GTC GAC TTA TCA    1152
1153  AGT TGT ATT GTA AAG ATT ATG AAT AGC AGC ACA GTG ATG ATG GCA GCG    1200
1201  GAA GGA AGG ATA ATG AAG ATA GGG ATT GAT TAC TTT TAC TAT CAG CGG    1248
1249  TCA TCT TCT TGG TGG CCA TTG GCA TTT GTC ACA AAA CTA GAC CCG CAA    1296
1297  GAG TTG GCA GAC ACA AAC TCA ATA TGG CTG ACC AAT TCC ATA CCA ATC    1344
1345  CCG CAA TCA AAG TTC CCT CGG CCT TCA TAT TCA GAA AAT TAT TGC ACA    1392
1393  AAG CCA GCA GTT TGC CCT GCT ACT TGT GTC ACT GGT GTG TAC TCT GAT    1440
1441  ATT TGG CCC CTG ACC TCA TCT TCA TCA CTC CCG AGC ATA ATT TGG ATC    1488
1489  GGC CAG TAC CTT GAT GCT CCT GTT GGA AGG ACT TAT CCT AGA TTT GGA    1536
1537  ATT GCA AAT CAG TCA CAC TGG TAC CTC CAA GAA GAT ATT CTA CCC ACT    1584
1585  TCC ACC GCA AGT GCG TAT TCA ACC ACT ACA TGT TTT AAG AAT ACT GCC    1632
1633  AGG AAT AGA GTG TTC TGC GTC ACC ATT GCC GAA TTT GCA GAT GGG TTG    1680
1681  TTT GGA GAG TAC AGG ATA ACA CCT CAG TTG TAC GAA TTA GTG AGA AAT    1728
1729  AAT TGA                                                          1734
```

SEQ ID NO:11 Protein sequence of APMV-8 Hemagglutinin/neuraminidase (HN)

```
1     MSNIASSLENIVEQDSRKTTWRAIFRWSVLLITTGCLALSIVSIVQIG      48
49    NLKIPSVGDLADEVVTPLKTTLSDTLRNPINQINDIFRIVALDIPLQV      96
97    TSIQKDLASQFNMLIDSLNAIKLGNGTNLIIPTSDKEYAGGIGNPVFT     144
145   VDAGGSIGFKQFSLIEHPSFIAGPTTTRGCTRIPTFHMSESHWCYSHN     192
193   IIAAGCQDASASSMYISMGVLHVSSSGTPIFLTTASELIDDGVNRKSC     240
241   SIVATQFGCDILCSIVTEKEGDDYWSDTPTPMRHGRFSFNGSFVEAEL     288
289   PVSSMFSSFSANYPAVGSGEIVKDRILFPIYGGIKQTSPEFTELVKYG     336
337   LFVSTPTTVCQSSWTYDQVKAAYRPDYISGRFWAQVILSCALDAVDLS     384
385   SCIVKIMNSSTVMMAAEGRIMKIGIDYFYYQRSSSWWPLAFVTKLDPQ     432
433   ELADTNSIWLTNSIPIPQSKFPRPSYSENYCTKPAVCPATCVTGVYSD     480
481   IWPLTSSSSLPSIIWIGQYLDAPVGRTYPRFGIANQSHWYLQEDILPT     528
529   STASAYSTTTCFKNTARNRVFCVTIAEFADGLFGEYRITPQLYELVRN     576
577   N*                                                    578
```

Figure 17 (1/4)

SEQ ID NO:12 DNA sequence encoding APMV-8 Polymerase (L)

```
   1  ATG GAG GGC GAC CTC TAC ACA AAC ATG GAT ATA AAA CAA GTT GAC CTG    48
  49  ATA ATA CAA CCC GAG GTT CAT CTC GAT TCA CCC ATC ATA TTG AAT AAA    96
  97  CTG GCA CTA TTA TGG CGC TTG AGT GGT TTA CCC ATG CCT GCA GAC CTA   144
 145  CGA CAA AAA TCC GTA GTG ATG CAC ATC CCG GAC CAC ATC TTA GAA AAA   192
 193  TCA GAA TAT CGG ATC AAG CAC CGT CTA GGG AAA ATC AAG AGT GAC ATA   240
 241  ACA CAT TAC TGT CAG TAT TTT AAT ATT AAT TTG GCA AAT ATT GAT CCG   288
 289  ATA ACC CAC CCC AAA AGT TTG TAT TGG TTA TCC AGA CTA ACA ATA GCT   336
 337  AGT GCT GGA ACT TTT AGG CAT ATG AAA GAT AGA ATC TTG TGT ACA GTT   384
 385  GGC TCT GAA TTT GGA CAC AAA ATT CAA GAT TTA TTT TCA CTG CTG AGC   432
 433  CAT AAA CTA GTA GGT AAC GGG GAT TTA TTT AAT CAA AGT CTC TCA GGT   480
 481  ACA CGT TTG ACT GCA AGT CCG TTA TCC CCT TTA TGC AAT CAA TTT GTC   528
 529  TCT GAC ATC AAG TCT GCA GTC ACG ACA CCC TGG TCA GAA GCT CGT TGG   576
 577  TCT TGG CTT CAT ATC AAA CAA ACA ATG AGA TAT CTG ATA AAA CAA TCA   624
 625  CGC ACT ACA AAT TCG GCT CAT TTA ACA GAA ATC ATA AAA GAA GAA TGG   672
 673  GGT TTA GTA GGT ATT ACT CCA GAT CTT GTC ATT CTT TTT GAC AGA GTC   720
 721  AAT AAT AGT CTG ACT GCA TTA ACA TTT GAG ATG GTT CTA ATG TAT TCA   768
 769  GAT GTA TTA GAA TCC CGT GAC AAT ATT GTG TTA GTG GGG CGA CTA TCT   816
 817  ACC TTT CTA CAG CCA GTA GTT AGT AGA CTG GAG GTG TTG TTT GAT CTA   864
 865  GTA GAT TCA TTG GCA AAA ATC TTA GGT GAC ACA ATA TAT GAG ATT ATT   912
 913  GCA GTG TTA GAG AGC TTG TCT TAT GGG TCA GTT CAA CTA CAT GAT GCA   960
 961  AGT CAC TCT CAT GCA GGG TCT TTT TTT TCA TTT AAC ATG AAT GAA CTT  1008
1009  GAT AAC ACA CTA TCA AAG AGG GTA GAT CCG AAA CAC AAG AAC ACT ATA  1056
1057  ATG AGC ATT ATA AGA CAA TGC TTT TCT AAT CTA GAT GTT GAT CAA GCT  1104
1105  GCA GAG ATG CTA TGC CTG ATG AGA TTA TTC GGA CAC CCA ATG TTA ACT  1152
1153  GCA CCG GAT GCA GCA GCC AAA GTG AGG AAA GCA ATG TGT GCT CCA AAA  1200
1201  CTT GTT GAA CAC GAC ACC ATC TTG CAG ACA TTA TCT TTC TTC AAG GGG  1248
1249  ATA ATT ATA AAT GGG TAC AGA AGA TCA CAC TCT GGC CTG TGG CCC AAT  1296
1297  GTA GAG CCG TCT TCA ATT TAT GAT GAT GAT CTC AGA CAG CTG TAC TTA  1344
1345  GAG TCA GCA GAG ATT TCC CAT CAT TTT ATG CTT AAA AAC TAC AAG AGT  1392
1393  TTA AGC ATG ATA GAA TTC AAG AAG AGC ATA GAC TAC GAT CTT CAT GAT  1440
1441  GAC CTA AGT ACT TTC TTA AAG GAT AGA GCA ATT TGC CGG CCG AAA TCC  1488
1489  CAG TGG GAT GTC ATA TTT CGT AAG TCT TTA CGC AGA TCT CAT ACG CAG  1536
1537  TCC CAG TAT CTG GAC GAA ATT AAG AGC AAC CGA TTG CTA ATT GAT TTT  1584
1585  CTT GAT TCT GCT GAA TTT GAC CCT GGA AAA GAA TTT GCA TAT GTA ACC  1632
1633  ACA ATG GAT TAT TTG CAC GAT AAT GAA TTT TGT GCT TCA TAT TCT CTA  1680
1681  AAG GAA AAG GAG ATC AAA ACT ACT GGG AGG ATA TTT GCA AAA ATG ACA  1728
1729  CGC AAT ATG AGA AGT TGC CAA GTA ATA CTT GAA TCT TTG TTA TCA AAG  1776
1777  CAT ATA TGC AAG TTC TTC AAA GAG AAT GGC GTT TCG ATG GAG CAA TTG  1824
1825  TCA TTG ACC AAG AGT CTA CTT GCA ATG TCT CAA CTC TCA CCA AAA GTC  1872
1873  TCG ACT TTG CAG GAC ACT GCA TCA CGT CAT GTA GGT AAC TCA AAA TCT  1920
1921  CAG ATT GCA ACC AGC AAC CCA TCT CGG CAT CAC TCG ACA CCC AAT CAG  1968
1969  ATG TCA CTC TCA AAT CGA AAA ACG GTT GTA GCA ACT TTC TTA ACA ACT  2016
2017  GAC TTG GAA AAA TAC TGC CTG CAG TGG CGA TAT TCA ACT ATT AAA TTG  2064
2065  TTT GCA CAA GCT CTA AAT CAA CTC TTT GGG ATT GAT CAC GGA TTT GAA  2112
2113  TGG ATA CAT TTA AGA CTT ATG AAC AGC ACC TTA TTT GTT GGC GAT CCT  2160
2161  TAC TCG CCT CCT GAA GAT CCA ACA CTA GAA GAT ATA GAT AAA GCA CCA  2208
2209  AAT GAT GAT ATC TTC ATA GTT TCT CCA AGG GGA GGC ATA GAG GGT TTA  2256
2257  TGT CAG AAA ATG TGG ACC ATG ATA TCA ATT AGT GCT ATA CAC TGT GTA  2304
2305  GCA GAG AAA ATT GGT GCA CGA GTG GCA GCA ATG GTG CAG GGT GAT AAT  2352
2353  CAA GTA ATA GCT ATC ACC AAA GAA TTA TTC AGA GGA GAG AAA GCT TGT  2400
2401  GAT GTC AGA GAT GAG TTA GAC GAG CTT GGT CAA GTG TTT TTT GAT GAG  2448
2449  TTC AAG AGA CAC AAT TAT GCA ATT GGA CAC AAT CTT AAG CTA AAT GAG  2496
2497  ACA ATA CAA AGC CAA TCC TTT TTT GTA TAT TCC AAA CGA ATA TTC TTT  2544
2545  GAA GGG CGA TTG CTT AGT CAA GTC CTC AAA AAT GCT GCC AAG TTA TGT  2592
2593  ATG GTT GCT GAC CAT CTA GGT GAA AAC ACT GTA TCT TCC TGT AGC AAC  2640
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Figure 17 (2/4)

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2641  CTG AGC TCG ACA ATT GCC CGC TTA GTG GAA AAT GGG TTT GAG AAG GAC    2688
2689  ACT GCT TTT GTG TTG AAC CTA GTC TAC ATC ATG ACT CAG ATT CTT TTT    2736
2737  GAT GAG CAT TAC TCG ATT GTA TGC GAT CAC CAT AGT GTC AAA AGC TTG    2784
2785  ATT GGA TCA AAA AAC CAT CGG AAT TTA TTG TAT TCA TCT CTA ATA CCA    2832
2833  GGT CAG CTC GGC GGT TTC AAC TTC CTC AAT ATA AGT CGG TTG TTC ACT    2880
2881  AGG AAT ATA GGT GAC CCA GTA ACA TGT AGT CTG TCT GAT CTC AAA TGC    2928
2929  TTC ATA GCC GCA GGT CTC CTT CCA CCC TAT GTC CTA AAA AAT GTG GTT    2976
2977  CTG CGT GAG CCT GGT CCT GGG ACA TGG TTG ACG TTG TGC TCT GAT CCT    3024
3025  TAC ACC CTT AAC ATA CCA TAC ACA CAG CTT CCA ACC ACA TAT CTC AAA    3072
3073  AAG CAC ACC CAG CGA TCA TTG CTT TCA CGT GCA GTA AAT CCT TTA TTA    3120
3121  GCC GGT GTA CAA GTG CCA AAT CAG CAT GAG GAA GAA GAG ATG TTG GCT    3168
3169  CGC TTT CTC CTT GAT CGT GAA TAT GTG ATG CCC CGC GTT GCT CAT GTA    3216
3217  ATA CTA GAA TCA TCA GTC CTT GGC AAA CGG AAA CAA ATC CAA GGC TTA    3264
3265  ATT GAT ACA ACT CCA ACC ATC ATT AGA ACA TCT CTA GTT AAT CTG CCA    3312
3313  GTG TCT AGA AAG AAA TGC GAA AAA ATA ATC AAT TAC TCT CTC AAT TAT    3360
3361  ATT GCT GAG TGT CAT GAC TCC TTA CTT AGC CAG GTC TGC TTC AGT GAT    3408
3409  AAT AAG GAA TAC TTG TGG TCA ACC TCC TTA ATA TCA GTT GAG ACC TGT    3456
3457  AGT GTG ACA ATT GCG GAC TAT CTG AGA GCT GTC AGC TGG TCT AAT ATA    3504
3505  TTA GGG GGA AGA AAC ATA TCC GGG GTG ACT ACA CCT GAT ACT ATT GAA    3552
3553  TTA ATT CAA GGT TGT TTA ATA GGT GAA AAT TCT AGT TGT ACT CTT TGT    3600
3601  GAA TCG CAT GAT GAC GCA TTC ACG TGG ATG CAC TTG CCT GGC CCA CTT    3648
3649  TAC ATC CCT GAA CCA TCA GTT ACT AAC TCT AAA ATG CGT GTG CCA TAT    3696
3697  CTG GGT TCA AAA ACA GAG GAG CGG AAA ACA GCC TCA ATG GCA GCA ATA    3744
3745  AAA GGA ATG TCA CAT CAC CTG CGT GCA GTC TTA AGA GGC ACA TCC GTA    3792
3793  TTT ATT TGG GCA TTT GGG GAT ACA GAT ATC AAT TGG GAT AAT GCA TTG    3840
3841  CAG ATT GCC CAA TCA CGG TGT AAC ATC ACA TTG GAT CAA ATG AGA TTA    3888
3889  CTT ACA CCA ATT CCT AGC AGT TCA AAT ATT CAA CAT AGA CTC GAT GAC    3936
3937  GGA ATC AGC ACG CAG AAA TTT ACT CCT GCA AGC CTT GCT CGA ATC ACA    3984
3985  TCC TTC GTT CAC ATC TGT AAT GAC AGC CAG AGG TTA GAG AAG GAT GGC    4032
4033  TCA TCT GTC GAC TCA AAC TTG ATT TAC CAG CAA ATT ATG TTA CTT GGA    4080
4081  CTC AGC ATC TTT GAA ACA ATG TAC TCA ATG GAC CAA AAG TGG GTA TTC    4128
4129  AAT AAC CAT ACC TTG CAT TTG CAC ACT GGA CAC TCC TGT TGT CCA AGG    4176
4177  GAA CTA GAC ATA AGT TTG GTG AAC CCG CCG AGA CAT CAG ACC CCG GAG    4224
4225  CTG ACT AGC ACA ACA ACC AAC CCG TTC CTA TAT GAT CAG CTC CCA TTA    4272
4273  AAT CAA GAA AAC TTG ACA ACA CTT GAG ATT AAG ACA TTT AAA TTC AAT    4320
4321  GAG CTC AAC ATT GAT GGT TTA GAT TTT GGT GAA GGA ATA CAA TTA TTG    4368
4369  AGT CGT TGT ACT GCA AGA TTA ATG GCA GAA TGT ATT CTA GAG GAG GGA    4416
4417  ATA GGC TCG TCA GTT AAA AAT GAA GCA ATT GTC AAT TTT GAT AAT TCA    4464
4465  GTC AAT TGG ATT TCA GAG TGC CTA ATG TGT GAT ATT CGC TCA CTT TGT    4512
4513  GTT AAT TTA GGT CAA GAG ATA CTA TGT AGC CTG GCA TAC CAA ATG TAT    4560
4561  TAC TTG CGA ATC AGG GGT AGA CGG GCC ATT CTT AAT TAC TTG GAC ACA    4608
4609  ACT TTG CAA AGG ATC CCT GTG ATA CAA TTA GCC AAC ATT GCA CTC ACC    4656
4657  ATT TCG CAC CCT GAG ATA TTT CGC AGA ATT GTC AAC ACC GGG ATC CAT    4704
4705  AAC CAG ATT AAG GGC CCA TAT GTG GCA ACA ACG GAT TTC ATA GCT GCA    4752
4753  AGT AGA GAT ATC ATA TTA TCA GGT GCA AGG GAG TAT CTA TCT TAT TTA    4800
4801  AGC AGT GGG CAG GAA GAC TGT TAC ACA TTC TTC AAC TGT CAA GAT GGG    4848
4849  GAT CTT ACT CCA AAA ATG GAA CAG TAT CTT GCA AGG AGG GCA TGC CTT    4896
4897  TTA ACA TTA TTG TAT AAT ACT GGG CAC CAG ATC CCC GTT ATC CGA TCA    4944
4945  CTG ACG CCA ATA GAG AAG TGC AAG GTG CTC ACA GAA TAC AAT CAA CAA    4992
4993  ATT GAG TAC GCA GAT CAA GAG TTT AGC TCT GTA CTA AAA GTG GTC AAT    5040
5041  GCA CTA CTA CAA AAT CCT AAG ATA GAT GCA TTA GTT TCA AAT CTC TAC    5088
5089  TTC ACC ACC AGA CGT GTT CTA TCA AAC CTC AGA TCA TGT GAT AAG GCT    5136
5137  AGA TCA TAT ATT GAA TAT TTG TAC ACT GAG GAC TTC GGA GAG AAA GAG    5184
5185  GAT ACA GTA CAA TAT GAC ATC ATG ACA ACA AAC GAT ATC ATA CTT ACT    5232
5233  CAT GGT CTA TTC ACA CAG ATC GAA ATA TCT TAT CAA GGG AAT AGT CTC    5280
5281  CAT AAG TTC CTT ACT CCG GAT AAC GCG CCT GGA TCT TTG ATC CCA TTC    5328
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Figure 17 (3/4)

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5329  TCT ATT TCA CCA AAT TCA CTT GCA TGT GAC CCT CTT CAT CAC TTG CTC    5376
5377  AAG TCG GTC GGT ACA TCA AGC ACA AGT TGG TAC AAG TAT GCA ATC GCC    5424
5425  TAT GCA GTG TCT GAA AAG AGG TCA GCT CGA TTA GGA GGG AGC TTG TAC    5472
5473  ATT GGT GAA GGG AGC GGA AGT GTG ATG ACT TTA CTC GAG TAT CTT GAG    5520
5521  CCA TCT GTT GAC ATA TTT TAC AAT TCA CTC TTC TCA AAT GGT ATG AAC    5568
5569  CCA CCA CAA CGA AAT TAT GGG CTT ATG CCA CTA CAA TTT GTG AAT TCG    5616
5617  GTG GTT TAT AAG AAC TTA ACG GCT AAA TCA GAA TGT AAG CTA GGG TTT    5664
5665  GTC CAG CAA TTT AAA CCG TTG TGG AGA GAC ATA GAC ATT GAG ACT AAT    5712
5713  GTT ACA GAT CCA TCA TTT ATC AAT TTT GCA TTG AAT GAA ATC CCA ATG    5760
5761  CAA TCA TTA AAA CGA GTA AAT TGT GAT GTG GAA TTT GAC CGT GGT ATG    5808
5809  CCG ATT GAA CGG GTT ATT CAG GGT TAC ACC CAT ATC TTA CTT GTT GCC    5856
5857  ACT TAC GGA TTA CAG CAA GAT TCA ATA CTG TGG GTG AAG GTA TAT AGG    5904
5905  ACA TCT GAA AAA GTA TTT CAA TTC TTA CTG AGT GCC ATG ATC ATG ATC    5952
5953  TTT GGT TAT GTA AAA ATC CAC AGG AAT GGT TAT ATG TCG ACA AAG GAT    6000
6001  GAA GAG TAC ATA TTG ATG TCT GAC TGC AAG GAA CCT GTA AAC TAT ACA    6048
6049  GCT GTC CCT AAC ATT CTT ACA CGT GTA AGT GAT TTA GTG TCG AAG AAT    6096
6097  CTG AGT CTT ATC CAT CCA GAA GAC CTC AGA AAA GTA AGG TGT GAA ACA    6144
6145  GAT TCC CTG AAT TTG AAG TGC AAT CAT ATT TAT GAG AAA ATA ATT GCC    6192
6193  AGA AAA ATT CCA TTA CAG GTA TCA TCA ACT GAC TCT TTG CTC CTC CAA    6240
6241  TTA GGC GGT GTT ATC AAC TCG GTG GGC TCA ACT GAT CCT AGA GAG GTT    6288
6289  GCA ACA TTA TCT TCT ATT GAG TGT ATG GAC TAT GTT GTC TCA TCA ATT    6336
6337  GAT TTG GCT ATA TTG GAG GCA AAT ATT GTA ATC TCA GAG AGT GCT GGT    6384
6385  CTT GAC CTC GCT TTA ATG TTA GGC CCA TTC AAC TTA AAT AAG CTT AAG    6432
6433  AAA ATT GAC ACA ATC CTT AAG TCA AGC ACC TAT CAG CTA ATC CCG TAC    6480
6481  TGG TTG CGC TAT GAG TAC TCT ATT AAT CCG AGA TCT TTG TCA TTT CTA    6528
6529  ATC ACT AAA TTA CAA CAA TGC CGA ATT TCA TGG TCA GAT ATG ATC ACG    6576
6577  ATT TCT GAA TTT CGT AAG AAA TCC AAG CGG CCT ATA TTT ATC AAA CGA    6624
6625  GTA ATA GGG AAT CAA CAG CTA AAA TCA TTC TTT AAT GAA AGC TCA AGT    6672
6673  ATT GTT TTG ACT CGG GCT GAA GTT AAA GTC TGT ATA AAG TTC CTC GGT    6720
6721  GCA ATC ATC AAG TTG AAA TAA                                       6741
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There are two **ATG** codons (bold and underline) that could be the start codon for APMV 8 Polymerase (L).

Figure 17 (4/4)

SEQ ID NO:13 Protein sequence (1) of APMV-8 Polymerase (L)

```
1     MEGDLYTNMDIKQVDLIIQPEVHLDSPIILNKLALLWRLSGLPMPADL      48
49    RQKSVVMHIPDHILEKSEYRIKHRLGKIKSDITHYCQYFNINLANIDP      96
97    ITHPKSLYWLSRLTIASAGTFRHMKDRILCTVGSEFGHKIQDLFSLLS      144
145   HKLVGNGDLFNQSLSGTRLTASPLSPLCNQFVSDIKSAVTTPWSEARW      192
193   SWLHIKQTMRYLIKQSRTTNSAHLTEIIKEEWGLVGITPDLVILFDRV      240
241   NNSLTALTFEMVLMYSDVLESRDNIVLVGRLSTFLQPVVSRLEVLFDL      288
289   VDSLAKILGDTIYEIIAVLESLSYGSVQLHDASHSHAGSFFSFNMNEL      336
337   DNTLSKRVDPKHKNTIMSIIRQCFSNLDVDQAAEMLCLMRLFGHPMLT      384
385   APDAAAKVRKAMCAPKLVEHDTILQTLSFFKGIIINGYRRSHSGLWPN      432
433   VEPSSIYDDDLRQLYLESAEISHHFMLKNYKSLSMIEFKKSIDYDLHD      480
481   DLSTFLKDRAICRPKSQWDVIFRKSLRRSHTQSQYLDEIKSNRLLIDF      528
529   LDSAEFDPGKEFAYVTTMDYLHDNEFCASYSLKEKEIKTTGRIFAKMT      576
577   RNMRSCQVILESLLSKHICKFFKENGVSMEQLSLTKSLLAMSQLSPKV      624
625   STLQDTASRHVGNSKSQIATSNPSRHHSTPNQMSLSNRKTVVATFLTT      672
673   DLEKYCLQWRYSTIKLFAQALNQLFGIDHGFEWIHLRLMNSTLFVGDP      720
721   YSPPEDPTLEDIDKAPNDDIFIVSPRGGIEGLCQKMWTMISISAIHCV      768
769   AEKIGARVAAMVQGDNQVIAITKELFRGEKACDVRDELDELGQVFFDE      816
817   FKRHNYAIGHNLKLNETIQSQSFFVYSKRIFFEGRLLSQVLKNAAKLC      864
865   MVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFVLNLVYIMTQILF      912
913   DEHYSIVCDHHSVKSLIGSKNHRNLLYSSLIPGQLGGFNFLNISRLFT      960
961   RNIGDPVTCSLSDLKCFIAAGLLPPYVLKNVVLREPGPGTWLTLCSDP      1008
1009  YTLNIPYTQLPTTYLKKHTQRSLLSRAVNPLLAGVQVPNQHEEEEMLA      1056
1057  RFLLDREYVMPRVAHVILESSVLGKRKQIQGLIDTTPTIIRTSLVNLP      1104
1105  VSRKKCEKIINYSLNYIAECHDSLLSQVCFSDNKEYLWSTSLISVETC      1152
1153  SVTIADYLRAVSWSNILGGRNISGVTTPDTIELIQGCLIGENSSCTLC      1200
1201  ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSKTEERKTASMAAI      1248
1249  KGMSHHLRAVLRGTSVFIWAFGDTDINWDNALQIAQSRCNITLDQMRL      1296
1297  LTPIPSSSNIQHRLDDGISTQKFTPASLARITSFVHICNDSQRLEKDG      1344
1345  SSVDSNLIYQQIMLLGLSIFETMYSMDQKWVFNNHTLHLHTGHSCCPR      1392
1393  ELDISLVNPPRHQTPELTSTTTNPFLYDQLPLNQENLTTLEIKTFKFN      1440
1441  ELNIDGLDFGEGIQLLSRCTARLMAECILEEGIGSSVKNEAIVNFDNS      1488
1489  VNWISECLMCDIRSLCVNLGQEILCSLAYQMYYLRIRGRRAILNYLDT      1536
1537  TLQRIPVIQLANIALTISHPEIFRRIVNTGIHNQIKGPYVATTDFIAA      1584
1585  SRDIILSGAREYLSYLSSGQEDCYTFFNCQDGDLTPKMEQYLARRACL      1632
1633  LTLLYNTGHQIPVIRSLTPIEKCKVLTEYNQQIEYADQEFSSVLKVVN      1680
1681  ALLQNPKIDALVSNLYFTTRRVLSNLRSCDKARSYIEYLYTEDFGEKE      1728
1729  DTVQYDIMTTNDIILTHGLFTQIEISYQGNSLHKFLTPDNAPGSLIPF      1776
1777  SISPNSLACDPLHHLLKSVGTSSTSWYKYAIAYAVSEKRSARLGGSLY      1824
1825  IGEGSGSVMTLLEYLEPSVDIFYNSLFSNGMNPPQRNYGLMPLQFVNS      1872
1873  VVYKNLTAKSECKLGFVQQFKPLWRDIDIETNVTDPSFINFALNEIPM      1920
1921  QSLKRVNCDVEFDRGMPIERVIQGYTHILLVATYGLQQDSILWVKVYR      1968
1969  TSEKVFQFLLSAMIMIFGYVKIHRNGYMSTKDEEYILMSDCKEPVNYT      2016
2017  AVPNILTRVSDLVSKNLSLIHPEDLRKVRCETDSLNLKCNHIYEKIIA      2064
2065  RKIPLQVSSTDSLLLQLGGVINSVGSTDPREVATLSSIECMDYVVSSI      2112
2113  DLAILEANIVISESAGLDLALMLGPFNLNKLKKIDTILKSSTYQLIPY      2160
2161  WLRYEYSINPRSLSFLITKLQQCRISWSDMITISEFRKKSKRPIFIKR      2208
2209  VIGNQQLKSFFNESSSIVLTRAEVKVCIKFLGAIIKLK*               2247
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Figure 18

SEQ ID NO:14 Protein sequence (2) of APMV-8 Polymerase (L)

```
   1  MDIKQVDLII QPEVHLDSPI ILNKLALLWR LSGLPMPADL RQKSVVMHIP
  51  DHILEKSEYR IKHRLGKIKS DITHYCQYFN INLANIDPIT HPKSLYWLSR
 101  LTIASAGTFR HMKDRILCTV GSEFGHKIQD LFSLLSHKLV GNGDLFNQSL
 151  SGTRLTASPL SPLCNQFVSD IKSAVTTPWS EARWSWLHIK QTMRYLIKQS
 201  RTTNSAHLTE IIKEEWGLVG ITPDLVILFD RVNNSLTALT FEMVLMYSDV
 251  LESRDNIVLV GRLSTFLQPV VSRLEVLFDL VDSLAKILGD TIYEIIAVLE
 301  SLSYGSVQLH DASHSHAGSF FSFNMNELDN TLSKRVDPKH KNTIMSIIRQ
 351  CFSNLDVDQA AEMLCLMRLF GHPMLTAPDA AAKVRKAMCA PKLVEHDTIL
 401  QTLSFFKGII INGYRRSHSG LWPNVEPSSI YDDDLRQLYL ESAEISHHFM
 451  LKNYKSLSMI EFKKSIDYDL HDDLSTFLKD RAICRPKSQW DVIFRKSLRR
 501  SHTQSQYLDE IKSNRLLIDF LDSAEFDPGK EFAYVTTMDY LHDNEFCASY
 551  SLKEKEIKTT GRIFAKMTRN MRSCQVILES LLSKHICKFF KENGVSMEQL
 601  SLTKSLLAMS QLSPKVSTLQ DTASRHVGNS KSQIATSNPS RHHSTPNQMS
 651  LSNRKTVVAT FLTTDLEKYC LQWRYSTIKL FAQALNQLFG IDHGFEWIHL
 701  RLMNSTLFVG DPYSPPEDPT LEDIDKAPND DIFIVSPRGG IEGLCQKMWT
 751  MISISAIHCV AEKIGARVAA MVQGDNQVIA ITKELFRGEK ACDVRDELDE
 801  LGQVFFDEFK RHNYAIGHNL KLNETIQSQS FFVYSKRIFF EGRLLSQVLK
 851  NAAKLCMVAD HLGENTVSSC SNLSSTIARL VENGFEKDTA FVLNLVYIMT
 901  QILFDEHYSI VCDHHSVKSL IGSKNHRNLL YSSLIPGQLG GFNFLNISRL
 951  FTRNIGDPVT CSLSDLKCFI AAGLLPPYVL KNVVLREPGP GTWLTLCSDP
1001  YTLNIPYTQL PTTYLKKHTQ RSLLSRAVNP LLAGVQVPNQ HEEEEMLARF
1051  LLDREYVMPR VAHVILESSV LGKRKQIQGL IDTTPTIIRT SLVNLPVSRK
1101  KCEKIINYSL NYIAECHDSL LSQVCFSDNK EYLWSTSLIS VETCSVTIAD
1151  YLRAVSWSNI LGGRNISGVT TPDTIELIQG CLIGENSSCT LCESHDDAFT
1201  WMHLPGPLYI PEPSVTNSKM RVPYLGSKTE ERKTASMAAI KGMSHHLRAV
1251  LRGTSVFIWA FGDTDINWDN ALQIAQSRCN ITLDQMRLLT PIPSSSNIQH
1301  RLDDGISTQK FTPASLARIT SFVHICNDSQ RLEKDGSSVD SNLIYQQIML
1351  LGLSIFETMY SMDQKWVFNN HTLHLHTGHS CCPRELDISL VNPPRHQTPE
1401  LTSTTTNPFL YDQLPLNQEN LTTLEIKTFK FNELNIDGLD FGEGIQLLSR
1451  CTARLMAECI LEEGIGSSVK NEAIVNFDNS VNWISECLMC DIRSLCVNLG
1501  QEILCSLAYQ MYYLRIRGRR AILNYLDTTL QRIPVIQLAN IALTISHPEI
1551  FRRIVNTGIH NQIKGPYVAT TDFIAASRDI ILSGAREYLS YLSSGQEDCY
1601  TFFNCQDGDL TPKMEQYLAR RACLLTLLYN TGHQIPVIRS LTPIEKCKVL
1651  TEYNQQIEYA DQEFSSVLKV VNALLQNPKI DALVSNLYFT TRRVLSNLRS
1701  CDKARSYIEY LYTEDFGEKE DTVQYDIMTT NDIILTHGLF TQIEISYQGN
1751  SLHKFLTPDN APGSLIPFSI SPNSLACDPL HHLLKSVGTS STSWYKYAIA
1801  YAVSEKRSAR LGGSLYIGEG SGSVMTLLEY LEPSVDIFYN SLFSNGMNPP
1851  QRNYGLMPLQ FVNSVVYKNL TAKSECKLGF VQQFKPLWRD IDIETNVTDP
1901  SFINFALNEI PMQSLKRVNC DVEFDRGMPI ERVIQGYTHI LLVATYGLQQ
1951  DSILWVKVYR TSEKVFQFLL SAMIMIFGYV KIHRNGYMST KDEEYILMSD
2001  CKEPVNYTAV PNILTRVSDL VSKNLSLIHP EDLRKVRCET DSLNLKCNHI
2051  YEKIIARKIP LQVSSTDSLL LQLGGVINSV GSTDPREVAT LSSIECMDYV
2101  VSSIDLAILE ANIVISESAG LDLALMLGPF NLNKLKKIDT ILKSSTYQLI
2151  PYWLRYEYSI NPRSLSFLIT KLQQCRISWS DMITISEFRK KSKRPIFIKR
2201  VIGNQQLKSF FNESSSIVLT RAEVKVCIKF LGAIIKLK
```

Figure 19A (1/2)

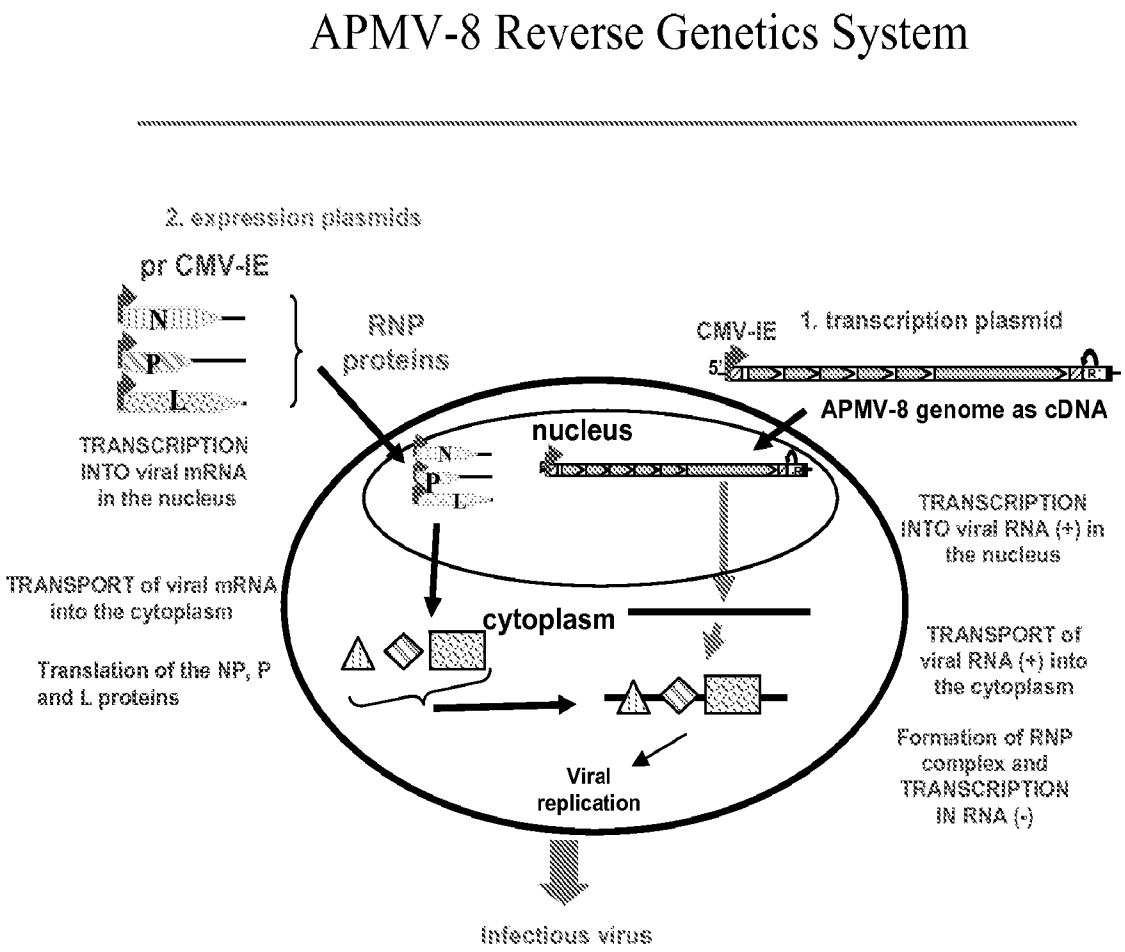


Figure 19B (2/2)

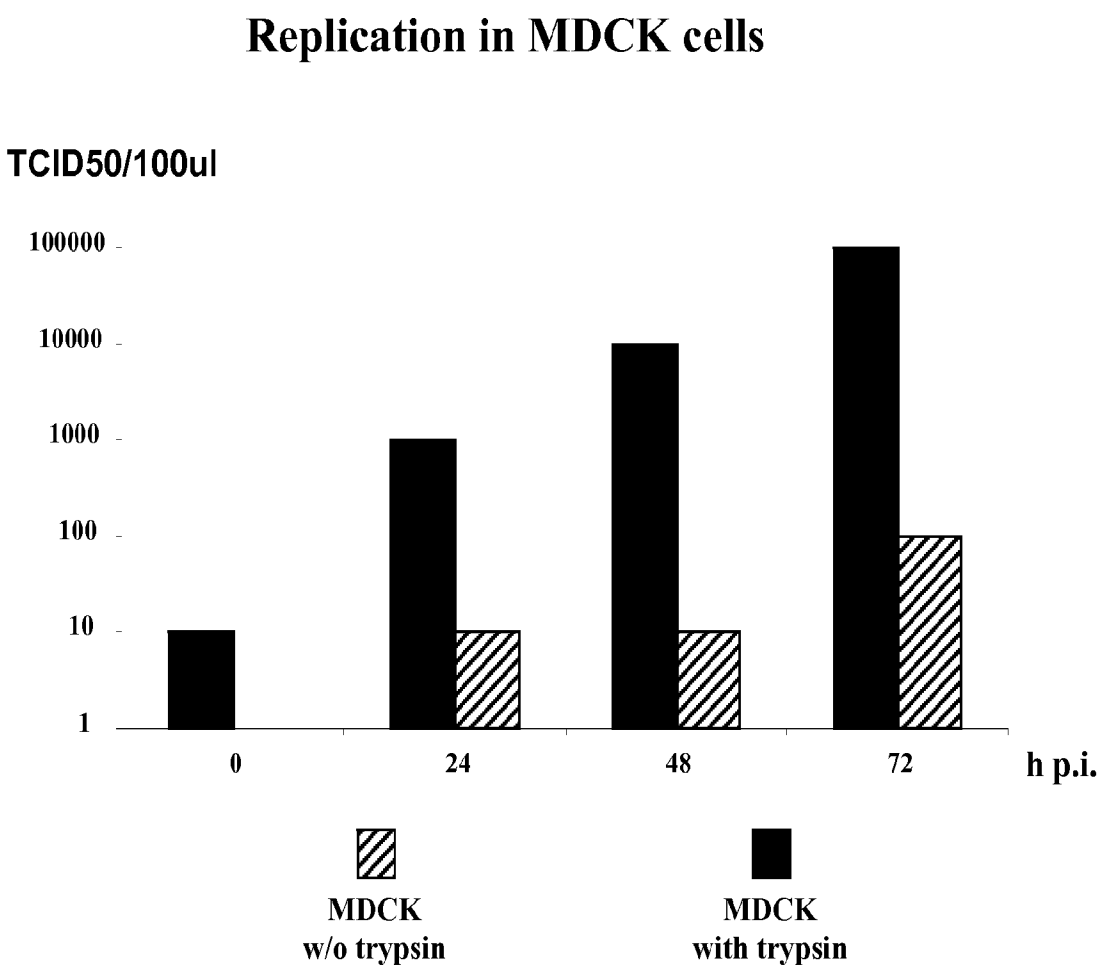


Figure 20

Commercial broiler 2 weeks after APMV-8 vaccination

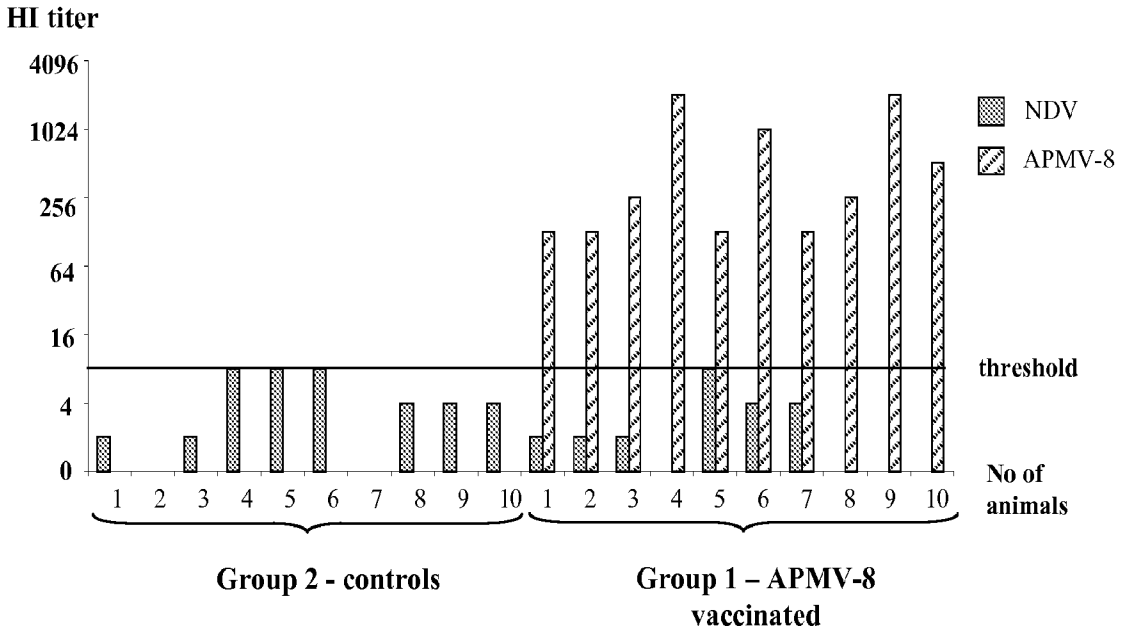


Figure 21

Commercial broiler 4 weeks after APMV-8 vaccination

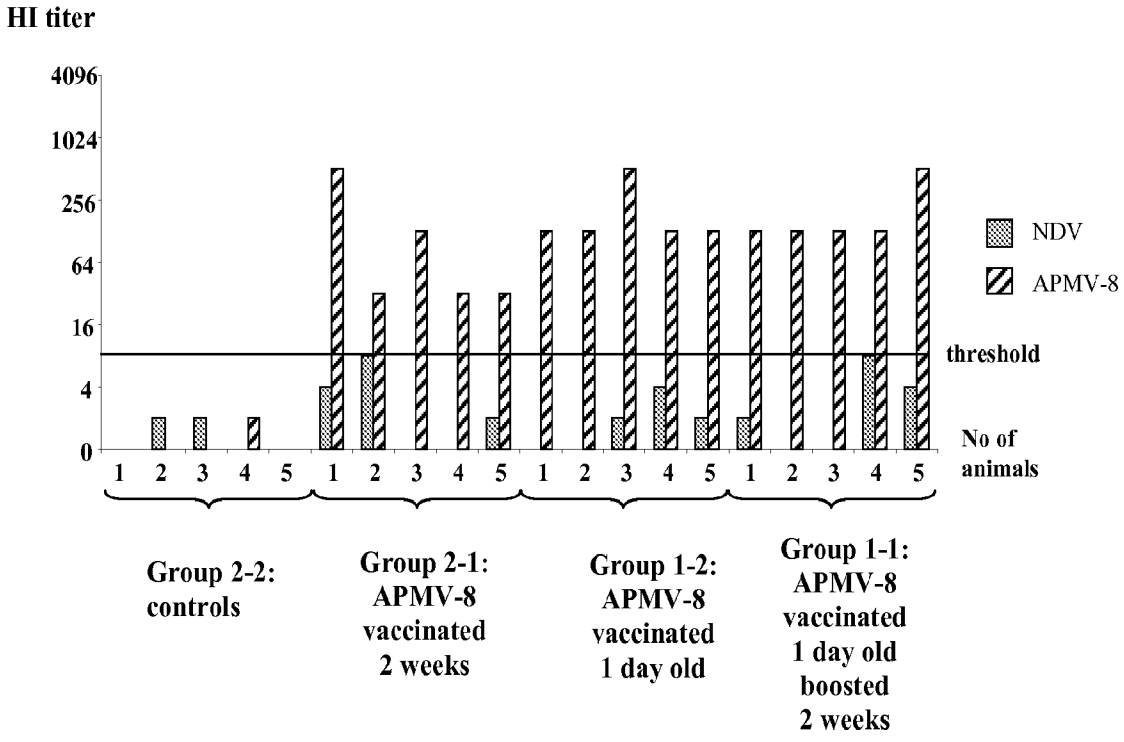
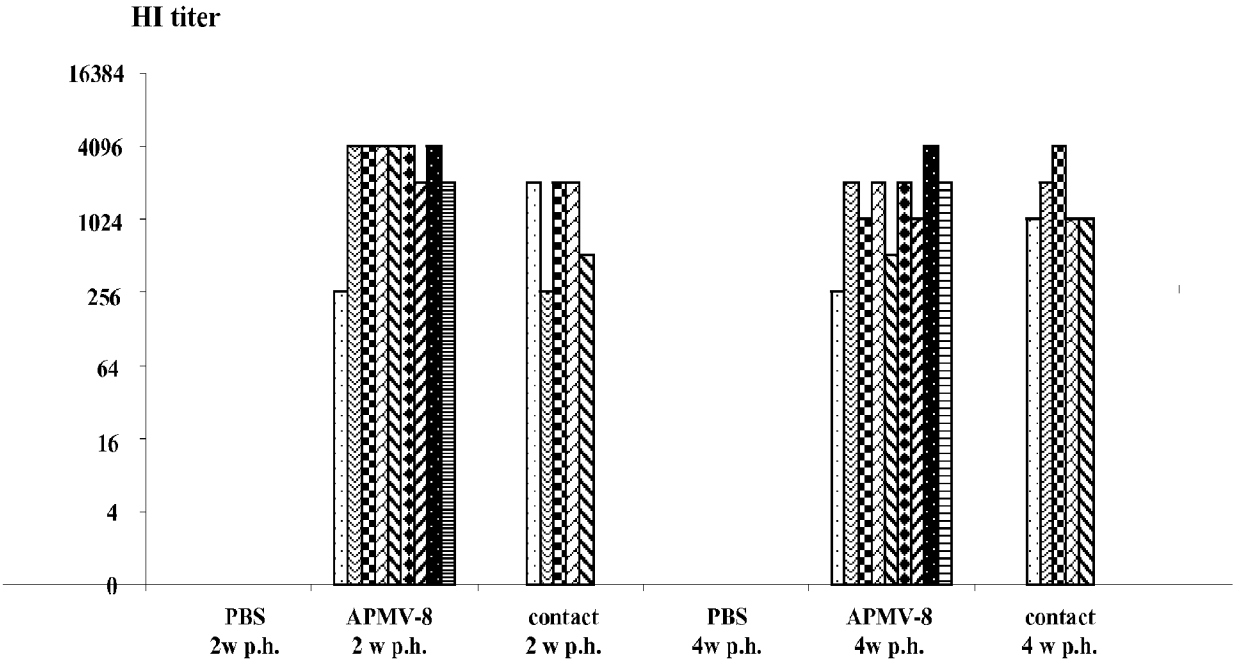


Figure 22

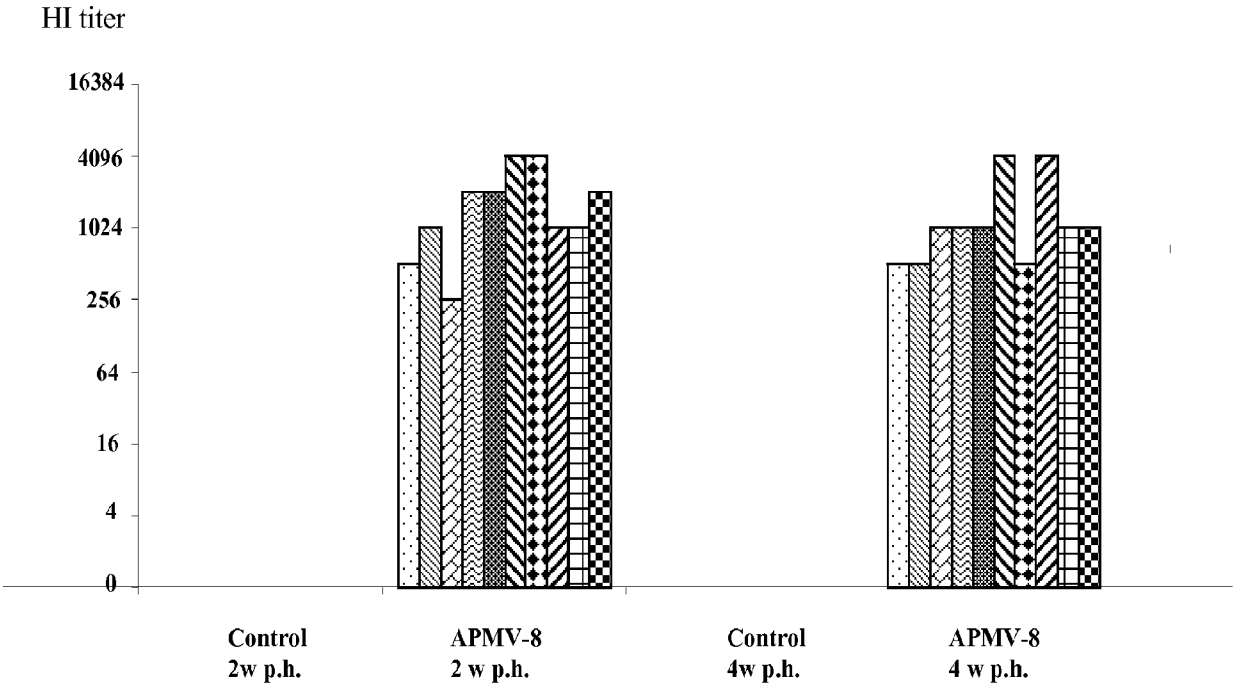
Study 1, *in ovo* vaccinated at day 18



p.h. = post hatch
w = weeks

Figure 23

Study 2: *in ovo* vaccinated at day 19



p.h. = post hatch
w = weeks

Figure 24

Study 3: *in ovo* vaccinated at day 18

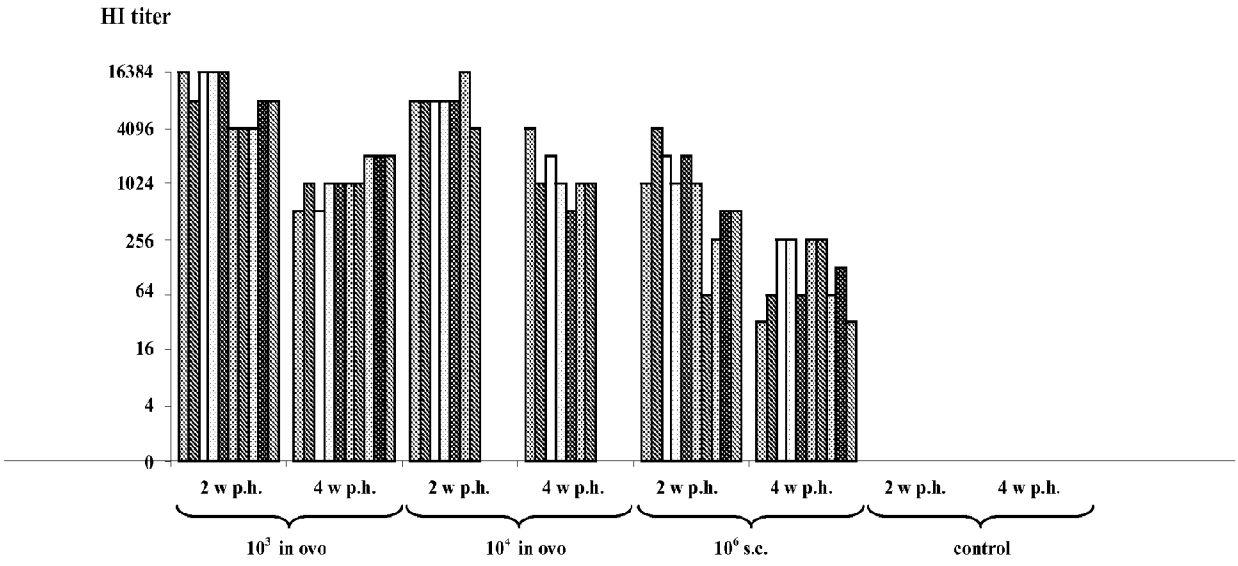


Figure 25 (1/5)

5'-part, full length genome (5'-FLG) SEQ ID NO:47:

ggGCGGCCGC*GTTGACATTGATTATTGACTAGTTATTAATAGTAATCAATTACGGGGTCATTAGTTCATAGCCCATATA*
TGGAGTTCCGCGTTACATAACTTACGGTAAATGGCCCGCCTGGCTGACCGCCCAACGACCCCCGCCCATTGACGTCAAT
AATGACGTATGTTCCCATAGTAACGCCAATAGGGACTTTCCATTGACGTCAATGGGTGGAGTATTTACGGTAAACTGCC
CACTTGGCAGTACATCAAGTGTATCATATGCCAAGTACGCCCCCTATTGACGTCAATGACGGTAAATGGCCCGCCTGGC
ATTATGCCCAGTACATGACCTTATGGGACTTTCCTACTTGGCAGTACATCTACGTATTAGTCATCGCTATTACCATGGT
GATGCGGTTTTGGCAGTACATCAATGGGCGTGGATAGCGGTTTGACTCACGGGGATTTCCAAGTCTCCACCCCATTGAC
GTCAATGGGAGTTTGTTTTGGCACCAAAATCAACGGGACTTTCCAAAATGTCGTAACAACTCCGCCCCATTGACGCAAA
*TGGGCGGTAGGCGTGTACGGTGGGAGGTCTATATAAGCAGAGCT*CCCGGGtgttaagcgtctgatgagtccgtgaggac
gaaactataggaaaggaattcctatagtcACCAAACAAGGAATGCAAGACCAACGGGAACTTTAAATAAAACAATCGAA
TTATTGGGGGCGAAGCAAGTGGATCTCGAGCTCGAGGCCGAAACCCTGAATTTCACTGGAGGTTTTGAATAGGTCGCTA
TAGGACTCAATATGTCATCTGTGTTCAATGAGTATCAGGCGCTTCAAGAACAACTTGTGAAGCCGGCTGTCAGGAGACC
TGATGTTGCCTCAACGGGTTTACTCAGAGCGGAAATACCTGTCTGTGTTACATTATCTCAAGACCCCGGTGAGAGATGG
AGCCTTGCTTGCTTGAATATTAGATGGCTTGCGAGTGATTCATCAACCACACCAATGAAGCAAGGAGCAATATTGTCAC
TGCTGAGTCTACATTCAGACAATATGCGAGCTCACGCAACATTAGCAGCAAGGTCTGCAGATGCTTCACTCACCATACT
TGAGGTAGATGAAGTAGATATTAGCAACTCACTAATCAAATTCAACGCCAGAAGTGGTGTATCTGACAAACGCTCAAAT
CAATTGCTTGCAATTGCGGATGACATCCCCAAAAGTTGCAGTAATGGGCATCCATTTCTTGACACAGACATTGAGACCA
GAGACCCGCTCGATCTATCAGAGACTATAGATCGCCTGCAGGGTATTGCAGCTCAGATATGGGTGTCAGCCATAAAGAG
CATGACAGCGCCTGACACCGCATCAGAGTCAGAAAGTAAGAGGCTGGCCAAATATCAACAACAAGGCCGACTGGTTAAG
CAAGTACTCTTGCATTCTGTAGTCAGGACAGAATTTATGAGAGTTATTCGGGGCAGCTTGGTACTGCGCCAGTTTATGG
TTAGCGAGTGCAAGAGGGCTTCAGCCATGGGCGGAGACACATCTAGGTACTATGCTATGGTGGGTGACATCAGTCTTTA
CATCAAGAATGCAGGATTGACTGCATTTTTCCTCACCCTGAAGTTCGGAGTTGGTACCCAGTATCCAACCTTAGCAATG
AGTGTTTTCTCCAGTGACCTTAAAAGGCTTGCTGCACTCATCAGGCTATACAAAACCAAGGGAGACAATGCACCATACA
TGGCATTCCTGGAGGACTCCGATATGGGAAATTTTGCTCCAGCAAATTATAGCACAATGTACTCTTATGCCATGGGCAT
TGGGACAATTCTGGAAGCATCTGTATCTCGATACCAGTATGCCAGAGACTTTACCAGTGAGAATTATTTCCGTCTTGGA
GTTGAGACAGCCCAAAGCCAGCAGGGAGCATTTGACGAGAGAACAGCCCGAGAAATGGGCTTGACTGAGGAATCAAAAC
AGCAGGTTAGATCACTGCTAATGTCAGTAGACATGGGTCCCAGTTCAATTCATGAGCCATCTCGCCCTGCATTTATCAG
TCAAGAAGAAAATAGGCAGCCTGCCCAGAACTTGTCAGATACTCAGGGTCAGACCAAGCCAGTCCCGAAGCAGCCCGCA
CCAAGGGCCGACTCAGATGACATTGATCCATACGAGAACGGGCTAGAATGGTAATTCAACCACCCCGACACATCCACCT
ATACACCAATTCCGTGACATATTAACCCAATCAAACATTTCATAAACTATAGTAGTCATTGATTTAAGAAAAAATTGGG
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GCCCTCGCATCCAGAATCTCCCTGGGTCCCAGGCGGCAACTCAACAGGCGACCCACCCATTGGCAGGGGACACCCCGAA
CATGCAAGCACAGACAAAAGCCCTGGCGAAGCCACATCAAGAGGCAATCAATCCTGGCAACCAGGACACAGGAGAGAGT
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GCCAAAGCTCAGACTTCTTCCGGTGTGAGTAAGGGTGAAATAGAAGGATTGATTGCATTGGTGGAAACATTAGTTGACA
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CGTCTTCGCTCCTATCATTCCCGTTGGTACTAAAAGAGACAGACAGAGGCACAAAGGAGCTTCAACCACAGGTAAGGGT
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TAGGTGCGATCCGAATGATGGCTGATGTTAATACCATCTCTAATGACGCACTAGCGCTGGAGATCACTGTTAAGAAATC
TGCAACTTCTCAAGAGAAAATGACGGTGATGTTCCACAATAGCCCCCCTTCATTGAGAACTGCAATAACTATCCGAGCA
GGAGGTTTCATCTCGAATGCAGACGAGAATATAAAATGTGCCAGCAAATTGACTGCAGGAGTGCAGTACATATTCCGCC
CAATGTTTGTTTCAATCACTAAATTACACAATGGCAAACTATATAGGGTGCCCAAAAGCATCCACAGCATCTCATCCAC
TCTACTGTATAGTGTGATGTTGGAGGTAGGATTCAAAGTGGATATTGGGAAGGATCATCCCCAGGCAAAGATGCTGAAG

Figure 25 (2/5)

AAGGTCACAATCGGCGATGCAGACACATACTGGGGGTTTGCATGGTTCCACCTGTGCAATTTCAAAAAGACATCCTCTA
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GGGTCCGACTATTGTGGTCCAAATCACTGGCAAGAGCAGCAAATATGCTCAAGGATTTTTTTCCTCCAATGGTACTTGT
TGTCTCCCAATCAGCAGATCTGCACCAGAGCTTGGGAAGCTTCTGTGGTCTTGTTCAGCAACTATAGGTGACGCAACAG
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CAATTTCCTAATTATAAAAAATTGCTTTAAAGGTTATTGACGAGTCGGGGGCGAAATCTTGCCACTTAGTCTGCAGTCA
ATCTTAGAATCTACATATTGAACT**ATGGGTCAAATATCAGTATATCTAATTAATAGCGTGCTATTATTGCTGGTATATC**
CTGTGAATTCGATTGACAATACACTCATTGCCCCAATCGGAGTTGCCAGCGCAAATGAATGGCAGCTTGCTGCATATAC
AACATCACTTTCAGGGACAATTGCCGTGCGATTCCTACCTGTGCTCCCGGATAATATGACTACCTGTCTTAAAGAAACA
ATCACTACATACAATAATACTGTCAACAACATCTTAGGCCCACTCAAATCCAATCTGGATGCACTGCTCTCATCTGAGA
CTTATCCCCAGACAAGATTAATTGGGGCAGTTATAGGTTCAATTGCTCTCGGTGTTGCAACATCGGCTCAAATCACTGC
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GCGGTCAAGGAGCTTAGTAGTGGGTTACAACAAACAGCTATTGCACTTGGTAAGATACAGAGTTTTGTGAATGAGGAAA
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GGTGGCAACATGGCAATGCTTACTCAGAAGATTGGAATTAAACAGCAAGACGTTAATTCGCTATATGAAGCCGGACTAA
TCACAGGACAAGTCATTGGTTATGACTCTCATTACCAGCTGCTGGTCATCCAGGTCAATTATCCAAGCATTTCTGAGGT
CACTGGTGTACGTGCGACAGAATTAGTCACTGTTAGTGTAACAACAGACAAGGGTGAAGGGAAAGCAATTGTACCCCAA
TTTGTAGCTGAAAGTCGGGTGACTATTGAAGAGCTTGATGTCGCATCTTGTAAATTCAGCAGCACGACCCTATATTGCA
GGCAGGTCAACACAAGGGCACTTCCCCCGCTAGTAGCTAGCTGTCTTCGAGGTAACTATGATGCCGCGG

Restriction enzyme cleavage sites: upper case letter, bold and underlined
Human cytomegalovirus immediate early promoter: upper case letter, bold, italics
Hammerhead ribozyme sequence: lower case
Open reading frame for the viral proteins: upper case letter, bold
Non-coding sequences: upper case letter

Not I: **GCGGCCGC**
Bmt I: **GCTAGC**
Sac II: **CCGCGG**

3'-part, full length genome (3'-FLG) SEQ ID NO:48:

GCGGCCGCCAGGTCAACACAAGGGCACTTCCCCCGCTAGTAGCTAGCTGTCTTCGAGGTAACTATGATGATTGTCAATA
TACCACAGAGATTGGAGCATTATCATCCCGGTATATAACACTAGATGGGGGGGTCTTAGTTAATTGCAAGTCAATTGTT
TGTAGGTGCCTTAATCCAAGTAAGATCATCTCTCAAAATACAAACGCTGCAGTAACATATGTTGATGCCACAATCTGCA
AAACAATTCAATTGGATGATATACAACTCCAGCTGGAAGGGTCACTATCATCAGTTTATGCAAGAAACATCTCAATTGA
GATCAGTCAGGTGACCACATCCGGGTCTTTAGATATCAGCAGTGAGATAGGAAACATCAATAATACGGTGAATCGTGTG
GAGGATTTAATTCACCAATCAGAGGAATGGCTGGCAAAGGTTAACCCACACATTGTTAATAATACAACACTAATTGTAC
TCTGTGTGTTAAGTGCGCTTGCTGTGATCTGGCTGGCAGTATTAACGGCTATTATAATATACTTGAGAACAAAGTTGAA
GACTATATCGGCATTAGCTGTAACCAATACAATACAGTCTAACCCCTATGTTAACCAAACGAAACATGAATCTAAGTTT
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CACTAATTATTAATATACTCGTGATTAGATGATAACGTTAAAAGTCTTAGATATTTAATAAAAAATGTAACCTGGGGGC
GACCCATTTATAGGTGAGTATATATTAGGAAGTCCTTATATTGCACTGTGATTTCAAACAATTATATTACCTCATATCT
ACCTTGTCTAAAGACATC**ATGAGTAACATTGCATCCAGTTTAGAAAACATTGTAGAGCAGGATAGTCGAAAAACAACTT**
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TGGAAATTTGAAAATTCCTTCTGTAGGGGATCTGGCTGATGAAGTGGTGACACCCTTGAAAACCACTCTGTCAGATACA
CTCAGGAATCCAATTAACCAGATAAATGATATATTTAGGATTGTTGCCCTTGATATTCCATTGCAAGTGACCAGTATCC
AAAAAGACCTTGCAAGTCAATTTAACATGTTGATAGATAGTTTAAATGCTATCAAATTAGGCAACGGGACCAACCTTAT
CATACCTACATCAGACAAGGAGTATGCAGGAGGAATTGGAAACCCTGTATTTACTGTCGATGCTGGAGGTTCTATAGGA
TTCAAACAGTTTAGCTTAATAGAACATCCGAGCTTTATTGCTGGACCTACAACGACCCGAGGCTGTACAAGAATACCCA
CTTTTCACATGTCAGAAAGTCATTGGTGCTACTCACACAACATCATCGCTGCTGGCTGTCAAGATGCCAGTGCATCCAG
TATGTATATCTCAATGGGAGTTCTCCATGTGTCCTCATCTGGCACTCCCATTTTTCTTACTACTGCAAGTGAGCTGATA
GACGATGGAGTTAACCGTAAGTCATGCAGCATTGTAGCAACCCAATTTGGCTGTGACATTTTGTGCAGTATTGTCACAG

Figure 25 (3/5)

AGAAGGAGGGAGATGATTACTGGTCTGATACTCCGACTCCAATGCGCCACGGCCGTTTTTCATTCAATGGTAGTTTTGT
AGAAGCCGAACTACCAGTGTCCAGTATGTTCTCATCATTCTCTGCCAACTACCCTGCTGTGGGATCAGGCGAAATTGTA
AAAGATAGAATATTATTCCCAATTTACGGAGGTATAAAGCAGACTTCACCAGAGTTTACCGAATTAGTGAAATACGGAC
TCTTTGTATCAACACCTACAACTGTGTGCCAGAGTAGCTGGACTTATGACCAGGTAAAAGCTGCGTATAGGCCAGATTA
CATATCAGGCCGGTTCTGGGCACAAGTGATACTCAGCTGCGCTCTTGATGCAGTCGACTTATCAAGTTGTATTGTAAAG
ATTATGAATAGCAGCACAGTGATGATGGCAGCGGAAGGAAGGATAATGAAGATAGGGATTGATTACTTTTACTATCAGC
GGTCATCTTCTTGGTGGCCATTGGCATTTGTCACAAAACTAGACCCGCAAGAGTTGGCAGACACAAACTCAATATGGCT
GACCAATTCCATACCAATCCCGCAATCAAAGTTCCCTCGGCCTTCATATTCAGAAAATTATTGCACAAAGCCAGCAGTT
TGCCCTGCTACTTGTGTCACTGGTGTGTACTCTGATATTTGGCCCCTGACCTCATCTTCATCACTCCCGAGCATAATTT
GGATCGGCCAGTACCTTGATGCTCCTGTTGGAAGGACTTATCCTAGATTTGGAATTGCAAATCAGTCACACTGGTACCT
CCAAGAAGATATTCTACCCACTTCCACCGCAAGTGCGTATTCAACCACTACATGTTTTAAGAATACTGCCAGGAATAGA
GTGTTCTGCGTCACCATTGCCGAATTTGCAGATGGGTTGTTTGGAGAGTACAGGATAACACCTCAGTTGTACGAATTAG
TGAGAAATAATTGAATAACAATAATTTTGGGACTCATTTTGTCGCAAAGTGAAATTGTCATCTTTAAAAATAATCAATT
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GGGTCAGTTCAACTACATGATGCAAGTCACTCTCATGCAGGGTCTTTTTTTTCATTTAACATGAATGAACTTGATAACA
CACTATCAAAGAGGGTAGATCCGAAACACAAGAACACTATAATGAGCATTATAAGACAATGCTTTTCTAATCTAGATGT
TGATCAAGCTGCAGAGATGCTATGCCTGATGAGATTATTCGGACACCCAATGTTAACTGCACCGGATGCAGCAGCCAAA
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AGTGGGATGTCATATTTCGTAAGTCTTTACGCAGATCTCATACGCAGTCCCAGTATCTGGACGAAATTAAGAGCAACCG
ATTGCTAATTGATTTTCTTGATTCTGCTGAATTTGACCCTGGAAAAGAATTTGCATATGTAACCACAATGGATTATTTG
CACGATAATGAATTTTGTGCTTCATATTCTCTAAAGGAAAAGGAGATCAAAACTACTGGGAGGATATTTGCAAAAATGA
CACGCAATATGAGAAGTTGCCAAGTAATACTTGAATCTTTGTTATCAAAGCATATATGCAAGTTCTTCAAAGAGAATGG
CGTTTCGATGGAGCAATTGTCATTGACCAAGAGTCTACTTGCAATGTCTCAACTCTCACCAAAAGTCTCGACTTTGCAG
GACACTGCATCACGTCATGTAGGTAACTCAAAATCTCAGATTGCAACCAGCAACCCATCTCGGCATCACTCGACACCCA
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TTAGCCAGGTCTGCTTCAGTGATAATAAGGAATACTTGTGGTCAACCTCCTTAATATCAGTTGAGACCTGTAGTGTGAC
AATTGCGGACTATCTGAGAGCTGTCAGCTGGTCTAATATATTAGGGGGAAGAAACATATCCGGGGTGACTACACCTGAT

Figure 25 (4/5)

ACTATTGAATTAATTCAAGGTTGTTTAATAGGTGAAAATTCTAGTTGTACTCTTTGTGAATCGCATGATGACGCATTCA
CGTGGATGCACTTGCCTGGCCCACTTTACATCCCTGAACCATCAGTTACTAACTCTAAAATGCGTGTGCCATATCTGGG
TTCAAAAACAGAGGAGCGGAAAACAGCCTCAATGGCAGCAATAAAAGGAATGTCACATCACCTGCGTGCAGTCTTAAGA
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AATCAGCACGCAGAAATTTACTCCTGCAAGCCTTGCTCGAATCACATCCTTCGTTCACATCTGTAATGACAGCCAGAGG
TTAGAGAAGGATGGCTCATCTGTCGACTCAAACTTGATTTACCAGCAAATTATGTTACTTGGACTCAGCATCTTTGAAA
CAATGTACTCAATGGACCAAAAGTGGGTATTCAATAACCATACCTTGCATTTGCACACTGGACACTCCTGTTGTCCAAG
GGAACTAGACATAAGTTTGGTGAACCCGCCGAGACATCAGACCCCGGAGCTGACTAGCACAACAACCAACCCGTTCCTA
TATGATCAGCTCCCATTAAATCAAGAAAACTTGACAACACTTGAGATTAAGACATTTAAATTCAATGAGCTCAACATTG
ATGGTTTAGATTTTGGTGAAGGAATACAATTATTGAGTCGTTGTACTGCAAGATTAATGGCAGAATGTATTCTAGAGGA
GGGAATAGGCTCGTCAGTTAAAAATGAAGCAATTGTCAATTTTGATAATTCAGTCAATTGGATTTCAGAGTGCCTAATG
TGTGATATTCGCTCACTTTGTGTTAATTTAGGTCAAGAGATACTATGTAGCCTGGCATACCAAATGTATTACTTGCGAA
TCAGGGGTAGACGGGCCATTCTTAATTACTTGGACACAACTTTGCAAAGGATCCCTGTGATACAATTAGCCAACATTGC
ACTCACCATTTCGCACCCTGAGATATTTCGCAGAATTGTCAACACCGGGATCCATAACCAGATTAAGGGCCCATATGTG
GCAACAACGGATTTCATAGCTGCAAGTAGAGATATCATATTATCAGGTGCAAGGGAGTATCTATCTTATTTAAGCAGTG
GGCAGGAAGACTGTTACACATTCTTCAACTGTCAAGATGGGGATCTTACTCCAAAAATGGAACAGTATCTTGCAAGGAG
GGCATGCCTTTTAACATTATTGTATAATACTGGGCACCAGATCCCCGTTATCCGATCACTGACGCCAATAGAGAAGTGC
AAGGTGCTCACAGAATACAATCAACAAATTGAGTACGCAGATCAAGAGTTTAGCTCTGTACTAAAAGTGGTCAATGCAC
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ATGTGATAAGGCTAGATCATATATTGAATATTTGTACACTGAGGACTTCGGAGAGAAAGAGGATACAGTACAATATGAC
ATCATGACAACAAACGATATCATACTTACTCATGGTCTATTCACACAGATCGAAATATCTTATCAAGGGAATAGTCTCC
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TCTTCATCACTTGCTCAAGTCGGTCGGTACATCAAGCACAAGTTGGTACAAGTATGCAATCGCCTATGCAGTGTCTGAA
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AGCCATCTGTTGACATATTTTACAATTCACTCTTCTCAAATGGTATGAACCCACCACAACGAAATTATGGGCTTATGCC
ACTACAATTTGTGAATTCGGTGGTTTATAAGAACTTAACGGCTAAATCAGAATGTAAGCTAGGGTTTGTCCAGCAATTT
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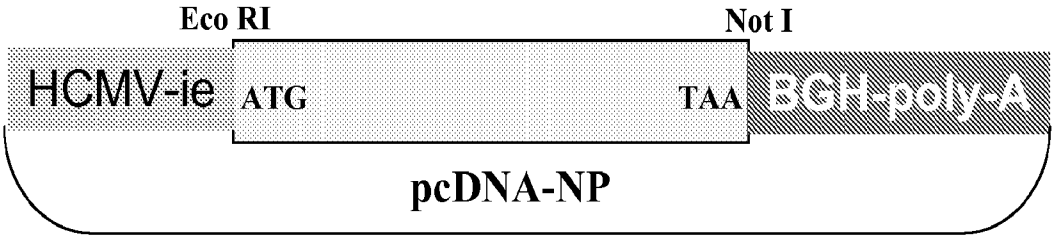
CAAAGGATGAAGAGTACATATTGATGTCTGACTGCAAGGAACCTGTAAACTATACAGCTGTCCCTAACATTCTTACACG
TGTAAGTGATTTAGTGTCGAAGAATCTGAGTCTTATCCATCCAGAAGACCTCAGAAAAGTAAGGTGTGAAACAGATTCC
CTGAATTTGAAGTGCAATCATATTTATGAGAAAATAATTGCCAGAAAAATTCCATTACAGGTATCATCAACTGACTCTT
TGCTCCTCCAATTAGGCGGTGTTATCAACTCGGTGGGCTCAACTGATCCTAGAGAGGTTGCAACATTATCTTCTATTGA
GTGTATGGACTATGTTGTCTCATCAATTGATTTGGCTATATTGGAGGCAAATATTGTAATCTCAGAGAGTGCTGGTCTT
GACCTCGCTTTAATGTTAGGCCCATTCAACTTAAATAAGCTTAAGAAAATTGACACAATCCTTAAGTCAAGCACCTATC
AGCTAATCCCGTACTGGTTGCGCTATGAGTACTCTATTAATCCGAGATCTTTGTCATTTCTAATCACTAAATTACAACA
ATGCCGAATTTCATGGTCAGATATGATCACGATTTCTGAATTTCGTAAGAAATCCAAGCGGCCTATATTTATCAAACGA
GTAATAGGGAATCAACAGCTAAAATCATTCTTTAATGAAAGCTCAAGTATTGTTTTGACTCGGGCTGAAGTTAAAGTCT
GTATAAAGTTCCTCGGTGCAATCATCAAGTTGAAATAATTTCTGCGATTTTAAAGGGGTGTAATGTTCTAATTTGCACT
TGAAGTAATATAGCTTGTAATCATTCGCTAGGGGATAGGATAATTTCTCTAACCTCTGAATCTATATTCCTAGAGTATA
ACAAATATATACATAATAAAAATGATTTTAAGAAAAAATCCGACACTCAAAGAAAATTGGTGCCTGTAATATTCTTCTT
GCCAAATGATTGTGAAGTGTCTAGCCTAACTTAAAACAATCGTATTCGATAGGGAAGAATGATATATAAAATAACTAAT
AAAAAATTGTATTAGTAAAAATTACCGTATTTCCTGTATTCCATTTCTGGTgggtcggcatggcatctccacctcctcg
cggtccgacctgggcatccgaaggaggacgcacgtccactcggatggctaagggagggcg**ctagagctcgctgatcagc**
ctcgactgtgccttctagttgccagccatctgttgtttgcccctcccccgtgccttccttgaccctggaaggtgccact
cccactgtcctttcctaataaaatgaggaaattgcatcgcattgtctgagtaggtgtcattctattctgggggggtgggg
tggggcaggacagcaagggggaggattgggaagacaatagcaggcatgctggggatgcggtgggctctatgCCGCGG

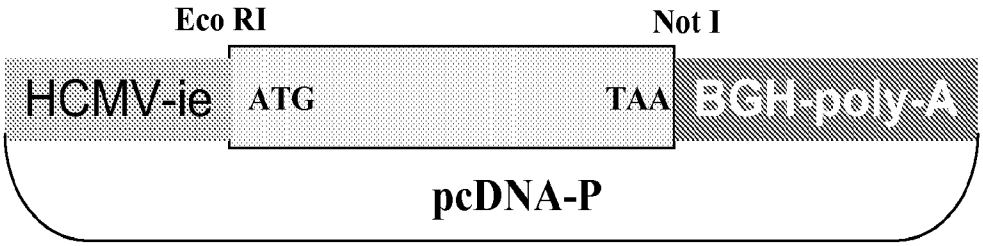
Restriction enzyme cleavage sites: upper case letter, bold and underlined
Human cytomegalovirus immediate early promoter: upper case letter, bold, italics
Hepatitis delta ribozyme sequence: lower case
Open reading frame for the viral proteins: upper case letter, bold typed
Non-coding sequences: upper case letter
Bovine growth hormone poly A sequence: lower case letter, underlined

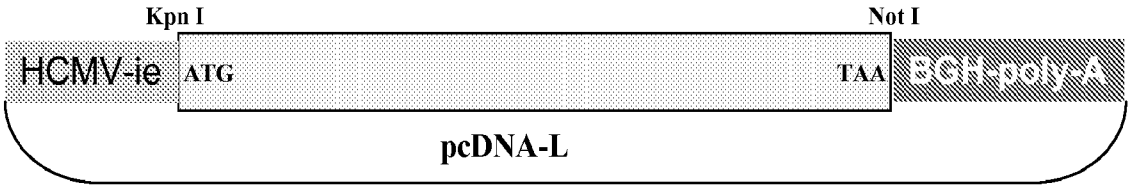
Not I: **GCGGCCGC**
Bmt I: **GCTAGC**
Sac II: **CCGCGG**

Figure 26

Plasmid encoding the proteins which are part of the riboprotein complex of APMV-8







Plasmid encoding the T7 polymerase

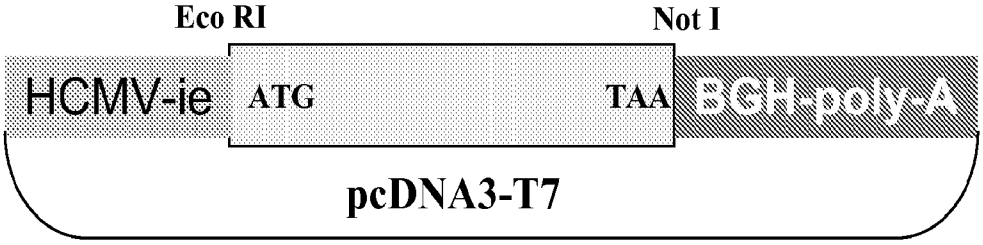
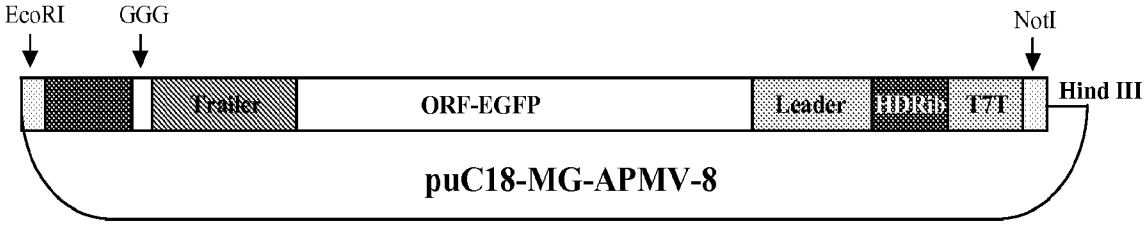


Figure 27

Plasmid containing a minigenome for APMV-8



T7Pro:	T7 promoter
GGG:	base triplet consisting of three G
Trailer:	complete sequence of the trailer sequence of the APMV-8 virus
Leader:	complete sequence of the leader sequence of the APMV-8 virus
ORF-EGFP:	open reading frame of the enhanced green fluorescent protein
HDRib:	hepatitis delta ribozyme sequence
T7T:	T7 terminator

Restriction enzyme cleavage sites: EcoRI, NotI, HindIII

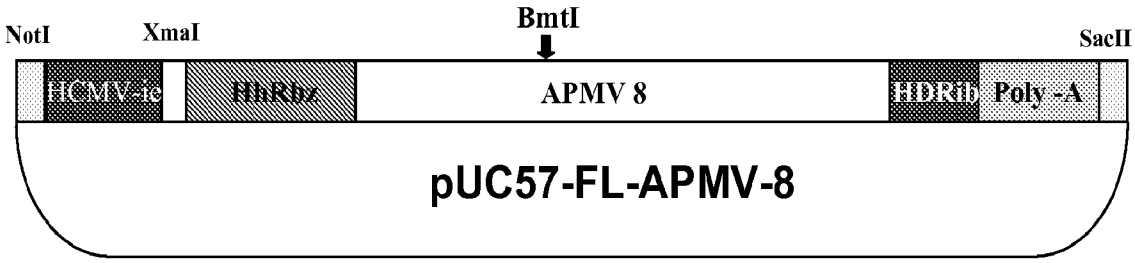
Plasmid encoding the EGFP under the control of the SITE promoter

T7Pro:	T7 promoter
Site:	internal ribosome entry site
ORF-EGFP:	open reading frame of the enhanced green fluorescent protein

Restriction enzyme cleavage sites: BamHI, NotI

Figure 28

Plasmid containing the full length sequence of APMV-8



HCMV-ie:	human cytomegalovirus immediate early promoter
AMPV 8:	full length sequence of APMV 8 in antigenomic orientation
HhRbz:	hammerhead ribozyme sequence
HDRib:	hepatitis delta ribozyme sequence
Poly A:	bovine growth hormone polyadenylation signal sequence

Restriction enzyme cleavage sites: Not I, XmaI, BmtI, SacII

Figure 29

Construction of the minigenome

Eco RI

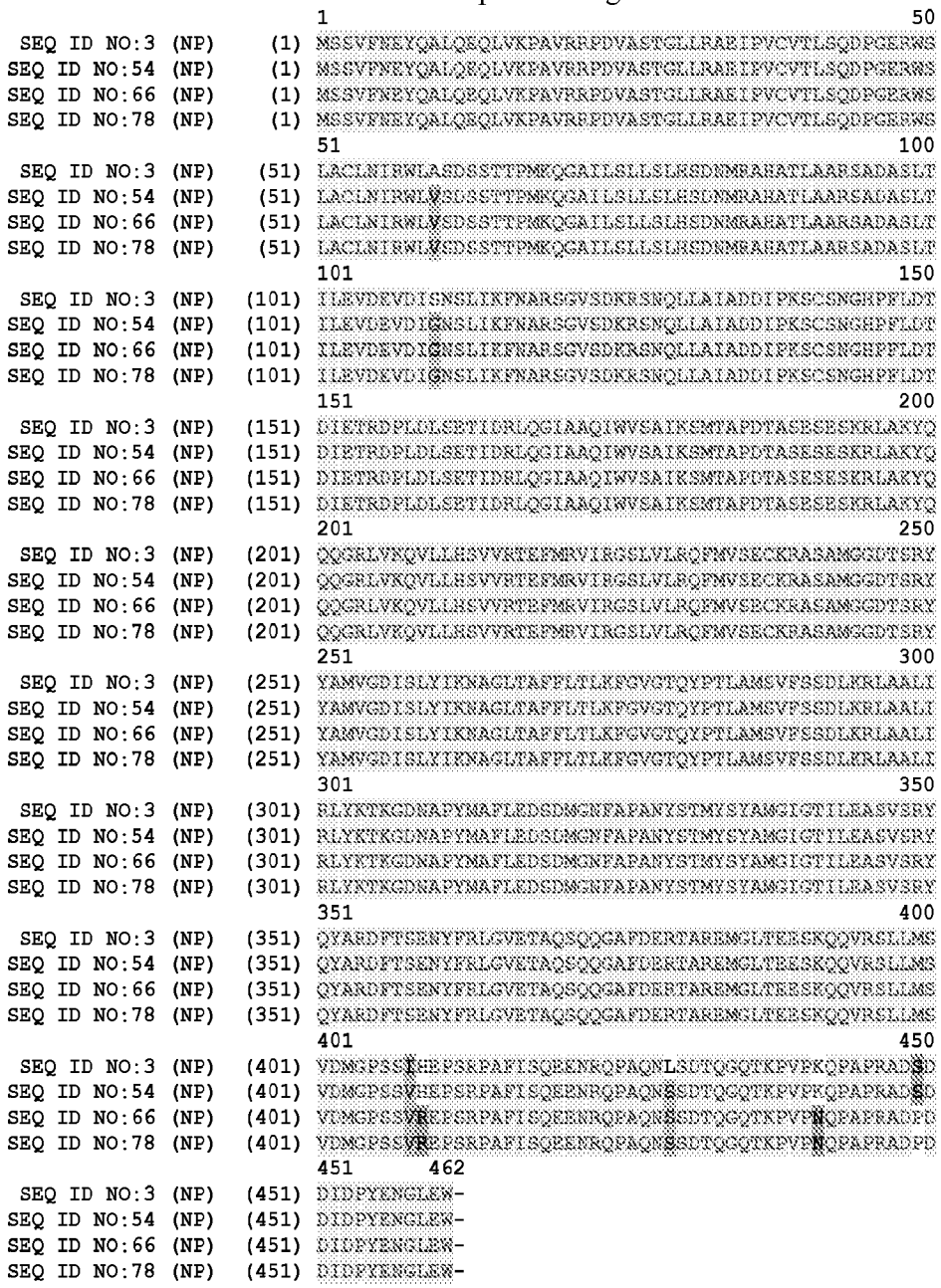
*GAATTC***TAATACGACTCACTATA**GGGaccagaaatggaatacaggaaatacggtaatttttactaatacaatttttttat
tagttattttatatatcattcttccctatcgaatacgattgttttaagttaggctagacacttcacaatcatttggcaa
gaagaatattacaggcaccaatttttctttgagtgtcggatttttttcttaaaatcatttttattatgtatatatttgtta
tactctaggaatatagattcagaggttagagaaattatcctatcccctagcgaatgattacaagctatattacttcaag
tgcaaattagaacattacacccctttaaaatcgcagaaa**TTACAAGCTATATTACTTCAAGTGCAAATTAGAACATTAC**
ACCCCTTTAAAATCGCAGAAATTACTTGTACAGCTCGTCCATGCCGAGAGTGATCCCGGCGGCGGTCACGAACTCCAGC
AGGACCATGTGATCGCGCTTCTCGTTGGGGTCTTTGCTCAGGGCGGACTGGGTGCTCAGGTAGTGGTTGTCGGGCAGCA
GCACGGGGCCGTCGCCGATGGGGGTGTTCTGCTGGTAGTGGTCGGCGAGCTGCACGCTGCCGTCCTCGATGTTGTGGCG
GATCTTGAAGTTCACCTTGATGCCGTTCTTCTGCTTGTCGGCCATGATATAGACGTTGTGGCTGTTGTAGTTGTACTCC
AGCTTGTGCCCCAGGATGTTGCCGTCCTCCTTGAAGTCGATGCCCTTCAGCTCGATGCGGTTCACCAGGGTGTCGCCCT
CGAACTTCACCTCGGCGCGGGTCTTGTAGTTGCCGTCGTCCTTGAAGAAGATGGTGCGCTCCTGGACGTAGCCTTCGGG
CATGGCGGACTTGAAGAAGTCGTGCTGCTTCATGTGGTCGGGGTAGCGGCTGAAGCACTGCACGCCGTAGGTCAGGGTG
GTCACGAGGGTGGGCCAGGGCACGGGCAGCTTGCCGGTGGTGCAGATGAACTTCAGGGTCAGCTTGCCGTAGGTGGCAT
CGCCCTCGCCCTCGCCGGACACGCTGAACTTGTGGCCGTTTACGTCGCCGTCCAGCTCGACCAGGATGGGCACCACCCC
GGTGAACAGCTCCTCGCCCTTGCTCACCATattgagtcctatagcgacctattcaaaacctccagtgaaattcagggtt
tcggcctcgagctcgagatccacttgcttcgcccccaataattcgattgttttatttaaagttcccgttggtcttgcat
tccttgtttggt**gggtcggcatggcatctccacctcctcgcggtccgacctgggcatccgaaggaggacgcacgtccac**
tcggatggctaagggagggcgTAGCATAACCCCTTGGGGCCTCTAAACGGGTCTTGAGGGGTTTTTTG*GCGGCCGC*

Not I

Restriction enzymes: italics and underlined
T7 polymerase promoter: upper case letter, bold and underlined
Additional three G nucleotides: upper case letter and underlined
Trailer sequence with genomic sequence: lower case letter
Sequence of the open reading frame of the enhanced green fluorescent protein in antisense orientation: upper case letter, bold
Leader sequence with genomic sequence: lower case letter and underlined
Hepatitis delta ribozyme sequence: lower case letter , underlined, and bold
T7 terminator sequence: upper case letter

Figure 30

NP protein alignment



Protein sequence identity:

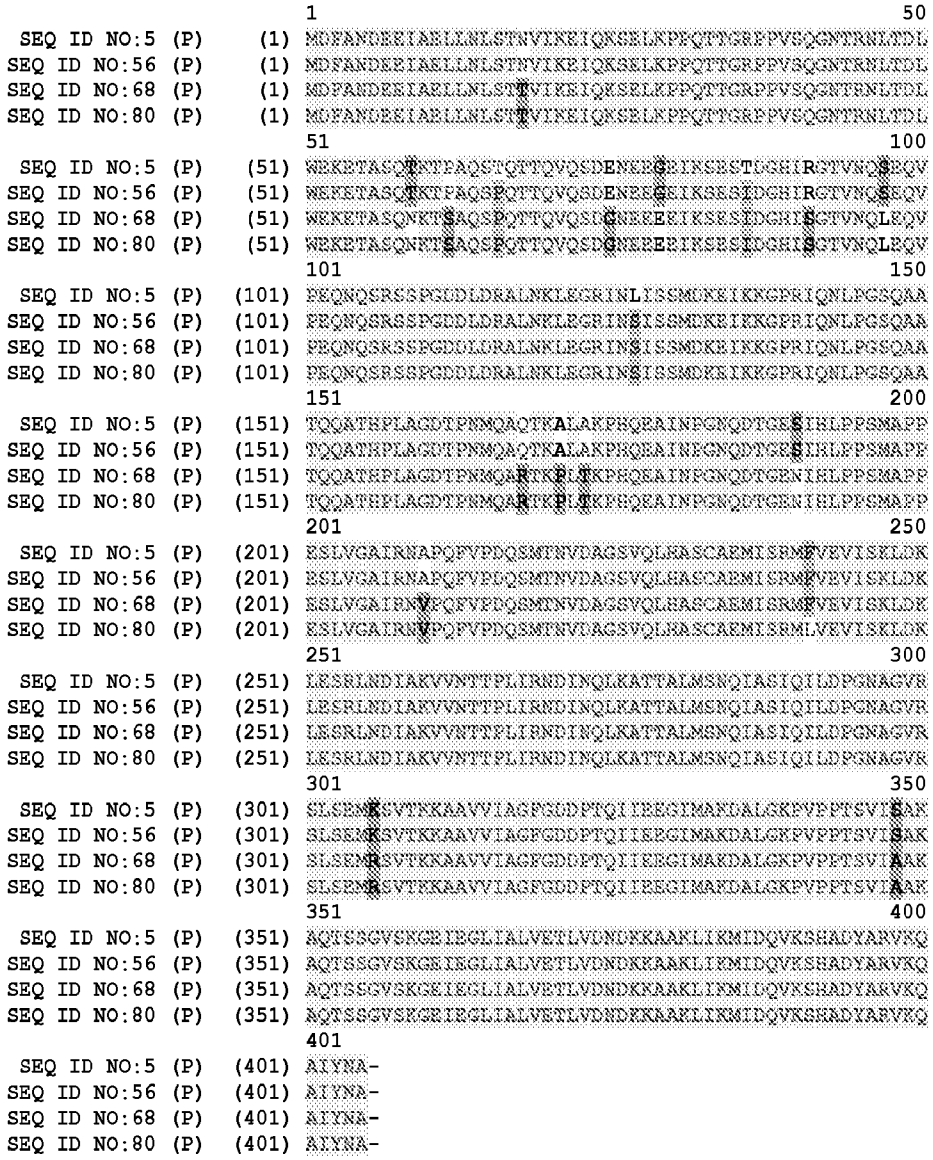
SEQ ID NO:3 v. SEQ ID NO:54: 99% sequence identity
SEQ ID NO:3 v. SEQ ID NO:66: 98% sequence identity
SEQ ID NO:3 v. SEQ ID NO:78: 98% sequence identity

DNA sequence identity:

SEQ ID NO:2 v. SEQ ID NO:53: 99% sequence identity
SEQ ID NO:2 v. SEQ ID NO:65: 97% sequence identity
SEQ ID NO:2 v. SEQ ID NO:77: 97% sequence identity

Figure 31

P protein alignment



Protein sequence identity:

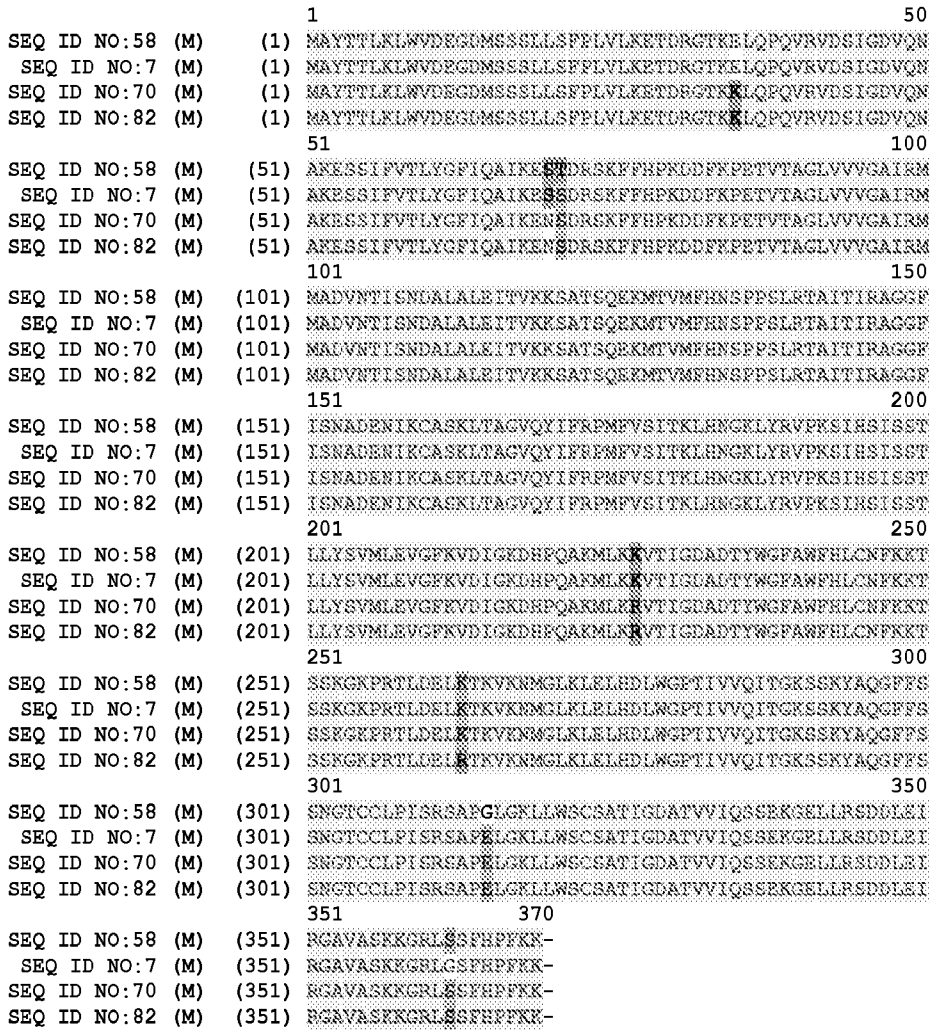
SEQ ID NO:5 v. SEQ ID NO:56: 99% sequence identity
SEQ ID NO:5 v. SEQ ID NO:68: 96% sequence identity
SEQ ID NO:5 v. SEQ ID NO:80: 95% sequence identity

DNA sequence identity:

SEQ ID NO:4 v. SEQ ID NO:55: 99% sequence identity
SEQ ID NO:4 v. SEQ ID NO:67: 96% sequence identity
SEQ ID NO:4 v. SEQ ID NO:79: 96% sequence identity

Figure 32

M protein alignment



Protein sequence identity:

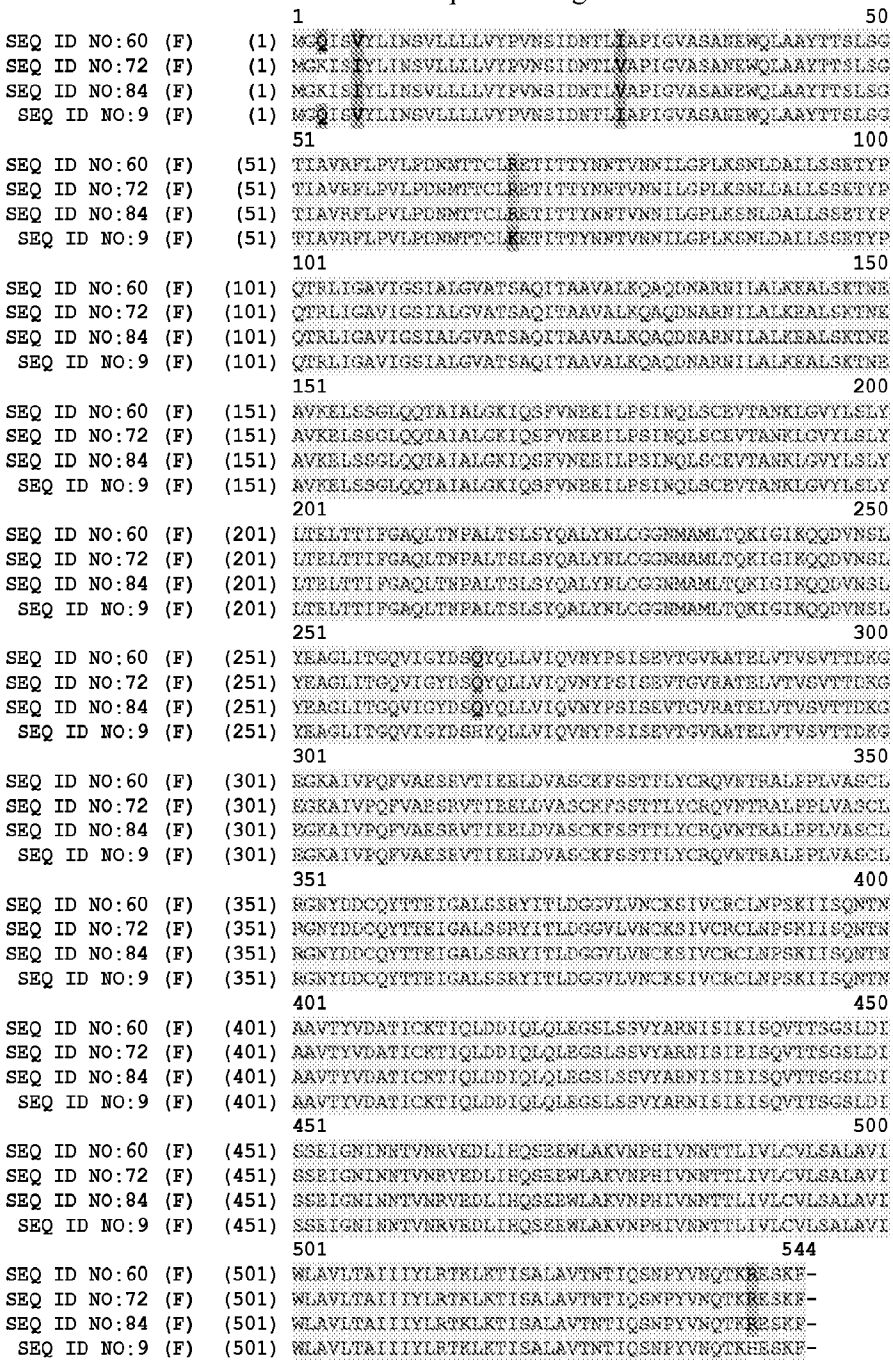
SEQ ID NO:7 v. SEQ ID NO:58: 99% sequence identity
SEQ ID NO:7 v. SEQ ID NO:70: 98% sequence identity
SEQ ID NO:7 v. SEQ ID NO:82: 98% sequence identity

DNA sequence identity:

SEQ ID NO:6 v. SEQ ID NO:57: 99% sequence identity
SEQ ID NO:6 v. SEQ ID NO:69: 97% sequence identity
SEQ ID NO:6 v. SEQ ID NO:81: 97% sequence identity

Figure 33

F protein alignment



Protein sequence identity:

SEQ ID NO:9 v. SEQ ID NO:60: 99% sequence identity
SEQ ID NO:9 v. SEQ ID NO:72: 98% sequence identity
SEQ ID NO:9 v. SEQ ID NO:84: 98% sequence identity

DNA sequence identity:

SEQ ID NO:8 v. SEQ ID NO:59: 99% sequence identity
SEQ ID NO:8 v. SEQ ID NO:71: 97% sequence identity
SEQ ID NO:8 v. SEQ ID NO:83: 97% sequence identity

Figure 34 (1/2)

HN protein alignment

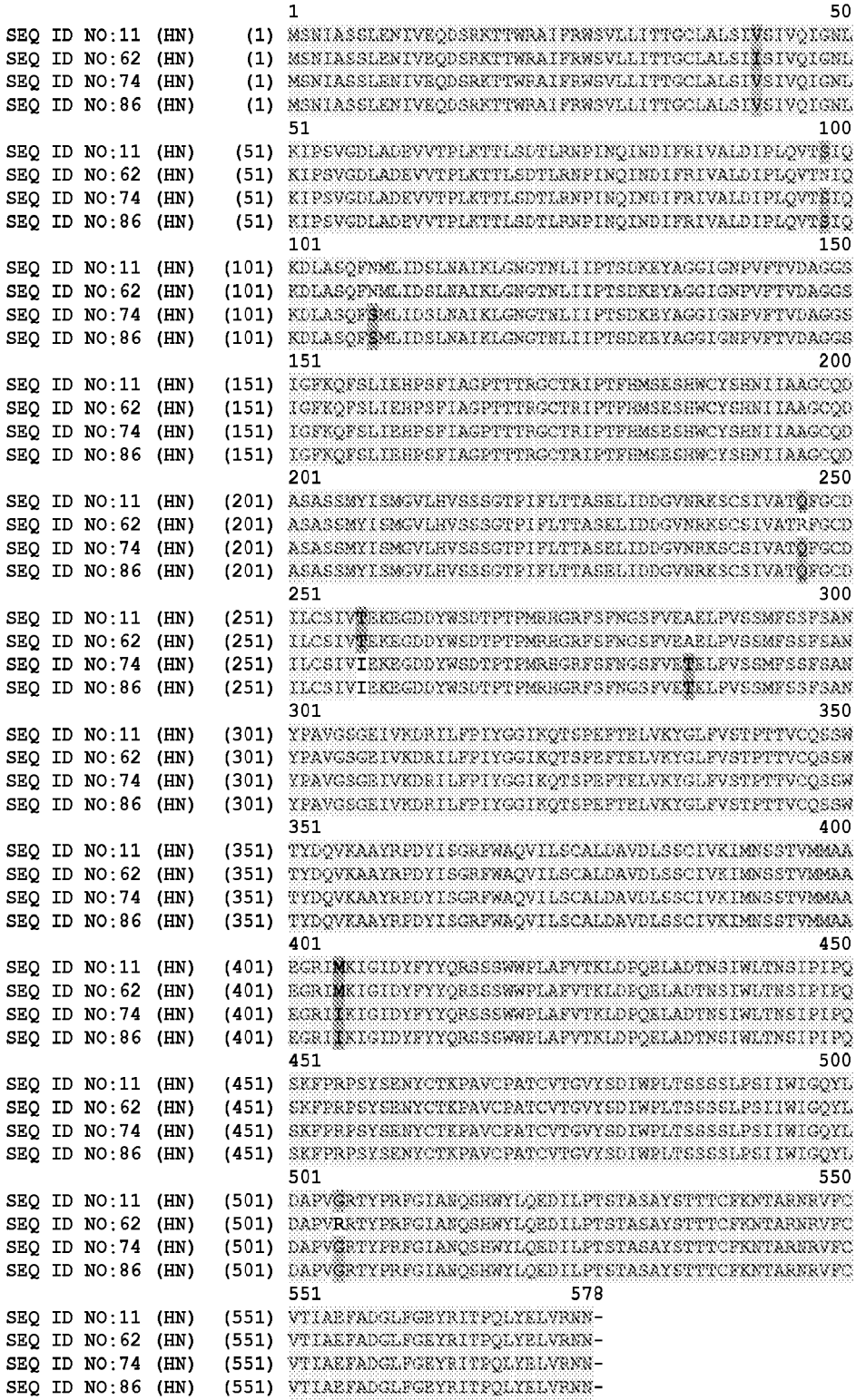


Figure 34 (2/2)

Protein sequence identity:

SEQ ID NO:11 v. SEQ ID NO:62: 99% sequence identity
SEQ ID NO:11 v. SEQ ID NO:74: 99% sequence identity
SEQ ID NO:11 v. SEQ ID NO:86: 99% sequence identity

DNA sequence identity:

SEQ ID NO:10 v. SEQ ID NO:61: 99% sequence identity
SEQ ID NO:10 v. SEQ ID NO:73: 97% sequence identity
SEQ ID NO:10 v. SEQ ID NO:85: 97% sequence identity

Figure 35 (1/5)

L protein alignment

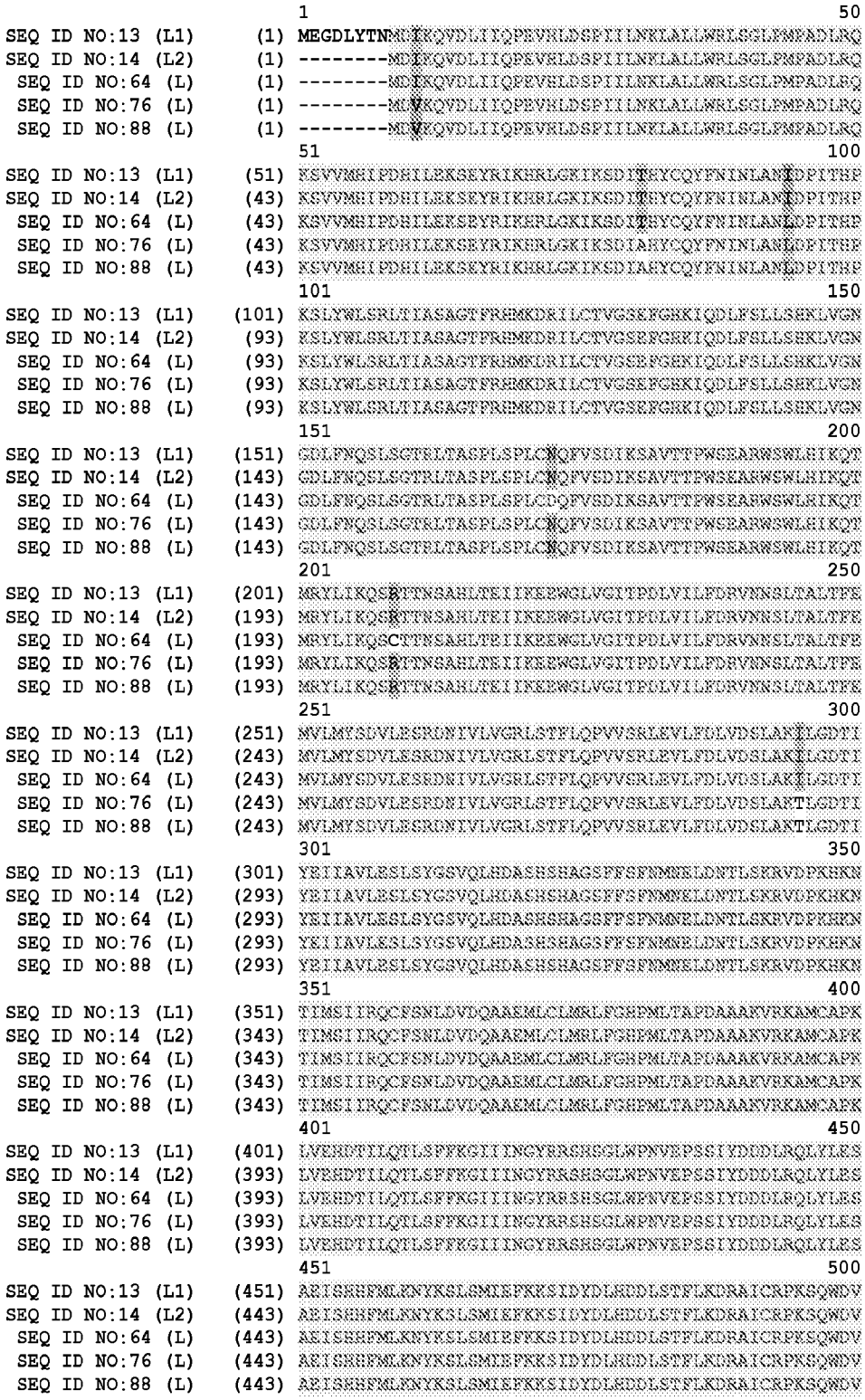


Figure 35 (2/5)

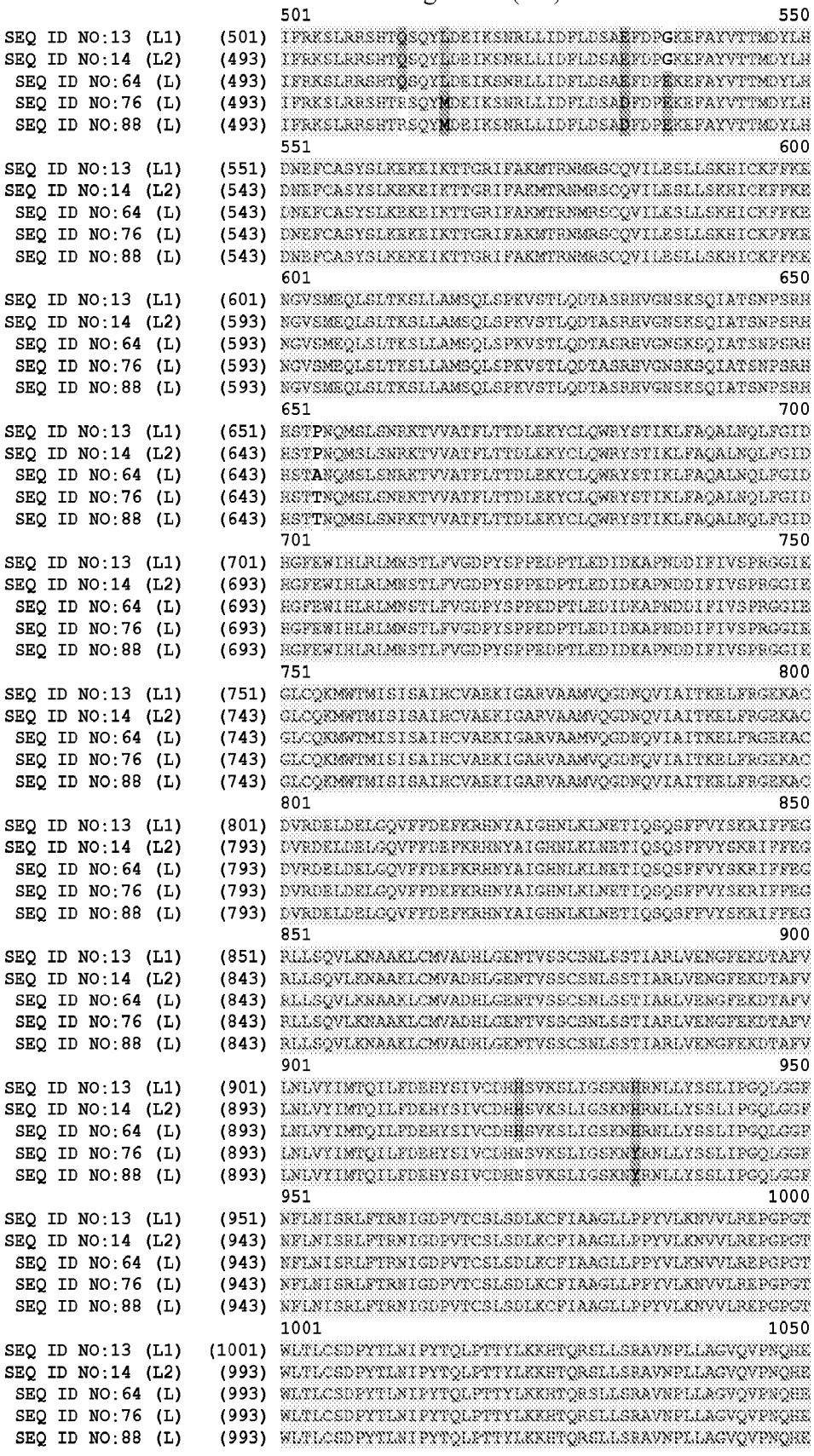

501 550
SEQ ID NO:13 (L1) (501) IFRESLRRSHTQSQYLDEIKSNRLLIDFLDSAEFDPGKEFAYVTTMDYLH
SEQ ID NO:14 (L2) (493) IFRESLRRSHTQSQYLDEIKSNRLLIDFLDSAEFDPGKEFAYVTTMDYLH
SEQ ID NO:64 (L) (493) IFRESLRRSHTQSQYLDEIKSNRLLIDFLDSAEFDPEKEFAYVTTMDYLH
SEQ ID NO:76 (L) (493) IFRESLRRSHTESQYMDEIKSNRLLIDFLDSADFDPEKEFAYVTTMDYLH
SEQ ID NO:88 (L) (493) IFRESLRRSHTPSQYMDEIKSNRLLIDFLDSADFDPEKEFAYVTTMDYLH
551 600
SEQ ID NO:13 (L1) (551) DNEFCASYSLKEKEIKTTGRIFAKMTRNMRSCQVILESLLSKHICKFFKE
SEQ ID NO:14 (L2) (543) DNEFCASYSLKEKEIKTTGRIFAKMTRNMRSCQVILESLLSKHICKFFKE
SEQ ID NO:64 (L) (543) DNEFCASYSLKEKEIKTTGRIFAKMTRNMRSCQVILESLLSKHICKFFKE
SEQ ID NO:76 (L) (543) DNEFCASYSLKEKEIKTTGRIFAKMTRNMRSCQVILESLLSKHICKFFKE
SEQ ID NO:88 (L) (543) DNEFCASYSLKEKEIKTTGRIFAKMTRNMRSCQVILESLLSKHICKFFKE
601 650
SEQ ID NO:13 (L1) (601) NGVSMEQLSLTKSLLAMSQLSPKVSTLQDTASREVGNSKSQIATSNPSRH
SEQ ID NO:14 (L2) (593) NGVSMEQLSLTKSLLAMSQLSPKVSTLQDTASREVGNSKSQIATSNPSRH
SEQ ID NO:64 (L) (593) NGVSMEQLSLTKSLLAMSQLSPKVSTLQDTASREVGNSKSQIATSNPSRH
SEQ ID NO:76 (L) (593) NGVSMEQLSLTKSLLAMSQLSPKVSTLQDTASREVGNSKSQIATSNPSRH
SEQ ID NO:88 (L) (593) NGVSMEQLSLTKSLLAMSQLSPKVSTLQDTASREVGNSKSQIATSNPSRH
651 700
SEQ ID NO:13 (L1) (651) KSTPNQMSLSNRKTVVATFLTTDLEKYCLQWRYSTIKLFAQALNQLFGID
SEQ ID NO:14 (L2) (643) KSTPNQMSLSNRKTVVATFLTTDLEKYCLQWRYSTIKLFAQALNQLFGID
SEQ ID NO:64 (L) (643) KSTANQMSLSNRKTVVATFLTTDLEKYCLQWRYSTIKLFAQALNQLFGID
SEQ ID NO:76 (L) (643) KSTTNQMSLSNRKTVVATFLTTDLEKYCLQWRYSTIKLFAQALNQLFGID
SEQ ID NO:88 (L) (643) KSTTNQMSLSNRKTVVATFLTTDLEKYCLQWRYSTIKLFAQALNQLFGID
701 750
SEQ ID NO:13 (L1) (701) KGFEWIHLRLMNSTLFVGDPYSPPEDPTLEDIDKAPNDDIFIVSPRGGIE
SEQ ID NO:14 (L2) (693) KGFEWIHLRLMNSTLFVGDPYSPPEDPTLEDIDKAPNDDIFIVSPRGGIE
SEQ ID NO:64 (L) (693) KGFEWIHLRLMNSTLFVGDPYSPPEDPTLEDIDKAPNDDIFIVSPRGGIE
SEQ ID NO:76 (L) (693) KGFEWIHLRLMNSTLFVGDPYSPPEDPTLEDIDKAPNDDIFIVSPRGGIE
SEQ ID NO:88 (L) (693) KGFEWIHLRLMNSTLFVGDPYSPPEDPTLEDIDKAPNDDIFIVSPRGGIE
751 800
SEQ ID NO:13 (L1) (751) GLCQKMWTMISISAIKCVAEKIGARVAAMVQGDNQVIAITKELFRGEKAC
SEQ ID NO:14 (L2) (743) GLCQKMWTMISISAIKCVAEKIGARVAAMVQGDNQVIAITKELFRGEKAC
SEQ ID NO:64 (L) (743) GLCQKMWTMISISAIKCVAEKIGARVAAMVQGDNQVIAITKELFRGEKAC
SEQ ID NO:76 (L) (743) GLCQKMWTMISISAIKCVAEKIGARVAAMVQGDNQVIAITKELFRGEKAC
SEQ ID NO:88 (L) (743) GLCQKMWTMISISAIKCVAEKIGARVAAMVQGDNQVIAITKELFRGEKAC
801 850
SEQ ID NO:13 (L1) (801) DVRDELDELGQVFFDEFKRHNYAIGHNLKLNETIQSQSFFVYSKRIFFEG
SEQ ID NO:14 (L2) (793) DVRDELDELGQVFFDEFKRHNYAIGHNLKLNETIQSQSFFVYSKRIFFEG
SEQ ID NO:64 (L) (793) DVRDELDELGQVFFDEFKRHNYAIGHNLKLNETIQSQSFFVYSKRIFFEG
SEQ ID NO:76 (L) (793) DVRDELDELGQVFFDEFKRHNYAIGHNLKLNETIQSQSFFVYSKRIFFEG
SEQ ID NO:88 (L) (793) DVRDELDELGQVFFDEFKRHNYAIGHNLKLNETIQSQSFFVYSKRIFFEG
851 900
SEQ ID NO:13 (L1) (851) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV
SEQ ID NO:14 (L2) (843) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV
SEQ ID NO:64 (L) (843) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV
SEQ ID NO:76 (L) (843) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV
SEQ ID NO:88 (L) (843) RLLSQVLKNAAKLCMVADHLGENTVSSCSNLSSTIARLVENGFEKDTAFV
901 950
SEQ ID NO:13 (L1) (901) LNLVYIMTQILFDEHYSIVCDHRSVKSLIGSKNRRNLLYSSLIPGQLGGF
SEQ ID NO:14 (L2) (893) LNLVYIMTQILFDEHYSIVCDHRSVKSLIGSKNRRNLLYSSLIPGQLGGF
SEQ ID NO:64 (L) (893) LNLVYIMTQILFDEHYSIVCDHRSVKSLIGSKNRRNLLYSSLIPGQLGGF
SEQ ID NO:76 (L) (893) LNLVYIMTQILFDEHYSIVCDHNSVKSLIGSKNTRNLLYSSLIPGQLGGF
SEQ ID NO:88 (L) (893) LNLVYIMTQILFDEHYSIVCDHNSVKSLIGSKNTRNLLYSSLIPGQLGGF
951 1000
SEQ ID NO:13 (L1) (951) KFLNISRLFTRNIGDPVTCSLSDLKCFIAAGLLPPYVLKNVVLREPGPGT
SEQ ID NO:14 (L2) (943) KFLNISRLFTRNIGDPVTCSLSDLKCFIAAGLLPPYVLKNVVLREPGPGT
SEQ ID NO:64 (L) (943) KFLNISRLFTRNIGDPVTCSLSDLKCFIAAGLLPPYVLKNVVLREPGPGT
SEQ ID NO:76 (L) (943) KFLNISRLFTRNIGDPVTCSLSDLKCFIAAGLLPPYVLKNVVLREPGPGT
SEQ ID NO:88 (L) (943) KFLNISRLFTRNIGDPVTCSLSDLKCFIAAGLLPPYVLKNVVLREPGPGT
1001 1050
SEQ ID NO:13 (L1) (1001) WLTLCSDPYTLNIPYTQLPTTYLKKHTQRSLLSRAVNPLLAGVQVPNQHE
SEQ ID NO:14 (L2) (993) WLTLCSDPYTLNIPYTQLPTTYLKKHTQRSLLSRAVNPLLAGVQVPNQHE
SEQ ID NO:64 (L) (993) WLTLCSDPYTLNIPYTQLPTTYLKKHTQRSLLSRAVNPLLAGVQVPNQHE
SEQ ID NO:76 (L) (993) WLTLCSDPYTLNIPYTQLPTTYLKKHTQRSLLSRAVNPLLAGVQVPNQHE
SEQ ID NO:88 (L) (993) WLTLCSDPYTLNIPYTQLPTTYLKKHTQRSLLSRAVNPLLAGVQVPNQHE

Figure 35 (3/5)

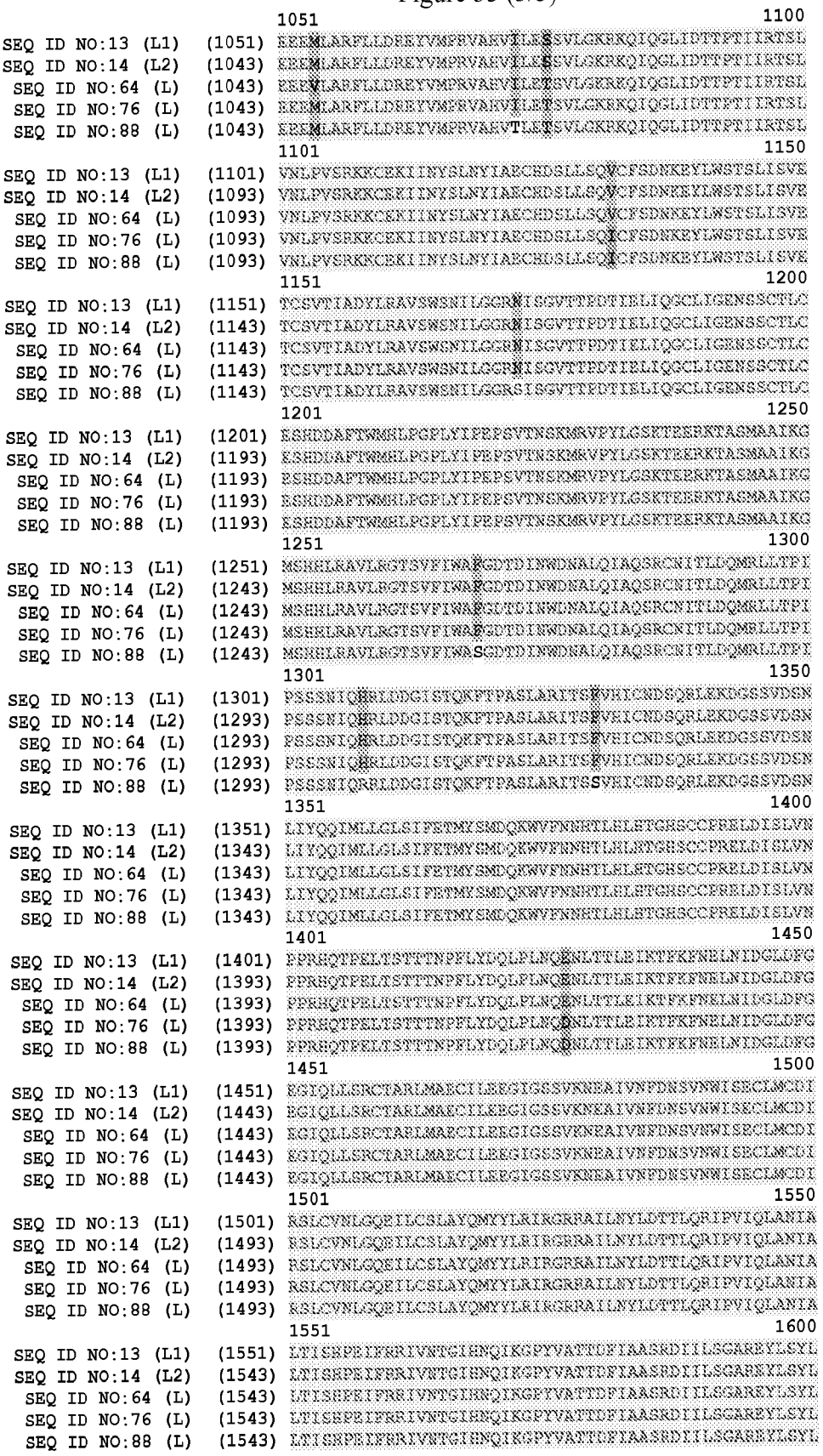

1051 1100
SEQ ID NO:13 (L1) (1051) EEEMLARFLLDEEYVMPRVAEVILESSVLGKEKQIQGLIDTTPTIIRTSL
SEQ ID NO:14 (L2) (1043) EEEMLARFLLDEEYVMPRVAEVILESSVLGKEKQIQGLIDTTPTIIRTSL
SEQ ID NO:64 (L) (1043) EEEVLARFLLDEEYVMPRVAEVILETSVLGKEKQIQGLIDTTPTIIRTSL
SEQ ID NO:76 (L) (1043) EEEMLARFLLDEEYVMPRVAEVILETSVLGKEKQIQGLIDTTPTIIRTSL
SEQ ID NO:88 (L) (1043) EEEMLARFLLDEEYVMPRVAEVTLETSVLGKEKQIQGLIDTTPTIIRTSL
1101 1150
SEQ ID NO:13 (L1) (1101) VNLPVSEKKCEKIINYSLNYIAECHDSLLSQVCFSDNKEYLWSTSLISVE
SEQ ID NO:14 (L2) (1093) VNLPVSEKKCEKIINYSLNYIAECHDSLLSQVCFSDNKEYLWSTSLISVE
SEQ ID NO:64 (L) (1093) VNLPVSEKKCEKIINYSLNYIAECHDSLLSQVCFSDNKEYLWSTSLISVE
SEQ ID NO:76 (L) (1093) VNLPVSEKKCEKIINYSLNYIAECHDSLLSQICFSDNKEYLWSTSLISVE
SEQ ID NO:88 (L) (1093) VNLPVSEKKCEKIINYSLNYIAECHDSLLSQICFSDNKEYLWSTSLISVE
1151 1200
SEQ ID NO:13 (L1) (1151) TCSVTIADYLRAVSWSNILGGRNISGVTTPDTIELIQGCLIGENSSCTLC
SEQ ID NO:14 (L2) (1143) TCSVTIADYLRAVSWSNILGGRNISGVTTPDTIELIQGCLIGENSSCTLC
SEQ ID NO:64 (L) (1143) TCSVTIADYLRAVSWSNILGGRNISGVTTPDTIELIQGCLIGENSSCTLC
SEQ ID NO:76 (L) (1143) TCSVTIADYLRAVSWSNILGGRNISGVTTPDTIELIQGCLIGENSSCTLC
SEQ ID NO:88 (L) (1143) TCSVTIADYLRAVSWSNILGGRSISGVTTPDTIELIQGCLIGENSSCTLC
1201 1250
SEQ ID NO:13 (L1) (1201) ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSKTEERKTASMAAIKG
SEQ ID NO:14 (L2) (1193) ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSKTEERKTASMAAIKG
SEQ ID NO:64 (L) (1193) ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSKTEERKTASMAAIKG
SEQ ID NO:76 (L) (1193) ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSKTEERKTASMAAIKG
SEQ ID NO:88 (L) (1193) ESHDDAFTWMHLPGPLYIPEPSVTNSKMRVPYLGSKTEERKTASMAAIKG
1251 1300
SEQ ID NO:13 (L1) (1251) MSHHLRAVLRGTSVFIWAPGDTDINWDNALQIAQSRCNITLDQMRLLTPI
SEQ ID NO:14 (L2) (1243) MSHHLRAVLRGTSVFIWAPGDTDINWDNALQIAQSRCNITLDQMRLLTPI
SEQ ID NO:64 (L) (1243) MSHHLRAVLRGTSVFIWAPGDTDINWDNALQIAQSRCNITLDQMRLLTPI
SEQ ID NO:76 (L) (1243) MSHHLRAVLRGTSVFIWAPGDTDINWDNALQIAQSRCNITLDQMRLLTPI
SEQ ID NO:88 (L) (1243) MSHHLRAVLRGTSVFIWASGDTDINWDNALQIAQSRCNITLDQMRLLTPI
1301 1350
SEQ ID NO:13 (L1) (1301) PSSSNIQPRLDDGISTQKFTPASLARITSPVHICNDSQRLEKDGSSVDSN
SEQ ID NO:14 (L2) (1293) PSSSNIQPRLDDGISTQKFTPASLARITSPVHICNDSQRLEKDGSSVDSN
SEQ ID NO:64 (L) (1293) PSSSNIQPRLDDGISTQKFTPASLARITSPVHICNDSQRLEKDGSSVDSN
SEQ ID NO:76 (L) (1293) PSSSNIQPRLDDGISTQKFTPASLARITSPVHICNDSQRLEKDGSSVDSN
SEQ ID NO:88 (L) (1293) PSSSNIQPRLDDGISTQKFTPASLARITSSVHICNDSQRLEKDGSSVDSN
1351 1400
SEQ ID NO:13 (L1) (1351) LIYQQIMLLGLSIFETMYSMDQKWVFNNHTLELETGHSCCPRELDISLVN
SEQ ID NO:14 (L2) (1343) LIYQQIMLLGLSIFETMYSMDQKWVFNNHTLELETGHSCCPRELDISLVN
SEQ ID NO:64 (L) (1343) LIYQQIMLLGLSIFETMYSMDQKWVFNNHTLELETGHSCCPRELDISLVN
SEQ ID NO:76 (L) (1343) LIYQQIMLLGLSIFETMYSMDQKWVFNNHTLELETGHSCCPRELDISLVN
SEQ ID NO:88 (L) (1343) LIYQQIMLLGLSIFETMYSMDQKWVFNNHTLELETGHSCCPRELDISLVN
1401 1450
SEQ ID NO:13 (L1) (1401) PPRHQTPELTSTTTNPFLYDQLPLNQENLTTLEIKTFKFNELNIDGLDFG
SEQ ID NO:14 (L2) (1393) PPRHQTPELTSTTTNPFLYDQLPLNQENLTTLEIKTFKFNELNIDGLDFG
SEQ ID NO:64 (L) (1393) PPRHQTPELTSTTTNPFLYDQLPLNQENLTTLEIKTFKFNELNIDGLDFG
SEQ ID NO:76 (L) (1393) PPREQTPELTSTTTNPFLYDQLPLNQENLTTLEIKTFKFNELNIDGLDFG
SEQ ID NO:88 (L) (1393) PPRHQTPELTSTTTNPFLYDQLPLNQENLTTLEIKTFKFNELNIDGLDFG
1451 1500
SEQ ID NO:13 (L1) (1451) EGIQLLSRCTARLMAECILEEGIGSSVKNEAIVNFDNSVNWISECLMCDI
SEQ ID NO:14 (L2) (1443) EGIQLLSRCTARLMAECILEEGIGSSVKNEAIVNFDNSVNWISECLMCDI
SEQ ID NO:64 (L) (1443) EGIQLLSRCTARLMAECILEEGIGSSVKNEAIVNFDNSVNWISECLMCDI
SEQ ID NO:76 (L) (1443) EGIQLLSRCTARLMAECILEEGIGSSVKNEAIVNFDNSVNWISECLMCDI
SEQ ID NO:88 (L) (1443) EGIQLLSRCTARLMAECILEEGIGSSVKNEAIVNFDNSVNWISECLMCDI
1501 1550
SEQ ID NO:13 (L1) (1501) RSLCVNLGQEILCSLAYQMYYLRIRGRRAILNYLDTTLQRIPVIQLANIA
SEQ ID NO:14 (L2) (1493) RSLCVNLGQEILCSLAYQMYYLRIRGRRAILNYLDTTLQRIPVIQLANIA
SEQ ID NO:64 (L) (1493) RSLCVNLGQEILCSLAYQMYYLRIRGRRAILNYLDTTLQRIPVIQLANIA
SEQ ID NO:76 (L) (1493) RSLCVNLGQEILCSLAYQMYYLRIRGRRAILNYLDTTLQRIPVIQLANIA
SEQ ID NO:88 (L) (1493) RSLCVNLGQEILCSLAYQMYYLRIRGRRAILNYLDTTLQRIPVIQLANIA
1551 1600
SEQ ID NO:13 (L1) (1551) LTISRPEIFERIVNTGIHNQIKGPYVATTDFIAASRDIILSGARELSYL
SEQ ID NO:14 (L2) (1543) LTISRPEIFERIVNTGIHNQIKGPYVATTDFIAASRDIILSGARELSYL
SEQ ID NO:64 (L) (1543) LTISRPEIFERIVNTGIHNQIKGPYVATTDFIAASRDIILSGARELSYL
SEQ ID NO:76 (L) (1543) LTISRPEIFERIVNTGIHNQIKGPYVATTDFIAASRDIILSGARELSYL
SEQ ID NO:88 (L) (1543) LTISRPEIFERIVNTGIHNQIKGPYVATTDFIAASRDIILSGARELSYL

Figure 35 (4/5)

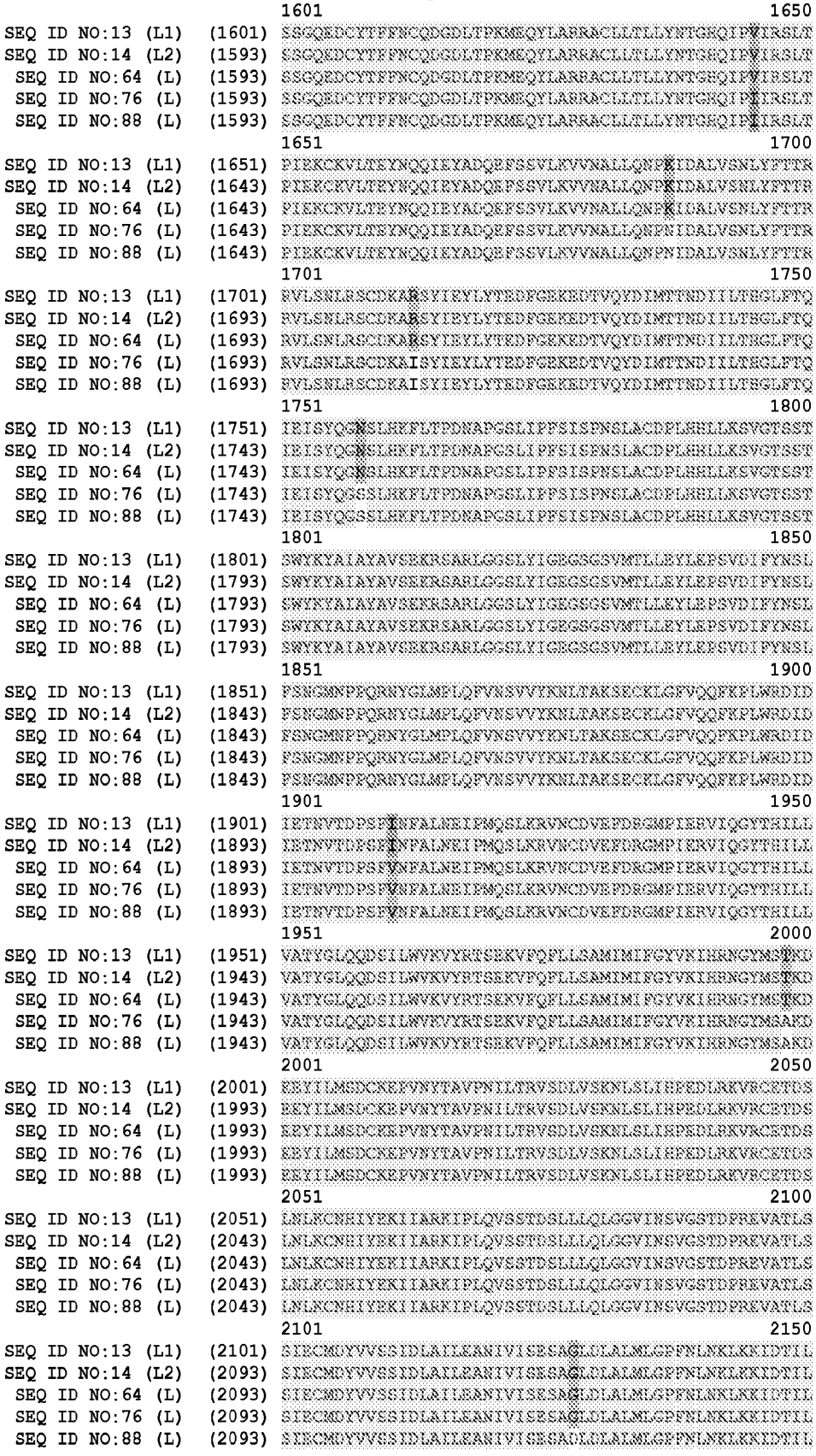
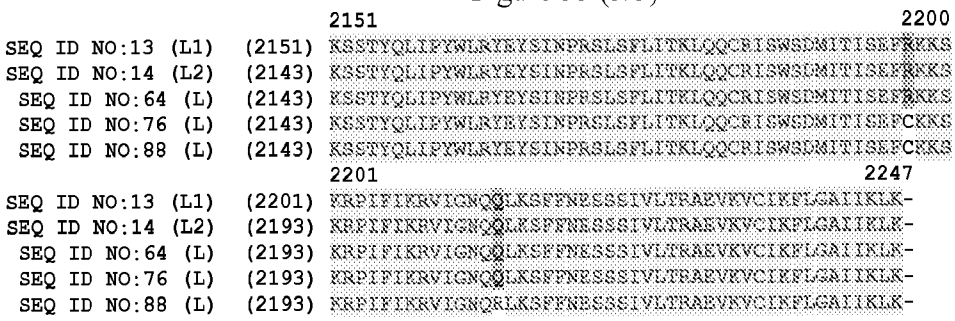

1601 1650
SEQ ID NO:13 (L1) (1601)
SEQ ID NO:14 (L2) (1593)
SEQ ID NO:64 (L) (1593)
SEQ ID NO:76 (L) (1593)
SEQ ID NO:88 (L) (1593)
1651 1700
SEQ ID NO:13 (L1) (1651)
SEQ ID NO:14 (L2) (1643)
SEQ ID NO:64 (L) (1643)
SEQ ID NO:76 (L) (1643)
SEQ ID NO:88 (L) (1643)
1701 1750
SEQ ID NO:13 (L1) (1701)
SEQ ID NO:14 (L2) (1693)
SEQ ID NO:64 (L) (1693)
SEQ ID NO:76 (L) (1693)
SEQ ID NO:88 (L) (1693)
1751 1800
SEQ ID NO:13 (L1) (1751)
SEQ ID NO:14 (L2) (1743)
SEQ ID NO:64 (L) (1743)
SEQ ID NO:76 (L) (1743)
SEQ ID NO:88 (L) (1743)
1801 1850
SEQ ID NO:13 (L1) (1801)
SEQ ID NO:14 (L2) (1793)
SEQ ID NO:64 (L) (1793)
SEQ ID NO:76 (L) (1793)
SEQ ID NO:88 (L) (1793)
1851 1900
SEQ ID NO:13 (L1) (1851)
SEQ ID NO:14 (L2) (1843)
SEQ ID NO:64 (L) (1843)
SEQ ID NO:76 (L) (1843)
SEQ ID NO:88 (L) (1843)
1901 1950
SEQ ID NO:13 (L1) (1901)
SEQ ID NO:14 (L2) (1893)
SEQ ID NO:64 (L) (1893)
SEQ ID NO:76 (L) (1893)
SEQ ID NO:88 (L) (1893)
1951 2000
SEQ ID NO:13 (L1) (1951)
SEQ ID NO:14 (L2) (1943)
SEQ ID NO:64 (L) (1943)
SEQ ID NO:76 (L) (1943)
SEQ ID NO:88 (L) (1943)
2001 2050
SEQ ID NO:13 (L1) (2001)
SEQ ID NO:14 (L2) (1993)
SEQ ID NO:64 (L) (1993)
SEQ ID NO:76 (L) (1993)
SEQ ID NO:88 (L) (1993)
2051 2100
SEQ ID NO:13 (L1) (2051)
SEQ ID NO:14 (L2) (2043)
SEQ ID NO:64 (L) (2043)
SEQ ID NO:76 (L) (2043)
SEQ ID NO:88 (L) (2043)
2101 2150
SEQ ID NO:13 (L1) (2101)
SEQ ID NO:14 (L2) (2093)
SEQ ID NO:64 (L) (2093)
SEQ ID NO:76 (L) (2093)
SEQ ID NO:88 (L) (2093)

Figure 35 (5/5)



Protein sequence identity:

SEQ ID NO:14 v. SEQ ID NO:64: 99% sequence identity
SEQ ID NO:14 v. SEQ ID NO:76: 99% sequence identity
SEQ ID NO:14 v. SEQ ID NO:88: 98% sequence identity

DNA sequence identity:

SEQ ID NO:12 v. SEQ ID NO:63: 99% sequence identity
SEQ ID NO:12 v. SEQ ID NO:75: 97% sequence identity
SEQ ID NO:12 v. SEQ ID NO:87: 97% sequence identity

REFERENCES CITED IN THE DESCRIPTION

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Patent documents cited in the description

- US 6719979 B **[0003] [0058]**
- WO 0236617 A **[0009]**
- WO 2007104782 A **[0009]**
- WO 2009101149 A **[0009]**
- US 4708871 A **[0034]**
- US 4769330 A **[0058]**
- US 4722848 A **[0058]**
- US 4603112 A **[0058]**
- US 5174993 A **[0058]**
- US 5756103 A **[0058]**
- US 6919084 B **[0064]**
- US 6358500 B **[0064]**
- US 7371395 B **[0064]**
- WO 9816247 A, Klinman **[0065]**
- US 2909462 A **[0066]**
- US 61235912 B **[0134]**

Non-patent literature cited in the description

- **PEETERS et al.** *Vaccine,* 2001, vol. 19, 1616-1627 **[0009]**
- **PAULDURAI et al.** *Virus Research,* 2009, vol. 142, 144-153 **[0009]**
- **BENJAMIN LEWIN ; GENES V.** molecular biology. Oxford University Press, 1994 **[0024]**
- The Encyclopedia of Molecular Biolog. Blackwell Science Ltd, 1994 **[0024]**
- Molecular Biology and Biotechnology: a Comprehensive Desk Reference. VCH Publishers, Inc, 1995 **[0024]**
- Epitope Mapping Protocols in Methods in Molecular Biology. 1996, vol. 66 **[0034]**
- **M. POWELL ; M. NEWMAN.** Vaccine Design, The Subunit and Adjuvant Approach. Plenum Press, 1995, 147 **[0065]**
- *Pharmeuropa,* June 1996, vol. 8 (2 **[0066]**
- **REED, LJ et al.** *Am. J. Epidemiol.,* 1938, vol. 27, 493-497 **[0075]**
- **CONZELMANN et al.** *J Virol.,* 1994, vol. 68, 713-719 **[0120]**
- **COLLINS et al.** *PNAS USA,* 1991, vol. 88, 9663-9667 **[0120]**
- Newcastle disease. **ALEXANDER.** Developments in veterinary virology. Kluwer Academic, 1988, x, , 378 **[0133]**
- **ALEXANDER.** Characterization of viruses which represent further distinct serotypes (PMV-8 and PMV-9) of avian paramyxoviruses. *Arch Virol,* vol. 78, 29-36 **[0133]**
- **ALEXANDER et al.** Properties of a newly isolated, serologically distinct avian paramyxovirus. *Arch Virol,* 1979, vol. 60, 105-13 **[0133]**
- Newcastle Disease, other Paramyxoviruses, and Pneumovirus Avian Paramyxoviruses 2-9. **ALEXANDER.** Diseases of poultry. Iowa State Press, 2003, 63-99 **[0133]**
- **ANDRAL et al.** Isolation of avian paramyxovirus 2 and 3 from turkeys in Brittany. *Vet Rec,* 1984, vol. 114, 570-1 **[0133]**
- **BANKOWSKI et al.** Effect of paramyxovirus yucaipa on fertility, hatchability, and poult yield of turkeys. *Avian Dis,* 1981, vol. 25, 517-20 **[0133]**
- **BANKOWSKI et al.** Isolation of an Unidentified Agent from the Respiratory Tract of Chickens. *Science,* 1960, vol. 132, 292-293 **[0133]**
- **BRADSHAW et al.** The Epidemiology of Yucaipa Virus in Relationship to the Acute Respiratory Disease Syndrome in Turkeys. *Avian Diseases,* 1979, vol. 23, 539-542 **[0133]**
- **CAPUA et al.** Isolation of an avian paramyxovirus type 9 from migratory waterfowl in Italy. *Vet Rec,* 2004, vol. 155, 156 **[0133]**
- **CHAMBERS et al.** Protection of chickens from lethal influenza infection by vaccineexpressed hemagglutinin. *Virology,* 1988, vol. 167, 414-421 **[0133]**
- **COLLINS, P. L. et al.** Rescue of synthetic analogs of respiratory syncytial virus genomic RNA and effect of truncations and mutations on the expression of a foreign reporter gene. *Proc. Natl. Acad. Sci. USA,* 1991, vol. 88, 9663-9667 **[0133]**
- **CONZELMANN KK ; SCHNELL M.** Rescue of synthetic genomic RNA analogs of rabies virus by plasmid-encoded proteins. *J Virol.,* 1994, vol. 68, 713-719 **[0133]**
- **DARTEIL, R. ; M. BUBLOT ; E. LAPLACE ; J.F. BOUQUET ; J.C. AUDONNET ; M. RIVIERE.** Herpesvirus of turkey recombinant viruses expressing infectious bursal disease virus (IBDV) VP2 immunogen induce protection against an IBDV virulent challenge in chickens. *Virology,* 1995, vol. 211, 481-490 **[0133]**

- **DE LEEUW et al.** Complete nucleotide sequence of Newcastle disease virus: evidence for the existence of a new genus within the subfamily Paramyxovirinae. *J Gen Virol,* 1999, vol. 80, 131-136 **[0133]**
- **FLEURY et al.** Isolation of twenty-three Yucaipa-like viruses from 616 wild birds in Senegal, West Africa. *Avian Dis,* 1979, vol. 23, 742-4 **[0133]**
- **GAO et al.** Protection of mice and poultry from lethal H5N1 avian influenza virus through adenovirus-based immunization. *J Virol,* 2006, vol. 80, 1959-1964 **[0133]**
- **GE et al.** Newcastle disease virus-based live attenuated vaccine completely protects chickens and mice from lethal challenge of homologous and heterologous H5N1 avian influenza viruses. *Journal of Virology,* 2007, vol. 81 (1), 150-158 **[0133]**
- **GOODMAN et al.** Isolation of avian paramyxovirus-2 from domestic and wild birds in Costa Rica. *Avian Dis,* 1988, vol. 32, 713-7 **[0133]**
- **GOUGH et al.** Avian paramyxovirus type 4 isolated from a ringed teal (Calonetta leucophrys). *Vet Rec,* 1984, vol. 115, 653 **[0133]**
- **HOELSCHER et al.** A broadly protective vaccine against globally dispersed clade 1 and clade 2 H5N1 influenza viruses. *J Infect Dis.,* 2008, vol. 197, 1185-1188 **[0133]**
- **HUANG et al.** A recombinant Newcastle Disease Virus (NDV) expressing VP2 protein of Infectious Bursal Disease Virus (IBDV) protects against NDV and IBDV. *Journal of Virology,* 2004, vol. 78, 10054-10063 **[0133]**
- **HUNT et al.** Retrovirus-expressed hemagglutinin protects against lethal influenza virus infections. *J Virol,* 1988, vol. 62, 3014-3019 **[0133]**
- **INOUE K ; SHOJI Y ; KURANE I ; IIJIMA T ; SAKAI T ; MORIMOTO K.** An improved method for recovering rabies virus from cloned cDNA. *J Virol Methods,* 2003, vol. 107, 229-236 **[0133]**
- **KRISHNAMURTHY et al.** Nucleotide sequences of the trailer, nucleocapsid protein gene and intergenic regions of Newcastle disease virus strain Beaudette C and completion of the entire genome sequence. *J Gen Virol,* 1998, vol. 79, 2419-2424 **[0133]**
- **KRISHNAMURTHY, S. ; HUANG, Z. ; SAMAL, S. K.** Recovery of a virulent strain of Newcastle disease virus from cloned cDNA: expression of a foreign gene results in growth retardation and attenuation. *Virology,* 2000, vol. 278, 168-182 **[0133]**
- **LAMB et al.** *Paramyxoviridae: The viruses and Their Replication,* 2007, 1449-1496 **[0133]**
- Fields' virology. Wolters Kluwer Health/Lippincott Williams & Wilkins **[0133]**
- **LANG, G. ; A. GAGNON ; J. HOWELL.** The occurrence of Paramyxovirus yucaipa in Canadian poultry. *Can Vet J,* 1975, vol. 16, 233-7 **[0133]**
- **LIPKIND et al.** Isolation of yucaipa-like avian paramyxovirus from a wild mallard duck (Anas platyrhinchos) wintering in Israel. *Vet Rec,* 1982, vol. 110, 15-6 **[0133]**
- **LIPKIND et al.** The isolation of yucaipa-like paramyxoviruses from epizootics of a respiratory disease in turkey poultry farms in Israel. *Vet Rec,* 1979, vol. 105, 577-8 **[0133]**
- **MALDONADO et al.** Serological survey for avian paramyxoviruses from wildfowl in aquatic habitats in Andalusia. *Journal of Wildlife Diseases,* 1995, vol. 31 (1), 66-69 **[0133]**
- **MAYO et al.** A summary of taxonomic changes recently approved by ICTV. *Arch Virol,* 2002, vol. 147, 1655-63 **[0133]**
- **NAYAK B et al.** Molecular characterization and complete genome sequence of avian paramyxovirus type 4 prototype strain duck/Hong Kong/D3/75. *Virol J.,* 2008, vol. 20 (5), 124 **[0133]**
- **PARK et al.** Engineered viral vaccine constructs with dual specificity: Avian influenza and Newcastle disease. *Proceedings of the National Academy of Sciences,* 2006, vol. 103 (21), 8203-8208 **[0133]**
- **PEETERS et al.** Rescue of Newcastle disease virus from cloned cDNA: evidence that cleavability of the fusion protein is a major determinant for virulence. *Journal of Virology,* 1999, vol. 73 (6), 5001-5009 **[0133]**
- **REDMANN et al.** Isolation of a paramyxovirus-3 from turkeys with respiratory tract disease in Germany. *Dtsch Tierarztl Wochenschr,* 1991, vol. 98, 138-41 **[0133]**
- **REED et al.** A SIMPLE METHOD OF ESTIMATING FIFTY PER CENT ENDPOINTS. *Am. J. Epidemiol.,* 1938, vol. 27, 493-497 **[0133]**
- **RÖMER-OBERDÖRFER et al.** Generation of recombinant lentogenic Newcastle disease virus from cDNA. *Journal of General Virology,* 1999, vol. 80, 2987-2995 **[0133]**
- **ROSENBERGER et al.** Isolation of Newcastle disease and type-A influenza viruses from migratory waterfowl in the Atlantic flyway. *Avian Diseases,* 1974, vol. 18 (4), 610-613 **[0133]**
- **SAIF et al.** Natural and Experimental Infection of Turkeys with Avian Paramyxovirus-7. *Avian Diseases,* 1997, vol. 41, 326-329 **[0133]**
- **SHIHMANTER et al.** Isolation of avian serotype 3 paramyxoviruses from imported caged birds in Israel. *Avian Dis,* 1998, vol. 42, 829-31 **[0133]**
- **SHIHMANTER et al.** Avian paramyxoviruses serotype 3 isolated from captive birds in Israel: clinical signs, pathology, and antigenic characterization. *Avian Dis,* 1998, vol. 42, 418-22 **[0133]**
- **SHORTRIDGE et al.** Isolation and properties of viruses from poultry in Hong Kong which represent a new (sixth) distinct group of avian paramyxoviruses. *J Gen Virol,* 1980, vol. 49, 255-262 **[0133]**

- **SCHULTZ-CHERRY et al.** Influenza virus (A/HK/156/97) hemagglutinin expressed by an alphavirus replicon system protects chickens against lethal infection with Hong Kong-origin H5N1 viruses. *Virology,* 2000, vol. 278, 55-59 **[0133]**
- **STALLKNECHT et al.** Avian paramyxoviruses from migrating and resident ducks in coastal Louisiana. *Journal af Wildlive Diseases,* 1991, vol. 27, 123-128 **[0133]**
- **STANISLAWEK et al.** Avian paramyxoviruses and influenza viruses isolated from mallard ducks (Anas platyrhynchos) in New Zealand. *Archives of Virology,* 2002, vol. V147, 1287-1302 **[0133]**
- **TANG M et al.** Recombinant adenovirus encoding the HA gene from swine H3N2 influenza virus partially protects mice from challenge with heterologous virus: A/HK/I/68 (H3N2). *Arch Virol,* 2002, vol. 147, 2125-2141 **[0133]**
- **TAYLOR et al.** Protective immunity against avian influenza induced by a fowlpox virus recombinant. *Vaccine,* 1998, vol. 6, 504-508 **[0133]**
- **TORO et al.** Protective avian influenza in ovo vaccination with non-replicating human adenovirus vector. *Vaccine,* 2007, vol. 25, 2886-2891 **[0133]**
- **TUMOVA et al.** A hitherto unreported paramyxovirus of turkeys. *Res Vet Sci,* 1979, vol. 27, 135-40 **[0133]**
- **TUMOVA et al.** Further evidence of the circulation of PMV-4 and influenza viruses with N2-1957 enzyme in the migratory waterfowls. *Acta Virol,* 1989, vol. 33, 573-6 **[0133]**
- **VEITS et al.** Deletion of the non-essential UL0 gene of infectious laryngotracheitis (ILT) virus leads to attenuation in chickens, and UL0 mutants expressing influenza virus haemagglutinin (H7) protect against ILT and fowl plague. *J Gen Virol,* 2003, vol. 84, 3343-3352 **[0133]**
- **VEITS et al.** Newcastle disease virus expressing H5 hemagglutinin gene protects chickens against Newcastle disease and avian influenza. *Proceedings of the National Academy of Sciences,* 2006, vol. 103 (21), 8197-8202 **[0133]**
- **WEBSTER et al.** Ortho- and paramyxoviruses from migrating feral ducks: characterization of a new group of influenza A viruses. *J Gen Virol,* 1976, vol. 32, 217-25 **[0133]**
- **YAMANE et al.** Characterization of avian paramyxoviruses isolated from feral ducks in northern Japan: the presence of three distinct viruses in nature. *Microbiol Immunol,* 1982, vol. 26, 557-68 **[0133]**
- **ZHANG et al.** Serological survey on prevalence of antibodies to avian paramyxovirus serotype 2 in China. *Avian Dis,* 2007, vol. 51, 137-9 **[0133]**
- **ZHANG et al.** Isolation, identification, and comparison of four isolates of avian paramyxovirus serotype 2 in China. *Avian Dis,* 2006, vol. 50, 386-90 **[0133]**
- **ZOU et al.** Complete Genome Sequence and Biological Characterizations of A Novel Goose Paramyxovirus-SF02 Isolated in China. *Virus Genes,* 2005, vol. 30, 13-21 **[0133]**

REKOMBINÁNS MADÁR-PARAMYXOVÍRUS-OLTÓANYAG ÉS ELJÁRÁS ELŐÁLLÍTÁSÁRA ÉS ALKALMAZÁSÁRA

Szabadalmi igénypontok

1. Oltóanyag, amely tartalmaz: (i) rekombináns APMV virális vektort és (ii) gyógyászatilag vagy állatgyógyászatilag elfogadható hordozót, ahol az APMV virális vektor APMV-8, és ahol az APMV virális vektor tartalmaz egy olyan polinukleotidot, melynek szekvenciája legalább 90%-ban azonos egy SEQ ID NO:1 szerinti szekvenciájú polinukleotid szekvenciájával vagy egy olyan polinukleotidot, amely komplementer olyan polinukleotiddal, melynek szekvenciája legalább 90%-ban azonos egy SEQ ID NO:1 szerinti szekvenciájú polinukleotid szekvenciájával; ahol az APMV virális vektor tartalmaz továbbá antigént vagy patogént kódoló izolált polinukleotidot, ahol a patogén madár-, macskaféle-, kutyaféle-, lóféle, szarvasmarhaféle-, juhféle-, kecskeféle- vagy sertésféle-patogén, ahol a polinukleotid az APMV genomjának nem esszenciális régiójába inszertált, és ahol továbbá a nem esszenciális régió a következőkből álló régiókból választott: az NP nyitott leolvasási kerettől 5'irányban elhelyezkedő nem transzlálódó régió, az APMV genom két nyitott leolvasási kerete közötti intergenikus régiók és az L nyitott leolvasási kerettől 3' irányban elhelyezkedő nem transzlálódó régió.

2. Gyógyászati készítmény vagy oltóanyag, amely rekombináns APMV virális vektort tartalmaz, ahol a rekombináns APMV virális vektor állati antigént vagy patogént kódoló és expresszáló heterológ polinukleotidot tartalmaz, állatban az antigénre immunológiai válasz indukálásában történő alkalmazásra, ahol az alkalmazás magában foglalja az állat inokulálását a gyógyászati készítménnyel vagy oltóanyaggal,

ahol az APMV virális vektor APMV-8 és ahol az APMV virális vektor tartalmaz egy olyan polinukleotidot, melynek szekvenciája legalább 90%-ban azonos SEQ ID NO:1 szerinti szekvenciájú polinukleotid szekvenciájával vagy egy olyan polinukleotidot, amely komplementer olyan polinukleotiddal, melynek szekvenciája legalább 90%-ban azonos SEQ ID NO:1 szerinti szekvenciájú polinukleotid szekvenciájával;

ahol a patogén madár-, macskaféle-, kutyaféle-, lóféle, szarvasmarhaféle-, juhféle-, kecskeféle- vagy sertésféle-patogén, és ahol a heterológ polinukleotid az APMV genomjának a következőkből álló régiókból választott nem esszenciális régiójába inszertált: NP nyitott leolvasási kerettől 5' irányban elhelyezkedő nem transzlálódó régió, az APMV genom két nyitott leolvasási kerete közötti intergenikus régiók és az L nyitott leolvasási kerettől 3' irányban elhelyezkedő nem transzlálódó régió.

3. A 2. igénypont szerinti gyógyászati készítmény vagy oltóanyag az ott meghatározott alkalmazásra, ahol az immunológiai válasz az antigénre egy állatban prímer-emlékeztető rendszerben indukált.

4. A 2. vagy 3. igénypont szerinti gyógyászati készítmény vagy oltóanyag az ott meghatározott alkalmazásra, ahol az állat madár, lóféle, kutyaféle, macskaféle, sertésféle, szarvasmarhaféle vagy juhféle.

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