INFLUENZA VIRUS VACCINE COMPOSITION AND METHODS OF USE

BACKGROUND OF THE INVENTION

[0001] The present invention relates to influenza virus vaccine compositions and methods of treating or preventing influenza infection and disease in mammals. Influenza is an acute febrile illness caused by infection of the respiratory tract. There are three types of influenza viruses: A, B, and C "IAV," "IBV" or "IAC," respectively, or generally "IV". Type A, which includes several subtypes, causes widespread epidemics and global pandemics such as those that occurred in 1918, 1957 and 1968. Type B causes regional epidemics. Type C causes sporadic cases and minor, local outbreaks. These virus types are distinguished in part on the basis of differences in two structural proteins, the nucleoprotein, found in the center of the virus, and the matrix protein, which forms the viral shell.

[0002] The disease can cause significant systemic symptoms, severe illness requiring hospitalization (such as viral pneumonia), and complications such as secondary bacterial pneumonia. More than 20 million people died during the pandemic flu season of 1918/1919, the largest pandemic of the 20th century. Recent epidemics in the United States are believed to have resulted in greater than 10,000 (up to 40,000) excess deaths per year and 5,000-10,000 deaths per year in non-epidemic years.

[0003] The best strategy for prevention of morbidity and mortality associated with influenza is vaccination. Vaccination is especially recommended for people in high-risk groups, such as residents of nursing or residential homes, as well as for diabetes, chronic renal failure, or chronic respiratory conditions.

[0004] Traditional methods of producing influenza vaccines involve growth of an isolated strain in embryonated hens' eggs. Initially, the virus is recovered

from a throat swab or similar source and isolated in eggs. The initial isolation in egg is difficult, but the virus adapts to its egg host and subsequent propagation in eggs takes place relatively easily. It is widely recognized, however, that the egg-derived production of IV for vaccine purposes has several disadvantages. One disadvantage is that such production process is rather vulnerable due to the varying (micro)biological quality of the eggs. Another disadvantage is that the process completely lacks flexibility if demand suddenly increases, *i.e.*, in case of a serious epidemic or pandemic, because of the logistical problems due to the non-availability of large quantities of suitable eggs. Also, vaccines thus produced are contra-indicated for persons with a known hypersensitivity to chicken and/or egg proteins.

[0005] The influenza vaccines currently in use are designated whole virus (WV) vaccine or subvirion (SV) (also called "split" or "purified surface antigen"). The WV vaccine contains intact, inactivated virus, whereas the SV vaccine contains purified virus disrupted with detergents that solubilize the lipid-containing viral envelope, followed by chemical inactivation of residual virus. Attenuated viral vaccines against influenza are also in development. A discussion of methods of preparing conventional vaccine may be found in Wright, P.F. & Webster, R.G., FIELDS VIROLOGY, 4d Ed. (Knipe, D.M. *et al.* Ed.), 1464-65 (2001), for example.

Virus Structures

[0006] An IV is roughly spherical, but it can also be elongated or irregularly shaped. Inside the virus, eight segments of single-stranded RNA contain the genetic instructions for making the virus. The most striking feature of the virus is a layer of spikes projecting outward over its surface. There are two different types of spikes: one is composed of the molecule hemagglutinin (HA), the other of neuraminidase (NA). The HA molecule allows the virus to "stick" to a cell, initiating infection. The NA molecule allows newly formed viruses to exit their host cell without sticking to the cell surface or to each

other. The viral capsid is comprised of viral ribonucleic acid and several so called "internal" proteins (polymerases (PB1, PB2, and PA, matrix protein (M1) and nucleoprotein (NP)). Because antibodies against HA and NA have traditionally proved the most effective in fighting infection, much research has focused on the structure, function, and genetic variation of those molecules. Researchers are also interested in a two non-structural proteins M2 and NS1; both molecules play important roles in viral infection.

[0007] Type A subtypes are described by a nomenclature system that includes the geographic site of discovery, a lab identification number, the year of discovery, and in parentheses the type of HA and NA it possesses, for example, A/Hong Kong/156/97 (H5N1). If the virus infects non-humans, the host species is included before the geographical site, as in A/Chicken/Hong Kong/G9/97 (H9N2).

[0008] Virions contain 7 segments (influenza C virus) to 8 segments (influenza A and B virus) of linear negative-sense single stranded RNA. Most of the segments of the virus genome code for a single protein. For many influenza viruses, the whole genome is now known. Genetic reassortment of the virus results from intermixing of the parental gene segments in the progeny of the viruses when a cell is co-infected by two different viruses of a given type. This phenomenon is facilitated by the segmental nature of the genome of influenza virus. Genetic reassortment is manifested as sudden changes in the viral surface antigens.

[0009] Antigenic changes in HA and NA allow the influenza virus to have tremendous variability. Antigenic drift is the term used to indicate minor antigenic variations in HA and NA of the influenza virus from the original parent virus, while major changes in HA and NA which make the new virions significantly different, are called Antigenic shift. The difference between the two phenomena is a matter of degree.

[0010] Antigenic drift (minor changes) occurs due to accumulation of point mutations in the gene which results in changes in the amino acids in the proteins. Changes which are extreme, and drastic (too drastic to be explained

by mutation alone) result in antigenic shift of the virus. The segmented genomes of the influenza viruses reassort readily in double infected cells. Genetic reassortment between human and non-human influenza virus has been suggested as a mechanism for antigenic shift. Influenza is a zoonotic disease, and an important pathogen in a number of animal species, including swine, horses, and birds, both wild and domestic. Influenza viruses are transferred to humans from other species.

[0011] Because of antigenic shift and antigenic drift, immunity to an IV carrying a particular HA and/or NA protein does not necessarily confer protective immunity against IV strains carrying variant, or different HA and/or NA proteins. Because antibodies against HA and NA have traditionally proved the most effective in fighting IV infection, much research has focused on the structure, function and genetic variation of those molecules.

Recent IV Vaccine Candidates

[0012] During the past few years, there has been substantial interest in testing DNA-based vaccines for a number of infectious diseases where the need for a vaccine, or an improved vaccine, exists. Several well-recognized advantages of DNA-based vaccines include the speed, ease and cost of manufacture, the versatility of developing and testing multivalent vaccines, the finding that DNA vaccines can produce a robust cellular response in a wide variety of animal models as well as in humans, and the proven safety of using plasmid DNA as a delivery vector (Donnelly, J.J., *et al., Annu. Rev. Immunol. 15*:617-648 (1997); Manickan, E., *et al., Crit. Rev. Immunol. 17*(2):139-154 (1997); U.S. Patent No. 6,214,804). DNA vaccines represent the next generation in the development of vaccines (Nossal, G., *Nat. Med. 4*(5 Supple):475-476 (1998)) and numerous DNA vaccines are in clinical trials. The above references are herein incorporated by reference in their entireties.

[0013] Studies have already been performed using DNA-based vaccines in animals. Ulmer, J.B. *et al., Science 259*:1745-9 (1993) revealed that mice

could be protected by an IV nucleoprotein DNA vaccine alone against severe disease and death resulting from either a homologous or a heterologous IV challenge. Further studies have substantiated this model, and comparative studies of live influenza vaccines versus DNA influenza vaccines show them to be relatively equivalent in immune induction and protection in the murine model.

[0014] WO 94/21797, incorporated herein by reference in its entirety, discloses IV vaccine compositions comprising DNA constructs encoding NP, HA, M1, PB1 and NS1. WO 94/21797 also discloses methods of protecting against IV infection comprising immunization with a prophylactically effective amount of these DNA vaccine compositions.

[0015] The IV nucleoprotein is relatively conserved (*see* Shu, L.L. *et al.*, *J. Virol. 67*:2723-9 (1993)), but just as conserved are the M1 matrix protein (which is a major T-cell target), and the M2 protein, which are encoded by separate reading frames of RNA segment 7. *See* Neirynck, S. *et al.*, *Nat. Med. 5*:1157-63 (1999); Lamb, R.A. & Lai, C.J., *Virology 112*:746-51 (1981); Ito, T. *et al.*, *J. Virol. 65*:5491-8 (1991). Animal DNA vaccine trials have been performed with DNA constructs encoding these genes alone or in combination, usually with success. *See* Okuda, K., *et al.*, *Vaccine 19*:3681-91 (2001); Watabe, S. *et al.*, *Vaccine* 19:4434-44 (2001). Of interest, the M2 protein is involved as part of an ion channel, is critical in resistance to the antiviral agents amantadine and rimantidine, and approximately 24 amino acids are extracellular (eM2). *See* Fischer, W.B., *Biochim Biophys Acta 1561*:27-45 (2002); Zhong, Q., *FEBS Lett 434*:265-71 (1998). Antibodies to this extracellular, highly conserved protein (eM2), which is highly expressed in infected cells (Lamb, R.A., *et al.*, *Cell 40*:627-33 (1985)), have been shown to be involved in animal models. Treanor, J.J., *J. Virol. 64*:1375-7 (1990); Slepushkin, V.A. *et al.*, *Vaccine 13*:1399-402 (1995). An approach using a conjugate hepatitis B core-eM2 protein has been evaluated in an animal model and proposed as a pandemic influenza vaccine. Neirynck, S. *et al.*, *Nat. Med. 5*:1157-63 (1999). However, in one study vaccination of pigs with a DNA

construct expressing eM2-NP fusion protein exacerbated disease after challenge with influenza A virus. Heinen, P.P., *J. Gen. Virol. 83*:1851-59 (2002). All of the above references are herein incorporated by reference in their entireties.

[0016] Heterologous "prime boost" strategies have been effective for enhancing immune responses and protection against numerous pathogens. Schneider *et al., Immunol. Rev.* 170:29-38 (1999); Robinson, H.L., *Nat. Rev. Immunol.* 2:239-50 (2002); Gonzalo, R.M. *et al., Vaccine 20*:1226-31 (2002); Tanghe, A., *Infect. Immun. 69*:3041-7 (2001). Providing antigen in different forms in the prime and the boost injections appears to maximize the immune response to the antigen. DNA vaccine priming followed by boosting with protein in adjuvant or by viral vector delivery of DNA encoding antigen appears to be the most effective way of improving antigen specific antibody and CD4+ T-cell responses or CD8+ T-cell responses respectively. Shiver J.W. *et al., Nature 415*: 331-5 (2002); Gilbert, S.C. *et al., Vaccine* 20:1039-45 (2002); Billaut-Mulot, O. *et al., Vaccine 19*:95-102 (2000); Sin, J.I. *et al.,* DNA Cell Biol. 18:771-9 (1999). Recent data from monkey vaccination studies suggests that adding CRL1005 poloxamer (12 kDa, 5% POE), to DNA encoding the HIV gag antigen enhances T-cell responses when monkeys are vaccinated with an HIV gag DNA prime followed by a boost with an adenoviral vector expressing HIV gag (Ad5-gag). The cellular immune responses for a DNA/poloxamer prime followed by an Ad5-gag boost were greater than the responses induced with a DNA (without poloxamer) prime followed by Ad5-gag boost or for Ad5-gag only. Shiver, J.W. *et al. Nature* 415:331-5 (2002). U.S. Patent Appl. Publication No. US 2002/0165172 A1 describes simultaneous administration of a vector construct encoding an immunogenic portion of an antigen and a protein comprising the immunogenic portion of an antigen such that an immune response is generated. The document is limited to hepatitis B antigens and HIV antigens. Moreover, U.S. Patent No. 6,500,432 is directed to methods of enhancing an immune response of nucleic acid vaccination by simultaneous administration of a polynucleotide

and polypeptide of interest. According to the patent, simultaneous administration means administration of the polynucleotide and the polypeptide during the same immune response, preferably within 0-10 or 3-7 days of each other. The antigens contemplated by the patent include, among others, those of Hepatitis (all forms), HSV, HIV, CMV, EBV, RSV, VZV, HPV, polio, influenza, parasites (*e.g.*, from the genus *Plasmodium*), and pathogenic bacteria (including but not limited to *M. tuberculosis*, *M. leprae*, *Chlamydia*, *Shigella*, *B. burgdorferi*, enterotoxigenic *E. coli*, *S. typhosa*, *H. pylori*, *V. cholerae*, *B. pertussis*, etc.). All of the above references are herein incorporated by reference in their entireties.

SUMMARY OF THE INVENTION

[0017] The present invention is directed to enhancing the immune response of a vertebrate in need of protection against IV infection by administering *in vivo*, into a tissue of the vertebrate, at least one polynucleotide, wherein the polynucleotide comprises one or more nucleic acid fragments, where the one or more nucleic acid fragments are optionally fragments of codon-optimized coding regions operably encoding one or more IV polypeptides, or fragments, variants, or derivatives thereof. The present invention is further directed to enhancing the immune response of a vertebrate in need of protection against IV infection by administering, *in vivo*, into a tissue of the vertebrate, a polynucleotide described above plus at least one isolated IV polypeptide or a fragment, a variant, or derivative thereof. The isolated IV polypeptide can be, for example, a purified subunit, a recombinant protein, a viral vector expressing an isolated IV polypeptide, or can be an inactivated or attentuated IV, such as those present in conventional IV vaccines. According to either method, the polynucleotide is incorporated into the cells of the vertebrate *in vivo*, and an immunologically effective amount of an immunogenic epitope of the encoded IV polypeptide, or a fragment, variant, or derivative thereof, is produced *in vivo*. When utilized, an isolated IV polypeptide or a fragment,

variant, or derivative thereof is also administered in an immunologically effective amount.

[0018] According to the present invention, the polynucleotide can be administered either prior to, at the same time (simultaneously), or subsequent to the administration of the isolated IV polypeptide. The IV polypeptide or fragment, variant, or derivative thereof encoded by the polynucleotide comprises at least one immunogenic epitope capable of eliciting an immune response to influenza virus in a vertebrate. In addition, an isolated IV polypeptide or fragment, variant, or derivative thereof, when used, comprises at least one immunogenic epitope capable of eliciting an immune response in a vertebrate. The IV polypeptide or fragment, variant, or derivative thereof encoded by the polynucleotide can, but need not, be the same protein or fragment, variant, or derivative thereof as the isolated IV polypeptide which can be administered according to the method.

[0019] The polynucleotide of the invention can comprise a nucleic acid fragment, where the nucleic acid fragment is a fragment of a codon-optimized coding region operably encoding any IV polypeptide or fragment, variant, or derivative thereof, including, but not limited to, HA, NA, NP, M1 or M2 proteins or fragments (*e.g.*, eM2), variants or derivatives thereof. A polynucleotide of the invention can also encode a derivative fusion protein, wherein two or more nucleic acid fragments, at least one of which encodes an IV polypeptide or fragment, variant, or derivative thereof, are joined in frame to encode a single polypeptide, *e.g.*, NP fused to eM2. Additionally, a polynucleotide of the invention can further comprise a heterologous nucleic acid or nucleic acid fragment. Such heterologous nucleic acid or nucleic acid fragment may encode a heterologous polypeptide fused in frame with the polynucleotide encoding the IV polypeptide, *e.g.*, a hepatitis B core protein or a secretory signal peptide. Preferably, the polynucleotide encodes an IV polypeptide or fragment, variant, or derivative thereof comprising at least one immunogenic epitope of IV, wherein the epitope elicits a B-cell (antibody) response, a T-cell (*e.g.*, CTL) response, or both.

[0020] Similarly, the isolated IV polypeptide or fragment, variant, or derivative thereof to be delivered (either a recombinant protein, a purified subunit, or viral vector expressing an isolated IV polypeptide, or in the form of an inactivated IV vaccine) can be any isolated IV polypeptide or fragment, variant, or derivative thereof, including but not limited to the HA, NA, NP, M1 or M2 proteins or fragments (*e.g.*, eM2), variants or derivatives thereof. In certain embodiments, a derivative protein can be a fusion protein, *e.g.*, NP-eM2. In other embodiments, the isolated IV polypeptide or fragment, variant, or derivative thereof can be fused to a heterologous protein, *e.g.*, a secretory signal peptide or the hepatitis B virus core protein. Preferably, the isolated IV polypeptide or fragment, variant, or derivative thereof comprises at least one immunogenic epitope of IV, wherein the antigen elicits a B-cell antibody response, a T-cell antibody response, or both.

[0021] Nucleic acids and fragments thereof of the present invention can be altered from their native state in one or more of the following ways. First, a nucleic acid or fragment thereof which encodes an IV polypeptide or fragment, variant, or derivative thereof can be part or all of a codon-optimized coding region, optimized according to codon usage in the animal in which the vaccine is to be delivered. In addition, a nucleic acid or fragment thereof which encodes an IV polypeptide can be a fragment which encodes only a portion of a full-length polypeptide, and/or can be mutated so as to, for example, remove from the encoded polypeptide non-desired protein motifs present in the encoded polypeptide or virulence factors associated with the encoded polypeptide. For example, the nucleic acid sequence could be mutated so as not to encode a membrane anchoring region that would prevent release of the polypeptide from the cell as with, *e.g.*, eM2. Upon delivery, the polynucleotide of the invention is incorporated into the cells of the vertebrate *in vivo*, and a prophylactically or therapeutically effective amount of an immunologic epitope of an IV is produced *in vivo*.

[0022] Similarly, the proteins of the invention can be a fragment of a full-length IV polypeptide and/or can be altered so as to, for example, remove

from the polypeptide non-desired protein motifs present in the polypeptide or virulence factors associated with the polypeptide. For example, the polypeptide could be altered so as not to encode a membrane anchoring region that would prevent release of the the polypeptide from the cell.

[0023] The invention further provides immunogenic compositions comprising at least one polynucleotide, wherein the polynucleotide comprises one or more nucleic acid fragments, where each nucleic acid fragment is a fragment of a codon-optimized coding region encoding an IV polypeptide or a fragment, a variant, or a derivative thereof; and immunogenic compositions comprising a polynucleotide as described above and at least one isolated IV polypeptide or a fragment, a variant, or derivative thereof. Such compositions can further comprise, for example, carriers, excipients, transfection facilitating agents, and/or adjuvants as described herein.

[0024] The immunogenic compositions comprising a polynucleotide and an isolated IV polypeptide or fragment, variant, or derivative thereof as described above can be provided so that the polynucleotide and protein formulation are administered separately, for example, when the polynucleotide portion of the composition is administered prior (or subsequent) to the isolated IV polypeptide portion of the composition. Alternatively, immunogenic compositions comprising the polynucleotide and the isolated IV polypeptide or fragment, variant, or derivative thereof can be provided as a single formulation, comprising both the polynucleotide and the protein, for example, when the polynucleotide and the protein are administered simultaneously. In another alternative, the polynucleotide portion of the composition and the isolated IV polypeptide portion of the composition can be provided simultaneously, but in separate formulations.

[0025] Compositions comprising at least one polynucleotide comprising one or more nucleic acid fragments, where each nucleic acid fragment is optionally a fragment of a codon-optimized coding region operably encoding an IV polypeptide or fragment, variant, or derivative thereof together with and one or more isolated IV polypeptides or fragments, variants or derivatives thereof

(as either a recombinant protein, a purified subunit, a viral vector expressing the protein, or in the form of an inactivated or attenuated IV vaccine) will be referred to herein as "combinatorial polynucleotide (*e.g.*, DNA) vaccine compositions" or "single formulation heterologous prime-boost vaccine compositions."

[0026] The compositions of the invention can be univalent, bivalent, trivalent or mulitvalent. A univalent composition will comprise only one polynucleotide comprising a nucleic acid fragment, where the nucleic acid fragment is optionally a fragment of a codon-optimized coding region encoding an IV polypeptide or a fragment, variant, or derivative thereof, and optionally the same IV polypeptide or a fragment, variant, or derivative thereof in isolated form. In a single formulation heterologous prime-boost vaccine composition, a univalent composition can include a polynucleotide comprising a nucleic acid fragment, where the nucleic acid fragment is optionally a fragment of a codon-optimized coding region encoding an IV polypeptide or a fragment, variant, or derivative thereof and an isolated polypeptide having the same antigenic region as the polynucleotide. A bivalent composition will comprise, either in polynucleotide or protein form, two different IV polypeptides or fragments, variants, or derivatives thereof, each capable of eliciting an immune response. The polynucleotide(s) of the composition can encode two IV polypeptides or alternatively, the polynucleotide can encode only one IV polypeptide and the second IV polypeptide would be provided by an isolated IV polypeptide of the invention as in, for example, a single formulation heterologous prime-boost vaccine composition. In the case where both IV polypeptides of a bivalent composition are delivered in polynucleotide form, the nucleic acid fragments operably encoding those IV polypeptides need not be on the same polynucleotide, but can be on two different polynucleotides. A trivalent or further multivalent composition will comprise three IV polypeptides or fragments, variants or derivatives thereof, either in isolated form or encoded by one or more polynucleotides of the invention.

[0027] The present invention further provides plasmids and other polynucleotide constructs for delivery of nucleic acid fragments of the invention to a vertebrate, *e.g.*, a human, which provide expression of IV polypeptides, or fragments, variants, or derivatives thereof. The present invention further provides carriers, excipients, transfection-facilitating agents, immunogenicity-enhancing agents, *e.g.*, adjuvants, or other agent or agents to enhance the transfection, expression or efficacy of the administered gene and its gene product.

[0028] In one embodiment, a mulitvalent composition comprises a single polynucleotide, *e.g.*, plasmid, comprising one or more nucleic acid regions operably encoding IV polypeptides or fragments, variants, or derivatives thereof. Reducing the number of polynucleotides, *e.g.*, plasmids in the compositions of the invention can have significant impacts on the manufacture and release of product, thereby reducing the costs associated with manufacturing the compositions. There are a number of approaches to include more than one expressed antigen coding sequence on a single plasmid. These include, for example, the use of Internal Ribosome Entry Site (IRES) sequences, dual promoters/expression cassettes, and fusion proteins.

[0029] The invention also provides methods for enhancing the immune response of a vertebrate to IV infection by administering to the tissues of a vertebrate one or more polynucleotides each comprising one or more nucleic acid fragments, where each nucleic acid fragment is optionally a fragment of a codon-optimized coding region encoding an IV polypeptide or fragment, variant, or derivative thereof; and optionally administering to the tissues of the vertebrate one or more isolated IV polypeptides, or fragments, variants, or derivatives thereof. The isolated IV polypeptide can be administered prior to, at the same time (simultaneously), or subsequent to administration of the polynucleotides encoding IV polypeptides.

[0030] In addition, the invention provides consensus amino acid sequences for IV polypeptides, or fragments, variants or derivatives thereof, including, but not limited to the HA, NA, NP, M1 or M2 proteins or fragments (*e.g.* eM2),

variants or derivatives thereof. Polynucleotides which encode the consensus polypeptides or fragments, variants or derivatives thereof, are also embodied in this invention. Such polynucleotides can be obtained by known methods, for example by backtranslation of the amino acid sequence and PCR synthesis of the corresponding polynucleotide as described below.

BRIEF DESCRIPTION OF THE FIGURES

[0031] Figure 1 shows an alignment of nucleotides 46-1542 of SEQ ID NO:1 (native NP coding region) with a coding region fully codon-optimized for human usage (SEQ ID NO:23).

[0032] Figure 2 shows the protocol for the preparation of a formulation comprising 0.3 mM BAK, 7.5 mg/ml CRL 1005 and 5 mg/ml of DNA in a final volume of 3.6 ml, through the use of thermal cycling.

[0033] Figure 3 shows the protocol for the preparation of a formulation comprising 0.3 mM BAK, 34 mg/ml or 50 mg/ml CRL 1005 and 2.5 mg/ml DNA in a final volumne of 4.0 ml, through the use of thermal cycling.

[0034] Figure 4 shows the protocol for the simplified preparation (without thermal cycling) of a formulation comprising 0.3 mM BAK, 7.5 mg/ml CRL 1005 and 5 mg/ml DNA.

[0035] Figure 5 shows the anti-NP antibody response three weeks after a single administration of a combinatorial prime-boost vaccine formulation against the influenza virus NP protein.

[0036] Figure 6 shows the anti-NP antibody response twelve days after a second administration of a combinatorial prime-boost vaccine formulation against the influenza virus NP protein.

[0037] Figure 7 shows the CD8+ T Cell response to a combinatorial prime-boost vaccine formulation against the influenza virus NP protein.

[0038] Figure 8 shows the CD4+ T Cell response to a combinatorial prime-boost vaccine formulation against the influenza virus NP protein.

[0039] Figures 9A and 9B show the results of a two dose mouse immunization regimen study with plasmid DNA encoding IAV HA (H3).

[0040] Figures 10A and 10B show the *in vitro* expression of M1 and M2 from segment 7 and an M1M2 fusion.

[0041] Figures 11A and 11B show the *in vitro* expression of eM2-NP and codon-optimized influenza virus NP protein.

[0042] Figure 12 shows the influenza A NP protein consensus amino acid sequence aligned with 22 full length NP sequences.

[0043] Figure 13 is a schematic diagram of various vectors encoding influenza proteins described herein.

[0044] Figure 14 are the results of western blot experiments as described in Example 13, Experiment 3. The blots show lysates of VM92 cells transfected with plasmids which express M2 or NP to compare expression of the influenza protein from different expression vectors.

[0045] Figure 15 are the results of western blot experiments as described in Example 13, Experiment 3. The blots show lysates of VM92 cells transfected with plasmids which express M1, M2 or NP to compare expression of the influenza protein from expression vectors.

DETAILED DESCRIPTION OF THE INVENTION

[0046] The present invention is directed to compositions and methods for enhancing the immune response of a vertebrate in need of protection against IV infection by administering *in vivo*, into a tissue of a vertebrate, at least one polynucleotide comprising one or more nucleic acid fragments, where each nucleic acid fragment is optionally a fragment of a codon-optimized coding region operably encoding an IV polypeptide, or a fragment, variant, or derivative thereof in cells of the vertebrate in need of protection. The present invention is also directed to administering *in vivo*, into a tissue of the vertebrate the above described polynucleotide and at least one isolated IV polypeptide, or a fragment, variant, or derivative thereof. The isolated IV

polypeptide or fragment, variant, or derivative thereof can be, for example, a recombinant protein, a purified subunit protein, a protein expressed and carried by a heterologous live or inactivated or attentuated viral vector expressing the protein, or can be an inactivated IV, such as those present in conventional, commercially available, inactivated IV vaccines. According to either method, the polynucleotide is incorporated into the cells of the vertebrate *in vivo*, and an immunologically effective amount of the influenza protein, or fragment or variant encoded by the polynucleotide is produced *in vivo*. The isolated protein or fragment, variant, or derivative thereof is also administered in an immunologically effective amount. The polynucleotide can be administered to the vertebrate in need thereof either prior to, at the same time (simultaneously), or subsequent to the administration of the isolated IV polypeptide or fragment, variant, or derivative thereof.

[0047] Non-limiting examples of IV polypeptides within the scope of the invention include, but are not limited to, NP, HA, NA, M1 and M2 polypeptides, and fragments, *e.g.*, eM2, derivatives, *e.g.*, an NP-eM2 fusion, and variants thereof. Nucleotide and amino acid sequences of IV polypeptides from a wide variety of IV types and subtypes are known in the art. The nucleotide sequences set out below are the wild-type sequences. For example, the nucleotide sequence of the NP protein of Influenza A/PR/8/34 (H1N1) is available as GenBank Accession Number M38279.1, and has the following sequence, referred to herein as SEQ ID NO:1:

AGCAAAAGCAGGGTAGATAATCACTCACTGAGTGACATCAAAATCATGGCGTCTCAAGGCACC
AAACGATCTTACGAACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATCAGAGCA
TCCGTCGGAAAAATGATTGGTGGAATTGGACGATTCTACATCCAAATGTGCACCGAACTCAAA
CTCAGTGATTATGAGGGACGGTTGATCCAAAACAGCTTAACAATAGAGAGAATGGTGCTCTCT
GCTTTTGACGAAAGGAGAAATAAATACCTTGAAGAACATCCCAGTGCGGGGAAAGATCCTAAG
AAAACTGGAGGACCTATATACAGGAGAGTAAACGGAAAGTGGATGAGAGAACTCATCCTTTAT
GACAAAGAAGAAATAAGGCGAATCTGGCGCCAAGCTAATAATGGTGACGATGCAACGGCTGGT
CTGACTCACATGATGATCTGGCATTCCAATTTGAATGATGCAACTTATCAGAGGACAAGAGCT
CTTGTTCGCACCGGAATGGATCCCAGGATGTGCTCTCTGATGCAAGGTTCAACTCTCCCTAGG
AGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGAGTTGGAACAATGGTGATGGAATTGGTCAGA
ATGATCAAACGTGGGATCAATGATCGGAACTTCTGGAGGGGTGAGAATGGACGAAAAACAAGA
ATTGCTTATGAAAGAATGTGCAACATTCTCAAAGGGAAATTTCAAACTGCTGCACAAAAAGCA
ATGATGGATCAAGTGAGAGAGAGCCGGAACCCAGGGAATGCTGAGTTCGAAGATCTCACTTTT
CTAGCACGGTCTGCACTCATATTGAGAGGGTCGGTTGCTCACAAGTCCTGCCTGCCTGCCTGT
GTGTATGGACCTGCCGTAGCCAGTGGGTACGACTTTGAAAGGGAGGGATACTCTCTAGTCGGA
ATAGACCCTTTCAGACTGCTTCAAAACAGCCAAGTGTACAGCCTAATCAGACCAAATGAGAAT
CCAGCACACAAGAGTCAACTGGTGTGGATGGCATGCCATTCTGCCGCATTTGAAGATCTAAGA

GTATTAAGCTTCATCAAAGGGACGAAGGTGCTCCCAAGAGGGAAGCTTTCCACTAGAGGAGTT
CAAATTGCTTCCAATGAAAATATGGAGACTATGGAATCAAGTACACTTGAACTGAGAAGCAGG
TACTGGGCCATAAGGACCAGAAGTGGAGGAAACACCAATCAACAGAGGGCATCTGCGGGCCAA
ATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCTTTTGACAGAACAACCGTTATG
GCAGCATTCAGTGGGAATACAGAGGGGAGAACATCTGACATGAGGACCGAAATCATAAGGATG
ATGGAAAGTGCAAGACCAGAAGATGTGTCTTTCCAGGGGCGGGGAGTCTTCGAGCTCTCGGAC
GAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATGAGTAATGAAGGATCTTATTTCTTC
GGAGACAATGCAGAGGAATACGATAATTAAAGAAAAATACCCTTGTTTCTACT

[0048] The amino acid sequence of the NP protein of Influenza A/PR/8/34 (H1N1), encoded by nucleotides 46-1494 of SEQ ID NO:1 is as follows, referred to herein as SEQ ID NO:2:

MASQGTKRSYEQMETDGERQNATEIRASVGKMIGGIGRFYIQMCTELKLSDYEGRLIQNSLTI
ERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYRRVNGKWMRELILYDKEEIRRIWRQANNG
DDATAGLTHMMIWHSNLNDATYQRTRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTM
VMELVRMIKRGINDRNFWRGENGRKTRIAYERMCNILKGKFQTAAQKAMMDQVRESRNPGNAE
FEDLTFLARSALILRGSVAHKSCLPACVYGPAVASGYDFEREGYSLVGIDPFRLLQNSQVYSL
IRPNENPAHKSQLVWMACHSAAFEDLRVLSFIKGTKVLPRGKLSTRGVQIASNENMETMESST
LELRSRYWAIRTRSGGNTNQQRASAGQISIQPTFSVQRNLPFDRTTVMAAFSGNTEGRTSDMR
TEIIRMMESARPEDVSFQGRGVFELSDEKAASPIVPSFDMSNEGSYFFGDNAEEYDN

[0049] Segment 7 of the IAV genome encodes both M1 and M2. Seqment 7 of Influenza A virus (A/Puerto Rico/8/34/Mount Sinai (H1N1)), is available as GenBank Accession No. AF389121.1, and has the following sequence, referred to herein as SEQ ID NO:3:

AGCGAAAGCAGGTAGATATTGAAAGATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTC
TATCATCCCGTCAGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAGG
GAAGAACACTGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACCAATCCTGTCACCTCT
GACTAAGGGGATTTTAGGATTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAGCG
TAGACGCTTTGTCCAAAATGCCCTTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGT
TAAACTGTATAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCACTCAG
TTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAACAGGATGGGGGCTGTGAC
CACTGAAGTGGCATTTGGCCTGGTATGTGCAACCTGTGAACAGATTGCTGACTCCCAGCATCG
GTCTCATAGGCAAATGGTGACAACAACCAATCCACTAATCAGACATGAGAACAGAATGGTTTT
AGCCAGCACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCAGCAGAGGC
CATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGATGAGAACCATTGGGACTCATCC
TAGCTCCAGTGCTGGTCTGAAAAATGATCTTCTTGAAAATTTGCAGGCCTATCAGAAACGAAT
GGGGGTGCAGATGCAACGGTTCAAGTGATCCTCTCGCTATTGCCGCAAATATCATTGGGATCT
TGCACTTGACATTGTGGATTCTTGATCGTCTTTTTTTCAAATGCATTTACCGTCGCTTTAAAT
ACGGACTGAAAGGAGGGCCTTCTACGGAAGGAGTGCCAAAGTCTATGAGGGAAGAATATCGAA
AGGAACAGCAGAGTGCTGTGGATGCTGACGATGGTCATTTTGTCAGCATAGAGCTGGAGTAAA
AAACTACCTTGTTTCTACT

[0050] The amino acid sequence of the M1 protein of Influenza A/Puerto Rico/8/34/Mount Sinai(H1N1), encoded by nucleotides 26 to 784 of SEQ ID NO:3 is as follows, referred to herein as SEQ ID NO:4:

MSLLTEVETYVLSIIPSGPLKAEIAQRLEDVFAGKNTDLEVLMEWLKTRPILSPLTKGIL
GFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDKAVKLYRKLKREITFHGAKEISL
SYSAGALASCMGLIYNRMGAVTTEVAFGLVCATCEQIADSQHRSHRQMVTTTNPLIR
HENRMVLASTTAKAMEQMAGSSEQAAEAMEVASQARQMVQAMRTIGTHPSSSAGL
KNDLLENLQAYQKRMGVQMQRFK

[0051] The amino acid sequence of the M2 protein of Influenza A/Puerto Rico/8/34/Mount Sinai (H1N1), encoded (in spliced form) by nucleotides 26 to 51 and 740 to 1007 of SEQ ID NO:3 is as follows, referred to herein as SEQ ID NO:5:

MSLLTEVETPIRNEWGCRCNGSSDPLAIAANIIGILHLTLWILDRLFFKCIYRRFKYGLK
GGPSTEGVPKSMREEYRKEQQSAVDADDGHFVSIELE

[0052] The Extracellular region of the M2 protein (eM2) corresponds to the first 24 amino acids of the N-terminal end of the protein, and is underlined above. See Fischer, W.B. *et al., Biochim. Biophys. Acta. 1561*:27-45 (2002); Zhong, Q. *et al., FEBS Lett. 434*:265-71 (1998).

[0053] A derivative of NP and eM2 described herein is encoded by a construct which encodes the first 24 amino acids of M2 and all or a portion of NP. The fusion constructs may be constructed with the eM2 sequences followed by the NP sequences, or with the NP sequences followed by the eM2 sequences. Exemplary fusion constructs using the NP and M2 sequences from Influenza A/PR/8/34 (H1N1) are set out below. A sequence, using the original influenza virus nucleotide sequences, which encodes the first 24 amino acids of M2 fused at its 3' end to a sequence which encodes NP in its entirety eM2-NP is referred to herein as SEQ ID NO:6:

```
   1 ATGAGTCTTC TAACCGAGGT CGAAACGCCT ATCAGAAACG AATGGGGGTG CAGATGCAAC
  61 GGTTCAAGTG ATATGGCGTC TCAAGGCACC AAACGATCTT ACGAACAGAT GGAGACTGAT
 121 GGAGAACGCC AGAATGCCAC TGAAATCAGA GCATCCGTCG GAAAAATGAT TGGTGGAATT
 181 GGACGATTCT ACATCCAAAT GTGCACCGAA CTCAAACTCA GTGATTATGA GGGACGGTTG
 241 ATCCAAAACA GCTTAACAAT AGAGAGAATG GTGCTCTCTG CTTTTGACGA AAGGAGAAAT
 301 AAATACCTTG AAGAACATCC CAGTGCGGGG AAAGATCCTA AGAAAACTGG AGGACCTATA
 361 TACAGGAGAG TAAACGGAAA GTGGATGAGA GAACTCATCC TTTATGACAA AGAAGAAATA
 421 AGGCGAATCT GGCGCCAAGC TAATAATGGT GACGATGCAA CGGCTGGTCT GACTCACATG
 481 ATGATCTGGC ATTCCAATTT GAATGATGCA ACTTATCAGA GGACAAGAGC TCTTGTTCGC
 541 ACCGGAATGG ATCCCAGGAT GTGCTCTCTG ATGCAAGGTT CAACTCTCCC TAGGAGGTCT
 601 GGAGCCGCAG GTGCTGCAGT CAAAGGAGTT GGAACAATGG TGATGGAATT GGTCAGAATG
 661 ATCAAACGTG GGATCAATGA TCGGAACTTC TGGAGGGGTG AGAATGGACG AAAAACAAGA
 721 ATTGCTTATG AAAGAATGTG CAACATTCTC AAAGGGAAAT TTCAAACTGC TGCACAAAAA
 781 GCAATGATGG ATCAAGTGAG AGAGAGCCGG AACCCAGGGA ATGCTGAGTT CGAAGATCTC
 841 ACTTTTCTAG CACGGTCTGC ACTCATATTG AGAGGGTCGG TTGCTCACAA GTCCTGCCTG
 901 CCTGCCTGTG TGTATGGACC TGCCGTAGCC AGTGGGTACG ACTTTGAAAG GGAGGGATAC
 961 TCTCTAGTCG GAATAGACCC TTTCAGACTG CTTCAAAACA GCCAAGTGTA CAGCCTAATC
1021 AGACCAAATG AGAATCCAGC ACACAAGAGT CAACTGGTGT GGATGGCATG CCATTCTGCC
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1081 GCATTTGAAG ATCTAAGAGT ATTAAGCTTC ATCAAAGGGA CGAAGGTGCT CCCAAGAGGG
1141 AAGCTTTCCA CTAGAGGAGT TCAAATTGCT TCCAATGAAA ATATGGAGAC TATGGAATCA
1201 AGTACACTTG AACTGAGAAG CAGGTACTGG GCCATAAGGA CCAGAAGTGG AGGAAACACC
1261 AATCAACAGA GGGCATCTGC GGGCCAAATC AGCATACAAC CTACGTTCTC AGTACAGAGA
1321 AATCTCCCTT TTGACAGAAC AACCGTTATG GCAGCATTCA GTGGGAATAC AGAGGGGAGA
1381 ACATCTGACA TGAGGACCGA AATCATAAGG ATGATGGAAA GTGCAAGACC AGAAGATGTG
1441 TCTTTCCAGG GGCGGGGAGT CTTCGAGCTC TCGGACGAAA AGGCAGCGAG CCCGATCGTG
1501 CCTTCCTTTG ACATGAGTAA TGAAGGATCT TATTTCTTCG GAGACAATGC AGAGGAATAC
1561 GATAAT

[0054] The amino acid sequence of the eM2-NP fusion protein of Influenza A/PR/8/34/ (H1N1), encoded by nucleotides 1 to 1566 SEQ ID NO:6 is as follows, referred to herein as SEQ ID NO:7 (eM2 amino acid sequence underlined):

MSLLTEVETPIRNEWGCRCNGSSDMASQGTKRSYEQMETDGERQNATEIRASVGKMIGGIGRF
YIQMCTELKLSDYEGRLIQNSLTIERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYRRVNG
KWMRELILYDKEEIRRIWRQANNGDDATAGLTHMMIWHSNLNDATYQRTRALVRTGMDPRMCS
LMQGSTLPRRSGAAGAAVKGVGTMVMELVRMIKRGINDRNFWRGENGRKTRIAYERMCNILKG
KFQTAAQKAMMDQVRESRNPGNAEFEDLTFLARSALILRGSVAHKSCLPACVYGPAVASGYDF
EREGYSLVGIDPFRLLQNSQVYSLIRPNENPAHKSQLVWMACHSAAFEDLRVLSFIKGTKVLP
RGKLSTRGVQIASNENMETMESSTLELRSRYWAIRTRSGGNTNQQRASAGQISIQPTFSVQRN
LPFDRTTVMAAFSGNTEGRTSDMRTEIIRMMESARPEDVSFQGRGVFELSDEKAASPIVPSFD
MSNEGSYFFGDNAEEYDN

[0055] A sequence, using the original influenza virus nucleotide sequences, which encodes NP in its entirety fused at its 3' end to the first 24 amino acids of M2 fused to a sequence which encodes NP in its entirety is referred to herein as SEQ ID NO:8:

ATGGCGTCTCAAGGCACCAAACGATCTTACGAACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTG
AAATCAGAGCATCCGTCGGAAAAATGATTGGTGGAATTGGACGATTCTACATCCAAATGTGCACCGAACT
CAAACTCAGTGATTATGAGGGACGGTTGATCCAAAACAGCTTAACAATAGAGAGAATGGTGCTCTCTGCT
TTTGACGAAAGGAGAAATAAATACCTTGAAGAACATCCCAGTGCGGGGAAAGATCCTAAGAAAACTGGAG
GACCTATATATACAGGAGAGTAAACGGAAAGTGGATGAGAGAACTCATCCTTTATGACAAAGAAGAAATAAG
GCGAATCTGGCGCCAAGCTAATAATGGTGACGATGCAACGGCTGGTCTGACTCACATGATGATCTGGCAT
TCCAATTTGAATGATGCAACTTATCAGAGGACAAGAGCTCTTGTTCGCACCGGAATGGATCCCAGGATGT
GCTCTCTGATGCAAGGTTCAACTCTCCCTAGGAGGTCTGGAGCCGCAGGTGCTGCAGTCAAAGGAGTTGG
AACAATGGTGATGGAATTGGTCAGAATGATCAAACGTGGGATCAATGATCGGAACTTCTGGAGGGGTGAG
AATGGACGAAAAACAAGAATTGCTTATGAAAGAATGTGCAACATTCTCAAAGGGAAATTTCAAACTGCTG
CACAAAAAGCAATGATGGATCAAGTGAGAGAGAGCCGGAACCCAGGGAATGCTGAGTTCGAAGATCTCAC
TTTTCTAGCACGGTCTGCACTCATATTGAGAGGGTCGGTTGCTCACAAGTCCTGCCTGCCTGCCTGTGTG
TATGGACCTGCCGTAGCCAGTGGGTACGACTTTGAAAGGGAGGGATACTCTCTAGTCGGAATAGACCCTT
TCAGACTGCTTCAAAACAGCCAAGTGTACAGCCTAATCAGACCAAATGAGAATCCAGCACACAAGAGTCA
ACTGGTGTGGATGGCATGCCATTCTGCCGCATTTGAAGATCTAAGAGTATTAAGCTTCATCAAAGGGACG
AAGGTGCTCCCAAGAGGGAAGCTTTCCACTAGAGGAGTTCAAATTGCTTCCAATGAAAATATGGAGACTA
TGGAATCAAGTACACTTGAACTGAGAAGCAGGTACTGGGCCATAAGGACCAGAAGTGGAGGAAACACCAA
TCAACAGAGGGCATCTGCGGGCCAAATCAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCTTTT
GACAGAACAACCGTTATGGCAGCATTCAGTGGGAATACAGAGGGGAGAACATCTGACATGAGGACCGAAA
TCATAAGGATGATGGAAAGTGCAAGACCAGAAGATGTGTCTTTCCAGGGGCGGGGAGTCTTCGAGCTCTC
GGACGAAAAGGCAGCGAGCCCGATCGTGCCTTCCTTTGACATGAGTAATGAAGGATCTTATTTCTTCGGA
GACAATGCAGAGGAATACGATAATATGAGTCTTCTAACCGAGGTCGAAACGCCTATCAGAAACGAATGGG
GGTGCAGATGCAACGGTTCAAGTGAT

[0056] The amino acid sequence of the NP-eM2 fusion protein of Influenza A/PR/8/34/ (H1N1), encoded by nucleotides 1 to 1566 of SEQ ID NO:8 is as follows, referred to herein as SEQ ID NO:9 (eM2 amino acid sequence underlined):

MASQGTKRSYEQMETDGERQNATEIRASVGKMIGGIGRFYIQMCTELKLSDYEGRLIQNSLTI
ERMVLSAFDERRNKYLEEHPSAGKDPKKTGGPIYRRVNGKWMRELILYDKEEIRRIWRQANNG
DDATAGLTHMMIWHSNLNDATYQRTRALVRTGMDPRMCSLMQGSTLPRRSGAAGAAVKGVGTM
VMELVRMIKRGINDRNFWRGENGRKTRIAYERMCNILKGKFQTAAQKAMMDQVRESRNPGNAE
FEDLTFLARSALILRGSVAHKSCLPACVYGPAVASGYDFEREGYSLVGIDPFRLLQNSQVYSL
IRPNENPAHKSQLVWMACHSAAFEDLRVLSFIKGTKVLPRGKLSTRGVQIASNENMETMESST
LELRSRYWAIRTRSGGNTNQQRASAGQISIQPTFSVQRNLPFDRTTVMAAFSGNTEGRTSDMR
TEIIRMMESARPEDVSFQGRGVFELSDEKAASPIVPSFDMSNEGSYFFGDNAEEYDNMSLLTE
VETPIRNEWGCRCNGSSD

[0057] The construction of functional fusion proteins often requires a linker sequence between the two fused fragments, in order to adopt an extended conformation to allow maximal flexibility. We used program LINKER (Chiquita J. Crasto C.J. and Feng, J. *Protein Engineering 13*:309-312 (2000), program publicly available at http://chutney.med.yale.edu/linker/linker.html (visited April 16, 2003)), that can automatically generate a set of linker sequences, which are known to adopt extended conformations as determined by X-ray crystallography and NMR. Examples of suitable linkers to use in various eM2-NP or NP-eM2 fusion proteins are as follows:

1. GYNTRA (SEQ ID NO:10)
2. FQMGET (SEQ ID NO:11)
3. FDRVKHLK (SEQ ID NO:12)
4. GRNTNGVIT (SEQ ID NO:13)
5. VNEKTIPDHD (SEQ ID NO:14)

[0058] The nucleotide sequence of the NP protein of Influenza B/LEE/40 is available as GenBank Accession Number K01395, and has the following sequence, referred to herein as SEQ ID NO:15:

```
   1 ATGTCCAACA TGGATATTGA CAGTATAAAT ACCGGAACAA TCGATAAAAC ACCAGAAGAA
  61 CTGACTCCCG GAACCAGTGG GGCAACCAGA CCAATCATCA AGCCAGCAAC CCTTGCTCCG
 121 CCAAGCAACA AACGAACCCG AAATCCATCT CCAGAAAGGA CAACCACAAG CAGTGAAACC
 181 GATATCGGAA GGAAAATCCA AAAGAAACAA ACCCCAACAG AGATAAAGAA GAGCGTCTAC
 241 AAAATGGTGG TAAAACTGGG TGAATTCTAC AACCAGATGA TGGTCAAAGC TGGACTTAAT
 301 GATGACATGG AAAGGAATCT AATTCAAAAT GCACAAGCTG TGGAGAGAAT CCTATTGGCT
 361 GCAACTGATG ACAAGAAAAC TGAATACCAA AAGAAAAGGA ATGCCAGAGA TGTCAAAGAA
 421 GGGAAGGAAG AAATAGACCA CAACAAGACA GGAGGCACCT TTTATAAGAT GGTAAGAGAT
 481 GATAAAACCA TCTACTTCAG CCCTATAAAA ATTACCTTTT TAAAAGAAGA GGTGAAAACA
 541 ATGTACAAGA CCACCATGGG GAGTGATGGT TTCAGTGGAC TAAATCACAT TATGATTGGA
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 601 CATTCACAGA TGAACGATGT CTGTTTCCAA AGATCAAAGG GACTGAAAAG GGTTGGACTT
 661 GACCCTTCAT TAATCAGTAC TTTTGCCGGA AGCACACTAC CCAGAAGATC AGGTACAACT
 721 GGTGTTGCAA TCAAAGGAGG TGGAACTTTA GTGGATGAAG CCATCCGATT TATAGGAAGA
 781 GCAATGGCAG ACAGAGGGCT ACTGAGAGAC ATCAAGGCCA AGACGGCCTA TGAAAAGATT
 841 CTTCTGAATC TGAAAAACAA GTGCTCTGCG CCGCAACAAA AGGCTCTAGT TGATCAAGTG
 901 ATCGGAAGTA GGAACCCAGG GATTGCAGAC ATAGAAGACC TAACTCTGCT TGCCAGAAGC
 961 ATGGTAGTTG TCAGACCCTC TGTAGCGAGC AAAGTGGTGC TTCCCATAAG CATTTATGCT
1021 AAAATACCTC AACTAGGATT CAATACCGAA GAATACTCTA TGGTTGGGTA TGAAGCCATG
1081 GCTCTTTATA ATATGGCAAC ACCTGTTTCC ATATTAAGAA TGGGAGATGA CGCAAAAGAT
1141 AAATCTCAAC TATTCTTCAT GTCGTGCTTC GGAGCTGCCT ATGAAGATCT AAGAGTGTTA
1201 TCTGCACTAA CGGGCACCGA ATTTAAGCCT AGATCAGCAC TAAAATGCAA GGGTTTCCAT
1261 GTCCCGGCTA AGGAGCAAGT AGAAGGAATG GGGGCAGCTC TGATGTCCAT CAAGCTTCAG
1321 TTCTGGGCCC CAATGACCAG ATCTGGAGGG AATGAAGTAA GTGGAGAAGG AGGGTCTGGT
1381 CAAATAAGTT GCAGCCCTGT GTTTGCAGTA GAAAGACCTA TTGCTCTAAG CAAGCAAGCT
1441 GTAAGAAGAA TGCTGTCAAT GAACGTTGAA GGACGTGATG CAGATGTCAA AGGAAATCTA
1501 CTCAAAATGA TGAATGATTC AATGGCAAAG AAAACCAGTG GAAATGCTTT CATTGGGAAG
1561 AAAATGTTTC AAATATCAGA CAAAAACAAA GTCAATCCCA TTGAGATTCC AATTAAGCAG
1621 ACCATCCCCA ATTTCTTCTT TGGGAGGGAC ACAGCAGAGG ATTATGATGA CCTCGATTAT
1681 TAA
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[0059] The amino acid sequence of the NP protein of IBV B/LEE/40, encoded by nucleotides 1-1680 of SEQ ID NO:1 is as follows, referred to herein as SEQ ID NO:16:

```
MSNMDIDSINTGTIDKTPEELTPGTSGATRPIIKPATLAPPSNKRTRNPSPERTTTSSET
DIGRKIQKKQTPTEIKKSVYKMVVKLGEFYNQMMVKAGLNDDMERNLIQNAQAVERILLA
ATDDKKTEYQKKRNARDVKEGKEEIDHNKTGGTFYKMVRDDKTIYFSPIKITFLKEEVKT
MYKTTMGSDGFSGLNHIMIGHSQMNDVCFQRSKGLKRVGLDPSLISTFAGSTLPRRSGTT
GVAIKGGGTLVDEAIRFIGRAMADRGLLRDIKAKTAYEKILLNLKNKCSAPQQKALVDQV
IGSRNPGIADIEDLTLLARSMVVVRPSVASKVVLPISIYAKIPQLGFNTEEYSMVGYEAM
ALYNMATPVSILRMGDDAKDKSQLFFMSCFGAAYEDLRVLSALTGTEFKPRSALKCKGFH
VPAKEQVEGMGAALMSIKLQFWAPMTRSGGNEVSGEGGSGQISCSPVFAVERPIALSKQA
VRRMLSMNVEGRDADVKGNLLKMMNDSMAKKTSGNAFIGKKMFQISDKNKVNPIEIPIKQ
TIPNFFFGRDTAEDYDDLDY
```

[0060] Non limiting examples of nucleotide sequences encoding the IAV hemagglutinin (HA) are as follows. It should be noted that HA sequences vary significantly between IV subtypes. Virtually any nucleotide sequence encoding an IV HA is suitable for the present invention. In fact, HA sequences included in vaccines and therapeutic formulations of the present invention (discussed in more detail below) might change from year to year depending on the prevalent strain or strains of IV.

[0061] The partial nucleotide sequence of the HA protein of IAV A/New_York/1/18(H1N1) is available as GenBank Accession Number AF116576, and has the following sequence, referred to herein as SEQ ID NO:17:

```
  1 atggaggcaa gactactggt cttgttatgt gcatttgcag ctacaaatgc agacacaata
 61 tgtataggct accatgcgaa taactcaacc gacactgttg acacagtact cgaaaagaat
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 121 gtgaccgtga cacactctgt taacctgctc gaagacagcc acaacggaaa actatgtaaa
 181 ttaaaaggaa tagccccatt acaattgggg aaatgtaata tcgccggatg gctcttggga
 241 aacccggaat gcgatttact gctcacagcg agctcatggt cctatattgt agaaacatcg
 301 aactcagaga atggaacatg ttacccagga gatttcatcg actatgaaga actgagggag
 361 caattgagct cagtgtcatc gtttgaaaaa ttcgaaatat ttcccaagac aagctcgtgg
 421 cccaatcatg aaacaaccaa aggtgtaacg gcagcatgct cctatgcggg agcaagcagt
 481 ttttacagaa atttgctgtg gctgacaaag aagggaagct catacccaaa gcttagcaag
 541 tcctatgtga acaataaagg gaaagaagtc cttgtactat ggggtgttca tcatccgcct
 601 accggtactg atcaacagag tctctatcag aatgcagatg cttatgtctc tgtagggtca
 661 tcaaaatata acaggagatt caccccggaa atagcagcga gacccaaagt aagaggtcaa
 721 gctgggagga tgaactatta ctggacatta ctagaacccg gagacacaat aacatttgag
 781 gcaactggaa atctaatagc accatggtat gctttcgcac tgaatagagg ttctggatcc
 841 ggtatcatca cttcagacgc accagtgcat gattgtaaca cgaagtgtca aacaccccat
 901 ggtgctataa acagcagtct ccctttccag aatatacatc cagtcacaat aggagagtgc
 961 ccaaaatacg tcaggagtac caaattgagg atggctacag gactaagaaa cattccatct
1021 attcaatcca ggggtctatt tggagccatt gccggtttta ttgaggggg atggactgga
1081 atgatagatg gatggtatgg ttatcatcat cagaatgaac agggatcagg ctatgcagcg
1141 gatcaaaaaa gcacacaaaa tgccattgac gggattacaa acaaggtgaa ttctgttatc
1201 gagaaaatga acacccaatt
```

[0062] The amino acid sequence of the partial HA protein of IAV A/New_York/1/18(H1N1), encoded by nucleotides 1 to 1218 of SEQ ID NO:17 is as follows, referred to herein as SEQ ID NO:18:

MEARLLVLLCAFAATNADTICIGYHANNSTDTVDTVLEKNVTVTHSVNLLEDSHNGK
LCKLKGIAPLQLGKCNIAGWLLGNPECDLLLTASSWSYIVETSNSENGTCYPGDFIDY
EELREQLSSVSSFEKFEIFPKTSSWPNHETTKGVTAACSYAGASSFYRNLLWLTKKGSS
YPKLSKSYVNNKGKEVLVLWGVHHPPTGTDQQSLYQNADAYVSVGSSKYNRRFTPE
IAARPKVRGQAGRMNYYWTLLEPGDTITFEATGNLIAPWYAFALNRGSGSGIITSDAP
VHDCNTKCQTPHGAINSSLPFQNIHPVTIGECPKYVRSTKLRMATGLRNIPSIQSRGLF
GAIAGFIEGGWTGMIDGWYGYHHQNEQGSGYAADQKSTQNAIDGITNKVNSVIEKM
NTQ

[0063] The nucleotide sequence of the IAV A/Hong Kong/482/97 hemagglutinin (H5) is available as GenBank Accession Number AF046098, and has the following sequence, referred to herein as SEQ ID NO:19:

```
   1 ctgtcaaaat ggagaaaata gtgcttcttc ttgcaacagt cagtcttgtt aaaagtgatc
  61 agatttgcat tggttaccat gcaaacaact cgacagagca ggttgacaca ataatggaaa
 121 agaatgttac tgttacacat gcccaagaca tactggaaag gacacacaac gggaagctct
 181 gcgatctaaa tggagtgaaa cctctcattt tgagggattg tagtgtagct ggatggctcc
 241 tcggaaaccc tatgtgtgac gaattcatca atgtgccgga atggtcttac atagtggaga
 301 aggccagtcc agccaatgac ctctgttatc cagggaattt caacgactat gaagaactga
 361 aacacctatt gagcagaata aaccattttg agaaaattca gatcatcccc aaaagttctt
 421 ggtccaatca tgatgcctca tcaggggtga gctcagcatg tccatacctt gggaggtcct
 481 ccttttcag aaatgtggta tggcttatca aaaagaacag tgcataccca acaataaaga
 541 ggagctacaa taataccaac caagaagatc ttttggtact gtgggggatt caccatccta
 601 atgatgcggc agagcagaca aagctctatc aaaatccaac cacctacatt tccgttggaa
 661 catcaacact gaaccagaga ttggttccag aaatagctac tagacccaaa gtaaacgggc
 721 aaagtggaag aatggagttc ttctggacaa ttttaaagcc gaatgatgcc atcaatttcg
 781 agagtaatgg aaatttcatt gccccagaat atgcatacaa aattgtcaag aaaggggact
 841 caacaattat gaaaagtgaa ttggaatatg gtaactgcaa caccaagtgt caaactccaa
 901 tgggggcgat aaactctagt atgccattcc acaacataca ccccctcacc atcggggaat
 961 gccccaaata tgtgaaatca aacagattag ttcttgcgac tggactcaga aataccctc
1021 aaagggagag aagaagaaaa aagagaggac tatttggagc tatagcaggt tttatagagg
1081 gaggatggca gggcatggta gatggttggt atgggtacca ccatagcaat gagcagggga
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1141 gtggatacgc tgcagacaaa gaatccactc aaaaggcaat agatggagtc accaataagg
1201 tcaactcgat cattaacaaa atgaacactc agtttgaggc cgttggaagg gaatttaata
1261 acttagaaag gagaatagag aatttaaaca agaaaatgga agacggattc ctagatgtct
1321 ggacttacaa tgctgaactt ctggttctca tggaaaatga gagaactctc gactttcatg
1381 actcaaatgt caagaacctt tacgacaagg tccgactaca gcttagggat aatgcaaagg
1441 aactgggtaa tggttgtttc gaattctatc acaaatgtga taatgaatgt atggaaagtg
1501 taaaaaacgg aacgtatgac tacccgcagt attcagaaga agcaagacta aacagagagg
1561 aaataagtgg agtaaaattg gaatcaatgg gaacttacca aatactgtca atttattcaa
1621 cagtggcgag ttccctagca ctggcaatca tggtagctgg tctatcttta tggatgtgct
1681 ccaatggatc gttacaatgc agaatttgca tttaaatttg tgagttcaga ttgtagttaa
1741 a
```

[0064] The amino acid sequence of the HA protein of IAV A/Hong Kong/482/97 (H5), encoded by nucleotides 9 to 1715 of SEQ ID NO:19 is as follows, referred to herein as SEQ ID NO:20:

MEKIVLLLATVSLVKSDQICIGYHANNSTEQVDTIMEKNVTVTHAQDILERTHNGKLCDLN
GVKPLILRDCSVAGWLLGNPMCDEFINVPEWSYIVEKASPANDLCYPGNFNDYEELKHLLS
RINHFEKIQIIPKSSWSNHDASSGVSSACPYLGRSSFFRNVVWLIKKNSAYPTIKRSYNNTNQ
EDLLVLWGIHHPNDAAEQTKLYQNPTTYISVGTSTLNQRLVPEIATRPKVNGQSGRMEFFW
TILKPNDAINFESNGNFIAPEYAYKIVKKGDSTIMKSELEYGNCNTKCQTPMGAINSSMPFH
NIHPLTIGECPKYVKSNRLVLATGLRNTPQRERRRKKRGLFGAIAGFIEGGWQGMVDGWY
GYHHSNEQGSGYAADKESTQKAIDGVTNKVNSIINKMNTQFEAVGREFNNLERRIENLNK
KMEDGFLDVWTYNAELLVLMENERTLDFHDSNVKNLYDKVRLQLRDNAKELGNGCFEF
YHKCDNECMESVKNGTYDYPQYSEEARLNREEISGVKLESMGTYQILSIYSTVASSLALAI
MVAGLSLWMCSNGSLQCRICI

[0065] The nucleotide sequence of the IAV A/Hong Kong/1073/99(H9N2) is available as GenBank Accession Number INA404626, and has the following sequence, referred to herein as SEQ ID NO:21:

```
   1 gcaaaagcag gggaattact taactagcaa aatggaaaca atatcactaa taactatact
  61 actagtagta acagcaagca atgcagataa aatctgcatc ggccaccagt caacaaactc
 121 cacagaaact gtggacacgc taacagaaac caatgttcct gtgacacatg ccaaagaatt
 181 gctccacaca gagcataatg gaatgctgtg tgcaacaagc ctgggacatc ccctcattct
 241 agacacatgc actattgaag gactagtcta tggcaaccct tcttgtgacc tgctgttggg
 301 aggaagagaa tggtcctaca tcgtcgaaag atcatcagct gtaaatggaa cgtgttaccc
 361 tgggaatgta gaaaacctag aggaactcag gacacttttt agttccgcta gttcctacca
 421 aagaatccaa atcttcccag acacaacctg gaatgtgact tacactggaa caagcagagc
 481 atgttcaggt tcattctaca ggagtatgag atggctgact caaaagagcg gtttttaccc
 541 tgttcaagac gcccaataca caaataacag gggaaagagc attcttttcg tgtggggcat
 601 acatcaccca cccacctata ccgagcaaac aaatttgtac ataagaaacg acacaacaac
 661 aagcgtgaca acagaagatt tgaataggac cttcaaacca gtgatagggc caaggcccct
 721 tgtcaatggt ctgcagggaa gaattgatta ttattggtcg gtactaaaac caggccaaac
 781 attgcgagta cgatccaatg ggaatctaat tgctccatgg tatggacacg ttctttcagg
 841 agggagccat ggaagaatcc tgaagactga tttaaaaggt ggtaattgtg tagtgcaatg
 901 tcagactgaa aaaggtggct taaacagtac attgccattc cacaatatca gtaaatatgc
 961 atttggaacc tgccccaaat atgtaagagt taatagtctc aaactggcag tcggtctgag
1021 gaacgtgcct gctagatcaa gtagaggact atttggagcc atagctggat tcatagaagg
1081 aggttggcca ggactagtcg ctggctggta tggtttccag cattcaaatg atcaaggggt
1141 tggtatggct gcagataggg attcaactca aaaggcaatt gataaaataa catccaaggt
1201 gaataatata gtcgacaaga tgaacaagca atatgaaata attgatcatg aattcagtga
1261 ggttgaaact agactcaata tgatcaataa taagattgat gaccaaatac aagacgtatg
1321 ggcatataat gcagaattgc tagtactact tgaaaatcaa aaaacactcg atgagcatga
1381 tgcgaacgtg aacaatctat ataacaaggt gaagagggca ctgggctcca atgctatgga
1441 agatgggaaa ggctgtttcg agctatacca taaatgtgat gatcagtgca tggaaacaat
1501 tcggaacggg acctataata ggagaaagta tagagaggaa tcaagactag aaaggcagaa
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1561 aatagagggg gttaagctgg aatctgaggg aacttacaaa atcctcacca tttattcgac
1621 tgtcgcctca tctcttgtgc ttgcaatggg gtttgctgcc ttcctgttct gggccatgtc
1681 caatggatct tgcagatgca acatttgtat ataa
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[0066] The amino acid sequence of the HA protein of IAV A/Hong Kong/1073/99 (H9N2), encoded by nucleotides 32 to 1711 of SEQ ID NO:21 is as follows, referred to herein as SEQ ID NO:22:

METISLITILLVVTASNADKICIGHQSTNSTETVDTLTETNVPVTHAKELLHTEHNGMLCATSLG
HPLILDTCTIEGLVYGNPSCDLLLGGREWSYIVERSSAVNGTCYPGNVENLEELRTLFSSASSYQ
RIQIFPDTTWNVTYTGTSRACSGSFYRSMRWLTQKSGFYPVQDAQYTNNRGKSILFVWGIHHPP
TYTEQTNLYIRNDTTTSVTTEDLNRTFKPVIGPRPLVNGLQGRIDYYWSVLKPGQTLRVRSNGN
LIAPWYGHVLSGGSHGRILKTDLKGGNCVVQCQTEKGGLNSTLPFHNISKYAFGTCPKYVRVNS
LKLAVGLRNVPARSSRGLFGAIAGFIEGGWPGLVAGWYGFQHSNDQGVGMAADRDSTQKAID
KITSKVNNIVDKMNKQYEIIDHEFSEVETRLNMINNKIDDQIQDVWAYNAELLVLLENQKTLDE
HDANVNNLYNKVKRALGSNAMEDGKGCFELYHKCDDQCMETIRNGTYNRRKYREESRLERQ
KIEGVKLESEGTYKILTIYSTVASSLVLAMGFAAFLFWAMSNGSCRCNICI

[0067] The present invention also provides vaccine compositions and methods for delivery of IV coding sequences to a vertebrate with optimal expression and safety conferred through codon optimization and/or other manipulations. These vaccine compositions are prepared and administered in such a manner that the encoded gene products are optimally expressed in the vertebrate of interest. As a result, these compositions and methods are useful in stimulating an immune response against IV infection. Also included in the invention are expression systems, delivery systems, and codon-optimized IV coding regions.

[0068] In a specific embodiment, the invention provides combinatorial polynucleotide (*e.g.*, DNA) vaccines which combine both a polynucleotide vaccine and polypeptide (*e.g.*, either a recombinant protein, a purified subunit protein, a viral vector expressing an isolated IV polypeptide, or in the form of an inactivated or attenuated IV vaccine) vaccine in a single formulation. The single formulation comprises an IV polypeptide-encoding polynucleotide vaccine as described herein, and optionally, an effective amount of a desired isolated IV polypeptide or fragment, variant, or derivative thereof. The polypeptide may exist in any form, for example, a recombinant protein, a purified subunit protein, a viral vector expressing an isolated IV polypeptide, or in the form of an inactivated or attenuated IV vaccine. The IV polypeptide or fragment, variant, or derivative thereof encoded by the polynucleotide vaccine may be identical to the isolated IV polypeptide or fragment, variant, or

derivative thereof. Alternatively, the IV polypeptide or fragment, variant, or derivative thereof encoded by the polynucleotide may be different from the isolated IV polypeptide or fragment, variant, or derivative thereof.

[0069] It is to be noted that the term "a" or "an" entity refers to one or more of that entity; for example, "a polynucleotide," is understood to represent one or more polynucleotides. As such, the terms "a" (or "an"), "one or more," and "at least one" can be used interchangeably herein.

[0070] The term "polynucleotide" is intended to encompass a singular nucleic acid or nucleic acid fragment as well as plural nucleic acids or nucleic acid fragments, and refers to an isolated molecule or construct, *e.g.*, a virus genome (*e.g.*, a non-infectious viral genome), messenger RNA (mRNA), plasmid DNA (pDNA), or derivatives of pDNA (*e.g.*, minicircles as described in (Darquet, A-M *et al.*, *Gene Therapy* 4:1341-1349 (1997)) comprising a polynucleotide. A polynucleotide may comprise a conventional phosphodiester bond or a non-conventional bond (*e.g.*, an amide bond, such as found in peptide nucleic acids (PNA)).

[0071] The terms "nucleic acid" or "nucleic acid fragment" refer to any one or more nucleic acid segments, *e.g.*, DNA or RNA fragments, present in a polynucleotide or construct. A nucleic acid or fragment thereof may be provided in linear (*e.g.*, mRNA) or circular (*e.g.*, plasmid) form as well as double-stranded or single-stranded forms. By "isolated" nucleic acid or polynucleotide is intended a nucleic acid molecule, DNA or RNA, which has been removed from its native environment. For example, a recombinant polynucleotide contained in a vector is considered isolated for the purposes of the present invention. Further examples of an isolated polynucleotide include recombinant polynucleotides maintained in heterologous host cells or purified (partially or substantially) polynucleotides in solution. Isolated RNA molecules include *in vivo* or *in vitro* RNA transcripts of the polynucleotides of the present invention. Isolated polynucleotides or nucleic acids according to the present invention further include such molecules produced synthetically.

[0072] As used herein, a "coding region" is a portion of nucleic acid which consists of codons translated into amino acids. Although a "stop codon" (TAG, TGA, or TAA) is not translated into an amino acid, it may be considered to be part of a coding region, but any flanking sequences, for example promoters, ribosome binding sites, transcriptional terminators, and the like, are not part of a coding region. Two or more nucleic acids or nucleic acid fragments of the present invention can be present in a single polynucleotide construct, *e.g.*, on a single plasmid, or in separate polynucleotide constructs, *e.g.*, on separate (different) plasmids. Furthermore, any nucleic acid or nucleic acid fragment may encode a single IV polypeptide or fragment, derivative, or variant thereof, *e.g.*, or may encode more than one polypeptide, *e.g.*, a nucleic acid may encode two or more polypeptides. In addition, a nucleic acid may include a regulatory element such as a promoter, ribosome binding site, or a transcription terminator, or may encode heterologous coding regions fused to the IV coding region, *e.g.*, specialized elements or motifs, such as a secretory signal peptide or a heterologous functional domain.

[0073] The terms "fragment," "variant," "derivative" and "analog" when referring to IV polypeptides of the present invention include any polypeptides which retain at least some of the immunogenicity or antigenicity of the corresponding native polypeptide. Fragments of IV polypeptides of the present invention include proteolytic fragments, deletion fragments and in particular, fragments of IV polypeptides which exhibit increased secretion from the cell or higher immunogenicity or reduced pathogenicity when delivered to an animal. Polypeptide fragments further include any portion of the polypeptide which comprises an antigenic or immunogenic epitope of the native polypeptide, including linear as well as three-dimensional epitopes. Variants of IV polypeptides of the present invention include fragments as described above, and also polypeptides with altered amino acid sequences due to amino acid substitutions, deletions, or insertions. Variants may occur naturally, such as an allelic variant. By an "allelic variant" is intended alternate forms of a gene occupying a given locus on a chromosome or genome of an organism or

virus. *Genes II*, Lewin, B., ed., John Wiley & Sons, New York (1985), which is incorporated herein by reference. For example, as used herein, variations in a given gene product. When referring to IV NA or HA proteins, each such protein is a "variant," in that native IV strains are distinguished by the type of NA and HA proteins encoded by the virus. However, within a single HA or NA variant type, further naturally or non-naturally occurring variations such as amino acid deletions, insertions or substitutions may occur. Non-naturally occurring variants may be produced using art-known mutagenesis techniques. Variant polypeptides may comprise conservative or non-conservative amino acid substitutions, deletions or additions. Derivatives of IV polypeptides of the present invention, are polypeptides which have been altered so as to exhibit additional features not found on the native polypeptide. Examples include fusion proteins. An analog is another form of an IV polypeptide of the present invention. An example is a proprotein which can be activated by cleavage of the proprotein to produce an active mature polypeptide.

[0074] The terms "infectious polynucleotide" or "infectious nucleic acid" are intended to encompass isolated viral polynucleotides and/or nucleic acids which are solely sufficient to mediate the synthesis of complete infectious virus particles upon uptake by permissive cells. Thus, "infectious nucleic acids" do not require pre-synthesized copies of any of the polypeptides it encodes, *e.g.*, viral replicases, in order to initiate its replication cycle in a permissive host cell.

[0075] The terms "non-infectious polynucleotide" or "non-infectious nucleic acid" as defined herein are polynucleotides or nucleic acids which cannot, without additional added materials, *e.g,* polypeptides, mediate the synthesis of complete infectious virus particles upon uptake by permissive cells. An infectious polynucleotide or nucleic acid is not made "non-infectious" simply because it is taken up by a non-permissive cell. For example, an infectious viral polynucleotide from a virus with limited host range is infectious if it is capable of mediating the synthesis of complete infectious virus particles when taken up by cells derived from a permissive host (*i.e.*, a host permissive for the

virus itself). The fact that uptake by cells derived from a non-permissive host does not result in the synthesis of complete infectious virus particles does not make the nucleic acid "non-infectious." In other words, the term is not qualified by the nature of the host cell, the tissue type, or the species taking up the polynucleotide or nucleic acid fragment.

[0076] In some cases, an isolated infectious polynucleotide or nucleic acid may produce fully-infectious virus particles in a host cell population which lacks receptors for the virus particles, *i.e.*, is non-permissive for virus entry. Thus viruses produced will not infect surrounding cells. However, if the supernatant containing the virus particles is transferred to cells which are permissive for the virus, infection will take place.

[0077] The terms "replicating polynucleotide" or "replicating nucleic acid" are meant to encompass those polynucleotides and/or nucleic acids which, upon being taken up by a permissive host cell, are capable of producing multiple, *e.g.*, one or more copies of the same polynucleotide or nucleic acid. Infectious polynucleotides and nucleic acids are a subset of replicating polynucleotides and nucleic acids; the terms are not synonymous. For example, a defective virus genome lacking the genes for virus coat proteins may replicate, *e.g.*, produce multiple copies of itself, but is NOT infectious because it is incapable of mediating the synthesis of complete infectious virus particles unless the coat proteins, or another nucleic acid encoding the coat proteins, are exogenously provided.

[0078] In certain embodiments, the polynucleotide, nucleic acid, or nucleic acid fragment is DNA. In the case of DNA, a polynucleotide comprising a nucleic acid which encodes a polypeptide normally also comprises a promoter and/or other transcription or translation control elments operably associated with the polypeptide-encoding nucleic acid fragment. An operable association is when a nucleic acid fragment encoding a gene product, *e.g.*, a polypeptide, is associated with one or more regulatory sequences in such a way as to place expression of the gene product under the influence or control of the regulatory sequence(s). Two DNA fragments (such as a polypeptide-encoding nucleic

acid fragment and a promoter associated with the 5' end of the nucleic acid fragment) are "operably associated" if induction of promoter function results in the transcription of mRNA encoding the desired gene product and if the nature of the linkage between the two DNA fragments does not (1) result in the introduction of a frame-shift mutation, (2) interfere with the ability of the expression regulatory sequences to direct the expression of the gene product, or (3) interfere with the ability of the DNA template to be transcribed. Thus, a promoter region would be operably associated with a nucleic acid fragment encoding a polypeptide if the promoter was capable of effecting transcription of that nucleic acid fragment. The promoter may be a cell-specific promoter that directs substantial transcription of the DNA only in predetermined cells. Other transcription control elements, besides a promoter, for example enhancers, operators, repressors, and transcription termination signals, can be operably associated with the polynucleotide to direct cell-specific transcription. Suitable promoters and other transcription control regions are disclosed herein.

[0079] A variety of transcription control regions are known to those skilled in the art. These include, without limitation, transcription control regions which function in vertebrate cells, such as, but not limited to, promoter and enhancer segments from cytomegaloviruses (the immediate early promoter, in conjunction with intron-A), simian virus 40 (the early promoter), and retroviruses (such as Rous sarcoma virus). Other transcription control regions include those derived from vertebrate genes such as actin, heat shock protein, bovine growth hormone and rabbit ß-globin, as well as other sequences capable of controlling gene expression in eukaryotic cells. Additional suitable transcription control regions include tissue-specific promoters and enhancers as well as lymphokine-inducible promoters (*e.g.*, promoters inducible by interferons or interleukins).

[0080] Similarly, a variety of translation control elements are known to those of ordinary skill in the art. These include, but are not limited to ribosome binding sites, translation initiation and termination codons, elements from

picornaviruses (particularly an internal ribosome entry site, or IRES, also referred to as a CITE sequence).

[0081] A DNA polynucleotide of the present invention may be a circular or linearized plasmid or vector, or other linear DNA which may also be non-infectious and nonintegrating (*i.e.*, does not integrate into the genome of vertebrate cells). A linearized plasmid is a plasmid that was previously circular but has been linearized, for example, by digestion with a restriction endonuclease. Linear DNA may be advantageous in certain situations as discussed, *e.g.*, in Cherng, J.Y., *et al., J. Control. Release 60*:343-53 (1999), and Chen, Z.Y., *et al. Mol. Ther. 3*:403-10 (2001), both of which are incorporated herein by reference. As used herein, the terms plasmid and vector can be used interchangeably

[0082] Alternatively, DNA virus genomes may be used to administer DNA polynucleotides into vertebrate cells. In certain embodiments, a DNA virus genome of the present invention is nonreplicative, noninfectious, and/or nonintegrating. Suitable DNA virus genomes include without limitation, herpesvirus genomes, adenovirus genomes, adeno-associated virus genomes, and poxvirus genomes. References citing methods for the *in vivo* introduction of non-infectious virus genomes to vertebrate tissues are well known to those of ordinary skill in the art, and are cited *supra*.

[0083] In other embodiments, a polynucleotide of the present invention is RNA, for example, in the form of messenger RNA (mRNA). Methods for introducing RNA sequences into vertebrate cells are described in U.S. Patent No. 5,580,859, the disclosure of which is incorporated herein by reference in its entirety.

[0084] Polynucleotides, nucleic acids, and nucleic acid fragments of the present invention may be associated with additional nucleic acids which encode secretory or signal peptides, which direct the secretion of a polypeptide encoded by a nucleic acid fragment or polynucleotide of the present invention. According to the signal hypothesis, proteins secreted by mammalian cells have a signal peptide or secretory leader sequence which is cleaved from the mature

protein once export of the growing protein chain across the rough endoplasmic reticulum has been initiated. Those of ordinary skill in the art are aware that polypeptides secreted by vertebrate cells generally have a signal peptide fused to the N-terminus of the polypeptide, which is cleaved from the complete or "full length" polypeptide to produce a secreted or "mature" form of the polypeptide. In certain embodiments, the native leader sequence is used, or a functional derivative of that sequence that retains the ability to direct the secretion of the polypeptide that is operably associated with it. Alternatively, a heterologous mammalian leader sequence, or a functional derivative thereof, may be used. For example, the wild-type leader sequence may be substituted with the leader sequence of human tissue plasminogen activator (TPA) or mouse ß-glucuronidase.

[0085] In accordance with one aspect of the present invention, there is provided a polynucleotide construct, for example, a plasmid, comprising a nucleic acid fragment, where the nucleic acid fragment is a fragment of a codon-optimized coding region operably encoding an IV-derived polypeptide, where the coding region is optimized for expression in vertebrate cells, of a desired vertebrate species, *e.g.*, humans, to be delivered to a vertebrate to be treated or immunized. Suitable IV polypeptides, or fragments, variants, or derivatives thereof may be derived from, but are not limited to, the IV HA, NA, NP, M1, or M2 proteins. Additional IV-derived coding sequences, *e.g.*, coding for HA, NA, NP, M1, M2 or eM2, may also be included on the plasmid, or on a separate plasmid, and expressed, either using native IV codons or codons optimized for expression in the vertebrate to be treated or immunized. When such a plasmid encoding one or more optimized influenza sequences is delivered, *in vivo* to a tissue of the vertebrate to be treated or immunized, one or more of the encoded gene products will be expressed, *i.e.*, transcribed and translated. The level of expression of the gene product(s) will depend to a significant extent on the strength of the associated promoter and the presence and activation of an associated enhancer element, as well as the degree of optimization of the coding region.

[0086] As used herein, the term "plasmid" refers to a construct made up of genetic material (*i.e.*, nucleic acids). Typically a plasmid contains an origin of replication which is functional in bacterial host cells, *e.g.*, *Escherichia coli*, and selectable markers for detecting bacterial host cells comprising the plasmid. Plasmids of the present invention may include genetic elements as described herein arranged such that an inserted coding sequence can be transcribed and translated in eukaryotic cells. Also, the plasmid may include a sequence from a viral nucleic acid. However, such viral sequences normally are not sufficient to direct or allow the incorporation of the plasmid into a viral particle, and the plasmid is therefore a non-viral vector. In certain embodiments described herein, a plasmid is a closed circular DNA molecule.

[0087] The term "expression" refers to the biological production of a product encoded by a coding sequence. In most cases a DNA sequence, including the coding sequence, is transcribed to form a messenger-RNA (mRNA). The messenger-RNA is then translated to form a polypeptide product which has a relevant biological activity. Also, the process of expression may involve further processing steps to the RNA product of transcription, such as splicing to remove introns, and/or post-translational processing of a polypeptide product.

[0088] As used herein, the term "polypeptide" is intended to encompass a singular "polypeptide" as well as plural "polypeptides," and comprises any chain or chains of two or more amino acids. Thus, as used herein, terms including, but not limited to "peptide," "dipeptide," "tripeptide," "protein," "amino acid chain," or any other term used to refer to a chain or chains of two or more amino acids, are included in the definition of a "polypeptide," and the term "polypeptide" can be used instead of, or interchangeably with any of these terms. The term further includes polypeptides which have undergone post-translational modifications, for example, glycosylation, acetylation, phosphorylation, amidation, derivatization by known protecting/blocking groups, proteolytic cleavage, or modification by non-naturally occurring amino acids.

[0089] Also included as polypeptides of the present invention are fragments, derivatives, analogs, or variants of the foregoing polypeptides, and any combination thereof. Polypeptides, and fragments, derivatives, analogs, or variants thereof of the present invention can be antigenic and immunogenic polypeptides related to IV polypeptides, which are used to prevent or treat, *i.e.*, cure, ameliorate, lessen the severity of, or prevent or reduce contagion of infectious disease caused by the IV.

[0090] As used herein, an "antigenic polypeptide" or an "immunogenic polypeptide" is a polypeptide which, when introduced into a vertebrate, reacts with the vertebrate's immune system molecules, *i.e.*, is antigenic, and/or induces an immune response in the vertebrate, *i.e.*, is immunogenic. It is quite likely that an immunogenic polypeptide will also be antigenic, but an antigenic polypeptide, because of its size or conformation, may not necessarily be immunogenic. Examples of antigenic and immunogenic polypeptides of the present invention include, but are not limited to, *e.g.*, HA or fragments or variants thereof, *e.g.* NP, or fragments thereof, *e.g.*, PB1, or fragments or variants thereof, *e.g.*, NS1 or fragments or variants thereof, *e.g.*, M1 or fragments or variants thereof, and *e.g.* M2 or fragments or variants thereof including the extracellular fragment of M2 (eM2), or *e.g.*, any of the foregoing polypeptides or fragments fused to a heterologous polypeptide, for example, a hepatitis B core antigen. Isolated antigenic and immunogenic polypeptides of the present invention in addition to those encoded by polynucleotides of the invention, may be provided as a recombinant protein, a purified subunit, a viral vector expressing the protein, or may be provided in the form of an inactivated IV vaccine, *e.g.*, a live-attenuated virus vaccine, a heat-killed virus vaccine, etc.

[0091] By an "isolated" IV polypeptide or a fragment, variant, or derivative thereof is intended an IV polypeptide or protein that is not in its natural form. No particular level of purification is required. For example, an isolated IV polypeptide can be removed from its native or natural environment. Recombinantly produced IV polypeptides and proteins expressed in host cells

are considered isolated for purposed of the invention, as are native or recombinant IV polypeptides which have been separated, fractionated, or partially or substantially purified by any suitable technique, including the separation of IV virions from eggs or culture cells in which they have been propagated. In addition, an isolated IV polypeptide or protein can be provided as a live or inactivated viral vector expressing an isolated IV polypeptide and can include those found in inactivated IV vaccine compositions. Thus, isolated IV polypeptides and proteins can be provided as, for example, recombinant IV polypeptides, a purified subunit of IV, a viral vector expressing an isolated IV polypeptide, or in the form of an inactivated or attenuated IV vaccine.

[0092] The term "epitopes," as used herein, refers to portions of a polypeptide having antigenic or immunogenic activity in a vertebrate, for example a human. An "immunogenic epitope," as used herein, is defined as a portion of a protein that elicits an immune response in an animal, as determined by any method known in the art. The term "antigenic epitope," as used herein, is defined as a portion of a protein to which an antibody or T-cell receptor can immunospecifically bind as determined by any method well known in the art. Immunospecific binding excludes non-specific binding but does not exclude cross-reactivity with other antigens. Where all immunogenic epitopes are antigenic, antigenic epitopes need not be immunogenic.

[0093] The term "immunogenic carrier" as used herein refers to a first polypeptide or fragment, variant, or derivative thereof which enhances the immunogenicity of a second polypeptide or fragment, variant, or derivative thereof. Typically, an "immunogenic carrier" is fused to or conjugated to the desired polypeptide or fragment thereof. An example of an "immunogenic carrier" is a recombinant hepatitis B core antigen expressing, as a surface epitope, an immunogenic epitope of interest. See, *e.g.*, European Patent No. EP 0385610 B1, which is incorporated herein by reference in its entirety.

[0094] In the present invention, antigenic epitopes preferably contain a sequence of at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at

least 10, at least 15, at least 20, at least 25, or between about 8 to about 30 amino acids contained within the amino acid sequence of an IV polypeptide of the invention, *e.g.*, an NP polypeptide, an M1 polypeptide or an M2 polypeptide. Certain polypeptides comprising immunogenic or antigenic epitopes are at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues in length. Antigenic as well as immunogenic epitopes may be linear, *i.e.*, be comprised of contiguous amino acids in a polypeptide, or may be three dimensional, *i.e.*, where an epitope is comprised of non-contiguous amino acids which come together due to the secondary or tertiary structure of the polypeptide, thereby forming an epitope.

[0095] As to the selection of peptides or polypeptides bearing an antigenic epitope (*e.g.*, that contain a region of a protein molecule to which an antibody or T cell receptor can bind), it is well known in that art that relatively short synthetic peptides that mimic part of a protein sequence are routinely capable of eliciting an antiserum that reacts with the partially mimicked protein. *See, e.g.*, Sutcliffe, J. G., *et al.*, *Science 219*:660-666 (1983), which is herein incorporated by reference.

[0096] Peptides capable of eliciting an immunogenic response are frequently represented in the primary sequence of a protein, can be characterized by a set of simple chemical rules, and are confined neither to immunodominant regions of intact proteins nor to the amino or carboxyl terminals. Peptides that are extremely hydrophobic and those of six or fewer residues generally are ineffective at inducing antibodies that bind to the mimicked protein; longer peptides, especially those containing proline residues, usually are effective. Sutcliffe *et al.*, *supra*, at 661. For instance, 18 of 20 peptides designed according to these guidelines, containing 8-39 residues covering 75% of the sequence of the IV hemagglutinin HA1 polypeptide chain, induced antibodies that reacted with the HA1 protein or intact virus; and 12/12 peptides from the MuLV polymerase and 18/18 from the rabies glycoprotein induced antibodies that precipitated the respective proteins.

Codon Optimization

[0097] "Codon optimization" is defined as modifying a nucleic acid sequence for enhanced expression in the cells of the vertebrate of interest, *e.g.* human, by replacing at least one, more than one, or a significant number, of codons of the native sequence with codons that are more frequently or most frequently used in the genes of that vertebrate. Various species exhibit particular bias for certain codons of a particular amino acid.

[0098] In one aspect, the present invention relates to polynucleotides comprising nucleic acid fragments of codon-optimized coding regions which encode IV polypeptides, or fragments, variants, or derivatives thereof, with the codon usage adapted for optimized expression in the cells of a given vertebrate, *e.g.*, humans. These polynucleotides are prepared by incorporating codons preferred for use in the genes of the vertebrate of interest into the DNA sequence. Also provided are polynucleotide expression constructs, vectors, and host cells comprising nucleic acid fragments of codon-optimized coding regions which encode IV polypeptides, and fragments, variants, or derivatives thereof, and various methods of using the polynucleotide expression constructs, vectors, host cells to treat or prevent influenza disease in a vertebrate.

[0099] As used herein the term "codon-optimized coding region" means a nucleic acid coding region that has been adapted for expression in the cells of a given vertebrate by replacing at least one, or more than one, or a significant number, of codons with one or more codons that are more frequently used in the genes of that vertebrate.

[0100] Deviations in the nucleotide sequence that comprise the codons encoding the amino acids of any polypeptide chain allow for variations in the sequence coding for the gene. Since each codon consists of three nucleotides, and the nucleotides comprising DNA are restricted to four specific bases, there are 64 possible combinations of nucleotides, 61 of which encode amino acids (the remaining three codons encode signals ending translation). The "genetic code" which shows which codons encode which amino acids is reproduced

herein as Table 1. As a result, many amino acids are designated by more than one codon. For example, the amino acids alanine and proline are coded for by four triplets, serine and arginine by six, whereas tryptophan and methionine are coded by just one triplet. This degeneracy allows for DNA base composition to vary over a wide range without altering the amino acid sequence of the proteins encoded by the DNA.

TABLE 1: The Standard Genetic Code

	T	C	A	G
T	TTT Phe (F)	TCT Ser (S)	TAT Tyr (Y)	TGT Cys (C)
	TTC "	TCC "	TAC "	TGC
	TTA Leu (L)	TCA "	TAA **Ter**	TGA **Ter**
	TTG "	TCG "	TAG **Ter**	TGG Trp (W)
C	CTT Leu (L)	CCT Pro (P)	CAT His (H)	CGT Arg (R)
	CTC "	CCC "	CAC "	CGC "
	CTA "	CCA "	CAA Gln (Q)	CGA "
	CTG "	CCG "	CAG "	CGG "
A	ATT Ile (I)	ACT Thr (T)	AAT Asn (N)	AGT Ser (S)
	ATC "	ACC "	AAC "	AGC "
	ATA "	ACA "	AAA Lys (K)	AGA Arg (R)
	ATG Met (M)	ACG "	AAG "	AGG "
G	GTT Val (V)	GCT Ala (A)	GAT Asp (D)	GGT Gly (G)
	GTC "	GCC "	GAC "	GGC "
	GTA "	GCA "	GAA Glu (E)	GGA "
	GTG "	GCG "	GAG "	GGG "

[0101] Many organisms display a bias for use of particular codons to code for insertion of a particular amino acid in a growing peptide chain. Codon preference or codon bias, differences in codon usage between organisms, is afforded by degeneracy of the genetic code, and is well documented among many organisms. Codon bias often correlates with the efficiency of translation

of messenger RNA (mRNA), which is in turn believed to be dependent on, *inter alia*, the properties of the codons being translated and the availability of particular transfer RNA (tRNA) molecules. The predominance of selected tRNAs in a cell is generally a reflection of the codons used most frequently in peptide synthesis. Accordingly, genes can be tailored for optimal gene expression in a given organism based on codon optimization.

[0102] Given the large number of gene sequences available for a wide variety of animal, plant and microbial species, it is possible to calculate the relative frequencies of codon usage. Codon usage tables are readily available, for example, at the "Codon Usage Database" available at http://www.kazusa.or.jp/codon/ (visited July 9, 2002), and these tables can be adapted in a number of ways. *See* Nakamura, Y., *et al.* "Codon usage tabulated from the international DNA sequence databases: status for the year 2000" *Nucl. Acids Res.* 28:292 (2000), which is incorporated by reference. As examples, the codon usage tables for human, mouse, domestic cat, and cow, calculated from GenBank Release 128.0 (15 February 2002), are reproduced below as Tables 2-5. These Tables use mRNA nomenclature, and so instead of thymine (T) which is found in DNA, the Tables use uracil (U) which is found in RNA. The Tables have been adapted so that frequencies are calculated for each amino acid, rather than for all 64 codons.

TABLE 2: Codon Usage Table for Human Genes (*Homo sapiens*)

Amino Acid	Codon	Number	Frequency
Phe	UUU	326146	0.4525
Phe	UUC	394680	0.5475
Total		720826	
Leu	UUA	139249	0.0728
Leu	UUG	242151	0.1266
Leu	CUU	246206	0.1287
Leu	CUC	374262	0.1956
Leu	CUA	133980	0.0700
Leu	CUG	777077	0.4062
Total		1912925	

Amino Acid	Codon	Number	Frequency
Ile	AUU	303721	0.3554
Ile	AUC	414483	0.4850
Ile	AUA	136399	0.1596
Total		854603	
Met	AUG	430946	1.0000
Total		430946	
Val	GUU	210423	0.1773
Val	GUC	282445	0.2380
Val	GUA	134991	0.1137
Val	GUG	559044	0.4710
Total		1186903	
Ser	UCU	282407	0.1840
Ser	UCC	336349	0.2191
Ser	UCA	225963	0.1472
Ser	UCG	86761	0.0565
Ser	AGU	230047	0.1499
Ser	AGC	373362	0.2433
Total		1534889	
Pro	CCU	333705	0.2834
Pro	CCC	386462	0.3281
Pro	CCA	322220	0.2736
Pro	CCG	135317	0.1149
Total		1177704	
Thr	ACU	247913	0.2419
Thr	ACC	371420	0.3624
Thr	ACA	285655	0.2787
Thr	ACG	120022	0.1171
Total		1025010	
Ala	GCU	360146	0.2637
Ala	GCC	551452	0.4037
Ala	GCA	308034	0.2255
Ala	GCG	146233	0.1071
Total		1365865	
Tyr	UAU	232240	0.4347
Tyr	UAC	301978	0.5653
Total		534218	

Amino Acid	Codon	Number	Frequency
His	CAU	201389	0.4113
His	CAC	288200	0.5887
Total		489589	
Gln	CAA	227742	0.2541
Gln	CAG	668391	0.7459
Total		896133	
Asn	AAU	322271	0.4614
Asn	AAC	376210	0.5386
Total		698481	
Lys	AAA	462660	0.4212
Lys	AAG	635755	0.5788
Total		1098415	
Asp	GAU	430744	0.4613
Asp	GAC	502940	0.5387
Total		933684	
Glu	GAA	561277	0.4161
Glu	GAG	787712	0.5839
Total		1348989	
Cys	UGU	190962	0.4468
Cys	UGC	236400	0.5532
Total		427362	
Trp	UGG	248083	1.0000
Total		248083	
Arg	CGU	90899	0.0830
Arg	CGC	210931	0.1927
Arg	CGA	122555	0.1120
Arg	CGG	228970	0.2092
Arg	AGA	221221	0.2021
Arg	AGG	220119	0.2011
Total		1094695	
Gly	GGU	209450	0.1632
Gly	GGC	441320	0.3438
Gly	GGA	315726	0.2459
Gly	GGG	317263	0.2471
Total		1283759	

Amino Acid	Codon	Number	Frequency
Stop	UAA	13963	
Stop	UAG	10631	
Stop	UGA	24607	

TABLE 3: Codon Usage Table for Mouse Genes (*Mus musculus*)

Amino Acid	Codon	Number	Frequency
Phe	UUU	150467	0.4321
Phe	UUC	197795	0.5679
Total		348262	
Leu	UUA	55635	0.0625
Leu	UUG	116210	0.1306
Leu	CUU	114699	0.1289
Leu	CUC	179248	0.2015
Leu	CUA	69237	0.0778
Leu	CUG	354743	0.3987
Total		889772	
Ile	AUU	137513	0.3367
Ile	AUC	208533	0.5106
Ile	AUA	62349	0.1527
Total		408395	
Met	AUG	204546	1.0000
Total		204546	
Val	GUU	93754	0.1673
Val	GUC	140762	0.2513
Val	GUA	64417	0.1150
Val	GUG	261308	0.4664
Total		560241	
Ser	UCU	139576	0.1936
Ser	UCC	160313	0.2224
Ser	UCA	100524	0.1394
Ser	UCG	38632	0.0536
Ser	AGU	108413	0.1504
Ser	AGC	173518	0.2407
Total		720976	
Pro	CCU	162613	0.3036
Pro	CCC	164796	0.3077
Pro	CCA	151091	0.2821
Pro	CCG	57032	0.1065
Total		535532	
Thr	ACU	119832	0.2472

Amino Acid	Codon	Number	Frequency
Thr	ACC	172415	0.3556
Thr	ACA	140420	0.2896
Thr	ACG	52142	0.1076
Total		484809	
Ala	GCU	178593	0.2905
Ala	GCC	236018	0.3839
Ala	GCA	139697	0.2272
Ala	GCG	60444	0.0983
Total		614752	
Tyr	UAU	108556	0.4219
Tyr	UAC	148772	0.5781
Total		257328	
His	CAU	88786	0.3973
His	CAC	134705	0.6027
Total		223491	
Gln	CAA	101783	0.2520
Gln	CAG	302064	0.7480
Total		403847	
Asn	AAU	138868	0.4254
Asn	AAC	187541	0.5746
Total		326409	
Lys	AAA	188707	0.3839
Lys	AAG	302799	0.6161
Total		491506	
Asp	GAU	189372	0.4414
Asp	GAC	239670	0.5586
Total		429042	
Glu	GAA	235842	0.4015
Glu	GAG	351582	0.5985
Total		587424	
Cys	UGU	97385	0.4716
Cys	UGC	109130	0.5284
Total		206515	
Trp	UGG	112588	1.0000
Total		112588	
Arg	CGU	41703	0.0863
Arg	CGC	86351	0.1787
Arg	CGA	58928	0.1220
Arg	CGG	92277	0.1910

Amino Acid	Codon	Number	Frequency
Arg	AGA	101029	0.2091
Arg	AGG	102859	0.2129
Total		483147	
Gly	GGU	103673	0.1750
Gly	GGC	198604	0.3352
Gly	GGA	151497	0.2557
Gly	GGG	138700	0.2341
Total		592474	
Stop	UAA	5499	
Stop	UAG	4661	
Stop	UGA	10356	

TABLE 4: Codon Usage Table for Domestic Cat Genes (*Felis cattus*)

Amino Acid	Codon	Number	Frequency of usage
Phe	UUU	1204.00	0.4039
Phe	UUC	1777.00	0.5961
Total		2981	
Leu	UUA	404.00	0.0570
Leu	UUG	857.00	0.1209
Leu	CUU	791.00	0.1116
Leu	CUC	1513.00	0.2135
Leu	CUA	488.00	0.0688
Leu	CUG	3035.00	0.4282
Total		7088	
Ile	AUU	1018.00	0.2984
Ile	AUC	1835.00	0.5380
Ile	AUA	558.00	0.1636
Total		3411	
Met	AUG	1553.00	0.0036
Total		1553	
Val	GUU	696.00	0.1512
Val	GUC	1279.00	0.2779
Val	GUA	463.00	0.1006
Val	GUG	2164.00	0.4702
Total		4602	
Ser	UCU	940.00	0.1875
Ser	UCC	1260.00	0.2513
Ser	UCA	608.00	0.1213
Ser	UCG	332.00	0.0662
Ser	AGU	672.00	0.1340

Amino Acid	Codon	Number	Frequency of usage
Ser	AGC	1202.00	0.2397
Total		5014	
Pro	CCU	958.00	0.2626
Pro	CCC	1375.00	0.3769
Pro	CCA	850.00	0.2330
Pro	CCG	465.00	0.1275
Total		3648	
Thr	ACU	822.00	0.2127
Thr	ACC	1574.00	0.4072
Thr	ACA	903.00	0.2336
Thr	ACG	566.00	0.1464
Total		3865	
Ala	GCU	1129.00	0.2496
Ala	GCC	1951.00	0.4313
Ala	GCA	883.00	0.1952
Ala	GCG	561.00	0.1240
Total		4524	
Tyr	UAU	837.00	0.3779
Tyr	UAC	1378.00	0.6221
Total		2215	
His	CAU	594.00	0.3738
His	CAC	995.00	0.6262
Total		1589	
Gln	CAA	747.00	0.2783
Gln	CAG	1937.00	0.7217
Total		2684	
Asn	AAU	1109.00	0.3949
Asn	AAC	1699.00	0.6051
Total		2808	
Lys	AAA	1445.00	0.4088
Lys	AAG	2090.00	0.5912
Total		3535	
Asp	GAU	1255.00	0.4055
Asp	GAC	1840.00	0.5945
Total		3095	
Glu	GAA	1637.00	0.4164
Glu	GAG	2294.00	0.5836
Total		3931	

Amino Acid	Codon	Number	Frequency of usage
Cys	UGU	719.00	0.4425
Cys	UGC	906.00	0.5575
Total		1625	
Trp	UGG	1073.00	1.0000
Total		1073	
Arg	CGU	236.00	0.0700
Arg	CGC	629.00	0.1865
Arg	CGA	354.00	0.1050
Arg	CGG	662.00	0.1963
Arg	AGA	712.00	0.2112
Arg	AGG	779.00	0.2310
Total		3372	
Gly	GGU	648.00	0.1498
Gly	GGC	1536.00	0.3551
Gly	GGA	1065.00	0.2462
Gly	GGG	1077.00	0.2490
Total		4326	
Stop	UAA	55	
Stop	UAG	36	
Stop	UGA	110	

TABLE 5: Codon Usage Table for Cow Genes (*Bos taurus*)

Amino Acid	Codon	Number	Frequency of usage
Phe	UUU	13002	0.4112
Phe	UUC	18614	0.5888
Total		31616	
Leu	UUA	4467	0.0590
Leu	UUG	9024	0.1192
Leu	CUU	9069	0.1198
Leu	CUC	16003	0.2114
Leu	CUA	4608	0.0609
Leu	CUG	32536	0.4298
Total		75707	
Ile	AUU	12474	0.3313
Ile	AUC	19800	0.5258
Ile	AUA	5381	0.1429
Total		37655	
Met	AUG	17770	1.0000
Total		17770	

Amino Acid	Codon	Number	Frequency of usage
Val	GUU	8212	0.1635
Val	GUC	12846	0.2558
Val	GUA	4932	0.0982
Val	GUG	24222	0.4824
Total		50212	
Ser	UCU	10287	0.1804
Ser	UCC	13258	0.2325
Ser	UCA	7678	0.1347
Ser	UCG	3470	0.0609
Ser	AGU	8040	0.1410
Ser	AGC	14279	0.2505
Total		57012	
Pro	CCU	11695	0.2684
Pro	CCC	15221	0.3493
Pro	CCA	11039	0.2533
Pro	CCG	5621	0.1290
Total		43576	
Thr	ACU	9372	0.2203
Thr	ACC	16574	0.3895
Thr	ACA	10892	0.2560
Thr	ACG	5712	0.1342
Total		42550	
Ala	GCU	13923	0.2592
Ala	GCC	23073	0.4295
Ala	GCA	10704	0.1992
Ala	GCG	6025	0.1121
Total		53725	
Tyr	UAU	9441	0.3882
Tyr	UAC	14882	0.6118
Total		24323	
His	CAU	6528	0.3649
His	CAC	11363	0.6351
Total		17891	
Gln	CAA	8060	0.2430
Gln	CAG	25108	0.7570
Total		33168	
Asn	AAU	12491	0.4088
Asn	AAC	18063	0.5912
Total		30554	

Amino Acid	Codon	Number	Frequency of usage
Lys	AAA	17244	0.3897
Lys	AAG	27000	0.6103
Total		44244	
Asp	GAU	16615	0.4239
Asp	GAC	22580	0.5761
Total		39195	
Glu	GAA	21102	0.4007
Glu	GAG	31555	0.5993
Total		52657	
Cys	UGU	7556	0.4200
Cys	UGC	10436	0.5800
Total		17992	
Trp	UGG	10706	1.0000
Total		10706	
Arg	CGU	3391	0.0824
Arg	CGC	7998	0.1943
Arg	CGA	4558	0.1108
Arg	CGG	8300	0.2017
Arg	AGA	8237	0.2001
Arg	AGG	8671	0.2107
Total		41155	
Gly	GGU	8508	0.1616
Gly	GGC	18517	0.3518
Gly	GGA	12838	0.2439
Gly	GGG	12772	0.2427
Total		52635	
Stop	UAA	555	
Stop	UAG	394	
Stop	UGA	392	

[0103] By utilizing these or similar tables, one of ordinary skill in the art can apply the frequencies to any given polypeptide sequence, and produce a nucleic acid fragment of a codon-optimized coding region which encodes the polypeptide, but which uses codons more optimal for a given species. Codon-optimized coding regions can be designed by various different methods.

[0104] In one method, termed "uniform optimization," a codon usage table is used to find the single most frequent codon used for any given amino acid, and that codon is used each time that particular amino acid appears in the

polypeptide sequence. For example, referring to Table 2 above, for leucine, the most frequent codon in humans is CUG, which is used 41% of the time. Thus all the leucine residues in a given amino acid sequence would be assigned the codon CUG. A coding region for IAV NP (SEQ ID NO:2) optimized by the "uniform optimization" method is presented herein as SEQ ID NO:24:

```
   1 ATGGCCAGCC AGGGCACCAA GCGGAGCTAC GAGCAGATGG AGACCGACGG CGAGCGGCAG
  61 AACGCCACCG AGATCCGGGC CAGCGTGGGC AAGATGATCG GCGGCATCGG CCGGTTCTAC
 121 ATCCAGATGT GCACCGAGCT GAAGCTGAGC GACTACGAGG GCCGGCTGAT CCAGAACAGC
 181 CTGACCATCG AGCGGATGGT GCTGAGCGCC TTCGACGAGC GGCGGAACAA GTACCTGGAG
 241 GAGCACCCCA GCGCCGGCAA GGACCCCAAG AAGACCGGCG GCCCCATCTA CCGGCGGGTG
 301 AACGGCAAGT GGATGCGGGA GCTGATCCTG TACGACAAGG AGGAGATCCG GCGGATCTGG
 361 CGGCAGGCCA ACAACGGCGA CGACGCCACC GCCGGCCTGA CCCACATGAT GATCTGGCAC
 421 AGCAACCTGA ACGACGCCAC CTACCAGCGG ACCCGGGCCC TGGTGCGGAC CGGCATGGAC
 481 CCCCGGATGT GCAGCCTGAT GCAGGGCAGC ACCCTGCCCC GGCGGAGCGG CGCCGCCGGC
 541 GCCGCCGTGA AGGGCGTGGG CACCATGGTG ATGGAGCTGG TGCGGATGAT CAAGCGGGGC
 601 ATCAACGACC GGAACTTCTG GCGGGGCGAG AACGGCCGGA AGACCCGGAT CGCCTACGAG
 661 CGGATGTGCA ACATCCTGAA GGGCAAGTTC CAGACCGCCG CCCAGAAGGC CATGATGGAC
 721 CAGGTGCGGG AGAGCCGGAA CCCCGGCAAC GCCGAGTTCG AGGACCTGAC CTTCCTGGCC
 781 CGGAGCGCCC TGATCCTGCG GGGCAGCGTG GCCCACAAGA GCTGCCTGCC CGCCTGCGTG
 841 TACGGCCCCG CCGTGGCCAG CGGCTACGAC TTCGAGCGGG AGGGCTACAG CCTGGTGGGC
 901 ATCGACCCCT TCCGGCTGCT GCAGAACAGC CAGGTGTACA GCCTGATCCG GCCCAACGAG
 961 AACCCCGCCC ACAAGAGCCA GCTGGTGTGG ATGGCCTGCC ACAGCGCCGC CTTCGAGGAC
1021 CTGCGGGTGC TGAGCTTCAT CAAGGGCACC AAGGTGCTGC CCCGGGGCAA GCTGAGCACC
1081 CGGGGCGTGC AGATCGCCAG CAACGAGAAC ATGGAGACCA TGGAGAGCAG CACCCTGGAG
1141 CTGCGGAGCC GGTACTGGGC CATCCGGACC CGGAGCGGCG GCAACACCAA CCAGCAGCGG
1201 GCCAGCGCCG GCCAGATCAG CATCCAGCCC ACCTTCAGCG TGCAGCGGAA CCTGCCCTTC
1261 GACCGGACCA CCGTGATGGC CGCCTTCAGC GGCAACACCG AGGGCCGGAC CAGCGACATG
1321 CGGACCGAGA TCATCCGGAT GATGGAGAGC GCCCGGCCCG AGGACGTGAG CTTCCAGGGC
1381 CGGGGCGTGT TCGAGCTGAG CGACGAGAAG GCCGCCAGCC CCATCGTGCC CAGCTTCGAC
1441 ATGAGCAACG AGGGCAGCTA CTTCTTCGGC GACAACGCCG AGGAGTACGA CAACTGA
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[0105] In another method, termed "full-optimization," the actual frequencies of the codons are distributed randomly throughout the coding region. Thus, using this method for optimization, if a hypothetical polypeptide sequence had 100 leucine residues, referring to Table 2 for frequency of usage in humans, about 7, or 7% of the leucine codons would be UUA, about 13, or 13% of the leucine codons would be UUG, about 13, or 13% of the leucine codons would be CUU, about 20, or 20% of the leucine codons would be CUC, about 7, or 7% of the leucine codons would be CUA, and about 41, or 41% of the leucine codons would be CUG. These frequencies would be distributed randomly throughout the leucine codons in the coding region encoding the hypothetical polypeptide. As will be understood by those of ordinary skill in the art, the

distribution of codons in the sequence can vary significantly using this method; however, the sequence always encodes the same polypeptide.

[0106] As an example, a nucleotide sequence for NP (SEQ ID NO:2) fully optimized for human codon usage, is shown as SEQ ID NO:23. An alignment of nucleotides 46-1542 of SEQ ID NO:1 (native NP coding region) with the codon-optimized coding region (SEQ ID NO:23) is presented in Figure 1.

[0107] In using the "full-optimization" method, an entire polypeptide sequence may be codon-optimized as described above. With respect to various desired fragments, variants or derivatives of the complete polypeptide, the fragment variant, or derivative may first be designed, and is then codon-optimized individually. Alternatively, a full-length polypeptide sequence is codon-optimized for a given species resulting in a codon-optimized coding region encoding the entire polypeptide, and then nucleic acid fragments of the codon-optimized coding region, which encode fragments, variants, and derivatives of the polypeptide are made from the original codon-optimized coding region. As would be well understood by those of ordinary skill in the art, if codons have been randomly assigned to the full-length coding region based on their frequency of use in a given species, nucleic acid fragments encoding fragments, variants, and derivatives would not necessarily be fully codon-optimized for the given species. However, such sequences are still much closer to the codon usage of the desired species than the native codon usage. The advantage of this approach is that synthesizing codon-optimized nucleic acid fragments encoding each fragment, variant, and derivative of a given polypeptide, although routine, would be time consuming and would result in significant expense.

[0108] When using the "full-optimization" method, the term "about" is used precisely to account for fractional percentages of codon frequencies for a given amino acid. As used herein, "about" is defined as one amino acid more or one amino acid less than the value given. The whole number value of amino acids is rounded up if the fractional frequency of usage is 0.50 or greater, and is rounded down if the fractional frequency of use is 0.49 or less.

Using again the example of the frequency of usage of leucine in human genes for a hypothetical polypeptide having 62 leucine residues, the fractional frequency of codon usage would be calculated by multiplying 62 by the frequencies for the various codons. Thus, 7.28 percent of 62 equals 4.51 UUA codons, or "about 5," *i.e.*, 4, 5, or 6 UUA codons, 12.66 percent of 62 equals 7.85 UUG codons or "about 8," *i.e.*, 7, 8, or 9 UUG codons, 12.87 percent of 62 equals 7.98 CUU codons, or "about 8," *i.e.*, 7, 8, or 9 CUU codons, 19.56 percent of 62 equals 12.13 CUC codons or "about 12," *i.e.*, 11, 12, or 13 CUC codons, 7.00 percent of 62 equals 4.34 CUA codons or "about 4," *i.e.*, 3, 4, or 5 CUA codons, and 40.62 percent of 62 equals 25.19 CUG codons, or "about 25," *i.e.*, 24, 25, or 26 CUG codons.

[0109] In a third method termed "minimal optimization," coding regions are only partially optimized. For example, the invention includes a nucleic acid fragment of a codon-optimized coding region encoding a polypeptide in which at least about 1%, 2%, 3%, 4%, 5%, 10%, 15%, 20%, 25%, 30%, 35%, 40%, 45%, 50%, 55%, 60%, 65%, 70%, 75%, 80%, 85%, 90%, 95% or 100% of the codon positions have been codon-optimized for a given species. That is, they contain a codon that is preferentially used in the genes of a desired species, *e.g.*, a vertebrate species, *e.g.*, humans, in place of a codon that is normally used in the native nucleic acid sequence. Codons that are rarely found in the genes of the vertebrate of interest are changed to codons more commonly utilized in the coding regions of the vertebrate of interest.

[0110] Thus, those codons which are used more frequently in the IV gene of interest than in genes of the vertebrate of interest are substituted with more frequently-used codons. The difference in frequency at which the IV codons are substituted may vary based on a number factors as discussed below. For example, codons used at least twice more per thousand in IV genes as compared to genes of the vertebrate of interest are substituted with the most frequently used codon for that amino acid in the vertebrate of interest. This ratio may be adjusted higher or lower depending on various factors such as those discussed below. Accordingly, a codon in an IV native coding region

would be substituted with a codon used more frequently for that amino acid in coding regions of the vertebrate of interest if the codon is used 1.1 times, 1.2 times, 1.3 times, 1.4 times, 1.5 times, 1.6 times, 1.7 times, 1.8 times, 1.9 times, 2.0 times, 2.1 times, 2.2 times, 2.3 times, 2.4 times, 2.5 times, 2.6 times, 2.7 times, 2.8 times, 2.9 times, 3.0 times, 3.1 times, 3.2 times, 3.3. times, 3.4 times, 3.5 times, 3.6 times. 3.7 times, 3.8 times, 3.9 times, 4.0 times, 4.1 times, 4.2 times, 4.3 times, 4.4 times, 4.5 times, 4.6 times, 4.7 times, 4.8 times, 4.9 times, 5.0 times, 5.5 times, 6.0 times, 6.5 times, 7.0 times, 7.5 times, 8.0 times, 8.5 times, 9.0 times, 9.5 times, 10.0 times, 10.5 times, 11.0 times, 11.5 times, 12.0 times, 12.5 times, 13.0 times, 13.5 times, 14.0 times, 14.5 times, 15.0 times, 15.5 times, 16.0 times, 16.5 times, 17.0 times, 17.5 times, 18.0 times, 18.5 times, 19.0 times, 19.5 times, 20 times, 21 times, 22 times, 23 times, 24 times, 25 times, or greater more frequently in IV coding regions than in coding regions of the vertebrate of interest.

[0111] This minimal human codon optimization for highly variant codons has several advantages, which include but are not limited to the following examples. Since fewer changes are made to the nucleotide sequence of the gene of interest, fewer manipulations are required, which leads to reduced risk of introducing unwanted mutations and lower cost, as well as allowing the use of commercially available site-directed mutagenesis kits, and reducing the need for expensive oligonucleotide synthesis. Further, decreasing the number of changes in the nucleotide sequence decreases the potential of altering the secondary structure of the sequence, which can have a significant impact on gene expression in certain host cells. The introduction of undesirable restriction sites is also reduced, facilitating the subcloning of the genes of interest into the plasmid expression vector.

[0112] The present invention also provides isolated polynucleotides comprising coding regions of IV polypeptides, *e.g.*, NP, M1, M2, HA, NA, PB1, PB2, PA, NS1 or NS2, or fragments, variants, or derivatives thereof. The isolated polynucleotides can also be codon-optimized.

[0113] In certain embodiments described herein, a codon-optimized coding region encoding SEQ ID NO:2 is optimized according to codon usage in humans (*Homo sapiens*). Alternatively, a codon-optimized coding region encoding SEQ ID NO:2 may be optimized according to codon usage in any plant, animal, or microbial species. Codon-optimized coding regions encoding SEQ ID NO:2, optimized according to codon usage in humans are designed as follows. The amino acid composition of SEQ ID NO:2 is shown in Table 6.

TABLE 6

AMINO ACID		Number in SEQ ID NO:2
A	Ala	39
R	Arg	49
C	Cys	6
G	Gly	41
H	His	6
I	Ile	26
L	Leu	33
K	Lys	21
M	Met	25
F	Phe	18
P	Pro	17
S	Ser	40
T	Thr	28
W	Trp	6
Y	Tyr	15
V	Val	23
N	Asn	26
D	Asp	22
Q	Gln	21
E	Glu	36

[0114] Using the amino acid composition shown in Table 6, a human codon-optimized coding region which encodes SEQ ID NO:2 can be designed by any of the methods discussed herein. For "uniform" optimization, each amino acid is assigned the most frequent codon used in the human genome for that amino acid. According to this method, codons are assigned to the coding region encoding SEQ ID NO:2 as follows: the 18 phenylalanine codons are TTC, the 33 leucine codons are CTG, the 26 isoleucine codons are ATC, the 25 methionine codons are ATG, the 23 valine codons are GTG, the 40 serine

codons are AGC, the 17 proline codons are CCC, the 28 threonine codons are ACC, the 39 alanine codons are GCC, the 15 tyrosine codons are TAC, the 6 histidine codons are CAC, the 21 glutamine codons are CAG, the 26 asparagine codons are AAC, the 21 lysine codons are AAG, the 22 aspartic acid codons are GAC, the 36 glutamic acid codons are GAG, the 6 tryptophan codons are TGG, the 49 arginine codons are CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 41 glycine codons are GGC.

[0115] Alternatively, a human codon-optimized coding region which encodes SEQ ID NO:2 can be designed by the "full optimization" method, where each amino acid is assigned codons based on the frequency of usage in the human genome. These frequencies are shown in Table 6 above. Using this latter method, codons are assigned to the coding region encoding SEQ ID NO:2 as follows: about 8 of the 18 phenylalanine codons are TTT, and about 10 of the phenylalanine codons are TTC; about 2 of the 33 leucine codons are TTA, about 4 of the leucine codons are TTG, about 4 of the leucine codons are CTT, about 6 of the leucine codons are CTC, about 2 of the leucine codons are CTA, and about 13 of the leucine codons are CTG; about 9 of the 26 isoleucine codons are ATT, about 13 of the isoleucine codons are ATC, and about 4 of the isoleucine codons are ATA; the 25 methionine codons are ATG; about 4 of the 23 valine codons are GTT, about 5 of the valine codons are GTG, about 3 of the valine codons are GTA, and about 11 of the valine codons are GTG; about 7 of the 40 serine codons are TCT, about 9 of the serine codons are TCC, about 6 of the serine codons are TCA, about 2 of the serine codons are TCG, about 6 of the serine codons are AGT, and about 10 of the serine codons are AGC; about 5 of the 17 proline codons are CCT, about 6 of the proline codons are CCC, about 5 of the proline codons are CCA, and about 2 of the proline codons are CCG; about 7 of the 28 threonine codons are ACT, about 10 of the threonine codons are ACC, about 8 of the threonine codons are ACA, and about 3 of the threonine codons are ACG; about 10 of the 39 alanine codons are GCT, about 16 of the alanine codons are GCC,

about 9 of the alanine codons are GCA, and about 4 of the alanine codons are GCG; about 7 of the 15 tyrosine codons are TAT and about 8 of the tyrosine codons are TAC; about 2 of the 6 histidine codons are CAT and about 4 of the histidine codons are CAC; about 5 of the 21 glutamine codons are CAA and about 16 of the glutamine codons are CAG; about 12 of the 26 asparagine codons are AAT and about 14 of the asparagine codons are AAC; about 9 of the 21 lysine codons are AAA and about 12 of the lysine codons are AAG; about 10 of the 22 aspartic acid codons are GAT and about 12 of the aspartic acid codons are GAC; about 11 of the 26 glutamic acid codons are GAA and about 15 of the glutamic acid codons are GAG; about 3 of the 6 cysteine codons are TGT and about 3 of the cysteine codons are TGC; the 6 tryptophan codons are TGG; about 4 of the 49 arginine codons are CGT, about 9 of the arginine codons are CGC, about 5 of the arginine codons are CGA, about 10 of the arginine codons are CGG, about 10 of the arginine codons are AGA, and about 10 of the arginine codons are AGG; and about 7 of the 41 glycine codons are GGT, about 14 of the glycine codons are GGC, about 10 of the glycine codons are GGA, and about 10 of the glycine codons are GGG.

[0116] As described above, the term "about" means that the number of amino acids encoded by a certain codon may be one more or one less than the number given. It would be understood by those of ordinary skill in the art that the total number of any amino acid in the polypeptide sequence must remain constant, therefore, if there is one "more" of one codon encoding a give amino acid, there would have to be one "less" of another codon encoding that same amino acid.

[0117] A representative "fully optimized" codon-optimized coding region encoding SEQ ID NO:2, optimized according to codon usage in humans is presented herein as SEQ ID NO:23.

[0118] Additionally, a minimally codon-optimized nucleotide sequence encoding SEQ ID NO:2 can be designed by changing only certain codons found more frequently in IV genes than in human genes, as shown in Table 7. For example, if it is desired to substitute more frequently used codons in

humans for those codons that occur at least 2 times more frequently in IV genes (designated with an asterisk in Table 7), Arg AGA, which occurs 2.3 times more frequently in IV genes than in human genes, is changed to, e.g., CGG; Asn AAT, which occurs 2.0 times more frequently in IV genes than in human genes, is changed to, e.g., AAC; Ile ATA, which occurs 3.6 times more frequently in IV genes than in human genes, is changed to, e.g., ATC; and Leu CTA, which occurs 2.0 times more frequently in IV genes than is human, is changed to, e.g., CTG.

TABLE 7: Codon Usage Table for Human Genes and IV Genes

Amino Acid		Codon	Human	IV
Ala	A	GCA	16	25
		GCG	8	5
		GCC	19	11
		GCT	19	15
Arg	R	AGA	12	28*
		AGG	11	14
		CGA	6	7
		CGG	12	4
		CGC	11	3
		CGT	5	3
Asn	N	AAC	20	27
		AAT	17	34*
Asp	D	GAC	26	20
		GAT	22	25
Cys	C	TGC	12	13
		TGT	10	12
Gln	Q	CAA	12	18
		CAG	35	20
Glu	E	GAA	30	39
		GAG	40	28
Gly	G	GGA	16	30
		GGG	16	19
		GGC	23	9
		GGT	11	13
His	H	CAC	15	13
		CAT	11	7
Ile	I	ATA	7	25*
		ATC	22	18
		ATT	16	23

Leu	L	CTA	7	14*
		CTG	40	17
		CTC	20	14
		CTT	13	14
		TTA	7	8
		TTG	13	14
Lys	K	AAA	24	35
		AAG	33	20
Met	M	ATG	22	30
Phe	F	TTC	21	17
		TTT	17	19
Pro	P	CCA	17	12
		CCG	7	4
		CCC	20	8
		CCT	17	13
Ser	S	AGC	19	14
		AGT	12	16
		TCA	12	23
		TCG	5	4
		TCC	18	12
		TCT	15	15
Thr	T	ACA	15	24
		ACG	6	4
		ACC	19	13
		ACT	13	19
Trp	W	TGG	13	18
Tyr	Y	TAC	16	12
		TAT	12	19
Val	V	GTA	7	13
		GTG	29	20
		GTC	15	12
		GTT	11	15
Term		TAA	1	2
		TAG	0.5	0.4
		TGA	1	1

[0119] In another form of minimal optimization, a Codon Usage Table (CUT) for the specific IV sequence in question is generated and compared to CUT for human genomic DNA (see Table 7, *supra*). Amino acids are identified for which there is a difference of at least 10 percentage points in codon usage between human and IV DNA (either more or less). Then the wild type IV codon is modified to conform to predominant human codon for each such amino acid. Furthermore, the remainder of codons for that amino acid are also

modified such that they conform to the predominant human codon for each such amino acid.

[0120] A representative "minimally optimized" codon-optimized coding region encoding SEQ ID NO:2, minimally optimized according to codon usage in humans by this latter method, is presented herein as SEQ ID NO:25:

```
   1 ATGGCCTCAC AGGGCACCAA GCGGAGTTAT GAGCAGATGG AGACCGATGG CGAGAGACAG
  61 AACGCCACAG AGATCAGAGC CTCAGTTGGC AAGATGATCG GCGGCATCGG CCGGTTCTAT
 121 ATCCAGATGT GCACGGAGCT GAAGCTGAGC GACTACGAGG GCAGACTGAT TCAGAACTCT
 181 CTGACCATCG AGAGAATGGT CCTGAGTGCC TTCGATGAGA GACGAAACAA GTATCTGGAG
 241 GAGCATCCCT CCGCCGGCAA GGACCCCAAG AAGACGGGCG GCCCCATATA TAGAAGAGTT
 301 AACGGCAAGT GGATGAGAGA GCTGATCCTG TACGATAAGG AGGAGATCCG CAGAATATGG
 361 AGGCAGGCCA ACAACGGCGA CGATGCCACT GCCGGCCTGA CACATATGAT GATATGGCAC
 421 AGTAACCTGA ACGACGCCAC CTACCAGAGA ACAAGGGCCC TGGTTCGCAC GGGCATGGAT
 481 CCCAGAATGT GTTCACTGAT GCAGGGCTCT ACACTGCCCA GAAGGTCTGG CGCCGCCGGC
 541 GCCGCCGTCA AGGGCGTTGG CACAATGGTG ATGGAGCTGG TGCGGATGAT CAAGAGAGGC
 601 ATTAACGATC GGAACTTTTG GAGGGGCGAG AACGGCAGAA AGACCAGGAT AGCCTACGAG
 661 CGAATGTGCA ACATTCTGAA GGGCAAGTTC CAGACTGCCG CCCAGAAGGC CATGATGGAT
 721 CAGGTGCGGG AGAGCAGAAA CCCCGGCAAC GCCGAGTTCG AGGACCTGAC TTTCCTGGCC
 781 AGATCTGCCC TGATACTGAG GGGCTCTGTA GCCCACAAGT CCTGCCTGCC CGCCTGCGTG
 841 TACGGCCCCG CCGTGGCCTC CGGCTATGAC TTCGAGCGAG AGGGCTACTC CCTGGTAGGC
 901 ATCGATCCCT TTAGACTGCT GCAGAACTCT CAGGTCTACA GTCTGATTAG ACCCAACGAG
 961 AACCCCGCCC ATAAGAGCCA GCTGGTGTGG ATGGCCTGCC ACAGTGCCGC CTTCGAGGAC
1021 CTGAGGGTGC TGTCTTTTAT AAAGGGCACA AAGGTGCTGC CCCGCGGCAA GCTGTCTACT
1081 AGGGGCGTCC AGATAGCCTC CAACGAGAAC ATGGAGACAA TGGAGTCTAG TACTCTGGAG
1141 CTGAGGTCTA GGTACTGGGC CATCAGGACT AGGAGCGGCG GCAACACCAA CCAGCAGAGG
1201 GCCAGCGCCG GCCAGATCAG CATTCAGCCC ACCTTCAGTG TACAGAGAAA CCTGCCCTTT
1261 GATAGAACTA CTGTTATGGC CGCCTTCTCT GGCAACACTG AGGGCAGAAC TAGTGACATG
1321 CGAACAGAGA TCATAAGAAT GATGGAGTCG GCCCGTCCCG AGGATGTGTC CTTTCAGGGC
1381 AGGGGCGTCT TCGAGCTGAG CGACGAGAAG GCCGCCAGCC CCATCGTACC CTCTTTCGAT
1441 ATGAGTAACG AGGGCTCGTA CTTTTTTGGC GACAACGCCG AGGAGTATGA TAACTGA
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[0121] In certain embodiments described herein, a codon-optimized coding region encoding SEQ ID NO:4 is optimized according to codon usage in humans (*Homo sapiens*). Alternatively, a codon-optimized coding region encoding SEQ ID NO:4 may be optimized according to codon usage in any plant, animal, or microbial species. Codon-optimized coding regions encoding SEQ ID NO:4, optimized according to codon usage in humans are designed as follows. The amino acid composition of SEQ ID NO:4 is shown in Table 8.

TABLE 8

AMINO ACID		Number in SEQ ID NO:4
A	Ala	25
R	Arg	17

C	Cys	3
G	Gly	16
H	His	5
I	Ile	11
L	Leu	26
K	Lys	13
M	Met	14
F	Phe	7
P	Pro	8
S	Ser	18
T	Thr	18
W	Trp	1
Y	Tyr	5
V	Val	16
N	Asn	11
D	Asp	6
Q	Gln	15
E	Glu	17

[0122] Using the amino acid composition shown in Table 8, a human codon-optimized coding region which encodes SEQ ID NO:4 can be designed by any of the methods discussed herein. For "uniform" optimization, each amino acid is assigned the most frequent codon used in the human genome for that amino acid. According to this method, codons are assigned to the coding region encoding SEQ ID NO:4 as follows: the 7 phenylalanine codons are TTC, the 26 leucine codons are CTG, the 11 isoleucine codons are ATC, the 14 methionine codons are ATG, the 16 valine codons are GTG, the 18 serine codons are AGC, the 8 proline codons are CCC, the 18 threonine codons are ACC, the 25 alanine codons are GCC, the 5 tyrosine codons are TAC, the 5 histidine codons are CAC, the 15 glutamine codons are CAG, the 11 asparagine codons are AAC, the 13 lysine codons are AAG, the 6 aspartic acid codons are GAC, the 17 glutamic acid codons are GAG, the 1 tryptophan codon is TGG, the 17 arginine codons are CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 16 glycine codons are GGC. The codon-optimized coding region designed by this method is presented herein as SEQ ID NO:27:

ATGAGCCTGCTGACCGAGGTGGAGACCTACGTGCTGAGCATCATCCCCAGCGGCCC
CCTGAAGGCCGAGATCGCCCAGAGGCTGGAGGACGTGTTCGCCGGCAAGAACACCG
ACCTGGAGGTGCTGATGGAGTGGCTGAAGACCAGGCCCATCCTGAGCCCCCTGACC
AAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTGCCCAGCGAGAGGGGCCTGCA

GAGGAGGAGGTTCGTGCAGAACGCCCTGAACGGCAACGGCGACCCCAACAACATGG
ACAAGGCCGTGAAGCTGTACAGGAAGCTGAAGAGGGAGATCACCTTCCACGGCGCC
AAGGAGATCAGCCTGAGCTACAGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGAT
CTACAACAGGATGGGCGCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCA
CCTGCGAGCAGATCGCCGACAGCCAGCACAGGAGCCACAGGCAGATGGTGACCACC
ACCAACCCCCTGATCAGGCACGAGAACAGGATGGTGCTGGCCAGCACCACCGCCAA
GGCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAGGTGG
CCAGCCAGGCCAGGCAGATGGTGCAGGCCATGAGGACCATCGGCACCCACCCCAGC
AGCAGCGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTACCAGAAGAG
GATGGGCGTGCAGATGCAGAGGTTCAAG

[0123] Alternatively, a human codon-optimized coding region which encodes SEQ ID NO:4 can be designed by the "full optimization" method, where each amino acid is assigned codons based on the frequency of usage in the human genome. These frequencies are shown in Table 8 above. Using this latter method, codons are assigned to the coding region encoding SEQ ID NO:4 as follows: about 3 of the 7 phenylalanine codons are TTT, and about 4 of the phenylalanine codons are TTC; about 2 of the 26 leucine codons are TTA, about 3 of the leucine codons are TTG, about 3 of the leucine codons are CTT, about 5 of the leucine codons are CTC, about 2 of the leucine codons are CTA, and about 11 of the leucine codons are CTG; about 4 of the 11 isoleucine codons are ATT, about 5 of the isoleucine codons are ATC, and about 2 of the isoleucine codons are ATA; the 14 methionine codons are ATG; about 3 of the 16 valine codons are GTT, about 4 of the valine codons are GTG, about 2 of the valine codons are GTA, and about 8 of the valine codons are GTG; about 3 of the 18 serine codons are TCT, about 4 of the serine codons are TCC, about 3 of the serine codons are TCA, about 1 of the serine codons is TCG, about 3 of the serine codons are AGT, and about 4 of the serine codons are AGC; about 2 of the 8 proline codons are CCT, about 3 of the proline codons are CCC, about 2 of the proline codons are CCA, and about 1 of the proline codons is CCG; about 4 of the 18 threonine codons are ACT, about 7 of the threonine codons are ACC, about 5 of the threonine codons are ACA, and about 2 of the threonine codons are ACG; about 7 of the 25 alanine codons are GCT, about 10 of the alanine codons are GCC, about 6 of the alanine codons are GCA, and about 3 of the alanine codons are GCG; about 2 of the 5 tyrosine codons are TAT and about 3 of the tyrosine codons are TAC; about 2 of the 5 histidine codons are CAT and about 3 of the

histidine codons are CAC; about 4 of the 15 glutamine codons are CAA and about 11 of the glutamine codons are CAG; about 5 of the 11 asparagine codons are AAT and about 6 of the asparagine codons are AAC; about 5 of the 13 lysine codons are AAA and about 8 of the lysine codons are AAG; about 3 of the 6 aspartic acid codons are GAT and about 3 of the aspartic acid codons are GAC; about 7 of the 17 glutamic acid codons are GAA and about 10 of the glutamic acid codons are GAG; about 1 of the 3 cysteine codons is TGT and about 2 of the cysteine codons are TGC; the 1 tryptophan codons is TGG; about 1 of the 17 arginine codons are CGT, about 3 of the arginine codons are CGC, about 2 of the arginine codons are CGA, about 4 of the arginine codons are CGG, about 3 of the arginine codons are AGA, and about 3 of the arginine codons are AGG; and about 3 of the 16 glycine codons are GGT, about 6 of the glycine codons are GGC, about 4 of the glycine codons are GGA, and about 4 of the glycine codons are GGG.

[0124] As described above, the term "about" means that the number of amino acids encoded by a certain codon may be one more or one less than the number given. It would be understood by those of ordinary skill in the art that the total number of any amino acid in the polypeptide sequence must remain constant, therefore, if there is one "more" of one codon encoding a give amino acid, there would have to be one "less" of another codon encoding that same amino acid.

[0125] A representative "fully optimized" codon-optimized coding region encoding SEQ ID NO:4, optimized according to codon usage in humans is presented herein as SEQ ID NO:26:

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ATGAGCTTGCTAACAGAAGTGGAAACCTATGTCCTCAGTATCATTCCTAGCGGCCC
CTTAAAAGCCGAAATCGCTCAGCGGCTCGAGGATGTTTTTGCCGGCAAGAACACCG
ACCTGGAGGTATTGATGGAGTGGCTGAAAACGCGACCTATTCTGAGCCCCCTGACT
AAGGGAATACTCGGCTTCGTTTTTACATTGACCGTGCCCTCAGAGAGGGGTCTCCA
AAGGAGGCGCTTCGTGCAGAACGCCTTAAACGGGAACGGGGACCCAAATAATATGG
ATAAGGCAGTGAAACTGTATCGCAAATTAAAGCGGGAGATAACCTTCCATGGAGCC
AAGGAGATCTCCCTGTCTTACTCTGCAGGTGCTCTCGCGTCGTGTATGGGACTTAT
CTACAACCGAATGGGCGCCGTCACAACAGAAGTGGCTTTCGGGCTGGTGTGCGCAA
CTTGCGAACAGATTGCTGACAGTCAGCACCGGTCCCACCGTCAAATGGTCACCACC
ACCAATCCGCTGATTAGACATGAAAATCGCATGGTTCTAGCATCAACTACAGCCAA
AGCAATGGAACAAATGGCCGGAAGCTCCGAGCAGGCTGCCGAGGCGATGGAGGTGG
CGTCCCAGGCCAGACAGATGGTACAGGCTATGAGAACTATCGGTACGCACCCAAGT
TCTTCAGCTGGGCTGAAGAATGATCTTCTTGAGAACCTGCAGGCCTACCAAAAGCG
GATGGGCGTCCAGATGCAGAGATTTAAA
```

[0126] Additionally, a minimally codon-optimized nucleotide sequence encoding SEQ ID NO:4 can be designed by changing only certain codons found more frequently in IV genes than in human genes, as shown in Table 7. For example, if it is desired to substitute more frequently used codons in humans for those codons that occur at least 2 times more frequently in IV genes (designated with an asterisk in Table 7), Arg AGA, which occurs 2.3 times more frequently in IV genes than in human genes, is changed to, e.g., CGG; Asn AAT, which occurs 2.0 times more frequently in IV genes than in human genes, is changed to, e.g., AAC; Ile ATA, which occurs 3.6 times more frequently in IV genes than in human genes, is changed to, e.g., ATC; and Leu CTA, which occurs 2.0 times more frequently in IV genes than is human, is changed to, e.g., CTG.

[0127] In another form of minimal optimization, a Codon Usage Table (CUT) for the specific IV sequence in question is generated and compared to CUT for human genomic DNA (see Table 7, *supra*). Amino acids are identified for which there is a difference of at least 10 percentage points in codon usage between human and IV DNA (either more or less). Then the wild type IV codon is modified to conform to predominant human codon for each such amino acid. Furthermore, the remainder of codons for that amino acid are also modified such that they conform to the predominant human codon for each such amino acid.

[0128] A representative "minimally optimized" codon-optimized coding region encoding SEQ ID NO:4, minimally optimized according to codon usage in humans by this latter method, is presented herein as SEQ ID NO:28:

```
ATGAGTCTGCTGACAGAGGTTGAGACGTACGTGCTGTCCATCATTCCCTCAGGCCC
CCTGAAGGCCGAGATTGCCCAGAGACTGGAGGACGTCTTCGCCGGCAAGAACACCG
ATCTGGAGGTGCTGATGGAGTGGCTGAAGACTCGCCCCATCCTGTCTCCCCTGACA
AAGGGCATCCTGGGCTTCGTATTTACACTGACCGTCCCCTCCGAGAGAGGCCTGCA
GCGGAGGAGGTTCGTTCAGAACGCCCTGAACGGCAACGGCGATCCCAACAACATGG
ATAAGGCCGTGAAGCTGTATAGAAAGCTGAAGCGAGAGATCACATTTCATGGCGCC
AAGGAGATATCGCTGAGCTACAGTGCCGGCGCCCTGGCCTCTTGCATGGGCCTGAT
ATACAACAGAATGGGCGCCGTTACTACAGAGGTAGCCTTTGGCCTGGTCTGCGCCA
CTTGCGAGCAGATCGCCGACTCTCAGCATAGATCTCACAGACAGATGGTGACGACT
ACAAACCCCCTGATACGGCACGAGAACAGGATGGTGCTGGCCTCTACTACCGCCAA
GGCCATGGAGCAGATGGCCGGCAGCAGTGAGCAGGCCGCCGAGGCCATGGAGGTAG
CCTCACAGGCCAGGCAGATGGTGCAGGCCATGCGAACCATCGGCACTCACCCCTCC
AGCTCTGCCGGCCTGAAGAACGACCTGCTGGAGAACCTGCAGGCCTATCAGAAGAG
AATGGGCGTACAGATGCAGAGGTTCAAG
```

[0129] In certain embodiments described herein, a codon-optimized coding region encoding SEQ ID NO:5 is optimized according to codon usage in humans (*Homo sapiens*). Alternatively, a codon-optimized coding region encoding SEQ ID NO:5 may be optimized according to codon usage in any plant, animal, or microbial species. Codon-optimized coding regions encoding SEQ ID NO:5, optimized according to codon usage in humans are designed as follows. The amino acid composition of SEQ ID NO:5 is shown in Table 9.

TABLE 9

AMINO ACID		Number in SEQ ID NO:5
A	Ala	5
R	Arg	7
C	Cys	3
G	Gly	8
H	His	2
I	Ile	8
L	Leu	10
K	Lys	5
M	Met	2
F	Phe	4
P	Pro	4
S	Ser	7
T	Thr	4
W	Trp	2
Y	Tyr	3
V	Val	4
N	Asn	3
D	Asp	5
Q	Gln	2
E	Glu	9

[0130] Using the amino acid composition shown in Table 9, a human codon-optimized coding region which encodes SEQ ID NO:5 can be designed by any of the methods discussed herein. For "uniform" optimization, each amino acid is assigned the most frequent codon used in the human genome for that amino acid. According to this method, codons are assigned to the coding region encoding SEQ ID NO:5 as follows: the 4 phenylalanine codons are TTC, the 10 leucine codons are CTG, the 8 isoleucine codons are ATC, the 2

methionine codons are ATG, the 4 valine codons are GTG, the 7 serine codons are AGC, the 4 proline codons are CCC, the 4 threonine codons are ACC, the 5 alanine codons are GCC, the 3 tyrosine codons are TAC, the 2 histidine codons are CAC, the 2 glutamine codons are CAG, the 3 asparagine codons are AAC, the 5 lysine codons are AAG, the 5 aspartic acid codons are GAC, the 9 glutamic acid codons are GAG, the 2 tryptophan codons are TGG, the 7 arginine codons are CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 8 glycine codons are GGC. The codon-optimized PA coding region designed by this method is presented herein as SEQ ID NO:30:

```
  1 ATGAGCCTGC TGACCGAGGT GGAGACCCCC ATCCGGAACG AGTGGGGCTG CCGGTGCAAC
 61 GGCAGCAGCG ACCCCCTGGC CATCGCCGCC AACATCATCG GCATCCTGCA CCTGACCCTG
121 TGGATCCTGG ACCGGCTGTT CTTCAAGTGC ATCTACCGGC GGTTCAAGTA CGGCCTGAAG
181 GGCGGCCCCA GCACCGAGGG CGTGCCCAAG AGCATGCGGG AGGAGTACCG GAAGGAGCAG
241 CAGAGCGCCG TGGACGCCGA CGACGGCCAC TTCGTGAGCA TCGAGCTGGA GTGA
```

[0131] Alternatively, a human codon-optimized coding region which encodes SEQ ID NO:5 can be designed by the "full optimization" method, where each amino acid is assigned codons based on the frequency of usage in the human genome. These frequencies are shown in Table 9 above. Using this latter method, codons are assigned to the coding region encoding SEQ ID NO:5 as follows: about 2 of the 4 phenylalanine codons are TTT, and about 2 of the phenylalanine codons are TTC; about 1 of the 10 leucine codons are TTA, about 1 of the leucine codons are TTG, about 1 of the leucine codons are CTT, about 2 of the leucine codons are CTC, about 1 of the leucine codons are CTA, and about 4 of the leucine codons are CTG; about 3 of the 8 isoleucine codons are ATT, about 4 of the isoleucine codons are ATC, and about 1 of the isoleucine codons are ATA; the 2 methionine codons are ATG; about 1 of the 4 valine codons are GTT, about 1 of the valine codons are GTG, about 0 of the valine codons are GTA, and about 2 of the valine codons are GTG; about 1 of the 7 serine codons are TCT, about 2 of the serine codons are TCC, about 1 of the serine codons are TCA, about 0 of the serine codons are TCG, about 1 of the serine codons are AGT, and about 2 of the serine codons are AGC; about 1 of the 4 proline codons are CCT, about 1 of the proline codons are CCC, about

2 of the proline codons are CCA, and about 0 of the proline codons are CCG; about 1 of the 4 threonine codons are ACT, about 1 of the threonine codons are ACC, about 1 of the threonine codons are ACA, and about 0 of the threonine codons are ACG; about 1 of the 5 alanine codons are GGT, about 2 of the alanine codons are GCC, about 1 of the alanine codons are GCA, and about 1 of the alanine codons are GCG; about 1 of the 3 tyrosine codons are TAT and about 2 of the tyrosine codons are TAC; about 1 of the 2 histidine codons are CAT and about 1 of the histidine codons are CAC; about 1 of the 2 glutamine codons are CAA and about 1 of the glutamine codons are CAG; about 1 of the 3 asparagine codons are AAT and about 2 of the asparagine codons are AAC; about 2 of the 5 lysine codons are AAA and about 3 of the lysine codons are AAG; about 2 of the 5 aspartic acid codons are GAT and about 3 of the aspartic acid codons are GAC; about 4 of the 9 glutamic acid codons are GAA and about 5 of the glutamic acid codons are GAG; about 1 of the 3 cysteine codons are TGT and about 2 of the cysteine codons are TGC; the 2 tryptophan codons are TGG; about 1 of the 7 arginine codons are CGT, about 1 of the arginine codons are CGC, about 1 of the arginine codons are CGA, about 1 of the arginine codons are CGG, about 1 of the arginine codons are AGA, and about 1 of the arginine codons are AGG; and about 1 of the 8 glycine codons are GGT, about 3 of the glycine codons are GGC, about 2 of the glycine codons are GGA, and about 2 of the glycine codons are GGG.

[0132] As described above, the term "about" means that the number of amino acids encoded by a certain codon may be one more or one less than the number given. It would be understood by those of ordinary skill in the art that the total number of any amino acid in the polypeptide sequence must remain constant, therefore, if there is one "more" of one codon encoding a give amino acid, there would have to be one "less" of another codon encoding that same amino acid.

[0133] A representative "fully optimized" codon-optimized coding region encoding SEQ ID NO:5, optimized according to codon usage in humans is presented herein as SEQ ID NO:29:

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1 ATGAGTCTTC TAACCGAGGT CGAAACGCCT ATCAGAAACG AATGGGGGTG CAGATGCAAC
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 61 GGTTCAAGTG ATCCTCTCGC TATTGCCGCA AATATCATTG GGATCTTGCA CTTGACATTG
121 TGGATTCTTG ATCGTCTTTT TTTCAAATGC ATTTACCGTC GCTTTAAATA CGGACTGAAA
181 GGAGGGCCTT CTACGGAAGG AGTGCCAAAG TCTATGAGGG AAGAATATCG AAAGGAACAG
241 CAGAGTGCTG TGGATGCTGA CGATGGTCAT TTTGTCAGCA TAGAGCTGGA GTAA
```

[0134] Additionally, a minimally codon-optimized nucleotide sequence encoding SEQ ID NO:5 can be designed by changing only certain codons found more frequently in IV genes than in human genes, as shown in Table 7. For example, if it is desired to substitute more frequently used codons in humans for those codons that occur at least 2 times more frequently in IV genes (designated with an asterisk in Table 7), Arg AGA, which occurs 2.3 times more frequently in IV genes than in human genes, is changed to, e.g., CGG; Asn AAT, which occurs 2.0 times more frequently in IV genes than in human genes, is changed to, e.g., AAC; Ile ATA, which occurs 3.6 times more frequently in IV genes than in human genes, is changed to, e.g., ATC; and Leu CTA, which occurs 2.0 times more frequently in IV genes than is human, is changed to, e.g., CTG.

[0135] In another form of minimal optimization, a Codon Usage Table (CUT) for the specific IV sequence in question is generated and compared to CUT for human genomic DNA (see Table 7, *supra*). Amino acids are identified for which there is a difference of at least 10 percentage points in codon usage between human and IV DNA (either more or less). Then the wild type IV codon is modified to conform to predominant human codon for each such amino acid. Furthermore, the remainder of codons for that amino acid are also modified such that they conform to the predominant human codon for each such amino acid.

[0136] A representative "minimally optimized" codon-optimized coding region encoding SEQ ID NO:5, minimally optimized according to codon usage in humans by this latter method, is presented herein as SEQ ID NO:31:

```
  1 ATGTCTCTGC TGACAGAGGT GGAGACACCC ATAAGGAACG AGTGGGGCTG CAGGTGCAAC
 61 GGCTCTAGTG ATCCCCTGGC CATCGCCGCC AACATCATTG GCATACTGCA TCTGACCCTG
121 TGGATCCTGG ATAGACTGTT CTTTAAGTGC ATTTACAGAC GATTTAAGTA TGGCCTGAAG
181 GGCGGCCCCT CAACTGAGGG CGTGCCCAAG AGTATGAGAG AGGAGTACCG GAAGGAGCAG
241 CAGAGCGCCG TTGACGCCGA TGACGGCCAC TTCGTCTCCA TCGAGCTGGA GTGA
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[0137] In certain embodiments described herein, a codon-optimized coding region encoding SEQ ID NO:7 is optimized according to codon usage in

humans (*Homo sapiens*). Alternatively, a codon-optimized coding region encoding SEQ ID NO:7 may be optimized according to codon usage in any plant, animal, or microbial species. Codon-optimized coding regions encoding SEQ ID NO:7, optimized according to codon usage in humans are designed as follows. The amino acid composition of SEQ ID NO:7 is shown in Table 10.

TABLE 10

AMINO ACID		Number in SEQ ID NO:7
A	Ala	39
R	Arg	51
C	Cys	8
G	Gly	43
H	His	6
I	Ile	27
L	Leu	35
K	Lys	21
M	Met	26
F	Phe	18
P	Pro	18
S	Ser	43
T	Thr	30
W	Trp	7
Y	Tyr	15
V	Val	24
N	Asn	28
D	Asp	23
Q	Gln	21
E	Glu	39

[0138] Using the amino acid composition shown in Table 10, a human codon-optimized coding region which encodes SEQ ID NO:7 can be designed by any of the methods discussed herein. For "uniform" optimization, each amino acid is assigned the most frequent codon used in the human genome for that amino acid. According to this method, codons are assigned to the coding region encoding SEQ ID NO:7 as follows: the 18 phenylalanine codons are TTC, the 35 leucine codons are CTG, the 27 isoleucine codons are ATC, the 26 methionine codons are ATG, the 24 valine codons are GTG, the 43 serine codons are AGC, the 18 proline codons are CCC, the 30 threonine codons are

ACC, the 39 alanine codons are GCC, the 15 tyrosine codons are TAC, the 6 histidine codons are CAC, the 21 glutamine codons are CAG, the 28 asparagine codons are AAC, the 21 lysine codons are AAG, the 23 aspartic acid codons are GAC, the 39 glutamic acid codons are GAG, the 7 tryptophan codons are TGG, the 51 arginine codons are CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 43 glycine codons are GGC. The codon-optimized PA coding region designed by this method is presented herein as SEQ ID NO:33:

ATGAGCCTGCTGACCGAGGTGGAGACCCCCATCAGGAACGAGTGGGGCTGCAGGTGCAACGGCAGCAGCG
ACATGGCCAGCCAGGGCACCAAGAGGAGCTACGAGCAGATGGAGACCGACGGCGAGAGGCAGAACGCCAC
CGAGATCAGGGCCAGCGTGGGCAAGATGATCGGCGGCATCGGCAGGTTCTACATCCAGATGTGCACCGAG
CTGAAGCTGAGCGACTACGAGGGCAGGCTGATCCAGAACAGCCTGACCATCGAGAGGATGGTGCTGAGCG
CCTTCGACGAGAGGAGGAACAAGTACCTGGAGGAGCACCCCAGCGCCGGCAAGGACCCCAAGAAGACCGG
CGGCCCCATCTACAGGAGGGTGAACGGCAAGTGGATGAGGGAGCTGATCCTGTACGACAAGGAGGAGATC
AGGAGGATCTGGAGGCAGGCCAACAACGGCGACGACGCCACCGCCGGCCTGACCCACATGATGATCTGGC
ACAGCAACCTGAACGACGCCACCTACCAGAGGACCAGGGCCCTGGTGAGGACCGGCATGGACCCCAGGAT
GTGCAGCCTGATGCAGGGCAGCACCCTGCCCAGGAGGAGCGGCGCCGCCGGCGCCGCCGTGAAGGGCGTG
GGCACCATGGTGATGGAGCTGGTGAGGATGATCAAGAGGGGCATCAACGACAGGAACTTCTGGAGGGGCG
AGAACGGCAGGAAGACCAGGATCGCCTACGAGAGGATGTGCAACATCCTGAAGGGCAAGTTCCAGACCGC
CGCCCAGAAGGCCATGATGGACCAGGTGAGGGAGAGCAGGAACCCCGGCAACGCCGAGTTCGAGGACCTG
ACCTTCCTGGCCAGGAGCGCCCTGATCCTGAGGGGCAGCGTGGCCCACAAGAGCTGCCTGCCCGCCTGCG
TGTACGGCCCCGCCGTGGCCAGCGGCTACGACTTCGAGAGGGAGGGCTACAGCCTGGTGGGCATCGACCC
CTTCAGGCTGCTGCAGAACAGCCAGGTGTACAGCCTGATCAGGCCCAACGAGAACCCCGCCCACAAGAGC
CAGCTGGTGTGGATGGCCTGCCACAGCGCCGCCTTCGAGGACCTGAGGGTGCTGAGCTTCATCAAGGGCA
CCAAGGTGCTGCCCAGGGGCAAGCTGAGCACCAGGGGCGTGCAGATCGCCAGCAACGAGAACATGGAGAC
CATGGAGAGCAGCACCCTGGAGCTGAGGAGCAGGTACTGGGCCATCAGGACCAGGAGCGGCGGCAACACC
AACCAGCAGAGGGCCAGCGCCGGCCAGATCAGCATCCAGCCCACCTTCAGCGTGCAGAGGAACCTGCCCT
TCGACAGGACCACCGTGATGGCCGCCTTCAGCGGCAACACCGAGGGCAGGACCAGCGACATGAGGACCGA
GATCATCAGGATGATGGAGAGCGCCAGGCCCGAGGACGTGAGCTTCCAGGGCAGGGGCGTGTTCGAGCTG
AGCGACGAGAAGGCCGCCAGCCCCATCGTGCCCAGCTTCGACATGAGCAACGAGGGCAGCTACTTCTTCG
GCGACAACGCCGAGGAGTACGACAAC

[0139] Alternatively, a human codon-optimized coding region which encodes SEQ ID NO:7 can be designed by the "full optimization" method, where each amino acid is assigned codons based on the frequency of usage in the human genome. These frequencies are shown in Table 10 above. Using this latter method, codons are assigned to the coding region encoding SEQ ID NO:7 as follows: about 8 of the 18 phenylalanine codons are TTT, and about 10 of the phenylalanine codons are TTC; about 3 of the 35 leucine codons are TTA, about 4 of the leucine codons are TTG, about 5 of the leucine codons are CTT, about 7 of the leucine codons are CTC, about 2 of the leucine codons are CTA, and about 14 of the leucine codons are CTG; about 10 of the 27

isoleucine codons are ATT, about 13 of the isoleucine codons are ATC, and about 4 of the isoleucine codons are ATA; the 26 methionine codons are ATG; about 4 of the 24 valine codons are GTT, about 6 of the valine codons are GTG, about 3 of the valine codons are GTA, and about 11 of the valine codons are GTG; about 8 of the 43 serine codons are TCT, about 9 of the serine codons are TCC, about 6 of the serine codons are TCA, about 2 of the serine codons are TCG, about 6 of the serine codons are AGT, and about 10 of the serine codons are AGC; about 5 of the 18 proline codons are CCT, about 6 of the proline codons are CCC, about 5 of the proline codons are CCA, and about 2 of the proline codons are CCG; about 7 of the 30 threonine codons are ACT, about 11 of the threonine codons are ACC, about 8 of the threonine codons are ACA, and about 4 of the threonine codons are ACG; about 10 of the 39 alanine codons are GGT, about 16 of the alanine codons are GCC, about 9 of the alanine codons are GCA, and about 4 of the alanine codons are GCG; about 7 of the 15 tyrosine codons are TAT and about 8 of the tyrosine codons are TAC; about 2 of the 6 histidine codons are CAT and about 4 of the histidine codons are CAC; about 5 of the 21 glutamine codons are CAA and about 16 of the glutamine codons are CAG; about 13 of the 28 asparagine codons are AAT and about 15 of the asparagine codons are AAC; about 9 of the 21 lysine codons are AAA and about 12 of the lysine codons are AAG; about 11 of the 23 aspartic acid codons are GAT and about 12 of the aspartic acid codons are GAC; about 16 of the 39 glutamic acid codons are GAA and about 23 of the glutamic acid codons are GAG; about 4 of the 8 cysteine codons are TGT and about 4 of the cysteine codons are TGC; the 7 tryptophan codons are TGG; about 4 of the 51 arginine codons are CGT, about 10 of the arginine codons are CGC, about 6 of the arginine codons are CGA, about 11 of the arginine codons are CGG, about 10 of the arginine codons are AGA, and about 10 of the arginine codons are AGG; and about 7 of the 43 glycine codons are GGT, about 15 of the glycine codons are GGC, about 11 of the glycine codons are GGA, and about 11 of the glycine codons are GGG.

[0140] As described above, the term "about" means that the number of amino acids encoded by a certain codon may be one more or one less than the number given. It would be understood by those of ordinary skill in the art that the total number of any amino acid in the polypeptide sequence must remain constant, therefore, if there is one "more" of one codon encoding a give amino acid, there would have to be one "less" of another codon encoding that same amino acid.

[0141] A representative "fully optimized" codon-optimized coding region encoding SEQ ID NO:7, optimized according to codon usage in humans is presented herein as SEQ ID NO:32:

ATGAGCCTTCTCACAGAAGTGGAAACACCTATCAGAAATGAATGGGGATGCAGATGCAATGGGTCGAGTG
ATATGGCCTCTCAAGGTACGAAAAGAAGCTACGAGCAAATGGAAACGGATGGAGAAAGACAAAACGCGAC
CGAAATCAGAGCATCCGTCGGGAAGATGATTGGAGGAATCGGACGATTCTACATCCAGATGTGCACAGAG
CTAAAGCTATCGGATTATGAAGGGAGACTAATACAAAATAGCCTAACTATCGAGAGAATGGTGCTGTCTG
CATTTGACGAAAGGAGAAACAAATACCTGGAAGAACACCCCTCTGCAGGGAAAGACCCAAAAAAAACTGG
AGGTCCGATATACCGGAGAGTCAACGGTAAATGGATGAGAGAGCTGATCTTGTATGATAAGGAAGAAATA
AGACGCATCTGGCGGCAAGCTAATAATGGAGACGACGCTACTGCAGGGCTCACGCATATGATGATCTGGC
ACTCTAATTTGAATGATGCAACGTACCAAAGAACCCGCGCACTTGTGCGGACCGGAATGGACCCTCGTAT
GTGCAGCCTTATGCAGGGGTCCACACTGCCCAGAAGGTCCGGAGCAGCTGGAGCAGCAGTAAAGGGGGTT
GGAACCATGGTGATGGAGCTGGTGAGAATGATTAAGAGGGGGATCAATGACAGGAACTTCTGGCGAGGAG
AAAACGGGAGAAAAACTAGGATAGCATATGAGAGGATGTGTAACATCCTCAAAGGAAAATTCCAAACCGC
TGCTCAGAAAGCAATGATGGATCAAGTACGCGAAAGTAGAAATCCTGGAAATGCAGAGTTTGAAGATCTC
ACTTTCCTCGCGCGAAGCGCTCTCATCCTCAGAGGGAGTGTCGCTCATAAAAGTTGCCTGCCTGCCTGCG
TATATGGTCCTGCCGTGGCAAGTGGATACGACTTTGAGAGAGAGGGGTACTCTCTTGTTGGAATAGATCC
ATTCAGATTACTTCAGAATTCCCAGGTGTACAGTTTAATAAGGCCAAACGAAAATCCTGCACACAAATCA
CAACTTGTTTGGATGGCATGCCATAGTGCCGCATTCGAAGATCTAAGAGTTCTCTCTTTCATCAAAGGTA
CAAAGGTCCTTCCAAGGGGAAAACTCTCTACCAGAGGGGTACAAATAGCTTCAAATGAGAACATGGAGAC
AATGGAATCTAGCACATTGGAATTGAGAAGTAGGTATTGGGCCATTAGAACCAGGAGTGGAGGCAATACT
AATCAACAGCGGGCTTCTGCCGGTCAAATTAGCATACAACCTACTTTTTCAGTGCAACGGAATCTCCCTT
TTGATAGGACAACTGTCATGGCGGCATTCTCTGGAAATACCGAAGGAAGGACTTCCGATATGAGGACTGA
GATCATTAGGATGATGGAAAGTGCCCGACCTGAAGACGTCAGTTTTCAAGGAAGAGGTGTGTTCGAACTC
TCTGACGAAAAGGCAGCTAGCCCAATCGTTCCTTCTTTTGATATGTCAAATGAAGGATCCTACTTCTTCG
GCGATAATGCGGAGGAATATGACAAC

[0142] In certain embodiments described herein, a codon-optimized coding region encoding SEQ ID NO:9 is optimized according to codon usage in humans (*Homo sapiens*). Alternatively, a codon-optimized coding region encoding SEQ ID NO:9 may be optimized according to codon usage in any plant, animal, or microbial species. Codon-optimized coding regions encoding SEQ ID NO:9, optimized according to codon usage in humans are designed as follows. The amino acid composition of SEQ ID NO:9 is shown in Table 11.

TABLE 11

AMINO ACID		Number in SEQ ID NO:9
A	Ala	39
R	Arg	51
C	Cys	8
G	Gly	43
H	His	6
I	Ile	27
L	Leu	35
K	Lys	21
M	Met	26
F	Phe	18
P	Pro	18
S	Ser	43
T	Thr	30
W	Trp	7
Y	Tyr	15
V	Val	24
N	Asn	28
D	Asp	23
Q	Gln	21
E	Glu	39

[0143] Using the amino acid composition shown in Table 11, a human codon-optimized coding region which encodes SEQ ID NO:9 can be designed by any of the methods discussed herein. For "uniform" optimization, each amino acid is assigned the most frequent codon used in the human genome for that amino acid. According to this method, codons are assigned to the coding region encoding SEQ ID NO:9 as follows: the 18 phenylalanine codons are TTC, the 35 leucine codons are CTG, the 27 isoleucine codons are ATC, the 26 methionine codons are ATG, the 24 valine codons are GTG, the 43 serine codons are AGC, the 18 proline codons are CCC, the 30 threonine codons are ACC, the 39 alanine codons are GCC, the 15 tyrosine codons are TAC, the 6 histidine codons are CAC, the 21 glutamine codons are CAG, the 28 asparagine codons are AAC, the 21 lysine codons are AAG, the 23 aspartic acid codons are GAC, the 39 glutamic acid codons are GAG, the 7 tryptophan codons are TGG, the 51 arginine codons are CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 43 glycine codons are GGC. The codon-

optimized PA coding region designed by this method is presented herein as SEQ ID NO:35:

ATGGCCAGCCAGGGCACCAAGAGGAGCTACGAGCAGATGGAGACCGACGGCGAGAGGCA
GAACGCCACCGAGATCAGGGCCAGCGTGGGCAAGATGATCGGCGGCATCGGCAGGTTCTA
CATCCAGATGTGCACCGAGCTGAAGCTGAGCGACTACGAGGGCAGGCTGATCCAGAACAG
CCTGACCATCGAGAGGATGGTGCTGAGCGCCTTCGACGAGAGGAGGAACAAGTACCTGGA
GGAGCACCCCAGCGCCGGCAAGGACCCCAAGAAGACCGGCGGCCCCATCTACAGGAGGGT
GAACGGCAAGTGGATGAGGGAGCTGATCCTGTACGACAAGGAGGAGATCAGGAGGATCTG
GAGGCAGGCCAACAACGGCGACGACGCCACCGCCGGCCTGACCCACATGATGATCTGGCA
CAGCAACCTGAACGACGCCACCTACCAGAGGACCAGGGCCCTGGTGAGGACCGGCATGGA
CCCCAGGATGTGCAGCCTGATGCAGGGCAGCACCCTGCCCAGGAGGAGCGGCGCCGCCGG
CGCCGCCGTGAAGGGCGTGGGCACCATGGTGATGGAGCTGGTGAGGATGATCAAGAGGGG
CATCAACGACAGGAACTTCTGGAGGGGCGAGAACGGCAGGAAGACCAGGATCGCCTACGA
GAGGATGTGCAACATCCTGAAGGGCAAGTTCCAGACCGCCGCCCAGAAGGCCATGATGGA
CCAGGTGAGGGAGAGCAGGAACCCCGGCAACGCCGAGTTCGAGGACCTGACCTTCCTGGC
CAGGAGCGCCCTGATCCTGAGGGGCAGCGTGGCCCACAAGAGCTGCCTGCCCGCCTGCGTG
TACGGCCCCGCCGTGGCCAGCGGCTACGACTTCGAGAGGGAGGGCTACAGCCTGGTGGGCA
TCGACCCCTTCAGGCTGCTGCAGAACAGCCAGGTGTACAGCCTGATCAGGCCCAACGAGAA
CCCCGCCCACAAGAGCCAGCTGGTGTGGATGGCCTGCCACAGCGCCGCCTTCGAGGACCTG
AGGGTGCTGAGCTTCATCAAGGGCACCAAGGTGCTGCCCAGGGGCAAGCTGAGCACCAGG
GGCGTGCAGATCGCCAGCAACGAGAACATGGAGACCATGGAGAGCAGCACCCTGGAGCTG
AGGAGCAGGTACTGGGCCATCAGGACCAGGAGCGGCGGCAACACCAACCAGCAGAGGGCC
AGCGCCGGCCAGATCAGCATCCAGCCCACCTTCAGCGTGCAGAGGAACCTGCCCTTCGACA
GGACCACCGTGATGGCCGCCTTCAGCGGCAACACCGAGGGCAGGACCAGCGACATGAGGA
CCGAGATCATCAGGATGATGGAGAGCGCCAGGCCCGAGGACGTGAGCTTCCAGGGCAGGG
GCGTGTTCGAGCTGAGCGACGAGAAGGCCGCCAGCCCCATCGTGCCCAGCTTCGACATGAG
CAACGAGGGCAGCTACTTCTTCGGCGACAACGCCGAGGAGTACGACAACATGAGCCTGCTG
ACCGAGGTGGAGACCCCCATCAGGAACGAGTGGGGCTGCAGGTGCAACGGCAGCAGCGAC

[0144] Alternatively, a human codon-optimized coding region which encodes SEQ ID NO:9 can be designed by the "full optimization" method, where each amino acid is assigned codons based on the frequency of usage in the human genome. These frequencies are shown in Table 11 above. Using this latter method, codons are assigned to the coding region encoding SEQ ID NO:9 as follows: about 8 of the 18 phenylalanine codons are TTT, and about 10 of the phenylalanine codons are TTC; about 3 of the 35 leucine codons are TTA, about 4 of the leucine codons are TTG, about 5 of the leucine codons are CTT, about 7 of the leucine codons are CTC, about 2 of the leucine codons are CTA, and about 14 of the leucine codons are CTG; about 10 of the 27 isoleucine codons are ATT, about 13 of the isoleucine codons are ATC, and about 4 of the isoleucine codons are ATA; the 26 methionine codons are ATG; about 4 of the 24 valine codons are GTT, about 6 of the valine codons are GTG, about 3 of the valine codons are GTA, and about 11 of the valine codons are GTG; about 8 of the 43 serine codons are TCT, about 9 of the serine codons are TCC, about 6 of the serine codons are TCA, about 2 of the

serine codons are TCG, about 6 of the serine codons are AGT, and about 10 of the serine codons are AGC; about 5 of the 18 proline codons are CCT, about 6 of the proline codons are CCC, about 5 of the proline codons are CCA, and about 2 of the proline codons are CCG; about 7 of the 30 threonine codons are ACT, about 11 of the threonine codons are ACC, about 8 of the threonine codons are ACA, and about 4 of the threonine codons are ACG; about 10 of the 39 alanine codons are GGT, about 16 of the alanine codons are GCC, about 9 of the alanine codons are GCA, and about 4 of the alanine codons are GCG; about 7 of the 15 tyrosine codons are TAT and about 8 of the tyrosine codons are TAC; about 2 of the 6 histidine codons are CAT and about 4 of the histidine codons are CAC; about 5 of the 21 glutamine codons are CAA and about 16 of the glutamine codons are CAG; about 13 of the 28 asparagine codons are AAT and about 15 of the asparagine codons are AAC; about 9 of the 21 lysine codons are AAA and about 12 of the lysine codons are AAG; about 11 of the 23 aspartic acid codons are GAT and about 12 of the aspartic acid codons are GAC; about 16 of the 39 glutamic acid codons are GAA and about 23 of the glutamic acid codons are GAG; about 4 of the 8 cysteine codons are TGT and about 4 of the cysteine codons are TGC; the 7 tryptophan codons are TGG; about 4 of the 51 arginine codons are CGT, about 10 of the arginine codons are CGC, about 6 of the arginine codons are CGA, about 11 of the arginine codons are CGG, about 10 of the arginine codons are AGA, and about 10 of the arginine codons are AGG; and about 7 of the 43 glycine codons are GGT, about 15 of the glycine codons are GGC, about 11 of the glycine codons are GGA, and about 11 of the glycine codons are GGG.

[0145] As described above, the term "about" means that the number of amino acids encoded by a certain codon may be one more or one less than the number given. It would be understood by those of ordinary skill in the art that the total number of any amino acid in the polypeptide sequence must remain constant, therefore, if there is one "more" of one codon encoding a give amino acid, there would have to be one "less" of another codon encoding that same amino acid.

[0146] A representative "fully optimized" codon-optimized coding region encoding SEQ ID NO:9, optimized according to codon usage in humans is presented herein as SEQ ID NO:34:

ATGGCAAGCCAGGGCACAAAACGCAGTTACGAGCAGATGGAGACTGATGGTGAGAGGCAGAACGCCACCG
AAATCCGGGCCTCCGTCGGCAAGATGATTGGTGGCATCGGAAGATTCTATATCCAGATGTGCACGGAGCT
TAAGCTGTCCGATTACGAGGGGCGCTTAATACAGAACTCTCTGACTATCGAGCGAATGGTCTTGAGCGCC
TTTGATGAGCGGCGTAATAAGTATCTCGAAGAGCACCCTTCTGCTGGAAAAGACCCCAAAAAGACCGGGG
GACCTATCTACCGACGTGTGAACGGAAAATGGATGCGCGAACTGATACTGTACGACAAGGAGGAGATCCG
TAGGATCTGGAGACAGGCTAATAACGGAGATGATGCCACAGCTGGGCTGACCCATATGATGATATGGCAT
AGCAACCTGAACGACGCAACCTATCAACGCACTAGAGCACTCGTGAGGACCGGTATGGACCCACGCATGT
GCTCATTGATGCAAGGTAGCACATTGCCTCGGAGGTCAGGCGCCGCCGGTGCCGCCGTAAAGGGGGTGGG
CACAATGGTGATGGAACTGGTCCGAATGATCAAAAGAGGCATCAATGACAGGAACTTTTGGCGCGGAGAA
AACGGGCGCAAGACCCGCATTGCCTACGAGCGCATGTGTAACATTTTAAAAGGCAAATTCCAGACTGCAG
CCCAGAAAGCAATGATGGACCAAGTTAGAGAAAGTAGAAATCCCGGGAATGCCGAGTTTGAAGACCTGAC
TTTCCTGGCTAGAAGCGCCTTGATCCTGCGGGGCTCTGTCGCCCACAAGAGCTGCCTCCCCGCTTGCGTT
TACGGCCCCGCGGTCGCAAGTGGCTACGATTTCGAGAGGGAGGGGTATTCCCTAGTTGGGATCGATCCCT
TCCGGCTCCTACAGAATTCTCAGGTGTATAGTCTGATTAGACCCAACGAAAACCCGGCTCACAAGAGTCA
GCTTGTTTGGATGGCATGTCACTCAGCAGCTTTCGAAGACCTGCGGGTACTCAGCTTTATTAAAGGCACC
AAGGTCCTGCCAAGAGGAAAGCTCTCCACGAGGGGAGTACAGATCGCCTCAAACGAGAACATGGAGACAA
TGGAAAGCTCCACCCTTGAGCTTAGGTCGCGGTATTGGGCTATTAGAACACGATCTGGGGGGAATACCAA
TCAGCAACGAGCGAGTGCTGGTCAGATTTCCATTCAGCCTACTTTCTCTGTGCAACGGAATCTACCATTT
GACAGGACAACTGTGATGGCAGCGTTCTCCGGCAATACAGAAGGACGAACATCAGACATGAGGACCGAAA
TTATCCGGATGATGGAGAGCGCTCGGCCAGAAGATGTGTCGTTCCAGGGCCGGGGCGTGTTTGAGCTCAG
CGACGAGAAGGCCGCGTCTCCAATTGTGCCTTCCTTTGATATGAGCAATGAGGGGTCATACTTTTTCGGA
GACAATGCCGAAGAGTATGATAATATGTCTCTGCTTACCGAGGTGGAAACGCCGATACGCAACGAATGGG
GTTGTCGTTGTAACGGCTCCAGTGAT

[0147] In certain embodiments described herein, a codon-optimized coding region encoding SEQ ID NO:16 is optimized according to codon usage in humans (*Homo sapiens*). Alternatively, a codon-optimized coding region encoding SEQ ID NO:16 may be optimized according to codon usage in any plant, animal, or microbial species. Codon-optimized coding regions encoding SEQ ID NO:16, optimized according to codon usage in humans are designed as follows. The amino acid composition of SEQ ID NO:16 is shown in Table 12.

TABLE 12

AMINO ACID		Number in SEQ ID NO:16
A	Ala	41
R	Arg	30
C	Cys	5
G	Gly	44
H	His	4

I	Ile	38
L	Leu	39
K	Lys	52
M	Met	27
F	Phe	21
P	Pro	26
S	Ser	40
T	Thr	38
W	Trp	1
Y	Tyr	14
V	Val	32
N	Asn	25
D	Asp	34
Q	Gln	19
E	Glu	30

[0148] Using the amino acid composition shown in Table 12, a human codon-optimized coding region which encodes SEQ ID NO:16 can be designed by any of the methods discussed herein. For "uniform" optimization, each amino acid is assigned the most frequent codon used in the human genome for that amino acid. According to this method, codons are assigned to the coding region encoding SEQ ID NO:16 as follows: the 21 phenylalanine codons are TTC, the 39 leucine codons are CTG, the 38 isoleucine codons are ATC, the 27 methionine codons are ATG, the 32 valine codons are GTG, the 40 serine codons are AGC, the 26 proline codons are CCC, the 38 threonine codons are ACC, the 41 alanine codons are GCC, the 14 tyrosine codons are TAC, the 4 histidine codons are CAC, the 19 glutamine codons are CAG, the 25 asparagine codons are AAC, the 52 lysine codons are AAG, the 34 aspartic acid codons are GAC, the 30 glutamic acid codons are GAG, the 1 tryptophan codon is TGG, the 30 arginine codons are CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 44 glycine codons are GGC. The codon-optimized PA coding region designed by this method is presented herein as SEQ ID NO:37:

ATGAGCAACATGGACATCGACAGCATCAACACCGGCACCATCGACAAGACCCCCGAGGAG
CTGACCCCCGGCACCAGCGGCGCCACCCGGCCCATCATCAAGCCCGCCACCCTGGCCCCCC
CCAGCAACAAGCGGACCCGGAACCCCAGCCCCGAGCGGACCACCACCAGCAGCGAGACCG
ACATCGGCCGGAAGATCCAGAAGAAGCAGACCCCCACCGAGATCAAGAAGAGCGTGTACA
AGATGGTGGTGAAGCTGGGCGAGTTCTACAACCAGATGATGGTGAAGGCCGGCCTGAACG
ACGACATGGAGCGGAACCTGATCCAGAACGCCCAGGCCGTGGAGCGGATCCTGCTGGCCG
CCACCGACGACAAGAAGACCGAGTACCAGAAGAAGCGGAACGCCCGGGACGTGAAGGAG

GGCAAGGAGGAGATCGACCACAACAAGACCGGCGGCACCTTCTACAAGATGGTGCGGGAC
GACAAGACCATCTACTTCAGCCCCATCAAGATCACCTTCCTGAAGGAGGAGGTGAAGACCA
TGTACAAGACCACCATGGGCAGCGACGGCTTCAGCGGCCTGAACCACATCATGATCGGCCA
CAGCCAGATGAACGACGTGTGCTTCCAGCGGAGCAAGGGCCTGAAGCGGGTGGGCCTGGA
CCCCAGCCTGATCAGCACCTTCGCCGGCAGCACCCTGCCCCGGCGGAGCGGCACCACCGGC
GTGGCCATCAAGGGCGGCGGCACCCTGGTGGACGAGGCCATCCGGTTCATCGGCCGGGCCA
TGGCCGACCGGGGCCTGCTGCGGGACATCAAGGCCAAGACCGCCTACGAGAAGATCCTGCT
GAACCTGAAGAACAAGTGCAGCGCCCCCCAGCAGAAGGCCCTGGTGGACCAGGTGATCGG
CAGCCGGAACCCCGGCATCGCCGACATCGAGGACCTGACCCTGCTGGCCCGGAGCATGGTG
GTGGTGCGGCCCAGCGTGGCCAGCAAGGTGGTGCTGCCCATCAGCATCTACGCCAAGATCC
CCCAGCTGGGCTTCAACACCGAGGAGTACAGCATGGTGGGCTACGAGGCCATGGCCCTGTA
CAACATGGCCACCCCCGTGAGCATCCTGCGGATGGGCGACGACGCCAAGGACAAGAGCCA
GCTGTTCTTCATGAGCTGCTTCGGCGCCGCCTACGAGGACCTGCGGGTGCTGAGCGCCCTGA
CCGGCACCGAGTTCAAGCCCCGGAGCGCCCTGAAGTGCAAGGGCTTCCACGTGCCCGCCAA
GGAGCAGGTGGAGGGCATGGGCGCCGCCCTGATGAGCATCAAGCTGCAGTTCTGGGCCCCC
ATGACCCGGAGCGGCGGCAACGAGGTGAGCGGCGAGGGCGGCAGCGGCCAGATCAGCTGC
AGCCCCGTGTTCGCCGTGGAGCGGCCCATCGCCCTGAGCAAGCAGGCCGTGCGGCGGATGC
TGAGCATGAACGTGGAGGGCCGGGACGCCGACGTGAAGGGCAACCTGCTGAAGATGATGA
ACGACAGCATGGCCAAGAAGACCAGCGGCAACGCCTTCATCGGCAAGAAGATGTTCCAGA
TCAGCGACAAGAACAAGGTGAACCCCATCGAGATCCCCATCAAGCAGACCATCCCCAACTT
CTTCTTCGGCCGGGACACCGCCGAGGACTACGACGACCTGGACTACTGA

[0149] Alternatively, a human codon-optimized coding region which encodes SEQ ID NO:16 can be designed by the "full optimization" method, where each amino acid is assigned codons based on the frequency of usage in the human genome. These frequencies are shown in Table 12 above. Using this latter method, codons are assigned to the coding region encoding SEQ ID NO:16 as follows: about 10 of the 21 phenylalanine codons are TTT, and about 12 of the phenylalanine codons are TTC; about 3 of the 39 leucine codons are TTA, about 5 of the leucine codons are TTG, about 5 of the leucine codons are CTT, about 8 of the leucine codons are CTC, about 3 of the leucine codons are CTA, and about 16 of the leucine codons are CTG; about 14 of the 38 isoleucine codons are ATT, about 18 of the isoleucine codons are ATC, and about 6 of the isoleucine codons are ATA; the 27 methionine codons are ATG; about 6 of the 32 valine codons are GTT, about 8 of the valine codons are GTG, about 4 of the valine codons are GTA, and about 15 of the valine codons are GTG; about 7 of the 40 serine codons are TCT, about 9 of the serine codons are TCC, about 6 of the serine codons are TCA, about 2 of the serine codons are TCG, about 6 of the serine codons are AGT, and about 10 of the serine codons are AGC; about 7 of the 26 proline codons are CCT, about 9 of the proline codons are CCC, about 7 of the proline codons are CCA, and about 3 of the proline codons are CCG; about 9 of the 38 threonine codons are

ACT, about 14 of the threonine codons are ACC, about 11 of the threonine codons are ACA, and about 4 of the threonine codons are ACG; about 11 of the 41 alanine codons are GGT, about 17 of the alanine codons are GCC, about 9 of the alanine codons are GCA, and about 4 of the alanine codons are GCG; about 6 of the 14 tyrosine codons are TAT and about 8 of the tyrosine codons are TAC; about 2 of the 4 histidine codons are CAT and about 2 of the histidine codons are CAC; about 5 of the 19 glutamine codons are CAA and about 14 of the glutamine codons are CAG; about 12 of the 25 asparagine codons are AAT and about 13 of the asparagine codons are AAC; about 22 of the 52 lysine codons are AAA and about 30 of the lysine codons are AAG; about 16 of the 34 aspartic acid codons are GAT and about 18 of the aspartic acid codons are GAC; about 12 of the 30 glutamic acid codons are GAA and about 18 of the glutamic acid codons are GAG; about 2 of the 5 cysteine codons are TGT and about 3 of the cysteine codons are TGC; the single tryptophan codon is TGG; about 2 of the 30 arginine codons are CGT, about 6 of the arginine codons are CGC, about 3 of the arginine codons are CGA, about 6 of the arginine codons are CGG, about 6 of the arginine codons are AGA, and about 6 of the arginine codons are AGG; and about 7 of the 44 glycine codons are GGT, about 15 of the glycine codons are GGC, about 11 of the glycine codons are GGA, and about 11 of the glycine codons are GGG.

[0150] As described above, the term "about" means that the number of amino acids encoded by a certain codon may be one more or one less than the number given. It would be understood by those of ordinary skill in the art that the total number of any amino acid in the polypeptide sequence must remain constant, therefore, if there is one "more" of one codon encoding a give amino acid, there would have to be one "less" of another codon encoding that same amino acid.

[0151] A representative "fully optimized" codon-optimized coding region encoding SEQ ID NO:16, optimized according to codon usage in humans is presented herein as SEQ ID NO:36:

ATGTCGAACATGGACATCGACAGCATTAACACAGGTACTATTGACAAAACCCCCGAAGAACTAACCCCTG
GAACCTCAGGAGCAACACGCCCAATAATCAAACCGGCCACCCTCGCGCCCCCTAGCAATAAGAGGACCCG
CAATCCAAGTCCTGAGAGAACCACTACTTCATCTGAAACGGATATCGGTCGGAAAATTCAAAAAAAGCAG

ACGCCCACAGAGATAAAGAAGTCTGTTTACAAAATGGTGGTAAAGCTCGGTGAGTTTTATAACCAGATGA
TGGTCAAGGCGGGGCTTAACGACGATATGGAACGAAATCTTATACAGAATGCACAGGCAGTAGAGAGAAT
ACTGCTGGCCGCTACTGATGACAAGAAAACGGAGTACCAAAAAAAACGGAATGCTCGAGATGTGAAAGAA
GGAAAAGAAGAAATTGACCATAACAAAACTGGGGGGACATTCTATAAGATGGTGCGGGACGATAAGACAA
TCTATTTTAGCCCGATAAAGATTACCTTCCTGAAGGAGGAGGTTAAAACAATGTACAAGACGACGATGGG
CAGCGATGGGTTTTCCGGACTTAATCATATAATGATTGGTCACTCGCAGATGAACGATGTATGTTTCCAG
CGCTCCAAGGGCTTAAAGAGGGTAGGTCTTGACCCGTCTCTAATATCAACTTTCGCAGGATCCACTTTGC
CGAGGCGTTCTGGCACGACAGGCGTGGCTATCAAGGGCGGGGGGACGCTGGTCGATGAGGCCATTCGCTT
TATTGGTAGGGCCATGGCCGATAGAGGGCTTCTACGAGACATCAAAGCAAAAACAGCATATGAGAAGATA
TTATTAAACTTAAAGAACAAATGCTCCGCTCCTCAGCAAAAAGCGCTCGTTGACCAAGTAATCGGTTCGA
GAAATCCAGGCATTGCCGATATCGAAGATCTTACACTCTTGGCGCGAAGCATGGTCGTTGTCCGTCCCAG
TGTCGCTAGTAAGGTGGTACTACCAATCTCGATTTACGCAAAAATTCCACAACTCGGCTTTAATACAGAG
GAATATTCTATGGTAGGTTATGAAGCCATGGCGTTGTATAATATGGCTACACCAGTCTCCATATTGCGTA
TGGGAGATGACGCAAAAGATAAGAGTCAACTCTTTTTCATGTCATGTTTCGGCGCAGCGTACGAAGATCT
GAGAGTACTATCCGCCTTGACTGGAACGGAATTTAAACCACGGTCAGCCTTAAAGTGTAAGGGTTTTCAC
GTCCCTGCTAAGGAGCAAGTTGAGGGAATGGGCGCGGCACTGATGAGTATAAAATTACAATTTTGGGCTC
CAATGACGCGTTCGGGAGGGAATGAAGTTTCTGGTGAGGGAGGGAGTGGACAGATATCATGCTCGCCCGT
GTTCGCGGTTGAACGTCCGATTGCTTTGAGTAAGCAGGCGGTTAGGCGGATGTTAAGTATGAATGTGGAG
GGCCGCGATGCCGACGTCAAAGGCAACTTATTAAAAATGATGAACGACAGCATGGCAAAGAAGACTAGTG
GGAATGCTTTTATAGGGAAAAAAATGTTCCAAATAAGTGACAAAAACAAAGTGAACCCCATCGAAATACC
TATCAAGCAAACCATCCCGAATTTCTTTTTCGGTCGAGACACCGCGGAGGACTACGATGACCTAGATTAC
TAA

[0152] Additionally, a minimally codon-optimized nucleotide sequence encoding SEQ ID NO:16 can be designed by changing only certain codons found more frequently in IV genes than in human genes, as shown in Table 7. For example, if it is desired to substitute more frequently used codons in humans for those codons that occur at least 2 times more frequently in IV genes (designated with an asterisk in Table 7), Arg AGA, which occurs 2.3 times more frequently in IV genes than in human genes, is changed to, e.g., CGG; Asn AAT, which occurs 2.0 times more frequently in IV genes than in human genes, is changed to, e.g., AAC; Ile ATA, which occurs 3.6 times more frequently in IV genes than in human genes, is changed to, e.g., ATC; and Leu CTA, which occurs 2.0 times more frequently in IV genes than is human, is changed to, e.g., CTG.

[0153] In another form of minimal optimization, a Codon Usage Table (CUT) for the specific IV sequence in question is generated and compared to CUT for human genomic DNA (see Table 7, *supra*). Amino acids are identified for which there is a difference of at least 10 percentage points in codon usage between human and IV DNA (either more or less). Then the wild type IV codon is modified to conform to predominant human codon for each such amino acid. Furthermore, the remainder of codons for that amino acid are also

modified such that they conform to the predominant human codon for each such amino acid.

[0154] A representative "minimally optimized" codon-optimized coding region encoding SEQ ID NO:16, minimally optimized according to codon usage in humans by this latter method, is presented herein as SEQ ID NO:38:

ATGTCTAACATGGACATCGACTCTATAAACACAGGCACGATCGATAAGACCCCCGAGGAGC
TGACACCCGGCACTTCAGGCGCCACCAGACCCATAATAAAGCCCGCCACTCTGGCCCCCCC
CTCTAACAAGAGGACGAGGAACCCCTCTCCCGAGCGCACCACAACGAGTAGCGAGACGGA
CATCGGCAGGAAGATACAGAAGAAGCAGACTCCCACTGAGATTAAGAAGTCCGTGTATAA
GATGGTGGTTAAGCTGGGCGAGTTTTACAACCAGATGATGGTGAAGGCCGGCCTGAACGAT
GACATGGAGAGGAACCTGATACAGAACGCCCAGGCCGTGGAGAGGATTCTGCTGGCCGCC
ACCGATGACAAGAAGACTGAGTATCAGAAGAAGAGAAACGCCCGGGACGTTAAGGAGGGC
AAGGAGGAGATCGATCACAACAAGACAGGCGGCACTTTCTATAAGATGGTCCGTGATGAC
AAGACAATCTACTTTTCTCCCATCAAGATCACATTCCTGAAGGAGGAGGTAAAGACTATGT
ACAAGACAACTATGGGCTCCGATGGCTTCAGTGGCCTGAACCACATAATGATAGGCCATAG
TCAGATGAACGATGTGTGCTTCCAGAGAAGCAAGGGCCTGAAGAGGGTCGGCCTGGATCCC
TCGCTGATTAGTACCTTCGCCGGCAGCACTCTGCCCAGAAGATCTGGCACTACTGGCGTAGC
CATAAAGGGCGGCGGCACACTGGTAGACGAGGCCATAAGGTTTATTGGCAGAGCCATGGC
CGACCGCGGCCTGCTGAGAGATATCAAGGCCAAGACCGCCTACGAGAAGATACTGCTGAA
CCTGAAGAACAAGTGCTCAGCCCCCCAGCAGAAGGCCCTGGTGGATCAGGTGATCGGCAGT
AGAAACCCCGGCATCGCCGACATCGAGGATCTGACTCTGCTGGCCAGAAGCATGGTAGTCG
TAAGACCCTCTGTGGCCTCTAAGGTTGTGCTGCCCATCTCCATCTACGCCAAGATTCCCCAG
CTGGGCTTTAACACTGAGGAGTACTCCATGGTGGGCTATGAGGCCATGGCCCTGTATAACA
TGGCCACACCCGTCTCTATCCTGCGGATGGGCGACGATGCCAAGGACAAGTCTCAGCTGTT
TTTTATGAGTTGTTTCGGCGCCGCCTATGAGGATCTGAGAGTCCTGTCAGCCCTGACAGGCA
CTGAGTTCAAGCCCAGGTCCGCCCTGAAGTGCAAGGGCTTTCATGTGCCCGCCAAGGAGCA
GGTGGAGGGCATGGGCGCCGCCCTGATGAGCATCAAGCTGCAGTTCTGGGCCCCCATGACC
CGGTCTGGCGGCAACGAGGTCTCGGGCGAGGGCGGCAGTGGCCAGATAAGTTGCAGCCCC
GTTTTTGCCGTTGAGAGACCCATCGCCCTGTCTAAGCAGGCCGTTAGACGAATGCTGAGTAT
GAACGTCGAGGGCCGAGACGCCGATGTGAAGGGCAACCTGCTGAAGATGATGAACGATTC
CATGGCCAAGAAGACAAGCGGCAACGCCTTCATTGGCAAGAAGATGTTCCAGATAAGCGA
TAAGAACAAGGTTAACCCCATCGAGATTCCCATCAAGCAGACCATCCCCAACTTCTTCTTCG
GCAGGGATACCGCCGAGGATTACGATGACCTGGACTACTGA

[0155] Randomly assigning codons at an optimized frequency to encode a given polypeptide sequence using the "full-optimization" or "minimal optimization" methods, can be done manually by calculating codon frequencies for each amino acid, and then assigning the codons to the polypeptide sequence randomly. Additionally, various algorithms and computer software programs are readily available to those of ordinary skill in the art. For example, the "EditSeq" function in the Lasergene Package, available from DNAstar, Inc., Madison, WI, the backtranslation function in the VectorNTI Suite, available from InforMax, Inc., Bethesda, MD, and the "backtranslate" function in the GCG--Wisconsin Package, available from Accelrys, Inc., San Diego, CA. In addition, various resources are publicly

available to codon-optimize coding region sequences. For example, the "backtranslation" function found at http://www.entelechon.com/eng/backtranslation.html (visited July 9, 2002), and the "backtranseq" function available at http://bioinfo.pbi.nrc.ca:8090/EMBOSS/index.html (visited October 15, 2002). Constructing a rudimentary algorithm to assign codons based on a given frequency can also easily be accomplished with basic mathematical functions by one of ordinary skill in the art.

[0156] A number of options are available for synthesizing codon-optimized coding regions designed by any of the methods described above, using standard and routine molecular biological manipulations well known to those of ordinary skill in the art. In one approach, a series of complementary oligonucleotide pairs of 80-90 nucleotides each in length and spanning the length of the desired sequence are synthesized by standard methods. These oligonucleotide pairs are synthesized such that upon annealing, they form double stranded fragments of 80-90 base pairs, containing cohesive ends, *e.g.*, each oligonucleotide in the pair is synthesized to extend 3, 4, 5, 6, 7, 8, 9, 10, or more bases beyond the region that is complementary to the other oligonucleotide in the pair. The single-stranded ends of each pair of oligonucleotides is designed to anneal with the single-stranded end of another pair of oligonucleotides. The oligonucleotide pairs are allowed to anneal, and approximately five to six of these double-stranded fragments are then allowed to anneal together via the cohesive single stranded ends, and then they ligated together and cloned into a standard bacterial cloning vector, for example, a TOPO® vector available from Invitrogen Corporation, Carlsbad, CA. The construct is then sequenced by standard methods. Several of these constructs consisting of 5 to 6 fragments of 80 to 90 base pair fragments ligated together, *i.e.*, fragments of about 500 base pairs, are prepared, such that the entire desired sequence is represented in a series of plasmid constructs. The inserts of these plasmids are then cut with appropriate restriction enzymes and ligated together to form the final construct. The final construct is then cloned into a standard bacterial cloning vector, and sequenced. Additional methods would

be immediately apparent to the skilled artisan. In addition, gene synthesis is readily available commercially.

[0157] The codon-optimized coding regions can be versions encoding any gene products from any strain, derivative, or variant of IV, or fragments, variants, or derivatives of such gene products. For example, nucleic acid fragments of codon-optimized coding regions encoding the NP, M1 and M2 polypeptides, or fragments, variants or derivatives thereof. Codon-optimized coding regions encoding other IV polypeptides or fragments, variants, or derivatives thereof (*e.g.* HA, NA, PB1, PB2, PA, NS1 or NS2), are included within the present invention. Additional, non-codon-optimized polynucleotides encoding IV polypeptides or other polypeptides are included as well.

Consensus Sequences

[0158] The present invention is further directed to specific consensus sequences of influenza virus proteins, and fragments, derivatives and variants thereof. A "consensus sequence" is, *e.g.*, an idealized sequence that represents the amino acids most often present at each position of two or more sequences which have been compared to each other. A consensus sequence is a theoretical representative amino acid sequence in which each amino acid is the one which occurs most frequently at that site in the different sequences which occur in nature. The term also refers to an actual sequence which approximates the theoretical consensus. A consensus sequence can be derived from sequences which have, *e.g.*, shared functional or structural purposes. It can be defined by aligning as many known examples of a particular structural or functional domain as possible to maximize the homology. A sequence is generally accepted as a consensus when each particular amino acid is reasonably predominant at its position, and most of the sequences which form the basis of the comparison are related to the consensus by rather few substitutions, *e.g.*, from 0 to about 100 substitutions. In general, the wild-type comparison sequences are at least about 50%, 75%, 80%, 90%, 95%, 96%,

97%, 98% or 99% identical to the consensus sequence. Accordingly, polypeptides of the invention are about 50%, 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, 99% or 100% identical to the consensus sequence. Consensus amino acid sequences can be prepared for any of the influenza antigens. By analyzing amino acid sequences from influenza A strains sequenced since 1990, consensus amino acid sequences were derived for the influenza A NP (SEQ ID NO: 76), M1 (SEQ ID NO:77) and M2 (SEQ ID NO:78) proteins (Example 3).

[0159] A "consensus amino acid" is an amino acid chosen to occupy a given position in the consensus protein. A system which is organized to select consensus amino acids can be a computer program, or a combination of one or more computer programs with "by hand" analysis and calculation. When a consensus amino acid is obtained for each position of the aligned amino acid sequences, then these consensus amino acids are "lined up" to obtain the amino acid sequence of the consensus protein.

[0160] Another embodiment of this invention is directed to a process for the preparation of a consensus protein comprising a process to calculate an amino acid residue for nearly all positions of a so-called consensus protein and to synthesize a complete gene from this sequence that could be expressed in a prokaryotic or eukaryotic expression system.

[0161] Polynucleotides which encode the consensus influenza polypeptides, or fragments, variants or derivatives thereof, are also part of this invention. Such polynucleotides can be obtained by known methods, for example by backtranslation of the amino acid sequence and PCR synthesis of the corresponding polynucleotide.

Compositions and Methods

[0162] In certain embodiments, the present invention is directed to compositions and methods of enhancing the immune response of a vertebrate in need of protection against IV infection by administering *in vivo*, into a tissue of a vertebrate, one or more polynucleotides comprising at least one

codon-optimized coding region encoding an IV polypeptide, or a fragment, variant, or derivative thereof. In addition, the present invention is directed to compositions and methods of enhancing the immune response of a vertebrate in need of protection against IV infection by administering to the vertebrate a composition comprising one or more polynucleotides as described herein, and at least one isolated IV polypeptide, or a fragment, variant, or derivative thereof. The polynucleotide may be administered either prior to, at the same time (simultaneously), or subsequent to the administration of the isolated polypeptide.

[0163] The coding regions encoding IV polypeptides or fragments, variants, or derivatives thereof may be codon optimized for a particular vertebrate. Codon optimization is carried out by the methods described herein, for example, in certain embodiments codon-optimized coding regions encoding polypeptides of IV, or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof are optimized according to the codon usage of the particular vertebrate. The polynucleotides of the invention are incorporated into the cells of the vertebrate *in vivo*, and an immunologically effective amount of an IV polypeptide or a fragment, variant, or derivative thereof is produced *in vivo*. The coding regions encoding an IV polypeptide or a fragment, variant, or derivative thereof may be codon optimized for mammals, *e.g.*, humans, apes, monkeys (*e.g.*, owl, squirrel, cebus, rhesus, African green, patas, cynomolgus, and cercopithecus), orangutans, baboons, gibbons, and chimpanzees, dogs, wolves, cats, lions, and tigers, horses, donkeys, zebras, cows, pigs, sheep, deer, giraffes, bears, rabbits, mice, ferrets, seals, whales; birds, *e.g.*, ducks, geese, terns, shearwaters, gulls, turkeys, chickens, quail, pheasants, geese, starlings and budgerigars, or other vertebrates.

[0164] In one embodiment, the present invention relates to codon-optimized coding regions encoding polypeptides of IV, or nucleic acid fragments of such coding regions fragments, variants, or derivatives thereof which have been optimized according to human codon usage. For example, human codon-

optimized coding regions encoding polypeptides of IV, or fragments, variants, or derivatives thereof are prepared by substituting one or more codons preferred for use in human genes for the codons naturally used in the the DNA sequence encoding the IV polypeptide or a fragment, variant, or derivative thereof. Also provided are polynucleotides, vectors, and other expression constructs comprising codon-optimized coding regions encoding polypeptides of IV, or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof; pharmaceutical compositions comprising polynucleotides, vectors, and other expression constructs comprising codon-optimized coding regions encoding polypeptides of IV, or nucleic acid fragments of such coding regions encoding fragments, variants, or derivatives thereof; and various methods of using such polynucleotides, vectors and other expression constructs. Coding regions encoding IV polypeptides can be uniformly optimized, fully optimized, minimally optimized, codon-optimized by region and/or not codon-optimized, as described herein.

[0165] The present invention is further directed towards polynucleotides comprising codon-optimized coding regions encoding polypeptides of IV antigens, for example, HA, NA, NP, M1 and M2, optionally in conjunction with other antigens. The invention is also directed to polynucleotides comprising codon-optimized nucleic acid fragments encoding fragments, variants and derivatives of these polypeptides, *e.g.*, an eM2 or a fusion of NP and eM2.

[0166] In certain embodiments, the present invention provides an isolated polynucleotide comprising a nucleic acid fragment, where the nucleic acid fragment is a fragment of a codon-optimized coding region encoding a polypeptide at least 60%, 65%, 70%, 75%, 80%, 85%, 86%, 87%, 88%, 89%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical to an IV polypeptide, *e.g.*, HA, NA, NP, M1 or M2, and where the nucleic acid fragment is a variant of a codon-optimized coding region encoding an IV polypeptide, *e.g.*, HA, NA, NP, M1 or M2. The human codon-optimized

coding region can be optimized for any vertebrate species and by any of the methods described herein.

Isolated IV Polypeptides

[0167] The present invention is further drawn to compositions which include at least one polynucleotide comprising one or more nucleic acid fragments, where each nucleic acid fragment is optionally a fragment of a codon-optimized coding region operably encoding an IV polypeptide or fragment, variant, or derivative thereof; together with one or more isolated IV component or isolated polypeptide. The IV component may be inactivated virus, attenuated virus, a viral vector expressing an isolated influenza virus polypeptide, or an influenza virus protein, fragment, variant or derivative thereof.

[0168] The polypeptides or fragments, variants or derivatives thereof, in combination with the codon-optimized nucleic acid compositions may be referred to as "combinatorial polynucleotide vaccine compositions" or "single formulation heterologous prime-boost vaccine compositions."

[0169] The isolated IV polypeptides of the invention may be in any form, and are generated using techniques well known in the art. Examples include isolated IV proteins produced recombinantly, isolated IV proteins directly purified from their natural milieu, recombinant (non-IV) virus vectors expressing an isolated IV protein, or proteins delivered in the form of an inactivated IV vaccine, such as conventional vaccines

[0170] When utilized, an isolated IV polypeptide or fragment, variant or derivative thereof is administered in an immunologically effective amount. Conventional IV vaccines have been standardized to micrograms of viral antigens HA and NA. *See* Subbarao, K., *Advances in Viral Research 54*:349-373 (1999), incorporated herein by reference in its entirety. The recommended dose for these vaccines is 15 *u*g of each HA per 0.5 ml. *Id.* The effective amount of conventional IV vaccines is determinable by one of ordinary skill in the art based upon several factors, including the antigen being

expressed, the age and weight of the subject, and the precise condition requiring treatment and its severity, and route of administration.

[0171] In the instant invention, the combination of conventional antigen vaccine compositions with the codon-optimized nucleic acid compositions provides for therapeutically beneficial effects at dose sparing concentrations. For example, immunological responses sufficient for a therapeutically beneficial effect in patients predetermined for an approved commercial product, such as for the conventional product described above, can be attained by using less of the approved commercial product when supplemented or enhanced with the appropriate amount of codon-optimized nucleic acid. Thus, dose sparing is contemplated by administration of conventional IV vaccines administered in combination with the codon-optimized nucleic acids of the invention

[0172] In particular, the dose of conventional vaccine may be reduced by at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60% or at least 70% when administered in combination with the codon-optimized nucleic acid compositions of the invention.

[0173] Similarly, a desirable level of an immunological response afforded by a DNA based pharmaceutical alone may be attained with less DNA by including an aliquot of a conventional vaccine. Further, using a combination of conventional and DNA based pharmaceuticals may allow both materials to be used in lesser amounts while still affording the desired level of immune response arising from administration of either component alone in higher amounts (e.g. one may use less of either immunological product when they are used in combination). This may be manifest not only by using lower amounts of materials being delivered at any time, but also to reducing the number of administrations points in a vaccination regime (e.g. 2 versus 3 or 4 injections), and/or to reducing the kinetics of the immunological response (e.g. desired response levels are attained in 3 weeks in stead of 6 after immunization).

[0174] In particular, the dose of DNA based pharmaceuticals, may be reduced by at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least

50%, at least 60% or at least 70% when administered in combination with conventional IV vaccines.

[0175] Determining the precise amounts of DNA based pharmaceutical and conventional antigen is based on a number of factors as described above, and is readily determined by one of ordinary skill in the art.

[0176] In addition to dose sparing, the claimed combinatorial compositions provide for a broadening of the immune response and/or enhanced beneficial immune responses. Such broadened or enhanced immune responses are achieved by: adding DNA to enhance cellular responses to a conventional vaccine; adding a conventional vaccine to a DNA pharmaceutical to enhance humoral response; using a combination that induces additional epitopes (both humoral and/or cellular) to be recognized and/or more desirably responded to (epitope broadening); employing a DNA-conventional vaccine combination designed for a particular desired spectrum of immunological responses; obtaining a desirable spectrum by using higher amounts of either component. The broadened immune response is measurable by one of ordinary skill in the art by standard immunological assay specific for the desirable response spectrum.

[0177] Both broadening and dose sparing can be obtained simultaneously.

[0178] The isolated IV polypeptide or fragment, variant, or derivative thereof to be delivered (either a recombinant protein, a purified subunit, or viral vector expressing an isolated IV polypeptide, or in the form of an inactivated IV vaccine) can be any isolated IV polypeptide or fragment, variant, or derivative thereof, including but not limited to the HA, NA, NP, M1, or M2 proteins or fragments, variants or derivatives thereof. Fragments include, but are not limited to, the eM2 protein. In certain embodiments, a derivative protein can be a fusion protein, *e.g.*, NP-eM2. It should be noted that any isolated IV polypeptide or fragment, variant, or derivative thereof described herein can be combined in a composition with any polynucleotide comprising a nucleic acid fragment, where the nucleic acid fragment is optionally a fragment of a codon-optimized coding region operably encoding an IV polypeptide or fragment,

variant, or derivative thereof. The proteins can be different, the same, or can be combined in any combination of one or more isolated IV proteins and one or more polynucleotides.

[0179] In certain embodiments, the isolated IV polypeptides, or fragments, derivatives or variants thereof can be fused to or conjugated to a second isolated IV polypeptide, or fragment, derivative or variant thereof, or can be fused to other heterologous proteins, including for example, hepatitis B proteins including, but not limited to the hepatitis B core antigen (HBcAg), or those derived from diphtheria or tetanus. The second isolated IV polypeptide or other heterologous protein can act as a "carrier" that potentiates the immunogenicity of the IV polypeptide or a fragment, variant, or derivative thereof to which it is attached. Hepatitis B virus proteins and fragments and variants thereof useful as carriers within the scope of the invention are disclosed in U.S. Patent Nos. 6,231,864 and 5,143,726, which are incorporated by reference in their entireties. Polynucleotides comprising coding regions encoding said fused or conjugated proteins are also within the scope of the invention.

[0180] The use of recombinant particles comprising hepatitis B core antigen ("HBcAg") and heterologous protein sequences as potent immunogenic moieties is well documented. For example, addition of heterologous sequences to the amino terminus of a recombinant HBcAg results in the spontaneous assembly of particulate structures which express the heterologous epitope on their surface, and which are highly immunogenic when inoculated into experimental animals. *See* Clarke *et al.*, *Nature 330*:381-384 (1987). Heterologous epitopes can also be inserted into HBcAg particles by replacing approximately 40 amino acids of the carboxy terminus of the protein with the heterologous sequences. These recombinant HBcAg proteins also spontaneously form immunogenic particles. *See* Stahl and Murray, *Proc. Natl. Acad. Sci. USA*, *86*:6283-6287 (1989). Additionally, chimeric HBcAg particles may be constructed where the heterologous epitope is inserted in or replaces all or part of the sequence of amino acid residues in a more central

region of the HBcAg protein, in an immunodominant loop, thereby allowing the heterologous epitope to be displayed on the surface of the resulting particles. *See* EP Patent No. 0421635 B1. Shown below are the DNA and amino acid sequences of the human hepatitis B core protein (HBc), subtype ayw (SEQ ID NOs 39 and 40), as described in Galibert, F., *et al.*, *Nature 281:*646-650 (1979); *see also* U.S. Patent Nos. 4,818,527, 4,882,145 and 5,143,726. All of the above references are incorporated herein by reference in their entireties. The nucleotide and amino acid sequences are presented herein as SEQ ID NO 39:

ATGGACATCGACCCTTATAAAGAATTTGGAGCTACTGTGGAGTTACTCTC
GTTTTTGCCTTCTGACTTCTTTCCTTCAGTACGAGATCTTCTAGATACCGC
CTCAGCTCTGTATCGGGAAGCCTTAGAGTCTCCTGAGCATTGTTCACCTCA
CCATACTGCACTCAGGCAAGCAATTCTTTGCTGGGGGGGAACTAATGACTC
TAGCTACCTGGGTGGGTGTTAATTTGGAAGATCCAGCGTCTAGAGACCTA
GTAGTCAGTTATGTCAACACTAATATGGGCCTAAAGTTCAGGCAACTCTT
GTGGTTTCACATTTCTTGTCTCACTTTTGGAAGAGAAACAGTTATAGAGTA
TTTGGTGTCTTTCGGAGTGTGGATTCGCACTCCTCCAGCTTATAGACCACC
AAATGCCCCTATCCTATCAACACTTCCGGAGACTACTGTTGTTAGACGAC
GAGGCAGGTCCCCTAGAAGAAGAACTCCCTCGCCTCGCAGACGAAGGTC
TCAATCGCCGCGTCGCAGAAGATCTCAATCTCGGGAATCTCAATGTTAG

and SEQ ID NO:40:

MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHT
ALRQAILCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWF
HISCLTFGRETVIEYLVSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPRR
RTPSPRRRRSQSPRRRRSQSRESQC

[0181] A completely synthetic HBcAg has been synthesized as well. *See* Nassal, M. Gene 66:279-294 (1988). The nucleotide and amino acid sequences are presented herein as SEQ ID NO 41:

ATGGATATCGATCCTTATAAAGAATTCGGAGCTACTGGGAGTTACTCTCG
TTTCTCCCGAGTGACTTCTTTCCTTCAGTACGAGATCTTCTGGATACCGCC
AGCGCGCTGTATCGGGAAGCCTTGGAGTCTCCTGAGCACTGCAGCCCTCA
CCATACTGCCCTCAGGCAAGCAATTCTTTGCTGGGGGGAGCTCATGACTC
TGGCCACGTGGGTGGGTGTTAACTTGGAAGATCCAGCTAGCAGGGACCTG
GTAGTCAGTTATGTCAACACTAATATGGGTTTAAAGTTCAGGCAACTCTT
GTGGTTTCACATTAGCTGCCTCACTTTCGGCCGAGAAACAGTTCTAGAAT
ATTTGGTGTCTTTCGGAGTGTGGATCCGCACTCCTCCAGCTTATAGGCCTC
CGAATGCCCCTATCCTGTCGACACTCCCGGAGACTACTGTTGTTAGACGT
CGAGGCAGGTCACCTAGAAGAAGAACTCCTTCGCCTCGCAGGCGAAGGT

CTCAATCGCCGCGGCGCCGAAGATCTCAATCTCGGGAATCTCAATGTTAG
TGA

and SEQ ID NO:42:

MDIDPYKEFGATVELLSFLPSDFFPSVRDLLDTASALYREALESPEHCSPHHT
ALRQAILCWGELMTLATWVGVNLEDPASRDLVVSYVNTNMGLKFRQLLWF
HISCLTFGRETVLEYLVSFGVWIRTPPAYRPPNAPILSTLPETTVVRRRGRSPR
RRTPSPRRRRSQSPRRRRSQSRESQC

[0182] Chimaeric HBcAg particles comprising isolated IV proteins or variants, fragments or derivatives thereof are prepared by recombinant techniques well known to those of ordinary skill in the art. A polynucleotide, *e.g.*, a plasmid, which carries the coding region for the HBcAg operably associated with a promoter is constructed. Convenient restrictions sites are engineered into the coding region encoding the N-terminal, central, and/or C-terminal portions of the HBcAg, such that heterologous sequences may be inserted. A construct which expresses a HBcAg/IV fusion protein is prepared by inserting a DNA sequence encoding an IV protein or variant, fragment or derivative thereof, in frame, into a desired restriction site in the coding region of the HBcAg. The resulting construct is then inserted into a suitable host cell, *e.g.*, *E. coli*, under conditions where the chimeric HBcAg will be expressed. The chimaeric HBcAg self-assembles into particles when expressed, and can then be isolated, *e.g.*, by ultracentrifugation. The particles formed resemble the natural 27 nm HBcAg particles isolated from a hepatitis B virus, except that an isolated IV protein or fragment, variant, or derivative thereof is contained in the particle, preferably exposed on the outer particle surface.

[0183] The IV protein or fragment, variant, or derivative thereof expressed in a chimaeric HBcAg particle may be of any size which allows suitable particles of the chimeric HBcAg to self-assemble. As discussed above, even small antigenic epitopes may be immunogenic when expressed in the context of an immunogenic carrier, *e.g.*, a HBcAg. Thus, HBcAg particles of the invention may comprise at least 4, at least 5, at least 6, at least 7, at least 8, at least 9, at least 10, at least 15, at least 20, at least 25, or between about 15 to about 30

amino acids of an IV protein fragment of interest inserted therein. HBcAg particles of the invention may further comprise immunogenic or antigenic epitopes of at least 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, or 100 amino acid residues of an IV protein fragment of interest inserted therein.

[0184] The immunodominant loop region of HBcAg was mapped to about amino acid residues 75 to 83, to about amino acids 75 to 85 or to about amino acids 130 to140. *See* Colucci *et al.*, *J. Immunol. 141*:4376-4380 (1988), and Salfeld *et al. J. Virol. 63*:798 (1989), which are incorporated by reference. A chimeric HBcAg is still often able to form core particles when foreign epitopes are cloned into the immunodominant loop. Thus, for example, amino acids of the IV protein fragment may be inserted into the sequence of HBcAg amino acids at various positions, for example, at the N-terminus, from about amino acid 75 to about amino acid 85, from about amino acid 75 to about amino acid 83, from about amino acid 130 to about amino acid 140, or at the C-terminus. Where amino acids of the IV protein fragment replace all or part of the native core protein sequence, the inserted IV sequence is generally not shorter, but may be longer, than the HBcAg sequence it replaces.

[0185] Alternatively, if particle formation is not desired, full-length IV coding sequences can be fused to the coding region for the HBcAg. The HBcAg sequences can be fused either at the N- or C-terminus of any of the Influenza antigens described herein, including the eM2-NP constructs. Fusions could include flexible protein linkers as described for NP-eM2 fusions above. Examples of IV coding sequences fused to the HBcAg coding sequence of SEQ ID NO:41 include an IAV NP-HBcAg fusion (SEQ ID NO:43),

ATGGCGTCTCAAGGCACCAAACGATCTTACGAACAGATGGAGACTGATG
GAGAACGCCAGAATGCCACTGAAATCAGAGCATCCGTCGGAAAAATGAT
TGGTGGAATTGGACGATTCTACATCCAAATGTGCACCGAACTCAAACTCA
GTGATTATGAGGGACGGTTGATCCAAAACAGCTTAACAATAGAGAGAAT
GGTGCTCTCTGCTTTTGACGAAAGGAGAAATAAATACCTTGAAGAACATC
CCAGTGCGGGGAAAGATCCTAAGAAAACTGGAGGACCTATATACAGGAG
AGTAAACGGAAAGTGGATGAGAGAACTCATCCTTTATGACAAAGAAGAA
ATAAGGCGAATCTGGCGCCAAGCTAATAATGGTGACGATGCAACGGCTG
GTCTGACTCACATGATGATCTGGCATTCCAATTTGAATGATGCAACTTATC
AGAGGACAAGAGCTCTTGTTCGCACCGGAATGGATCCCAGGATGTGCTCT

CTGATGCAAGGTTCAACTCTCCCTAGGAGGTCTGGAGCCGCAGGTGCTGC
AGTCAAAGGAGTTGGAACAATGGTGATGGAATTGGTCAGAATGATCAAA
CGTGGGATCAATGATCGGAACTTCTGGAGGGGTGAGAATGGACGAAAAA
CAAGAATTGCTTATGAAAGAATGTGCAACATTCTCAAAGGGAAATTTCAA
ACTGCTGCACAAAAAGCAATGATGGATCAAGTGAGAGAGAGCCGGAACC
CAGGGAATGCTGAGTTCGAAGATCTCACTTTTCTAGCACGGTCTGCACTC
ATATTGAGAGGGTCGGTTGCTCACAAGTCCTGCCTGCCTGCCTGTGTGTA
TGGACCTGCCGTAGCCAGTGGGTACGACTTTGAAAGGGAGGGATACTCTC
TAGTCGGAATAGACCCTTTCAGACTGCTTCAAAACAGCCAAGTGTACAGC
CTAATCAGACCAAATGAGAATCCAGCACACAAGAGTCAACTGGTGTGGA
TGGCATGCCATTCTGCCGCATTTGAAGATCTAAGAGTATTAAGCTTCATC
AAAGGGACGAAGGTGCTCCCAAGAGGGAAGCTTTCCACTAGAGGAGTTC
AAATTGCTTCCAATGAAAATATGGAGACTATGGAATCAAGTACACTTGAA
CTGAGAAGCAGGTACTGGGCCATAAGGACCAGAAGTGGAGGAAACACCA
ATCAACAGAGGGCATCTGCGGGCCAAATCAGCATACAACCTACGTTCTCA
GTACAGAGAAATCTCCCTTTTGACAGAACAACCGTTATGGCAGCATTCAG
TGGGAATACAGAGGGGAGATGGCGTCTCAAGGCACCAAACGATCTTACG
AACAGATGGAGACTGATGGAGAACGCCAGAATGCCACTGAAATCAGAGC
ATCCGTCGGAAAAATGATTGGTGGAATTGGACGATTCTACATCCAAATGT
GCACCGAACTCAAACTCAGTGATTATGAGGGACGGTTGATCCAAAACAG
CTTAACAATAGAGAGAATGGTGCTCTCTGCTTTTGACGAAAGGAGAAATA
AATACCTTGAAGAACATCCCAGTGCGGGGAAAGATCCTAAGAAAACTGG
AGGACCTATATACAGGAGAGTAAACGGAAAGTGGATGAGAGAACTCATC
CTTTATGACAAAGAAGAAATAAGGCGAATCTGGCGCCAAGCTAATAATG
GTGACGATGCAACGGCTGGTCTGACTCACATGATGATCTGGCATTCCAAT
TTGAATGATGCAACTTATCAGAGGACAAGAGCTCTTGTTCGCACCGGAAT
GGATCCCAGGATGTGCTCTCTGATGCAAGGTTCAACTCTCCCTAGGAGGT
CTGGAGCCGCAGGTGCTGCAGTCAAAGGAGTTGGAACAATGGTGATGGA
ATTGGTCAGAATGATCAAACGTGGGATCAATGATCGGAACTTCTGGAGG
GGTGAGAATGGACGAAAAACAAGAATTGCTTATGAAAGAATGTGCAACA
TTCTCAAAGGGAAATTTCAAACTGCTGCACAAAAAGCAATGATGGATCA
AGTGAGAGAGAGCCGGAACCCAGGGAATGCTGAGTTCGAAGATCTCACT
TTTCTAGCACGGTCTGCACTCATATTGAGAGGGTCGGTTGCTCACAAGTC
CTGCCTGCCTGCCTGTGTGTATGGACCTGCCGTAGCCAGTGGGTACGACT
TTGAAAGGGAGGGATACTCTCTAGTCGGAATAGACCCTTTCAGACTGCTT
CAAAACAGCCAAGTGTACAGCCTAATCAGACCAAATGAGAATCCAGCAC
ACAAGAGTCAACTGGTGTGGATGGCATGCCATTCTGCCGCATTTGAAGAT
CTAAGAGTATTAAGCTTCATCAAAGGGACGAAGGTGCTCCCAAGAGGGA
AGCTTTCCACTAGAGGAGTTCAAATTGCTTCCAATGAAAATATGGAGACT
ATGGAATCAAGTACACTTGAACTGAGAAGCAGGTACTGGGCCATAAGGA
CCAGAAGTGGAGGAAACACCAATCAACAGAGGGCATCTGCGGGCCAAAT
CAGCATACAACCTACGTTCTCAGTACAGAGAAATCTCCCTTTTGACAGAA
CAACCGTTATGGCAGCATTCAGTGGGAATACAGAGGGGAGAACATCTGA
CATGAGGACCGAAATCATAAGGATGATGGAAAGTGCAAGACCAGAAGAT
GTGTCTTTCCAGGGGCGGGGAGTCTTCGAGCTCTCGGACGAAAAGGCAGC
GAGCCCGATCGTGCCTTCCTTTGACATGAGTAATGAAGGATCTTATTTCTT
CGGAGACAATGCAGAGGAATACGATAATATGGATATCGATCCTTATAAA
GAATTCGGAGCTACTGTGGAGTTACTCTCGTTTCTCCCGAGTGACTTCTTT
CCTTCAGTACGAGATCTTCTGGATACCGCCAGCGCGCTGTATCGGGAAGC
CTTGGAGTCTCCTGAGCACTGCAGCCCTCACCATACTGCCCTCAGGCAAG
CAATTCTTTGCTGGGGGGAGCTCATGACTCTGGCCACGTGGGTGGGTGTT
AACTTGGAAGATCCAGCTAGCAGGGACCTGGTAGTCAGTTATGTCAACAC
TAATATGGGTTTAAAGTTCAGGCAACTCTTGTGGTTTCACATTAGCTGCCT
CACTTTCGGCCGAGAAACAGTTCTAGAATATTTGGTGTCTTTCGGAGTGT
GGATCCGCACTCCTCCAGCTTATAGGCCTCCGAATGCCCCTATCCTGTCG
ACACTCCCGGAGACTACTGTTGTTAGACGTCGAGGCAGGTCACCTAGAAG

AAGAACTCCTTCGCCTCGCAGGCGAAGGTCTCAATCGCCGCGGCGCCGAA
GATCTCAATCTCGGGAATCTCAATGT

an IBV NP-HBcAg fusion (SEQ ID NO:44),

ATGTCCAACATGGATATTGACAGTATAAATACCGGAACAATCGATAAAA
CACCAGAAGAACTGACTCCCGGAACCAGTGGGGCAACCAGACCAATCAT
CAAGCCAGCAACCCTTGCTCCGCCAAGCAACAAACGAACCCGAAATCCA
TCTCCAGAAAGGACAACCACAAGCAGTGAAACCGATATCGGAAGGAAAA
TCCAAAAGAAACAAACCCCAACAGAGATAAAGAAGAGCGTCTACAAAAT
GGTGGTAAAACTGGGTGAATTCTACAACCAGATGATGGTCAAAGCTGGA
CTTAATGATGACATGGAAAGGAATCTAATTCAAAATGCACAAGCTGTGG
AGAGAATCCTATTGGCTGCAACTGATGACAAGAAAACTGAATACCAAAA
GAAAAGGAATGCCAGAGATGTCAAAGAAGGGAAGGAAGAAATAGACCA
CAACAAGACAGGAGGCACCTTTTATAAGATGGTAAGAGATGATAAAACC
ATCTACTTCAGCCCTATAAAAATTACCTTTTTAAAAGAAGAGGTGAAAAC
AATGTACAAGACCACCATGGGGAGTGATGGTTTCAGTGGACTAAATCAC
ATTATGATTGGACATTCACAGATGAACGATGTCTGTTTCCAAAGATCAAA
GGGACTGAAAAGGGTTGGACTTGACCCTTCATTAATCAGTACTTTTGCCG
GAAGCACACTACCCAGAAGATCAGGTACAACTGGTGTTGCAATCAAAGG
AGGTGGAACTTTAGTGGATGAAGCCATCCGATTTATAGGAAGAGCAATG
GCAGACAGAGGGCTACTGAGAGACATCAAGGCCAAGACGGCCTATGAAA
AGATTCTTCTGAATCTGAAAAACAAGTGCTCTGCGCCGCAACAAAAGGCT
CTAGTTGATCAAGTGATCGGAAGTAGGAACCCAGGGATTGCAGACATAG
AAGACCTAACTCTGCTTGCCAGAAGCATGGTAGTTGTCAGACCCTCTGTA
GCGAGCAAAGTGGTGCTTCCCATAAGCATTTATGCTAAAATACCTCAACT
AGGATTCAATACCGAAGAATACTCTATGGTTGGGTATGAAGCCATGGCTC
TTTATAATATGGCAACACCTGTTTCCATATTAAGAATGGGAGATGACGCA
AAAGATAAATCTCAACTATTCTTCATGTCGTGCTTCGGAGCTGCCTATGA
AGATCTAAGAGTGTTATCTGCACTAACGGGCACCGAATTTAAGCCTAGAT
CAGCACTAAAATGCAAGGGTTTCCATGTCCCGGCTAAGGAGCAAGTAGA
AGGAATGGGGGCAGCTCTGATGTCCATCAAGCTTCAGTTCTGGGCCCCAA
TGACCAGATCTGGAGGGAATGAAGTAAGTGGAGAAGGAGGGTCTGGTCA
AATAAGTTGCAGCCCTGTGTTTGCAGTAGAAAGACCTATTGCTCTAAGCA
AGCAAGCTGTAAGAAGAATGCTGTCAATGAACGTTGAAGGACGTGATGC
AGATGTCAAAGGAAATCTACTCAAAATGATGAATGATTCAATGGCAAAG
AAAACCAGTGGAAATGCTTTCATTGGGAAGAAAATGTTTCAAATATCAGA
CAAAAACAAAGTCAATCCCATTGAGATTCCAATTAAGCAGACCATCCCCA
ATTTCTTCTTTGGGAGGGACACAGCAGAGGATTATGATGACCTCGATTAT
ATGGATATCGATCCTTATAAAGAATTCGGAGCTACTGTGGAGTTACTCTC
GTTTCTCCCGAGTGACTTCTTTCCTTCAGTACGAGATCTTCTGGATACCGC
CAGCGCGCTGTATCGGGAAGCCTTGGAGTCTCCTGAGCACTGCAGCCCTC
ACCATACTGCCCTCAGGCAAGCAATTCTTTGCTGGGGGGAGCTCATGACT
CTGGCCACGTGGGTGGGTGTTAACTTGGAAGATCCAGCTAGCAGGGACCT
GGTAGTCAGTTATGTCAACACTAATATGGGTTTAAAGTTCAGGCAACTCT
TGTGGTTTCACATTAGCTGCCTCACTTTCGGCCGAGAAACAGTTCTAGAA
TATTTGGTGTCTTTCGGAGTGTGGATCCGCACTCCTCCAGCTTATAGGCCT
CCGAATGCCCCTATCCTGTCGACACTCCCGGAGACTACTGTTGTTAGACG
TCGAGGCAGGTCACCTAGAAGAAGAACTCCTTCGCCTCGCAGGCGAAGG
TCTCAATCGCCGCGGCGCCGAAGATCTCAATCTCGGGAATCTCAATGTT

or an IAV M1-HBcAg fusion (SEQ ID NO:45),

ATGAGTCTTCTAACCGAGGTCGAAACGTACGTACTCTCTATCATCCCGTC
AGGCCCCCTCAAAGCCGAGATCGCACAGAGACTTGAAGATGTCTTTGCAG
GGAAGAACACTGATCTTGAGGTTCTCATGGAATGGCTAAAGACAAGACC
AATCCTGTCACCTCTGACTAAGGGGATTTTAGGATTTGTGTTCACGCTCAC

CGTGCCCAGTGAGCGAGGACTGCAGCGTAGACGCTTTGTCCAAAATGCCC
TTAATGGGAACGGGGATCCAAATAACATGGACAAAGCAGTTAAACTGTA
TAGGAAGCTCAAGAGGGAGATAACATTCCATGGGGCCAAAGAAATCTCA
CTCAGTTATTCTGCTGGTGCACTTGCCAGTTGTATGGGCCTCATATACAAC
AGGATGGGGGCTGTGACCACTGAAGTGGCATTTGGCCTGGTATGTGCAAC
CTGTGAACAGATTGCTGACTCCCAGCATCGGTCTCATAGGCAAATGGTGA
CAACAACCAATCCACTAATCAGACATGAGAACAGAATGGTTTTAGCCAG
CACTACAGCTAAGGCTATGGAGCAAATGGCTGGATCGAGTGAGCAAGCA
GCAGAGGCCATGGAGGTTGCTAGTCAGGCTAGACAAATGGTGCAAGCGA
TGAGAACCATTGGGACTCATCCTAGCTCCAGTGCTGGTCTGAAAAATGAT
CTTCTTGAAAATTTGCAGGCCTATCAGAAACGAATGGGGGTGCAGATGCA
ACGGTTCAAGATGGATATCGATCCTTATAAAGAATTCGGAGCTACTGTGG
AGTTACTCTCGTTTCTCCCGAGTGACTTCTTTCCTTCAGTACGAGATCTTC
TGGATACCGCCAGCGCGCTGTATCGGGAAGCCTTGGAGTCTCCTGAGCAC
TGCAGCCCTCACCATACTGCCCTCAGGCAAGCAATTCTTTGCTGGGGGGA
GCTCATGACTCTGGCCACGTGGGTGGGTGTTAACTTGGAAGATCCAGCTA
GCAGGGACCTGGTAGTCAGTTATGTCAACACTAATATGGGTTTAAAGTTC
AGGCAACTCTTGTGGTTTCACATTAGCTGCCTCACTTTCGGCCGAGAAAC
AGTTCTAGAATATTTGGTGTCTTTCGGAGTGTGGATCCGCACTCCTCCAGC
TTATAGGCCTCCGAATGCCCCTATCCTGTCGACACTCCCGGAGACTACTG
TTGTTAGACGTCGAGGCAGGTCACCTAGAAGAAGAACTCCTTCGCCTCGC
AGGCGAAGGTCTCAATCGCCGCGGCGCCGAAGATCTCAATCTCGGGAAT
CTCAATGT

[0186] These fusion constructs could be codon optimized by any of the methods described.

[0187] The chimeric HBcAg can be used in the present invention in conjunction with a polynucleotide comprising a nucleic acid fragment, where each nucleic acid fragment is optionally a fragment of a codon-optimized coding region operably encoding an IV polypeptide, or a fragment, variant, or derivative thereof, as an influenza vaccine for a vertebrate.

Methods and Administration

[0188] The present invention also provides methods for delivering an IV polypeptide or a fragment, variant, or derivative thereof to a human, which comprise administering to a human one or more of the compositions described herein; such that upon administration of compositions such as those described herein, an IV polypeptide or a fragment, variant, or derivative thereof is expressed in human cells, in an amount sufficient to generate an immune response to the IV or administering the IV polypeptide or a fragment, variant, or derivative thereof itself to the human in an amount sufficient to generate an immune response.

[0189] The present invention further provides methods for delivering an IV polypeptide or a fragment, variant, or derivative thereof to a human, which comprise administering to a vertebrate one or more of the compositions described herein; such that upon administration of compositions such as those described herein, an immune response is generated in the vertebrate.

[0190] The term "vertebrate" is intended to encompass a singular "vertebrate" as well as plural "vertebrates" and comprises mammals and birds, as well as fish, reptiles, and amphibians.

[0191] The term "mammal" is intended to encompass a singular "mammal" and plural "mammals," and includes, but is not limited to humans; primates such as apes, monkeys (*e.g.*, owl, squirrel, cebus, rhesus, African green, patas, cynomolgus, and cercopithecus), orangutans, baboons, gibbons, and chimpanzees; canids such as dogs and wolves; felids such as cats, lions, and tigers; equines such as horses, donkeys, and zebras, food animals such as cows, pigs, and sheep; ungulates such as deer and giraffes; ursids such as bears; and others such as rabbits, mice, ferrets, seals, whales. In particular, the mammal can be a human subject, a food animal or a companion animal.

[0192] The term "bird" is intended to encompass a singular "bird" and plural "birds," and includes, but is not limited to feral water birds such as ducks, geese, terns, shearwaters, and gulls; as well as domestic avian species such as turkeys, chickens, quail, pheasants, geese, and ducks. The term "bird" also encompasses passerine birds such as starlings and budgerigars.

[0193] The present invention further provides a method for generating, enhancing or modulating an immune response to an IV comprising administering to a vertebrate one or more of the compositions described herein. In this method, the compositions may include one or more isolated polynucleotides comprising at least one nucleic acid fragment where the nucleic acid fragment is optionally a fragment of a codon-optimized coding region encoding an IV polypeptide, or a fragment, variant, or derivative thereof. In another embodiment, the compositions may include both a polynucleotide as described above, and also an isolated IV polypeptide, or a

fragment, variant, or derivative thereof, wherein the protein is provided as a recombinant protein, in particular, a fusion protein, a purified subunit, viral vector expressing the protein, or in the form of an inactivated IV vaccine. Thus, the latter compositions include both a polynucleotide encoding an IV polypeptide or a fragment, variant, or derivative thereof and an isolated IV polypeptide or a fragment, variant, or derivative thereof. The IV polypeptide or a fragment, variant, or derivative thereof encoded by the polynucleotide of the compositions need not be the same as the isolated IV polypeptide or a fragment, variant, or derivative thereof of the compositions. Compositions to be used according to this method may be univalent, bivalent, trivalent or multivalent.

[0194] The polynucleotides of the compositions may comprise a fragment of a human (or other vertebrate) codon-optimized coding region encoding a protein of the IV, or a fragment, variant, or derivative thereof. The polynucleotides are incorporated into the cells of the vertebrate *in vivo*, and an antigenic amount of the IV polypeptide, or fragment, variant, or derivative thereof, is produced *in vivo*. Upon administration of the composition according to this method, the IV polypeptide or a fragment, variant, or derivative thereof is expressed in the vertebrate in an amount sufficient to elicit an immune response. Such an immune response might be used, for example, to generate antibodies to the IV for use in diagnostic assays or as laboratory reagents, or as therapeutic or preventative vaccines as described herein.

[0195] The present invention further provides a method for generating, enhancing, or modulating a protective and/or therapeutic immune response to IV in a vertebrate, comprising administering to a vertebrate in need of therapeutic and/or preventative immunity one or more of the compositions described herein. In this method, the compositions include one or more polynucleotides comprising at least one nucleic acid fragment, where the nucleic acid fragment is optionally a fragment of a codon-optimized coding region encoding an IV polypeptide, or a fragment, variant, or derivative thereof. In a further embodiment, the composition used in this method

includes both an isolated polynucleotide comprising at least one nucleic acid fragment, where the nucleic acid fragment is optionally a fragment of a codon-optimized coding region encoding an IV polypeptide, or a fragment, variant, or derivative thereof; and at least one isolated IV polypeptide, or a fragment, variant, or derivative thereof. Thus, the latter composition includes both an isolated polynucleotide encoding an IV polypeptide or a fragment, variant, or derivative thereof and an isolated IV polypeptide or a fragment, variant, or derivative thereof, for example, a recombinant protein, a purified subunit, viral vector expressing the protein, or an inactivated virus vaccine. Upon administration of the composition according to this method, the IV polypeptide or a fragment, variant, or derivative thereof is expressed in the human in a therapeutically or prophylactically effective amount.

[0196] As used herein, an "immune response" refers to the ability of a vertebrate to elicit an immune reaction to a composition delivered to that vertebrate. Examples of immune responses include an antibody response or a cellular, *e.g.*, cytotoxic T-cell, response. One or more compositions of the present invention may be used to prevent influenza infection in vertebrates, *e.g.*, as a prophylactic vaccine, to establish or enhance immunity to IV in a healthy individual prior to exposure to influenza or contraction of influenza disease, thus preventing the disease or reducing the severity of disease symptoms.

[0197] As mentioned above, compositions of the present invention can be used both to prevent IV infection, and also to therapeutically treat IV infection. In individuals already exposed to influenza, or already suffering from influenza disease, the present invention is used to further stimulate the immune system of the vertebrate, thus reducing or eliminating the symptoms associated with that disease or disorder. As defined herein, "treatment " refers to the use of one or more compositions of the present invention to prevent, cure, retard, or reduce the severity of influenza disease symptoms in a vertebrate, and/or result in no worsening of influenza disease over a specified period of time in a vertebrate which has already been exposed to IV and is

thus in need of therapy. The term "prevention" refers to the use of one or more compositions of the present invention to generate immunity in a vertebrate which has not yet been exposed to a particular strain of IV, thereby preventing or reducing disease symptoms if the vertebrate is later exposed to the particular strain of IV. The methods of the present invention therefore may be referred to as therapeutic vaccination or preventative or prophylactic vaccination. It is not required that any composition of the present invention provide total immunity to influenza or totally cure or eliminate all influenza disease symptoms. As used herein, a "vertebrate in need of therapeutic and/or preventative immunity" refers to an individual for whom it is desirable to treat, *i.e.*, to prevent, cure, retard, or reduce the severity of influenza disease symptoms, and/or result in no worsening of influenza disease over a specified period of time. Vertebrates to treat and/or vaccinate include humans, apes, monkeys (*e.g.*, owl, squirrel, cebus, rhesus, African green, patas, cynomolgus, and cercopithecus), orangutans, baboons, gibbons, and chimpanzees, dogs, wolves, cats, lions, and tigers, horses, donkeys, zebras, cows, pigs, sheep, deer, giraffes, bears, rabbits, mice, ferrets, seals, whales, ducks, geese, terns, shearwaters, gulls, turkeys, chickens, quail, pheasants, geese, starlings and budgerigars.

[0198] One or more compositions of the present invention are utilized in a "prime boost" regimen. An example of a "prime boost" regimen may be found in Yang, Z. *et al. J. Virol. 77*:799-803 (2002), which is incorporated herein by reference in its entirety. In these embodiments, one or more polynucleotide vaccine compositions of the present invention are delivered to a vertebrate, thereby priming the immune response of the vertebrate to an IV, and then a second immunogenic composition is utilized as a boost vaccination. One or more compositions of the present invention are used to prime immunity, and then a second immunogenic composition, *e.g.*, a recombinant viral vaccine or vaccines, a different polynucleotide vaccine, or one or more purified subunit isolated IV polypeptides or fragments, variants or derivatives thereof is used to boost the anti-IV immune response.

[0199] In one embodiment, a priming composition and a boosting composition are combined in a single composition or single formulation. For example, a single composition may comprise an isolated IV polypeptide or a fragment, variant, or derivative thereof as the priming component and a polynucleotide encoding an influenza protein as the boosting component. In this embodiment, the compositions may be contained in a single vial where the priming component and boosting component are mixed together. In general, because the peak levels of expression of protein from the polynucleotide does not occur until later (*e.g.*, 7-10 days) after administration, the polynucleotide component may provide a boost to the isolated protein component. Compositions comprising both a priming component and a boosting component are referred to herein as "combinatorial vaccine compositions" or "single formulation heterologous prime-boost vaccine compositions." In addition, the priming composition may be administered before the boosting composition, or even after the boosting composition, if the boosting composition is expected to take longer to act.

[0200] In another embodiment, the priming composition may be administered simultaneously with the boosting composition, but in separate formulations where the priming component and the boosting component are separated.

[0201] The terms "priming" or "primary" and "boost" or "boosting" as used herein may refer to the initial and subsequent immunizations, respectively, *i.e.*, in accordance with the definitions these terms normally have in immunology. However, in certain embodiments, *e.g.*, where the priming component and boosting component are in a single formulation, initial and subsequent immunizations may not be necessary as both the "prime" and the "boost" compositions are administered simultaneously.

[0202] In certain embodiments, one or more compositions of the present invention are delivered to a vertebrate by methods described herein, thereby achieving an effective therapeutic and/or an effective preventative immune response. More specifically, the compositions of the present invention may be administered to any tissue of a vertebrate, including, but not limited to,

muscle, skin, brain tissue, lung tissue, liver tissue, spleen tissue, bone marrow tissue, thymus tissue, heart tissue, *e.g.*, myocardium, endocardium, and pericardium, lymph tissue, blood tissue, bone tissue, pancreas tissue, kidney tissue, gall bladder tissue, stomach tissue, intestinal tissue, testicular tissue, ovarian tissue, uterine tissue, vaginal tissue, rectal tissue, nervous system tissue, eye tissue, glandular tissue, tongue tissue, and connective tissue, *e.g.*, cartilage.

[0203] Furthermore, the compositions of the present invention may be administered to any internal cavity of a vertebrate, including, but not limited to, the lungs, the mouth, the nasal cavity, the stomach, the peritoneal cavity, the intestine, any heart chamber, veins, arteries, capillaries, lymphatic cavities, the uterine cavity, the vaginal cavity, the rectal cavity, joint cavities, ventricles in brain, spinal canal in spinal cord, the ocular cavities, the lumen of a duct of a salivary gland or a liver. When the compositions of the present invention is administered to the lumen of a duct of a salivary gland or liver, the desired polypeptide is expressed in the salivary gland and the liver such that the polypeptide is delivered into the blood stream of the vertebrate from each of the salivary gland or the liver. Certain modes for administration to secretory organs of a gastrointestinal system using the salivary gland, liver and pancreas to release a desired polypeptide into the bloodstream is disclosed in U.S. Patent Nos. 5,837,693 and 6,004,944, both of which are incorporated herein by reference in their entireties.

[0204] In certain embodiments, the compositions are administered into embryonated chicken eggs or by intra-muscular injection into the defeathered breast area of chicks as described in Kodihalli S. *et al.*, *Vaccine 18*:2592-9 (2000), which is incorporated herein by reference in its entirety.

[0205] In certain embodiments, the compositions are administered to muscle, either skeletal muscle or cardiac muscle, or to lung tissue. Specific, but non-limiting modes for administration to lung tissue are disclosed in Wheeler, C.J., *et al.*, *Proc. Natl. Acad. Sci. USA 93*:11454-11459 (1996), which is incorporated herein by reference in its entirety.

[0206] According to the disclosed methods, compositions of the present invention can be administered by intramuscular (i.m.), subcutaneous (s.c.), or intrapulmonary routes. Other suitable routes of administration include, but are not limited to intratracheal, transdermal, intraocular, intranasal, inhalation, intracavity, intravenous (i.v.), intraductal (*e.g.*, into the pancreas) and intraparenchymal (*i.e.*, into any tissue) administration. Transdermal delivery includes, but not limited to intradermal (*e.g.*, into the dermis or epidermis), transdermal (*e.g.*, percutaneous) and transmucosal administration (*i.e.*, into or through skin or mucosal tissue). Intracavity administration includes, but not limited to administration into oral, vaginal, rectal, nasal, peritoneal, or intestinal cavities as well as, intrathecal (*i.e.*, into spinal canal), intraventricular (*i.e.*, into the brain ventricles or the heart ventricles), inraatrial (*i.e.*, into the heart atrium) and sub arachnoid (*i.e.*, into the sub arachnoid spaces of the brain) administration.

[0207] Any mode of administration can be used so long as the mode results in the expression of the desired peptide or protein, in the desired tissue, in an amount sufficient to generate an immune response to IV and/or to generate a prophylactically or therapeutically effective immune response to IV in a human in need of such response. Administration means of the present invention include needle injection, catheter infusion, biolistic injectors, particle accelerators (*e.g.*, "gene guns" or pneumatic "needleless" injectors) Med-E-Jet (Vahlsing, H., *et al., J. Immunol. Methods 171*:11-22 (1994)), Pigjet (Schrijver, R., *et al., Vaccine 15*: 1908-1916 (1997)), Biojector (Davis, H., *et al., Vaccine 12*: 1503-1509 (1994); Gramzinski, R., *et al., Mol. Med. 4*: 109-118 (1998)), AdvantaJet (Linmayer, I., *et al., Diabetes Care 9:*294-297 (1986)), Medi-jector (Martins, J., and Roedl, E. J. *Occup. Med. 21:*821-824 (1979)), gelfoam sponge depots, other commercially available depot materials (*e.g.*, hydrogels), osmotic pumps (*e.g.*, Alza minipumps), oral or suppositorial solid (tablet or pill) pharmaceutical formulations, topical skin creams, and decanting, use of polynucleotide coated suture (Qin, Y., *et al., Life Sciences 65*: 2193-2203 (1999)) or topical applications during surgery. Certain modes

of administration are intramuscular needle-based injection and pulmonary application via catheter infusion. Energy-assisted plasmid delivery (EAPD) methods may also be employed to administer the compositions of the invention. One such method involves the application of brief electrical pulses to injected tissues, a procedure commonly known as electroporation. *See generally* Mir, L.M. *et al.*, *Proc. Natl. Acad. Sci USA 96*:4262-7 (1999); Hartikka, J. *et al.*, *Mol. Ther. 4*:407-15 (2001); Mathiesen, I., *Gene Ther. 6*:508-14(1999); Rizzuto G. *et al.*, *Hum. Gen. Ther. 11*:1891-900 (2000). Each of the references cited in this paragraph is incorporated herein by reference in its entirety.

[0208] Determining an effective amount of one or more compositions of the present invention depends upon a number of factors including, for example, the antigen being expressed or administered directly, *e.g.*, HA, NA, NP, M1 or M2, or fragments, *e.g.*, eM2, variants, or derivatives thereof, the age and weight of the subject, the precise condition requiring treatment and its severity, and the route of administration. Based on the above factors, determining the precise amount, number of doses, and timing of doses are within the ordinary skill in the art and will be readily determined by the attending physician or veterinarian.

[0209] Compositions of the present invention may include various salts, excipients, delivery vehicles and/or auxiliary agents as are disclosed, *e.g.*, in U.S. Patent Application Publication No. 2002/0019358, published February 14, 2002, which is incorporated herein by reference in its entirety.

[0210] Furthermore, compositions of the present invention may include one or more transfection facilitating compounds that facilitate delivery of polynucleotides to the interior of a cell, and/or to a desired location within a cell. As used herein, the terms "transfection facilitating compound," "transfection facilitating agent," and "transfection facilitating material" are synonymous, and may be used interchangeably. It should be noted that certain transfection facilitating compounds may also be "adjuvants" as described infra, *i.e.*, in addition to facilitating delivery of polynucleotides to the interior

of a cell, the compound acts to alter or increase the immune response to the antigen encoded by that polynucleotide. Examples of the transfection facilitating compounds include, but are not limited to inorganic materials such as calcium phosphate, alum (aluminum sulfate), and gold particles (*e.g.*, "powder" type delivery vehicles); peptides that are, for example, cationic, intercell targeting (for selective delivery to certain cell types), intracell targeting (for nuclear localization or endosomal escape), and ampipathic (helix forming or pore forming); proteins that are, for example, basic (*e.g.*, positively charged) such as histones, targeting (*e.g.*, asialoprotein), viral (*e.g.*, Sendai virus coat protein), and pore-forming; lipids that are, for example, cationic (*e.g.*, DMRIE, DOSPA, DC-Chol), basic (*e.g.*, steryl amine), neutral (*e.g.*, cholesterol), anionic (*e.g.*, phosphatidyl serine), and zwitterionic (*e.g.*, DOPE, DOPC); and polymers such as dendrimers, star-polymers, "homogenous" poly-amino acids (*e.g.*, poly-lysine, poly-arginine), "heterogeneous" poly-amino acids (*e.g.*, mixtures of lysine & glycine), co-polymers, polyvinylpyrrolidinone (PVP), poloxamers (*e.g.* CRL 1005) and polyethylene glycol (PEG). A transfection facilitating material can be used alone or in combination with one or more other transfection facilitating materials. Two or more transfection facilitating materials can be combined by chemical bonding (*e.g.*, covalent and ionic such as in lipidated polylysine, PEGylated polylysine) (Toncheva, *et al., Biochim. Biophys. Acta 1380(3)*:354-368 (1988)), mechanical mixing (*e.g.*, free moving materials in liquid or solid phase such as "polylysine + cationic lipids") (Gao and Huang, *Biochemistry 35*:1027-1036 (1996); Trubetskoy, *et al., Biochem. Biophys. Acta 1131*:311-313 (1992)), and aggregation (*e.g.*, co-precipitation, gel forming such as in cationic lipids + poly-lactide, and polylysine + gelatin). Each of the references cited in this paragraph is incorporated herein by reference in its entirety.

[0211] One category of transfection facilitating materials is cationic lipids. Examples of cationic lipids are 5-carboxyspermylglycine dioctadecylamide (DOGS) and dipalmitoyl-phophatidylethanolamine-5-carboxyspermylamide (DPPES). Cationic cholesterol derivatives are also useful, including {3ß-[N-

N',N'-dimethylamino)ethane]-carbomoyl}-cholesterol (DC-Chol). Dimethyldioctdecyl-ammonium bromide (DDAB), N-(3-aminopropyl)-N,N-(bis-(2-tetradecyloxyethyl))-N-methyl-ammonium bromide (PA-DEMO), N-(3-aminopropyl)-N,N-(bis-(2-dodecyloxyethyl))-N-methyl-ammonium bromide (PA-DELO), N,N,N-tris-(2-dodecyloxy)ethyl-N-(3-amino)propyl-ammonium bromide (PA-TELO), and N1-(3-aminopropyl)((2-dodecyloxy)ethyl)-N2-(2-dodecyloxy)ethyl-1-piperazinaminium bromide (GA-LOE-BP) can also be employed in the present invention.

[0212] Non-diether cationic lipids, such as DL-1,2-dioleoyl-3-dimethylaminopropyl-β-hydroxyethylammonium (DORI diester), 1-O-oleyl-2-oleoyl-3-dimethylaminopropyl-β-hydroxyethylammonium (DORI ester/ether), and their salts promote *in vivo* gene delivery. In some embodiments, cationic lipids comprise groups attached via a heteroatom attached to the quaternary ammonium moiety in the head group. A glycyl spacer can connect the linker to the hydroxyl group.

[0213] Specific, but non-limiting cationic lipids for use in certain embodiments of the present invention include DMRIE ((±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide), GAP-DMORIE ((±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(syn-9-tetradeceneyloxy)-1-propanaminium bromide), and GAP-DLRIE ((±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-(bis-dodecyloxy)-1-propanaminium bromide).

[0214] Other specific but non-limiting cationic surfactants for use in certain embodiments of the present invention include Bn-DHRIE, DhxRIE, DhxRIE-OAc, DhxRIE-OBz and Pr-DOctRIE-OAc. These lipids are disclosed in copending U.S. Patent Application No. 10/725,015. In another aspect of the present invention, the cationic surfactant is Pr-DOctRIE-OAc.

[0215] Other cationic lipids include (±)-N,N-dimethyl-N-[2-(sperminecarboxamido) ethyl]-2,3-bis(dioleyloxy)-1-propaniminium pentahydrochloride (DOSPA), (±)-N-(2-aminoethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propaniminium bromide (β-aminoethyl-DMRIE or βAE-

DMRIE) (Wheeler, *et al., Biochim. Biophys. Acta 1280*:1-11 (1996), and (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(dodecyloxy)-l-propaniminium bromide (GAP-DLRIE) (Wheeler, *et al., Proc. Natl. Acad. Sci. USA 93:*11454-11459 (1996)), which have been developed from DMRIE. Both of the references cited in this paragraph are incorporated herein by reference in their entirety.

[0216] Other examples of DMRIE-derived cationic lipids that are useful for the present invention are (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-(bis-decyloxy)-1-propanaminium bromide (GAP-DDRIE), (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-(bis-tetradecyloxy)-1-propanaminium bromide (GAP-DMRIE), (±)-N-((N"-methyl)-N'-ureyl)propyl-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide (GMU-DMRIE), (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(dodecyloxy)-1-propanaminium bromide (DLRIE), and (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis-([Z]-9-octadecenyloxy)propyl-1- propaniminium bromide (HP-DORIE).

[0217] In the embodiments where the immunogenic composition comprises a cationic lipid, the cationic lipid may be mixed with one or more co-lipids. For purposes of definition, the term "co-lipid" refers to any hydrophobic material which may be combined with the cationic lipid component and includes amphipathic lipids, such as phospholipids, and neutral lipids, such as cholesterol. Cationic lipids and co-lipids may be mixed or combined in a number of ways to produce a variety of non-covalently bonded macroscopic structures, including, for example, liposomes, multilamellar vesicles, unilamellar vesicles, micelles, and simple films. One non-limiting class of co-lipids are the zwitterionic phospholipids, which include the phosphatidylethanolamines and the phosphatidylcholines. Examples of phosphatidylethanolamines, include DOPE, DMPE and DPyPE. In certain embodiments, the co-lipid is DPyPE, which comprises two phytanoyl substituents incorporated into the diacylphosphatidylethanolamine skeleton. In other embodiments, the co-lipid is DOPE, CAS name 1,2-diolyeoyl-sn-glycero-3-phosphoethanolamine.

[0218] When a composition of the present invention comprises a cationic lipid and co-lipid, the cationic lipid:co-lipid molar ratio may be from about 9:1 to about 1:9, from about 4:1 to about 1:4, from about 2:1 to about 1:2, or about 1:1.

[0219] In order to maximize homogeneity, the cationic lipid and co-lipid components may be dissolved in a solvent such as chloroform, followed by evaporation of the cationic lipid/co-lipid solution under vacuum to dryness as a film on the inner surface of a glass vessel (*e.g.*, a Rotovap round-bottomed flask). Upon suspension in an aqueous solvent, the amphipathic lipid component molecules self-assemble into homogenous lipid vesicles. These lipid vesicles may subsequently be processed to have a selected mean diameter of uniform size prior to complexing with, for example, a codon-optimized polynucleotide of the present invention, according to methods known to those skilled in the art. For example, the sonication of a lipid solution is described in Felgner *et al., Proc. Natl. Acad. Sci. USA 8:*,7413-7417 (1987) and in U.S. Patent No. 5,264,618, the disclosures of which are incorporated herein by reference.

[0220] In those embodiments where the composition includes a cationic lipid, polynucleotides of the present invention are complexed with lipids by mixing, for example, a plasmid in aqueous solution and a solution of cationic lipid:co-lipid as prepared herein are mixed. The concentration of each of the constituent solutions can be adjusted prior to mixing such that the desired final plasmid/cationic lipid:co-lipid ratio and the desired plasmid final concentration will be obtained upon mixing the two solutions. The cationic lipid:co-lipid mixtures are suitably prepared by hydrating a thin film of the mixed lipid materials in an appropriate volume of aqueous solvent by vortex mixing at ambient temperatures for about 1 minute. The thin films are prepared by admixing chloroform solutions of the individual components to afford a desired molar solute ratio followed by aliquoting the desired volume of the solutions into a suitable container. The solvent is removed by

evaporation, first with a stream of dry, inert gas (*e.g.* argon) followed by high vacuum treatment.

[0221] Other hydrophobic and amphiphilic additives, such as, for example, sterols, fatty acids, gangliosides, glycolipids, lipopeptides, liposaccharides, neobees, niosomes, prostaglandins and sphingolipids, may also be included in compositions of the present invention. In such compositions, these additives may be included in an amount between about 0.1 mol % and about 99.9 mol % (relative to total lipid), about 1-50 mol %, or about 2-25 mol %.

[0222] Additional embodiments of the present invention are drawn to compositions comprising an auxiliary agent which is administered before, after, or concurrently with the polynucleotide. As used herein, an "auxiliary agent" is a substance included in a composition for its ability to enhance, relative to a composition which is identical *except* for the inclusion of the auxiliary agent, the entry of polynucleotides into vertebrate cells *in vivo*, and/or the *in vivo* expression of polypeptides encoded by such polynucleotides. Certain auxiliary agents may, in addition to enhancing entry of polynucleotides into cells, enhance an immune response to an immunogen encoded by the polynucleotide. Auxiliary agents of the present invention include nonionic, anionic, cationic, or zwitterionic surfactants or detergents, with nonionic surfactants or detergents being preferred, chelators, DNase inhibitors, poloxamers, agents that aggregate or condense nucleic acids, emulsifying or solubilizing agents, wetting agents, gel-forming agents, and buffers.

[0223] Auxiliary agents for use in compositions of the present invention include, but are not limited to non-ionic detergents and surfactants IGEPAL CA 630®, NONIDET NP-40, Nonidet® P40, Tween-20™, Tween-80™, Pluronic® F68 (ave. MW: 8400; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 80%), Pluronic F77® (ave. MW: 6600; approx. MW of hydrophobe, 2100; approx. wt. % of hydrophile, 70%), Pluronic P65®(ave. MW: 3400; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 50%), Triton X-100™, and Triton X-114™; the anionic detergent sodium

dodecyl sulfate (SDS); the sugar stachyose; the condensing agent DMSO; and the chelator/DNAse inhibitor EDTA, CRL 1005 (12 kDa, 5% POE), and BAK (Benzalkonium chloride 50% solution, available from Ruger Chemical Co. Inc.). In certain specific embodiments, the auxiliary agent is DMSO, Nonidet P40, Pluronic F68® (ave. MW: 8400; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 80%), Pluronic F77® (ave. MW: 6600; approx. MW of hydrophobe, 2100; approx. wt. % of hydrophile, 70%), Pluronic P65® (ave. MW: 3400; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 50%), Pluronic L64® (ave. MW: 2900; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 40%), and Pluronic F108® (ave. MW: 14600; approx. MW of hydrophobe, 3000; approx. wt. % of hydrophile, 80%). *See, e.g.*, U.S. Patent Application Publication No. 2002/0019358, published February 14, 2002, which is incorporated herein by reference in its entirety.

[0224] Certain compositions of the present invention can further include one or more adjuvants before, after, or concurrently with the polynucleotide. The term "adjuvant" refers to any material having the ability to (1) alter or increase the immune response to a particular antigen or (2) increase or aid an effect of a pharmacological agent. It should be noted, with respect to polynucleotide vaccines, that an "adjuvant," can be a transfection facilitating material. Similarly, certain "transfection facilitating materials" described *supra*, may also be an "adjuvant." An adjuvant may be used with a composition comprising a polynucleotide of the present invention. In a prime-boost regimen, as described herein, an adjuvant may be used with either the priming immunization, the booster immunization, or both. Suitable adjuvants include, but are not limited to, cytokines and growth factors; bacterial components (*e.g.*, endotoxins, in particular superantigens, exotoxins and cell wall components); aluminum-based salts; calcium-based salts; silica; polynucleotides; toxoids; serum proteins, viruses and virally-derived materials, poisons, venoms, imidazoquiniline compounds, poloxamers, and cationic lipids.

[0225] A great variety of materials have been shown to have adjuvant activity through a variety of mechanisms. Any compound which may increase the expression, antigenicity or immunogenicity of the polypeptide is a potential adjuvant. The present invention provides an assay to screen for improved immune responses to potential adjuvants. Potential adjuvants which may be screened for their ability to enhance the immune response according to the present invention include, but are not limited to: inert carriers, such as alum, bentonite, latex, and acrylic particles; pluronic block polymers, such as TiterMax® (block copolymer CRL-8941, squalene (a metabolizable oil) and a microparticulate silica stabilizer); depot formers, such as Freunds adjuvant, surface active materials, such as saponin, lysolecithin, retinal, Quil A, liposomes, and pluronic polymer formulations; macrophage stimulators, such as bacterial lipopolysaccharide; alternate pathway complement activators, such as insulin, zymosan, endotoxin, and levamisole; and non-ionic surfactants, such as poloxamers, poly(oxyethylene)-poly(oxypropylene) tri-block copolymers. Also included as adjuvants are transfection-facilitating materials, such as those described above.

[0226] Poloxamers which may be screened for their ability to enhance the immune response according to the present invention include, but are not limited to, commercially available poloxamers such as Pluronic® surfactants, which are block copolymers of propylene oxide and ethylene oxide in which the propylene oxide block is sandwiched between two ethylene oxide blocks. Examples of Pluronic® surfactants include Pluronic® L121 (ave. MW: 4400; approx. MW of hydrophobe, 3600; approx. wt. % of hydrophile, 10%), Pluronic® L101 (ave. MW: 3800; approx. MW of hydrophobe, 3000; approx. wt. % of hydrophile, 10%), Pluronic® L81 (ave. MW: 2750; approx. MW of hydrophobe, 2400; approx. wt. % of hydrophile, 10%), Pluronic® L61 (ave. MW: 2000; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 10%), Pluronic® L31 (ave. MW: 1100; approx. MW of hydrophobe, 900; approx. wt. % of hydrophile, 10%), Pluronic® L122 (ave. MW: 5000; approx. MW of hydrophobe, 3600; approx. wt. % of hydrophile, 20%), Pluronic® L92

(ave. MW: 3650; approx. MW of hydrophobe, 2700; approx. wt. % of hydrophile, 20%), Pluronic® L72 (ave. MW: 2750; approx. MW of hydrophobe, 2100; approx. wt. % of hydrophile, 20%), Pluronic® L62 (ave. MW: 2500; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 20%), Pluronic® L42 (ave. MW: 1630; approx. MW of hydrophobe, 1200; approx. wt. % of hydrophile, 20%), Pluronic® L63 (ave. MW: 2650; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 30%), Pluronic® L43 (ave. MW: 1850; approx. MW of hydrophobe, 1200; approx. wt. % of hydrophile, 30%), Pluronic® L64 (ave. MW: 2900; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 40%), Pluronic® L44 (ave. MW: 2200; approx. MW of hydrophobe, 1200; approx. wt. % of hydrophile, 40%), Pluronic® L35 (ave. MW: 1900; approx. MW of hydrophobe, 900; approx. wt. % of hydrophile, 50%), Pluronic® P123 (ave. MW: 5750; approx. MW of hydrophobe, 3600; approx. wt. % of hydrophile, 30%), Pluronic® P103 (ave. MW: 4950; approx. MW of hydrophobe, 3000; approx. wt. % of hydrophile, 30%), Pluronic® P104 (ave. MW: 5900; approx. MW of hydrophobe, 3000; approx. wt. % of hydrophile, 40%), Pluronic® P84 (ave. MW: 4200; approx. MW of hydrophobe, 2400; approx. wt. % of hydrophile, 40%), Pluronic® P105 (ave. MW: 6500; approx. MW of hydrophobe, 3000; approx. wt. % of hydrophile, 50%), Pluronic® P85 (ave. MW: 4600; approx. MW of hydrophobe, 2400; approx. wt. % of hydrophile, 50%), Pluronic® P75 (ave. MW: 4150; approx. MW of hydrophobe, 2100; approx. wt. % of hydrophile, 50%), Pluronic® P65 (ave. MW: 3400; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 50%), Pluronic® F127 (ave. MW: 12600; approx. MW of hydrophobe, 3600; approx. wt. % of hydrophile, 70%), Pluronic® F98 (ave. MW: 13000; approx. MW of hydrophobe, 2700; approx. wt. % of hydrophile, 80%), Pluronic® F87 (ave. MW: 7700; approx. MW of hydrophobe, 2400; approx. wt. % of hydrophile, 70%), Pluronic® F77 (ave. MW: 6600; approx. MW of hydrophobe, 2100; approx. wt. % of hydrophile, 70%), Pluronic® F108 (ave. MW: 14600; approx. MW of hydrophobe, 3000; approx. wt. % of hydrophile, 80%), Pluronic® F98 (ave.

MW: 13000; approx. MW of hydrophobe, 2700; approx. wt. % of hydrophile, 80%), Pluronic® F88 (ave. MW: 11400; approx. MW of hydrophobe, 2400; approx. wt. % of hydrophile, 80%), Pluronic® F68 (ave. MW: 8400; approx. MW of hydrophobe, 1800; approx. wt. % of hydrophile, 80%), Pluronic® F38 (ave. MW: 4700; approx. MW of hydrophobe, 900; approx. wt. % of hydrophile, 80%).

[0227] Reverse poloxamers which may be screened for their ability to enhance the immune response according to the present invention include, but are not limited to Pluronic® R 31R1 (ave. MW: 3250; approx. MW of hydrophobe, 3100; approx. wt. % of hydrophile, 10%), Pluronic® R 25R1 (ave. MW: 2700; approx. MW of hydrophobe, 2500; approx. wt. % of hydrophile, 10%), Pluronic® R 17R1 (ave. MW: 1900; approx. MW of hydrophobe, 1700; approx. wt. % of hydrophile, 10%), Pluronic® R 31R2 (ave. MW: 3300; approx. MW of hydrophobe, 3100; approx. wt. % of hydrophile, 20%), Pluronic® R 25R2 (ave. MW: 3100; approx. MW of hydrophobe, 2500; approx. wt. % of hydrophile, 20%), Pluronic® R 17R2 (ave. MW: 2150; approx. MW of hydrophobe, 1700; approx. wt. % of hydrophile, 20%), Pluronic® R 12R3 (ave. MW: 1800; approx. MW of hydrophobe, 1200; approx. wt. % of hydrophile, 30%), Pluronic® R 31R4 (ave. MW: 4150; approx. MW of hydrophobe, 3100; approx. wt. % of hydrophile, 40%), Pluronic® R 25R4 (ave. MW: 3600; approx. MW of hydrophobe, 2500; approx. wt. % of hydrophile, 40%), Pluronic® R 22R4 (ave. MW: 3350; approx. MW of hydrophobe, 2200; approx. wt. % of hydrophile, 40%), Pluronic® R 17R4 (ave. MW: 3650; approx. MW of hydrophobe, 1700; approx. wt. % of hydrophile, 40%), Pluronic® R 25R5 (ave. MW: 4320; approx. MW of hydrophobe, 2500; approx. wt. % of hydrophile, 50%), Pluronic® R 10R5 (ave. MW: 1950; approx. MW of hydrophobe, 1000; approx. wt. % of hydrophile, 50%), Pluronic® R 25R8 (ave. MW: 8550; approx. MW of hydrophobe, 2500; approx. wt. % of hydrophile, 80%), Pluronic® R 17R8 (ave. MW: 7000; approx. MW of hydrophobe, 1700;

approx. wt. % of hydrophile, 80%), and Pluronic® R 10R8 (ave. MW: 4550; approx. MW of hydrophobe, 1000; approx. wt. % of hydrophile, 80%).

[0228] Other commercially available poloxamers which may be screened for their ability to enhance the immune response according to the present invention include compounds that are block copolymer of polyethylene and polypropylene glycol such as Synperonic® L121 (ave. MW: 4400), Synperonic® L122 (ave. MW: 5000), Synperonic® P104 (ave. MW: 5850), Synperonic® P105 (ave. MW: 6500), Synperonic® P123 (ave. MW: 5750), Synperonic® P85 (ave. MW: 4600) and Synperonic® P94 (ave. MW: 4600), in which L indicates that the surfactants are liquids, P that they are pastes, the first digit is a measure of the molecular weight of the polypropylene portion of the surfactant and the last digit of the number, multiplied by 10, gives the percent ethylene oxide content of the surfactant; and compounds that are nonylphenyl polyethylene glycol such as Synperonic® NP10 (nonylphenol ethoxylated surfactant - 10% solution), Synperonic® NP30 (condensate of 1 mole of nonylphenol with 30 moles of ethylene oxide) and Synperonic® NP5 (condensate of 1 mole of nonylphenol with 5.5 moles of naphthalene oxide).

[0229] Other poloxamers which may be screened for their ability to enhance the immune response according to the present invention include: (a) a polyether block copolymer comprising an A-type segment and a B-type segment, wherein the A-type segment comprises a linear polymeric segment of relatively hydrophilic character, the repeating units of which contribute an average Hansch-Leo fragmental constant of about –0.4 or less and have molecular weight contributions between about 30 and about 500, wherein the B-type segment comprises a linear polymeric segment of relatively hydrophobic character, the repeating units of which contribute an average Hansch-Leo fragmental constant of about –0.4 or more and have molecular weight contributions between about 30 and about 500, wherein at least about 80% of the linkages joining the repeating units for each of the polymeric segments comprise an ether linkage; (b) a block copolymer having a polyether segment and a polycation segment, wherein the polyether segment comprises

at least an A-type block, and the polycation segment comprises a plurality of cationic repeating units; and (c) a polyether-polycation copolymer comprising a polymer, a polyether segment and a polycationic segment comprising a plurality of cationic repeating units of formula —NH—R^0, wherein R^0 is a straight chain aliphatic group of 2 to 6 carbon atoms, which may be substituted, wherein said polyether segments comprise at least one of an A-type of B-type segment. *See* U.S. Patent No. 5,656,611, by Kabonov, *et al.*, which is incorporated herein by reference in its entirety. Other poloxamers of interest include CRL1005 (12 kDa, 5% POE), CRL8300 (11 kDa, 5% POE), CRL2690 (12 kDa, 10% POE), CRL4505 (15 kDa, 5% POE) and CRL1415 (9 kDa, 10% POE).

[0230] Other auxiliary agents which may be screened for their ability to enhance the immune response according to the present invention include, but are not limited to Acacia (gum arabic); the poloxyethylene ether R-O-$(C_2H_4O)_x$-H (BRIJ®), *e.g.*, polyethylene glycol dodecyl ether (BRIJ® 35, x=23), polyethylene glycol dodecyl ether (BRIJ® 30, x=4), polyethylene glycol hexadecyl ether (BRIJ® 52 x=2), polyethylene glycol hexadecyl ether (BRIJ® 56, x=10), polyethylene glycol hexadecyl ether (BRIJ® 58P, x=20), polyethylene glycol octadecyl ether (BRIJ® 72, x=2), polyethylene glycol octadecyl ether (BRIJ® 76, x=10), polyethylene glycol octadecyl ether (BRIJ® 78P, x=20), polyethylene glycol oleyl ether (BRIJ® 92V, x=2), and polyoxyl 10 oleyl ether (BRIJ® 97, x=10); poly-D-glucosamine (chitosan); chlorbutanol; cholesterol; diethanolamine; digitonin; dimethylsulfoxide (DMSO), ethylenediamine tetraacetic acid (EDTA); glyceryl monosterate; lanolin alcohols; mono- and di-glycerides; monoethanolamine; nonylphenol polyoxyethylene ether (NP-40®); octylphenoxypolyethoxyethanol (NONIDET NP-40 from Amresco); ethyl phenol poly (ethylene glycol ether)^n, n=11 (Nonidet® P40 from Roche); octyl phenol ethylene oxide condensate with about 9 ethylene oxide units (nonidet P40); IGEPAL CA 630® ((octyl phenoxy) polyethoxyethanol; structurally same as NONIDET NP-40); oleic acid; oleyl alcohol; polyethylene glycol 8000; polyoxyl 20 cetostearyl ether;

polyoxyl 35 castor oil; polyoxyl 40 hydrogenated castor oil; polyoxyl 40 stearate; polyoxyethylene sorbitan monolaurate (polysorbate 20, or TWEEN-20®; polyoxyethylene sorbitan monooleate (polysorbate 80, or TWEEN-80®); propylene glycol diacetate; propylene glycol monstearate; protamine sulfate; proteolytic enzymes; sodium dodecyl sulfate (SDS); sodium monolaurate; sodium stearate; sorbitan derivatives (SPAN®), *e.g.*, sorbitan monopalmitate (SPAN® 40), sorbitan monostearate (SPAN® 60), sorbitan tristearate (SPAN® 65), sorbitan monooleate (SPAN® 80), and sorbitan trioleate (SPAN® 85); 2,6,10,15,19,23-hexamethyl-2,6,10,14,18,22-tetracosa-hexaene (squalene); stachyose; stearic acid; sucrose; surfactin (lipopeptide antibiotic from *Bacillus subtilis*); dodecylpoly(ethyleneglycolether)$_9$ (Thesit®) MW 582.9; octyl phenol ethylene oxide condensate with about 9-10 ethylene oxide units (Triton X-100™); octyl phenol ethylene oxide condensate with about 7-8 ethylene oxide units (Triton X-114™); tris(2-hydroxyethyl)amine (trolamine); and emulsifying wax.

[0231] In certain adjuvant compostions, the adjuvant is a cytokine. A composition of the present invention can comprise one or more cytokines, chemokines, or compounds that induce the production of cytokines and chemokines, or a polynucleotide encoding one or more cytokines, chemokines, or compounds that induce the production of cytokines and chemokines. Examples include, but are not limited to granulocyte macrophage colony stimulating factor (GM-CSF), granulocyte colony stimulating factor (G-CSF), macrophage colony stimulating factor (M-CSF), colony stimulating factor (CSF), erythropoietin (EPO), interleukin 2 (IL-2), interleukin-3 (IL-3), interleukin 4 (IL-4), interleukin 5 (IL-5), interleukin 6 (IL-6), interleukin 7 (IL-7), interleukin 8 (IL-8), interleukin 10 (IL-10), interleukin 12 (IL-12), interleukin 15 (IL-15), interleukin 18 (IL-18), interferon alpha (IFNα), interferon beta (IFNβ), interferon gamma (IFNγ), interferon omega (IFNω), interferon tau (IFNτ), interferon gamma inducing factor I (IGIF), transforming growth factor beta (TGF-β), RANTES (regulated upon activation, normal T-cell expressed and presumably secreted), macrophage inflammatory proteins

(*e.g.*, MIP-1 alpha and MIP-1 beta), *Leishmania* elongation initiating factor (LEIF), and Flt-3 ligand.

[0232] In certain compositions of the present invention, the polynucleotide construct may be complexed with an adjuvant composition comprising (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE). The composition may also comprise one or more co-lipids, *e.g.*, 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE), 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE), and/or 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE). An adjuvant composition comprising GAP-DMORIE and DPyPE at a 1:1 molar ratio is referred to herein as Vaxfectin™. *See, e.g.*, PCT Publication No. WO 00/57917, which is incorporated herein by reference in its entirety.

[0233] In other embodiments, the polynucleotide itself may function as an adjuvant as is the case when the polynucleotides of the invention are derived, in whole or in part, from bacterial DNA. Bacterial DNA containing motifs of unmethylated CpG-dinucleotides (CpG-DNA) triggers innate immune cells in vertebrates through a pattern recognition receptor (including toll receptors such as TLR 9) and thus possesses potent immunostimulatory effects on macrophages, dendritic cells and B-lymphocytes. *See, e.g.*, Wagner, H., *Curr. Opin. Microbiol. 5*:62-69 (2002); Jung, J. *et al., J. Immunol. 169:* 2368-73 (2002); *see also* Klinman, D.M. *et al., Proc. Natl Acad. Sci. U.S.A. 93*:2879-83 (1996). Methods of using unmethylated CpG-dinucleotides as adjuvants are described in, for example, U.S. Patent Nos. 6,207,646, 6,406,705 and 6,429,199, the disclosures of which are herein incorporated by reference.

[0234] The ability of an adjuvant to increase the immune response to an antigen is typically manifested by a significant increase in immune-mediated protection. For example, an increase in humoral immunity is typically manifested by a significant increase in the titer of antibodies raised to the antigen, and an increase in T-cell activity is typically manifested in increased cell proliferation, or cellular cytotoxicity, or cytokine secretion. An adjuvant

may also alter an immune response, for example, by changing a primarily humoral or Th_2 response into a primarily cellular, or Th_1 response.

[0235] Nucleic acid molecules and/or polynucleotides of the present invention, *e.g.*, plasmid DNA, mRNA, linear DNA or oligonucleotides, may be solubilized in any of various buffers. Suitable buffers include, for example, phosphate buffered saline (PBS), normal saline, Tris buffer, and sodium phosphate (*e.g.*, 150 mM sodium phosphate). Insoluble polynucleotides may be solubilized in a weak acid or weak base, and then diluted to the desired volume with a buffer. The pH of the buffer may be adjusted as appropriate. In addition, a pharmaceutically acceptable additive can be used to provide an appropriate osmolarity. Such additives are within the purview of one skilled in the art. For aqueous compositions used *in vivo*, sterile pyrogen-free water can be used. Such formulations will contain an effective amount of a polynucleotide together with a suitable amount of an aqueous solution in order to prepare pharmaceutically acceptable compositions suitable for administration to a human.

[0236] Compositions of the present invention can be formulated according to known methods. Suitable preparation methods are described, for example, in Remington's Pharmaceutical Sciences, 16th Edition, A. Osol, ed., Mack Publishing Co., Easton, PA (1980), and Remington's Pharmaceutical Sciences, 19th Edition, A.R. Gennaro, ed., Mack Publishing Co., Easton, PA (1995), both of which are incorporated herein by reference in their entireties. Although the composition may be administered as an aqueous solution, it can also be formulated as an emulsion, gel, solution, suspension, lyophilized form, or any other form known in the art. In addition, the composition may contain pharmaceutically acceptable additives including, for example, diluents, binders, stabilizers, and preservatives.

[0237] The following examples are included for purposes of illustration only and are not intended to limit the scope of the present invention, which is defined by the appended claims. All references cited in the Examples are incorporated herein by reference in their entireties.

EXAMPLES

Materials and Methods

[0238] The following materials and methods apply generally to all the examples disclosed herein. Specific materials and methods are disclosed in each example, as necessary.

[0239] The practice of the present invention will employ, unless otherwise indicated, conventional techniques of cell biology, cell culture, molecular biology (including PCR), vaccinology, microbiology, recombinant DNA, and immunology, which are within the skill of the art. Such techniques are explained fully in the literature. *See*, for example, *Molecular Cloning A Laboratory Manual*, 2nd Ed., Sambrook *et al.*, ed., Cold Spring Harbor Laboratory Press: (1989); *DNA Cloning*, Volumes I and II (D. N. Glover ed., 1985); *Oligonucleotide Synthesis* (M. J. Gait ed., 1984); Mullis *et al.* U.S. Pat. No: 4,683,195; *Nucleic Acid Hybridization* (B. D. Hames & S. J. Higgins eds. 1984); *Transcription And Translation* (B. D. Hames & S. J. Higgins eds. 1984); *Culture Of Animal Cells* (R. I. Freshney, Alan R. Liss, Inc., 1987); *Immobilized Cells And Enzymes* (IRL Press, 1986); B. Perbal, *A Practical Guide To Molecular Cloning* (1984); the treatise, *Methods In Enzymology* (Academic Press, Inc., N.Y.); *Gene Transfer Vectors For Mammalian Cells* (J. H. Miller and M. P. Calos eds., 1987, Cold Spring Harbor Laboratory); *Methods In Enzymology*, Vols. 154 and 155 (Wu *et al.* eds.), *Immunochemical Methods In Cell And Molecular Biology* (Mayer and Walker, eds., Academic Press, London, 1987); and in Ausubel *et al.*, *Current Protocols in Molecular Biology,* John Wiley and Sons, Baltimore, Maryland (1989). Each of the references cited in this paragraph is incorporated herein by reference in its entirety.

Gene Construction

[0240] Constructs of the present invention are constructed based on the sequence information provided herein or in the art utilizing standard molecular

biology techniques, including, but not limited to the following. First, a series complementary oligonucleotide pairs of 80-90 nucleotides each in length and spanning the length of the construct are synthesized by standard methods. These oligonucleotide pairs are synthesized such that upon annealing, they form double stranded fragments of 80-90 base pairs, containing cohesive ends. The single-stranded ends of each pair of oligonucleotides are designed to anneal with a single-stranded end of an adjacent oligonucleotide duplex. Several adjacent oligonucleotide pairs prepared in this manner are allowed to anneal, and approximately five to six adjacent oligonucleotide duplex fragments are then allowed to anneal together via the cohesive single stranded ends. This series of annealed oligonucleotide duplex fragments is then ligated together and cloned into a suitable plasmid, such as the TOPO® vector available from Invitrogen Corporation, Carlsbad, CA. The construct is then sequenced by standard methods. Constructs prepared in this manner, comprising 5 to 6 adjacent 80 to 90 base pair fragments ligated together, *i.e.*, fragments of about 500 base pairs, are prepared, such that the entire desired sequence of the construct is represented in a series of plasmid constructs. The inserts of these plasmids are then cut with appropriate restriction enzymes and ligated together to form the final construct. The final construct is then cloned into a standard bacterial cloning vector, and sequenced. The oligonucleotides and primers referred to herein can easily be designed by a person of skill in the art based on the sequence information provided herein and in the art, and such can be synthesized by any of a number of commercial nucleotide providers, for example Retrogen, San Diego, CA, and GENEART, Regensburg, Germany.

Plasmid Vectors

[0241] Constructs of the present invention can be inserted, for example, into eukaryotic expression vectors VR1012 or VR10551 . These vectors are built on a modified pUC18 background (*see* Yanisch-Perron, C., *et al. Gene 33*:103-119 (1985)), and contain a kanamycin resistance gene, the human

cytomegalovirus immediate early promoter/enhancer and intron A, and the bovine growth hormone transcription termination signal, and a polylinker for inserting foreign genes. *See* Hartikka, J., *et al.*, *Hum. Gene Ther.* 7:1205-1217 (1996). However, other standard commercially available eukaryotic expression vectors may be used in the present invention, including, but not limited to: plasmids pcDNA3, pHCMV/Zeo, pCR3.1, pEF1/His, pIND/GS, pRc/HCMV2, pSV40/Zeo2, pTRACER-HCMV, pUB6/V5-His, pVAX1, and pZeoSV2 (available from Invitrogen, San Diego, CA), and plasmid pCI (available from Promega, Madison, WI).

[0242] An optimized backbone plasmid, termed VR10551, has minor changes from the VR1012 backbone described above. The VR10551 vector is derived from and similar to VR1012 in that it uses the human cytomegalovirus immediate early (hCMV-IE) gene enhancer/promoter and 5' untranslated region (UTR), including the hCMV-IE Intron A. The changes from the VR1012 to the VR10551 include some modifications to the multiple cloning site, and a modified rabbit β globin 3' untranslated region/polyadenylation signal sequence/transcriptional terminator has been substituted for the same functional domain derived from the bovine growth hormone gene.

[0243] Additionally, constructs of the present invention can be inserted into other eukaryotic expression vector backbones such as VR10682 or VR10686. The VR10682 expression vector backbone (SEQ ID NO:94) contains a modified rous sarcoma virus (RSV) promoter from expression plasmid VCL1005, the bovine growth hormone (BGH) poly-adenylation site and a polylinker for inserting foreign genes and a kanamycin resistance gene. The RSV promoter in VCL1005 and VR10682 contains a XbaI endonuclease restriction site near the transcription start site in the sequence TAC TCT AGA CG (SEQ ID NO:82). The modified RSV promoter contained in VR10682 . Expression plasmid VCL1005 is described in U.S. Patent No. 5,561,064 and is incorporated herein by reference.

[0244] The VR10686 expression vector backbone (SEQ ID NO:112) was created by replacing the West Nile Virus (WNV) antigen insert in VR6430

(SEQ ID NO:89) with the multiple cloning site from the VR1012 vector. The VR10686 and VR6430 expression vector backbones contain the RSV promoter, derived from VCL1005, which has been modified back to the wild-type RSV sequence (TAC AAT AAA CG (SEQ ID NO:83)). The wild-type RSV promoter is fused to the "R" region plus the first 39 nucleotides of the U5 region from Human T-Cell Leukemia Virus I (HTLV-I), hereinafter refered to as the RU5 element. The R and U5 regions are portions of the long terminal repeat region (LTR) of HTLV-I which control expression of the HTLV-I transcript and is duplicated at either end of the integrated viral genome as a result of the retroviral integration mechanism. The LTR of HTLV-1 and most retroviruses are divided into three regions, U3, R and U5. Transcription from the intigrated viral genome commences at the U3-R boundary of the 5' LTR and the transcript is polyadenylated at the R-U5 boundary of the 3' LTR. (*See* Goff, S. P. Retroviridae, *Field's Virology* 4th ed. 2:1871-1939 (2001). This RU5 HTLV-I element has been shown to be a potent stimulator of translation when fused to the SV40 early gene promoter. *See* Takebe *et al.*, *Mol. Cell Biol.* 8:466-472 (1988). It has been proposed that the stimulation of translation by the HTLV-I RU5 element is due to its function, in part, as a translational enhancing internal ribosome entry site (IRES). See Attal *et al. FEBS Letters* 392:220-224 (1996). Additionally the HTLV-I RU5 element provides the 5'-splice donor site. Immediately downstream of the RU5 element is the 3'-end of the HCMV intron A sequence containing the splice acceptor sequence. The VR10686 and VR6430 expression vectors contain a hybrid intron composed of the 5'-HTLV I intron sequence fused to the 3'-end of the HCMV intron A, a bovine growth hormone poly-adenylation site, a polylinker for insertion of forign genes and a kanamycin resistance gene. The VR6430 vector expresses the prM and E West Nile Virus antigens (Genebank Accession No. AF202541).

[0245] The vector backbones described above may by used to create expression vectors which express multiple influenza proteins, fragments, variants or derivatives thereof. An expression vector as desribed herein may

contain an additional promoter. For example, construct VR4774 (described in Example 13), contains a CMV promoter and an RSV promoter. Thus, the vector backbones described herein may contain multiple expression cassettes which comprise a promoter and an influenza coding sequence including, *inter alia*, polynucleotides as described herein. The expression cassettes may encode the same or different influenza polypeptides. Additionally, the expression cassettes may be in the same or opposite orientation relative to each other. As such transcription from each cassette may be in the same or opposition direction (*i.e.* 5' to 3' in both expression cassettes or, alternatively, 5' to 3' in one expression cassette and 3' to 5' in the other expression cassette).

Plasmid DNA Purification

[0246] Plasmid DNA may be transformed into competent cells of an appropriate *Escherichia coli* strain (including but not limited to the DH5α strain) and highly purified covalently closed circular plasmid DNA was isolated by a modified lysis procedure (Horn, N.A., *et al., Hum. Gene Ther.* *6*:565-573 (1995)) followed by standard double CsCl-ethidium bromide gradient ultracentrifugation (Sambrook, J., *et al., Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, Plainview, New York (1989)). Alternatively, plasmid DNAs are purified using Giga columns from Qiagen (Valencia, CA) according to the kit instructions. All plasmid preparations were free of detectable chromosomal DNA, RNA and protein impurities based on gel analysis and the bicinchoninic protein assay (Pierce Chem. Co., Rockford IL). Endotoxin levels were measured using *Limulus* Amebocyte Lysate assay (LAL, Associates of Cape Cod, Falmouth, MA) and were less than 0.6 Endotoxin Units/mg of plasmid DNA. The spectrophotometric A_{260}/A_{280} ratios of the DNA solutions were typically above 1.8. Plasmids were ethanol precipitated and resuspended in an appropriate solution, *e.g.*, 150 mM sodium phosphate (for other appropriate excipients and auxiliary agents, see U.S. Patent Application Publication 2002/0019358, published February 14, 2002). DNA was stored at -20EC until

use. DNA was diluted by mixing it with 300 mM salt solutions and by adding appropriate amount of USP water to obtain 1 mg/ml plasmid DNA in the desired salt at the desired molar concentration.

Plasmid expression in mammalian cell lines

[0247] The expression plasmids were analyzed *in vitro* by transfecting the plasmids into a well characterized mouse melanoma cell line (VM-92, also known as UM-449). *See, e.g.,* Wheeler, C.J., Sukhu, L., Yang, G., Tsai, Y., Bustamente, C., Felgner, P. Norman, J & Manthorpe, M. "Converting an Alcohol to an Amine in a Cationic Lipid Dramatically Alters the Co-lipid Requirement, Cellular Transfection Activity and the Ultrastructure of DNA-Cytofectin Complexes," *Biochim. Biophys. Acta. 1280*:1-11 (1996). Other well-characterized human cell lines can also be used, *e.g.* MRC-5 cells, ATCC Accession No. CCL-171 or human rhabdomyosarcoma cell line RD (ATCC CCL-136). The transfection was performed using cationic lipid-based transfection procedures well known to those of skill in the art. Other transfection procedures are well known in the art and may be used, for example electroporation and calcium chloride-mediated transfection (Graham F.L.and A.J. van der Eb *Virology 52*:456-67 (1973)). Following transfection, cell lysates and culture supernatants of transfected cells were evaluated to compare relative levels of expression of IV antigen proteins. The samples were assayed by western blots and ELISAs, using commercially available polyclonal and/or monoclonal antibodies (available, *e.g.*, from Research Diagnostics Inc., Flanders NJ), so as to compare both the quality and the quantity of expressed antigen.

Injections of plasmid DNA

[0248] The quadriceps muscles of restrained awake mice (*e.g.*, female 6 - 12 week old BALB/c mice from Harlan Sprague Dawley, Indianapolis, IN) are injected bilaterally with 1-50 μg of DNA in 50 μl solution (100 μg in 100 μl total per mouse) using a disposable plastic insulin syringe and 28G 1/2 needle

(Becton-Dickinson, Franklin Lakes, NJ, Cat. No. 329430) fitted with a plastic collar cut from a micropipette tip, as previously described (Hartikka, J., *et al.*, *Hum. Gene Ther.* 7:1205-1217 (1996).

[0249] Animal care throughout the study was in compliance with the "Guide for the Use and Care of Laboratory Animals", Institute of Laboratory Animal Resources, Commission on Life Sciences, National Research Council, National Academy Press, Washington, D.C., 1996 as well as with Vical's Institutional Animal Care and Use Committee.

EXAMPLE 1

Construction of Expression Vectors

[0250] Plasmid constructs comprising the native coding regions encoding NP, M1, M2, HA, and eM2, IV proteins or fragments, variants or derivatives are constructed as follows. The NP, M1, and M2 genes from IV (A/PR/8/34) are isolated from viral RNA by RT PCR, or prepared by direct synthesis if the wildtype sequence is known, by standard methods and are inserted into the vector VR10551 via standard restriction sites, by standard methods.

[0251] Plasmid constructs comprising human codon-optimized coding regions encoding NP, M1, M2, HA, eM2, and/or an eM2-NP fusion; or other codon-optimized coding regions encoding other IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, are prepared as follows. The codon-optimized coding regions are generated using the full, minimal, or uniform codon optimization methods described herein. The codon optimized coding regions are constructed using standard PCR methods described herein, or are ordered commercially. Oligonucleotides representing about the first 23-24 aa extracellular region of M2 are constructed, and are used in an overlap PCR reaction with the NP coding regions described above, to create a coding region coding for an eM2/NP fusion protein, for example as shown in SEQ ID NOs 6 and 7. The codon-

optimized coding regions are inserted into the vector VR10551 via standard restriction sites, by standard methods.

[0252] Plasmids constructed as above are propagated in *Escherichia coli* and purified by the alkaline lysis method (Sambrook, J., *et al., Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, ed. 2 (1989)). CsCl-banded DNA are ethanol precipitated and resuspended in 0.9% saline or PBS to a final concentration of 2 mg/ml for injection. Alternately, plasmids are purified using any of a variety of commercial kits, or by other known procedures involving differential precipitation and/or chromatographic purification.

[0253] Expression is tested by formulating each of the plasmids in DMRIE/DOPE and transfecting VM92 cells. The supernatants are collected and the protein production tested by Western blot or ELISA. The relative expression of the wild type and codon optimized constructs are compared.

[0254] Examples of constructs made according to the above methods are listed in Table 13. The experimental procedure for generating the listed constructs is as described above, with particular parameters and materials employed as described herein.

TABLE 13

Plasmid #	Description
VR4700	TPA leader- NP (A/PR/34) in VR 1255
VR4707	TPA leader-M2 with transmembrane deletion, glycine linker inserted
VR4710	TPA leader -1st 24 amino acids of M2 from VR4707 fused to NP from VR4700
VR4750	full length HA from mouse adapted virus (H3, Hong Kong 68)
VR4752	full length HA from mouse adapted virus (H1, Puerto Rico 34)
VR4755	algorithm to codon optimize consensus amino acid sequence, direct fusion M2 to ATG of M1
VR4756	native sequence from A/Niigata/137/96 influenza strain (matches amino acid consensus sequence)
VR4757	Contracted codon optimized- 1st 24 amino acids of M2 from consensus fused to full-length NP consensus
VR4758	Applicants' codon optimized- 1st 24 amino acids of M2 from consensus fused to full-length NP consensus
VR4759	Full-length M2 derived from VR4755
VR4760	Full-length M1 derived from VR4755
VR4761	Full-length NP derived from VR4757
VR4762	Full-length NP derived from VR4758

VR4763	Selectively codon-optimized regions of segment 7

[0255] The pDNA expression vector VR4700 which encodes the influenza NP protein has been described in the art. *See, e.g.* Sankar, V., Baccaglilni, L., Sawddey, M., Wheeler, C. J., Pillemer, S. R., Baum, B. J. and Atkinson, J. C., "Salivary Gland Delivery of pDNA-Cationic Lipolplexes Elicits Systemic Immune Responses," *Oral Diseases 8*:275-281 (2002). The following is the open reading frame for TPA-NP (from VR4700), referred to herein as SEQ ID NO:46:

```
   1  atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt
  61  tcgcccagcg ctagaggatc gggaatggcg tcccaaggca ccaaacggtc ttacgaacag
 121  atggagactg atggagaacg ccagaatgcc actgaaatca gagcatccgt cggaaaaatg
 181  attggtggaa ttggacgatt ctacatccaa atgtgcaccg aactcaaact cagtgattat
 241  gagggacggt tgatccaaaa cagcttaaca atagagagaa tggtgctctc tgcttttgac
 301  gaaaggagaa ataaatacct ggaagaacat cccagtgcgg ggaaagatcc taagaaaact
 361  ggaggaccta tatacaggag agtaaacgga aagtggatga gagaactcat cctttatgac
 421  aaagaagaaa taaggcgaat ctggcgccaa gctaataatg gtgacgatgc aacggctggt
 481  ctgactcaca tgatgatctg gcattccaat ttgaatgatg caacttatca gaggacaaga
 541  gctcttgttc gcaccggaat ggatcccagg atgtgctctc tgatgcaagg ttcaactctc
 601  cctaggaggt ctggagccgc aggtgctgca gtcaaaggag ttggaacaat ggtgatggaa
 661  ttggtcagga tgatcaaacg tgggatcaat gatcggaact tctggagggg tgagaatgga
 721  cgaaaaacaa gaattgctta tgaaagaatg tgcaacattc tcaaagggaa atttcaaact
 781  gctgcacaaa aagcaatgat ggatcaagtg agagagagcc ggaacccagg gaatgctgag
 841  ttcgaagatc tcacttttct agcacggtct gcactcatat tgagagggtc ggttgctcac
 901  aagtcctgcc tgcctgcctg tgtgtatgga cctgccgtag ccagtgggta cgactttgaa
 961  agagagggat actctctagt cggaatagac cctttcagac tgcttcaaaa cagccaagtg
1021  tacagcctaa tcagaccaaa tgagaatcca gcacacaaga gtcaactggt gtggatggca
1081  tgccattctg ccgcatttga agatctaaga gtattaagct tcatcaaagg gacgaaggtg
1141  ctcccaagag ggaagctttc cactagagga gttcaaattg cttccaatga aaatatggag
1201  actatggaat caagtacact tgaactgaga agcaggtact gggccataag gaccagaagt
1261  ggaggaaaca ccaatcaaca gagggcatct gcgggccaaa tcagcataca acctacgttc
1321  tcagtacaga gaaatctccc ttttgacaga acaaccatta tggcagcatt caatgggaat
1381  acagagggaa gaacatctga catgaggacc gaaatcataa ggatgatgga aagtgcaaga
1441  ccagaagatg tgtctttcca ggggcgggga gtcttcgagc tctcggacga aaaggcagcg
1501  agcccgatcg tgccttcctt tgacatgagt aatgaaggat cttatttctt cggagacaat
1561  gcagatgagt acgacaatta a
```

[0256] Purified VR4700 DNA was used to transfect the murine cell line VM92 to determine expression of the NP protein. Expression of NP was confirmed with a Western Blot assay. Western blot analysis showed very low level expression of VR4700 *in vitro* as detected with mouse polyclonal anti-NP antibody. *In vivo* antibody response was detected by ELISA with an average titer of 62,578.

[0257] Plasmid VR4707 expresses a secreted form of M2, *i.e.*, TPA-M2. The sequence was assembled using synthetic oligonucleotides in which the oligos were annealed amongst themselves, and then ligated and gel purified. The purified product was then ligated (cloned) into Eco RI/Sal I of VR10551. The

M2 sequence lacks the transmembrane domain; the cloned sequence contains amino acids [TPA(1-23)]ARGSG[M2(1-25)]GGG[M2(44-97)]. Amino acid residues between TPA and M2 and between M2 domains were added as flexible linkers. The following mutations were introduced to generate appropriate T-cell epitopes: 74S->G and 78S->N. The following is the open reading frame for TPA-M2ΔTM (from VR4707), referred to herein as SEQ ID NO:47:

```
  1  atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt
 61  tcgcccagcg ctagaggatc gggaatgagt cttctgaccg aggtcgaaac ccctatcaga
121  aacgaatggg ggtgcagatg caacgattca agtgatcctg gcggcggcga tcggcttttt
181  ttcaaatgca tttatcggcg ctttaaatac ggcttgaaaa gagggccttc taccgaagga
241  gtgccagagt ctatgaggga agaatatcgg aaggaacagc agaatgctgt ggatgttgac
301  gatagccatt ttgtcagcat cgagctggag taa
```

[0258] Purified VR4707 DNA was used to transfect the murine cell line VM92 to determine expression of the M2 protein. Expression of M2 was confirmed with a Western Blot assay. Expression was visualized with a commercially available anti-M2 monoclonal antibody. *In vivo* M2 antibody response to VR4707, as assayed by ELISA, resulted in an average titer of 110, which is lower than the average titer of 9,240 for VR4756, encoding full-length M2 from segment 7. An IFNγ ELISPOT assay for M2-specific T cells resulted in an average of 61 SFU/10^6 cells versus an average of 121 SFU/10^6 cells for the segment 7 construct.

[0259] VR4710 was created by fusing the TPA leader and the first 24 amino acids of M2 from VR4707 to the full-length NP gene from VR4700. Primers 5'-GCCGAATCCATGGATGCAATGAAG-3' (SEQ ID NO:48) and 5'-GGTGCCTTGGGACGCCATATCACTTGAATCGTTGCA-3' (SEQ ID NO:49) were used to amplify the TPA-M2 fragment from VR4707. Primers 5'-TGCAACGATTCAAGTGATATGGCGTCCCAAGGCACC-3' (SEQ ID NO:50) and 5'-GCCGTCGACTTAATTGTCGTACTC-3' (SEQ ID NO:51) were used to amplify the NP gene from VR4700. Then the N-terminal and C-terminal primers were used to assemble the fusion, and the eM2NP fusion was cloned into VR10551 as an EcoRI-SalI fragment. The following is the open reading frame for TPA-M2-NP (from VR4710), referred to herein as SEQ ID NO:52:

```
   1  atggatgcaa tgaagagagg gctctgctgt gtgctgctgc tgtgtggagc agtcttcgtt
  61  tcgcccagcg ctagaggatc gggaatgagt cttctgaccg aggtcgaaac ccctatcaga
 121  aacgaatggg ggtgcagatg caacgattca agtgatatgg cgtcccaagg caccaaacgg
 181  tcttacgaac agatggagac tgatggagaa cgccagaatg ccactgaaat cagagcatcc
 241  gtcggaaaaa tgattggtgg aattggacga ttctacatcc aaatgtgcac cgaactcaaa
 301  ctcagtgatt atgagggacg gttgatccaa aacagcttaa caatagagag aatggtgctc
 361  tctgcttttg acgaaaggag aaataaatac ctggaagaac atcccagtgc ggggaaagat
 421  cctaagaaaa ctggaggacc tatatacagg agagtaaacg gaaagtggat gagagaactc
 481  atcctttatg acaaagaaga aataaggcga atctggcgcc aagctaataa tggtgacgat
 541  gcaacggctg gtctgactca catgatgatc tggcattcca atttgaatga tgcaacttat
 601  cagaggacaa gagctcttgt tcgcaccgga atggatccca ggatgtgctc tctgatgcaa
 661  ggttcaactc tccctaggag gtctggagcc gcaggtgctg cagtcaaagg agttggaaca
 721  atggtgatgg aattggtcag gatgatcaaa cgtgggatca atgatcggaa cttctggagg
 781  ggtgagaatg gacgaaaaac aagaattgct tatgaaagaa tgtgcaacat tctcaaaggg
 841  aaatttcaaa ctgctgcaca aaaagcaatg atggatcaag tgagagagag ccggaaccca
 901  gggaatgctg agttcgaaga tctcactttt ctagcacggt ctgcactcat attgagaggg
 961  tcggttgctc acaagtcctg cctgcctgcc tgtgtgtatg gacctgccgt agccagtggg
1021  tacgactttg aaagagaggg atactctcta gtcggaatag acccttttcag actgcttcaa
1081  aacagccaag tgtacagcct aatcagacca aatgagaatc cagcacacaa gagtcaactg
1141  gtgtggatgg catgccattc tgccgcattt gaagatctaa gagtattaag cttcatcaaa
1201  gggacgaagg tgctcccaag agggaagctt tccactagag gagttcaaat tgcttccaat
1261  gaaaatatgg agactatgga atcaagtaca cttgaactga gaagcaggta ctgggccata
1321  aggaccagaa gtggaggaaa caccaatcaa cagagggcat ctgcgggcca aatcagcata
1381  caacctacgt tctcagtaca gagaaatctc ccttttgaca gaacaaccat tatggcagca
1441  ttcaatggga atacagaggg aagaacatct gacatgagga ccgaaatcat aaggatgatg
1501  gaaagtgcaa gaccagaaga tgtgtctttc caggggcggg gagtcttcga gctctcggac
1561  gaaaaggcag cgagcccgat cgtgccttcc tttgacatga gtaatgaagg atcttatttc
1621  ttcggagaca atgcagatga gtacgacaat taa
```

[0260] Purified VR4710 DNA was used to transfect the murine cell line VM92 to determine expression of the eM2-NP fusion protein. Expression of eM2-NP was confirmed with a Western Blot assay. Expression was visualized with a commercially available monoclonal antibody to M2 and with mouse polyclonal antibody to NP. ELISA assay results following 2 injections of pDNA into mice revealed little antibody response to M2, but an average titer of 66,560 for anti-NP antibody.

[0261] VR4750 was created by first reverse transcribing RNA from the mouse-adapted A/Hong Kong/1/68 virus stock using random hexamer to create a cDNA library. Then primers 5' GGGCTAGCGCCGCCACCATGAAGACCATCATTGCT 3' (SEQ ID NO:53) and 5' CCGTCGACTCAAATGCAAATGTTGCA 3' (SEQ ID NO:54) were employed to PCR the HA gene. The gene was inserted into the Invitrogen TOPO-TA vector first, and then sub-cloned into VR10551 using restriction enzymes NheI and SalI. The following is the open reading frame for HA (H3N2) from mouse-adapted A/Hong Kong/68 (from VR4750), referred to herein as SEQ ID NO:55:

```
   1  atgaagacca tcattgcttt gagctacatt ttctgtctgg ctctcggcca agaccttcca
  61  ggaaatgaca acaacacagc aacgctgtgc ctgggacatc atgcggtgcc aaacggaaca
 121  ctagtgaaaa caatcacaga tgatcagatt gaagtgacta atgctactga gctagttcag
 181  agctcctcaa cggggaaaat atgcaacaat cctcatcgaa tccttgatgg aatagactgc
 241  acactgatag atgctctatt gggggaccct cattgtgatg tttttcaaaa tgagacatgg
 301  gacctttttcg ttgaacgcag caaagctttc agcaactgtt acccttatga tgtgccagat
 361  tatgcccccc ttaggtcact agttgcctcg tcaggcactc tggagtttat cactgagggt
 421  ttcacttgga ctggggtcac tcagaatggg ggaagcagtg cttgcaaaag gggacctggt
 481  agcggttttt tcagtagact gaactggttg accaaatcag gaagcacata tccagtgctg
 541  aacgtgacta tgccaaacaa tgacaatttt gacaaactat acatttgggg ggttcaccac
 601  ccgagcacga accaagaaca aaccagcctg tatgttcaag catcagggag agtcacagtc
 661  tctaccagga gaagccagca aactataatc ccgaatatcg agtccagacc ctgggtaagg
 721  ggtctgtcta gtagaataag catctattgg acaatagtta agccgggaga cgtactggta
 781  attaatagta atgggaacct aatcgctcct cggggttatt tcaagatgcg cactgggaaa
 841  agctcaataa tgaggtcaga tgcacctatt gatacctgta tttctgaatg catcactcca
 901  aatggaagca ttcccaatga caagcccttt caaaacgtaa acaaaatcac gtatggagca
 961  tgccccaagt atgttaagca aaacaccctg aagttggcaa cagggatgcg gaatgtacca
1021  gagaaacaaa ctagaggcct attcggcgca atagcaggtt tcatagaaaa tggttgggag
1081  ggaatgatag acggttggta cggtttcagg catcaaaatt ctgagggcac aggacaagca
1141  gcagatctta aaagcactca agcagccatc gaccaaatca atgggaaatt gaacaggata
1201  atcaagaaga cgaacgagaa attccatcaa atcgaaaagg aattctcaga agtagaaggg
1261  agaattcagg acctcgagaa atacgttgaa gacactaaaa tagatctctg gtcttacaat
1321  gcggagcttc ttgtcgctct ggagaatcaa catacaattg acctgactga ctcggaaatg
1381  aacaagctgt ttgaaaaaac aaggaggcaa ctgagggaaa atgctgaaga catgggcaat
1441  ggttgcttca aaatatacca caaatgtgac aacgcttgca tagagtcaat cagaactggg
1501  acttatgacc atgatgtata cagagacgaa gcattaaaca accggtttca gatcaaaggt
1561  gttgaactga agtctggata caaagactgg atcctgtgga tttcctttgc catatcatgc
1621  tttttgcttt gtgttgtttt gctggggttc atcatgtggg cctgccagaa aggcaacatt
1681  aggtgcaaca tttgcatttg a
```

[0262] While VR4750 expression was not clearly detected *in vitro* by Western blot assay, two 100 μg vaccinations of VR4750 have been shown to protect mice from intranasal challenge with mouse-adapted A/Hong Kong/68 virus.

[0263] VR4752 was created by first reverse transcribing RNA from the mouse-adapted A/Puerto Rico/8/34 virus stock using random hexamer to create a cDNA library. Then primers 5' GGGCTAGCGCCGCCACCATGAAGGCAAACCTACTG 3' (SEQ ID NO:56) and 5' CCGTCGACTCAGATGCATATTCTGCA 3' (SEQ ID NO:57) were employed to PCR the HA gene. The gene was then cloned into the TOPO-TA vector first, and then sub-cloned into VR10551 using restriction enzymes NheI and SalI. The following is the open reading frame for HA (H1N1) cloned from mouse-adapted A/Puerto Rico/34 (from VR4752), referred to herein as SEQ ID NO:58:

```
   1  atgaaggcaa acctactggt cctgttatgt gcacttgcag ctgcagatgc agacacaata
  61  tgtataggct accatgcgaa caattcaacc gacactgttg acacagtgct cgagaagaat
 121  gtgacagtga cacactctgt taacctgctc gaagacagcc acaacggaaa actatgtaga
 181  ttaaaaggaa tagccccact acaattgggg aaatgtaaca tcgccggatg gctcttggga
 241  aacccagaat gcgacccact gcttccagtg agatcatggt cctacattgt agaaacacca
 301  aactctgaga atggaatatg ttatccagga gatttcatcg actatgagga gctgagggag
 361  caattgagct cagtgtcatc attcgaaaga ttcgaaatat ttcccaaaga aagctcatgg
 421  cccaaccaca acacaaccaa aggagtaacg gcagcatgct cccatgcggg gaaaagcagt
 481  ttttacagaa atttgctatg gctgacggag aaggagggct catacccaaa gctgaaaaat
 541  tcttatgtga acaagaaagg gaaagaagtc cttgtactgt ggggtattca tcacccgtct
```

```
 601  aacagtaagg atcaacagaa tatctatcag aatgaaaatg cttatgtctc tgtagtgact
 661  tcaaattata acaggagatt taccccggaa atagcagaaa gacccaaagt aagagatcaa
 721  gctgggagga tgaactatta ctggaccttg ctaaaacccg gagacacaat aatatttgag
 781  gcaaatggaa atctaatagc accaaggtat gctttcgcac tgagtagagg ctttgggtcc
 841  ggcatcatca cctcaaacgc atcaatgcat gagtgtaaca cgaagtgtca aacacccctg
 901  ggagctataa acagcagtct ccctttccag aatatacacc cagtcacaat aggagagtgc
 961  ccaaaatacg tcaggagtgc caaattgagg atggttacag gactaaggaa cattccgtcc
1021  attcaatcca gaggtctatt tggagccatt gccggtttta ttgaaggggg atggactgga
1081  atgatagatg gatggtacgg ttatcatcat cagaatgaac agggatcagg ctatgcagcg
1141  gatcaaaaaa gcacacaaaa tgccattaac gggattacaa acaaggtgaa ctctgttatc
1201  gagaaaatga acattcaatt cacagctgtg ggtaaagaat tcaacaaatt agaaaaaagg
1261  atggaaaatt taaataaaaa agttgatgat ggatttctgg acatttggac atataatgca
1321  gaattgttag ttctactgga aaatgaaagg actctggatt tccatgactc aaatgtgaag
1381  aatctgtatg agaaagtaaa aagccaatta aagaataatg ccaaagaaat cggaaatgga
1441  tgttttgagt tctaccacaa gtgtgacaat gaatgcatgg aaagtgtaag aaatgggact
1501  tatgattatc ccaaatattc agaagagtca aagttgaaca gggaaaaggt agatggagtg
1561  aaattggaat caatggggat ctatcagatt ctggcgatct actcaactgt cgccagttca
1621  ctggtgcttt tggtctccct gggggcaatc agtttctgga tgtgttctaa tggatctttg
1681  cagtgcagaa tatgcatctg a
```

[0264] Purified VR4752 DNA was used to transfect the murine cell line VM92 to determine expression of the HA protein. Expression of HA was confirmed with a Western Blot assay. Expression was visualized with a commercially available goat anti-influenza A (H1N1) antibody.

[0265] A direct fusion of the M2 gene to the M1 gene was synthesized based on a codon-optimized sequence derived from methods described in Example 4 using the "universal" optimization strategy. The synthesized gene was received in the pUC119 vector and then sub-cloned into VR10551 as an EcoRI-SalI fragment. The following is the open reading frame for the M2M1 fusion (from VR4755), referred to herein as SEQ ID NO:59:

```
   1  atgagcctgc tgaccgaggt ggagaccccc atcagaaacg agtggggctg cagatgcaac
  61  gacagcagcg acccccctggt ggtggccgcc agcatcatcg gcatcctgca cctgatcctg
 121  tggatcctgg acagactgtt cttcaagtgc atctacagac tgttcaagca cggcctgaag
 181  agaggcccca gcaccgaggg cgtgcccgag agcatgagag aggagtacag aaaggagcag
 241  cagaacgccg tggacgccga cgacagccac ttcgtgagca tcgagctgga gatgtccctg
 301  ctgacagaag tggaaacata cgtgctgagc atcgtgccca gcggcccccct gaaggccgag
 361  atcgcccaga gactggagga cgtgttcgcc ggcaagaaca ccgacctgga ggccctgatg
 421  gagtggctga agaccagacc catcctgagc cccctgacca agggcatcct gggcttcgtg
 481  ttcaccctga ccgtgcccag cgagagaggc ctgcagagaa gaagattcgt gcagaacgcc
 541  ctgaacggca acggcgaccc caacaacatg gaccgggccg tgaagctgta ccggaagctg
 601  aagagagaga tcaccttcca cggcgccaag gagatcgccc tgagctacag cgccggcgcc
 661  ctggccagct gcatgggcct gatctacaac agaatgggcg ccgtgaccac cgaggtggcc
 721  ttcggcctgg tgtgcgccac ctgcgagcag atcgccgaca gccagcacag aagccacaga
 781  cagatggtgg ccaccaccaa ccccctgatc agacacgaga acagaatggt gctggccagc
 841  accaccgcca aggccatgga gcagatggcc ggcagcagcg agcaggccgc cgaggccatg
 901  gagatcgcca gccaggccag acagatggtg caggccatga gagccatcgg cacccacccc
 961  agcagcagcg ccggcctgaa ggacgacctg ctggagaacc tgcagaccta ccagaagaga
1021  atgggcgtgc agatgcagag attcaagtga
```

[0266] Purified VR4755 DNA was used to transfect the murine cell line VM92 to determine expression of the M2M1 fusion protein. Expression of

M2M1 was confirmed with a Western Blot assay. Expression of the M2M1 fusion was visualized with commercially available anti-M1 and anti-M2 monoclonal antibodies.

[0267] The segment 7 RNA of influenza A encodes both the M1 and M2 genes. A consensus amino acid sequence for M1 and M2 was derived according to methods described herein. The consensus sequences for both proteins, however, are identical to the M1 and M2 amino acid sequences derived from the IV strain A/Niigata/137/96, represented herein as SEQ ID NO:77 and SEQ ID NO:78, respectively. Accordingly, the native sequence for segment 7, A/Niigata/137/96, was synthesized and received as an insert in pUC119. The segment 7 insert was sub-cloned into VR10551 as an EcoRI-SalI fragment. The following is the open reading frame for segment 7 (from VR4756), referred to herein as SEQ ID NO:60:

```
   1  atgagccttc taaccgaggt cgaaacgtat gttctctcta tcgttccatc aggccccctc
  61  aaagccgaaa tcgcgcagag acttgaagat gtctttgctg ggaaaaacac agatcttgag
 121  gctctcatgg aatggctaaa gacaagacca atcctgtcac ctctgactaa ggggattttg
 181  gggtttgtgt tcacgctcac cgtgcccagt gagcgaggac tgcagcgtag acgctttgtc
 241  caaaatgccc tcaatgggaa tggggatcca aataacatgg acagagcagt taaactatat
 301  agaaaactta agagggagat tacattccat ggggccaaag aaatagcact cagttattct
 361  gctggtgcac ttgccagttg catgggcctc atatacaaca gaatgggggc tgtaaccact
 421  gaagtggcct ttggcctggt atgtgcaaca tgtgaacaga ttgctgactc ccagcacagg
 481  tctcataggc aaatggtggc aacaaccaat ccattaataa ggcatgagaa cagaatggtt
 541  ttggccagca ctacagctaa ggctatggag caaatggctg gatcaagtga gcaggcagcg
 601  gaggccatgg aaattgctag tcaggccagg caaatggtgc aggcaatgag agccattggg
 661  actcatccta gctccagtgc tggtctaaaa gatgatcttc ttgaaaattt gcagacctat
 721  cagaaacgaa tgggggtgca gatgcaacga ttcaagtgac ccgcttgttg ttgctgcgag
 781  tatcattggg atcttgcact tgatattgtg gattcttgat cgtctttttt tcaaatgcat
 841  ctatcgactc ttcaaacacg gtctgaaaag agggccttct acggaaggag tacctgagtc
 901  tatgagggaa gaatatcgaa aggaacagca gaatgctgtg gatgctgacg acagtcattt
 961  tgtcagcata gagctggagt aa
```

[0268] SEQ ID NO:77 ("consensus" (A/Niigata/137/96) M1):

MSLLTEVETYVLSIVPSGPLKAEIAQRLEDVFAGKNTDLEALMEWLKTRPILSPLTKGI
LGFVFTLTVPSERGLQRRRFVQNALNGNGDPNNMDRAVKLYRKLKREITFHGAKEIA
LSYSAGALASCMGLIYNRMGAVTTEVAFGLVCATCEQIADSQHRSHRQMVATTNPLI

RHENRMVLASTTAKAMEQMAGSSEQAAEAMEIASQARQMVQAMRAIGTHPSSSAG
LKDDLLENLQTYQKRMGVQMQRFK

[0269] SEQ ID NO:78 ("consensus" (A/Niigata/137/96) M2):

MSLLTEVETPIRNEWGCRCNDSSDPLVVAASIIGILHLILWILDRLFFKCIYRLFKHGLK
RGPSTEGVPESMREEYRKEQQNAVDADDSHFVSIELE

[0270] Purified VR4756 DNA was used to transfect the murine cell line VM92 to determine expression of the the proteins encoded by segment 7. Expression of both M1 and M2 was confirmed with a Western blot assay using commercially available anti-M1 and anti-M2 monoclonal antibodies. ELISA assay results following 2 injections of pDNA into mice revealed an average anti-M2 antibody titer of 9,240 versus a 110 average titer for VR4707. An IFNγ ELISPOT assay for M2-specific T cells resulted in an average of 121 SFU/106 cells for VR4756 injected mice versus an average of 61 SFU/106 cells for the VR4707 construct.

[0271] An additional segment 7 sequence is created, VR4763, which contains selectively codon-optimized regions of segment 7. Optimization of the coding regions in segment 7 is selective, because segment 7 contains two overlapping coding regions (*i.e.*, encoding M1 and M2,) and these coding regions are partially in different reading frames. From the AUG encoded by nucleotides 1 to 3 of segment 7, M1 is encoded by bp 1 through 759 of the segment 7 RNA, while M2 is encoded by a spliced messenger RNA which includes nucleotides 1 to 26 of segment 7 spliced to nucleotides 715 to 982 of segment 7. Optimization of the region from 715 to 759 is avoided because the M1 and M2 coding sequences (in different reading frames) overlap in that region. Due to the splicing that occurs to join bp 26 to an alternate frame at bp 715 of the segment 7 sequence, optimization in these splicing regions is also avoided; adjacent regions that arguably could also participate in splicing are likewise avoided. Optimization is done in a manner to insure that no new splicing sites are inadvertently introduced. The areas that are optimized are done so using

"universal" strategy, *e.g.* inserting the most frequently used codon for each amino acid. The following is the nucleotide sequence for codon-optimized segment 7 (from VR4763), referred to herein as SEQ ID NO:61:

```
   1  atgagcctgc tgaccgaggt cgaaacgtat gttctctcta tcgtgcccag cggccccctg
  61  aaggccgaga tcgcccagag actggaggac gtgttcgccg gcaagaacac cgacctggag
 121  gccctgatgg agtggctgaa gaccagaccc atcctgagcc ccctgaccaa gggcatcctg
 181  ggcttcgtgt tcaccctgac cgtgcccagc gagagaggcc tgcagagaag aagattcgtg
 241  cagaacgccc tgaacggcaa cggcgacccc aacaacatgg acagagccgt gaagctgtac
 301  agaaagctga agagagagat caccttccac ggcgccaagg agatcgccct gagctacagc
 361  gccggcgccc tggccagctg catgggcctg atctacaaca gaatgggcgc cgtgaccacc
 421  gaggtggcct tcggcctggt gtgcgccacc tgcgagcaga tcgccgacag ccagcacaga
 481  agccacagac agatggtggc caccaccaac cccctgatca gacacgagaa cagaatggtg
 541  ctggccagca ccaccgccaa ggccatggag cagatggccg gcagcagcga gcaggccgcc
 601  gaggccatgg agatcgccag ccaggccaga cagatggtgc aggccatgag agccatcggc
 661  acccacccca gcagcagcgc cggcctgaaa gatgatcttc ttgaaaattt gcagacctat
 721  cagaaacgaa tgggggtgca gatgcaacga ttcaagtgac cccctggtgg tggccgccag
 781  catcatcggc atcctgcacc tgatcctgtg gatcctggac agactgttct tcaagtgcat
 841  ctacagactg ttcaagcacg gcctgaagag aggccccagc accgagggcg tgcccgagag
 901  catgagagag gagtacagaa aggagcagca gaacgccgtg gacgccgacg acagccactt
 961  cgtgagcatc gagctggagt ga
```

[0272] The codon optimized coding region for M1 extends from nucleotide 1 to nucleotide 759 of SEQ ID NO:61 including the stop codon, and is represented herein as SEQ ID NO:79. The codon-optimized coding region for M2 extends from nucleotide 1 to nucleotide 26 of SEQ ID NO:61 spliced to nucleotide 715 through nucleotide 959 of SEQ ID NO:61, including the stop codon, and is represented herein as SEQ ID NO:80.

[0273] Optimized M1 Coding Region (SEQ ID NO:79):

```
ATGAGCCTGCTGACCGAGGTCGAAACGTATGTTCTCTCTATCGTGCCCAGC
GGCCCCCTGAAGGCCGAGATCGCCCAGAGACTGGAGGACGTGTTCGCCGGC
AAGAACACCGACCTGGAGGCCCTGATGGAGTGGCTGAAGACCAGACCCATC
CTGAGCCCCCTGACCAAGGGCATCCTGGGCTTCGTGTTCACCCTGACCGTG
CCCAGCGAGAGAGGCCTGCAGAGAAGAAGATTCGTGCAGAACGCCCTGAAC
GGCAACGGCGACCCCAACAACATGGACAGAGCCGTGAAGCTGTACAGAAAG
CTGAAGAGAGAGATCACCTTCCACGGCGCCAAGGAGATCGCCCTGAGCTAC
AGCGCCGGCGCCCTGGCCAGCTGCATGGGCCTGATCTACAACAGAATGGGC
```

GCCGTGACCACCGAGGTGGCCTTCGGCCTGGTGTGCGCCACCTGCGAGCAG

ATCGCCGACAGCCAGCACAGAAGCCACAGACAGATGGTGGCCACCACCAAC

CCCCTGATCAGACACGAGAACAGAATGGTGCTGGCCAGCACCACCGCCAAG

GCCATGGAGCAGATGGCCGGCAGCAGCGAGCAGGCCGCCGAGGCCATGGAG

ATCGCCAGCCAGGCCAGACAGATGGTGCAGGCCATGAGAGCCATCGGCACC

CACCCCAGCAGCAGCGCCGGCCTGAAAGATGATCTTCTTGAAAATTTGCAG

ACCTATCAGAAACGAATGGGGGTGCAGATGCAACGATTCAAGTGA

[0274] Optimized M2 Coding Region (SEQ ID NO:80):

ATGAGCCTGCTGACCGAGGTCGAAACACCTATCAGAAACGAATGGGGGTGC

AGATGCAACGATTCAAGTGACCCCCTGGTGGTGGCCGCCAGCATCATCGGC

ATCCTGCACCTGATCCTGTGGATCCTGGACAGACTGTTCTTCAAGTGCATC

TACAGACTGTTCAAGCACGGCCTGAAGAGAGGCCCCAGCACCGAGGGCGTG

CCCGAGAGCATGAGAGAGGAGTACAGAAAGGAGCAGCAGAACGCCGTGGAC

GCCGACGACAGCCACTTCGTGAGCATCGAGCTGGAGTGA

[0275] The eM2-NP fusion was codon-optimized, inserted in pUC119 and sub-cloned into VR10551 as an EcoRI-SalI fragment. The following is the open reading frame for eM2-NP: codon-optimized by Contract (from VR4757), referred to herein as SEQ ID NO:62:

```
   1  atgagcttgc tcactgaagt cgagacacca atcagaaacg aatggggatg tagatgcaac
  61  gatagctcag acatggcctc ccagggaacc aaaagaagct atgaacagat ggagactgac
 121  ggagagagac agaacgccac agagatcaga gctagtgtag gaaagatgat agacggtatc
 181  gggcgatttt acattcaaat gtgtacggaa ttgaaactca gcgactatga aggcagactt
 241  atccagaact cactcacaat tgagcgcatg gtactcagtg catttgatga aagaaggaat
 301  aggtacctcg aagaacaccc cagcgccggc aaagatccca agaagactgg cggcccaatt
 361  tacagaagag tggacggtaa gtggatgaga gagctggtat tgtacgataa agaagaaatt
 421  agaagaatct ggaggcaagc aaacaatgga gaggatgcta cagctggcct gacccacatg
 481  atgatttggc atagtaacct gaatgatacc acctaccagc ggacaagggc tctcgttcga
 541  accgggatgg atccccgcat gtgctcattg atgcagggta gtacactccc gaggaggtca
 601  ggcgcggccg gtgcagccgt gaaaggaatc ggcactatgg taatggaatt gataagaatg
 661  attaaaaggg ggattaatga caggaacttt tggagaggag aaaatggacg caaaacaagg
 721  agtgcgtatg aacggatgtg caatattttg aaaggaaaat tccaaactgc agcacagcgc
 781  gccatgatgg atcaggtacg agaaagtcgc aacccaggta atgctgaaat agaggacctt
 841  atatttctcg cccggagtgc tctcatactt agaggaagcg tggcccataa aagttgtctc
 901  cccgcatgcg tatacggtcc cgctgtgtct tccggatacg attttgaaaa agagggatat
 961  tcattggtgg gaatcgaccc ttttaagctg cttcagaact cacaggttta cagtttgatt
1021  agaccaaacg agaacccagc ccacaaatca caactcgtgt ggatggcatg ccactctgcc
1081  gctttcgaag atctgagact gctctcattt attagaggca ctaaagtgag cccgagggga
1141  aaactgagca cacgaggagt acagatagca tctaacgaaa atatggataa tatgggatct
1201  agcacactcg aattgaggtc acgatactgg gctattagaa cacggagcgg agggaacacc
1261  aaccagcaga gagcatccgc cggtcagata agcgttcagc ctacattttc agtacaacga
1321  aacctgccat ttgaaaagag tacagtgatg gccgcattta ctggcaacac cgagggacga
1381  acaagcgaca tgagagcaga gattattaga atgatggaag gagctaaacc agaggaggtt
1441  tcatttagag gaaggggagt cttcgaattg tccgatgaga aagccacaaa tcccatagta
1501  cctagcttcg acatgtccaa cgaaggctct tacttttttg gtgacaatgc cgaagagtac
1561  gacaattga
```

[0276] Purified VR4757 DNA was used to transfect the murine cell line VM92 to determine expression of the eM2-NP fusion protein. Expression of eM2-NP was confirmed with a Western Blot assay. Expression was visualized with a commercially available monoclonal antibody to M2 and with mouse polyclonal antibody to NP. *In vivo* antibody response to NP was detected by ELISA with an average titer of 51,200.

[0277] The eM2-NP fusion gene in VR4758 was codon-optimized and synthesized. The gene was inserted into pUC119 and sub-cloned into VR10551 as an EcoRI-SalI fragment. The following is the open reading frame for eM2-NP: codon-optimized by Applicants (from VR4758), referred to herein as SEQ ID NO:63:

```
   1  atgagcctgc tgaccgaggt ggagaccccc atcagaaacg agtggggctg cagatgcaac
  61  gacagcagcg acatggccag ccagggcacc aagagaagct acgagcagat ggagaccgac
 121  ggcgagagac agaacgccac cgagatcaga gccagcgtgg gcaagatgat cgacggcatc
 181  ggcagattct acatccagat gtgcaccgag ctgaagctga gcgactacga gggcagactg
 241  atccagaaca gcctgaccat cgagagaatg gtgctgagcg ccttcgacga gagaagaaac
 301  agatacctgg aggagcaccc cagcgccggc aaggacccca agaagaccgg cggccccatc
 361  tacagaagag tggacggcaa gtggatgaga gagctggtgc tgtacgacaa ggaggagatc
 421  agaagaatct ggagacaggc caacaacggc gaggacgcca ccgccggcct gacccacatg
 481  atgatctggc acagcaacct gaacgacacc acctaccaga gaaccagagc cctggtgcgg
 541  accggcatgg accccagaat gtgcagcctg atgcagggca gcaccctgcc cagaagaagc
 601  ggcgccgccg gcgccgccgt gaagggcatc ggcaccatgg tgatggagct gatcagaatg
 661  atcaagagag gcatcaacga cagaaacttc tggagaggcg agaacggcag aaagaccaga
 721  agcgcctacg agagaatgtg caacatcctg aagggcaagt tccagaccgc cgcccagaga
 781  gccatgatgg accaggtccg ggagagcaga aaccccggca acgccgagat cgaggacctg
 841  atcttcctgg ccagaagcgc cctgatcctg agaggcagcg tggcccacaa gagctgcctg
 901  cccgcctgcg tgtacggccc cgccgtgagc agcggctacg acttcgagaa ggagggctac
 961  agcctggtgg gcatcgaccc cttcaagctg ctgcagaaca gccaggtgta cagcctgatc
1021  agacccaacg agaaccccgc ccacaagagc cagctggtgt ggatggcctg ccacagcgcc
1081  gccttcgagg acctgagact gctgagcttc atcagaggca ccaaggtgtc ccccagaggc
1141  aagctgagca ccagaggcgt gcagatcgcc agcaacgaga acatggacaa catgggcagc
1201  agcaccctgg agctgagaag cagatactgg gccatcagaa ccagaagcgg cggcaacacc
1261  aaccagcaga gagccagcgc cggccagatc agcgtgcagc ccaccttcag cgtgcagaga
1321  aacctgccct tcgagaagag caccgtgatg gccgccttca ccggcaacac cgagggcaga
1381  accagcgaca tgagagccga gatcatcaga atgatggagg gcgccaagcc cgaggaggtg
1441  tccttcagag gcagaggcgt gttcgagctg agcgacgaga aggccaccaa ccccatcgtg
1501  cctagcttcg acatgagcaa cgagggcagc tacttcttcg gcgacaacgc cgaggagtac
1561  gacaactga
```

[0278] Purified VR4758 DNA was used to transfect the murine cell line VM92 to determine expression of the eM2-NP protein. Expression of eM2-NP was confirmed with a Western Blot assay. Expression was visualized with a commercially available monoclonal antibody to M2 and with mouse polyclonal antibody to NP. *In vivo* antibody response to NP was detected by ELISA with an average titer of 48,640.

[0279] The M2 gene was PCR-amplified from VR4755 using the primers 5'-GCCGAATTCGCCACCATGAGCCTGCTGACC-3' (SEQ ID NO:64) and 5'-GCCGTCGACTGATCACTCCAGCTCGATGCTCAC-3' (SEQ ID NO:65) and sub-cloned into VR10551 as an EcoRI-SalI fragment. The following is the open reading frame for M2 (from VR4759), referred to herein as SEQ ID NO:66:

```
  1  atgagcctgc tgaccgaggt ggagacccca atcagaaacg agtggggctg cagatgcaac
 61  gacagcagcg acccccctggt ggtggccgcc agcatcatcg gcatcctgca cctgatcctg
121  tggatcctgg acagactgtt cttcaagtgc atctacagac tgttcaagca cggcctgaag
181  agaggcccca gcaccgaggg cgtgcccgag agcatgagag aggagtacag aaaggagcag
241   cagaacgccg tggacgccga cgacagccac ttcgtgagca tcgagctgga gtga
```

[0280] Purified VR4759 DNA was used to transfect the murine cell line VM92 to determine expression of the M2 protein. Expression of M2 was confirmed with a Western Blot assay. Expression was visualized with a commercially available anti-M2 monoclonal antibody.

[0281] The M1 gene was PCR-amplified from VR4755 using the primers 5'-GCCGAATTCGCCACCATGTCCCTGCTGACAGAAGTG-3' (SEQ ID NO:67) and 5'-GCCGTCGACTGATCACTTGAATCTCTGCATC-3' (SEQ ID NO:68) and sub-cloned into VR10551 as an EcoRI-SalI fragment. The following is the open reading frame for M1 (from VR4760), referred to herein as SEQ ID NO:69:

```
  1  atgtccctgc tgacagaagt ggaaacatac gtgctgagca tcgtgcccag cggccccctg
 61  aaggccgaga tcgcccagag actggaggac gtgttcgccg gcaagaacac cgacctggag
121  gccctgatgg agtggctgaa gaccagaccc atcctgagcc ccctgaccaa gggcatcctg
181  ggcttcgtgt tcaccctgac cgtgcccagc gagagaggcc tgcagagaag aagattcgtg
241  cagaacgccc tgaacggcaa cggcgacccc aacaacatgg accgggccgt gaagctgtac
301  cggaagctga agagagagat caccttccac ggcgccaagg agatcgccct gagctacagc
361  gccggcgccc tggccagctg catgggcctg atctacaaca gaatgggcgc cgtgaccacc
421  gaggtggcct tcggcctggt gtgcgccacc tgcgagcaga tcgccgacag ccagcacaga
481  agccacagac agatggtggc caccaccaac cccctgatca gacacgagaa cagaatggtg
541  ctggccagca ccaccgccaa ggccatggag cagatggccg gcagcagcga gcaggccgcc
601  gaggccatgg agatcgccag ccaggccaga cagatggtgc aggccatgag agccatcggc
661  acccacccca gcagcagcgc cggcctgaag gacgacctgc tggagaacct gcagacctac
721  cagaagagaa tgggcgtgca gatgcagaga ttcaagtga
```

[0282] Purified VR4760 DNA was used to transfect the murine cell line VM92 to determine expression of the M1 protein. Expression of M1 was confirmed with a Western Blot assay. Expression was visualized with a commercially available anti-M1 monoclonal antibody.

[0283] The NP gene was PCR-amplified from VR4757 using primers 5'-GCCGAATTCGCCACCATGGCCTCCCAGGGAACCAAAAG-3' (SEQ ID NO:70) and 5'-GCCGTCGACTGATCAATTGTCGTACTCTTC-3' (SEQ ID NO:71) and sub-cloned into VR10551 as an EcoRI-SalI fragment. The following is the open reading frame for NP: codon-optimized by Contract (from VR4761), referred to herein as SEQ ID NO:72:

```
   1  atg gcc tcc cag gga acc aaa aga agc tat gaa cag atg gag act gac
  49  gga gag aga cag aac gcc aca gag atc aga gct agt gta gga aag atg
  97  ata gac ggt atc ggg cga ttt tac att caa atg tgt acg gaa ttg aaa
 145  ctc agc gac tat gaa ggc aga ctt atc cag aac tca ctc aca att gag
 193  cgc atg gta ctc agt gca ttt gat gaa aga agg aat agg tac ctc gaa
 241  gaa cac ccc agc gcc ggc aaa gat ccc aag aag act ggc ggc cca att
 289  tac aga aga gtg gac ggt aag tgg atg aga gag ctg gta ttg tac gat
 337  aaa gaa gaa att aga aga atc tgg agg caa gca aac aat gga gag gat
 385  gct aca gct ggc ctg acc cac atg atg att tgg cat agt aac ctg aat
 433  gat acc acc tac cag cgg aca agg gct ctc gtt cga acc ggg atg gat
 481  ccc cgc atg tgc tca ttg atg cag ggt agt aca ctc ccg agg agg tca
 529  ggc gcg gcc ggt gca gcc gtg aaa gga atc ggc act atg gta atg gaa
 577  ttg ata aga atg att aaa agg ggg att aat gac agg aac ttt tgg aga
 625  gga gaa aat gga cgc aaa aca agg agt gcg tat gaa cgg atg tgc aat
 673  att ttg aaa gga aaa ttc caa act gca gca cag cgc gcc atg atg gat
 721  cag gta cga gaa agt cgc aac cca ggt aat gct gaa ata gag gac ctt
 769  ata ttt ctc gcc cgg agt gct ctc ata ctt aga gga agc gtg gcc cat
 817  aaa agt tgt ctc ccc gca tgc gta tac ggt ccc gct gtg tct tcc gga
 865  tac gat ttt gaa aaa gag gga tat tca ttg gtg gga atc gac cct ttt
 913  aag ctg ctt cag aac tca cag gtt tac agt ttg att aga cca aac gag
 961  aac cca gcc cac aaa tca caa ctc gtg tgg atg gca tgc cac tct gcc
1009  gct ttc gaa gat ctg aga ctg ctc tca ttt att aga ggc act aaa gtg
1057  agc ccg agg gga aaa ctg agc aca cga gga gta cag ata gca tct aac
1105  gaa aat atg gat aat atg gga tct agc aca ctc gaa ttg agg tca cga
1153  tac tgg gct att aga aca cgg agc gga ggg aac acc aac cag cag aga
1201  gca tcc gcc ggt cag ata agc gtt cag cct aca ttt tca gta caa cga
1249  aac ctg cca ttt gaa aag agt aca gtg atg gcc gca ttt act ggc aac
1297  acc gag gga cga aca agc gac atg aga gca gag att att aga atg atg
1345  gaa gga gct aaa cca gag gag gtt tca ttt aga gga agg gga gtc ttc
1393  gaa ttg tcc gat gag aaa gcc aca aat ccc ata gta cct agc ttc gac
1441  atg tcc aac gaa ggc tct tac ttt ttt ggt gac aat gcc gaa gag tac
1489  gac aat tga
```

[0284] Purified VR4761 DNA was used to transfect the murine cell line VM92 to determine expression of the NP protein. Expression of NP was confirmed with a Western Blot assay. Expression was visualized with a mouse polyclonal anti-NP antibody. *In vitro* expression of VR4761 was significantly higher than VR4700 and comparable to VR4762.

[0285] The NP gene was PCR-amplified from VR4758 using primers 5'-GCCGAATTCGCCACCATGGCCAGCCAGGGCACCAAG-3' (SEQ ID NO:73) and 5'-GCCGTCGACTGATCAGTTGTCGTACTCC-3' (SEQ ID NO:74) and sub-cloned into VR10551 as an EcoRI-SalI fragment. The

following is the open reading frame for NP: codon-optimized by Applicants (from VR4762), referred to herein as SEQ ID NO:75:

```
   1  atg gcc agc cag ggc acc aag aga agc tac gag cag atg gag acc gac
  49  ggc gag aga cag aac gcc acc gag atc aga gcc agc gtg ggc aag atg
  97  atc gac ggc atc ggc aga ttc tac atc cag atg tgc acc gag ctg aag
 145  ctg agc gac tac gag ggc aga ctg atc cag aac agc ctg acc atc gag
 193  aga atg gtg ctg agc gcc ttc gac gag aga aga aac aga tac ctg gag
 241  gag cac ccc agc gcc ggc aag gac ccc aag aag acc ggc ggc ccc atc
 289  tac aga aga gtg gac ggc aag tgg atg aga gag ctg gtg ctg tac gac
 337  aag gag gag atc aga aga atc tgg aga cag gcc aac aac ggc gag gac
 385  gcc acc gcc ggc ctg acc cac atg atg atc tgg cac agc aac ctg aac
 433  gac acc acc tac cag aga acc aga gcc ctg gtg cgg acc ggc atg gac
 481  ccc aga atg tgc agc ctg atg cag ggc agc acc ctg ccc aga aga agc
 529  ggc gcc gcc ggc gcc gcc gtg aag ggc atc ggc acc atg gtg atg gag
 577  ctg atc aga atg atc aag aga ggc atc aac gac aga aac ttc tgg aga
 625  ggc gag aac ggc aga aag acc aga agc gcc tac gag aga atg tgc aac
 673  atc ctg aag ggc aag ttc cag acc gcc gcc cag aga gcc atg atg gac
 721  cag gtc cgg gag agc aga aac ccc ggc aac gcc gag atc gag gac ctg
 769  atc ttc ctg gcc aga agc gcc ctg atc ctg aga ggc agc gtg gcc cac
 817  aag agc tgc ctg ccc gcc tgc gtg tac ggc ccc gcc gtg agc agc ggc
 865  tac gac ttc gag aag gag ggc tac agc ctg gtg ggc atc gac ccc ttc
 913  aag ctg ctg cag aac agc cag gtg tac agc ctg atc aga ccc aac gag
 961  aac ccc gcc cac aag agc cag ctg gtg tgg atg gcc tgc cac agc gcc
1009  gcc ttc gag gac ctg aga ctg ctg agc ttc atc aga ggc acc aag gtg
1057  tcc ccc aga ggc aag ctg agc acc aga ggc gtg cag atc gcc agc aac
1105  gag aac atg gac aac atg ggc agc agc acc ctg gag ctg aga agc aga
1153  tac tgg gcc atc aga acc aga agc ggc ggc aac acc aac cag cag aga
1201  gcc agc gcc ggc cag atc agc gtg cag ccc acc ttc agc gtg cag aga
1249  aac ctg ccc ttc gag aag agc acc gtg atg gcc gcc ttc acc ggc aac
1297  acc gag ggc aga acc agc gac atg aga gcc gag atc atc aga atg atg
1345  gag ggc gcc aag ccc gag gag gtg tcc ttc aga ggc aga ggc gtg ttc
1393  gag ctg agc gac gag aag gcc acc aac ccc atc gtg cct agc ttc gac
1441  atg agc aac gag ggc agc tac ttc ttc ggc gac aac gcc gag gag tac
1489  gac aac tga
```

[0286] Purified VR4762 DNA was used to transfect the murine cell line VM92 to determine expression of the NP protein. Expression of NP was confirmed with a Western Blot assay. Expression was visualized with a mouse polyclonal anti-NP antibody. *In vitro* expression of VR4762 was significantly higher than VR4700 and comparable to VR4761.

[0287] In addition to plasmids encoding single IV proteins, single plasmids which contain two or more IV coding regions are constructed according to standard methods. For example, a polycistronic construct, where two or more IV coding regions are transcribed as a single transcript in eukaryotic cells may be constructed by separating the various coding regions with IRES sequences. Alternatively, two or more coding regions may be inserted into a single plasmid, each with their own promoter sequence.

EXAMPLE 2

Preparation of recombinant NP DNA and protein

[0288] Recombinant NP DNA and protein may be prepared using the following procedure. Eukaryotic cells may be used to express the NP protein from a transfected expression plasmid. Alternatively, a baculovirus system can be used wherein insect cells such as, but not limited to, Sf9, Sf21, or D.Mel-2 cells are infected with a recombinant baculovirus which can expresses the NP protein. Cells which have been infected with recombinant baculoviruses, or contain expression plasmids, encoding recombinant NP are collected by knocking and scraping cells off the bottom of the flask in which they are grown. Cells infected for 24 or 48 hours are less easy to detach from flask and may lyse, thus care must be taken with their removal. The flask containing the cells is then rinsed with PBS and the cells are transfered to 250 ml conical tubes. The tubes are spun at 1000 rpm in J-6 centrifuge (300 x g) for about 5-10 minutes. The cell pellets are washed two times with PBS and then resuspended in about 10-20 ml of PBS in order to count. The cells are finally resuspended at a concentration of about $2x10^7$ cells/ml in RSB (10mM Tris pH=7.5, 1.5mM $MgCl_2$, 10mM KCl).

[0289] Approximately 10^6 cells are used per lane of a standard SDS-PAGE mini-protein gel which is equivalent to the whole cell fraction for gel analysis purposes. 10% NP40 is added to the cells for a final concentration of 0.5%. The cell-NP40 mixture is vortexed and placed on ice for 10 minutes, vortexing occasionally. After ice incubation, the cells are spun at 1500 rpm in a J-6 centrifuge (600 x 1) for 10 minutes. The supernantant is removed which is the cytoplasmic fration. The remaining pellet, containing the nuclei, is washed two times with buffer C (20 mM HEPES pH = 7.9, 1.5 mM $MgCl_2$, 0.2 mM EDTA, 0.5 mM PMSF, 0.5 mM DTT) to remove cytoplasmic proteins. The nuclei are resuspended in buffer C to $5x10^7$ nuclei/ml. The nuclei are vortexed vigorously to break up particles and an aliquot is removed for the mini-protein gel which is the nuclei fraction.

[0290] To the remaining nuclei a quarter of the volume of 5M NaCl is added and the mixture is sonicated for 5 minutes at a maximum output in a bath-type sonicator at 4°C, in 1-2 minute bursts, resting 30 seconds between bursts. The sonicated mixture is stirred at 4°C, then spun at 12000 x g for 10 minutes. A sample is removed for the protein mini-gel equivalent to approximately 10^6 nuclei. The sample for the gel is centrifuged and the supernatant is the nuclear extract and the pellet is the nuclear pellet for gel analysis.

[0291] For gel analysis, a small amount (about 10^6 nuclear equivalents) of the nuclear pellet is resuspended directly in gel sample buffer and run with equivalent amounts of whole cells, cytoplasm, nuclei, nuclear extract and nuclear pellet. The above method gives relatively crude NP. To recover NP of a higher purity, 2.1M NaCl can be added to the nuclear pellet instead of 5M NaCl. This will bring the salt content to 0.42M NaCl. The supernatant will then contain about 60-70% of the total NP plus nuclear proteins. The resulting pellet is then extracted with 1M NaCl and centrifuged as above. The supernatant will contain NP at more than 95% purity.

EXAMPLE 3

Consensus Amino Acid Sequences of NP, M1 and M2

[0292] By analyzing amino acid sequences from influenza strains sequenced since 1990, consensus amino acid sequences were derived for influenza NP, M1 and M2 antigens.

NP Consensus Amino Acid Sequence

[0293] The method by which amino acid sequences for influenza NP (strain A) was chosen is as follows. The http://www.flu.lanl.gov database containing influenza sequences for each segment was searched for influenza A strains, human, NP, amino acids. Results gave about 400 sequences, the majority of which were only partial sequences. The sequences were subsequently narrowed down to 85 approximately full length sequences. If different

passages of the same strain were found, the earliest passage was chosen. The sequences were further narrowed down to 28 full length NP sequences isolated from 1990 to 2000 (no full-length sequences from 2001-2003). Five additional sequences were eliminated which were identical to another sequence isolated from the same year based on the assumption that sequences with the same year and identical amino acid sequences were likely to be the same virus strain (in order to avoid double weighting). If there were sequences from the same year with different amino acid sequences, both sequences were kept.

[0294] Sequences were aligned to the A/PR/8/34 strain in decending order by most recent, and the consensus sequence was determined by utilizing the amino acid with the majority (Figure 12). There are 32 amino acid changes between the A/PR/8/34 and the consensus sequence, and all amino acid changes are also present in the two year 2000 NP sequences. For one additional amino acid (aa 275) 15/23 have changed from E (in A/PR/34) to G/D or V (7G, 7D, 1V). Since the two 2000 strains both contain a G at this position, G was chosen. The changes total 33 amino acids, which is about a 7% difference from the A/PR/8/34 strain.

[0295] The dominant Balb/c epitope TYQRTRALV is still maintained in the new consensus; changes to other theoretical human epitopes have not been determined as yet.

[0296] The A strains used in the last 8 years of flu vaccines (USA) are as follows (no full length sequences are available on any of the these strains' NP genes):

a. 2002-2003 A/Moscow/10/99, A/New Caledonia/20/99
b. 2001-2002 A/Moscow/10/99, A/New Caledonia/20/99
c. 2000-2001 A/Panama/2007/99, A/New Caledonia/20/99
d. 1999-2000 A/Sydney/05/97, A/Beijing/262/95
e. 1998-1999 A/Sydney/05/97, A/Beijing/262/95
f. 1997-1998 A/Nanchang/933/95, A/Johannesburg/82/96
g. 1996-1997 A/Nanchang/933/95, A/Texas/36/91
h. 1995-1996 A/Johannesburg/33/94, A/Texas/36/91

[0297] The final NP consensus amino acid sequence derived using this method is referred to herein as SEQ ID NO:76:

```
  1  masqgtkrsy eqmetdgerq nateirasvg kmidgigrfy iqmctelkls dyegrliqns
 61  ltiermvlsa fderrnryle ehpsagkdpk ktggpiyrrv dgkwmrelvl ydkeeirriw
121  rqanngedat aglthmmiwh snlndttyqr tralvrtgmd prmcslmqgs tlprrsgaag
181  aavkgigtmv melirmikrg indrnfwrge ngrktrsaye rmcnilkgkf qtaaqrammd
241  qvresrnpgn aeiedlifla rsalilrgsv ahksclpacv ygpavssgyd fekegyslvg
301  idpfkllqns qvyslirpne npahksqlvw machsaafed lrllsfirgt kvsprgklst
361  rgvqiasnen mdnmgsstle lrsrywairt rsggntnqqr asagqisvqp tfsvqrnlpf
421  ekstvmaaft gntegrtsdm raeiirmmeg akpeevsfrg rgvfelsdek atnpivpsfd
481  msnegsyffg dnaeeydn
```

M1 and M2 Consensus Amino Acid Sequences

[0298] Consensus sequences for M1 and M2 were determined in a similar fashion, as follows. The search parameters on the http://www.flu.lanl.gov/ website were: influenza A strains, human, segment 7, nucleotide (both M1 and M2 are derived from segment 7). Full-length sequences from 1990-1999 (no 2000+ sequences were available) were chosen. For sequences with the same year and city, only the earliest passage was used. For entries for the same year, sequences were eliminated that were identical to another sequence isolated from the same year (even if different city). Twenty one sequences, full-length for both M1 and M2 from 1993-1999, were compared. At each position, the amino acid with the simple majority was used.

[0299] The M1 amino acid consensus sequence is referred to herein as SEQ ID NO:77:

```
  1  mslltevety vlsivpsgpl kaeiaqrled vfagkntdle almewlktrp ilspltkgil
 61  gfvftltvps erglqrrrfv qnalngngdp nnmdravkly rklkreitfh gakeialsys
121  agalascmgl iynrmgavtt evafglvcat ceqiadsqhr shrqmvattn plirhenrmv
181  lasttakame qmagsseqaa eameiasqar qmvqamraig thpsssaglk ddllenlqty
241  qkrmgvqmqr fk
```

[0300] The M2 amino acid consensus sequence is referred to herein as SEQ ID NO:78:

```
  1  mslltevetp irnewgcrcn dssdplvvaa siigilhlil wildrlffkc iyrlfkhglk
 61  rgpstegvpe smreeyrkeq qnavdaddsh fvsiele
```

EXAMPLE 4

Codon Optimization Algorithm

[0301] The following is an outline of the algorithm used to derive human codon-optimized sequences of influenza antigens.

Back Translation

[0302] Starting with the amino acid sequence, one can either (a) manually backtranslate using the human codon usage table from http://www.kazusa.or.jp/codon/

[0303] Homo sapiens [gbpri]: 55194 CDS's (24298072 codons)

[0304] Fields: [triplet] [frequency: per thousand] ([number])

UUU 17.1(415589) UCU 14.7(357770) UAU 12.1(294182) UGU 10.0(243198)
UUC 20.6(500964) UCC 17.6(427664) UAC 15.5(377811) UGC 12.2(297010)
UUA 7.5(182466) UCA 12.0(291788) UAA 0.7(17545) UGA 1.5(36163)
UUG 12.6(306793) UCG 4.4(107809) UAG 0.6(13416) UGG 12.7(309683)

CUU 13.0(315804) CCU 17.3(419521) CAU 10.5(255135) CGU 4.6(112673)
CUC 19.8(480790) CCC 20.1(489224) CAC 15.0(364828) CGC 10.7(259950)
CUA 7.8(189383) CCA 16.7(405320) CAA 12.0(292745) CGA 6.3(152905)
CUG 39.8(967277) CCG 6.9(168542) CAG 34.1(827754) CGG 11.6(281493)

AUU 16.1(390571) ACU 13.0(315736) AAU 16.7(404867) AGU 11.9(289294)
AUC 21.6(525478) ACC 19.4(471273) AAC 19.5(473208) AGC 19.3(467869)
AUA 7.7(186138) ACA 15.1(366753) AAA 24.1(585243) AGA 11.5(278843)
AUG 22.2(538917) ACG 6.1(148277) AAG 32.2(781752) AGG 11.4(277693)

GUU 11.0(266493) GCU 18.6(451517) GAU 21.9(533009) GGU 10.8(261467)
GUC 14.6(354537) GCC 28.4(690382) GAC 25.6(621290) GGC 22.5(547729)
GUA 7.2(174572) GCA 16.1(390964) GAA 29.0(703852) GGA 16.4(397574)
GUG 28.4(690428) GCG 7.5(181803) GAG 39.9(970417) GGG 16.3(396931)

* Coding GC 52.45% 1st letter GC 56.04% 2nd letter GC 42.37% 3rd letter GC 58.93%
(Table as of November 6, 2003)

[0305] Or (b) log on to www.syntheticgenes.com and use the backtranslation tool, as follows:

[0306] (1) Under Protein tab, paste amino acid sequence;

[0307] (2) Under download codon usage tab, highlight homo sapiens and then download CUT.

UUU 17.1(415589) UCU 14.7(357770) UAU 12.1(294182) UGU 10.0(243198)
UUC 20.6(500964) UCC 17.6(427664) UAC 15.5(377811) UGC 12.2(297010)
UUA 7.5(182466) UCA 12.0(291788) UAA 0.7(17545) UGA 1.5(36163)
UUG 12.6(306793) UCG 4.4(107809) UAG 0.6(13416) UGG 12.7(309683)

CUU 13.0(315804) CCU 17.3(419521) CAU 10.5(255135) CGU 4.6(112673)
CUC 19.8(480790) CCC 20.1(489224) CAC 15.0(364828) CGC 10.7(259950)
CUA 7.8(189383) CCA 16.7(405320) CAA 12.0(292745) CGA 6.3(152905)
CUG 39.8(967277) CCG 6.9(168542) CAG 34.1(827754) CGG 11.6(281493)

AUU 16.1(390571) ACU 13.0(315736) AAU 16.7(404867) AGU 11.9(289294)
AUC 21.6(525478) ACC 19.4(471273) AAC 19.5(473208) AGC 19.3(467869)
AUA 7.7(186138) ACA 15.1(366753) AAA 24.1(585243) AGA 11.5(278843)
AUG 22.2(538917) ACG 6.1(148277) AAG 32.2(781752) AGG 11.4(277693)

GUU 11.0(266493) GCU 18.6(451517) GAU 21.9(533009) GGU 10.8(261467)
GUC 14.6(354537) GCC 28.4(690382) GAC 25.6(621290) GGC 22.5(547729)
GUA 7.2(174572) GCA 16.1(390964) GAA 29.0(703852) GGA 16.4(397574)
GUG 28.4(690428) GCG 7.5(181803) GAG 39.9(970417) GGG 16.3(396931)

(Table as of November 6, 2003)

[0308] (3) Hit Apply button.

[0309] (4) Under Optimize TAB, open General TAB.

[0310] (5) Check use only most frequent codon box.

[0311] (6) Hit Apply button.

[0312] (7) Under Optimize TAB, open Motif TAB.

[0313] (8) Load desired cloning restriction sites into bad motifs; load any undesirable sequences, such as Pribnow Box sequences (TATAA), Chi sequences (GCTGGCGG), and restriction sites into bad motifs.

[0314] (9) Under Output TAB, click on Start box. Output will include sequence, motif search results (under Report TAB), and codon usage report.

[0315] The program did not always use the most frequent codon for amino acids such as cysteine proline, and arginine. To change this, go back to the Edit CUT TAB and manually drag the rainbow colored bar to 100% for the desired codon. Then re-do start under the Output TAB.

[0316] The use of CGG for arginine can lead to very high GC content, so AGA can be used for arginine as an alternative. The difference in codon usage is 11.6 per thousand for CGG vs. 11.5 per thousand for AGA.

Splice donor and acceptor site search

[0317] (1) Log on to Berkeley Drosophila Genome Project Website at http://www.fruitfly.org/seq_tools/splice.html\

[0318] (2) Check boxes for Human or other and both splice sites.

[0319] (3) Select minimum scores for 5' and 3' splice sites between 0 and 1.

Used the default setting at 0.4 where:

Default minimum score is 0.4, where:

	% splice sites recognized	% false positives
Human 5' Splice sites	93.2%	5.2%
Human 3' Splice sites	83.8%	3.1%

[0320] (4) Paste in sequence.

[0321] (5) Submit.

[0322] (6) Based on predicted donors or acceptors, change the individual codons until the sites are no longer predicted.

Add in 5' and 3' sequences.

[0323] On the 5' end of the gene sequence, the restriction enzyme site and Kozak sequence (gccacc) was added before ATG. On 3' end of the sequence, tca was added following the stop codon (tga on opposite strand) and then a restriction enzyme site. The GC content and Open Reading Frames were then checked in SEC Central.

EXAMPLE 5

Preparation of Vaccine Formulations

[0324] Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, HA, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives

either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, are formulated with the poloxamer CRL 1005 and BAK (Benzalkonium chloride 50% solution, available from Ruger Chemical Co. Inc.) by the following methods. Specific final concentrations of each component of the formulae are described in the following methods, but for any of these methods, the concentrations of each component may be varied by basic stoichiometric calculations known by those of ordinary skill in the art to make a final solution having the desired concentrations.

[0325] For example, the concentration of CRL 1005 is adjusted depending on, for example, transfection efficiency, expression efficiency, or immunogenicity, to achieve a final concentration of between about 1 mg/ml to about 75 mg/ml, for example, about 1 mg/ml, about 2 mg/ml, about 3 mg/ml, about 4 mg/ml, about 5 mg/ml, about 6.5 mg/ml, about 7 mg/ml, about 7.5 mg/ml, about 8 mg/ml, about 9 mg/ml, about 10 mg/ml, about 15 mg/ml, about 20 mg/ml, about 25 mg/ml, about 30 mg/ml, about 35 mg/ml, about 40 mg/ml, about 45 mg/ml, about 50 mg/ml, about 55 mg/ml, about 60 mg/ml, about 65 mg/ml, about 70 mg/ml, or about 75 mg/ml of CRL 1005.

[0326] Similarly the concentration of DNA is adjusted depending on many factors, including the amount of a formulation to be delivered, the age and weight of the subject, the delivery method and route and the immunogenicity of the antigen being delivered. In general, formulations of the present invention are adjusted to have a final concentration from about 1 ng/ml to about 30 mg/ml of plasmid (or other polynucleotide). For example, a formulation of the present invention may have a final concentration of about 1 ng/ml, about 5 ng/ml, about 10 ng/ml, about 50 ng/ml, about 100 ng/ml, about 500 ng/ml, about 1 μg/ml, about 5 μg/ml, about 10 μg/ml, about 50 μg/ml, about 200 μg/ml, about 400 μg/ml, about 600 μg/ml, about 800 μg/ml, about 1 mg/ml, about 2 mg/ml, about 2.5, about 3 mg/ml, about 3.5, about 4 mg/ml, about 4.5, about 5 mg/ml, about 5.5 mg/ml, about 6 mg/ml, about 7 mg/ml, about 8 mg/ml, about 9 mg/ml, about 10 mg/ml, about 20 mg/ml, or about 30 mg mg/ml of a plasmid.

[0327] Certain formulations of the present invention include a cocktail of plasmids (*see, e,g,*, Example 2 *supra*) of the present invention, *e.g.*, comprising coding regions encoding IV proteins NP, M1 and/or M2 and optionally, plasmids encoding immunity enhancing proteins, *e.g.*, cytokines. Various plasmids desired in a cocktail are combined together in PBS or other diluent prior to the addition to the other ingredients. Furthermore, plasmids may be present in a cocktail at equal proportions, or the ratios may be adjusted based on, for example, relative expression levels of the antigens or the relative immunogenicity of the encoded antigens. Thus, various plasmids in the cocktail may be present in equal proportion, or up to twice or three times as much of one plasmid may be included relative to other plasmids in the cocktail.

[0328] Additionally, the concentration of BAK may be adjusted depending on, for example, a desired particle size and improved stability. Indeed, in certain embodiments, formulations of the present invention include CRL 1005 and DNA, but are free of BAK. In general BAK-containing formulations of the present invention are adjusted to have a final concentration of BAK from about 0.05 mM to about 0.5 mM. For example, a formulation of the present invention may have a final BAK concentration of about 0.05 mM, 0.1 mM, 0.2 mM, 0.3 mM, 0.4 mM or 0.5 mM.

[0329] The total volume of the formulations produced by the methods below may be scaled up or down, by choosing apparatus of proportional size. Finally, in carrying out any of the methods described below, the three components of the formulation, BAK, CRL 1005, and plasmid DNA, may be added in any order. In each of these methods described below the term "cloud point" refers to the point in a temperature shift, or other titration, at which a clear solution becomes cloudy, *i.e.*, when a component dissolved in a solution begins to precipitate out of solution.

Thermal Cycling of a Pre-Mixed Formulation

[0330] This example describes the preparation of a formulation comprising 0.3 mM BAK, 7.5 mg/ml CRL 1005, and 5 mg/ml of DNA in a total volume of 3.6 ml. The ingredients are combined together at a temperature below the cloud point and then the formulation is thermally cycled to room temperature (above the cloud point) several times, according to the protocol outlined in Figure 2.

[0331] A 1.28 mM solution of BAK is prepared in PBS, 846 µl of the solution is placed into a 15 ml round bottom flask fitted with a magnetic stirring bar, and the solution is stirred with moderate speed, in an ice bath on top of a stirrer/hotplate (hotplate off) for 10 minutes. CRL 1005 (27 µl) is then added using a 100 µl positive displacement pipette and the solution is stirred for a further 60 minutes on ice. Plasmids comprising codon-optimized coding regions encoding, for example, NP, M1, and M2 as described herein, and optionally, additional plasmids comprising codon-optimized or non-codin-optimized coding regions encoding, *e.g.*, additional IV proteins, and or other proteins, *e.g.*, cytokines, are mixed together at desired proportions in PBS to achieve 6.4 mg/ml total DNA. This plasmid cocktail is added drop wise, slowly, to the stirring solution over 1 min using a 5 ml pipette. The solution at this point (on ice) is clear since it is below the cloud point of the poloxamer and is further stirred on ice for 15 min. The ice bath is then removed, and the solution is stirred at ambient temperature for 15 minutes to produce a cloudy solution as the poloxamer passes through the cloud point.

[0332] The flask is then placed back into the ice bath and stirred for a further 15 minutes to produce a clear solution as the mixture is cooled below the poloxamer cloud point. The ice bath is again removed and the solution stirred at ambient temperature for a further 15 minutes. Stirring for 15 minutes above and below the cloud point (total of 30 minutes), is defined as one thermal cycle. The mixture is cycled six more times. The resulting formulation may be used immediately, or may be placed in a glass vial, cooled below the cloud point, and frozen at -80 °C for use at a later time.

Thermal Cycling, Dilution and Filtration of a Pre-mixed Formulation, Using Increased Concentrations of CRL 1005

[0333] This example describes the preparation of a formulation comprising 0.3 mM BAK, 34 mg/ml or 50 mg/ml CRL 1005, and 5.0 mg/ml of DNA in a final volume of 4.0 ml. The ingredients are combined together at a temperature below the cloud point, then the formulation is thermally cycled to room temperature (above the cloud point) several times, diluted, and filtered according to the protocol outlined in Figure 3.

[0334] Plasmids comprising codon-optimized coding regions encoding, for example, NP, M1, and M2 as described herein, and optionally, additional plasmids comprising codon-optimized or non-codin-optimized coding regions encoding, *e.g.*, additional IV proteins, and or other proteins, *e.g.*, cytokines, are mixed together at desired proportions in PBS to achieve 6.4 mg/ml total DNA. This plasmid cocktail is placed into the 15 ml round bottom flask fitted with a magnetic stirring bar, and for the formulation containing 50 mg/ml CRL 1005, 3.13 ml of a solution containing about 3.2 mg/ml of NP encoding plasmid and about 3.2 mg/ml M2 encoding plasmid (about 6.4 mg/ml total DNA) is placed into the 15 ml round bottom flask fitted with a magnetic stirring bar, and the solutions are stirred with moderate speed, in an ice bath on top of a stirrer/hotplate (hotplate off) for 10 minutes. CRL 1005 (136 µl for 34 mg/ml final concentration, and 200 µl for 50 mg/ml final concentration) is then added using a 200 µl positive displacement pipette and the solution is stirred for a further 30 minutes on ice. Solutions of 1.6 mM and 1.8 mM BAK are prepared in PBS, and 734 µl of 1.6 mM and 670 µl of 1.8 mM are then added drop wise, slowly, to the stirring poloxamer solutions with concentrations of 34 mg/ml or 50 mg/ml mixtures, respectively, over 1 min using a 1ml pipette. The solutions at this point are clear since they are below the cloud point of the poloxamer and are stirred on ice for 30 min. The ice baths are then removed; the solutions stirred at ambient temperature for 15 minutes to produce cloudy solutions as the poloxamer passes through the cloud point.

[0335] The flasks are then placed back into the ice baths and stirred for a further 15 minutes to produce clear solutions as the mixtures cooled below the poloxamer cloud point. The ice baths are again removed and the solutions stirred for a further 15 minutes. Stirring for 15 minutes above and below the cloud point (total of 30 minutes), is defined as one thermal cycle. The mixtures are cycled two more times.

[0336] In the meantime, two Steriflip® 50 ml disposable vacuum filtration devices, each with a 0.22 μm Millipore Express® membrane (available from Millipore, cat # SCGP00525) are placed in an ice bucket, with a vacuum line attached and left for 1 hour to allow the devices to equilibrate to the temperature of the ice. The poloxamer formulations are then diluted to 2.5 mg/ml DNA with PBS and filtered under vacuum.

[0337] The resulting formulations may be used immediately, or may be transferred to glass vials, cooled below the cloud point, and frozen at -80 °C for use at a later time.

A Simplified Method Without Thermal Cycling

[0338] This example describes a simplified preparation of a formulation comprising 0.3 mM BAK, 7.5 mg/ml CRL 1005, and 5 mg/ml of DNA in a total volume of 2.0 ml. The ingredients are combined together at a temperature below the cloud point and then the formulation is simply filtered and then used or stored, according to the protocol outlined in Figure 4.

[0339] A 0.77 mM solution of BAK is prepared in PBS, and 780 μl of the solution is placed into a 15 ml round bottom flask fitted with a magnetic stirring bar, and the solution is stirred with moderate speed, in an ice bath on top of a stirrer/hotplate (hotplate off) for 15 minutes. CRL 1005 (15 μl) is then added using a 100 μl positive displacement pipette and the solution is stirred for a further 60 minutes on ice. Plasmids comprising codon-optimized coding regions encoding, for example, NP, M1, and M2 as described herein, and optionally, additional plasmids comprising codon-optimized or non-codin-optimized coding regions encoding, *e.g.*, additional IV proteins, and or other

proteins, *e.g.*, cytokines, are mixed together at desired proportions in PBS to achieve a final concentration of about 8.3 mg/ml total DNA. This plasmid cocktail is added drop wise, slowly, to the stirring solution over 1 min using a 5 ml pipette. The solution at this point (on ice) is clear since it is below the cloud point of the poloxamer and is further stirred on ice for 15 min.

[0340] In the meantime, one Steriflip® 50 ml disposable vacuum filtration devices, with a 0.22 μm Millipore Express® membrane (available from Millipore, cat # SCGP00525) is placed in an ice bucket, with a vacuum line attached and left for 1 hour to allow the device to equilibrate to the temperature of the ice. The poloxamer formulation is then filtered under vacuum, below the cloud point and then allowed to warm above the cloud point. The resulting formulations may be used immediately, or may be transferred to glass vials, cooled below the cloud point and then frozen at -80°C for use at a later time.

EXAMPLE 6

Animal Immunizations

[0341] The immunogenicity of the various IV expression products encoded by the codon-optimized polynucleotides described herein are initially evaluated based on each plasmid's ability to mount an immune response *in vivo*. Plasmids are tested individually and in combinations by injecting single constructs as well as multiple constructs. Immunizations are initially carried out in animals, such as mice, rabbits, goats, sheep, non-human primates, or other suitable animal, by intramuscular (IM) injections. Serum is collected from immunized animals, and the antigen specific antibody response is quantified by ELISA assay using purified immobilized antigen proteins in a protein – immunized subject antibody – anti-species antibody type assay, according to standard protocols. The tests of immunogenicity further include measuring antibody titer, neutralizing antibody titer, T-cell proliferation, T-cell secretion of cytokines, cytolytic T cell responses, and by direct

enumeration of antigen specific CD4+ and CD8+ T-cells. Correlation to protective levels of the immune responses in humans are made according to methods well known by those of ordinary skill in the art. *See* above.

A. DNA formulations

[0342] Plasmid DNA is formulated with a poloxamer by any of the methods described in Example 3. Alternatively, plasmid DNA is prepared as described above and dissolved at a concentration of about 0.1 mg/ml to about 10 mg/ml, preferably about 1 mg/ml, in PBS with or without transfection-facilitating cationic lipids, *e.g.*, DMRIE/DOPE at a 4:1 DNA:lipid mass ratio. Alternative DNA formulations include 150 mM sodium phosphate instead of PBS, adjuvants, *e.g.*, Vaxfectin™ at a 4:1 DNA: Vaxfectin™ mass ratio, mono-phosphoryl lipid A (detoxified endotoxin) from *S. minnesota* (MPL) and trehalosedicorynomycolateAF (TDM), in 2% oil (squalene)-Tween 80-water (MPL + TDM, available from Sigma/Aldrich, St. Louis, MO, (catalog # M6536)), a solubilized mono-phosphoryl lipid A formulation (AF, available from Corixa), or (±)-N-(3-Acetoxypropyl)-N,N-dimethyl-2,3-bis(octyloxy)-1-propanaminium chloride (compound # VC1240) (*see* Shriver, J.W. *et al.*, *Nature 415*:331-335 (2002), and P.C.T. Publication No. WO 02/00844 A2, each of which is incorporated herein by reference in its entirety).

B. Animal immunizations

[0343] Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, are injected into BALB/c mice as single plasmids or as cocktails of two or more plasmids, as either DNA in PBS or formulated with the poloxamer-based delivery system: 2 mg/ml DNA, 3

mg/ml CRL 1005, and 0.1 mM BAK. Groups of 10 mice are immunized three times, at biweekly intervals, and serum is obtained to determine antibody titers to each of the antigens. Groups are also included in which mice are immunized with a trivalent preparation, containing each of the three plasmid constructs in equal mass.

[0344] The immunization schedule is as follows:

Day –3	Pre-bleed
Day 0	Plasmid injections, intramuscular, bilateral in rectus femoris, 5- 50 μg/leg
Day 21	Plasmid injections, intramuscular, bilateral in rectus femoris, 5-50 μg/leg
Day 49	Plasmid injections, intramuscular, bilateral in rectus femoris, 5-50 μg/leg
Day 59	Serum collection

[0345] Serum antibody titers are determined by ELISA with recombinant proteins, peptides or transfection supernatants and lysates from transfected VM-92 cells live, inactivated, or lysed virus.

C. Immunization of Mice with Vaccine Formulations Using a Vaxfectin™ Adjuvant

[0346] Vaxfectin™ (a 1:1 molar ratio of the cationic lipid VC1052 and the neutral co-lipid DPyPE) is a synthetic cationic lipid formulation which has shown promise for its ability to enhance antibody titers against when administered with DNA intramuscularly to mice.

[0347] In mice, intramuscular injection of Vaxfectin™ formulated with NP DNA increased antibody titers up to 20-fold to levels that could not be reached with DNA alone. In rabbits, complexing DNA with Vaxfectin™ enhanced antibody titers up to 50-fold. Thus, Vaxfectin™ shows promise as a delivery system and as an adjuvant in a DNA vaccine.

[0348] Vaxfectin™ mixtures are prepared by mixing chloroform solutions of VC1052 cationic lipid with chloroform solutions of DpyPE neutral co-lipid.

Dried films are prepared in 2 ml sterile glass vials by evaporating the chloroform under a stream of nitrogen, and placing the vials under vacuum overnight to remove solvent traces. Each vial contains 1.5 μmole each of VC1052 and DPyPE. Liposomes are prepared by adding sterile water followed by vortexing. The resulting liposome solution is mixed with DNA at a phosphate mole:cationic lipid mole ratio of 4:1.

[0349] Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, are mixed together at desired proportions in PBS to achieve a final concentration of 1.0 mg/ml. The plasmid cocktail, as well as the controls, are formulated with Vaxfectin™. Groups of 5 BALB/c female mice are injected bilaterally in the rectus femoris muscle with 50 μl of DNA solution (100 μl total/mouse), on days 1 and 21 and 49 with each formulation. Mice are bled for serum on days 0 (prebleed), 20 (bleed 1), and 41 (bleed 2), and 62 (bleed 3), and up to 40 weeks post-injection. Antibody titers to the various IV proteins encoded by the plasmid DNAs are measured by ELISA as described elsewhere herein.

[0350] Cytolytic T-cell responses are measured as described in Hartikka *et al.* "Vaxfectin Enhances the Humoral Response to Plasmid DNA-encoded Antigens," *Vaccine 19*:1911-1923 (2001) and is incorporated herein in its entirety by reference. Standard ELISPOT technology is used for the CD4+ and CD8+ T-cell assays as described in Example 6, part A.

D. Production of NP, M1 or M2 antisera in animals

[0351] Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives

either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, are prepared according to the immunization scheme described above and injected into a suitable animal for generating polyclonal antibodies. Serum is collected and the antibody titered as above.

[0352] Monoclonal antibodies are also produced using hybridoma technology (Kohler, *et al., Nature 256*:495 (1975); Kohler, *et al., Eur. J. Immunol. 6*:511 (1976); Kohler, *et al., Eur. J. Immunol. 6*:292 (1976); Hammerling, *et al.*, in *Monoclonal Antibodies and T-Cell Hybridomas*, Elsevier, N.Y., (1981), pp. 563-681, each of which is incorporated herein by reference in its entirety). In general, such procedures involve immunizing an animal (preferably a mouse) as described above. The splenocytes of such mice are extracted and fused with a suitable myeloma cell line. Any suitable myeloma cell line may be employed in accordance with the present invention; however, it is preferable to employ the parent myeloma cell line (SP2O), available from the American Type Culture Collection, Rockville, Maryland. After fusion, the resulting hybridoma cells are selectively maintained in HAT medium, and then cloned by limiting dilution as described by Wands *et al., Gastroenterology 80*:225-232 (1981), incorporated herein by reference in its entirety. The hybridoma cells obtained through such a selection are then assayed to identify clones which secrete antibodies capable of binding the various IV proteins.

[0353] Alternatively, additional antibodies capable of binding to IV proteins described herein may be produced in a two-step procedure through the use of anti-idiotypic antibodies. Such a method makes use of the fact that antibodies are themselves antigens, and that, therefore, it is possible to obtain an antibody which binds to a second antibody. In accordance with this method, various IV-specific antibodies are used to immunize an animal, preferably a mouse. The splenocytes of such an animal are then used to produce hybridoma cells, and the hybridoma cells are screened to identify clones which produce an antibody whose ability to bind to the IV protein-specific antibody can be blocked by the cognate IV protein. Such antibodies comprise anti-idiotypic

antibodies to the IV protein-specific antibody and can be used to immunize an animal to induce formation of further IV-specific antibodies.

[0354] It will be appreciated that Fab and $F(ab')_2$ and other fragments of the antibodies of the present invention may be used according to the methods disclosed herein. Such fragments are typically produced by proteolytic cleavage, using enzymes such as papain (to produce Fab fragments) or pepsin (to produce $F(ab')_2$ fragments). Alternatively, NP, M1, M2, HA and eM2 binding fragments can be produced through the application of recombinant DNA technology or through synthetic chemistry.

[0355] It may be preferable to use "humanized" chimeric monoclonal antibodies. Such antibodies can be produced using genetic constructs derived from hybridoma cells producing the monoclonal antibodies described above. Methods for producing chimeric antibodies are known in the art. See, for review, Morrison, *Science 229*:1202 (1985); Oi, *et al., BioTechniques 4*:214 (1986); Cabilly, *et al.*, U.S. Patent No. 4,816,567; Taniguchi, *et al.*, EP 171496; Morrison, *et al.*, EP 173494; Neuberger, *et al.*, WO 8601533; Robinson, *et al.*, WO 8702671; Boulianne, *et al., Nature 312*:643 (1984); Neuberger, *et al., Nature 314*:268 (1985).

[0356] These antibodies are used, for example, in diagnostic assays, as a research reagent, or to further immunize animals to generate IV-specific anti-idiotypic antibodies. Non-limiting examples of uses for anti-IV antibodies include use in Western blots, ELISA (competitive, sandwich, and direct), immunofluorescence, immunoelectron microscopy, radioimmunoassay, immunoprecipitation, agglutination assays, immunodiffusion, immunoelectrophoresis, and epitope mapping (Weir, D. *Ed. Handbook of Experimental Immunology*, 4^{th} ed. Vols. I and II, Blackwell Scientific Publications (1986)).

EXAMPLE 7

Mucosal Vaccination and Electrically Assisted Plasmid Delivery

A. Mucosal DNA Vaccination

[0357] Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, HA, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, (100 μg/50 μl total DNA) are delivered to BALB/c mice at 0, 2 and 4 weeks via i.m., intranasal (i.n.), intravenous (i.v.), intravaginal (i.vag.), intrarectal (i.r.) or oral routes. The DNA is delivered unformulated or formulated with the cationic lipids DMRIE/DOPE (DD) or GAP-DLRIE/DOPE (GD). As endpoints, serum IgG titers against the various IV antigens are measured by ELISA and splenic T-cell responses are measured by antigen-specific production of IFN-gamma and IL-4 in ELISPOT assays. Standard chromium release assays are used to measure specific cytotoxic T lymphocyte (CTL) activity against the various IV antigens. Tetramer assays are used to detect and quantify antigen specific T-cells, with quantification being confirmed and phenotypic characterization accomplished by intracellular cytokine staining. In addition, IgG and IgA responses against the various IV antigens are analyzed by ELISA of vaginal washes.

B. Electrically-assisted plasmid delivery

[0358] *In vivo* gene delivery may be enhanced through the application of brief electrical pulses to injected tissues, a procedure referred to herein as electrically-assisted plasmid delivery. See, *e.g.*, Aihara, H. & Miyazaki, J. *Nat.* Biotechnol. *16:*867-70 (1998); Mir, L.M. *et al.*, *Proc. Natl Acad. Sci.* USA *96:*4262-67 (1999); Hartikka, J. *et al.*, *Mol. Ther. 4:*407-15 (2001); and

Mir, L.M. *et al.*; Rizzuto, G. *et al.*, *Hum Gene Ther 11:*1891-900 (2000); Widera, G. *et al, J. of Immuno. 164*: 4635-4640 (2000). The use of electrical pulses for cell electropermeabilization has been used to introduce foreign DNA into prokaryotic and eukaryotic cells *in vitro*. Cell permeabilization can also be achieved locally, *in vivo*, using electrodes and optimal electrical parameters that are compatible with cell survival.

[0359] The electroporation procedure can be performed with various electroporation devices. These devices include external plate type electrodes or invasive needle/rod electrodes and can possess two electrodes or multiple electrodes placed in an array. Distances between the plate or needle electrodes can vary depending upon the number of electrodes, size of target area and treatment subject.

[0360] The TriGrid needle array, used in examples described herein, is a three electrode array comprising three elongate electrodes in the approximate shape of a geometric triangle. Needle arrays may include single, double, three, four, five, six or more needles arranged in various array formations. The electrodes are connected through conductive cables to a high voltage switching device that is connected to a power supply.

[0361] The electrode array is placed into the muscle tissue, around the site of nucleic acid injection, to a depth of approximately 3 mm to 3 cm. The depth of insertion varys depending upon the target tissue and size of patient receiving electroporation. After injection of foreign nucleic acid, such as plasmid DNA, and a period of time sufficient for distribution of the nucleic acid, square wave electrical pulses are applied to the tissue. The amplitude of each pulse ranges from about 100 volts to about 1500 volts, *e.g.*, about 100 volts, about 200 volts, about 300 volts, about 400 volts, about 500 volts, about 600 volts, about 700 volts, about 800 volts, about 900 volts, about 1000 volts, about 1100 volts, about 1200 volts, about 1300 volts, about 1400 volts, or about 1500 volts or about 1-1.5kV/cm, based on the spacing between electrodes. Each pulse has a duration of about 1μs to about 1000μs, *e.g.*, about 1μs, about 10μs, about 50μs, about 100μs, about 200μs, about 300μs,

about 400μs, about 500μs, about 600μs, about 700μs, about 800μs, about 900μs, or about 1000μs, and a pulse frequency on the order of about 1-10 Hz. The polarity of the pulses may be reversed during the electroporation procedure by switching the connectors to the pulse generator. Pulses are repeated multiple times. The electroporation parameters (*e.g.* voltage amplitude, duration of pulse, number of pulses, depth of electrode insertion and frequency) will vary based on target tissue type, number of electrodes used and distance of electrode spacing, as would be understood by one of ordinary skill in the art.

[0362] Immediately after completion of the pulse regimen, subjects receiving electroporation can be optionally treated with membrane stabilizing agents to prolong cell membrane permeability as a result of the electroporation. Examples of membrane stabilizing agents include, but are not limited to, steroids (e.g. dexamethasone, methylprednisone and progesterone), angiotensin II and vitamin E. A single dose of dexamethasone, approximately 0.1 mg per kilogram of body weight, should be sufficient to achieve a beneficial affect.

[0363] EAPD techniques such as electroporation can also be used for plasmids contained in liposome formulations. The liposome – plasmid suspension is administered to the animal or patient and the site of injection is treated with a safe but effective electrical field generated, for example, by a TriGrid needle array. The electroporation may aid in plasmid delivery to the cell by destabilizing the liposome bilayer so that membrane fusion between the liposome and the target cellular structure occurs. Electroporation may also aid in plasmid delivery to the cell by triggering the release of the plasmid, in high concentrations, from the liposome at the surface of the target cell so that the plasmid is driven across the cell membrane by a concentration gradient via the pores created in the cell membrane as a result of the electroporation.

[0364] Female BALB/c mice aged 8-10 weeks are anesthetized with inhalant isoflurane and maintained under anesthesia for the duration of the electroporation procedure. The legs are shaved prior to treatment. Plasmid

constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, HA, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, are administered to BALB/c mice (n = 10) via unilateral injection in the quadriceps with 25 μg total of a plasmid DNA per mouse using an 0.3 cc insulin syringe and a 26 gauge, 1/2 length needle fitted with a plastic collar to regulate injection depth. Approximately one minute after injection, electrodes are applied. Modified caliper electrodes are used to apply the electrical pulse. *See* Hartikka J. *et al. Mol Ther 188*:407-415 (2001). The caliper electrode plates are coated with conductivity gel and applied to the sides of the injected muscle before closing to a gap of 3 mm for administration of pulses. EAPD is applied using a square pulse type at 1-10 Hz with a field strength of 100-500 V/cm, 1-10 pulses, of 10-100 ms each.

[0365] Mice are vaccinated ± EAPD at 0, 2 and 4 weeks. As endpoints, serum IgG titers against the various IV antigens are measured by ELISA and splenic T-cell responses are measured by antigen-specific production of IFN-gamma and IL-4 in ELISPOT assays. Standard chromium release assays are used to measure specific cytotoxic T lymphocyte (CTL) activity against the various IV antigens.

[0366] Rabbits (n = 3) are given bilateral injections in the quadriceps muscle with plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, HA, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector. The implantation area is shaved and the TriGrid electrode array is implanted into the target region of the muscle. 3.0 mg of plasmid DNA is administered per dose through the injection port of the electrode array. An injection collet is used to control the depth of injection.

Electroporation begins approximately one minute after injection of the plasmid DNA is complete. Electroporation is administered with a TriGrid needle array, with eletrodes evenly spaced 7mm apart, using an Ichor TGP-2 pulse generator. The array is inserted into the target muscle to a depth of about 1 to 2 cm. 4-8 pulses are administered. Each pulse has a duration of about 50-100 μs, an amplitude of about 1-1.2kV/cm and a pulse frequency of 1 Hz. The injection and electroporation may be repeated.

[0367] Sera are collected from vaccinated rabbits at various time point. As endpoints, serum IgG titers against the various IV antigens are measured by ELISA and PBMC T-cell proliferative responses.

[0368] To test the effect of electroporation on therapeutic protein expression in non-human primates, male or female rhesus monkeys are given either 2 or 6 i.m. injections of plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, (0.1 to 10 mg DNA total per animal). Target muscle groups include, but are not limited to, bilateral rectus fermoris, cranial tibialis, biceps, gastrocenemius or deltoid muscles. The target area is shaved and a needle array, comprising between 4 and 10 electrodes, spaced between 0.5-1.5 cm apart, is implanted into the target muscle. Once injections are complete, a sequence of brief electrical pulses are applied to the electrodes implanted in the target muscle using an Ichor TGP-2 pulse generator. The pulses have an amplitude of approximately 120 – 200V. The pulse sequence is completed within one second. During this time, the target muscle may make brief contractions or twitches. The injection and electroporation may be repeated.

[0369] Sera are collected from vaccinated monkeys at various time points. As endpoints, serum IgG titers against the various IV antigens are measured by ELISA and PBMC T-cell proliferative responses are measured by antigen-

specific production of IFN-gamma and IL-4 in ELISPOT assays or by tetramer assays to detect and quantify antigen specific T-cells, with quantification being confirmed and phenotypic characterization accomplished by intracellular cytokine staining. Standard chromium release assays are used to measure specific cytotoxic T lymphocyte (CTL) activity against the various IV antigens.

EXAMPLE 8

Combinatorial DNA Vaccine Using Heterologous Prime-Boost Vaccination

[0370] This Example describes vaccination with a combinatorial formulation including one or more polynucleotides comprising one codon-optimized coding regions encoding an IV protein or fragment, variant, or derivative thereof prepared with an adjuvant and/or transfection facilitating agent; and also an isolated IV protein or fragment, variant, or derivative thereof. Thus, antigen is provided in two forms. The exogenous isolated protein stimulates antigen specific antibody and CD4+ T-cell responses, while the polynucleotide-encoded protein, produced as a result of cellular uptake and expression of the coding region, stimulates a CD8+ T-cell response. Unlike conventional "prime-boost" vaccination strategies, this approach provides different forms of antigen in the same formulation. Because antigen expression from the DNA vaccine doesn't peak until 7-10 days after injection, the DNA vaccine provides a boost for the protein component. Furthermore, the formulation takes advantage of the immunostimulatory properties of the bacterial plasmid DNA.

A. Non-Codon Optimized NP Gene

[0371] This example demonstrates the efficacy of this procedure using a non-codon-optimized polynucleotide encoding NP, however, the methods described herein are applicable to any IV polynucleotide vaccine formulation. Because only a small amount of protein is needed in this method, it is

conceivable that the approach could be used to reduce the dose of conventional vaccines, thus increasing the availability of scarce or expensive vaccines. This feature would be particularly important for vaccines against pandemic influenza or biological warfare agents.

[0372] An injection dose of 10 μg influenza A/PR/8/34 nucleoprotein (NP) DNA per mouse, prepared essentially as described in Ulmer, J.B., *et al.*, *Science 259:*1745-49 (1993) and Ulmer, J.B. *et al.*, *J Virol. 72:*5648-53 (1998) was pre-determined in dose response studies to induce T cell and antibody responses in the linear range of the dose response and results in a response rate of greater than 95% of mice injected. Each formulation, NP DNA alone, or NP DNA +/- NP protein formulated with Ribi I or the cationic lipids, DMRIE:DOPE or Vaxfectin™, was prepared in the recommended buffer for that vaccine modality. For injections with NP DNA formulated with cationic lipid, the DNA was diluted in 2X PBS to 0.2 mg/ml +/- purified recombinant NP protein (produced in baculovirus as described in Example 2) at 0.08 mg/ml. Each cationic lipid was reconstituted from a dried film by adding 1 ml of sterile water for injection (SWFI) to each vial and vortexing continuously for 2 min., then diluted with SWFI to a final concentration of 0.15 mM. Equal volumes of NP DNA (+/- NP protein) and cationic lipid were mixed to obtain a DNA to cationic lipid molar ratio of 4:1. For injections with DNA containing Ribi I adjuvant (Sigma), Ribi I was reconstituted with saline to twice the final concentration. Ribi I (2X) was mixed with an equal volume of NP DNA at 0.2 mg/ml in saline +/- NP protein at 0.08 mg/ml. For immunizations without cationic lipid or Ribi, NP DNA was prepared in 150 mM sodium phosphate buffer, pH 7.2. For each experiment, groups of 9 BALB/c female mice at 7-9 weeks of age were injected with 50 μl of NP DNA +/- NP protein, cationic lipid or Ribi I. Injections were given bilaterally in each rectus femoris at day 0 and day 21. The mice were bled by OSP on day 20 and day 33 and serum titers of individual mice were measured.

[0373] NP specific serum antibody titers were determined by indirect binding ELISA using 96 well ELISA plates coated overnight at 4°C with purified

recombinant NP protein at 0.5 μg per well in BBS buffer pH 8.3. NP coated wells were blocked with 1% bovine serum albumin in BBS for 1 h at room temperature. Two-fold serial dilutions of sera in blocking buffer were incubated for 2 h at room temperature and detected by incubating with alkaline phosphatase conjugated (AP) goat anti-mouse IgG-Fc (Jackson Immunoresearch, West Grove, PA) at 1:5000 for 2 h at room temperature. Color was developed with 1 mg/ml para-nitrophenyl phosphate (Calbiochem, La Jolla, CA) in 50 mM sodium bicarbonate buffer, pH 9.8 and 1 mM $MgCl_2$ and the absorbance read at 405 nm. The titer is the reciprocal of the last dilution exhibiting an absorbance value 2 times that of pre-bleed samples.

[0374] Standard ELISPOT technology, used to identify the number of interferon gamma (IFN-γ) secreting cells after stimulation with specific antigen (spot forming cells per million splenocytes, expressed as SFU/million), was used for the CD4+ and CD8+ T-cell assays. For the screening assays, 3 mice from each group were sacrificed on day 34, 35, and 36. At the time of collection, spleens from each group were pooled, and single cell suspensions made in cell culture media using a dounce homogenizer. Red blood cells were lysed, and cells washed and counted. For the CD4+ and CD8+ assays, cells were serially diluted 3- fold, starting at 10^6 cells per well and transferred to 96 well ELISPOT plates pre-coated with anti-murine IFN-γ monoclonal antibody. Spleen cells were stimulated with the H-$2K^d$ binding peptide, TYQRTRALV (SEQ ID NO:81), at 1 μg/ml and recombinant murine IL-2 at 1 U/ml for the CD8+ assay and with purified recombinant NP protein at 20 μg/ml for the CD4+ assay. Cells were stimulated for 20-24 hours at 37°C in 5% CO_2, then the cells were washed out and biotin labeled anti-IFN-γ monoclonal antibody added for a 2 hour incubation at room temperature. Plates were washed and horseradish peroxidase-labeled avidin was added. After a 1-hour incubation at room temperature, AEC substrate was added and "spots" developed for 15 min. Spots were counted using the Immunospot automated spot counter (C.T.L. Inc., Cleveland OH). Thus, CD4+ and CD8+

responses were measured in three separate assays, using spleens collected on each of three consecutive days.

[0375] Three weeks after a single injection, antibody responses in mice receiving vaccine formulations containing purified protein were 6 to 8-fold higher than for mice receiving NP DNA only (Figure 5, Table 15). The titers for mice receiving DNA and protein formulated with a cationic lipid were similar to those for mice receiving protein in Ribi adjuvant or DNA and protein in Ribi adjuvant. These data indicate that the levels of antibody seen when protein is injected with an adjuvant can be obtained with DNA vaccines containing DNA and protein formulated with a cationic lipid, without the addition of conventional adjuvant.

[0376] Twelve days after a second injection, antibody responses in mice receiving vaccine formulations containing purified protein were 9 to 129-fold higher than for mice receiving NP DNA only (Figure 6, Table 15). With a mean anti-NP antibody titer of 750,933 at day 33, the titers for mice receiving DNA and protein formulated with Vaxfectin™ were 25-fold higher than for mice receiving DNA alone (mean titer = 30,578), and nearly as high as those for mice injected with protein in Ribi adjuvant (mean titer = 1,748,133).

TABLE 15. Fold increase in antibody response over DNA alone

Formulation	**20 days after one injection**	**12 days after second injection**
protein+Ribi	7X (p=0.0002)	57X (p=0.002)
DNA+protein+DMRIE: DOPE	6X (p=0.00005)	9X (p=0.0002)
DNA+protein+Vaxfectin™	8X (p=0.00003)	25X (p=0.0004)
DNA+protein+Ribi	7X (p=0.01)	129X (p=0.003)

*protein = purified recombinant NP protein

[0377] As expected, an NP specific CD8+ T-cell IFN-γ response was not detected in spleens of mice injected with NP protein in Ribi (Figure 7). All of the other groups had detectable NP specific CD8+ T-cell responses. The CD8+ T-cell responses for all groups receiving vaccine formulations containing NP DNA were not statistically different from each other.

[0378] Mice from all of the groups had detectable NP specific CD4+ T-cell responses (Figure 8). The CD4+ T-cell responses of splenocytes from groups receiving vaccine formulations containing NP DNA and NP protein formulated with cationic lipid were 2-6 fold higher than the group injected with DNA alone.

B. Codon-Optimized IV Constructs

[0379] Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, are used in the prime-boost compositions described herein. For the prime-boost modalities, the same protein may be used for the boost, *e.g.*, DNA encoding NP with NP protein, or a heterologous boost may be used, *e.g.*, DNA encoding NP with an M1 protein boost. Each formulation, the plasmid comprising a coding region for the IV protein alone, or the plasmid comprising a coding region for the IV protein plus the isolated protein are formulated with Ribi I or the cationic lipids, DMRIE:DOPE or Vaxfectin™. The formulations are prepared in the recommended buffer for that vaccine modality. Exemplary formulations, using NP as an example, are described herein. Other plasmid/protein formulations, including multivalent formulations, can be easily prepared by one of ordinary skill in the art by following this example. For injections with DNA formulated with cationic lipid, the DNA is diluted in 2X PBS to 0.2 mg/ml +/- purified recombinant NP protein at 0.08 mg/ml. Each cationic lipid is reconstituted from a dried film by adding 1 ml of sterile water for injection (SWFI) to each vial and vortexing continuously for 2 min., then diluted with SWFI to a final concentration of 0.15 mM. Equal volumes of NP DNA (+/- NP protein) and cationic lipid are mixed to obtain a DNA to cationic lipid molar ratio of 4:1. For injections with DNA containing Ribi I adjuvant (Sigma), Ribi I is reconstituted with saline to

twice the final concentration. Ribi I (2X) is mixed with an equal volume of NP DNA at 0.2 mg/ml in saline +/- NP protein at 0.08 mg/ml. For immunizations without cationic lipid or Ribi, NP DNA is prepared in 150 mM sodium phosphate buffer, pH 7.2. For each experiment, groups of 9 BALB/c female mice at 7-9 weeks of age are injected with 50 μl of NP DNA +/- NP protein, cationic lipid or Ribi I. The formulations are administered to BALB/c mice (n = 10) via bilateral injection in each rectus femoris at day 0 and day 21.

[0380] The mice are bled on day 20 and day 33 and serum titers of individual mice to the various IV antigens are measured. Serum antibody titers specific for the various IV antigens are determined by ELISA. Standard ELISPOT technology, used to identify the number of interferon gamma (IFN-γ) secreting cells after stimulation with specific antigen (spot forming cells per million splenocytes, expressed as SFU/million), is used for the CD4+ and CD8+ T-cell assays using 3 mice from each group vaccinated above, sacrificed on day 34, 35 and 36, post vaccination.

EXAMPLE 9

Murine Challenge Model of Influenza

General Experimental Procedure

[0381] A murine challenge model with influenza A virus is used to test the efficacy of the immunotherapies. The model used is based on that described in Ulmer, J.B., *et al.*, *Science 259:*1745-49 (1993) and Ulmer, J.B. *et al.*, *J Virol. 72:*5648-53 (1998), both of which are incorporated herein by reference in their entireties. This model utilizes a mouse-adapted strain of influenza A/HK/8/68 which replicates in mouse lungs and is titered in tissue culture in Madin Darby Canine Kidney cells. The LD_{90} of this mouse-adapted influenza virus is determined in female BALB/c mice age 13-15 weeks. In this model, two types of challenge study can be conducted: lethal challenge, where the

virus is administered intranasally to heavily sedated mice under ketamine anesthesia; and a sub-lethal challenge, where mice are not anesthetized when the viral inoculum is administered (also intranasally). The endpoint for lethal challenge is survival, but loss in body mass and body temperature can also be monitored. The read-outs for the sublethal challenge include lung virus titer and loss in body mass and body temperature.

[0382] In the studies described here, mice are subjected to lethal challenge. Mice that are previously vaccinated with DNA encoding IV antigens are anesthetized and challenged intranasally with 0.02 mL of mouse-adapted influenza A/HK/8/68 (mouse passage #6), diluted 1 to 10,000 (500 PFU) in PBS containing 0.2% wt/vol BSA.

[0383] These challenge studies utilize groups of 10 mice. The route of administration is intramuscular in rectus femoris (quadriceps), using 0.1 μg up to 1 mg total plasmid DNA. Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, are tested singly and in multivalent cocktails for the ability to protect against challenge. The plasmids are formulated with an adjuvant and/or a transfection facilitating agent, *e.g.*, Vaxfectin™ by methods described elsewhere herein. Mice are vaccinated on days 0 and 21 using amounts of plasmids as described in Example 6. Subsequent injections can be administered. Nasal challenge of mice takes place 3 weeks after the final immunization, and animals are monitored daily for body mass, hypothermia, general appearance and then death.

[0384] For each group of mice that are studied, blood is taken at 2 weeks following the second injection, and/or any subsequent injection, and the animals are terminally bled two weeks following the last injection. Antibody titers are determined for M2, M1, and NP using ELISAs as previously described.

Plasmids

[0385] As described above, constructs of the present invention were inserted into the expression vector VR10551. VR10551 is an expression vector without any transgene insert.

[0386] VR4750 contains the coding sequence for hemagglutinin (HA) (H3N2) from mouse adapted A/Hong Kong/68. The DNA was prepared using Qiagen plasmid purification kits.

Experimental Procedure

[0387] The experimental procedure for the following example is as described above, with particular parameters and materials employed as described herein. In order to provide a pDNA control for protection in the mouse influenza challenge model, the hemagglutinin (HA) gene was cloned from the influenza A/HK/8/68 challenge virus stock, which was passaged 6 times in mice.

[0388] Mice were vaccinated twice at 3 week intervals with either 100 μg pDNA VR4750 encoding the HA gene cloned directly from the mouse-adapted influenza A/HK/8/68 strain, or with 100 μg blank vector pDNA (VR10551). An additional control group was immunized intranasally with live A/HK/8/68 virus (500 PFU). Three weeks after the last injection, mice were challenged intranasally with mouse-adapted influenza A/HK/8/68 with one of 3 doses (50, 500 and 5,000 PFU). Following viral challenge, mice were monitored daily for symptoms of disease, loss in body mass and survival.

[0389] Figure 9 shows that homologous HA-pDNA vaccinated mice are completely protected over a range of viral challenge doses (Figure 9A) and did not suffer significant weight loss (Figure 9B) during the 3 week period following challenge.

[0390] Based on these results, future mouse flu challenge studies can include VR4750 (HA) pDNA as a positive control for protection and utilize 500 PFU, which is the LD90 for this mouse-adapted virus, as the challenge dose.

EXAMPLE 10

Challenge in Non-Human Primates

[0391] The purpose of these studies is to evaluate three or more of the optimal plasmid DNA vaccine formulations for immunogenicity in non-human primates. Rhesus or cynomologus monkeys (6/group) are vaccinated with plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, HA, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, intramuscularly 0.1 to 2 mg DNA combined with cationic lipid, and/or poloxamer and/or aluminum phosphate based or other adjuvants at 0, 1 and 4 months.

[0392] Blood is drawn twice at baseline and then again at the time of and two weeks following each vaccination, and then again 4 months following the last vaccination. At 2 weeks post-vaccination, plasma is analyzed for humoral response and PBMCs are monitored for cellular responses, by standard methods described herein. Animals are monitored for 4 months following the final vaccination to determine the durability of the immune response.

[0393] Animals are challenged within 2-4 weeks following the final vaccination. Animals are challenged intratracheally with the suitable dose of virus based on preliminary challege studies. Nasal swabs, pharyngeal swabs and lung lavages are collected at days 0, 2, 4, 6, 8 and 11 post-challenge and will be assayed for cell-free virus titers on monkey kidney cells. After challenge, animals are monitored for clinical symptoms, *e.g.*, rectal temperature, body weight, leukocyte counts, and in addition, hematocrit and respiratory rate. Oropharyngeal swab samples are taken to allow determination of the length of viral shedding. Illness is scored using the system developed by

Berendt & Hall (*Infect Immun 16*:476-479 (1977)), and will be analyzed by analysis of variance and the method of least significant difference.

EXAMPLE 11

Challenge in Birds

[0394] In this example, various vaccine formulations of the present invention are tested in the chicken influenza model. For these studies an IV H5N1 virus, known to infect birds, is used. Plasmid constructs comprising codon-optimized and non-codon-optimized coding regions encoding NP, M1, M2, eM2, and/or an eM2-NP fusion; or alternatively coding regions (either codon-optimized or non-codon optimized) encoding various IV proteins or fragments, variants or derivatives either alone or as fusions with a carrier protein, *e.g.*, HBcAg, as well as various controls, *e.g.*, empty vector, are formulated with cationic lipid, and/or poloxamer and/or aluminum phosphate based or other adjuvants. The vaccine formulations are delivered at a dose of about 1-10 μg, delivered IM into the defeathered breast area, at 0 and 1 month. The animals are bled for antibody results 3 weeks following the second vaccine. Antibody titers against the various IV antigens are determined using techniques described in the literature. See, *e.g.*, Kodihalli S. *et al.*, *Vaccine 18*:2592-9 (2000). The birds are challenged intranasally with 0.1 mL containing 100 LD_{50} 3 weeks post second vaccination. The birds are monitored daily for 10 days for disease symptoms, which include loss of appetite, diarrhea, swollen faces, cyanosis, paralysis and death. Tracheal and cloacal swabs are taken 4 days following challenge for virus titration.

EXAMPLE 12

Formulation Selection Studies

[0395] The potency of different vaccine formulations was evaluated in different experimental studies using the NP protein of Influenza A/PR/8/34.

Vaccination Regimen

[0396] Groups of nine, six- to eight-week old BALB/c mice (Harlan-Sprague-Dawley) received bilateral (50 μL/leg) intramuscular (rectus femoris) injections of plasmid DNA. Control mice received DNA in PBS alone. Mice received injections on days 0, 20 and 49. Mice were bled by OSP on day 62, and NP-specific antibodies analyzed by ELISA. Splenocytes were harvested from 3 mice/group/day for three sequential days beginning day 63, and NP-specific specific T cells were analyzed by IFNγ ELISPOT using overlapping peptide stimulation.

Cell Culture Media

[0397] Splenocyte cultures were grown in RPMI-1640 medium containing 25 mM HEPES buffer and L-glutamine and supplemented with 10% (v/v) FBS, 55 μM β-mercaptoethanol, 100 U/mL of penicillin G sodium salt, and 100 μg/mL of streptomycin sulfate.

Standard Influenza NP Indirect Binding Assay

[0398] NP specific serum antibody titers were determined by indirect binding ELISA using 96 well ELISA plates coated overnight at 4°C with purified recombinant NP protein at 0.5 μg per well in BBS buffer, pH 8.3. NP coated wells were blocked with 1% bovine serum albumin in BBS for 1 hour at room temperature. Two-fold serial dilutions of sera in blocking buffer were incubated for 2 hours at room temperature and detected by incubating with

alkaline phosphatase conjugated (AP) goat anti-mouse IgG-Fc (Jackson Immunoresearch, West Grove, PA) at 1:5000 for 2 hours at room temperature. Color was developed with 1 mg/ml para-nitrophenyl phosphate (Calbiochem, La Jolla, CA) in 50 mM sodium bicarbonate buffer, pH 9.8 and 1 mM $MgCl_2$ and the absorbance read at 405 nm. The titer is the reciprocal of the last dilution exhibiting an absorbance value 2 times that of pre-bleed samples.

Standard NP CD8+ and CD4+ T-Cell ELISPOT Assay

[0399] Standard ELISPOT technology, used to identify the number of interferon gamma (IFN-γ) secreting cells after stimulation with specific antigen (spot forming cells per million splenocytes, expressed as SFU/million), was used for the CD4+ and CD8+ T-cell assays. Three mice from each group were sacrificed on each of three consecutive days. At the time of collection, spleens from each group were pooled, and single cell suspensions were made in cell culture media using a dounce homogenizer. Red blood cells were lysed, and cells were washed and counted. For the CD4+ and CD8+ assays, cells were serially diluted 3- fold, starting at 10^6 cells per well and transferred to 96 well ELISPOT plates pre-coated with anti-murine IFN-γ monoclonal antibody. Spleen cells were stimulated with the H-$2K^d$ binding peptide, TYQRTRALV, at 1 μg/ml and recombinant murine IL-2 at 1 U/ml for the CD8+ assay and with purified recombinant NP protein at 20 μg/ml for the CD4+ assay. Cells were stimulated for 20-24 hours at 37°C in 5% CO_2, and then the cells were washed out and biotin labeled anti-IFN-γ monoclonal antibody added for a 2 hour incubation at room temperature. Plates were washed and horseradish peroxidase-labeled avidin was added. After a 1-hour incubation at room temperature, AEC substrate was added and "spots" developed for 15 minutes. Spots were counted using the Immunospot automated spot counter (C.T.L. Inc., Cleveland OH).

Experiment 1

[0400] The purpose of this experiment was to determine a dose response to naked pDNA (VR4700) and for pDNA formulated with VF-P1205-02A. VR4700 is a plasmid encoding influenza A/PR/8/34 nucleoprotein (NP) in a VR10551 backbone. VR10551 is an expression vector without any transgene insert. VF-P1205-02A is a formulation containing a poloxamer with a POP molecular weight of 12 KDa and POE of 5 % (CRL1005) at a DNA:poloxamer:BAK ratio of 5 mg/ml:7.5 mg/ml:0.3 mM. The results of this experiment are shown in the following Table:

TABLE 16

DNA dose (μg)	CRL1005 dose (μg)	BAK conc. (μM)	Serum Ab titers (total IgG, n=9)	$CD8^+T$ cells ($SFU/10^6$)	$CD4^+T$ cells ($SFU/10^6$)
1			11,206	28	24
10			31,289	77	99
100			65,422	243	304
1	1.5	0.06	9,956	48	57
10	15	0.6	45,511	174	220
100	150	6	79,644	397	382

[0401] The results of this experiment indicate that increasing the dose of DNA increases both the humoral and cell mediated immune responses. When the DNA is formulated with poloxamer and BAK, increasing the dose also increases both the humoral and cell mediated immune responses.

Experiment 2

[0402] The purpose of this experiment was to determine a dose response to CRL1005, with a fixed pDNA (VR4700) dose and no BAK. The results of this experiment are shown in the following Table:

TABLE 17

DNA dose (μg)	CRL1005 dose (μg)	Serum Ab titers (total IgG, n=9)	$CD8^+$T cells ($SFU/10^6$)	$CD4^+$T cells ($SFU/10^6$)
10		27,733	45	46
10	15	38,400	69	86
10	50	46,933	66	73
10	150	54,044	90	97
10	450	76,800	90	92
10	750	119,467	83	60

[0403] The results of this experiment indicate that increasing the dose of CRL1005 increases both the humoral and cell mediated immune responses.

Experiment 3

[0404] The purpose of this experiment was to compare immune responses of DMRIE:DOPE (1:1, mol:mol) and Vaxfectin™ cationic lipid formulations at different pDNA/cationic lipid molar ratios. The results of this experiement are shown in the following Table:

TABLE 18

DNA dose (μg)	DMRIE:DOPE pDNA/cationic lipid molar ratios	Vaxfectin™ pDNA/cationic lipid molar ratios	Serum Ab titers (total IgG, n=9)	$CD8^+$T cells ($SFU/10^6$)	$CD4^+$T cells ($SFU/10^6$)
10			17,778	57	54
10	4:1		48,356	47	112
10	2:1		49,778	44	133
10		4:1	88,178	68	464
10		2:1	150,756	46	363

[0405] The results of this experiment indicate that formulating the plasmid with DMRIE:DOPE or Vaxfectin™ increases both the humoral and cell mediated immune responses.

Experiment 4

[0406] The purpose of this experiment was first to compare immune responses of DMRIE:DOPE (1:1, mol:mol) at pDNA/cationic lipid molar ratios of 4:1 as an MLV (multi lamellar vesicle formulation - multi-vial) or SUV (small unilamellar vesicles - single-vial) formulation. Second, it was to compare sucrose (lyophilized and frozen) and PBS based formulations. The results of this experiment are shown in the following Table:

TABLE 19

DNA dose (μg)	Formulation	Buffer	Serum Ab titers (total IgG, n=9)	$CD8^+T$ cells ($SFU/10^6$)	$CD4^+T$ cells ($SFU/10^6$)
10		PBS, pH 7.2	21,333	107	118
10	SUV	PBS, pH 7.2	15,644	144	169
10	SUV	PBS, pH 7.8	13,511	114	173
10	SUV Frozen/thawed	Sucrose pH 7.8	15,644	103	119
10	SUV Lyophilized	Sucrose pH 7.8	10,311	ND	246
10	MLV	PBS, pH7.2	29,867	170	259

* ND - could not be counted due to high background

[0407] The results of this experiment indicate that formulating the plasmid with DMRIE:DOPE stimulates both the humoral and cell mediated immune responses.

Experiment 5

[0408] The purpose of this experiment was first to determine what effect changing the ratio of DMRIE to DOPE has on immune response at pDNA/cationic lipid molar ratios of 4:1 as an MLV (multi-vial, in PBS) or SUV (single-vial in PBS) formulation. Second, it was to compare the effect of

changing the co-lipid from DOPE to cholesterol. The results of this experiment are shown in the following Table:

TABLE 20

DNA dose (μg)	Formulation	DMRIE:DOPE	Serum Ab titers (total IgG, n=9)	$CD8^+T$ cells ($SFU/10^6$)	$CD4^+T$ cells ($SFU/10^6$)
10			19,342	65	98
10	MLV, DM:DP	1:0	38,684	70	126
10	MLV, DM:DP	3:1	75,093	82	162
10	MLV, DM:DP	1:1	53,476	78	186
10	SUV, DM:DP	1:1	36,409	96	106
10	MLV, DM:Chol	1:1	52,338	65	154

[0409] The results of this experiment indicate that formulating the plasmid with DMRIE:DOPE stimulates both the humoral and cell mediated immune responses. Changing the co-lipid from DOPE to cholesterol also stimulates both the humoral and cell mediated immune responses.

Experiment 6

[0410] The purpose of this experiment was to obtain a dose response to pDNA formulated with DMRIE:DOPE (1:1, mol:mol) at a 4:1 pDNA/cationic lipid molar ratio. The results of this experiemtn are shown in the following Table:

TABLE 21

DNA dose (μg)	Formulation	Serum Ab titers (total IgG, n=9)	$CD8^+$T cells ($SFU/10^6$)	$CD4^+$T cells ($SFU/10^6$)
10		22,044	119	154
1	MLV	5,600	22	67
3	MLV	22,756	46	97
10	MLV	45,511	199	250
30	MLV	60,444	274	473
100	MLV	91,022	277	262

[0411] The results of this experiment indicate that when the plasmid is formulated with DMRIE:DOPE, increasing the dose also increases both the humoral and cell mediated immune responses.

EXAMPLE 13

In vitro expression of influenza antigens

Plasmid Vector

[0412] Polynucleotides of the present invention were inserted into eukaryotic expression vector backbones VR10551, VR10682 and VR6430 all of which are described previously. The VR10551 vector is built on a modified pUC18 background (*see* Yanisch-Perron, C., *et al. Gene 33*:103-119 (1985)), and contains a kanamycin resistance gene, the human cytomegalovirus immediate early 1 promoter/enhancer and intron A, and the bovine growth hormone transcription termination signal, and a polylinker for inserting foreign genes. *See* Hartikka, J., *et al.*, *Hum. Gene Ther. 7*:1205-1217 (1996). However, other standard commercially available eukaryotic expression vectors may be used in the present invention, including, but not limited to: plasmids pcDNA3, pHCMV/Zeo, pCR3.1, pEF1/His, pIND/GS, pRc/HCMV2, pSV40/Zeo2, pTRACER-HCMV, pUB6/V5-His, pVAX1, and pZeoSV2 (available from Invitrogen, San Diego, CA), and plasmid pCI (available from Promega, Madison, WI).

[0413] Various plasmids were generated by cloning the nucleotide sequence for the following influenza A antigens: segment 7 (encodes both M1 and M2 proteins via differential splicing), M2 and NP into expression constructions as described below and pictured in Figure 13.

[0414] Plasmids VR4756 (SEQ ID NO:91), VR4759 (SEQ ID NO:92) and VR4762 (SEQ ID NO:93) were created by cloning the nucleotide sequence encoding the consensus sequence for the following influenza A antigens respectively: segment 7 (encoding both the M1 and M2 proteins by differential splicing), M2 and NP into the VR10551 backbone. The VR4756, VR4759 and VR4762 plasmids are also described in Table 13.

[0415] The VR4764 (SEQ ID NO:95) and VR4765 (SEQ ID NO:96) plasmids were constructed by ligating the segment 7 and NP coding regions from VR4756 and VR4762 respectively into the VR10682 vector. Specifically, the VR4756 vector was digested with EcoRV and SalI restriction endonucleases and the blunted fragment was ligated into the VR10682 backbone, which had been digested with the EcoRV restriction endonuclease. The VR4765 vector was constructed by digesting the VR4762 vector with EcoRV and NotI and ligating the NP coding region into the VR10682 backbone digested with the same restriction endonucleases.

[0416] VR4766 (SEQ ID NO:97) and VR4767 (SEQ ID NO:98) contain a CMV promoter/intron A-NP expression cassette and a RSV promoter (from VCL1005)-segment 7 expression cassette in the same orientation (VR4766) or opposite orientation (VR4767). These plasmids were generated by digesting VR4762 with the DraIII restriction endonuclease and cutting the RSV-segment 7-mRBG cassette from VR4764 with EcoRV and BamHI restriction endonucleases. After exonuclease digestion with the Klenow fragment of DNA polymerase I, the the EcoRV/BamHI fragment was cloned into the DraIII digested VR4762 vector. Both insert orientations were obtained by this blunt end cloning method.

[0417] VR4768 (SEQ ID NO:99) and VR4769 (SEQ ID NO:100), containing a CMV promoter/intron A-segment 7 expression cassette and a RSV

promoter-NP expression cassette, were similarly derived. VR4756 was digested with the DraIII restriction endonuclease and blunted by treatment with the Klenow fragment of DNA Polymerase I. The cassette containing the RSV promoter, NP coding region and mRBG terminator was removed from VR4765 by digesting with KpnI and NdeI restriction endonucleases. The fragment was also blunted with the Klenow fragment of DNA polymerase I and ligated into the DraIII-digested VR4756 vector in both gene orientations.

[0418] VR4770 (SEQ ID NO:101), VR4771 (SEQ ID NO:102) and VR4772 (SEQ ID NO:103) were constructed by cloning the coding regions from VR4756, VR4762 and VR4759 respectively into the VR6430 vector backbone. Specifically, the segment 7 gene from VR4756 was removed using SalI and EcoRV restriction endonucleases and blunted with the Klenow fragment of DNA polymerase I. The VR6430 plasmid was digested with EcoRV and BamHI and the vector backbone fragment was blunted with the Klenow fragment of DNA polymerase I. The segment 7 gene fragment was then ligated into the VR6430 vector backbone. VR4771 was derived by removing the NP insert from VR4762 following EcoRV and BglII restriction endonuclease digestion and the fragment was ligated into the VR6430 vector backbone which had been digested the same restriction endonucleases. VR4772 was derived by subcloning the M2 coding region from VR4759 as a blunted SalI-EcoRV fragment and ligating into the VR6430 vector backbone from a blunted EcoRV-BamHI digest.

[0419] VR4773 (SEQ ID NO:104) and VR4774 (SEQ ID NO:105) contain a CMV promoter/intron A-segment 7 expression cassette and a RSV/R-NP expression cassette with the genes in the same or opposite orientation. These plasmids were generated by digesting VR4756 with the DraIII restriction endonuclease, blunting, and ligating to the RSV/R-NP-BGH fragment from VR4771 (VR4771 digested with NdeI and SfiI and then blunted).

[0420] VR4775 (SEQ ID NO:106) and VR4776 (SEQ ID NO:107) contain a CMV promoter/intron A-NP expression cassette and a RSV/R-segment 7 expression cassette with the genes in the same or opposite orientation. These

plasmids were generated by digesting VR4762 with the DraIII restriction enzyme and blunting with the Klenow fragment of DNA polymerase. The RSV/R-segment 7-BGH fragment was generated by digesting VR4770 with NdeI and SfiI restriction endonucleases and ligating the blunted fragment with the DraIII restriction endonuclease digested VR4762.

[0421] VR4777 (SEQ ID NO:108) and VR4778 (SEQ ID NO:109) contain a CMV promoter/intron A-NP expression cassette and a RSV/R-M2 expression cassette in the same or opposite orientation. These plasmids were generated by digesting VR4762 with the MscI restriction endonuclease, digesting VR4772 with NdeI and SfiI restriction endonucleases and treating the RSV/R-M2-BGH with the Klenow fragment of DNA polymerase, followed by ligation of these two gel purified fragments.

[0422] VR4779 and VR4780 contain a CMV promoter/intron A-M2 expression cassette and a RSV/R-NP expression cassette in the same or opposite orientation. These plasmids were generated by digesting VR4759 with the MscI restriction endonuclease, digesting VR4771 with NdeI and SfiI restriction endonucleases and treating the RSV/R-NP-BGH segment with the Klenow fragment of DNA polymerase, followed by ligation of these two gel purified fragments.

Plasmid DNA purification

[0423] Plasmid DNA was transformed into *Escherichia coli* DH5α competent cells, and highly purified covalently closed circular plasmid DNA was isolated by a modified lysis procedure (Horn, N.A., *et al., Hum. Gene Ther.* 6:565-573 (1995)) followed by standard double CsCl-ethidium bromide gradient ultracentrifugation (Sambrook, J., *et al., Molecular Cloning: A Laboratory Manual*, 2nd Ed., Cold Spring Harbor Laboratory Press, Plainview, New York (1989)). All plasmid preparations were free of detectable chromosomal DNA, RNA and protein impurities based on gel analysis and the bicinchoninic protein assay (Pierce Chem. Co., Rockford IL). Endotoxin levels were measured using *Limulus* Amebocyte Lysate assay (LAL, Associates of Cape

Cod, Falmouth, MA) and were less than 0.6 Endotoxin Units/mg of plasmid DNA. The spectrophotometric A_{260}/A_{280} ratios of the DNA solutions were typically above 1.8. Plasmids were ethanol precipitated and resuspended in an appropriate solution, *e.g.*, 150 mM sodium phosphate (for other appropriate excipients and auxiliary agents, *see* U.S. Patent Application Publication 2002/0019358, published February 14, 2002). DNA was stored at -20°C until use. DNA was diluted by mixing it with 300 mM salt solutions and by adding appropriate amount of USP water to obtain 1 mg/ml plasmid DNA in the desired salt at the desired molar concentration.

Plasmid expression in mammalian cell lines

[0424] The expression plasmids were analyzed *in vitro* by transfecting the plasmids into a well characterized mouse melanoma cell line (VM-92, also known as UM-449) and the human rhabdomyosarcoma cell line RD (ATCC CCL-136) both available from the American Type Culture Collection, Manassas, VA. Other well-characterized human cell lines may also be used, *e.g.* MRC-5 cells, ATCC Accession No. CCL-171. The transfection was performed using cationic lipid-based transfection procedures well known to those of skill in the art. Other transfection procedures are well known in the art and may be used, for example electroporation and calcium chloride-mediated transfection (Graham F.L.and A.J. van der Eb *Virology 52*:456-67 (1973)). Following transfection, cell lysates and culture supernatants of transfected cells were evaluated to compare relative levels of expression of IV antigen proteins. The samples were assayed by western blots and ELISAs, using commercially available monoclonal antibodies (available, *e.g.*, from Research Diagnostics Inc., Flanders, NJ), so as to compare both the quality and the quantity of expressed antigen.

[0425] Genes encoding the consensus amino acid sequences (described above) derived for NP, M1 and M2 antigens were cloned in several configurations into several plasmid vector backbones. The pDNAs were tested for *in vitro*

expression and are being assessed *in vivo* for immunogenicity, as well as for the ability to protect mice from influenza challenge.

Experiment 1

[0426] Following the derivation of an amino acid consensus for M1 and M2, a native segment 7 isolate was found to encode this consensus, and this nucleotide sequence was synthesized according to methods described above. An M2-M1 fusion gene was also created and the nucleotide sequence was human codon-optimized using the above described codon optimization algorithm of Example 4. The individual full-length M2 and M1 genes were also cloned via PCR from this fusion.

[0427] *In vitro* expression of influenza antigens in cell lysates was assessed 48 hours after transfection into a mouse melanoma cell line. M2 expression was detected following transfection of VR4756 (segment 7), VR4755 (M2-M1 fusion) and VR4759 (full-length M2) using the anti-M2 monoclonal antibody (14C2) from Affinity BioReagents. The data are shown in Figure 10 for VR4756 and VR4755. Expression of M1 was detected from transfected VR4756, VR4755 and VR4760 (full-length M1) pDNAs, as detected by anti-M1 monoclonal (Serotec) in Figure 10 for VR4756 and VR4755, or by anti-M1 goat polyclonal (Virostat, data not shown). VR10551 is the empty cloning vector.

Experiment 2

[0428] In order to compare alternative human codon-optimization methods, two versions of a fusion of the first 24 amino acids of M2 to full-length NP ("eM2-NP") were constructed. One nucleotide sequence was derived from the above codon optimization algorithm, while the other was done by an outside vendor. Comparison of expression levels from the two eM2-NP pDNAs was measured *in vitro*, and comparison of immunogenicity *in vivo* is on-going.

Additionally, the full-length NP genes for both codon-optimized versions were sub-cloned from the eM2-NP pDNAs and analyzed for expression *in vitro*.

[0429] *In vitro* expression was tested to compare eM2-NP and NP pDNAs derived from the above described codon-optimization algorithm and an outside vendor algorithm. The data are shown in Figure 11. Expression levels were approximately the same for VR4757 (eM2-NP vendor optimization) vs. VR4758 (eM2-NP Applicant optimization), as detected by anti-M2 monoclonal (Figure 11A) or anti-NP mouse polyclonal (data not shown). Similarly, NP expression was approximately equal for VR4761 (vendor optimization) vs. VR4762 (Applicant optimization), detected by anti-NP mouse polyclonal generated by Applicants (Figure 11B). NP consensus protein expression *in vitro* was also detected using a goat polyclonal antibody (Fitzgerald) generated against whole H1N1 or H3N2 virus (data not shown). Expression levels of both of these NP constructs were much higher than a pDNA containing A/PR/34 NP (VR4700).

Experiment 3

[0430] Influenza antigen-encoding plasmids were transfected into VM92 cells using methods described above. Cell lysates and media were collected 48 hours after transfection. Cells were lysed in 200 µl of Laemmli buffer, cell debris removed by microcentrifuge spin, and 20 µl was heated and loaded on a 4-12% Bis-Tris gel. To determine expression of those vectors encoding secreted NP protein, 15 µl of media was mixed with 5 µl of loading buffer, heated, and loaded on a gel. Western blots were processed as described above. Primary antibodies were as follows: monoclonal antibody MA1-082 (ABR) to detect M2 protein, monoclonal antibody MCA401 (Serotec) to detect M1 protein, and a polyclonal antibody against VR4762-injected rabbits generated in-house. All primary antibodies were used at a 1:500 dilution.

[0431] Figure 14 shows Western blot results wherein M2 protein expression from segment 7-enocoding plasmids are higher in CMV promoter/intron A-

segment 7 (VR4756) and RSV/R-segment 7 (VR4770) than VR4764 (RSV promoter). NP expression appeared highest from the RSV/R-NP plasmid (VR4771), followed by CMV/intron A-NP (VR4762) and then RSV- NP (VR4765). Similar results were seen in Western blots from human RD-transfected cells.

[0432] For dual promoter plasmids, containing RSV-segment 7 and CMV/intron A-NP (VR4766 and VR4767), M2 expression from segment 7 is very low, independent of orientation. The CMV/intron A-NP expression in these dual promoter plasmids does not differ significantly compared to VR4762. RSV-NP expression in dual promoter plasmids (VR4768 and VR4769), where segment 7 is expressed from CMV/intron A, NP expression decreases somewhat, but not as drastically as M2 expression in the dual promoter VR4766 and VR4767.

[0433] Figure 15 shows expression of the M1 and M2 proteins from segment 7, as well as NP, from CMV promoter/intron A, RSV promoter, and RSV/R-containing plasmids. For these Western blots, dual promoter plasmids contain the CMV promoter/intron A and RSV/R driving either NP or segment 7. Similar results were seen in Western blots from human RD-transfected cells.

[0434] Western blot results confirm that the M1 and M2 protein expression from both CMV promoter/intron A-segment 7 (VR4756) and RSV/R-segment 7 (VR4770) is superior to RSV-segment 7 (VR4764). M1 and M2 expression decrease slightly when RSV/R-segment 7 or CMV/intron A-segment 7 is combined with CMV/intron A-NP or RSV/R-NP in a dual promoter plasmid (VR4773, VR4774, VR4775, and VR4776). Results were similar in Western blots from human RD transfected cells. Human RD cells transfected with M2 antigen encoding plasmids, RSV/R-M2 (VR4772) and CMV/intron A-M2 (VR4759), showed a similar level of M2 expression, which was decreased in dual promoter plasmids (VR4777, VR4778, VR4779, and VR4780). Human RD cells transfected with NP antigen-encoding plasmids, VR4762, VR4771, VR4777, VR4778, VR4779, and VR4780, all showed similar NP expression levels.

EXAMPLE 14

Murine Influenza A Challenge Model

[0435] A model *influenza A* challenge model has been established utilizing a mouse-adapted A/HK/8/68 strain. Positive and negative control Hemagluttinin (HA)-containing plasmids were generated by PCR of the HA genes directly from mouse-adapted A/Hong Kong/68 (H3N2) and A/Puerto Rico/34 (H1N1) viruses, respectively.

[0436] For all experiments, plasmid DNA vaccinations are given as bilateral, rectus femoris injections at 0 and 3 weeks, followed by orbital sinus puncture (OSP) bleed at 5 weeks and intranasal viral challenge at 6 weeks with 500 pfu (1 LD_{90}) of virus. Mice are monitored for morbidity and weight loss for about 3 weeks following viral challenge. Endpoint antibody titers for NP and M2 were determined by ELISA. For study GSJ08, 5 additional mice per test group were vaccinated and interferon-γ ELISPOT assays were performed at week number 5.

Study CL88:

[0437] A mouse influenza challenge study was initiated to test the M1, M2, Segment 7, and NP-encoding plamids alone, or in combination. In addition to HA pDNAs, sub-lethal infection and naïve mice serve as additional positive and negative controls, respectively. Mice received 100 μg of each plasmid formulated in poloxamer CRL1005, 02A formulation. The test groups and 21 day post-challenge survival are shown in Table 21:

TABLE 21

Group	Construct(s)	Total pDNA per vaccination	# mice/ group	21 day Survival (%)
A	VR4762 (NP)	100 µg	12	**17**
B	VR4759 (M2)	100 µg	12	**25**
C	VR4760 (M1)	100 µg	12	**0**
D	VR4756 (S7)	100 µg	12	**50**
E	VR4762 (NP)+VR4759 (M2)	200 µg	12	**100**
F	VR4762 (NP) +VR4760 (M1)	200 µg	12	**17**
G	VR4762 (NP) +VR4756 (S7)	200 µg	12	**75**
H	VR4750 (HA, H3N2, + control)	100 µg	12	**100**
I	VR4752 (HA, H1N1, - control)	100 µg	12	**8**
J	Naïve mice (- control)	N/A	12	**8**
K	Sub-lethal (+ control)	N/A	12	**100**

CL88 Results:

[0438] The performance criteria for this study was survival of >90% for the positive controls, ≤ 10% for the negative controls, and > 75% for the experimental groups. Table 21 shows that all of the control groups, as well as two experimental groups met the performance criteria. The M2 + NP and S7 + NP plamsid DNA combinations resulted in 100% and 75% survival, respectively. There was no statistically significant difference ($p < 0.05$) between the two lead plasmid combinations, but there was statistical significance in the S7, S7 + NP, and M2 + NP groups vs. the negative controls.

[0439] Weight loss data showed that the positive control groups did not exhibit any weight loss following viral challenge, as opposed to the weight loss seen in all of the experimental groups. Mice that survived the viral challenge recovered to their starting weight by the end of the study. Tables 22 and 23 show endpoint antibody titers for test groups containing M2, Segment 7, and NP antigens. Shaded boxes represent mice that died following viral challenge.

TABLE 22: CL88 M2 Antibody Titers

mouse	Group D (seg 7)	Group G (NP + seg7)	Group B (M2)	Group E (NP + M2)
1	800	1600	25600	1600
2	3200	1600	200	6400
3	3200	6400	3200	200
4	6400	800	12800	6400
5	12800	0	3200	3200
6	800	12800	12800	3200
7	12800	0	3200	3200
8	6400	0	3200	6400
9	800	3200	400	1600
10	12800	3200	6400	800
11	12800	1600	200	3200
12	6400	12800	12800	400

** An M2 antibody titer of 0 represents a titer of <100.

Table 23: CL88 NP Antibody Titers

mouse	Group A (NP)	Group E (NP + M2)	Group F (NP + M1)	Group G (NP + seg7)
1	204800	51200	102400	25600
2	204800	51200	204800	51200
3	204800	51200	102400	51200
4	204800	25600	51200	25600
5	102400	102400	102400	25600
6	102400	51200	102400	102400
7	204800	204800	51200	102400
8	409600	102400	51200	102400
9	<6400	102400	102400	51200
10	409600	102400	25600	102400
11	204800	51200	204800	25600
12	204800	51200	102400	25600

Study GSJ05:

[0440] In order to attempt to distinguish between the two antigen combinations, S7 + NP and M2 + NP, a dose ranging challenge experiment was undertaken with these two plasmid combinations. Mice were injected with 100 μg, 30 μg, or 10 μg per plasmid in the 02A poloxamer formulation at 0 and 3 weeks, followed by bleed at 5 weeks and viral challenge at 6 weeks. Sixteen mice per group were vaccinated for test groups A-H, while 12 mice per group were vaccinated for the controls. Poloxamer 02A-formulated HA

plasmids, VR4750 (HA H3) and VR4752 (HA H1), were included as positive and negative controls, respectively. The test groups and 21 day survival post-challenge are shown in Table 24:

TABLE 24

Group	Construct(s)	Total pDNA per vaccination	# mice/ group	21 day Survival (%)
A	VR4756 (Seg 7) + VR4762 (NP)	200μg	16	73
B	VR4756 (Seg 7) + VR4762 (NP)	60 μg	16	81
C	VR4756 (Seg 7) + VR4762 (NP)	20 μg	16	69
D	VR4759 (M2) + VR4762 (NP)	200μg	16	94
E	VR4759 (M2) + VR4762 (NP)	60 μg	16	81
F	VR4759 (M2) + VR4762 (NP)	20 μg	16	75
G	VR4750 (Positive DNA control)	100 μg	12	100
H	VR4752 (Negative DNA control)	100 μg	12	8

Results

[0441] The performance criteria of >90% survival with the HA positive control and ≤ 10% for the HA negative control plasmid again were met. The performance criteria for the experimental groups, > 75% survival at the 30 μg per plasmid dose, was met by both M2 + NP and S7 + NP (Table 24). In fact, at a dose of 10 μg per plasmid, S7 + NP and M2 + NP resulted in 69% and 75% survival, respectively. There was no statistical significance ($p < 0.05$) between the three doses of M2 + NP or between the 3 doses of S7 + NP, nor was there statistical significance when comparing M2 + NP to S7 + NP at the 200 μg, 60 μg, or 20 μg doses. However, there was a statistical difference for the HA positive control vs. S7 + NP at 200 μg and 20 μg. Body mass data shows weight loss and recovery by all surviving experimental plasmid DNA-vaccinated groups, while the HA positive control mice did not experience weight loss. Antibody data for M2 and NP are shown in Tables 25 and 26.

TABLE 25: GSJ05 M2 Antibody Titers

mouse #	Group A	Group B	Group C	Group D	Group E	Group F
1	800	400	3200	6400	800	3200
2	200	0	0	25600	1600	0
3	0	0	0	3200	3200	3200
4	100	0	0	6400	1600	400
5	0	0	0	3200	800	1600
6	3200	400	0	6400	200	100
7	25600	800	0	6400	0	0
8	0	100	0	1600	0	400
9	0	0	800	3200	12800	0
10	0	800	0	1600	800	1600
11	100	1600	0	3200	200	1600
12	3200	0	100	6400	800	1600
13	800	0	400	3200	400	800
14	0	0	1600	3200	400	100
15	0	1600	800	1600	3200	200
16	0	0	800	800	3200	800

TABLE 26: GSJ05 NP Antibody Titers

mouse #	Group A	Group B	Group C	Group D	Group E	Group F
1	25600	51200	51200	51200	25600	25600
2	25600	51200	12800	51200	25600	6400
3	102400	25600	51200	12800	51200	25600
4	25600	12800	25600	25600	12800	12800
5	51200	102400	6400	25600	12800	12800
6	25600	51200	25600	25600	12800	6400
7	102400	51200	6400	6400	3200	800
8	51200	25600	12800	12800	51200	6400
9	12800	51200	25600	102400	12800	12800
10	25600	25600	25600	25600	12800	25600
11	51200	25600	51200	25600	25600	3200
12	51200	51200	3200	25600	12800	12800
13	51200	51200	25600	51200	25600	12800
14	51200	12800	25600	51200	6400	12800
15	25600	6400	25600	25600	25600	12800
16	51200	51200	25600	12800	12800	6400

Gray shading represents mice that died post-challenge. Group A, mouse 9 (spotted box) died during the OSP bleed procedure.

Study GSJ06

[0442] The plasmid combination VR4759 (M2) and VR4762 (NP) was utilized in further mouse influenza challenge studies to examine additional formulations.

[0443] Using the experimental protocol described above, 12 mice per group were vaccinated with equal weight VR4759 (M2) and VR4762 (NP) in the following formulations:

- Poloxamer 02A used in the previous two challenge experiments.
- DMRIE + Cholesterol (DM:Chol) at a 4:1 molar ratio of DNA to DMRIE, the molar ratio of DM:Chol is 3:1.
- Vaxfectin™ (VC1052 + DPyPE) at a 4:1 molar ratio of DNA: VC1052, the molar ratio of VC1052: DpyPE is 1:1.

GSJ06 study design and 21 day survival post-challenge is found in Table 27.

Table 27

Group	pDNA	Total pDNA	21 day Survival (%)
A	Poloxamer 02A	20 ug	92
B	Poloxamer 02A	2 ug	58
C	DMRIE:Cholesterol	20 ug	58
D	DMRIE:Cholesterol	2 ug	17
E	Vaxfectin	20 ug	100
F	Vaxfectin	2 ug	75
G	VR4750 (HA,positive)	100 ug	100
H	VR4752 (HA,negative)	100 ug	0

Results

[0444] Poloxamer 02A and Vaxfectin™-formulated plasmid DNA led to 92% and 100% survival at the 20 μg pDNA dose, and 58% and 75% at the 2 μg dose, respectively (Table 27).

[0445] Average weights were tracked for each group of mice starting at the day of challenge. As shown in Table 28, it was noted in this experiment that the weight recovery for group E (Vaxfectin™-formulated pDNA, 20 μg total) began after day 4, as opposed to the other groups' recovery beginning at day 7.

Antibody titers, Tables 29 and 30, were determined for M2 and NP and shaded boxes represent mice that died following viral challenge.

TABLE 28: GSJ06 Average Body Weights Post-Challenge

Group	pDNA	Total pDNA	Avg Body Weights (g) - Days post-challenge									
			0	2	4	7	9	11	14	16	18	2
A	Poloxamer 02A	20 ug	20.73	19.98	17.98	16.14	17.36	18.74	19.94	20.45	20.60	2
B	Poloxamer 02A	2 ug	21.08	19.91	17.96	15.17	15.16	16.03	16.77	17.41	18.10	1
C	DMRIE:Cholesterol	20 ug	21.43	20.24	18.14	16.41	18.68	19.24	20.14	20.50	20.90	2
D	DMRIE:Cholesterol	2 ug	21.28	20.24	17.58	14.83	16.18	17.45	18.80	19.84	20.13	2
E	Vaxfectin	20 ug	21.41	19.97	17.83	18.10	19.12	19.82	20.39	20.87	20.93	2
F	Vaxfectin	2 ug	20.47	18.97	16.86	15.10	16.22	16.84	17.87	18.60	19.08	2
G	VR4750 (HA,positive)	100 ug	21.30	20.97	21.60	21.21	21.57	21.79	21.84	22.13	21.94	2
H	VR4752 (HA,negative)	100 ug	20.89	20.25	17.57	14.67						

Shading represents the lowest group average post-challenge for each test group. Group H (negative control) weight averages are not recorded once the percentage survival has dropped below 50%.

TABLE 29: GSJ06 M2 Antibody Titers

mouse #	Group A	Group B	Group C	Group D	Group E	Group F
1	800	400	200	0	1600	6400
2	6400	800	1600	0	400	800
3	6400	0	400	0	12800	3200
4	1600	0	400	0	25600	1600
5	6400	3200	1600	400	100	400
6	3200	100	100	0	12800	1600
7	800	1600	1600	0	800	3200
8	400	100	3200	200	6400	100
9	1600	0	100	0	6400	100
10	100	400	1600	100	3200	400
11	3200	0	800	0	1600	1600
12	6400	0	0	0	6400	1600

TABLE 30: GSJ06 NP Antibody Titers

mouse #	Group A	Group B	Group C	Group D	Group E	Group F
1	6400	6400	12800	1600	51200	51200
2	51200	6400	6400	3200	102400	102400
3	12800	1600	6400	200	51200	25600
4	25600	1600	6400	3200	204800	102400
5	25600	6400	25600	3200	51200	51200
6	51200	12800	25600	12800	102400	51200
7	25600	25600	12800	100	51200	51200
8	25600	3200	12800	6400	25600	25600
9	25600	6400	51200	400	51200	25600
10	51200	6400	12800	3200	51200	51200
11	25600	12800	25600	6400	102400	51200
12	51200	6400	12800	400	51200	51200

Study GSJ08

[0446] Further formulation comparisons were done with utilizing VR4759 (M2) and VR4762 (NP). Seventeen mice per test group (A-G) were vaccinated with equal weight VR4759 (M2) and VR4762 (NP) vectors in the following formulations:

- Poloxamer 02A
- Vaxfectin™ (preparations A and B represent different purifications)
- DMRIE :DOPE at a 4:1 molar ratio of DNA to DMRIE
- DMRIE: DOPE at a 2.5:1 molar ratio of DNA to DMRIE
- PBS (unformulated pDNA)

Twelve mice per test group were challenged with influenza virus at week number 6. Five mice per test group were sacrificed at days 36-38 for T cell assays (IFN-γ ELISPOT). The test groups and 21 day survival post-challenge are shown in Table 31. Groups A-D, and F-G were vaccinated with 20 μg total plasmid DNA per injection to further explore the weight loss/recovery phenomena seen in study GSJ06 with the Vaxfectin™-formulated pDNA.

TABLE 31:

Group	Construct(s)	Total pDNA per vaccination	21 Day Survival (%)
A	Poloxamer 02A	20 µg	50
B	DMRIE:DOPE 4:1	20 µg	92
C	DMRIE:DOPE 2.5:1	20 µg	92
D	Vaxfectin - prep A	20 µg	92
E	Vaxfectin - prep A	2 µg	75
F	Vaxfectin - prep B	20 µg	100
G	PBS	20 µg	42
H	VR4750 (HA, H3N2, + control)	100 µg	100
I	VR4752 (HA, H1N1, - control)	100 µg	17

Results

[0447] The DMRIE:DOPE and Vaxfectin™ formulated groups resulted in 92-100% survival at a 20 µg pDNA dose. Group A (Poloxamer 02A) and Group G (PBS) survival results were not statistically different than the negative control (as measured by Fisher exact p, one-tailed), while the Vaxfectin™ and DMIRE:DOPE Groups (Groups B-F) were shown to be statistically superior ($p<0.05$) as compared to the negative control. Therefore, the plasmid DNA formulated with lipids appear to provide superior protection in the mouse influenza model challenge.

[0448] A repeated measures ANOVA mixed model analysis of weight data for groups B, C, and D of the weight loss and recovery data showed that Group B and Group D were not statistically different, while Group C and Group D were statistically different.

[0449] T cell responses, as measured by IFN-γ ELISPOT assay, were conducted on the last 5 mice per group using an M2 peptide encompassing the first 24 amino acids of M2 (TABLE 33), an NP protein expressed in baculovirus (TABLE 34), and an NP CD8+ Balb/c immunodominant peptide (TABLE 35).

[0450] Antibody titers, Tables 36 and 37, were determined for M2 and NP proteins. The first 12 mice listed for each group were challenge at day 42 and

the last 5 mice per group were sacrificed for IFN-γ ELISPOT. The shaded boxes represent mice that died following viral challenge.

TABLE 32: GSJ06 Average Body Weights Post-Challenge

Group	Construct(s)	Total pDNA per vaccination	Avg Body Weights (g) - Days post-challenge										
			0	2	4	5	6	7	9	11	14	16	18	22
A	Poloxamer 02A	20 µg	20.47	18.97	16.30	15.43	14.75	14.31	14.35	14.44	16.63	17.64	18.36	20.53
B	DMRIE:DOPE 4:1	20 µg	21.58	19.94	17.43	16.75	16.17	15.86	16.43	17.28	18.45	19.50	20.22	20.89
C	DMRIE:DOPE 2.5:1	20 µg	19.95	18.58	16.44	15.77	15.46	15.56	15.75	16.22	16.78	17.16	17.31	18.04
D	Vaxfectin - prep A	20 µg	20.87	19.22	16.81	16.47	16.40	16.92	17.94	19.48	20.06	20.19	20.64	21.17
E	Vaxfectin - prep A	2 µg	20.40	19.59	17.97	17.47	17.27	17.23	18.96	19.83	20.24	20.49	20.57	21.06
F	Vaxfectin - prep B	20 µg	21.33	20.01	17.88	17.61	17.74	18.21	18.86	19.85	20.29	20.77	20.88	21.39
G	PBS	20 µg	20.84	19.46	16.97	16.00	15.38	14.79	15.80	16.39	17.35			
H	VR4750 (HA, H3N2, + control)	100 µg	21.25	21.15	21.27	20.77	20.92	21.24	20.74	21.16	21.33	21.40	21.64	21.64
I	VR4752 (HA, H1N1, - control)	100 µg	21.67	20.65	17.87	16.77	16.05	15.17	15.09					

Shading represents the lowest group average post-challenge for each test group. Group G and I weight averages are not recorded once the percentage survival has dropped below 50%.

TABLE 33: M2 peptide Interferon-γ ELISPOT

M2 peptide IFN gamma ELISPOT (SFU/10E6 cells)							
Mouse	A	B	C	D	E	F	G
1	66	88	145	189	283	253	31
2	11	115	150	269	62	282	47
3	115	247	190	233	99	283	112
4	20	6	51	67	73	93	45
5	93	277	397	248	202	399	93
AVG	**61**	**147**	**187**	**201**	**144**	**262**	**66**

TABLE 34: NP CD4 peptide Interferon-γ ELISPOT

NP CD4 peptide IFN gamma ELISPOT (SFU/10E6 cells)							
Mouse	A	B	C	D	E	F	G
1	7	32	3	52	72	108	18
2	8	83	34	125	8	34	8
3	22	91	106	293	26	51	73
4	9	15	80	39	53	10	12
5	37	150	374	117	40	217	43
AVG	**17**	**74**	**119**	**125**	**40**	**84**	**31**

TABLE 35: NP CD8 peptide Interferon-γ ELISPOT

NP CD8 peptide IFN gamma ELISPOT (SFU/10E6 cells)							
Mouse	A	B	C	D	E	F	G
1	11	37	4	14	20	67	8
2	0	3	4	6	1	0	2
3	31	19	15	26	23	51	34
4	1	0	0	12	1	38	3
5	46	36	39	21	13	15	18
AVG	18	19	12	16	12	34	13

TABLE 36: GSJ08 M2 Antibody Titers

mouse #	Group A	Group B	Group C	Group D	Group E	Group F	Group G	Group H	ELISPOT #
1	1600	3200	3200	6400	400	12800	800	6400	
2	12800	12800	6400	1600	3200	800	1600	800	
3	100	3200	6400	25600	800	3200	1600	800	
4	800	0	6400	1600	400	800	1600	0	
5	1600	0	800	12800	1600	800	800	200	
6	6400	3200	1600	6400	200	12800	400	800	
7	12800	3200	12800	800	1600	3200	1600	6400	
8	12800	6400	3200	12800	12800	12800	12800	400	
9	1600	1600	0	12800	6400	12800	100	200	
10	3200	1600	12800	12800	1600	800	100	12800	
11	1600	6400	3200	3200	0	6400	800	400	
12	200	800	6400	25600	1600	800	6400	6400	
13	1600	800	6400	12800	3200	6400	6400	6400	1
14	3200	6400	1600	1600	800	12800	3200	12800	2
15	0	1600	3200	3200	12800	12800	6400	12800	3
16	3200	3200	1600	12800	0	12800	200	6400	4
17	3200	200	400	6400	800	400	1600	3200	5

TABLE 37: GSJ08 NP Antibody Titers

mouse #	Group A	Group B	Group C	Group D	Group E	Group F	Group G	Group H	ELISPOT #
1	51200	25600	6400	51200	12800	51200	51200	25600	
2	6400	25600	51200	51200	25600	102400	12800	25600	
3	<3200	51200	12800	25600	6400	102400	25600	12800	
4	3200	25600	51200	102400	12800	25600	25600	25600	
5	25600	12800	12800	51200	51200	102400	25600	3200	
6	25600	12800	51200	102400	25600	51200	25600	12800	
7	51200	51200	51200	51200	25600	204800	102400	51200	
8	25600	51200	25600	51200	12800	51200	25600	51200	
9	25600	12800	25600	51200	51200	51200	12800	3200	
10	6400	12800	51200	51200	25600	204800	6400	25600	
11	12800	51200	25600	204800	12800	102400	51200	25600	
12	102400	102400	51200	102400	25600	204800	12800	51200	
13	25600	25600	12800	51200	51200	102400	25600	25600	1
14	51200	25600	12800	51200	25600	102400	25600	51200	2
15	51200	51200	51200	51200	25600	25600	102400	12800	3
16	25600	6400	25600	51200	25600	102400	25600	51200	4
17	25600	25600	51200	51200	12800	51200	25600	25600	5

* * *

[0451] The present invention is not to be limited in scope by the specific embodiments described which are intended as single illustrations of individual aspects of the invention, and any compositions or methods which are functionally equivalent are within the scope of this invention. Indeed, various modifications of the invention in addition to those shown and described herein will become apparent to those skilled in the art from the foregoing description and accompanying drawings. Such modifications are intended to fall within the scope of the appended claims.

[0452] All publications and patent applications mentioned in this specification are herein incorporated by reference to the same extent as if each individual publication or patent application was specifically and individually indicated to be incorporated by reference.

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:2, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:2;

wherein about 8 of the 18 phenylalanine codons in said coding region are TTT, and about 10 of said phenylalanine codons are TTC;

wherein about 2 of the 33 leucine codons in said coding region are TTA, about 4 of said leucine codons are TTG, about 4 of said leucine codons are CTT, about 6 of said leucine codons are CTC, about 2 of said leucine codons are CTA, and about 13 of said leucine codons are CTG;

wherein about 9 of the 26 isoleucine codons in said coding region are ATT, about 13 of said isoleucine codons are ATC, and about 4 of said isoleucine codons are ATA;

wherein the 25 methionine codons in said coding region are ATG;

wherein about 4 of the 23 valine codons in said coding region are GTT, about 5 of said valine codons are GTG, about 3 of said valine codons are GTA, and about 11 of said valine codons are GTG;

wherein about 7 of the 40 serine codons in said coding region are TCT, about 9 of said serine codons are TCC, about 6 of said serine codons are TCA, about 2 of said serine codons are TCG, about 6 of said serine codons are AGT, and about 10 of said serine codons are AGC;

wherein about 5 of the 17 proline codons in said coding region are CCT, about 6 of said proline codons are CCC, about 5 of said proline codons are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 28 threonine codons in said coding region are ACT, about 10 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 3 of said threonine codons are ACG;

wherein about 10 of the 39 alanine codons in said coding region are GCT, about 16 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 7 of the 15 tyrosine codons in said coding region are TAT and about 8 of said tyrosine codons are TAC;

wherein about 2 of the 6 histidine codons in said coding region are CAT and about 4 of said histidine codons are CAC;

wherein about 5 of the 21 glutamine codons in said coding region are CAA and about 16 of said glutamine codons are CAG;

wherein about 12 of the 26 asparagine codons in said coding region are AAT and about 14 of said asparagine codons are AAC;

wherein about 9 of the 21 lysine codons in said coding region are AAA and about 12 of said lysine codons are AAG;

wherein about 10 of the 22 aspartic acid codons in said coding region are GAT and about 12 of said aspartic acid codons are GAC;

wherein about 11 of the 26 glutamic acid codons in said coding region are GAA and about 15 of said glutamic acid codons are GAG;

wherein about 3 of the 6 cysteine codons in said coding region are TGT and about 3 of said cysteine codons are TGC; the 6 tryptophan codons are TGG;

wherein about 4 of the 49 arginine codons in said coding region are CGT, about 9 of said arginine codons are CGC, about 5 of said arginine codons are CGA, about 10 of said arginine codons are CGG, about 10 of said arginine codons are AGA, and about 10 of said arginine codons are AGG; and

wherein about 7 of the 41 glycine codons in said coding region are GGT, about 14 of said glycine codons are GGC, about 10 of said glycine codons are GGA, and about 10 of said glycine codons are GGG; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

2. The polynucleotide of claim 1, wherein said codon optimized coding region comprises SEQ ID NO:23.

3. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:2, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:2;

wherein the 18 phenylalanine codons in said coding region are TTC, the 33 leucine codons in said coding region are CTG, the 26 isoleucine codons in said coding region are ATC, the 25 methionine codons in said coding region are ATG, the 23 valine codons in said coding region are GTG, the 40 serine

codons in said coding region are AGC, the 17 proline codons in said coding region are CCC, the 28 threonine codons in said coding region are ACC, the 39 alanine codons in said coding region are GCC, the 15 tyrosine codons in said coding region are TAC, the 6 histidine codons in said coding region are CAC, the 21 glutamine codons in said coding region are CAG, the 26 asparagine codons in said coding region are AAC, the 21 lysine codons in said coding region are AAG, the 22 aspartic acid codons in said coding region are GAC, the 36 glutamic acid codons in said coding region are GAG, the 6 tryptophan codons in said coding region are TGG, the 49 arginine codons in said coding region are selected from the group consisting of CGG, AGA, and AGG, and the 41 glycine codons in said coding region are GGC; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

4. The polynucleotide of claim 3, wherein said codon optimized coding region comprises SEQ ID NO:24.

5. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:2, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:2;

wherein said codon-optimized coding region consists of nucleotides 46-1542 of SEQ ID NO:1 except that the 33 leucine codons are CTG, the 17 proline codons are CCC, the 39 alanine codons are GCC, the 21 glutamine

codons are CAG, the 26 asparagine codons are AAC, the 21 lysine codons are AAG, and the 36 glutamic acid codons are GAG; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

6. The polynucleotide of claim 5, wherein said codon optimized coding region comprises SEQ ID NO:25.

7. The polynucleotide of any one of claims 1-6, wherein said nucleic acid fragment encodes at least 50 contiguous amino acids of SEQ ID NO:2.

8. The polynucleotide of any one of claims 1-6, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:2.

9. The polynucleotide of claim 8, wherein said nucleic acid fragment encodes SEQ ID NO:2.

10. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:2, wherein said nucleic acid fragment is a variant fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:2;

wherein about 8 of the 18 phenylalanine codons in said coding region are TTT, and about 10 of said phenylalanine codons are TTC;

wherein about 2 of the 33 leucine codons in said coding region are TTA, about 4 of said leucine codons are TTG, about 4 of said leucine codons are CTT, about 6 of said leucine codons are CTC, about 2 of said leucine codons are CTA, and about 13 of said leucine codons are CTG;

wherein about 9 of the 26 isoleucine codons in said coding region are ATT, about 13 of said isoleucine codons are ATC, and about 4 of said isoleucine codons are ATA;

wherein the 25 methionine codons in said coding region are ATG;

wherein about 4 of the 23 valine codons in said coding region are GTT, about 5 of said valine codons are GTG, about 3 of said valine codons are GTA, and about 11 of said valine codons are GTG;

wherein about 7 of the 40 serine codons in said coding region are TCT, about 9 of said serine codons are TCC, about 6 of said serine codons are TCA, about 2 of said serine codons are TCG, about 6 of said serine codons are AGT, and about 10 of said serine codons are AGC;

wherein about 5 of the 17 proline codons in said coding region are CCT, about 6 of said proline codons are CCC, about 5 of said proline codons are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 28 threonine codons in said coding region are ACT, about 10 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 3 of said threonine codons are ACG;

wherein about 10 of the 39 alanine codons in said coding region are GCT, about 16 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 7 of the 15 tyrosine codons in said coding region are TAT and about 8 of said tyrosine codons are TAC;

wherein about 2 of the 6 histidine codons in said coding region are CAT and about 4 of said histidine codons are CAC;

wherein about 5 of the 21 glutamine codons in said coding region are CAA and about 16 of said glutamine codons are CAG;

wherein about 12 of the 26 asparagine codons in said coding region are AAT and about 14 of said asparagine codons are AAC;

wherein about 9 of the 21 lysine codons in said coding region are AAA and about 12 of said lysine codons are AAG;

wherein about 10 of the 22 aspartic acid codons in said coding region are GAT and about 12 of said aspartic acid codons are GAC;

wherein about 11 of the 26 glutamic acid codons in said coding region are GAA and about 15 of said glutamic acid codons are GAG;

wherein about 3 of the 6 cysteine codons in said coding region are TGT and about 3 of said cysteine codons are TGC; the 6 tryptophan codons are TGG;

wherein about 4 of the 49 arginine codons in said coding region are CGT, about 9 of said arginine codons are CGC, about 5 of said arginine codons are CGA, about 10 of said arginine codons are CGG, about 10 of said arginine codons are AGA, and about 10 of said arginine codons are AGG; and

wherein about 7 of the 41 glycine codons in said coding region are GGT, about 14 of said glycine codons are GGC, about 10 of said glycine codons are GGA, and about 10 of said glycine codons are GGG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

11. The polynucleotide of claim 10, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:2.

12. The polynucleotide of claim 11, wherein said nucleic acid fragment encodes SEQ ID NO:2.

13. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:2, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:2;

wherein the 18 phenylalanine codons in said coding region are TTC, the 33 leucine codons in said coding region are CTG, the 26 isoleucine codons in said coding region are ATC, the 25 methionine codons in said coding region are ATG, the 23 valine codons in said coding region are GTG, the 40 serine codons in said coding region are AGC, the 17 proline codons in said coding region are CCC, the 28 threonine codons in said coding region are ACC, the 39 alanine codons in said coding region are GCC, the 15 tyrosine codons in said coding region are TAC, the 6 histidine codons in said coding region are

CAC, the 21 glutamine codons in said coding region are CAG, the 26 asparagine codons in said coding region are AAC, the 21 lysine codons in said coding region are AAG, the 22 aspartic acid codons in said coding region are GAC, the 36 glutamic acid codons in said coding region are GAG, the 6 tryptophan codons in said coding region are TGG, the 49 arginine codons in said coding region are selected from the group consisting of CGG, AGA, and AGG, and the 41 glycine codons in said coding region are GGC; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

14. The polynucleotide of claim 13, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:2.

15. The polynucleotide of claim 14, wherein said nucleic acid fragment encodes SEQ ID NO:2.

16. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:2, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:2;

wherein said codon-optimized coding region consists of nucleotides 46-1542 of SEQ ID NO:1 except that the 33 leucine codons are CTG, the 17 proline codons are CCC, the 39 alanine codons are GCC, the 21 glutamine

codons are CAG, the 26 asparagine codons are AAC, the 21 lysine codons are AAG, and the 36 glutamic acid codons are GAG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

17. The polynucleotide of claim 16, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:2.

18. The polynucleotide of claim 17, wherein said nucleic acid fragment encodes SEQ ID NO:2.

19. The polynucleotide of any one of claims 1-18, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

20. The polynucleotide of claim 19, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

21. The polynucleotide of claim 20, wherein said heterologous polypeptide is a hepatitis B core antigen.

22. The polynucleotide of claim 21, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

23. The polynucleotide of claim 22, comprising SEQ ID NO:43.

24. The polynucleotide of claim 20, wherein said heterologous polypeptide is the extracellular domain of an influenza virus M2 protein.

25. The polynucleotide of claim 24, wherein said extracellular domain of an influenza virus M2 protein comprises amino acids 1 to 24 of SEQ ID NO:5.

26. The polynucleotide of any one of claims 1 to 25, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

27. The polynucleotide of any one of claims 1 to 25, which is RNA.

28. The polynucleotide of claim 27, which is messenger RNA (mRNA).

29. A vector comprising the polynucleotide of any one of claims 1 to 28.

30. The vector of claim 29, which is a plasmid.

31. A composition comprising the polynucleotide of any one of claims 1 to 28, and a carrier.

32. The composition of claim 31, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

33. The composition of claim 32, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(c) a solubilized mono-phosphoryl lipid A formulation; and

(d) CRL1005/BAK.

34. The composition of claim 33, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

35. The composition of claim 34, wherein said neutral lipid is DPyPE.

36. The composition of claim 32, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

37. The composition of claim 32, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

38. The composition of claim 37, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

39. The composition of claim 37 or claim 38, which is formulated by combining together the CRL1005, BAK, and polynucleotide at a

temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

40. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 1 to 29.

41. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:4, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 3 of the 7 phenylalanine codons in said coding region are TTT, and about 4 of said phenylalanine codons are TTC;

wherein about 2 of the 26 leucine codons in said coding region are TTA, about 3 of said leucine codons are TTG, about 3 of said leucine codons are CTT, about 5 of said leucine codons are CTC, about 2 of said leucine codons are CTA, and about 11 of said leucine codons are CTG;

wherein about 4 of the 11 isoleucine codons in said coding region are ATT, about 5 of said isoleucine codons are ATC, and about 2 of said isoleucine codons are ATA;

wherein the 14 methionine codons in said coding region are ATG;

wherein about 3 of the 16 valine codons in said coding region are GTT, about 4 of said valine codons are GTG, about 2 of said valine codons are GTA, and about 8 of said valine codons are GTG;

wherein about 3 of the 18 serine codons in said coding region are TCT, about 4 of said serine codons are TCC, about 3 of said serine codons are TCA, about 1 of said serine codons is TCG, about 3 of said serine codons are AGT, and about 4 of said serine codons are AGC;

wherein about 2 of the 8 proline codons are CCT, about 3 of said proline codons are CCC, about 2 of said proline codons are CCA, and about 1 of said proline codons is CCG;

wherein about 4 of the 18 threonine codons in said coding region are ACT, about 7 of said threonine codons are ACC, about 5 of said threonine codons are ACA, and about 2 of said threonine codons are ACG;

wherein about 7 of the 25 alanine codons in said coding region are GCT, about 10 of said alanine codons are GCC, about 6 of said alanine codons are GCA, and about 3 of said alanine codons are GCG;

wherein about 2 of the 5 tyrosine codons in said coding region are TAT and about 3 of said tyrosine codons are TAC;

wherein about 2 of the 5 histidine codons in said coding region are CAT and about 3 of said histidine codons are CAC;

wherein about 4 of the 15 glutamine codons in said coding region are CAA and about 11 of said glutamine codons are CAG;

wherein about 5 of the 11 asparagine codons in said coding region are AAT and about 6 of said asparagine codons are AAC;

wherein about 5 of the 13 lysine codons in said coding region are AAA and about 8 of said lysine codons are AAG;

wherein about 3 of the 6 aspartic acid codons in said coding region are GAT and about 3 of said aspartic acid codons are GAC;

wherein about 7 of the 17 glutamic acid codons in said coding region are GAA and about 10 of said glutamic acid codons are GAG;

wherein about 1 of the 3 cysteine codons in said coding region is TGT and about 2 of said cysteine codons are TGC;

wherein the 1 tryptophan codon in said coding region is TGG;

wherein about 1 of the 17 arginine codons in said coding region are CGT, about 3 of said arginine codons are CGC, about 2 of said arginine codons are CGA, about 4 of said arginine codons are CGG, about 3 of said arginine codons are AGA, and about 3 of said arginine codons are AGG; and

wherein about 3 of the 16 glycine codons in said coding region are GGT, about 6 of said glycine codons are GGC, about 4 of said glycine codons are GGA, and about 4 of said glycine codons are GGG; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:4.

42. The polynucleotide of claim 41, wherein said codon optimized coding region comprises SEQ ID NO:26.

43. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:4, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:4;

wherein the 7 phenylalanine codons in said coding region are TTC, the 26 leucine codons in said coding region are CTG, the 11 isoleucine codons in said coding region are ATC, the 14 methionine codons in said coding region are ATG, the 16 valine codons in said coding region are GTG, the 18 serine codons in said coding region are AGC, the 8 proline codons in said coding region are CCC, the 18 threonine codons in said coding region are ACC, the 25 alanine codons in said coding region are GCC, the 5 tyrosine codons in said coding region are TAC, the 5 histidine codons in said coding region are CAC, the 15 glutamine codons in said coding region are CAG, the 11 asparagine codons in said coding region are AAC, the 13 lysine codons in said coding region are AAG, the 6 aspartic acid codons in said coding region are GAC, the 17 glutamic acid codons in said coding region are GAG, the 1 tryptophan codon in said coding region is TGG, the 17 arginine codons in said coding region are selected from the group consisting of CGG, AGA, and AGG, and the 16 glycine codons are GGC; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:4.

44. The polynucleotide of claim 43, wherein said codon optimized coding region comprises SEQ ID NO:27.

45. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:4, wherein

said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:4;

wherein said codon-optimized coding region consists of nucleotides 26-784 of SEQ ID NO:3 except that the 26 leucine codons are CTG, the 8 proline codons are CCC, the 25 alanine codons are GCC, the 15 glutamine codons are CAG, the 11 asparagine codons are AAC, the 13 lysine codons are AAG, and the 17 glutamic acid codons are GAG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:4.

46. The polynucleotide of claim 45, wherein said codon optimized coding region comprises SEQ ID NO:28.

47. The polynucleotide any one of claims 41 to 46, wherein said nucleic acid fragment encodes at least 50 contiguous amino acids of SEQ ID NO:4.

48. The polynucleotide any one of claims 41 to 47, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:4.

49. The polynucleotide of any one of claims 41 to 48, wherein said nucleic acid fragment encodes SEQ ID NO:4.

50. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:4, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:4;

wherein about 3 of the 7 phenylalanine codons in said coding region are TTT, and about 4 of said phenylalanine codons are TTC;

wherein about 2 of the 26 leucine codons in said coding region are TTA, about 3 of said leucine codons are TTG, about 3 of said leucine codons are CTT, about 5 of said leucine codons are CTC, about 2 of said leucine codons are CTA, and about 11 of said leucine codons are CTG;

wherein about 4 of the 11 isoleucine codons in said coding region are ATT, about 5 of said isoleucine codons are ATC, and about 2 of said isoleucine codons are ATA;

wherein the 14 methionine codons in said coding region are ATG;

wherein about 3 of the 16 valine codons in said coding region are GTT, about 4 of said valine codons are GTG, about 2 of said valine codons are GTA, and about 8 of said valine codons are GTG;

wherein about 3 of the 18 serine codons in said coding region are TCT, about 4 of said serine codons are TCC, about 3 of said serine codons are TCA, about 1 of said serine codons is TCG, about 3 of said serine codons are AGT, and about 4 of said serine codons are AGC;

wherein about 2 of the 8 proline codons are CCT, about 3 of said proline codons are CCC, about 2 of said proline codons are CCA, and about 1 of said proline codons is CCG;

wherein about 4 of the 18 threonine codons in said coding region are ACT, about 7 of said threonine codons are ACC, about 5 of said threonine codons are ACA, and about 2 of said threonine codons are ACG;

wherein about 7 of the 25 alanine codons in said coding region are GCT, about 10 of said alanine codons are GCC, about 6 of said alanine codons are GCA, and about 3 of said alanine codons are GCG;

wherein about 2 of the 5 tyrosine codons in said coding region are TAT and about 3 of said tyrosine codons are TAC;

wherein about 2 of the 5 histidine codons in said coding region are CAT and about 3 of said histidine codons are CAC;

wherein about 4 of the 15 glutamine codons in said coding region are CAA and about 11 of said glutamine codons are CAG;

wherein about 5 of the 11 asparagine codons in said coding region are AAT and about 6 of said asparagine codons are AAC;

wherein about 5 of the 13 lysine codons in said coding region are AAA and about 8 of said lysine codons are AAG;

wherein about 3 of the 6 aspartic acid codons in said coding region are GAT and about 3 of said aspartic acid codons are GAC;

wherein about 7 of the 17 glutamic acid codons in said coding region are GAA and about 10 of said glutamic acid codons are GAG;

wherein about 1 of the 3 cysteine codons in said coding region is TGT and about 2 of said cysteine codons are TGC;

wherein the 1 tryptophan codon in said coding region is TGG;

wherein about 1 of the 17 arginine codons in said coding region are CGT, about 3 of said arginine codons are CGC, about 2 of said arginine codons are CGA, about 4 of said arginine codons are CGG, about 3 of said arginine codons are AGA, and about 3 of said arginine codons are AGG; and

wherein about 3 of the 16 glycine codons in said coding region are GGT, about 6 of said glycine codons are GGC, about 4 of said glycine codons are GGA, and about 4 of said glycine codons are GGG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:4.

51. The polynucleotide of claim 50, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:2.

52. The polynucleotide of claim 51, wherein said nucleic acid fragment encodes SEQ ID NO:4.

53. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:4, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:4;

wherein the 7 phenylalanine codons in said coding region are TTC, the 26 leucine codons in said coding region are CTG, the 11 isoleucine codons in said coding region are ATC, the 14 methionine codons in said coding region are ATG, the 16 valine codons in said coding region are GTG, the 18 serine

codons in said coding region are AGC, the 8 proline codons in said coding region are CCC, the 18 threonine codons in said coding region are ACC, the 25 alanine codons in said coding region are GCC, the 5 tyrosine codons in said coding region are TAC, the 5 histidine codons in said coding region are CAC, the 15 glutamine codons in said coding region are CAG, the 11 asparagine codons in said coding region are AAC, the 13 lysine codons in said coding region are AAG, the 6 aspartic acid codons in said coding region are GAC, the 17 glutamic acid codons in said coding region are GAG, the 1 tryptophan codon in said coding region is TGG, the 17 arginine codons in said coding region are selected from the group consisting of CGG, AGA, and AGG, and the 16 glycine codons are GGC; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:4.

54. The polynucleotide of claim 53, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:4.

55. The polynucleotide of claim 54, wherein said nucleic acid fragment encodes SEQ ID NO:4.

56. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:4, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:4;

wherein said codon-optimized coding region consists of nucleotides 26-784 of SEQ ID NO:3 except that the 26 leucine codons are CTG, the 8 proline codons are CCC, the 25 alanine codons are GCC, the 15 glutamine codons are CAG, the 11 asparagine codons are AAC, the 13 lysine codons are AAG, and the 17 glutamic acid codons are GAG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:4.

57. The polynucleotide of claim 56, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:4.

58. The polynucleotide of claim 57, wherein said nucleic acid fragment encodes SEQ ID NO:4.

59. The polynucleotide of any one of claims 41 to 58, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

60. The polynucleotide of claim 59, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

61. The polynucleotide of claim 60, wherein said heterologous polypeptide is a hepatitis B core antigen.

62. The polynucleotide of claim 8, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

63. The polynucleotide of claim 62, comprising SEQ ID NO:41.

64. The polynucleotide of any one of claims 41 to 63, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

65. The polynucleotide of any one of claims 41 to 63, which is RNA.

66. The polynucleotide of claim 65, which is messenger RNA (mRNA).

67. A vector comprising the polynucleotide of any one of claims 41 to 66.

68. The vector of claim 67, which is a plasmid.

69. A composition comprising the polynucleotide of any one of claims 41 to 66, and a carrier.

70. The composition of claim 69, further comprising a component selected from the group consisting of an adjuvant and a transfection facilitating compound.

71. The composition of claim 70, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

72. The composition of claim 71, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

73. The composition of claim 72, wherein said neutral lipid is DPyPE.

74. The composition of claim 70, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

75. The composition of claim 70, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

76. The composition of claim 75, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

77. The composition of claim 75 or claim 76, which is formulated by combining together the CRL1005, BAK, and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

78. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 41 to 66.

79. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:5, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:5;

wherein about 2 of the 4 phenylalanine codons in said coding region are TTT, and about 2 of said phenylalanine codons are TTC;

wherein about 1 of the 10 leucine codons in said coding region are TTA, about 1 of said leucine codons are TTG, about 1 of said leucine codons are CTT, about 2 of said leucine codons are CTC, about 1 of said leucine codons are CTA, and about 4 of said leucine codons are CTG;

wherein about 3 of the 8 isoleucine codons in said coding region are ATT, about 4 of said isoleucine codons are ATC, and about 1 of said isoleucine codons are ATA;

wherein the 2 methionine codons are ATG;

wherein about 1 of the 4 valine codons in said coding region are GTT, about 1 of said valine codons are GTG, about 0 of said valine codons are GTA, and about 2 of said valine codons are GTG;

wherein about 1 of the 7 serine codons in said coding region are TCT, about 2 of said serine codons are TCC, about 1 of said serine codons are TCA,

about 0 of said serine codons are TCG, about 1 of said serine codons are AGT, and about 2 of said serine codons are AGC;

wherein about 1 of the 4 proline codons in said coding region are CCT, about 1 of said proline codons are CCC, about 2 of said proline codons are CCA, and about 0 of said proline codons are CCG;

wherein about 1 of the 4 threonine codons in said coding region are ACT, about 1 of said threonine codons are ACC, about 1 of said threonine codons are ACA, and about 0 of said threonine codons are ACG;

wherein about 1 of the 5 alanine codons in said coding region are GGT, about 2 of said alanine codons are GCC, about 1 of said alanine codons are GCA, and about 1 of said alanine codons are GCG;

wherein about 1 of the 3 tyrosine codons in said coding region are TAT and about 2 of said tyrosine codons are TAC;

wherein about 1 of the 2 histidine codons in said coding region are CAT and about 1 of said histidine codons are CAC;

wherein about 1 of the 2 glutamine codons in said coding region are CAA and about 1 of said glutamine codons are CAG;

wherein about 1 of the 3 asparagine codons in said coding region are AAT and about 2 of said asparagine codons are AAC;

wherein about 2 of the 5 lysine codons in said coding region are AAA and about 3 of said lysine codons are AAG;

wherein about 2 of the 5 aspartic acid codons in said coding region are GAT and about 3 of said aspartic acid codons are GAC;

wherein about 4 of the 9 glutamic acid codons in said coding region are GAA and about 5 of said glutamic acid codons are GAG;

wherein about 1 of the 3 cysteine codons in said coding region are TGT and about 2 of said cysteine codons are TGC; the 2 tryptophan codons are TGG;

wherein about 1 of the 7 arginine codons in said coding region are CGT, about 1 of said arginine codons are CGC, about 1 of said arginine codons are CGA, about 1 of said arginine codons are CGG, about 1 of said arginine codons are AGA, and about 1 of said arginine codons are AGG; and

wherein about 1 of the 8 glycine codons in said coding region are GGT, about 3 of said glycine codons are GGC, about 2 of said glycine codons are GGA, and about 2 of said glycine codons are GGG; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:5.

80. The polynucleotide of claim 79, wherein said codon optimized coding region comprises SEQ ID NO:29.

81. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:5, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:5;

wherein the 4 phenylalanine codons in said coding region are TTC, the 10 leucine codons in said coding region are CTG, the 8 isoleucine codons in

said coding region are ATC, the 2 methionine codons in said coding region are ATG, the 4 valine codons in said coding region are GTG, the 7 serine codons in said coding region are AGC, the 4 proline codons in said coding region are CCC, the 4 threonine codons in said coding region are ACC, the 5 alanine codons in said coding region are GCC, the 3 tyrosine codons in said coding region are TAC, the 2 histidine codons in said coding region are CAC, the 2 glutamine codons in said coding region are CAG, the 3 asparagine codons in said coding region are AAC, the 5 lysine codons in said coding region are AAG, the 5 aspartic acid codons in said coding region are GAC, the 9 glutamic acid codons in said coding region are GAG, the 2 tryptophan codons in said coding region are TGG, the 7 arginine codons in said coding region are selected from the group consisting of CGG, AGA, and AGG, and the 8 glycine codons in said coding region are GGC; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:5.

82. The polynucleotide of claim 81, wherein said codon optimized coding region comprises SEQ ID NO:30.

83. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:5, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:5;

wherein said codon-optimized coding region consists of nucleotides 26 to51 of SEQ ID NO:3 fused in frame to nucleotides 740 to 1007 of SEQ ID NO:3, except that the 10 leucine codons are CTG, the 4 proline codons are CCC, the 5 alanine codons are GCC, the 2 glutamine codons are CAG, the 3 asparagine codons are AAC, the 5 lysine codons are AAG, and the 9 glutamic acid codons are GAG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:5.

84. The polynucleotide of claim 83, wherein said codon optimized coding region comprises SEQ ID NO:31.

85. The polynucleotide of any one of claims 79 to 83, wherein said nucleic acid fragment encodes amino acids 1 to 24 of SEQ ID NO:5.

86. The polynucleotide of any one of claims 79 to 81, wherein said nucleic acid fragment encodes at least 50 amino acids of SEQ ID NO:5.

87. The polynucleotide any one of claims 79 to 86, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:5.

88. The polynucleotide of any one of claims 79 to 87, wherein said nucleic acid fragment encodes SEQ ID NO:5.

89. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:5, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:5;

wherein about 2 of the 4 phenylalanine codons in said coding region are TTT, and about 2 of said phenylalanine codons are TTC;

wherein about 1 of the 10 leucine codons in said coding region are TTA, about 1 of said leucine codons are TTG, about 1 of said leucine codons are CTT, about 2 of said leucine codons are CTC, about 1 of said leucine codons are CTA, and about 4 of said leucine codons are CTG;

wherein about 3 of the 8 isoleucine codons in said coding region are ATT, about 4 of said isoleucine codons are ATC, and about 1 of said isoleucine codons are ATA;

wherein the 2 methionine codons are ATG;

wherein about 1 of the 4 valine codons in said coding region are GTT, about 1 of said valine codons are GTG, about 0 of said valine codons are GTA, and about 2 of said valine codons are GTG;

wherein about 1 of the 7 serine codons in said coding region are TCT, about 2 of said serine codons are TCC, about 1 of said serine codons are TCA, about 0 of said serine codons are TCG, about 1 of said serine codons are AGT, and about 2 of said serine codons are AGC;

wherein about 1 of the 4 proline codons in said coding region are CCT, about 1 of said proline codons are CCC, about 2 of said proline codons are CCA, and about 0 of said proline codons are CCG;

wherein about 1 of the 4 threonine codons in said coding region are ACT, about 1 of said threonine codons are ACC, about 1 of said threonine codons are ACA, and about 0 of said threonine codons are ACG;

wherein about 1 of the 5 alanine codons in said coding region are GGT, about 2 of said alanine codons are GCC, about 1 of said alanine codons are GCA, and about 1 of said alanine codons are GCG;

wherein about 1 of the 3 tyrosine codons in said coding region are TAT and about 2 of said tyrosine codons are TAC;

wherein about 1 of the 2 histidine codons in said coding region are CAT and about 1 of said histidine codons are CAC;

wherein about 1 of the 2 glutamine codons in said coding region are CAA and about 1 of said glutamine codons are CAG;

wherein about 1 of the 3 asparagine codons in said coding region are AAT and about 2 of said asparagine codons are AAC;

wherein about 2 of the 5 lysine codons in said coding region are AAA and about 3 of said lysine codons are AAG;

wherein about 2 of the 5 aspartic acid codons in said coding region are GAT and about 3 of said aspartic acid codons are GAC;

wherein about 4 of the 9 glutamic acid codons in said coding region are GAA and about 5 of said glutamic acid codons are GAG;

wherein about 1 of the 3 cysteine codons in said coding region are TGT and about 2 of said cysteine codons are TGC; the 2 tryptophan codons are TGG;

wherein about 1 of the 7 arginine codons in said coding region are CGT, about 1 of said arginine codons are CGC, about 1 of said arginine codons are CGA, about 1 of said arginine codons are CGG, about 1 of said arginine codons are AGA, and about 1 of said arginine codons are AGG; and

wherein about 1 of the 8 glycine codons in said coding region are GGT, about 3 of said glycine codons are GGC, about 2 of said glycine codons are GGA, and about 2 of said glycine codons are GGG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:5.

90. The polynucleotide of claim 89, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:5.

91. The polynucleotide of claim 90, wherein said nucleic acid fragment encodes SEQ ID NO:5.

92. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:5, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:5;

wherein the 4 phenylalanine codons in said coding region are TTC, the 10 leucine codons in said coding region are CTG, the 8 isoleucine codons in said coding region are ATC, the 2 methionine codons in said coding region are ATG, the 4 valine codons in said coding region are GTG, the 7 serine codons in said coding region are AGC, the 4 proline codons in said coding region are CCC, the 4 threonine codons in said coding region are ACC, the 5 alanine codons in said coding region are GCC, the 3 tyrosine codons in said coding region are TAC, the 2 histidine codons in said coding region are CAC, the 2 glutamine codons in said coding region are CAG, the 3 asparagine codons in said coding region are AAC, the 5 lysine codons in said coding region are AAG, the 5 aspartic acid codons in said coding region are GAC, the 9 glutamic acid codons in said coding region are GAG, the 2 tryptophan codons in said coding region are TGG, the 7 arginine codons in said coding region are selected from the group consisting of CGG, AGA, and AGG, and the 8 glycine codons in said coding region are GGC; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:5.

93. The polynucleotide of claim 92, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:5.

94. The polynucleotide of claim 93, wherein said nucleic acid fragment encodes SEQ ID NO:5.

95. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:5, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:5;

wherein said codon-optimized coding region consists of nucleotides 26 to51 of SEQ ID NO:3 fused in frame to nucleotides 740 to 1007 of SEQ ID NO:3, except that the 10 leucine codons are CTG, the 4 proline codons are CCC, the 5 alanine codons are GCC, the 2 glutamine codons are CAG, the 3 asparagine codons are AAC, the 5 lysine codons are AAG, and the 9 glutamic acid codons are GAG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:5.

96. The polynucleotide of claim 95, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:2.

97. The polynucleotide of claim 96, wherein said nucleic acid fragment encodes SEQ ID NO:5.

98. The polynucleotide of any one of claims 79 to 97, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

99. The polynucleotide of claim 98, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

100. The polynucleotide of claim 99, wherein said heterologous polypeptide is a hepatitis B core antigen.

101. The polynucleotide of claim 100, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

102. The polynucleotide of claim 100, wherein said heterologous polypeptide is the influenza A virus NP protein.

103. The polynucleotide of claim 102, wherein said influenza A virus NP protein comprises SEQ ID NO:2.

104. The polynucleotide of any one of claims 79 to 103, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

105. The polynucleotide of any one of claims 79 to 103, which is RNA.

106. The polynucleotide of claim 105, which is messenger RNA (mRNA).

107. A vector comprising the polynucleotide of any one of claims 79 to 106.

108. The vector of claim 107, which is a plasmid.

109. A composition comprising the polynucleotide of any one of claims 79 to 106, and a carrier.

110. The composition of claim 109, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

111. The composition of claim 110, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

112. The composition of claim 111, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

113. The composition of claim 112, wherein said neutral lipid is DPyPE.

114. The composition of claim 110, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

115. The composition of claim 110, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

116. The composition of claim 115, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

117. The composition of claim 115 or claim 116, which is formulated by combining together the CRL1005, BAK, and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

118. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 79 to 106.

119. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:7, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:7;

wherein about 8 of the 18 phenylalanine codons in said coding region are TTT, and about 10 of said phenylalanine codons are TTC;

wherein about 3 of the 35 leucine codons in said coding region are TTA, about 4 of said leucine codons are TTG, about 5 of said leucine codons are CTT, about 7 of said leucine codons are CTC, about 2 of said leucine codons are CTA, and about 14 of said leucine codons are CTG;

wherein about 10 of the 27 isoleucine codons in said coding region are ATT, about 13 of said isoleucine codons are ATC, and about 4 of said isoleucine codons are ATA;

wherein the 26 methionine codons in said coding region are ATG;

wherein about 4 of the 24 valine codons in said coding region are GTT, about 6 of said valine codons are GTG, about 3 of said valine codons are GTA, and about 11 of said valine codons are GTG;

wherein about 8 of the 43 serine codons in said coding region are TCT, about 9 of said serine codons are TCC, about 6 of said serine codons are TCA, about 2 of said serine codons are TCG, about 6 of said serine codons are AGT, and about 10 of said serine codons are AGC;

wherein about 5 of the 18 proline codons in said coding region are CCT, about 6 of said proline codons are CCC, about 5 of said proline codons are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 30 threonine codons in said coding region are ACT, about 11 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 4 of said threonine codons are ACG;

wherein about 10 of the 39 alanine codons in said coding region are GGT, about 16 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 7 of the 15 tyrosine codons in said coding region are TAT and about 8 of said tyrosine codons are TAC;

wherein about 2 of the 6 histidine codons in said coding region are CAT and about 4 of said histidine codons are CAC;

wherein about 5 of the 21 glutamine codons in said coding region are CAA and about 16 of said glutamine codons are CAG;

wherein about 13 of the 28 asparagine codons in said coding region are AAT and about 15 of said asparagine codons are AAC;

wherein about 9 of the 21 lysine codons in said coding region are AAA and about 12 of said lysine codons are AAG;

wherein about 11 of the 23 aspartic acid codons in said coding region are GAT and about 12 of said aspartic acid codons are GAC;

wherein about 16 of the 39 glutamic acid codons in said coding region are GAA and about 23 of said glutamic acid codons are GAG;

wherein about 4 of the 8 cysteine codons in said coding region are TGT and about 4 of said cysteine codons are TGC;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 4 of the 51 arginine codons in said coding region are CGT, about 10 of said arginine codons are CGC, about 6 of said arginine codons are CGA, about 11 of said arginine codons are CGG, about 10 of said arginine codons are AGA, and about 10 of said arginine codons are AGG; and

wherein about 7 of the 43 glycine codons in said coding region are GGT, about 15 of said glycine codons are GGC, about 11 of said glycine codons are GGA, and about 11 of said glycine codons are GGG; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:7.

120. The polynucleotide of claim 119, wherein said codon optimized coding region comprises SEQ ID NO:32.

121. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:7, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:7;

wherein the 18 phenylalanine codons in said coding region are TTC, the 35 leucine codons in said coding region are CTG, the 27 isoleucine codons in said coding region are ATC, the 26 methionine codons in said coding region are ATG, the 24 valine codons in said coding region are GTG, the 43 serine codons in said coding region are AGC, the 18 proline codons in said coding region are CCC, the 30 threonine codons in said coding region are ACC, the 39 alanine codons in said coding region are GCC, the 15 tyrosine codons in said coding region are TAC, the 6 histidine codons in said coding region are CAC, the 21 glutamine codons in said coding region are CAG, the 28 asparagine codons in said coding region are AAC, the 21 lysine codons in said coding region are AAG, the 23 aspartic acid codons in said coding region are GAC, the 39 glutamic acid codons in said coding region are GAG, the 7 tryptophan codons in said coding region are TGG, the 51 arginine codons in said coding region are CGG, AGA, or AGG, and the 43 glycine codons in said coding region are GGC; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:7.

122. The polynucleotide of claim 121, wherein said codon optimized coding region comprises SEQ ID NO:33.

123. The polynucleotide of any one of claims 119 to 122, wherein said nucleic acid fragment encodes at least 50 amino acids of SEQ ID NO:7.

124. The polynucleotide any one of claims 119 to 123, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:7.

125. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:7, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:7;

wherein about 8 of the 18 phenylalanine codons in said coding region are TTT, and about 10 of said phenylalanine codons are TTC;

wherein about 3 of the 35 leucine codons in said coding region are TTA, about 4 of said leucine codons are TTG, about 5 of said leucine codons are CTT, about 7 of said leucine codons are CTC, about 2 of said leucine codons are CTA, and about 14 of said leucine codons are CTG;

wherein about 10 of the 27 isoleucine codons in said coding region are ATT, about 13 of said isoleucine codons are ATC, and about 4 of said isoleucine codons are ATA;

wherein the 26 methionine codons in said coding region are ATG;

wherein about 4 of the 24 valine codons in said coding region are GTT, about 6 of said valine codons are GTG, about 3 of said valine codons are GTA, and about 11 of said valine codons are GTG;

wherein about 8 of the 43 serine codons in said coding region are TCT, about 9 of said serine codons are TCC, about 6 of said serine codons are TCA, about 2 of said serine codons are TCG, about 6 of said serine codons are AGT, and about 10 of said serine codons are AGC;

wherein about 5 of the 18 proline codons in said coding region are CCT, about 6 of said proline codons are CCC, about 5 of said proline codons are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 30 threonine codons in said coding region are ACT, about 11 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 4 of said threonine codons are ACG;

wherein about 10 of the 39 alanine codons in said coding region are GGT, about 16 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 7 of the 15 tyrosine codons in said coding region are TAT and about 8 of said tyrosine codons are TAC;

wherein about 2 of the 6 histidine codons in said coding region are CAT and about 4 of said histidine codons are CAC;

wherein about 5 of the 21 glutamine codons in said coding region are CAA and about 16 of said glutamine codons are CAG;

wherein about 13 of the 28 asparagine codons in said coding region are AAT and about 15 of said asparagine codons are AAC;

wherein about 9 of the 21 lysine codons in said coding region are AAA and about 12 of said lysine codons are AAG;

wherein about 11 of the 23 aspartic acid codons in said coding region are GAT and about 12 of said aspartic acid codons are GAC;

wherein about 16 of the 39 glutamic acid codons in said coding region are GAA and about 23 of said glutamic acid codons are GAG;

wherein about 4 of the 8 cysteine codons in said coding region are TGT and about 4 of said cysteine codons are TGC;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 4 of the 51 arginine codons in said coding region are CGT, about 10 of said arginine codons are CGC, about 6 of said arginine codons are CGA, about 11 of said arginine codons are CGG, about 10 of said arginine codons are AGA, and about 10 of said arginine codons are AGG; and

wherein about 7 of the 43 glycine codons in said coding region are GGT, about 15 of said glycine codons are GGC, about 11 of said glycine codons are GGA, and about 11 of said glycine codons are GGG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:7.

126. The polynucleotide of claim 125, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:7.

127. The polynucleotide of claim 126, wherein said nucleic acid fragment encodes SEQ ID NO:7.

128. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:5, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:7;

wherein the 18 phenylalanine codons in said coding region are TTC, the 35 leucine codons in said coding region are CTG, the 27 isoleucine codons in said coding region are ATC, the 26 methionine codons in said coding region are ATG, the 24 valine codons in said coding region are GTG, the 43 serine codons in said coding region are AGC, the 18 proline codons in said coding region are CCC, the 30 threonine codons in said coding region are ACC, the 39 alanine codons in said coding region are GCC, the 15 tyrosine codons in said coding region are TAC, the 6 histidine codons in said coding region are CAC, the 21 glutamine codons in said coding region are CAG, the 28 asparagine codons in said coding region are AAC, the 21 lysine codons in said coding region are AAG, the 23 aspartic acid codons in said coding region are GAC, the 39 glutamic acid codons in said coding region are GAG, the 7 tryptophan codons in said coding region are TGG, the 51 arginine codons in said coding region are CGG, AGA, or AGG, and the 43 glycine codons in said coding region are GGC; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:7.

129. The polynucleotide of claim 128, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:7.

130. The polynucleotide of claim 129, wherein said nucleic acid fragment encodes SEQ ID NO:7.

131. The polynucleotide of any one of claims 119 to 130, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

132. The polynucleotide of claim 131, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

133. The polynucleotide of claim 132, wherein said heterologous polypeptide is a hepatitis B core antigen.

134. The polynucleotide of claim 133, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

135. The polynucleotide of any one of claims 119 to 134, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

136. The polynucleotide of any one of claims 119 to 134, which is RNA.

137. The polynucleotide of claim 136, which is messenger RNA (mRNA).

138. A vector comprising the polynucleotide of any one of claims 119 to 137.

139. The vector of claim 138, which is a plasmid.

140. A composition comprising the polynucleotide of any one of claims 119 to 137, and a carrier.

141. The composition of claim 140, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

142. The composition of claim 141, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

143. The composition of claim 142, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

144. The composition of claim 143, wherein said neutral lipid is DPyPE.

145. The composition of claim 141, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

146. The composition of claim 141, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

147. The composition of claim 146, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

148. The composition of claim 146 or claim 147, which is formulated by combining together the CRL1005, BAK, and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

149. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 119 to 137.

150. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:9, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:9;

wherein about 8 of the 18 phenylalanine codons in said coding region are TTT, and about 10 of said phenylalanine codons are TTC;

wherein about 3 of the 35 leucine codons in said coding region are TTA, about 4 of said leucine codons are TTG, about 5 of said leucine codons are CTT, about 7 of said leucine codons are CTC, about 2 of said leucine codons are CTA, and about 14 of said leucine codons are CTG;

wherein about 10 of the 27 isoleucine codons in said coding region are ATT, about 13 of said isoleucine codons are ATC, and about 4 of said isoleucine codons are ATA;

wherein the 26 methionine codons in said coding region are ATG;

wherein about 4 of the 24 valine codons in said coding region are GTT, about 6 of said valine codons are GTG, about 3 of said valine codons are GTA, and about 11 of said valine codons are GTG;

wherein about 8 of the 43 serine codons in said coding region are TCT, about 9 of said serine codons are TCC, about 6 of said serine codons are TCA, about 2 of said serine codons are TCG, about 6 of said serine codons are AGT, and about 10 of said serine codons are AGC;

wherein about 5 of the 18 proline codons in said coding region are CCT, about 6 of said proline codons are CCC, about 5 of said proline codons are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 30 threonine codons in said coding region are ACT, about 11 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 4 of said threonine codons are ACG;

wherein about 10 of the 39 alanine codons in said coding region are GGT, about 16 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 7 of the 15 tyrosine codons in said coding region are TAT and about 8 of said tyrosine codons are TAC;

wherein about 2 of the 6 histidine codons in said coding region are CAT and about 4 of said histidine codons are CAC;

wherein about 5 of the 21 glutamine codons in said coding region are CAA and about 16 of said glutamine codons are CAG;

wherein about 13 of the 28 asparagine codons in said coding region are AAT and about 15 of said asparagine codons are AAC;

wherein about 9 of the 21 lysine codons in said coding region are AAA and about 12 of said lysine codons are AAG;

wherein about 11 of the 23 aspartic acid codons in said coding region are GAT and about 12 of said aspartic acid codons are GAC;

wherein about 16 of the 39 glutamic acid codons in said coding region are GAA and about 23 of said glutamic acid codons are GAG;

wherein about 4 of the 8 cysteine codons in said coding region are TGT and about 4 of said cysteine codons are TGC;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 4 of the 51 arginine codons in said coding region are CGT, about 10 of said arginine codons are CGC, about 6 of said arginine codons are CGA, about 11 of said arginine codons are CGG, about 10 of said arginine codons are AGA, and about 10 of said arginine codons are AGG; and

wherein about 7 of the 43 glycine codons in said coding region are GGT, about 15 of said glycine codons are GGC, about 11 of said glycine codons are GGA, and about 11 of said glycine codons are GGG; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:9.

151. The polynucleotide of claim 150, wherein said codon optimized coding region comprises SEQ ID NO:34.

152. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:9, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:9;

wherein the 18 phenylalanine codons in said coding region are TTC, the 35 leucine codons in said coding region are CTG, the 27 isoleucine codons in said coding region are ATC, the 26 methionine codons in said coding region are ATG, the 24 valine codons in said coding region are GTG, the 43 serine codons in said coding region are AGC, the 18 proline codons in said coding region are CCC, the 30 threonine codons in said coding region are ACC, the 39 alanine codons in said coding region are GCC, the 15 tyrosine codons in said coding region are TAC, the 6 histidine codons in said coding region are CAC, the 21 glutamine codons in said coding region are CAG, the 28 asparagine codons in said coding region are AAC, the 21 lysine codons in said coding region are AAG, the 23 aspartic acid codons in said coding region are

GAC, the 39 glutamic acid codons in said coding region are GAG, the 7 tryptophan codons in said coding region are TGG, the 51 arginine codons in said coding region are CGG, AGA, or AGG, and the 43 glycine codons in said coding region are GGC; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:9.

153. The polynucleotide of claim 152, wherein said codon optimized coding region comprises SEQ ID NO:35.

154. The polynucleotide of any one of claims 150 to 153, wherein said nucleic acid fragment encodes at least 50 amino acids of SEQ ID NO:9.

155. The polynucleotide any one of claims 150 to 154, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:9.

156. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:9, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:9;

wherein about 8 of the 18 phenylalanine codons in said coding region are TTT, and about 10 of said phenylalanine codons are TTC;

wherein about 3 of the 35 leucine codons in said coding region are TTA, about 4 of said leucine codons are TTG, about 5 of said leucine codons are CTT, about 7 of said leucine codons are CTC, about 2 of said leucine codons are CTA, and about 14 of said leucine codons are CTG;

wherein about 10 of the 27 isoleucine codons in said coding region are ATT, about 13 of said isoleucine codons are ATC, and about 4 of said isoleucine codons are ATA;

wherein the 26 methionine codons in said coding region are ATG;

wherein about 4 of the 24 valine codons in said coding region are GTT, about 6 of said valine codons are GTG, about 3 of said valine codons are GTA, and about 11 of said valine codons are GTG;

wherein about 8 of the 43 serine codons in said coding region are TCT, about 9 of said serine codons are TCC, about 6 of said serine codons are TCA, about 2 of said serine codons are TCG, about 6 of said serine codons are AGT, and about 10 of said serine codons are AGC;

wherein about 5 of the 18 proline codons in said coding region are CCT, about 6 of said proline codons are CCC, about 5 of said proline codons are CCA, and about 2 of said proline codons are CCG;

wherein about 7 of the 30 threonine codons in said coding region are ACT, about 11 of said threonine codons are ACC, about 8 of said threonine codons are ACA, and about 4 of said threonine codons are ACG;

wherein about 10 of the 39 alanine codons in said coding region are GGT, about 16 of said alanine codons are GCC, about 9 of said alanine codons are GCA, and about 4 of said alanine codons are GCG;

wherein about 7 of the 15 tyrosine codons in said coding region are TAT and about 8 of said tyrosine codons are TAC;

wherein about 2 of the 6 histidine codons in said coding region are CAT and about 4 of said histidine codons are CAC;

wherein about 5 of the 21 glutamine codons in said coding region are CAA and about 16 of said glutamine codons are CAG;

wherein about 13 of the 28 asparagine codons in said coding region are AAT and about 15 of said asparagine codons are AAC;

wherein about 9 of the 21 lysine codons in said coding region are AAA and about 12 of said lysine codons are AAG;

wherein about 11 of the 23 aspartic acid codons in said coding region are GAT and about 12 of said aspartic acid codons are GAC;

wherein about 16 of the 39 glutamic acid codons in said coding region are GAA and about 23 of said glutamic acid codons are GAG;

wherein about 4 of the 8 cysteine codons in said coding region are TGT and about 4 of said cysteine codons are TGC;

wherein the 7 tryptophan codons in said coding region are TGG;

wherein about 4 of the 51 arginine codons in said coding region are CGT, about 10 of said arginine codons are CGC, about 6 of said arginine codons are CGA, about 11 of said arginine codons are CGG, about 10 of said arginine codons are AGA, and about 10 of said arginine codons are AGG; and

wherein about 7 of the 43 glycine codons in said coding region are GGT, about 15 of said glycine codons are GGC, about 11 of said glycine codons are GGA, and about 11 of said glycine codons are GGG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:9.

157. The polynucleotide of claim 156, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:9.

158. The polynucleotide of claim 157, wherein said nucleic acid fragment encodes SEQ ID NO:9.

159. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:9, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:9;

wherein the 18 phenylalanine codons in said coding region are TTC, the 35 leucine codons in said coding region are CTG, the 27 isoleucine codons in said coding region are ATC, the 26 methionine codons in said coding region are ATG, the 24 valine codons in said coding region are GTG, the 43 serine codons in said coding region are AGC, the 18 proline codons in said coding region are CCC, the 30 threonine codons in said coding region are ACC, the 39 alanine codons in said coding region are GCC, the 15 tyrosine codons in said coding region are TAC, the 6 histidine codons in said coding region are CAC, the 21 glutamine codons in said coding region are CAG, the 28 asparagine codons in said coding region are AAC, the 21 lysine codons in said coding region are AAG, the 23 aspartic acid codons in said coding region are

GAC, the 39 glutamic acid codons in said coding region are GAG, the 7 tryptophan codons in said coding region are TGG, the 51 arginine codons in said coding region are CGG, AGA, or AGG, and the 43 glycine codons in said coding region are GGC; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:9.

160. The polynucleotide of claim 159, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:9.

161. The polynucleotide of claim 160, wherein said nucleic acid fragment encodes SEQ ID NO:9.

162. The polynucleotide of any one of claims 150 to 161, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

163. The polynucleotide of claim 162, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

164. The polynucleotide of claim 163, wherein said heterologous polypeptide is a hepatitis B core antigen.

165. The polynucleotide of claim 164, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

166. The polynucleotide of any one of claims 150 to 165, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

167. The polynucleotide of any one of claims 150 to 165, which is RNA.

168. The polynucleotide of claim 167, which is messenger RNA (mRNA).

169. A vector comprising the polynucleotide of any one of claims 150 to 168.

170. The vector of claim 169, which is a plasmid.

171. A composition comprising the polynucleotide of any one of claims 150 to 168, and a carrier.

172. The composition of claim 171, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

173. The composition of claim 172, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

174. The composition of claim 173, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

175. The composition of claim 174, wherein said neutral lipid is DPyPE.

176. The composition of claim 172, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

177. The composition of claim 172, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

178. The composition of claim 172, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

179. The composition of claim 176 or claim 178, which is formulated by combining together the CRL1005, BAK, and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

180. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 150 to 168.

181. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:16, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:16;

wherein about 10 of the 21 phenylalanine codons are TTT, and about 12 of the phenylalanine codons are TTC;

wherein about 3 of the 39 leucine codons are TTA, about 5 of the leucine codons are TTG, about 5 of the leucine codons are CTT, about 8 of the leucine codons are CTC, about 3 of the leucine codons are CTA, and about 16 of the leucine codons are CTG;

wherein about 14 of the 38 isoleucine codons are ATT, about 18 of the isoleucine codons are ATC, and about 6 of the isoleucine codons are ATA;

wherein the 27 methionine codons are ATG;

wherein about 6 of the 32 valine codons are GTT, about 8 of the valine codons are GTG, about 4 of the valine codons are GTA, and about 15 of the valine codons are GTG;

wherein about 7 of the 40 serine codons are TCT, about 9 of the serine codons are TCC, about 6 of the serine codons are TCA, about 2 of the

serine codons are TCG, about 6 of the serine codons are AGT, and about 10 of the serine codons are AGC;

wherein about 7 of the 26 proline codons are CCT, about 9 of the proline codons are CCC, about 7 of the proline codons are CCA, and about 3 of the proline codons are CCG; about 9 of the 38 threonine codons are ACT, about 14 of the threonine codons are ACC, about 11 of the threonine codons are ACA, and about 4 of the threonine codons are ACG;

wherein about 11 of the 41 alanine codons are GGT, about 17 of the alanine codons are GCC, about 9 of the alanine codons are GCA, and about 4 of the alanine codons are GCG;

wherein about 6 of the 14 tyrosine codons are TAT and about 8 of the tyrosine codons are TAC; about 2 of the 4 histidine codons are CAT and about 2 of the histidine codons are CAC;

wherein about 5 of the 19 glutamine codons are CAA and about 14 of the glutamine codons are CAG; about 12 of the 25 asparagine codons are AAT and about 13 of the asparagine codons are AAC; about 22 of the 52 lysine codons are AAA and about 30 of the lysine codons are AAG;

wherein about 16 of the 34 aspartic acid codons are GAT and about 18 of the aspartic acid codons are GAC;

wherein about 12 of the 30 glutamic acid codons are GAA and about 18 of the glutamic acid codons are GAG;

wherein about 2 of the 5 cysteine codons are TGT and about 3 of the cysteine codons are TGC;

wherein the single tryptophan codon is TGG;

wherein about 2 of the 30 arginine codons are CGT, about 6 of the arginine codons are CGC, about 3 of the arginine codons are CGA, about 6 of the arginine codons are CGG, about 6 of the arginine codons are AGA, and about 6 of the arginine codons are AGG;

wherein about 7 of the 44 glycine codons are GGT, about 15 of the glycine codons are GGC, about 11 of the glycine codons are GGA, and about 11 of the glycine codons are GGG;

and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

182. The polynucleotide of claim 181, wherein said codon-optimized coding region comprises SEQ ID NO:36.

183. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:16, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:16;

wherein the 21 phenylalanine codons is said coding region are TTC, the 39 leucine codons is said coding region are CTG, the 38 isoleucine codons in said coding region are ATC, the 27 methionine codons is said coding region are ATG, the 32 valine codons in said coding region are GTG, the 40 serine codons in said coding region are AGC, the 26 proline codons in said coding region are CCC, the 38 threonine codons in said coding region are ACC, the

41 alanine codons in said coding region are GCC, the 14 tyrosine codons in said coding region are TAC, the 4 histidine codons in said coding region are CAC, the 19 glutamine codons in said coding region are CAG, the 25 asparagine codons in said coding region are AAC, the 52 lysine codons in said coding region are AAG, the 34 aspartic acid codons in said coding region are GAC, the 30 glutamic acid codons in said coding region are GAG, the 1 tryptophan codon in said coding region is TGG, the 30 arginine codons in said coding region are selected from the group consisting of CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 44 glycine codons in said coding region are GGC; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

184. The polynucleotide of claim 183, wherein said codon optimized coding region comprises SEQ ID NO:37.

185. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 20 contiguous amino acids of SEQ ID NO:16, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:16;

wherein said codon-optimized coding region consists of nucleotides 1-1680 of SEQ ID NO:1 except that the 39 leucine codons are CTG, the 26 proline codons are CCC, the 41 alanine codons are GCC, the 19 glutamine

codons are CAG, the 25 asparagine codons are AAC, the 52 lysine codons are AAG, and the 30 glutamic acid codons are GAG; and

wherein said at least 20 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:16.

186. The polynucleotide of claim 185, wherein said codon optimized coding region comprises SEQ ID NO:38.

187. The polynucleotide of any one of claims 181 to 186, wherein said nucleic acid fragment encodes at least 50 contiguous amino acids of SEQ ID NO:16.

188. The polynucleotide of any one of claims 181 to 186, wherein said nucleic acid fragment encodes at least 100 contiguous amino acids of SEQ ID NO:16.

189. The polynucleotide of of claim 188, wherein said nucleic acid fragment encodes SEQ ID NO:16.

190. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:16, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:2;

wherein about 10 of the 21 phenylalanine codons are TTT, and about 12 of the phenylalanine codons are TTC;

wherein about 3 of the 39 leucine codons are TTA, about 5 of the leucine codons are TTG, about 5 of the leucine codons are CTT, about 8 of the leucine codons are CTC, about 3 of the leucine codons are CTA, and about 16 of the leucine codons are CTG;

wherein about 14 of the 38 isoleucine codons are ATT, about 18 of the isoleucine codons are ATC, and about 6 of the isoleucine codons are ATA;

wherein the 27 methionine codons are ATG;

wherein about 6 of the 32 valine codons are GTT, about 8 of the valine codons are GTG, about 4 of the valine codons are GTA, and about 15 of the valine codons are GTG;

wherein about 7 of the 40 serine codons are TCT, about 9 of the serine codons are TCC, about 6 of the serine codons are TCA, about 2 of the serine codons are TCG, about 6 of the serine codons are AGT, and about 10 of the serine codons are AGC;

wherein about 7 of the 26 proline codons are CCT, about 9 of the proline codons are CCC, about 7 of the proline codons are CCA, and about 3 of the proline codons are CCG; about 9 of the 38 threonine codons are ACT, about 14 of the threonine codons are ACC, about 11 of the threonine codons are ACA, and about 4 of the threonine codons are ACG;

wherein about 11 of the 41 alanine codons are GGT, about 17 of the alanine codons are GCC, about 9 of the alanine codons are GCA, and about 4 of the alanine codons are GCG;

wherein about 6 of the 14 tyrosine codons are TAT and about 8 of the tyrosine codons are TAC; about 2 of the 4 histidine codons are CAT and about 2 of the histidine codons are CAC;

wherein about 5 of the 19 glutamine codons are CAA and about 14 of the glutamine codons are CAG; about 12 of the 25 asparagine codons are AAT and about 13 of the asparagine codons are AAC; about 22 of the 52 lysine codons are AAA and about 30 of the lysine codons are AAG;

wherein about 16 of the 34 aspartic acid codons are GAT and about 18 of the aspartic acid codons are GAC;

wherein about 12 of the 30 glutamic acid codons are GAA and about 18 of the glutamic acid codons are GAG;

wherein about 2 of the 5 cysteine codons are TGT and about 3 of the cysteine codons are TGC;

wherein the single tryptophan codon is TGG;

wherein about 2 of the 30 arginine codons are CGT, about 6 of the arginine codons are CGC, about 3 of the arginine codons are CGA, about 6 of the arginine codons are CGG, about 6 of the arginine codons are AGA, and about 6 of the arginine codons are AGG;

wherein about 7 of the 44 glycine codons are GGT, about 15 of the glycine codons are GGC, about 11 of the glycine codons are GGA, and about 11 of the glycine codons are GGG;

and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

191. The polynucleotide of claim 190, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:16.

192. The polynucleotide of claim 191, wherein said nucleic acid fragment encodes SEQ ID NO:16.

193. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:16, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:16;

wherein the 21 phenylalanine codons is said coding region are TTC, the 39 leucine codons is said coding region are CTG, the 38 isoleucine codons in said coding region are ATC, the 27 methionine codons is said coding region are ATG, the 32 valine codons in said coding region are GTG, the 40 serine codons in said coding region are AGC, the 26 proline codons in said coding region are CCC, the 38 threonine codons in said coding region are ACC, the 41 alanine codons in said coding region are GCC, the 14 tyrosine codons in said coding region are TAC, the 4 histidine codons in said coding region are CAC, the 19 glutamine codons in said coding region are CAG, the 25 asparagine codons in said coding region are AAC, the 52 lysine codons in said

coding region are AAG, the 34 aspartic acid codons in said coding region are GAC, the 30 glutamic acid codons in said coding region are GAG, the 1 tryptophan codon in said coding region is TGG, the 30 arginine codons in said coding region are selected from the group consisting of CGG, AGA, or AGG (the frequencies of usage of these three codons in the human genome are not significantly different), and the 44 glycine codons in said coding region are GGC; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:2.

194. The polynucleotide of claim 193, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:16.

195. The polynucleotide of claim 194, wherein said nucleic acid fragment encodes SEQ ID NO:16.

196. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:16, wherein said nucleic acid fragment is a variant fragment of an codon-optimized coding region for the polypeptide of SEQ ID NO:16;

wherein said codon-optimized coding region consists of nucleotides 1-1680 of SEQ ID NO:1 except that the 33 leucine codons are CTG, the 17 proline codons are CCC, the 39 alanine codons are GCC, the 21 glutamine

codons are CAG, the 26 asparagine codons are AAC, the 21 lysine codons are AAG, and the 36 glutamic acid codons are GAG; and

wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:16.

197. The polynucleotide of claim 196, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:16.

198. The polynucleotide of claim 197, wherein said nucleic acid fragment encodes SEQ ID NO:2.

199. The polynucleotide of any one of claims 181 to 198, wherein said nucleic acid fragment is ligated to a heterologous nucleic acid.

200. The polynucleotide of claim 199, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

201. The polynucleotide of claim 200, wherein said heterologous polypeptide is a hepatitis B core antigen.

202. The polynucleotide of claim 201, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

203. The polynucleotide of claim 202, comprising SEQ ID NO:43.

204. The polynucleotide of claim 200, wherein said heterologous polypeptide is the extracellular domain of an influenza virus M2 protein.

205. The polynucleotide of claim 204, wherein said extracellular domain of an influenza virus M2 protein comprises amino acids 1 to 24 of SEQ ID NO:5.

206. The polynucleotide of any one of claims 181 to 205, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

207. The polynucleotide of any one of claims 181 to 205, which is RNA.

208. The polynucleotide of claim 207, which is messenger RNA (mRNA).

209. A vector comprising the polynucleotide of any one of claims 181 to 208.

210. The vector of claim 209, which is a plasmid.

211. A composition comprising the polynucleotide of any one of claims 181 to 208, and a carrier.

212. The composition of claim 211, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

213. The composition of claim 212, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

214. The composition of claim 213, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

215. The composition of claim 214, wherein said neutral lipid is DPyPE.

216. The composition of claim 212, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

217. The composition of claim 212, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

218. The composition of claim 217, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

219. The composition of claim 217 or claim 218, which is formulated by combining together the CRL1005, BAK, and polynucleotide at

a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

220. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 181 to 209.

221. The composition of any one of claims 31-39, 69-77, 109-117, 140-148, 171-179 or 211-219, further comprising a conventional vaccine component selected from the group consisting of inactivated virus, attenuated virus, a viral vector expressing an isolated influenza virus polypeptide, and isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof

222. The composition of claim 221, wherein said isolated polypeptide is any isolated influenza virus polypeptide fragment, variant or derivative thereof, selected from the group consisting of influenza A virus NP protein fragment, variant or derivative thereof, influenza A virus M1 protein fragment, variant or derivative thereof, an influenza M2 protein fragment, variant or derivative thereof, a polypeptide comprising an influenza A virus NP protein fused to the extracellular domain of influenza A virus M2 protein, a polypeptide comprising an influenza A virus M1 protein fused to an influenza A virus M2 protein, and an influenza B virus NP protein, or fragment, variant or derivative thereof.

223. The composition of claim 221, wherein said isolated polypeptide comprises at least one immunogenic epitope capable of eliciting an immune response in a vertebrate.

224. The composition of claim 221, wherein the codon-optimized nucleic acid composition and said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof are in the same formulation.

225. The composition of claim 224, wherein said composition is a combinatorial polynucleotide vaccine composition or single formulation heterologous prime-boost vaccine composition.

226. The composition of claim 221, wherein the codon-optimized nucleic acid composition and said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof are in different formulations, wherein said different formulations are administered sequentially or simultaneously.

227. The composition of claim 221, wherein the combination of the codon-optimized nucleic acid composition and said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, provides an equivalent or higher immunological response than the individual components administered alone.

228. The composition of claim 221, wherein the combination of the codon-optimized nucleic acid composition and said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, provides a broadened immune response.

229. The composition of claim 221, wherein the combination of the codon-optimized nucleic acid composition and the isolated polypeptide provides therapeutic benefit at lower doses than a therapeutically beneficial amount of either component administered alone.

230. The composition of claim 229, wherein the combination of the codon-optimized nucleic acid composition and the isolated polypeptide provides therapeutic benefit at a dose of isolated polypeptide that is at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60% or at least 70% less than administration of the polypeptide alone.

231. The composition of claim 221, wherein the combination of the codon-optimized nucleic acid composition and the isolated polypeptide provides a broadened immune response at lower doses than a therapeutically beneficial amount of either component administered alone.

232. A method of eliciting an immune response by administration of the composition of claim 221, wherein said immune response is an equivalent

or higher response than provided by administration of the composition in any one of claims 32-39,70-78,111-119,143-151,175-183 or said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof.

233. The method of claim 232, wherein said immune response is a broadened immune response.

234. The method of claim 232, wherein said immune response is achieved by administration of dose sparing amounts of said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, wherein said dose sparing amount is a concentration that is lower than conventionally administered.

235. The method of claim 234, wherein said immune response is be achieved by administration of dose sparing amounts of said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, and wherein said immune response is a broadened immune response.

236. The method of claim 234, wherein said dose sparing amounts of isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, are at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60% or at least 70% less than administration of polypeptide alone.

237. The method of claim 232, wherein said immune response is an enhanced cellular immune response.

238. The method of claim 232, wherein said immune response is an enhanced humoral immune response.

239. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 1 to 28, 41 to 66, 79 to 106, 150 to 168 or the composition of any one of claims 31 to 39, 69 to 77, 109 to 117, 171 to 179, 221-231 in any combination or permutation with any one of the polynucleotides of claims 181 to 208 or the composition of any one of claims 211 to 219.

240. An isolated polypeptide comprising at least 20 contiguous amino acids of the consensus amino acid sequence of SEQ ID NO:76, wherein said at least 150 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:76.

241. The polypeptide of claim 240, wherein said polypeptide comprises at least 200 contiguous amino acids of the consensus amino acid sequence of SEQ ID NO:76.

242. The polypeptide of claim 240, wherein said polypeptide comprises at least 250 contiguous amino acids of the consensus amino acid sequence of SEQ ID NO:76.

243. An isolated polypeptide comprising an amino acid sequence at least 90% identical to SEQ ID NO:76, wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:76.

244. The polypeptide of claim 243, wherein said amino acid sequence is at least 95% identical to SEQ ID NO:76.

245. The polypeptide of claim 240, wherein said polypeptide comprises the consensus amino acid sequence of SEQ ID NO:76.

246. The polypeptide of any one of claims 240 to 245, further comprising a heterologous polypeptide ligated to said polypeptide.

247. The polypeptide of claim 246, wherein said heterologous polypeptide is a hepatitis B core antigen.

248. The polypeptide of claim 247, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

249. The polypeptide of claim 246, wherein said heterologous polypeptide comprises at least the extracellular domain of an influenza virus M2 protein.

250. The polypeptide of claim 249, wherein said extracellular domain of an influenza virus M2 protein is selected from the group consisting of amino acids 1 to 24 of SEQ ID NO:5 and amino acids 1 to 24 of SEQ ID NO:78.

251. A composition comprising the polypeptide of any one of claims 240 to 250, and a carrier.

252. The composition of claim 251, further comprising an adjuvant.

253. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polypeptide of any one of claims 240 to 250.

254. An isolated polynucleotide comprising a nucleic acid fragment which encodes at least 150 contiguous amino acids of the consensus amino acid sequence of SEQ ID NO:76, wherein said at least 150 contiguous amino acids, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:76.

255. The polynucleotide of claim 254, wherein said nucleic acid fragment encodes at least 200 contiguous amino acids of SEQ ID NO:76.

256. The polynucleotide of claim 255, wherein said nucleic acid fragment encodes at least 250 contiguous amino acids of SEQ ID NO:76.

257. An isolated polynucleotide comprising a nucleic acid fragment which encodes a polypeptide at least 90% identical to SEQ ID NO:76, wherein said polypeptide, upon administration to a vertebrate, elicits a detectable immune response against SEQ ID NO:76.

258. The isolated polynucleotide of claim 257, wherein said nucleic acid fragment encodes a polypeptide at least 95% identical to SEQ ID NO:76.

259. The polynucleotide of claim 254, wherein said nucleic acid fragment encodes the consensus amino acid sequence of SEQ ID NO:76.

260. The polynucleotide of any one of claims 254 to 259, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:76.

261. The polynucleotide of claim 260, wherein said nucleic acid fragment comprises SEQ ID NO:75.

262. The polynucleotide of any one of claims 254 to 261, further comprising a heterologous nucleic acid ligated to said nucleic acid fragment.

263. The polynucleotide of claim 262, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

264. The polynucleotide of claim 263, wherein said heterologous polypeptide is a hepatitis B core antigen.

265. The polynucleotide of claim 264, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

266. The polynucleotide of claim 265, comprising SEQ ID NO:43.

267. The polynucleotide of claim 263, wherein said heterologous polypeptide comprises at least the extracellular domain of an influenza virus M2 protein.

268. The polynucleotide of claim 267, wherein said extracellular domain of an influenza virus M2 protein is selected from the group consisting of amino acids 1 to 24 of SEQ ID NO:5 and amino acids 1 to 24 of SEQ ID NO:78.

269. The polynucleotide of any one of claims 254 to 268, which is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

270. The polynucleotide of any one of claims 254 to 268, which is RNA.

271. The polynucleotide of claim 270, which is messenger RNA (mRNA).

272. A vector comprising the polynucleotide of any one of claims 254 to 271.

273. The vector of claim 272, wherein said vector is a plasmid.

274. A composition comprising the polynucleotide of any one of claims 254 to 292, and a carrier.

275. The composition of claim 274, further comprising a component selected from the group consisting of an adjuvant and a transfection facilitating compound.

276. The composition of claim 275, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

277. The composition of claim 276, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

278. The composition of claim 277, wherein said neutral lipid is DPyPE.

279. The composition of claim 275, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

280. The composition of claim 275, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

281. The composition of claim 280, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

282. The composition of claim 280 or claim 282, which is formulated by combining together the CRL1005, BAK and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

283. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 254 to 271.

284. A vector comprising an isolated polynucleotide comprising a nucleic acid fragment which encodes the consensus amino acid sequence of SEQ ID NO:77, wherein said vector, upon administration to a vertebrate, expresses said amino acid sequence and elicits a detectable immune response against SEQ ID NO:77.

285. The vector of claim 284, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:77.

286. The vector of claim 285, wherein said nucleic acid fragment comprises SEQ ID NO:79.

287. The vector of any one of claims 284 to 286, further comprising a heterologous nucleic acid ligated to said nucleic acid fragment.

288. The vector of claim 287, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

289. The vector of claim 288, wherein said heterologous polypeptide is a hepatitis B core antigen.

290. The vector of claim 289, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

291. The vector of claim 287, wherein said heterologous polypeptide is the extracellular domain of an influenza virus M2 protein.

292. The vector of claim 291, wherein said extracellular domain of an influenza virus M2 protein is selected from the group consisting of amino acids 1 to 24 of SEQ ID NO:5 and amino acids 1 to 24 of SEQ ID NO:78.

293. The vector of any one of claims 284 to 292, wherein said polynucleotide is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

294. The vector of any one of claims 284 to 292, wherein said polynucleotide is RNA.

295. The vector of claim 294, wherein said polynucleotide is messenger RNA (mRNA).

296. The vector of any one of claims 284 to 293, which is a plasmid.

297. A composition comprising the vector of any one of claims 284 to 296, and a carrier.

298. The composition of claim 297, further comprising a component selected from the group consisting of an adjuvant and a transfection facilitating compound.

299. The composition of claim 298, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

300. The composition of claim 299, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

301. The composition of claim 300, wherein said neutral lipid is DPyPE.

302. The composition of claim 298, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

303. The composition of claim 298, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

304. The composition of claim 303, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

305. The composition of claim 303 or claim 304, which is formulated by combining together the CRL1005, BAK and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

306. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the vector of any one of claims 284 to 296.

307. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof an isolated polypeptide comprising the consensus amino acid sequence of SEQ ID NO:77.

308. The method of claim 307, wherein said polypeptide is encoded by a nucleic acid fragment comprising a codon-optimized coding region for the polypeptide of SEQ ID NO:77.

309. The method of claim 308, wherein said polypeptide is encoded by a nucleic acid fragment comprising SEQ ID NO:79.

310. A vector comprising an isolated polynucleotide comprising a nucleic acid fragment which encodes the consensus amino acid sequence of SEQ ID NO:78, wherein said vector, upon administration to a vertebrate, expresses said amino acid sequence and elicits a detectable immune response against SEQ ID NO:78.

311. The vector of claim 310, wherein said nucleic acid fragment is a fragment of a codon-optimized coding region for the polypeptide of SEQ ID NO:78.

312. The vector of claim 311, wherein said nucleic acid fragment comprises SEQ ID NO:80.

313. The vector of any one of claims 310 to 312, further comprising a heterologous nucleic acid ligated to said nucleic acid fragment.

314. The vector of claim 313, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

315. The vector of claim 314, wherein said heterologous polypeptide is a hepatitis B core antigen.

316. The vector of claim 315, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

317. The vector of claim 313, wherein said heterologous polypeptide is an influenza virus M1 protein or a fragment thereof.

318. The vector of any one of claims 310 to 318, wherein said polynucleotide is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

319. The vector of any one of claims 310 to 318, wherein said polynucleotide is RNA.

320. The vector of claim 319, wherein said polynucleotide is messenger RNA (mRNA).

321. The vector of any one of claims 310 to 318, which is a plasmid.

322. A composition comprising the vector of any one of claims 310 to 321, and a carrier.

323. The composition of claim 322, further comprising a component selected from the group consisting of an adjuvant and a transfection facilitating compound.

324. The composition of claim 323, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

325. The composition of claim 324, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

326. The composition of claim 325, wherein said neutral lipid is DPyPE.

327. The composition of claim 323, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

328. The composition of claim 323 wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

329. The composition of claim 328, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

330. The composition of claim 328 or claim 329, which is formulated by combining together the CRL1005, BAK and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

331. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the vector of any one of claims 310 to 321.

332. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof an isolated polypeptide comprising the consensus amino acid sequence of SEQ ID NO:78.

333. The method of claim 332, wherein said polypeptide is encoded by a nucleic acid fragment comprising a codon-optimized coding region for the polypeptide of SEQ ID NO:78.

334. The method of claim 333, wherein said polypeptide is encoded by a nucleic acid fragment comprising SEQ ID NO:80.

335. A vector comprising an isolated polynucleotide comprising a nucleic acid fragment of SEQ ID NO:60, wherein said nucleic acid fragment

upon administration to a vertebrate expresses a fragment of a polypeptide selected from the group consisting of SEQ ID NO:77, SEQ ID NO:78 and mixtures thereof, and wherein said polypeptide fragment elicits a detectable immune response against said polypeptide selected from the group consisting of SEQ ID NO:77, SEQ ID NO:78 and mixtures thereof.

336. The vector of claim 335, wherein said nucleic acid fragment is codon-optimized.

337. The vector of claim 336, wherein said nucleic acid fragment comprises SEQ ID NO:79.

338. The vector of claim 336, wherein said nucleic acid fragment comprises SEQ ID NO:80.

339. The vector of claim 336, wherein said nucleic acid fragment comprises SEQ ID NO:61.

340. The vector of any one of claims 335 to 339, further comprising a heterologous nucleic acid ligated to said nucleic acid fragment.

341. The vector of claim 340, wherein said heterologous nucleic acid encodes a heterologous polypeptide fused to the polypeptide encoded by said nucleic acid fragment.

342. The vector of claim 341, wherein said heterologous polypeptide is a hepatitis B core antigen.

343. The vector of claim 342, wherein said hepatitis B core antigen comprises at least 50 amino acids of a polypeptide selected from the group consisting of SEQ ID NO:40 and SEQ ID NO:42.

344. The vector of any one of claims 335 to 343, wherein said polynucleotide is DNA, and wherein said nucleic acid fragment is operably associated with a promoter.

345. The vector of any one of claims 335 to 343, wherein said polynucleotide is RNA.

346. The vector of claim 345, wherein said polynucleotide is messenger RNA (mRNA).

347. The vector of any one of claims 335 to 344, which is a plasmid.

348. A composition comprising the vector of any one of claims 335 to 347, and a carrier.

349. The composition of claim 348, further comprising a component selected from the group consisting of an adjuvant and a transfection facilitating compound.

350. The composition of claim 349, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

351. The composition of claim 350, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

352. The composition of claim 351, wherein said neutral lipid is DPyPE.

353. The composition of claim 349, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

354. The composition of claim 349, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

355. The composition of claim 354, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

356. The composition of claim 354 or claim 355, which is formulated by combining together the CRL1005, BAK and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

357. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the vector of any one of claims 335 to 347.

358. The composition of any one of claims 251, 252, 274-282, 297-305, 322-330 or 348-356, further comprising a conventional vaccine component selected from the group consisting of inactivated virus, attenuated virus, a viral vector expressing an isolated influenza virus polypeptide, and isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof

359. The composition of claim 358, wherein said isolated polypeptide is any isolated influenza virus polypeptide fragment, variant or derivative thereof, selected from the group consisting of influenza A virus NP protein fragment, variant or derivative thereof, influenza A virus M1 protein fragment, variant or derivative thereof, an influenza M2 protein fragment, variant or derivative thereof, a polypeptide comprising an influenza A virus NP protein fused to the extracellular domain of influenza A virus M2 protein, a polypeptide comprising an influenza A virus M1 protein fused to the influenza A virus M2 protein, and an influenza B virus NP protein, or fragment, variant or derivative thereof.

360. The composition of claim 358, wherein said isolated polypeptide comprises at least one immunogenic epitope capable of eliciting an immune response in a vertebrate.

361. The composition of claim 358, wherein the consensus amino acid composition and said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof are in the same formulation.

362. The composition of claim 361, wherein said composition is a combinatorial polynucleotide vaccine composition or single formulation heterologous prime-boost vaccine composition.

363. The composition of claim 358, wherein the consensus amino acid composition and said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof are in different formulations, wherein said different formulations are administered sequentially or simultaneously.

364. The composition of claim 358, wherein the combination of the consensus amino acid composition and said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, provides an equivalent or higher immunological response than the individual components administered alone.

365. The composition of claim 358, wherein the combination of the consensus amino acid composition and said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, provides a broadened immune response.

366. The composition of claim 358, wherein the combination of the consensus amino acid composition and the isolated polypeptide provides therapeutic benefit at lower doses than a therapeutically beneficial amount of either component administered alone.

367. The composition of claim 366, wherein the combination of the consensus amino acid composition and the isolated polypeptide provides therapeutic benefit at a dose of isolated polypeptide that is at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60% or at least 70% less than administration of the polypeptide alone.

368. The composition of claim 358, wherein the combination of the consensus amino acid composition and the isolated polypeptide provides a broadened immune response at lower doses than a therapeutically beneficial amount of either component administered alone.

369. A method of eliciting an immune response by administration of the composition of claim 358, wherein said immune response is an equivalent or higher response than provided by administration of the composition in any

one of claims 251, 252, 274-282, 297-305, 322-330 or 348-356 or said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof.

370. The method of claim 369, wherein said immune response is a broadened immune response.

371. The method of claim 369, wherein said immune response is achieved by administration of dose sparing amounts of said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, wherein said dose sparing amount is a concentration that is lower than conventionally administered.

372. The method of claim 371, wherein said immune response is be achieved by administration of dose sparing amounts of said isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, and wherein said immune response is a broadened immune response.

373. The method of claim 371, wherein said dose sparing amounts of isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof, are at least 5%, at least 10%, at least 20%, at least 30%, at least 40%, at least 50%, at least 60% or at least 70% less than administration of polypeptide alone.

374. The method of claim 370, wherein said immune response is an enhanced cellular immune response.

375. The method of claim 370, wherein said immune response is an enhanced humoral immune response.

376. A method of treating or preventing influenza infection in a vertebrate comprising: administering to a vertebrate in need thereof the polynucleotide of any one of claims 254-271 or the polypeptide of any one of claims 240-250 in any combination or permutation with any one of the compositions of any one of claims 251, 252, 274-282, 297-305, 322-330 or 348-356.

377. The plasmid of any one of claims 30, 68, 108, 139, 170, 210, 273, 321 and 347 wherein the plasmid backbone is selected from the group consisting of the VR10551 backbone, VR10682 backbone and VR10686 backbone.

378. The plasmid of any one of claims 30, 68, 108, 139, 170, 210, 273, 321 and 347 wherein the plasmid backbone comprises a promoter selected from the group consisting of the human cytomegalovirus promoter, a rous sarcoma virus promoter, a modified rous sarcoma virus promoter from plasmid VCL1005 and a rous sarcoma virus promoter fused to an Human T-cell Leukemia Virus-I RU5 element.

379. The plasmid of any one of claims 30, 68, 108, 139, 170, 210, 273, 321 and 347 further comprising an additional promoter.

380. The plasmid of claim 379 further comprising an additional polynucleotide of any one of claims 1-26, 41-64, 79-104, 119-135, 150-166, 181-206 and 254-269.

381. The plasmid of claim 379 further comprising a polynucleotide selected from the group consisting of:

SEQ ID NO:60;

SEQ ID NO:61;

SEQ ID NO:77;

SEQ ID NO:78;

SEQ ID NO:79; and

SEQ ID NO:80.

382. A composition comprising the plasmid of any one of claims 377-381 and a carrier.

383. The composition of claim 382, further comprising a component selected from the group consisting of an adjuvant, and a transfection facilitating compound.

384. The composition of claim 383, wherein said adjuvant is selected from the group consisting of:

(a) (±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE) and a neutral lipid;

(b) a cytokine;

(c) mono-phosphoryl lipid A and trehalosedicorynomycolateAF (MPL + TDM);

(d) a solubilized mono-phosphoryl lipid A formulation; and

(e) CRL1005/BAK.

385. The composition of claim 384, wherein said adjuvant comprises(±)-N-(3-aminopropyl)-N,N-dimethyl-2,3-bis(*syn*-9-tetradeceneyloxy)-1-propanaminium bromide (GAP-DMORIE), and wherein said neutral lipid is selected from the group consisting of:

(a) 1,2-dioleoyl-*sn*-glycero-3-phosphoethanolamine (DOPE);

(b) 1,2-diphytanoyl-*sn*-glycero-3-phosphoethanolamine (DPyPE); and

(c) 1,2-dimyristoyl-glycer-3-phosphoethanolamine (DMPE).

386. The composition of claim 385, wherein said neutral lipid is DPyPE.

387. The composition of claim 383, comprising the transfection facilitating compound (±)-N-(2-hydroxyethyl)-N,N-dimethyl-2,3-bis(tetradecyloxy)-1-propanaminium bromide) (DMRIE).

388. The composition of claim 383, wherein said adjuvant or said transfection facilitating compound comprises CRL1005 and benzalkonium chloride (BAK).

389. The composition of claim 388, wherein said CRL1005 and BAK are present at concentrations selected from the group consisting of:

(a) 0.3 mM BAK and 7.5 mg/ml CRL 1005;

(b) 0.3 mM BAK and 34 mg/ml CRL 1005; and

(c) 0.3 mM BAK and 50 mg/ml CRL 1005.

390. The composition of claim 388 or claim 389, which is formulated by combining together the CRL1005, BAK, and polynucleotide at a temperature below the cloud point, without thermal cycling to a temperature above the cloud point.

391. The composition of any one of claims 382-390, further comprising a conventional vaccine component selected from the group consisting of inactivated virus, attenuated virus, a viral vector expressing an isolated influenza virus polypeptide, and an isolated polypeptide from an influenza virus protein, fragment, variant or derivative thereof

392. A method of treating of preventing influenza infection in a vertbrate comprising: administering to a vertebrate in need thereof the vector of any one of claims 377-380 or the composition of claims 382-391.