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(54) Title: SELF-ASSSEMBLING NANOSTRUCTURE VACCINES

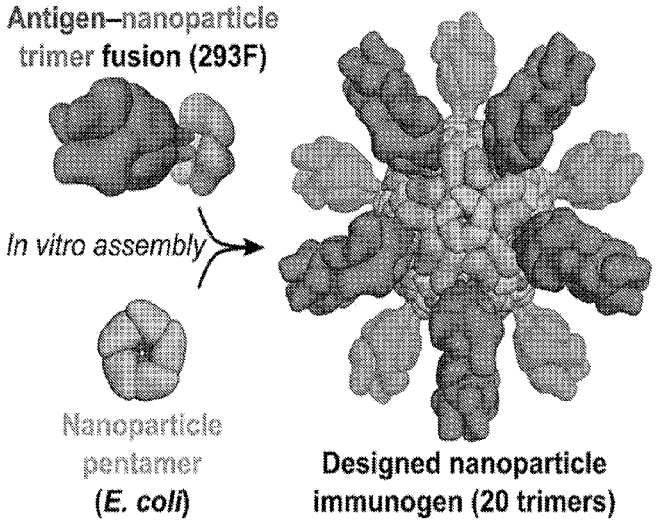

FIG. 1A

(57) Abstract: The present disclosure provides nanostructures and nanostructure-based vaccines. Some nanostructures of the present disclosure display antigens capable of eliciting immune responses to infectious agents such as bacteria, viruses, and pathogens. Some vaccines of the present disclosure are useful for preventing or decreasing the severity of infection with an infectious agent, including, for example and without limitation, lyme disease, pertussis, herpes virus, orthomyxovirus, paramyxovirus, pneumovirus, filovirus, flavivirus, reovirus, retrovirus, meningococcus, or malaria. The antigens may be attached to the core of the nanostructure either non-covalently or covalently, including as a fusion protein or by other means disclosed herein. Multimeric antigens may optionally be displayed along a symmetry axis of the nanostructure. Also provided are proteins and nucleic acid molecules encoding such proteins, vaccine compositions, and methods of administration.

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SELF-ASSSEMBLING NANOSTRUCTURE VACCINES

CROSS REFRENCE

[0001] This application claims priority to U.S. Provisional Patent Application Serial Nos. 62/636,757 filed February 28, 2018 and 62/724,721 filed August 30, 2018, each incorporated by reference herein in its entirety.

DESCRIPTION OF THE TEXT FILE SUBMITTED ELECTRONICALLY

[0002] This application is being filed electronically via EFS-Web and includes an electronically submitted sequence listing in .txt format. The .txt file contains a sequence listing entitled "ICVX_001_02WO_SeqList_ST25.txt" created on February 27, 2019 and having a size of ~ 373 kilobytes.

FIELD OF THE INVENTION

[0003] The present disclosure relates generally to vaccines and methods of use thereof. Specifically, the disclosure relates to nanostructure-based vaccines capable of eliciting immune responses to antigens, such as antigenic proteins of various infectious agents, including bacteria, viruses, and parasites.

BACKGROUND OF THE INVENTION

[0004] Vaccination is a treatment modality used to prevent or decrease the severity of infection with various infectious agents, including bacteria, viruses, and parasites. Development of new vaccines has important commercial and public health implications. In particular, lyme disease, pertussis, herpes virus, orthomyxovirus, paramyxovirus, pneumovirus, filovirus, flavivirus, reovirus, retrovirus, and malaria are infectious agents for which vaccines already exist, are being developed, or would be desirable.

[0005] Subunit vaccines are vaccines made from isolated antigens, usually proteins expressed recombinantly in bacterial, insect, or mammalian cell hosts. Typically, the antigenic component of a subunit vaccine is selected from among the proteins of an infectious

agent observed to elicit a natural immune response upon infection, although in some cases other components of the infectious agent can be used. Typical antigens for use in subunit vaccines include protein expressed on the surface of the target infectious agent, as such surface-expressed envelope glycoproteins of viruses. Preferably, the antigen is a target for neutralizing antibodies. More preferably, the antigen is a target for broadly neutralizing antibodies, such that the immune response to the antigen covers immunity against multiple strains of the infectious agent. In some cases, glycans that are N-linked or O-linked to the subunit vaccine may also be important in vaccination, either by contributing to the epitope of the antigen or by guiding the immune response to particular epitopes on the antigen by steric hindrance. The immune response that occurs in response to vaccination may be direct to the protein itself, to the glycan, or to both the protein and linked glycans. Subunit vaccines have various advantages including that they contain no live pathogen, which eliminates concerns about infection of the patient by the vaccine; they may be designed using standard genetic engineering techniques; they are more homogenous than other forms of vaccine; and they can be manufactured in standardized recombinant protein expression production systems using well-characterized expression systems. In some cases, the antigen may be genetically engineered to favor generation of desirable antibodies, such as neutralizing or broadly neutralizing antibodies. In particular, structural information about an antigen of interest, obtained by X-ray crystallography, electron microscopy, or nuclear magnetic resonance experiments, can be used to guide rational design of subunit vaccines.

[0006] A known limitation of subunit vaccines is that the immune response elicited may sometimes be weaker than the immune response to other types of vaccines, such as whole virus, live, or live attenuated vaccines. The present inventors have recognized and herein disclose that nanostructure-based vaccines have the potential to harness the advantages of subunit vaccines while increasing the potency and breadth of the vaccine-induced immune response through multivalent display of the antigen in symmetrically ordered arrays. Nanostructure-based vaccines are one form of "nanoparticle vaccine." In the present disclosure, nanostructure-based vaccines are distinguished from nanoparticle vaccines, because the term nanoparticle vaccine has been used in the art to refer to protein-based or glycoprotein-based vaccines (*see, e.g.* U.S. Patent No. US 9,441,019), polymerized liposomes (*see, e.g.*, US Patent No. 7,285,289), surfactant micelles (*see, e.g.*, US Patent Pub. No. US 2004/0038406 A1), and synthetic biodegradable particles (*see, e.g.*, US Patent No. US 8,323,696). Nanostructure-based vaccination represents a paradigm in vaccination with

significant commercial and public health implications. Thus, there exists a need for nanostructure-based vaccines and methods of use thereof for eliciting immune responses to infectious agents, such as bacteria, viruses, and parasites; and for preventing or decreasing the severity of infection with an infectious agent including, for example and without limitation, lyme disease, pertussis, herpes virus, orthomyxovirus, paramyxovirus, pneumovirus, filovirus, flavivirus, reovirus, retrovirus, meningococcus, and malaria.

SUMMARY OF THE INVENTION

[0007] Described herein are nanostructures, vaccines, methods of use thereof, and methods of making said nanostructures.

[0008] In one aspect, the present disclosure provides nanostructures comprising a first plurality of polypeptides, wherein the first plurality of polypeptides are arranged according to at least one symmetry operator; the nanostructure comprises a first plurality of antigens; each of the first plurality of the antigens has a proximal end and a distal end; and the proximal ends of the antigens are each attached to a member of the first plurality of polypeptides.

[0009] In another aspect, the present disclosure provides vaccines comprising any of the nanostructures of the present disclosure, wherein the vaccine is capable of eliciting a neutralizing antibody response to an infectious agent. In an embodiment, the vaccine is provided in a pharmaceutical composition.

[0010] In another aspect, the present disclosure provides methods of generating immunity to an infectious agent in a subject, comprising administering any of the vaccines of the present disclosure.

[0011] In another aspect, the present disclosure provides methods of making any of the nanostructures of the present disclosure by *in vitro* assembly of component purified from one or more recombinant expression systems. In another aspect, the present disclosure provides methods of making any of the nanostructures of the present disclosure by co-expression of all components in a recombinant expression system, thereby generating the nanostructure, and purifying the nanostructure.

[0012] In an embodiment of the nanostructures of the present disclosure, the nanostructure further comprises a second plurality of polypeptides, wherein the second

plurality of polypeptides is attached to the first plurality of polypeptides. In an embodiment, the nanostructure further comprises a second plurality of antigens. In an embodiment, the nanostructure further comprises a second plurality of antigens, each of the second plurality of second antigens has a proximal end and a distal end, and the proximal ends of the second antigens are each attached to a member of the second plurality of polypeptides; and optionally, the proximal ends of the antigens are the N termini of the antigens or the C termini of the antigens.

[0013] In an embodiment of the nanostructures of the present disclosure, the plurality of antigens is a plurality of antigenic proteins or antigenic fragments thereof. In an embodiment, the antigenic protein of the nanostructure is selected from SEQ ID NOs: 52-88 and 90-113 or a variant thereof; or the antigenic protein is at least 75, 80, 85, 90, 95, or 99% identical to a polypeptide selected from SEQ ID NOs: 52-88 and 90-97; or the antigenic protein is any of the following: HIV Env, RSV F, Influenza HA, EBV gp350, CMV gB, CMV UL128, CMV UL130, CMV UL131A, CMV gH, CMV gL, Lyme OspA, Pertussis toxin, Dengue E, SARS S, MERS S, Zaire ebolavirus GP, Sudan ebolavirus GP, Marburg virus GP, Hanta virus Gn, Hanta virus Gc, HepB surface antigen, Measles H, Zika envelope domain III, Malaria CSP, Malaria Pfs25, MenB fHbp, MenB NadA, MenB NHBA, Nipah virus F, Nipah virus G, Rotavirus VP4, Rotavirus VP8*, hMPV F, hMPV G, PV F, or PV HN 8.

[0014] In an embodiment, the nanostructure is configured to display a target epitope of the antigen; and optionally, the target epitope is accessible to an antibody as defined herein below. In any embodiment where the nanostructure comprises a plurality of antigenic proteins, optionally the nanostructure is configured to elicit an immune response to the first plurality of antigenic proteins, which immune response is preferentially directed to a target epitope of the antigenic protein. In embodiments of the present disclosure, the target epitope is conserved, it is an epitope for neutralizing antibodies, it is an epitope for cross-reactive antibodies, or it is an epitope for a broadly-neutralizing antibody.

[0015] In an embodiment of the nanostructures of the present disclosure, the plurality of antigens comprises at least one mutation selected from the group consisting of an interface-stabilizing mutation, complementary cysteine mutations configured to result in a disulfide bond, deletion of a loop, addition of an N-linked glycosylation site, removal of an N-linked glycosylation site, an epitope-destroying mutation, and an epitope-creating mutation. In an embodiment, the plurality of antigens comprises an antigenic oligosaccharide.

[0016] In an embodiment of the vaccines of the present disclosure, the neutralizing antibody response is protective against infection by an infectious agent. In an embodiment, the neutralizing antibody response is broadly-neutralizing against diverse strains of an infectious agent. In an embodiment, the infectious agent is any of the following: lyme disease, pertussis, herpesvirus, orthomyxovirus, paramyxovirus, pneumovirus, filovirus, flavivirus, reovirus, retrovirus, meningococcus, or malaria. In an embodiment, the infectious agent is a virus selected from the following: HIV, RSV, Influenza, EBV, CMV, Dengue, Severe Acute Respiratory Syndrome (SARS) virus, Middle East Respiratory Syndrome (MERS) virus, Ebola virus, Marburg virus, Hanta virus, Hepatitis B, HPV, Measles, Nipah virus, Rotavirus, Metapneumo virus, Parainfluenza virus, and Zika. In an embodiment, the infectious agent is lyme disease or pertussis. In an embodiment, the infectious agent is malaria. In an embodiment, the infectious agent is meningococcus.

[0017] In an embodiment of the methods of generating immunity of the present disclosure, the method further comprises administering an adjuvant. In an embodiment, the method further comprises administering the vaccine repeatedly. In an embodiment, the method further comprises administering a second vaccine which is selected from following: a nanoparticle-based vaccine, a protein-based vaccine, a live vaccine, a live attenuated vaccine, a whole germ vaccine, a DNA vaccine, or a RNA vaccine; and optionally the first vaccine is a prime and the second vaccine is a boost, or optionally the second vaccine is a prime and the first vaccine is a boost. In an embodiment, the method induces directed affinity maturation. In an embodiment, the method results in a broadly-neutralizing immune response.

[0018] In an embodiment of the methods of making any of the nanostructures of the present disclosure, the method achieves *in vitro* assembly of the nanostructure by sequentially or non-sequentially expressing the first plurality of polypeptides in a first recombinant expression system, expressing the first plurality of antigens in a second recombinant expression system, purifying the first plurality of polypeptides, purifying the first plurality of antigens, provided that expression of each component precedes purification of that component; and then mixing the first plurality of polypeptides and the first plurality of antigens; thereby generating the nanostructure.

[0019] In an embodiment of the methods of making a nanostructure, the method achieves *in vitro* assembly of the nanostructure by sequentially or non-sequentially expressing the first plurality of polypeptides in a first recombinant expression system, expressing the first

plurality of antigens in a second recombinant expression system, expressing the second plurality of polypeptides in a third recombinant expression system, purifying the first plurality of polypeptides, purifying the first plurality of antigens, purifying the second plurality of polypeptides, provided that expression of each component precedes purification of that component; and mixing the first plurality of polypeptides, the first plurality of antigens, and the second plurality of polypeptides; thereby generating the nanostructure. Optionally, the first recombinant expression system and the second recombinant expression system are the same, and the first plurality of polypeptides and the first plurality of antigens are purified together.

[0020] In an embodiment of the methods of making a nanostructure, the method comprises expressing the first plurality of polypeptides and the first plurality of antigens in a single recombinant expression system, thereby generating the nanostructure, and purifying the nanostructure. In an embodiment, the method comprises expressing the first plurality of polypeptides, the first plurality of antigens, and the second plurality of polypeptides in a single recombinant expression system, thereby generating the nanostructure, and purifying the nanostructure. In an embodiment, optionally, the first plurality of polypeptides and the first plurality of antigens are encoded by a single open reading frame; and optionally, the single open reading frame encodes a fusion protein of the polypeptide and the antigen; and optionally, the single open reading frame encodes a self-cleaving peptide.

[0021] The foregoing paragraphs are not intended to define every aspect of the invention, and additional aspects are described in other sections, such as the Detailed Description. The entire document is intended to be related as a unified disclosure, and it should be understood that all combinations of features described herein are contemplated, even if the combination of features are not found together in the same sentence, or paragraph, or section of this document. The invention includes, as an additional aspect, all embodiments of the invention narrower in scope in any way than the variations defined by specific paragraphs above. For example, where certain aspects of the invention that are described as a genus, it should be understood that every member of a genus is, individually, an aspect of the invention.

BRIEF DESCRIPTION OF THE DRAWINGS

[0022] FIG. 1A shows a schematic diagram of the production of antigen-bearing nanostructures by *in vitro* assembly. The two components or building blocks of a given

nanostructure can be expressed and purified individually, which allows assembly of the nanostructure to be initiated by mixing the purified components *in vitro*, a process referred to as *in vitro* assembly. In some embodiments, the two components of the nanostructure may be expressed in different expression hosts (e.g., human HEK293F cells or bacterial *E. coli* cells). The figure schematically depicts assembly of a 120-subunit nanostructure bearing 20 trimeric antigens (60 antigen subunits) via *in vitro* assembly of an antigen-nanostructure trimer fusion protein produced in HEK293F cells and a nanostructure pentamer protein produced in *E. coli*.

[0023] FIG. 1B depicts example nanostructure architectures.

[0024] FIGs. 2A-2C shows graphs illustrating detection of secreted DS-Cav1 (FIG. 2A), DS-Cav1-foldon-T33-31A (FIG. 2B), and DS-Cav1-T33-31A (FIG. 2C) fusion proteins in tissue culture supernatants. ELISA assays were performed on tissue culture supernatants from cells expressing DS-Cav1 (top), DS-Cav-1-foldon-T33-31A/T33-31B (bottom left), and DS-Cav-1-T33-31A/T33-31B (bottom right). Four different monoclonal antibodies that bind RSV F were used to evaluate the presence of DS-Cav1 or DS-Cav1 fusion proteins in the supernatants. The results confirm the secretion of proteins comprising well-folded RSV F antigen.

[0025] FIG. 3 shows size-exclusion chromatography of DS-Cav1-I53-50A. Protein purified from tissue culture supernatants by immobilized metal affinity chromatography was applied to a Superose 6 10/300 GL size exclusion column. The protein eluted as a single, monodisperse species.

[0026] FIG. 4 shows size exclusion chromatography of *in vitro*-assembled DS-Cav1-I53-50 nanostructures. Purified DS-Cav1-I53-50A and I53-50B.4PT1 proteins were mixed at an approximately 1:1 molar ratio, incubated overnight at 4 °C, and then applied to a Sephacryl S-500 16/60 HR size exclusion column. The assembled nanostructure eluted as a single, monodisperse peak around 65 mL, while excess DS-Cav1-I53-50A trimeric component eluted around 90 mL.

[0027] FIG. 5 shows a negative stain electron micrograph and two-dimensional class averages of *in vitro*-assembled DS-Cav1-I53-50 nanostructures. In vitro-assembled DS-Cav1¬I53-50 nanostructures, purified by size exclusion chromatography, were imaged by negative stain electron microscopy (top). Averaging many nanostructures yielded two-dimensional class averages (bottom) that indicate that the I53-50 portion of the

nanostructures is highly ordered and consistent, while the precise three-dimensional position of the displayed antigen varies slightly due to the flexible nature of the linker between the DS-Cav1 and I53-50A domains of the DS-Cav1-I53-50A fusion protein.

[0028] FIGs. 6A-6C shows a series of graphs depicting the antigenicity of DS-Cav1-I53-50 nanostructures. Analysis of purified DS-Cav1-I53-50 nanostructures by ELISA (FIG. 6A) using four RSV F-specific monoclonal antibodies, including the prefusion-specific antibodies MPE8, D25, and RSD5, indicated that the DS-Cav1 antigen is correctly folded and maintained in the prefusion state when multivalently displayed on DS-Cav1-I53-50 nanostructures. This finding was confirmed by surface plasmon resonance measurements using multiple RSV F-specific antibodies, which, when compared to trimeric DS-Cav1 (FIG. 6C), further suggested that multivalent display of DS-Cav1 (FIG. 6B) results in an avidity effect that reduces the dissociation rate of the antibodies.

[0029] FIG. 7 is a graph depicting DS-Cav1-specific serum antibody titers from mice immunized with DS-Cav1-I53-50 nanostructures. Groups of mice were immunized with I53-50 nanostructures lacking additional antigen, trimeric DS-Cav1, or I53-50 nanostructures bearing DS-Cav1 antigen at 33%, 66%, or 100% valency. DS-Cav1-specific serum antibody titers were measured by ELISA on plates coated with DS-Cav1. Serum antibody titers for each mouse are plotted as circles, with the geometric mean within each group plotted as a horizontal line and reported numerically at bottom.

[0030] FIG. 8 is a graph depicting serum neutralization activity elicited by immunization with DS-Cav1-I53-50 nanostructures. Groups of mice were immunized with I53-50 nanostructures lacking additional antigen, trimeric DS-Cav1, or I53-50 nanostructures bearing DS-Cav1 antigen at 33%, 66%, or 100% valency. Neutralization titers for each mouse are plotted as circles, with the geometric mean within each group plotted as a horizontal line.

[0031] FIGs. 9A-9B are graphs depicting immunogenicity in a primate immune system elicited by immunization with DS-Cav1-foldon I53-50 nanostructures. Rhesus macaques were injected with DS-Cav1-foldon-I53-50 nanostructures intramuscularly at weeks 0 and 4 with either free DS-Cav1 trimer or DS-Cav1-foldon-I53-50 nanostructures displaying DS-Cav1 at 100% valency. In both cases, the dose of DS-Cav1 antigen was 50 μg, and the immunogens were formulated with the MF59-like, squalene-based oil-in-water emulsion

adjuvant SWE. Sera obtained from the animals at weeks 6 and 16 were evaluated for anti-DS-Cav1 antibody titers (FIG. 9A) and RSV-neutralizing antibody titers (FIG. 9A).

[0032] FIG. 10 is a graph depicting the physical stability of DS-Cav1 when fused to I53-50A and/or when further assembled into the icosahedral nanostructure. Samples of trimeric DS-Cav1, trimeric DS-Cav1-foldon–I53-50A, and DS-Cav1-foldon–I53-50 nanostructures containing equivalent concentrations (50 nM) of DS-Cav1 were split into four aliquots and incubated at 20, 50, 70 or 80 °C for 1 hour. After cooling to room temperature, D25 binding was assayed by surface plasmon resonance (SPR).

[0033] FIGs. 11A-11J are graphs depicting physical stability of the nanostructures. Chemical denaturation in guanidine hydrochloride (GdnHCl), monitored by intrinsic tryptophan fluorescence, was used as a second, antibody-independent technique to evaluate physical stability of trimeric DS-Cav1 (FIG. 1A and FIG. 1B), DS-Cav1-foldon–I53-50A (FIG. 1C and FIG. 1D), DS-Cav1-foldon-I53-50 (FIG. 1E and FIG. 1F), I53-50 (FIG. 1G and FIG. 1H), and I53-50A (FIG. 1I and FIG. 1J). The data indicate superior physical stability of the DS-Cav1 antigen when genetically fused to the I53-50A nanostructure component.

DETAILED DESCRIPTION

[0034] The present disclosure relates to nanostructures and nanostructure-based vaccines. Some nanostructures of the present disclosure display antigens capable of eliciting immune responses to infectious agents, such as bacteria, viruses, and parasites. Some vaccines of the present disclosure are useful for preventing or decreasing the severity of infection with an infectious agent including, for example and without limitation, lyme disease, pertussis, herpes virus, orthomyxovirus, paramyxovirus, pneumovirus, filovirus, flavivirus, reovirus, retrovirus, meningococcus, and malaria. The antigens may be attached to the core of the nanostructure either non-covalently or covalently, including as a fusion protein or by other means disclosed herein. Multimeric antigens may optionally be displayed along a symmetry axis of the nanostructure. Also provided are proteins and nucleic acid molecules encoding such proteins, formulations, and methods of use.

[0035] Before the present invention is further described, it is to be understood that this invention is not limited to particular embodiments described, as such may, of course, vary. It

is also to be understood that the terminology used herein is for the purpose of describing particular embodiments only, and is not intended to be limiting, since the scope of the present invention will be limited only by the claims.

1. Overview of Nanostructures

[0036] The nanostructures of the present invention may comprise multimeric protein assemblies adapted for display of antigens or antigenic fragments. The nanostructures of the present invention comprise at least a first plurality of polypeptides. The first plurality of polypeptides may be derived from a naturally-occurring protein sequence by substitution of at least one amino acid residue or by additional at the N- or C-terminus of one or more residues. In some cases, the first plurality of polypeptides comprises a gene sequence determined de novo by computational methods. This first plurality of polypeptides may form the entire nanostructure; or the nanostructure may comprise one or more additional polypeptides, such that the nanostructure comprises two, three, four, five, six, seven, or more pluralities of polypeptides. In some cases, the first plurality will form trimers related by 3-fold rotational symmetry and the second plurality will form pentamers related by 5-fold rotational symmetry. Together these one or more pluralities of polypeptides may be arranged such that the members of each plurality of polypeptides are related to one another by symmetry operators. A general computational method for designing self-assembling protein materials, involving symmetrical docking of protein building blocks in a target symmetric architecture, is disclosed in U.S. Patent Pub. No. US 2015/0356240 A1.

[0037] The "core" of the nanostructure is used herein to describe the central portion of the nanostructure that links together the antigens or antigenic fragments displayed by the nanostructure. In an embodiment, the core and the displayed antigens are the same polypeptide, meaning that antigens are themselves capable of self-assembly into a nanostructure. An advantage of designing the antigens themselves to self-assemble is that the entire nanostructure then acts as the antigenic component of the vaccine. But in an embodiment, the cores of the nanostructures of the present disclosure are generic platforms adaptable for display of any of various antigens that one might select for inclusion in a vaccine. An advantage of designing a core to be a generic platform is that the one or more pluralities of polypeptides that comprise the core can be designed and optimized in advance and then applied to different antigens. It will be understood that in some cases, the same polypeptide may form a portion of the "core" and then extend outward as either an adaptor

for attachment of an antigen and as the antigen itself (i.e., a fusion protein with the antigen). In embodiments of the present disclosure, the antigen is a protein, glycoprotein, or oligosaccharide of an infectious agent.

[0038] In some cases, self-assembly may be further promoted by multimerization of the antigen even though the core would, in absence of the antigen, be independently capable of self-assembly. This would be the case for example when a homo-trimeric antigen (such as HIV gp140, influenza HA, or RSV F protein) is the antigen, or one of several antigens, displayed on the particle. In some cases, a trimeric antigen placed along a 3-fold axis of the nanostructure promotes proper folding and conformation stability of the antigen and makes self-assembly of the nanostructure a cooperative process, in that the antigen is trimerized properly in part due to its display on a 3-fold axis of the core of the nanostructure, and the nanostructure is stabilized in its assembled form, at least in part, by non-covalent or covalent interactions amongst the trimer units. In some cases, introduction of mutations to the antigen or to the nanostructure components may optionally further stabilize assembly, in particular if cysteine residues are position to create intramolecular disulfide bonds. In some examples, a dimeric, trimeric, tetrameric, pentameric, or hexameric antigen is displayed upon a core designed to have a matching 2-fold, 3-fold, 4-fold, 5-fold, or 6-fold symmetry axis such that the core accommodates the arrangement of the multimeric antigen with the native symmetry of the antigen.

2. Various Non-Limiting Examples of Nanostructures

[0039] A non-limiting example of an embodiment is shown in **FIG. 1A**, which depicts the RSV F protein genetically fused to a component (a first plurality of polypeptides) of the nanostructure, which is expressed recombinantly in 293F cells; along with a pentameric protein assembly (a second plurality of polypeptides), which is expressed recombinantly in *E. coli* cells, these two pluralities of polypeptides self-assembling into a nanostructure (a "designed nanoparticle immunogen") displaying 20 F-protein trimers around an icosahedral core. In this embodiment, the core has a generic design. As explained below, in other embodiments, the RSV F protein is replaced with other another antigen protein, such as a trimeric glycoprotein from another virus. In some embodiments, the nanostructure comprises the trimeric glycoproteins of HIV-1, HIV-2, EBV, CMV, RSV, influenza, Ebola, Marburg, Dengue, SARS, MERS, Hantaan, or Zika virus. In some embodiments, the nanostructure comprises the trimeric glycoproteins of viruses that are related evolutionarily or in sequence

identity to any of these exemplary virus, including without limitation, a herpes virus, orthomyxovirus, paramyxovirus, pneumovirus, filovirus, flavivirus, reovirus, or retrovirus. In an embodiment, the nanostructure comprises the extracellular domain or domains of a transmembrane protein or glycoprotein, or an antigenic fragment thereof. In some embodiments, the nanostructure comprises the antigen proteins or protein fragments or antigenic oligosaccharides of a bacterial pathogen, including without limitation, *Neisseria meningitides* (also known as "meningococcus"), *Haemophilus influenzae* type B, *Streptococcus pneumonia*, and *Listeria monocytogenes*.

[0040] Trimeric antigens that may be used with this or similar nanostructures are in some cases, without limitation, HIV gp140, influenza HA, dengue E protein, or Ebola sGP. When other trimeric antigens are used, they may optionally be placed on the 3-fold symmetry axis of the nanostructure. In some cases, the antigen chosen is monomeric and nevertheless placed on a 3-fold axis. Thus, the nanostructure depicted in **FIG. 1A** is capable of displaying 20 timeric antigens or 60 monomeric antigens. Additionally or alternatively the pentameric complexes of the nanostructure is used to display a 12 pentameric antigens or 70 monomeric antigens. In an embodiment, the nanostructure comprises 20 copies of a trimeric antigen and 12 copies of a pentameric antigen.

2.1. Nanostructure Cores

[0041] Other potential arrangements of polypeptides of the present disclosure are shown in **FIG. 1B**. In some embodiments, the nanostructure is adapted for display of up to 8 trimers; 8 timers and 12 dimers; 6 tetramers and 12 dimers; 6 tetramers and 8 trimers; 20 trimers and 30 dimers; 4 trimers and 6 dimers; 4 first trimers and 4 second trimers, or 8 trimers; 12 pentamers and 20 trimers; or 12 pentamers and 30 dimers; or 4 trimers. In some cases, one of the symmetric axes is not used for antigen display, thus, in some embodiments the nanostructure is adapted for display of up to 8 trimers; 12 dimers; 6 tetramers; 20 trimers; 30 dimers; 4 trimers; 6 dimers; 8 trimers; or 12 pentamers. In some cases, monomeric antigens are displayed and thus, the nanostructure is adapted for display of up to 12, 24, 60, or 70 monomeric antigens. In some cases, the nanostructure comprises mixed pluralities of polypeptides such that otherwise identical polypeptides of the core of the nanostructure display different antigens or no antigen. Thus, depending on the ratio of polypeptides, the nanostructure is in some cases adapted for display of between 1 and 130 antigens (*e.g.*, on the I52 particle) where each of the antigens displayed may be the same or may be different

members of mixed population in proportion to any ratio chosen. The antigens may be co-expressed in a recombinant expression system and self-assembled before purification. Alternatively, the antigens may be expressed separately and then mixed together, either before or after purification from expression host and associated contaminants. In various embodiments, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, or more antigens are displayed. Non-limiting exemplary nanostructures are provided in Bale et al. *Science* 353:389-94 (2016); Heinze et al. *J. Phys. Chem B.* 120:5945-5952 (2016); King et al. *Nature* 510:103-108 (2014); and King et al. *Science* 336:1171-71 (2012).

2.2. Mixed Nanostructures

[0042] In some embodiments, the nanostructure displays two or more antigens from the same organism, such as without limitation HIV gp140 and HIV gp41; or Ebola virus GP_1 and GP_2; or Measles H and F proteins; or CMV gB and CMV UL128, UL130, UL131A, gH (UL75) and gL (UL115), on the same nanostructure. In some cases, the nanostructure displays two antigenic proteins or glycoproteins that are generated by post-transcriptional cleavage, such as cleavage of RSV F protein or influenza HA protein by proteases endogenous to the recombinant expression system, or by proteases supplied exogenously.

[0043] In some cases, the nanostructure is adapted to display the same antigen from two or more diverse strain of a pathogenic organism. In non-limiting examples, the same nanostructure displays mixed populations of homotrimeric protein antigens or mixed heterotrimers of protein antigens from different strains of the infectious agent. In an embodiment, the nanostructure displays the HA proteins of an H1N1 influenza A and of an H3N2 influenza A proteins. In an embodiment, the nanostructure displays the HA proteins of an influenza A and of an influenza B. In an embodiment, the gp140 proteins from diverse strains of HIV are displayed on a single nanostructure. Two, three, four, five, or six strains of HIV may be displayed by the same nanostructure. Without being bound by theory, an advantage of such a mixed nanostructure is that it promotes the generation of cross-reactive or broadly neutralizing immune responses. In some cases, the nanostructure-based vaccine of the present disclosure is a universal influenza vaccine. In some cases, the nanostructure-based vaccine of the present disclosure is an HIV vaccine. In some case, the nanostructure-based vaccine of the present disclosure provides enduring protection against HIV. In some case, the nanostructure-based vaccine of the present disclosure provides enduring protection against

influenza. In an embodiment, the nanostructure is adapted for display of the E proteins of Dengue type 1, type 2, type 3, and type 4. In an embodiment, the nanostructure-based vaccine comprises nanostructures that individually display the protein E from each of Dengue type 1, type 2, type 3, and type 4. In an embodiment, the nanostructure-based vaccine of the present disclosure provides immunity to Dengue virus without increased risk of dengue hemorrhagic fever or dengue shock syndrome.

[0044] When mixed nanostructures are made, it may be advantageous to ensure homomerization in a strain-specific manner rather than permit heterodimerization, such that, for example all H1N1 influenza A HA proteins are displayed on one 3-fold axis of a T33 particle whereas all H3N2 influenza A HA proteins are displayed on the other 3-fold axis of the T33 particle. This may be achieved by use a nanostructure comprising two or more pluralities of polypeptides as the core of the nanostructure with each plurality of polypeptides attached to a different antigen. Alternatively, a nanostructure may be engineered with one or more symmetry-breaking mutations, such as knob-in-hole mutations or intramolecular disulfide mutations, which have the effect of preventing trimer formation between the different antigens. In that case, the nanostructure displays multimeric antigens from different strains at symmetrically equivalent positions on the nanostructure, but each position on the nanostructure is occupied by homomers from the same strain, with only an insignificant proportion of inter-strain heteromeric antigens. In some cases, the antigen itself may be genetically engineered to prevent inter-strain heterodimerization. In an embodiment, the nanostructure is engineered to prevent heteromization of two antigenic proteins with conserved structure but divergent antigenicity, such as for example, an HA protein from the 2009 H1N1 California influenza and the HA protein from the 1999 H1N1 New Caledonia influenza. Furthermore, when mixed nanostructures are made and the antigens are displayed as fusion proteins, the nanostructure will comprise three or more different proteins, as the fusion proteins will share identical (or equivalent) domains used to form the core of the nanostructure with different antigenic domains, one for each antigen displayed on the nanostructure.

2.3. Attachment Modalities

[0045] The nanostructures of the present disclosure display antigens in various ways including as gene fusion or by other means disclosed herein. As used herein, "attached to" denotes any means known in the art for causing two polypeptides to associate. The

association may be direct or indirect, reversible or irreversible, weak or strong, covalent or non-covalent, and selective or nonselective.

[0046] In some embodiments, attachment is achieved by genetic engineering to create an N- or C-terminus fusion of an antigen to one of the pluralities of polypeptides composing the nanostructure. Thus, the nanostructure may consist of, or consist essentially of, one, two, three, four, five, six, seven, eight, nine, or ten pluralities of polypeptides displaying one, two, three, four, five, six, seven, eight, nine, or ten pluralities of antigens, where at least one of the pluralities of antigen is genetically fused to at least one of the plurality of polypeptides. In some cases, the nanostructure consists essentially of one plurality of polypeptides capable of self-assembly and comprising the plurality of antigens genetically fused thereto. In some cases, the nanostructure consists essentially of a first plurality of polypeptides comprising the plurality of antigens genetically fused thereto; and a second plurality of polypeptides capable of co-assembling into two-component nanostructure, one plurality of polypeptides linking the antigen to the nanostructure and the other plurality of polypeptides promoting self-assembly of the nanostructure.

[0047] In some embodiments, attachment is achieved by post-translational covalent attachment between one or more pluralities of polypeptides and one or more pluralities of antigen. In some cases, chemical cross-linking is used to non-specifically attach the antigen to the nanostructure polypeptide. In some cases, chemical cross-linking is used to specifically attach the antigen to the nanostructure polypeptide. Various specific and non-specific cross-linking chemistries are known in the art, such as Click chemistry and other methods. In general, any cross-linking chemistry used to link two proteins may be adapted for use in the presently disclosed nanostructures. In particular, chemistries used in creation of immunoconjugates or antibody drug conjugates may be used. In some cases, an antigen-nanostructure conjugate (ANC) is created using a cleavable or non-cleavable linker. Processes and methods for conjugation of antigens to carriers are provided by, e.g., U.S. Patent Pub. No. US 2008/0145373 A1. In an embodiment, the antigen is a polysaccharide. In some cases, the antigen is a polysaccharide and the nanostructure acts as a hapten. In an embodiment, the target antigen is a protein and conjugation of the target antigen to a polysaccharide is used to enhance the immune response. Processes for preparing protein-polysaccharide conjugates are provided in, e.g., U.S. Patent No. 6,248,334. The conjugation of proteins to polysaccharides in some cases converts a polysaccharide from a weakly

immunogenic T-cell independent antigen to a T-cell dependent antigen that recruits T-cell help, and thus stimulates heightened immune responses. *See* J. M. Cruse, et al. (Editors), Conjugate Vaccines, Karger, Basel, (1989); and R. W. Ellis, et al. (Editors), Development and Clinical Uses of Haemophilus B Conjugate Vaccines, Marcel Dekker, New York (1994).

[0048] In an embodiment, attachment is achieved by non-covalent attachment between one or more pluralities of polypeptides and one or more pluralities of antigen. In some cases, the antigen is engineered to be negatively charged on at least one surface and the polypeptide is engineered to be positively charged on at least one surface, or positively and negatively charged, respectively. This promotes intermolecular association between the antigen and the polypeptides of the nanostructure by electrostatic force. In some cases, shape complementarity is employed to cause linkage of antigen to nanostructure. Shape complementarity can be pre-existing or rationally designed. In some cases, computational designed of protein-protein interfaces is used to achieve attachment. In an embodiment, the antigen is biotin-labeled and the polypeptide comprises a streptavidin, or vice versa. In an embodiment, streptavidin is displayed by gene fusion or otherwise as a tetramer on a 4-fold axis of the nanostructure and the biotin-labeled antigen is monomeric, dimeric, or tetrameric, permitting association to the nanostructure in a configuration appropriate for native multimerization of the antigen. In some cases, a protein-based adaptor is used to capture the antigen. In some cases, the polypeptide is fused to a protein capable of binding a complementary protein, which is fused to the antigen. In an embodiment, the polypeptide is fused to the rotavirus VP6 protein, which forms a trimer, and the antigen is N-terminally fused to the N-terminal peptide of rotavirus VP7, permitting trimer-to-trimer association of antigen to nanostructure. *See* Chen et al. Molecular interactions in rotavirus assembly and uncoating seen by high-resolution cryo-EM. PNAS 2009 June, 106 (26) 10644-10648.

[0049] In an embodiment, each of the first plurality of the antigenic proteins has a proximal end and a distal end, and the proximal ends of the antigenic proteins are each attached to a member of the first plurality of polypeptides. Thus, the distal end of the antigenic protein is defined as the portion of the antigen furthest from the center of the nanostructure. In an embodiment, the antigenic protein comprises target epitope, and the nanostructure is configured to display the target epitope. In some cases, the antigenic protein may comprise more than one target epitope and the nanostructure is configured to display each of the target epitopes. Epitopes progressively closer to the distal end are (without being

bound by theory) in some cases preferentially accessible to the immune system. The distal end of the antigenic protein may be its N terminus, its C terminus, or neither terminus. Thus, depending on how the antigenic protein is attached to the nanostructure, the antigenic protein may be displayed in any orientation. In some cases, the antigenic protein is displayed so that one or more known epitopes are oriented at or towards the distal end of the antigenic protein, such that these epitope(s) are preferentially accessible to the immune system. In some cases, the orientation will recapitulate the orientation of a viral protein with respect to the virus. Thus, in the case of influenza HA, the antigenic protein HA may be oriented so that the receptor binding site is at the distal end of the protein, similar to the orientation of HA in the whole virus; or alternatively, the influenza HA protein may be oriented such that the stem epitope is preferentially accessible to the immune system. The choice of orientation may direct the immune system to one or the other epitope. In this example, the immune response to influenza may be guided to the receptor binding site or to the stem by choice of orientation. Similarly, the orientation of other antigens may influence the immune response. In some embodiments, orientation of the antigen results in an immune response targeted to a preferred epitope. In the case of HIV, the antigenic protein is in some embodiments the Env protein of HIV-1 or HIV-2, or an antigenic fragment thereof. The orientation of the Env or fragment thereof will in some cases recapitulate that the orientation of Env protein with respect to the HIV viron, such that the proximal end is the membrane-proximal end of the Env protein or fragment thereof. In some cases, the preferred epitope is selected from the group consisting of the CD4-binding site (CD4bs); the V2 proteoglycan moiety on the trimer apex of Env; the V3 proteoglycan moiety on the high mannose patch of Env; the membrane proximal external region (MPER) of the Env transmembrane domain; and the gp120-gp41 interface with or without fusion peptide. In some cases, epitope preference is control by other means, such as positioning of glycans on the nanostructure by addition or subtraction of the N-linked glycan sequence motif N-X-[T/S] at predetermined positions in the amino acid sequence of any of the polypeptides of the nanostructure including in the amino acid sequence of the antigen. In some cases, the epitopes found at intermediate distances from the proximal to the distal end will be the preferred over epitopes more distally located depending on various considerations including but not limited to the overall geometry of the nanostructure, surface hydrophobicity, surface charge, and competitive binding of proteins endogenously present in the subject or proteins exogenously provided in the vaccine composition. The present disclosure encompasses all known methods of rational design of protein structure and the foregoing is not intended to be limiting.

2.4. Nanostructure Polypeptide Sequences

[0050] The one or more pluralities of polypeptides of the present disclosure may have any of various amino acids sequences. U.S. Patent Pub No. US 2015/0356240 A1 describes various methods for designing nanostructures. As disclosed in US Patent Pub No. US 2016/0122392 A1 and in International Patent Pub. No. WO 2014/124301 A1, the isolated polypeptides of SEQ ID NOS:1-51 were designed for their ability to self-assemble in pairs to form nanostructures, such as icosahedral nanostructures. The design involved design of suitable interface residues for each member of the polypeptide pair that can be assembled to form the nanostructure. The nanostructures so formed include symmetrically repeated, non-natural, non-covalent polypeptide-polypeptide interfaces that orient a first assembly and a second assembly into a nanostructure, such as one with an icosahedral symmetry. Thus, in one embodiment the first and second polypeptides are selected from the group consisting of SEQ ID NOS:1-51. In each case, the N-terminal methionine residue is optional.

TABLE 1

Name	Amino Acid Sequence	Identified interface residues
I53-34A SEQ ID NO:1	MEGMDPLAVLAESRLLPLLTVRGGEDLAGLATVLELMGVGALEITLRTEKGLE ALKALRKSGLLLGAGTVRSPKEAEAALEAGAAFLVSPGLLEEVAALAQARGVP YLPGVLTPTEVERALALGLSALKFFPAEPFQGVRVLRAYAEVFPEVRFLPTGG IKEEHLPHYAALPNLLAVGGSWLLQGDLAAVMKKVKAAKALLSPQAPG	I53-34A: 28,32,36,37,186,188,191,192,195
I53-34B SEQ ID NO:2	MTKKVGIVDTTFARVDMAEAAIRTLKALSPNIKIIRKTVPGIKDLPVACKKLL EEEGCDIVMALGMPGKAEKDKVCAHEASLGLMLAQLMTNKHIIEVFVHEDEAK DDDELDILALVPAIEHAANVYYLLFKPEYLTRMAGKGLRQGREDAGPARE	I53-34B: 19,20,23,24,27,109,113,116,117,120,124,148
I53-40A SEQ ID NO:3	MTKKVGIVDTTFARVDMASAAILTLKMESPNIKIIRKTVPGIKDLPVACKKLL EEEGCDIVMALGMPGKAEKDKVCAHEASLGLMLAQLMTNKHIIEVFVHEDEAK DDAELKILAARRAIEHALNVYYLLFKPEYLTRMAGKGLRQGFEDAGPARE	I53-40A: 20,23,24,27,28,109,112,113,116,120,124
I53-40B SEQ ID NO:4	MSTINNQLKALKVIPVIAIDNAEDIIPLGKVLAENGLPAAEITFRSSAAVKAI MLLRSAQPEMLIGAGTILNGVQALAAKEAGATFVVSPGFNPNTVRACQIIGID IVPGVNNPSTVEAALEMGLTTLKFFPAEASGGISMVKSLVGPYGDIRLMPTGG ITPSNIDNYLAIPQVLACGGTWMVDKKLVTNGEWDEIARLTREIVEQVNP	I53-40B: 47,51,54,58,74,102
I53-47A SEQ ID NO:5	MPIPTLNTNIKATDVPSDFLSLTSRLVGLILSKPGSYVAVHINTDQQLSFGGS TNPAAFGTLMSIGGIEPSKNRDHSAVLFDHLNAMLGIPKNRMYIHFVNLNGDD VGWNGTTF	I53-47A: 22,25,29,72,79,86,87
I53-47B SEQ ID NO:6	MNQHSHKDYETVRIAVVRARWHADIVDACVEAFEIAMAAIGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLST GVPVLSAVLTPHRYRDSAEHHRFFAAHFAVKGVEAARACIEILAAREKIAA	I53-47B: 28,31,35,36,39,131,132,135,139,146
I53-50A SEQ ID NO:7	MKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIK ALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVF YMPGVMTPTELVKAMKLGHTILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGV NLDNVCEWFKAGVLAVGVGSALVKGTPDEVREKAKAFVEKIRGCTE	I53-50A: 25,29,33,54,57
I53-50B SEQ ID NO:8	MNQHSHKDYETVRIAVVRARWHAEIVDACVSAFEAAMADIGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLST GVPVLSAVLTPHRYRDSDAHTLLFLALFAVKGMEAARACVEILAAREKIAA	I53-50B: 24,28,36,124,125,127,128,129, 131,132,133,135,139
I53-51A SEQ ID NO:9	MFTKSGDDGNTNVINKRVGKDSPLVNFLGDLDELNSFIGFAISKIPWEDMKKD LERVQVELFEIGEDLSTQSSKKKIDESYVLWLLAATAIYRIESGPVKLFVIPG GSEEASVLHVTRSVARRVERNAVKYTKELPEINRMIIVYLNRLSSLLFAMALV	I53-51A: 80,83,86,87,88,90,91,94,1

	ANKRRNQSEKIYEIGKSW	66,172,176
I53-51B SEQ ID NO:10	MNQHSHKDYETVRIAVVRARWHADIVDQCVRAFEEAMADAGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLST GVPVLSAVLTPHRYRSSREHHEFFREHFMVKGVEAAAACITILAAREKIAA	I53-51B: 31,35,36,40,122,124,128,1 31,135,139,143,146,147
I52-03A SEQ ID NO:11	MGHTKGPTPQQHDGSALRIGIVHARWNKTIIMPLLIGTIAKLLECGVKASNIV VQSVPGSWELPIAVQRLYSASQLQTPSSGPSLSAGDLLGSSTTDLTALPTTTA SSTGPFDALIAIGVLIKGETMHFEYIADSVSHGLMRVQLDTGVPVIFGVLTVL TDDQAKARAGVIEGSHNHGEDWGLAAVEMGVRRRDWAAGKTE	I52-03A: 28,32,36,39,44,49
I52-03B SEQ ID NO:12	MYEVDHADVYDLFYLGRGKDYAAEASDIADLVRSRTPEASSLLDVACGTGTHL EHFTKEFGDTAGLELSEDMLTHARKRLPDATLHQGDMRDFQLGRKFSAVVSMF SSVGYLKTVAELGAAVASFAEHLEPGGVVVVEPWWFPETFADGWVSADVVRRD GRTVARVSHSVREGNATRMEVHFTVADPGKGVRHFSDVHLITLFHQREYEAAF MAAGLRVEYLEGGPSGRGLFVGVPA	I52-03B: 94,115,116,206,213
I52-32A SEQ ID NO:13	MGMKEKFVLIITHGDFGKGLLSGAEVIIGKQENVHTVGLNLGDNIEKVAKEVM RIIIAKLAEDKEIIIVVDLFGGSPFNIALEMMKTFDVKVITGINMPMLVELIT SINVYDTTELLENISKIGKDGIKVIEKSSLKM	I52-32A: 47,49,53,54,57,58,61,83,8 7,88
I52-32B SEQ ID NO:14	MKYDGSKLRIGILHARWNLEIIAALVAGAIKRLQEFGVKAENIIIETVPGSFE LPYGSKLFVEKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDSTTHQLMKLNFE LGIPVIFGVLTCLTDEQAEARAGLIEGKMHNHGEDWGAAAVEMATKFN	I52-32B: 19,20,23,30,40
I52-33A SEQ ID NO:15	MAVKGLGEVDQKYDGSKLRIGILHARWNRKIILALVAGAVLRLLEFGVKAENI IIETVPGSFELPYGSKLFVEKQKRLGKPLDAIIPIGVLIKGSTMHFEYICDST THQLMKLNFELGIPVIFGVLTCLTDEQAEARAGLIEGKMHNHGEDWGAAAVEM ATKFN	I52-33A: 33,41,44,50
I52-33B SEQ ID NO:16	MGANWYLDNESSRLSFTSTKNADIAEVHRFLVLHGKVDPKGLAEVEVETESIS TGIPLRDMLLRVLVFQVSKFPVAQINAQLDMRPINNLAPGAQLELRLPLTVSL RGKSHSYNAELLATRLDERRFQVVTLEPLVIHAQDFDMVRAFNALRLVAGLSA VSLSVPVGAVLIFTAR	I52-33B: 61,63,66,67,72,147,148,15 4,155
I32-06A SEQ ID NO:17	MTDYIRDGSAIKALSFAIILAEADLRHIPQDLQRLAVRVIHACGMVDVANDLA FSEGAGKAGRNALLAGAPILCDARMVAEGITRSRLPADNRVIYTLSDPSVPEL AKKIGNTRSAAALDLWLPHIEGSIVAIGNAPTALFRLFELLDAGAPKPALIIG MPVGFVGAAESKDELAANSRGVPYVIVRGRRGGSAMTAAAVNALASERE	I32-06A: 9,12,13,14,20,30,33,34
I32-06B SEQ ID NO:18	MITVFGLKSKLAPRREKLAEVIYSSLHLGLDIPKGKHAIRFLCLEKEDFYYPF DRSDDYTVIEINLMAGRSEETKMLLIFLLFIALERKLGIRAHDVEITIKEQPA HCWGFRGRTGDSARDLDYDIYV	I32-06B: 24,71,73,76,77,80,81,84,8 5,88,114,118
I32-19A SEQ ID NO:19	MGSDLQKLQRFSTCDISDGLLNVYNIPTGGYFPNLTAISPPQNSSIVGTAYTV LPAPIDDPRPAVNYIDSVPPNSILVLALEPHLQSQFHPFIKITQAMYGGLMST RAQYLKSNGTVVFGRIRDVDEHRTLNHPVFAYGVGSCAPKAVVKAVGTNVQLK ILTSDGVTQTICPGDYIAGDNNGIVRIPVQETDISKLVTYIEKSIEVDRLVSE AIKNGLPAKAAQTARRMVLKDYI	I32-19A: 208,213,218,222,225,226,2 29,233
I32-19B SEQ ID NO:20	MSGMRVYLGADHAGYELKQAIIAFLKMTGHEPIDCGALRYDADDDYPAFCIAA ATRTVADPGSLGIVLGGSGNGEQIAANKVPGARCALAWSVQTAALAREHNNAQ LIGIGGRMHTLEEALRIVKAFVTTPWSKAQRHQRRIDILAEYERTHEAPPVPG APA	I32-19B: 20,23,24,27,117,118,122,1 25
I32-28A SEQ ID NO:21	MGDDARIAAIGDVDELNSQIGVLLAEPLPDDVRAALSAIQHDLFDLGGELCIP GHAAITEDHLLRLALWLVHYNGQLPPLEEFILPGGARGAALAHVCRTVCRRAE RSIKALGASEPLNIAPAAYVNLLSDLLFVLARVLNRAAGGADVLWDRTRAH	I32-28A: 60,61,64,67,68,71,110,120 ,123,124,128
I32-28B SEQ ID NO:22	MILSAEQSFTLRHPHGQAAALAFVREPAAALAGVQRLRGLDSDSEQVWGELLV RVPLLGEVDLPFRSEIVRTPQGAELRPLTLTGERAWVAVSGQATAAEGGEMAF APQFQAHLATPSAEGEGGAAFEVMVQAAAGVTLLLVAMALPQGLAAGLPPA	I32-28B: 35,36,54,122,129,137,140, 141,144,148
I53-40A.1 SEQ ID NO:23	MTKKVGIVDTTFARVDMASAAILTLKMESPNIKIIRKTVPGIKDLPVACKKLL EEEGCDIVMALGMPGKKEKDKVCAHEASLGLMLAQLMTNKHIIEVFVHEDEAK DDAELKILAARRAIEHALNVYYLLPKPEYLTRMAGKGLRQGFEDAGPARE	I53-40A: 20,23,24,27,28,109,112,11 3,116,120,124
I53-40B.1 SEQ ID NO:24	MDDINNQLKRLKVIPVIAIDNAEDIIPLGKVLAENGLPAAEITFRSSAAVKAI MLLRSAQPEMLIGAGTILNGVQALAAKEAGADFVVSPGFNPNTVRACQIIGID IVPGVNNPSTVEQALEMGLTTLKFFPAEASGGISMVKSLVGPYGDIRLMPTGG ITPDNIDNYLAIPQVLACGGTWMVDKKLVRNGEWDEIARLTREIVEQVNP	I53-40B: 47,51,54,58,74,102
I53-47A.1 SEQ ID NO:25	MPIFTLNTNIKADDVPSDFLSLTSRLVGLILSKPGSYVAVHINTDQQLSFGGS TNPAAFGTLMSIGGIEPDKNRDHSAVLFDHLNAMLGIPKNRMYIHFVNLNGDD VGWNGTTF	I53-47A: 22,25,29,72,79,86,87

I53-47A.1NegT2 SEQ ID NO:26	MPIFTLNTNIKADDVPSDFLSLTSRLVGLILSEPGSYVAVHINTDQQLSFGGS TNPAAFGTLMSIGGIEPDKNEDHSAVLFDHLNAMLGIPKNRMYIHFVDLDGDD VGWNGTTF	I53-47A: 22,25,29,72,79,86,87
I53-47B.1 SEQ ID NO:27	MNQHSHKDHETVRIAVVRARWHADIVDACVEAFEIAMAAIGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLDT GVPVLSAVLTPHRYRDSDEHHRFFAAHFAVKGVEAARACIEILNAREKIAA	I53-47B: 28,31,35,36,39,131,132,13 5,139,146
I53-47B.1NegT2 SEQ ID NO:28	MNQHSHKDHETVRIAVVRARWHADIVDACVEAFEIAMAAIGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVDGGIYDHEFVASAVIDGMMNVQLDT GVPVLSAVLTPHEYEDSDEDHEFFAAHFAVKGVEAARACIEILNAREKIAA	I53-47B: 28,31,35,36,39,131,132,13 5,139,146
I53-50A.1 SEQ ID NO:29	MKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIK ALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVF YMPGVMTPTELVKAMKLGHDILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGV NLDNVCEWFKAGVLAVGVGDALVKGDPDEVREKAKKFVEKIRGCTE	I53-50A: 25,29,33,54,57
I53-50A.1NegT2 SEQ ID NO:30	MKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIK ALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVF YMPGVMTPTELVKAMKLGHDILKLFPGEVVGPEFVEAMKGPFPNVKFVPTGGV DLDDVCEWFDAGVLAVGVGDALVEGDPDEVREDAKEFVEEIRGCTE	I53-50A: 25,29,33,54,57
I53-50A.1PosT1 SEQ ID NO:31	MKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITSTVPDADTVIK ALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVF YMPGVMTPTELVKAMKLGHDILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGV NLDNVCKWFKAGVLAVGVGKALVKGKPDEVREKAKKFVKKIRGCTE	I53-50A: 25,29,33,54,57
I53-50B.1 SEQ ID NO:32	MNQHSHKDHETVRIAVVRARWHAEIVDACVSAFEAAMRDIGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVIDGMMNVQLDT GVPVLSAVLTPHRYRDSDAHTLLFLALFAVKGMEAARACVEILAAREKIAA	I53-50B: 24,28,36,124,125,127,128, 129,131,132,133,135,139
I53-50B.1NegT2 SEQ ID NO:33	MNQHSHKDHETVRIAVVRARWHAEIVDACVSAFEAAMRDIGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVDGGIYDHEFVASAVIDGMMNVQLDT GVPVLSAVLTPHEYEDSDADTLLFLALFAVKGMEAARACVEILAAREKIAA	I53-50B: 24,28,36,124,125,127,128, 129,131,132,133,135,139
I53-50B.4PosT1 SEQ ID NO:34	MNQHSHKDHETVRIAVVRARWHAEIVDACVSAFEAAMRDIGGDRFAVDVFDVP GAYEIPLHARTLAETGRYGAVLGTAFVVNGGIYRHEFVASAVINGMMNVQLNT GVPVLSAVLTPHNYDKSKAHTLLFLALFAVKGMEAARACVEILAAREKIAA	I53-50B: 24,28,36,124,125,127,128, 129,131,132,133,135,139
I53-40 A genus SEQ ID NO:35	MTKKVGIVDTTFARVDMASAAILTLKMESPNIKIIRKTVPGIKDLPVACKKLL EEEGCDIVMALGMPGK(A/K)EKDKVCAHEASLGLMLAQLMTNKHIIEVFVHE DEAKDDAELKILAARRAIEHALNVYYLLFKPEYLTRMAGKGLRQGFEDAGPAR E	
I53-40 B genus SEQ ID NO:36	M(S/D)(T/D)INNQLK(A/R)LKVIPVIAIDNAEDIIPLGKVLAENGLPAAE ITFRSSAAVKAIMLLRSAQPEMLIGAGTILNGVQALAAKEAGA(T/D)FVVSP GFNPNTVRACQIIGIDIVPGVNNPSTVE(A/Q)ALEMGLTTLKFFPAEASGGI SMVKSLVGPYGDIRLMPTGGITP(S/D)NIDNYLAIPQVLACGGTWMVDKKLV (T/R)NGEWDEIARLTREIVEQVNP	
I53-47A genus SEQ ID NO:37	MPIFTLNTNIKA(T/D)DVPSDFLSLTSRLVGLILS(K/E)PGSYVAVHINTD QQLSFGGSTNPAAFGTLMSIGGIEP(S/D)KN(R/E)DHSAVLFDHLNAMLGI PKNRMYIHFV(N/D)L(N/D)GDDVGWNGTTF	
I53-47B genus SEQ ID NO:38	MNQHSHKD(Y/H)ETVRIAVVRARWHADIVDACVEAFEIAMAAIGGDRFAVDV FDVPGAYEIPLHARTLAETGRYGAVLGTAFVV(N/D)GGIY(R/D)HEFVASA VIDGMMNVQL(S/D)TGVPVLSAVLTPH(R/E)Y(R/E)DS(A/D)E(H/D)H (R/E)FFAAHFAVKGVEAARACIEIL(A/N)AREKIAA	
I53-50A genus SEQ ID NO:39	MKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIK ALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVF YMPGVMTPTELVKAMKLGH(T/D)ILKLFPGEVVGP(Q/E)FV(K/E)AMKGP FPNVKFVPTGGV(N/D)LD(N/D)VC(E/K)WF(K/D)AGVLAVGVG(S/K/D)ALV(K/E)G(T/D/K)PDEVRE(K/D)AK(A/E/K)FV(E/K)(K/E)IRGC TE	
I53-50B genus SEQ ID NO:40	MNQHSHKD(Y/H)ETVRIAVVRARWHAEIVDACVSAFEAAM(A/R)DIGGDRF AVDVFDVPGAYEIPLHARTLAETGRYGAVLGTAFVV(N/D)GGIY(R/D)HEF VASAVI(D/N)GMMNVQL(S/D/N)TGVPVLSAVLTPH(R/E/N)Y(R/D/E) (D/K)S(D/K)A(H/D)TLLFLALFAVKGMEAARACVEILAAREKIAA	

T32-28A SEQ ID NO:41	MGEVPIGDPKELNGMEIAAVYLQPIEMEPPGIDLAASLADIHLEADIHALKNN PNGFPEGFWMPYLTIAYALANADTGAIKTGTLMPMVADDGPHYGANIAMEKDK KGGFGVGTYALTFLISNPEKQGFGRHVDEETGVGKWFEPFVVTYFPKYTGTPK	
T32-28B SEQ ID NO:42	MSQAIGILELTSIAKGMELGDAMLKSANVDLLVSKTISPGKFLLMLGGDIGAI QQAIETGTSQAGEMLVDSLVLANIHPSVLPAISGLNSVDKRQAVGIVETWSVA ACISAADLAVKGSNVTLVRVHMAFGIGGKCYMVVAGDVLDVAAAVATASLAAG AKGLLVYASIIPRPHEAMWRQMVEG	
T33-09A SEQ ID NO:43	MEEVVLITVPSALVAVKIAHALVEERLAACVNIVPGLTSIYRWQGSVVSDHEL LLLVKTTTHAFPKLKERVKALHPYTVPEIVALPIAEGNREYLDWLRENTG	
T33-09B SEQ ID NO:44	MVRGIRGAITVEEDTPAAILAATIELLLKMLEANGIQSYEELAAVIFTVTEDL TSAFPAEAARLIGMHRVPLLSAREVPVPGSLPRVIRVLALWNTDTPQDRVRHV YLNEAVRLRPDLESAQ	
T33-15A SEQ ID NO:45	MSKAKIGIVTVSDRASAGITADISGKAIILALNLYLTSEWEPIYQVIPDEQDV IETTLIKMADEQDCCLIVTTGGTGPAKRDVTPEATEAVCDRMMPGFGELMRAE SLKEVPTAILSRQTAGLRGDSLIVNLPGDPASISDCLLAVFPAIPYCIDLMEG PYLECNEAMIKPFRPKAK	
T33-15B SEQ ID NO:46	MVRGIRGAITVNSDTPTSIIIATILLLEKMLEANGIQSYEELAAVIFTVTEDL TSAFPAEAARQIGMHRVPLLSAREVPVPGSLPRVIRVLALWNTDTPQDRVRHV YLSEAVRLRPDLESAQ	
T33-21A SEQ ID NO:47	MRITTKVGDKGSTRLFGGEEVWKDSPIIEANGTLDELTSFIGEAKHYVDEEMK GILEEIQNDIYKIMGEIGSKGKIEGISEERIAWLLKLILRYMEMVNLKSFVLP GGTLESAKLDVCRTIARRALRKVLTVTREFGIGAEAAAYLLALSDLLFLLARV IEIEKNKLKEVRS	
T33-21B SEQ ID NO:48	MPHLVIEATANLRLETSPGELLEQANKALPASGQFGEADIKSRFVTLEAYRQG TAAVERAYLHACLSILDGRDIATRTLLGASLCAVLAEAVAGGGEEGVQVSVEV REMERLSYAKRVVARQR	
T33-28A SEQ ID NO:49	MESVNTSFLSPSLVTIRDFDNGQFAVLRIGRTGFPADKGDIDLCLDKMIGVRA AQIFLGDDTEDGFKGPHIRIRCVDIDDKHTYNAMVYVDLIVGTGASEVERETA EEEAKLALRVALQVDIADEHSCVTQFEMKLREELLSSDSFHPDKDEYYKDFL	
T33-28B SEQ ID NO:50	MPVIQTFVSTPLDHHKRLLLAIIYRIVTRVVLGKPEDLVMMTFHDSTPMHFFG STDPVACVRVEALGGYGPSEPEKVTSIVTAAITAVCGIVADRIFVLYFSPLHC GWNGTNF	
T33-31A SEQ ID NO:51	MEEVVLITVPSALVAVKIAHALVEERLAACVNIVPGLTSIYREEGSVVSDHEL LLLVKTTTDAFPKLKERVKELHPYEVPEIVALPIAEGNREYLDWLRENTG	

[0051] Table 1 provides the amino acid sequence of the first and second polypeptides from embodiments of the present disclosure. In each case, the pairs of sequences together from an I53 icosahedron. The right hand column in Table 1 identifies the residue numbers in each exemplary polypeptide that were identified as present at the interface of resulting assembled nanostructures (i.e.: "identified interface residues"). As can be seen, the number of interface residues for the exemplary polypeptides of SEQ ID NO:1-34 range from 4-13. In various embodiments, the first and second polypeptides comprise an amino acid sequence that is at least 75%, 80%, 85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical over its length, and identical at least at 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 13 identified interface positions (depending on the number of interface residues for a given polypeptide), to the amino acid sequence of a polypeptide selected from the group consisting of SEQ ID NOS: 1-34. SEQ ID NOs: 35-51 represent other amino acid sequences of the first and second polypeptides from embodiments of the present disclosure. In other embodiments, the first and second polypeptides comprise an amino acid sequence that is at least 75%, 80%,

85%, 90%, 91%, 92%, 93%, 94%, 95%, 96%, 97%, 98%, or 99% identical over its length, and identical at least at 20%, 25%, 33%, 40%, 50%, 60%, 70%, 75%, 80%, 90%, or 100% of the identified interface positions, to the amino acid sequence of a polypeptide selected from the group consisting of SEQ ID NOS:1-51.

[0052] As is the case with proteins in general, the polypeptides are expected to tolerate some variation in the designed sequences without disrupting subsequent assembly into nanostructures: particularly when such variation comprises conservative amino acid substitutions. As used here, "conservative amino acid substitution" means that: hydrophobic amino acids (Ala, Cys, Gly, Pro, Met, Val, Ile, Leu) can only be substituted with other hydrophobic amino acids; hydrophobic amino acids with bulky side chains (Phe, Tyr, Trp) can only be substituted with other hydrophobic amino acids with bulky side chains; amino acids with positively charged side chains (Arg, His, Lys) can only be substituted with other amino acids with positively charged side chains; amino acids with negatively charged side chains (Asp, Glu) can only be substituted with other amino acids with negatively charged side chains; and amino acids with polar uncharged side chains (Ser, Thr, Asn, Gln) can only be substituted with other amino acids with polar uncharged side chains.

[0053] In various embodiments of the nanostructure of the invention, the first polypeptides and the second polypeptides comprise polypeptides with the amino acid sequence selected from the following pairs, or modified versions thereof (i.e.: permissible modifications as disclosed for the polypeptides of the invention: isolated polypeptides comprising an amino acid sequence that is at least 75% identical over its length, and/or identical at least at one identified interface position, to the amino acid sequence indicated by the SEQ ID NO.):

SEQ ID NO:1 and SEQ ID NO:2 (I53-34A and I53-34B);
SEQ ID NO:3 and SEQ ID NO:4 (I53-40A and I53-40B);
SEQ ID NO:3 and SEQ ID NO:24 (I53-40A and I53-40B.1);
SEQ ID NO:23 and SEQ ID NO:4 (I53-40A.1 and I53-40B);
SEQ ID NO:35 and SEQ ID NO:36 (I53-40A genus and I53-40B genus);
SEQ ID NO:5 and SEQ ID NO:6 (I53-47A and I53-47B);
SEQ ID NO:5 and SEQ ID NO:27 (I53-47A and I53-47B.1);
SEQ ID NO:5 and SEQ ID NO:28 (I53-47A and I53-47B.1NegT2);
SEQ ID NO:25 and SEQ ID NO:6 (I53-47A.1 and I53-47B);

SEQ ID NO:25 and SEQ ID NO:27 (I53-47A.1 and I53-47B.1);
SEQ ID NO:25 and SEQ ID NO:28 (I53-47A.1 and I53-47B.1NegT2);
SEQ ID NO:26 and SEQ ID NO:6 (I53-47A.1NegT2 and I53-47B);
SEQ ID NO:26 and SEQ ID NO:27 (I53-47A.1NegT2 and I53-47B.1);
SEQ ID NO:26 and SEQ ID NO:28 (I53-47A.1NegT2 and I53-47B.1NegT2);
SEQ ID NO:37 and SEQ ID NO:38 (I53-47A genus and I53-47B genus);
SEQ ID NO:7 and SEQ ID NO:8 (I53-50A and I53-50B);
SEQ ID NO:7 and SEQ ID NO:32 (I53-50A and I53-50B.1);
SEQ ID NO:7 and SEQ ID NO:33 (I53-50A and I53-50B.1NegT2);
SEQ ID NO:7 and SEQ ID NO:34 (I53-50A and I53-50B.4PosT1);
SEQ ID NO:29 and SEQ ID NO:8 (I53-50A.1 and I53-50B);
SEQ ID NO:29 and SEQ ID NO:32 (I53-50A.1 and I53-50B.1);
SEQ ID NO:29 and SEQ ID NO:33 (I53-50A.1 and I53-50B.1NegT2);
SEQ ID NO:29 and SEQ ID NO:34 (I53-50A.1 and I53-50B.4PosT1);
SEQ ID NO:30 and SEQ ID NO:8 (I53-50A.1NegT2 and I53-50B);
SEQ ID NO:30 and SEQ ID NO:32 (I53-50A.1NegT2 and I53-50B.1);
SEQ ID NO:30 and SEQ ID NO:33 (I53-50A.1NegT2 and I53-50B.1NegT2);
SEQ ID NO:30 and SEQ ID NO:34 (I53-50A.1NegT2 and I53-50B.4PosT1);
SEQ ID NO:31 and SEQ ID NO:8 (I53-50A.1PosT1 and I53-50B);
SEQ ID NO:31 and SEQ ID NO:32 (I53-50A.1PosT1 and I53-50B.1);
SEQ ID NO:31 and SEQ ID NO:33 (I53-50A.1PosT1 and I53-50B.1NegT2);
SEQ ID NO:31 and SEQ ID NO:34 (I53-50A.1PosT1 and I53-50B.4PosT1);
SEQ ID NO:39 and SEQ ID NO:40 (I53-50A genus and I53-50B genus);
SEQ ID NO:9 and SEQ ID NO:10 (I53-51A and I53-51B);
SEQ ID NO:11 and SEQ ID NO:12 (I52-03A and I52-03B);
SEQ ID NO:13 and SEQ ID NO:14 (I52-32A and I52-32B);
SEQ ID NO:15 and SEQ ID NO:16 (I52-33A and I52-33B)
SEQ ID NO:17 and SEQ ID NO:18 (I32-06A and I32-06B);
SEQ ID NO:19 and SEQ ID NO:20 (I32-19A and I32-19B);
SEQ ID NO:21 and SEQ ID NO:22 (I32-28A and I32-28B);
SEQ ID NO:23 and SEQ ID NO:24 (I53-40A.1 and I53-40B.1);
SEQ ID NO:41 and SEQ ID NO:42 (T32-28A and T32-28B);
SEQ ID NO:43 and SEQ ID NO:44 (T33-09A and T33-09B);
SEQ ID NO:45 and SEQ ID NO:46 (T33-15A and T33-15B);

SEQ ID NO:47 and SEQ ID NO:48 (T33-21A and T33-21B);

SEQ ID NO:49 and SEQ ID NO:50 (T33-28A and T32-28B); and

SEQ ID NO:51 and SEQ ID NO:44 (T33-31A and T33-09B (also referred to as T33-31B))

[0054] In one embodiment, the one or more proteins, or antigenic fragments thereof, are expressed as a fusion protein with the first and/or second polypeptides. In these embodiments, one or more proteins, or antigenic fragments thereof are present at the N terminus of the fusion protein, whenever this configuration can facilitate presentation of the one or more proteins, or antigenic fragments thereof on an exterior of the nanostructure. A preference for the presence of the protein at the N terminus of the fusion protein occurs whenever from the location of the C terminus of the proteins is at proximal end of the protein. In these embodiments, one or more proteins, or antigenic fragments thereof are present at the C terminus of the fusion protein, whenever this configuration can facilitate presentation of the one or more proteins, or antigenic fragments thereof on an exterior of the nanostructure. A preference for the presence of the protein at the C terminus of the fusion protein occurs whenever from the location of the M terminus of the proteins is at proximal end of the protein.

[0055] Non-limiting examples of nanostructures useful in vaccines of the present disclosure include those disclosed in U.S. Patent No. 9,630,994 and U.S. Provisional Patent Application No. 62/481,331, which are incorporated herein in its entirety.

3. Antigens

[0056] The present disclosure provides nanostructure-based vaccines for any of the various known bacteria, viruses, or parasites relevant to human or animal disease. In particular, the present disclosure relates to vaccines for lyme disease, pertussis, herpes virus, orthomyxovirus, paramyxovirus, pneumovirus, filovirus, flavivirus, reovirus, retrovirus, malaria, viral meningitis, fungal meningitis, and bacterial meningitis including *Neisseria meningitides* (also known as "meningococcus"), *Haemophilus influenzae* type B, *Streptococcus pneumonia*, and *Listeria monocytogenes*. For each of these organism, antigens (proteins or polysaccharides) capable of generating protective immune responses are known. The present disclosure relates to incorporation of any of these antigens—particularly antigenic proteins—into nanostructure-based vaccines. Guidance is particularly available

from studies of the immune response to infection or vaccination, such as isolation of binding or neutralizing antibodies, genetic analysis of antigen sequence, structural studies of antigenic proteins and antibodies, and most particularly clinical and veterinary experience with subunit vaccines. With few limitations, any known subunit vaccine can be adapted for use with the nanostructures of the present disclosure by employing the display modalities provided above. In some embodiments, the nanostructure-based vaccines of the present disclosure comprise an oligosaccharide (*e.g.*, a meningococcal oligosaccharide) conjugated directly or through an intermediate protein (*e.g.*, diphtheria toxoid, tetanus toxoid, or CRM197) to the nanostructure. In some embodiments, the nanostructure-based vaccines of the present disclosure comprise antigens or antigenic fragments from the list provided in Table 2.

TABLE 2
Non-Limiting List of Antigens

Infectious Agent	Antigens	Citation
HIV	gp160, gp140, gp21, MPER	Sok, D., Le, K. M., Vadnais, M., Saye-Francisco, K. L., Jardine, J. G., Torres, J. L., et al. (2017). Rapid elicitation of broadly neutralizing antibodies to HIV by immunization in cows. Nature, 548(7665), 108–111.
RSV	F protein (prefusion)	US20160046675A1, US 2016/0031972 A1, US 2017/0182151 A1, WO 2010/149745 A1, WO 2012/158613 A1, WO 2013/139916 A1, WO 2014/079842 A1, WO 2014/174018 A1, WO 2014/202570 A1, WO 2015/013551 A1, WO 2017/040387 A2, WO2017172890A1
Influenza	HA – Influenza A and B	Nabel et al. Induction of unnatural immunity: prospects for a broadly protective universal influenza vaccine. Nat Med. 2010 Dec;16(12):1389-91.
EBV	glycoprotein 350/220 (gp350)	Kanekiyo et al. Rational Design of an Epstein-Barr Virus Vaccine Targeting the Receptor-Binding Site. Cell. 2015 Aug 27;162(5):1090-100.
CMV	gB; UL128, UL130, UL131A, gH (UL75) and gL (UL115)	Ciferri et al. Structural and biochemical studies of HCMV gH/gL/gO and Pentamer reveal mutually exclusive cell entry complexes. Proc. Natl. Acad. Sci. U.S.A. 112, 1767–1772 (2015). Chandramouli et al. Structure of HCMV glycoprotein B in the postfusion conformation bound to a neutralizing human antibody. Nat Commun. 2015 Sep 14;6:8176. Chandramouli et al. Structural basis for potent antibody-mediated neutralization of human cytomegalovirus Sci. Immunol. 2, eaan1457 (2017).
Lyme	Outer Surface Protein A (OspA)	Ma et al. Safety, efficacy, and immunogenicity of a recombinant Osp subunit canine Lyme disease vaccine. Volume 14, Issue 14, October 1996, Pages 1366-1374
Pertussis	Pertussis toxin (PT)	Seubert et al. Genetically detoxified pertussis toxin (PT-9K/129G): implications for immunization and vaccines. Expert Rev Vaccines. 2014 Oct;13(10):1191-204. doi: 10.1586/14760584.2014.942641. Epub 2014 Sep 3.
Dengue	E protein	Modis, Y., Ogata, S., Clements, D. & Harrison, S. C. (2003) Proc. Natl. Acad. Sci. USA 100, 6986–6991.pmid:12759475
SARS	Spike (S) glycoprotein	Structure of SARS coronavirus spike receptor-binding domain complexed with receptor. Science. 2005 Sep 16;309(5742):1864-8; WO2006068663A2

MERS	Spike (S) glycoprotein	Immunogenicity and structures of a rationally designed prefusion MERS-CoV spike antigen. PNAS 2017 August, 114 (35) E7348-E7357. https://doi.org/10.1073/pnas.1707304114
Ebola	EBOV GP or sGP [GP_1 and GP_2 subunits	Structures of Ebola virus GP and sGP in complex with therapeutic antibodies. Nat Microbiol. 2016 Aug 8;1(9):16128. doi: 10.1038/nmicrobiol.2016.128.
Marberg	Marberg GP or sGP	Hashiguchi et al. Structural basis for Marburg virus neutralization by a cross-reactive human antibody. Cell. 2015 Feb 26; 160(5): 904–912.
Hantaan virus	Gn and Gc envelope glycoproteins	Hantavirus Gn and Gc Envelope Glycoproteins: Key Structural Units for Virus Cell Entry and Virus Assembly. Viruses. 2014 Apr; 6(4): 1801–1822.
Hepatitis B	HepB surface antigen (HBs)	Raldao et al. Virus-like particles in vaccine development. Expert Rev Vaccines. 2010 Oct;9(10):1149-76.
Measles	H and F proteins	Lobanova et al. The recombinant globular head domain of the measles virus hemagglutinin protein as a subunit vaccine against measles. Vaccine. 2012 Apr 26;30(20):3061-7.
Nipah virus	G and F protein	Satterfield et al. Status of vaccine research and development of vaccines for Nipah virus. Vaccine. 34(26):2971-2975 (2016).
Rotatvirus	VP4 and VP8	O'Ryan et al. Parenteral protein-based rotavirus vaccine. Lancet Infectious Disease. 17(8):786-787 (2017).
Human Metapneumo virus	G and F proteins	Aertes et al. Adjuvant effect of the human metapneumovirus (HMPV) matrix protein in HMPV subunit vaccines. J Gen Virol. 2015 Apr;96(Pt 4):767-74; US 20180008697 A1.
Parainfluenza virus	HN and F proteins	Morein et al. Protein subunit vaccines of parainfluenza type 3 virus: immunogenic effect in lambs and mice. J Gen Virol. 1983 Jul;64 (Pt 7):1557-69.
Zika	Zika envelope domain III (ZEDIII)	Recurrent Potent Human Neutralizing Antibodies to Zika Virus in Brazil and Mexico. Cell. 2017 May 4;169(4):597-609.e11. doi: 10.1016/j.cell.2017.04.024.
Malaria	Pfs25, circumsporozoite protein (CSP)	Lee et al. Assessment of Pfs25 expressed from multiple soluble expression platforms for use as transmission-blocking vaccine candidates. Malar J. 2016; 15: 405. Plassmeyer et al. Structure of the Plasmodium falciparum circumsporozoite protein, a leading malaria vaccine candidate. J Biol Chem. 2009 Sep 25;284(39):26951-63.

MenB	fHbp, NadA and NHBA	Davide et al. The new multicomponent vaccine against meningococcal serogroup B, 4CMenB: immunological, functional and structural characterization of the antigens. Vaccine. 2012 May 30; 30(0 2): B87–B97.
MenA, C, W-135, and Y	oligosaccharide	Tontini et al. Comparison of CRM197, diphtheria toxoid and tetanus toxoid as protein carriers for meningococcal glycoconjugate vaccines. Vaccine. 2013 Oct 1;31(42):4827-33.

[0057] In some embodiments, the antigen is an antigenic protein is selected from a polypeptide of SEQ ID NOs: 52-88 and 90-113 or a variant thereof, as provided in Table 3.

TABLE 3
Non-Limiting List of Antigen Sequences

Antigen	Amino Acid Sequence (UniProt)	SEQ ID NO
Human immunodeficiency virus 1 (HIV-1) gp160	>tr|A0A1C9TBY8|A0A1C9TBY8_9HIV1 Envelope glycoprotein gp160 OS=Human immunodeficiency virus 1 GN=env PE=3 SV=1 MRVKGIKKNYQHWWRGGIMLLGMLMICSSAEKLWVTVYYGVPVW KEATTTLFCASDAKAQNPEMHNIWATHACVPTDPNPQEVILKNL TEEFNMWKNNMVEQMHEDIISLWDQSLKPCVKLTPLCVTLNCTN AESLNCTATNGTNNCSASTKPMEEMKNCSFNITTSVQDKKQQEY ALFYKLDIIPIDNNENDLNNTNYTSYRLISCNTSVITQACPKIT FEPIPIHYCAPAGFAILKCKDKRFNGTGPCKNVSTVQCTHGIRP VVSTQLLLNGSLAEEGVVLRSENFTDNAKNIIVQLKDPVNITCT RPNNNTRKSITIGPGRAFYATGQVIGDIRKAHCDLNGTEWDNAL KQIVEELRKQYGNNITIFNSSSGGDPEIVMHSFNCGGEFFYCNT AQLFNSTWLFNSTWNSTERLGNDTERTNDTITLPCKIKQVINMW QTVGKAMYAPPIRGLIRCSSNITGLILTRDGSGNTTGNETFRPG GGNMKDNWRSELYKYKVVKIEPLGVAPTRAKRRVVQREKRAAGL GALFLGFLGMAGSTMGAASLTLTVQARQLLSGIVQQQNNLLRAI EAQQHLLQLTVWGIKQLQARVLAVERYLRDQQLLGIWGCSGKLI CTTTVPWNASWSNKSLDNIWENMTWMQWEKEIDNYTDVIYKLLE ESQNQQEKNEQELLELDKWASLWNWFDITRWLWYIKIFIMIVGG LVGLRIVFAVLSIVNRVRQGYSPLSFQTLFPAPRGPDRPEGTEE GGGERGRDSSDRSAHGFLALIWGDLWSLCLFSYRRLRDLLLIAA RIVELLGRRGWEVLKYWWSLLQYWSQELKKSAVSLLNATAIAVA EGTDRIIEIVQRAGRAIIHIPRRIRQGAERALL	52
Human immunodeficiency virus 1 (HIV-1) gp120	gp120>tr|A0A1C9TBY8|33-524 LWVTVYYGVPVWKEATTTLFCASDAKAQNPEMHNIWATHACVPT DPNPQEVILKNLTEEFNMWKNNMVEQMHEDIISLWDQSLKPCVK LTPLCVTLNCTNAESLNCTATNGTNNCSASTKPMEEMKNCSFNI TTSVQDKKQQEYALFYKLDIIPIDNNENDLNNTNYTSYRLISCN TSVITQACPKITFEPIPIHYCAPAGFAILKCKDKRFNGTGPCKN VSTVQCTHGIRPVVSTQLLLNGSLAEEGVVLRSENFTDNAKNII VQLKDPVNITCTRPNNNTRKSITIGPGRAFYATGQVIGDIRKAH CDLNGTEWDNALKQIVEELRKQYGNNITIFNSSSGGDPEIVMHS FNCGGEFFYCNTAQLFNSTWLFNSTWNSTERLGNDTERTNDTIT LPCKIKQVINMWQTVGKAMYAPPIRGLIRCSSNITGLILTRDGS GNTTGNETFRPGGGNMKDNWRSELYKYKVVKIEPLGVAPTRAKR RVVQREKR	53
Human immunodeficiency virus 1 (HIV-1) gp41	gp41>tr|A0A1C9TBY8|543-733 MGAASLTLTVQARQLLSGIVQQQNNLLRAIEAQQHLLQLTVWGI KQLQARVLAVERYLRDQQLLGIWGCSGKLICTTTVPWNASWSNK SLDNIWENMTWMQWEKEIDNYTDVIYKLLEESQNQQEKNEQELL ELDKWASLWNWFDITRWLWYIKIFIMIVGGLVGLRIVFAVLSIV NRVRQGYSPLSFQTL	54
Human immunodeficiency virus	>tr|A0A1C9TBY8|675-696	55

1 (HIV-1) MPER	ELDKWASLWNWFDITRWLWYIK	
Respiratory syncytial virus (RSV) type A F protein	>tr|X4Y973|X4Y973_9MONO Fusion glycoprotein F0 OS=Respiratory syncytial virus type A GN=F PE=3 SV=1 MELPILKTNAITTILAAVTLCFASSQNITEEFYQSTCSAVSKGY LSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQELDKYKN AVTELQLLMQSTPAANNRARRELPRFMNYTLNNTKNNNVTLSKK RKRRFLGFLLGVGSAIASGIAVSKVLHLEGEVNKIKNALLSTNK AVVSLSNGVSVLTSKVLDLKNYIDKQLLPIVNKQSCSISNIETV IEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNSELLSLINDM PITNDQKKLMSNNVQIVRQQSYSIMSIIKEEVLAYVVQLPLYGV IDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGSVSFF PQAETCKVQSNRVFCDTMNSLTLPSEVNLCNIDIFNPKYDCKIM TSKTDVSSSVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCD YVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDPLVFP SDEFDASISQVNEKINQSLAFIRKSDELLHNVNVGKSTTNIMIT TIIIVIIVILLLLIAVGLFLYCKARSTPVTLSKDQLSGINNIAF SN	56
Influenza A virus HA	>tr|C3W5X2|C3W5X2_9INFA Hemagglutinin OS=Influenza A virus (A/California/07/2009(H1N1)) GN=HA PE=1 SV=1 MKAILVVLLYTFATANADTLCIGYHANNSTDTVDTVLEKNVTVT HSVNLLEDKHNGKLCKLRGVAPLHLGKCNIAGWILGNPECESLS TASSWSYIVETPSSDNGTCYPGDFIDYEELREQLSSVSSFERFE IFPKTSSWPNHDSNKGVTAACPHAGAKSFYKNLIWLVKKGNSYP KLSKSYINDKGKEVLVLWGIHHPSTSADQQSLYQNADAYVFVGS SRYSKKFKPEIAIRPKVRDQEGRMNYYWTLVEPGDKITFEATGN LVVPRYAFAMERNAGSGIIISDTPVHDCNTTCQTPKGAINTSLP FQNIHPITIGKCPKYVKSTKLRLATGLRNIPSIQSRGLFGAIAG FIEGGWTGMVDGWYGYHHQNEQGSGYAADLKSTQNAIDEITNKV NSVIEKMNTQFTAVGKEFNHLEKRIENLNKKVDDGFLDIWTYNA ELLVLLENERTLDYHDSNVKNLYEKVRSQLKNNAKEIGNGCFEF YHKCDNTCMESVKNGTYDYPKYSEEAKLNREEIDGVKLESTRIY QILAIYSTVASSLVLVVSLGAISFWMCSNGSLQCRICI	57
Influenza B virus HA	>tr|A0A140EM53|A0A140EM53_9INFB Hemagglutinin OS=Influenza B virus (B/Victoria/809/2012) GN=HA PE=3 SV=1 MKAIIVLLMVVTSNADRICTGITSSNSPHVVKTATQGEVNVTGV IPLTTTPTKSYFANLKGTKTRGKLCPDCLNCTDLDVALGRPMCV GTTPSAKASILHEVRPVTSGCFPIMHDRTKIRQLANLLRGYENI RLSTQNVIDAEKAPGGPYRLGTSGSCPNATSKSGFFATMAWAVP KDNNKNATNPLTVEVPYICAEGEDQITVWGFHSDNKTQMKNLYG DSNPQKFTSSANGVTTHYVSQIGGFPDQTEDGGLPQSGRIVVDY MMQKPGKTGTIVYQRGVLLPQKVWCASGRSKVIKGSLPLIGEAD CLHEKYGGLNKSKPYYTGEHAKAIGNCPIWVKTPLKLANGTKYR PPAKLLKERGFFGAIAGFLEGGWEGMIAGWHGYTSHGAHGVAVA ADLKSTQEAINKITKNLNSLSELEVKNLQRLSGAMDELHNEILE LDEKVDDLRADTISSQIELAVLLSNEGIINSEDEHLLALERKLK KMLGPSAVDIGNGCFETKHKCNQTCLDRIAAGTFNAGEFSLPTF DSLNITAASLNDDGLDNHTILLYYSTAASSLAVTLMLAIFIVYM VSRDNVSCSICL	58
Epstein-Barr virus (EBV) glycoprotein 350/220 (gp350)	>sp|P03200|GP350_EBVB9 Envelope glycoprotein GP350 OS=Epstein-Barr virus (strain B95-8) GN=BLLF1 PE=1 SV=1 MEAALLVCQYTIQSLIHLTGEDPGFFNVEIPEFPFYPTCNVCTA DVNVTINFDVGGKKHQLDLDFGQLTPHTKAVYQPRGAFGGSENA TNLFLLELLGAGELALTMRSKKLPINVTTGEEQQVSLESVDVYF QDVFGTMWCHHAEMQNPVYLIPETVPYIKWDNCNSTNITAVVRA QGLDVTLPLSLPTSAQDSNFSVKTEMLGNEIDIECIMEDGEISQ VLPGDNKFNITCSGYESHVPSGGILTSTSPVATPIPGTGYAYSL RLTPRPVSRFLGNNSILYVFYSGNGPKASGGDYCIQSNIVFSDE IPASQDMPTNTTDITYVGDNATYSVPMVTSEDANSPNVTVTAFW AWPNNTETDFKCKWTLTSGTPSGCENISGAFASNRTFDITVSGL GTAPKTLIITRTATNATTTHKVIFSKAPESTTTSPTLNTTGFA DPNTTTGLPSSTHVPTNLTAPASTGPTVSTADVTSPTPAGTTSG ASPVTPSPSPWDNGTESKAPDMTSSTSPVTTPTPNATSPTPAVT TPTPNATSPTPAVTTPTPNATSPTLGKTSPTSAVTTPTPNATSP TLGKTSPTSAVTTPTPNATSPTLGKTSPTSAVTTPTPNATGPTV GETSPQANATNHTLGGTSPTPVVTSQPKNATSAVTTGQHNITSS STSSMSLRPSSNPETLSPSTSDNSTSHMPLLTSAHPTGGENITQ VTPASISTHHVSTSSPAPRPGTTSQASGPGNSSTSTKPGEVNVT KGTPPQNATSPQAPSGQKTAVPTVTSTGGKANSTTGGKHTTGHG ARTSTEPTTDYGGDSTTPRPRYNATTYLPPSTSSKLRPRWTFTS PPVTTAQATVPVPPTSQPRFSNLSMLVLQWASLAVLTLLLLLVM	59

	ADCAFRRNLSTSHTYTTPPYDDAETYV	
Human cytomegalovirus gB	>sp|P06473|GB_HCMVA Envelope glycoprotein B OS=Human cytomegalovirus (strain AD169) GN=gB PE=1 SV=1 MESRIWCLVVCVNLCIVCLGAAVSSSSTSHATSSTHNGSHTSRT TSAQTRSVYSQHVTSSEAVSHRANETIYNTTLKYGDVVGVNTTK YPYRVCSMAQGTDLIRFERNIICTSMKPINEDLDEGIMVVYKRN IVAHTFKVRVYQKVLTFRRSYAYIYTTYLLGSNTEYVAPPMWEI HHINKFAQCYSSYSRVIGGTVFVAYHRDSYENKTMQLIPDDYSN THSTRYVTVKDQWHSRGSTWLYRETCNLNCMLTITTARSKYPYH FFATSTGDVVYISPFYNGTNRNASYFGENADKFFIFPNYTIVSD FGRPNAAPETHRLVAFLERADSVISWDIQDEKNVTCQLTFWEAS ERTIRSEAEDSYHFSSAKMTATFLSKKQEVNMSDSALDCVRDEA INKLQQIFNTSYNQTYEKYGNVSVFETSGGLVVFWQGIKQKSLV ELERLANRSSLNITHRTRRSTSDNNTTHLSSMESVHNLVYAQLQ FTYDTLRGYINRALAQIAEAWCVDQRRTLEVFKELSKINPSAIL SAIYNKPIAARFMGDVLGLASCVTINQTSVKVLRDMNVKESPGR CYSRPVVIFNFANSSYVQYGQLGEDNEILLGNHRTEECQLPSLK IFIAGNSAYEYVDYLFKRMIDLSSISTVDSMIALDIDPLENTDF RVLELYSQKELRSSNVFDLEEIMREFNSYKQRVKYVEDKVVDPL PPYLKGLDDLMSGLGAAGKAVGVAIGAVGGAVASVVEGVATFLK NPFGAFTIILVAIAVVIITYLIYTRQRRLCTQPLQNLFPYLVSA DGTTVTSGSTKDTSLQAPPSYEESVYNSGRKGPGPPSSDASTAA PPYTNEQAYQMLLALARLDAEQRAQQNGTDSLDGQTGTQDKGQK PNLLDRLRHRKNGYRHLKDSDEEENV	60
Human cytomegalovirus UL128	>sp|P16837|UL128_HCMVA Uncharacterized protein UL128 OS=Human cytomegalovirus (strain AD169) GN=UL128 PE=1 SV=2 MSPKDLTPFLTTLWLLLGHSRVPRVRAEECCEFINVNHPPERCY DFKMCNRFTVALRCPDGEVCYSPEKTAEIRGIVTTMTHSLTRQV VHNKLTSCNYNPLYLEADGRIRCGKVNDKAQYLLGAAGSVPYRW INLEYDKITRIVGLDQYLESVKKHKRLDVCRAKMGYMLQ	61
Human cytomegalovirus UL130	>sp|F5HCP3|UL130_HCMVM Envelope glycoprotein UL130 OS=Human cytomegalovirus (strain Merlin) GN=UL130 PE=1 SV=1 MLRLLLRHHFHCLLLCAVWATPCLASPWSTLTANQNPSPPWSKL TYSKPHDAATFYCPFLYPSPPRSPLQFSGFQRVSTGPECRNETL YLLYNREGQTLVERSSTWVKKVIWYLSGRNQTILQRMPRTASKP SDGNVQISVEDAKIFGAHMVPKQTKLLRFVVNDGTRYQMCVMKL ESWAHVFRDYSVSFQVRLTFTEANNQTYTFCTHPNLIV	62
Human cytomegalovirus UL131A	>sp|F5HET4|UL131A_HCMVM Protein UL131A OS=Human cytomegalovirus (strain Merlin) GN=UL131A PE=1 SV=1 MRLCRVWLSVCLCAVVLGQCQRETAEKNDYYRVPHYWDACSRAL PDQTRYKYVEQLVDLTLNYHYDASHGLDNFDVLKRINVTEVSLL ISDFRRQNRRGGTNKRTTFNAAGSLAPHARSLEFSVRLFAN	63
Human cytomegalovirus gH (UL75)	>sp|P12824|GH_HCMVA Envelope glycoprotein H OS=Human cytomegalovirus (strain AD169) GN=gH PE=1 SV=1 MRPGLPPYLTVFTVYLLSHLPSQRYGADAASEALDPHAFHLLLN TYGRPIRFLRENTTQCTYNSSLRNSTVVRENAISFNFFQSYNQY YVFHMPRCLFAGPLAEQFLNQVDLTETLERYQQRLNTYALVSKD LASYRSFSQQLKAQDSLGQQPTTVPPPIDLSIPHVWMPPQTTPH DWKGSHTTSGLHRPHFNQTCILFDGHDLLFSTVTPCLHQGFYLM DELRYVKITLTEDFFVVTVSIDDDTPMLLIFGHLPRVLFKAPYQ RDNFILRQTEKHELLVLVKKAQLNRHSYLKDSDFLDAALDFNYL DLSALLRNSFHRYAVDVLKSGRCQMLDRRTVEMAFAYALALFAA ARQEEAGTEISIPRALDRQAALLQIQEFMITCLSQTPPRTTLLL YPTAVDLAKRALWTPDQITDITSLVRLVYILSKQNQQHLIPQWA LRQIADFALQLHKTHLASFLSAFARQELYLMGSLVHSMLVHTTE RREIFIVETGLCSLAELSHFTQLLAHPHHEYLSDLYTPCSSSGR RDHSLERLTRLFPDATVPATVPAALSILSTMQPSTLETFPDLFC LPLGESFSALTVSEHVSYVVTNQYLIKGISYPVSTTVVGQSLII TQTDSQTKCELTRNMHTTHSITAALNISLENCAFCQSALLEYDD TQGVINIMYMHDSDDVLFALDPYNEVVVSSPRTHYLMLLKNGTV LEVTDVVVDATDSRLLMMSVYALSAIIGIYLLYRMLKTC	64
Human cytomegalovirus gL (UL115)	>sp|P16832|GL_HCMVA Envelope glycoprotein L OS=Human cytomegalovirus (strain AD169) GN=gL PE=1 SV=2 MCRRPDCGFSFSPGPVVLLWCCLLLPIVSSVAVSVAPTAAEKVP AECPELTRRCLLGEVFQGDKYESWLRPLVNVTRRDGPLSQLIRY RPVTPEAANSVLLDDAFLDTLALLYNNPDQLRALLTLLSSDTAP RWMTVMRGYSECGDGSPAVYTCVDDLCRGYDLTRLSYGRSIFTE HVLGFELVPPSLFNVVVAIRNEATRTNRAVRLPVSTAAAPEGIT LFYGLYNAVKEFCLRHQLDPPLLRHLDKYYAGLPPELKQTRVNL PAHSRYGPQAVDAR	65

Lyme Outer Surface Protein A (OspA)	>sp|Q04968|OSPA7_BORBG Outer surface protein A OS=Borreliella burgdorferi GN=ospA PE=3 SV=1 MKKYLLGIGLILALIACKQNVSSLDEKNSVSVDVPGGMKVLVSK EKNKDGKYDLMATVDNVDLKGTSDKNNGSGILEGVKADKSKVKL TVADDLSKTTLEVLKEDGTVVSRKVTSKDKSTTEAKFNEKGELS EKTMTRANGTTLEYSQMTNEDNAAKAVETLKNGIKFEGNLASGK TAVEIKEGTVTLKREIDKNGKVTVSLNDTASGSKKTASWQESTS TLTISANSKKTKDLVFLTNGTITVQNYDSAGTKLEGSAAEIKKL DELKNALR	66
Bordetella pertussis Pertussis toxin (PT) subunits 1-5	>sp|P04977|TOX1_BORPE Pertussis toxin subunit 1 OS=Bordetella pertussis (strain Tohama I / ATCC BAA-589 / NCTC 13251) GN=ptxA PE=1 SV=1 MRCTRAIRQTARTGWLTWLAILAVTAPVTSPAWADDPPATVYRY DSRPPEDVFQNGFTAWGNNDNVLDHLTGRSCQVGSSNSAFVSTS SSRRYTEVYLEHRMQEAVEAERAGRGTGHFIGYIYEVRADNNFY GAASSYFEYVDTYGDNAGRILAGALATYQSEYLAHRRIPPENIR RVTRVYHNGITGETTTTEYSNARYVSQGTRANPNPYTSRRSVAS IVGTLVRMAPVIGACMARQAESSEAMAAWSERAGEAMVLVYYES IAYSF	67
Dengue virus Envelope protein E	>sp|P17763|281-775 MRCVGIGNRDFVEGLSGATWVDVVLEHGSCVTTMAKDKPTLDIE LLKTEVTNPAVLRKLCIEAKISNTTTDSRCPTQGEATLVEEQDT NFVCRRTFVDRGWGNGCGLFGKGSLITCAKFKCVTKLEGKIVQY ENLKYSVIVTVHTGDQHQVGNETTEHGTTATITPQAPTSEIQLT DYGALTLDCSPRTGLDFNEMVLLTMEKKSWLVHKQWFLDLPLPW TSGASTSQETWNRQDLLVTFKTAHAKKQEVVVLGSQEGAMHTAL TGATEIQTSGTTTIFAGHLKCRLKMDKLTLKGMSYVMCTGSFKL EKEVAETQHGTVLVQVKYEGTDAPCKIPFSSQDEKGVTQNGRLI TANPIVTDKEKPVNIEAEPPFGESYIVVGAGEKALKLSWFKKGS SIGKMFEATARGARRMAILGDTAWDFGSIGGVFTSVGKLIHQIF GTAYGVLFSGVSWTMKIGIGILLTWLGLNSRSTSLSMTCIAVGM VTLYLGVMVQA	68
Human SARS coronavirus (SARS) Spike (S) glycoprotein	>sp|P59594|SPIKE_CVHSA Spike glycoprotein OS=Human SARS coronavirus GN=S PE=1 SV=1 MFIFLLFLTLTSGSDLDRCTTFDDVQAPNYTQHTSSMRGVYYPD EIFRSDTLYLTQDLFLPFYSNVTGFHTINHTFGNPVIPFKDGIY FAATEKSNVVRGWVFGSTMNNKSQSVIIINNSTNVVIRACNFEL CDNPFFAVSKPMGTQTHTMIFDNAFNCTFEYISDAFSLDVSEKS GNFKHLREFVFKNKDGFLYVYKGYQPIDVVRDLPSGFNTLKPIF KLPLGINITNFRAILTAFSPAQDIWGTSAAAYFVGYLKPTTFML KYDENGTITDAVDCSQNPLAELKCSVKSFEIDKGIYQTSNFRVV PSGDVVRFPNITNLCPFGEVFNATKFPSVYAWERKKISNCVADY SVLYNSTFFSTFKCYGVSATKLNDLCFSNVYADSFVVKGDDVRQ IAPGQTGVIADYNYKLPDDFMGCVLAWNTRNIDATSTGNYNYKY RYLRHGKLRPFERDISNVPFSPDGKPCTPPALNCYWPLNDYGFY TTTGIGYQPYRVVVLSFELLNAPATVCGPKLSTDLIKNQCVNFN FNGLTGTGVLTPSSKRFQPFQQFGRDVSDFTDSVRDPKTSEILD ISPCSFGGVSVITPGTNASSEVAVLYQDVNCTDVSTAIHADQLT PAWRIYSTGNNVFQTQAGCLIGAEHVDTSYECDIPIGAGICASY HTVSLLRSTSQKSIVAYTMSLGADSSIAYSNNTIAIPTNFSISI TTEVMPVSMAKTSVDCNMYICGDSTECANLLLQYGSFCTQLNRA LSGIAAEQDRNTREVFAQVKQMYKTPTLKYFGGFNFSQILPDPL KPTKRSFIEDLLFNKVTLADAGFMKQYGECLGDINARDLICAQK FNGLTVLPPLLTDDMIAAYTAALVSGTATAGWTFGAGAALQIPF AMQMAYRFNGIGVTQNVLYENQKQIANQFNKAISQIQESLTTTS TALGKLQDVVNQNAQALNTLVKQLSSNFGAISSVLNDILSRLDK VEAEVQIDRLITGRLQSLQTYVTQQLIRAAEIRASANLAATKMS ECVLGQSKRVDFCGKGYHLMSFPQAAPHGVVFLHVTYVPSQERN FTTAPAICHEGKAYFPREGVFVFNGTSWFITQRNFFSPQIITTD NTFVSGNCDVVIGIINNTVYDPLQPELDSFKEELDKYFKNHTSP DVDLGDISGINASVVNIQKEIDRLNEVAKNLNESLIDLQELGKY EQYIKWPWYVWLGFIAGLIAIVMVTILLCCMTSCCSCLKGACSC GSCCKFDEDDSEPVLKGVKLHYT	69
Middle East respiratory syndrome-related coronavirus (MERS) Spike (S) glycoprotein	>tr|R9UCW7|R9UCW7_9BETC Spike glycoprotein OS=Middle East respiratory syndrome-related coronavirus PE=4 SV=1 MIHSVFLLMFLLTPTESYVDVGPDSIKSACIEVDIQQTFFDKTW PRPIDVSKADGIIYPQGRTYSNITITYQGLFPYQGDHGDMYVYS AGHATGTTPQKLFVANYSQDVKQFANGFVVRIGAAANSTGTVII SPSTSATIRKIYPAFMLGSSVGNFSDGKMGRFFNHTLVLLPDGC GTLLRAFYCILEPRSGNHCPAGNSYTSFATYHTPATDCSDGNYN RNASLNSFKEYFNLRNCTFMYTYNITEDEILEWFGITQTAQGVH LFSSRYVDLYGGNMFQFATLPVYDTIKYYSIIPHSIRSIQSDRK AWAAFYVYKLQPLTFLLDFSVDGYIRRAIDCGFNDLSQLHCSYE	70

	SFDVESGVYSVSSFEAKPSGSVVEQAEGVECDFSPLLSGTPPQV YNFKRLVFTNCNYNLTKLLSLFSVNDFTCSQISPAAIASNCYSS LILDYFSYPLSMKSDLSVSSAGPISQFNYKQSFSNPTCLILATV PHNLTTITKPLKYSYINKCSRLLSDDRTEVPQLVNANQYSPCVS IVPSTVWEDGDYYRKQLSPLEGGGWLVASGSTVAMTEQLQMGFG ITVQYGTDTNSVCPKLEFANDTKIASQLGNCVEYSLYGVSGRGV FQNCTAVGVRQQRFVYDAYQNLVGYYSDDGNYYCLRACVSVPVS VIYDKETKTHATLFGSVACEHISSTMSQYSRSTRSMLKRRDSTY GPLQTPVGCVLGLVNSSLFVEDCKLPLGQSLCALPDTPSTLTPR SVRSVPGEMRLASIAFNHPIQVDQLNSSYFKLSIPTNFSFGVTQ EYIQTTIQKVTVDCKQYVCNGFQKCEQLLREYGQFCSKINQALH GANLRQDDSVRNLFASVKSSQSSPIIPGFGGDFNLTLLEPVSIS TGSRSARSAIEDLLFDKVTIADPGYMQGYDDCMQQGPASARDLI CAQYVAGYKVLPPLMDVNMEAAYTSSLLGSIAGVGWTAGLSSFA AIPFAQSIFYRLNGVGITQQVLSENQKLIANKFNQALGAMQTGF TTTNEAFHKVQDAVNNNAQALSKLASELSNTFGAISASIGDIIQ RLDVLEQDAQIDRLINGRLTTLNAFVAQQLVRSESAALSAQLAK DKVNECVKAQSKRSGFCGQGTHIVSFVVNAPNGLYFMHVGYYPS NHIEVVSAYGLCDAANPTNCIAPVNGYFIKTNNTRIVDEWSYTG SSFYAPEPITSLNTKYVAPQVTYQNISTNLPPPLLGNSTGIDFQ DELDEFFKNVSTSIPNFGSLTQINTTLLDLTYEMLSLQQVVKAL NESYIDLKELGNYTYYNKWPWYIWLGFIAGLVALALCVFFILCC TGCGTNCMGKLKCNRCCDRYEEYDLEPHKVHVH	
Zaire ebolavirus GP	>sp|Q05320|VGP_EBOZM Envelope glycoprotein OS=Zaire ebolavirus (strain Mayinga-76) GN=GP PE=1 SV=1 MGVTGILQLPRDRFKRTSFFLWVIILFQRTFSIPLGVIHNSTLQ VSDVDKLVCRDKLSSTNQLRSVGLNLEGNGVATDVPSATKRWGF RSGVPPKVVNYEAGEWAENCYNLEIKKPDGSECLPAAPDGIRGF PRCRYVHKVSGTGPCAGDFAFHKEGAFFLYDRLASTVIYRGTTF AEGVVAFLILPQAKKDFFSSHPLREPVNATEDPSSGYYSTTIRY QATGFGTNETEYLFEVDNLTYVQLESRFTPQFLLQLNETIYTSG KRSNTTGKLIWKVNPEIDTTIGEWAFWETKKNLTRKIRSEELSF TVVSNGAKNISGQSPARTSSDPGTNTTTEDHKIMASENSSAMVQ VHSQGREAAVSHLTTLATISTSPQSLTTKPGPDNSTHNTPVYKL DISEATQVEQHHRRTDNDSTASDTPSATTAAGPPKAENTNTSKS TDFLDPATTTSPQNHSETAGNNNTHHQDTGEESASSGKLGLITN TIAGVAGLITGGRRTRREAIVNAQPKCNPNLHYWTTQDEGAAIG LAWIPYFGPAAEGIYIEGLMHNQDGLICGLRQLANETTQALQLF LRATTELRTFSILNRKAIDFLLQRWGGTCHILGPDCCIEPHDWT KNITDKIDQIIHDFVDKTLPDQGDNDNWWTGWRQWIPAGIGVTG VIIAVIALFCICKFVF	71
Marburg virus GP	>sp|P35253|VGP_MABVM Envelope glycoprotein OS=Lake Victoria marburgvirus (strain Musoke-80) GN=GP PE=1 SV=1 MKTTCFLISLILIQGTKNLPILEIASNNQPQNVDSVCSGTLQKT EDVHLMGFTLSGQKVADSPLEASKRWAFRTGVPPKNVEYTEGEE AKTCYNISVTDPSGKSLLLDPPTNIRDYPKCKTIHHIQGQNPHA QGIALHLWGAFFLYDRIASTTMYRGKVFTEGNIAAMIVNKTVHK MIFSRQGQGYRHMNLTSTNKYWTSSNGTQTNDTGCFGALQEYNS TKNQTCAPSKIPPPLPTARPEIKLTSTPTDATKLNTTDPSSDDE DLATSGSGSGEREPHTTSDAVTKQGLSSTMPPTPSPQPSTPQQG GNNTNHSQDAVTELDKNNTTAQPSMPPHNTTTISTNNTSKHNFS TLSAPLQNTTNDNTQSTITENEQTSAPSITTLPPTGNPTTAKST SSKKGPATTAPNTTNEHFTSPPPTPSSTAQHLVYFRRKRSILWR EGDMFFFLDGLINAPIDFDPVPNTKTIFDESSSSGASAEEDQHA SPNISLTLSYFPNINENTAYSGENENDCDAELRIWSVQEDDLAA GLSWIPFFGPGIEGLYTAVLIKNQNNLVCRLRRLANQTAKSLEL LLRVTTEERTFSLINRHAIDFLLTRWGGTCKVLGPDCCIGIEDL SKNISEQIDQIKKDEQKEGTGWGLGGKWWTSDWGVLTNLGILLL LSIAVLIALSCICRIFTKYIG	72
Hanta virus Gn envelope glycoprotein	>sp|P08668|19-648 LRNVYDMKIECPHTVSFGENSVIGYVELPPVPLADTAQMVPESS CNMDNHQSLNTITKYTQVSWRGKADQSQSSQNSFETVSTEVDLK GTCVLKHKMVEESYRSRKSVTCYDLSCNSTYCKPTLYMIVPIHA CNMMKSCLIALGPYRVQVVYERSYCMTGVLIEGKCFVPDQSVVS IIKHGIFDIASVHIVCFFVAVKGNTYKIFEQVKKSFESTCNDTE NKVQGYYICIVGGNSAPIYVPTLDDFRSMEAFTGIFRSPHGEDH DLAGEEIASYSIVGPANAKVPHSASSDTLSLIAYSGIPSYSSLS ILTSSTEAKHVFSPGLFPKLNHTNCDKSAIPLIWTGMIDLPGYY EAVHPCTVFCVLSGPGASCEAFSEGGIFNITSPMCLVSKQNRFR LTEQQVNFVCQRVDMDIVVYCNGQRKVILTKTLVIGQCIYTITS LFSLLPGVAHSIAVELCVPGFHGWATAALLVTFCFGWVLIPAIT FIILTCVLKFIANIFHTSNQENRLKSVLRKIKEEFEKTKGSMVCD VCKYECETYKELKAHGVSCPQSQCPYCFTHCEPTEAAFQAHYKV CQVTHRFRDDLKKTVTPQNFTPGCYRTLNLFRYKSRCYIFTMWI	73

	FLLVLESILWAASA	
Hanta virus Gc envelope glycoprotein	>sp|P08668|649-1135 SETPLTPVWNDNAHGVGSVPMHTDLELDFSLTSSSKYTYRRKLT NPLEEAQSIDLHIEIEEQTIGVDVHALGHWFDGRLNLKTSFHCY GACTKYEYPWHTAKCHYERDYQYETSWGCNPSDCPGVGTGCTAC GLYLDQLKPVGSAYKIITIRYSRRVCVQFGEENLCKIIDMNDCF VSRHVKVCIIGTVSKFSQGDTLLFFGPLEGGGLIFKHWCTSTCQ FGDPGDIMSPRDKGFLCPEFPGSFRKKCNFATTPICEYDGNMVS GYKKVMATIDSFQSFNTSTMHFTDERIEWKDPDGMLRDHINILV TKDIDFDNLGENPCKIGLQTSSIEGAWGSGVGFTLTCLVSLTEC PTFLTSIKACDKAICYGAESVTLTRGQNTVKVSGKGGHSGSTFR CCHGEDCSQIGLHAAAPHLDKVNGISEIENSKVYDDGAPQCGIK CWEVKSGEWISGIFSGNWIVLIVLCVFLLFSLVLLSILCPVRKH KKS	74
Hepatitis B HepB surface antigen (HBs)	>tr|Q9DIX1|Q9DIX1_HBV Surface antigen HBsAg OS=Hepatitis B virus GN=S PE=4 SV=1 MENITSGFLGPLLVLQAGFFLLTKILTIPQSLNSWWTSLSFLGG NTVCLGQNSQSPTSNHSPTSCPPTCPGYRWMCLRRFIIFLFILL LCLIFLLVLLDYQGMLPVCPLIPGSSTTSTGPCRTCKTPAQGTS MYPSCCCTKPSDGNCTCIPIPSSWAFGKFLWEWASARFSWLSLI VPFVQWFVGLSPTVWLSVIWMMWYWGPSLYSILSPFLPLLPIFF CLWVYI	75
Measles H protein	>sp|P08362|HEMA_MEASE Hemagglutinin glycoprotein OS=Measles virus (strain Edmonston) GN=H PE=1 SV=1 MSPQRDRINAFYKDNPHPKGSRIVINREHLMIDRPYVLLAVLFV MFLSLIGLLAIAGIRLHRAAIYTAEIHKSLSTNLDVTNSIEHQV KDVLTPLFKIIGDEVGLRTPQRFTDLVKFISDKIKFLNPDREYD FRDLTWCINPPERIKLDYDQYCADVAAEELMNALVNSTLLETRT TNQFLAVSKGNCSGPTTIRGQFSNMSLSLLDLYLGRGYNVSSIV TMTSQGMYGGTYLVEKPNLSSKRSELSQLSMYRVFEVGVIRNPG LGAPVFHMTNYLEQPVSNDLSNCMVALGELKLAALCHGEDSITI PYQGSGKGVSFQLVKLGVWKSPTDMQSWVPLSTDDPVIDRLYLS SHRGVIADNQAKWAVPTTRTDDKLRMETCFQQACKGKIQALCEN PEWAPLKDNRIPSYGVLSVDLSLTVELKIKIASGFGPLITHGSG MDLYKSNHNNVYWLTIPPMKNLALGVINTLEWIPRFKVSPYLFN VPIKEAGEDCHAPTYLPAEVDGDVKLSSNLVILPGQDLQYVLAT YDTSRVEHAVVYYVYSPSRSFSYFYPFRLPIKGVPIELQVECFT WDQKLWCRHFCVLADSESGGHITHSGMEGMGVSCTVTREDGTNR R	76
Measles F protein	>sp|P69353|FUS_MEASE Fusion glycoprotein F0 OS=Measles virus (strain Edmonston) GN=F PE=3 SV=1 MGLKVNVSAIFMAVLLTLQTPTGQIHWGNLSKIGVVGIGSASYK VMTRSSHQSLVIKLMPNITLLNNCTRVEIAEYRRLLRTVLEPIR DALNAMTQNIRPVQSVASSRRHKRFAGVVLAGAALGVATAAQIT AGIALHQSMLNSQAIDNLRASLETTNQAIEAIRQAGQEMILAVQ GVQDYINNELIPSMNQLSCDLIGQKLGLKLLRYYTEILSLFGPS LRDPISAEISIQALSYALGGDINKVLEKLGYSGGDLLGILESRG IKARITHVDTESYFIVLSIAYPTLSEIKGVIVHRLEGVSYNIGS QEWYTTVPKYVATQGYLISNFDESSCTFMPEGTVCSQNALYPMS PLLQECLRGSTKSCARTLVSGSFGNRFILSQGNLIANCASILCK CYTTGTIINQDPDKILTYIAADHCPVVEVNGVTIQVGSRRYPDA VYLHRIDLGPPISLERLDVGTNLGNAIAKLEDAKELLESSDQIL RSMKGLSSTSIVYILIAVCLGGLIGIPALICCCRGRCNKKGEQV GMSRPGLKPDLTGTSKSYVRSL	77
Zika Zika envelope domain III (ZEDIII)	>sp|Q32ZE1|291-790 IRCIGVSNRDFVEGMSGGTWVDVVLEHGGCVTVMAQDKPTVDIE LVTTTVSNMAEVRSYCYEASISDMASDSRCPTQGEAYLDKQSDT QYVCKRTLVDRGWGNGCGLFGKGSLVTCAKFTCSKKMTGKSIQP ENLEYRIMLSVHGSQHSGMIGYETDEDRAKVEVTPNSPRAEATL GGFGSLGLDCEPRTGLDFSDLYYLTMNNKHWLVHKEWFHDIPLP WHAGADTGTPHWNNKEALVEFKDAHAKRQTVVVLGSQEGAVHTA LAGALEAEMDGAKGRLFSGHLKCRLKMDKLRLKGVSYSLCTAAF TFTKVPAETLHGTVTVEVQYAGTDGPCKIPVQMAVDMQTLTPVG RLITANPVITESTENSKMMLELDPPFGDSYIVIGVGDKKITHHW HRSGSTIGKAFEATVRGAKRMAVLGDTAWDFGSVGGVFNSLGKG IHQIFGAAFKSLFGGMSWFSQILIGTLLVWLGLNTKNGSISLTC LALGGVMIFLSTAVSA	78
Malaria circumsporozoite protein (CSP)	>sp|P08677|CSP_PLAVB Circumsporozoite protein OS=Plasmodium vivax (strain Belem) PE=3 SV=2 MKNFILLAVSSILLVDLFPTHCGHNVDLSKAINLNGVNFNNVDA SSLGAAHVGQSASRGRGLGENPDDEEGDAKKKKDGKKAEPKNPR ENKLKQPGDRADGQPAGDRADGQPAGDRADGQPAGDRAAGQPAG DRADGQPAGDRADGQPAGDRADGQPAGDRADGQPAGDRAAGQPA	79

	GDRAAGQPAGDRADGQPAGDRAAGQPAGDRADGQPAGDRAAGQP AGDRADGQPAGDRAAGQPAGDRAAGQPAGDRAAGQPAGDRAAGQ PAGNGAGGQAAGGNAGGGQGQNNEGANAPNEKSVKEYLDKVRAT VGTEWTPCSVTCGVGVRVRRRVNAANKKPEDLTLNDLETDVCTM DKCAGIFNVVSNSLGLVILLVLALFN	
Nipah virus F protein	>sp|Q9IH63|FUS_NIPAV Fusion glycoprotein F0 OS=Nipah virus GN=F PE=1 SV=1 MVVILDKRCYCNLLILLMISECSVGILHYEKLSKIGLVKGVTR KYKIKSNPLTKDIVIKMIPNVSNMSQCTGSVMENYKTRLNGILT PIKGALEIYKNNTHDLVGDVRLAGVIMAGVAIGIATAAQITAGV ALYEAMKNADNINKLKSSIESTNEAVVKLQETAEKTVYVLTALQ DYINTNLVPTIDKISCKQTELSLDLALSKYLSDLLFVFGPNLQD PVSNSMTIQAISQAFGGNYETLLRTLGYATEDFDDLLESDSITG QIIYVDLSSYYIIVRVYFPILTEIQQAYIQELLPVSFNNDNSEW ISIVPNFILVRNTLISNIEIGFCLITKRSVICNQDYATPMTNNM RECLTGSTEKCPRELVVSSHVPRFALSNGVLFANCISVTCQCQT TGRAISQSGEQTLLMIDNTTCPTAVLGNVIISLGKYLGSVNYNS EGIAIGPPVFTDKVDISSQISSMNQSLQQSKDYIKEAQRLLDTV NPSLISMLSMIILYVLSIASLCIGLITFISFIIVEKKRNTYSRL EDRRVRPTSSGDLYYIGT	80
Nipah virus G protein	>sp|Q9IH62|GLYCP_NIPAV Glycoprotein G OS=Nipah virus GN=G PE=1 SV=1 MPAENKKVRFENTTSDKGKIPSKVIKSYYGTMDIKKINEGLLDS KILSAFNTVIALLGSIVIIVMNIMIIQNYTRSTDNQAVIKDALQ GIQQQIKGLADKIGTEIGPKVSLIDTSSTITIPANIGLLGSKIS QSTASINENVNEKCKFTLPPLKIHECNISCPNPLPFREYRPQTE GVSNLVGLPNNICLQKTSNQILKPKLISYTLPVVGQSGTCITDP LLAMDEGYFAYSHLERIGSCSRGVSKQRIIGVGEVLDRGDEVPS LFMTNVWTPPNPNTVYHCSAVYNNEFYYVLCAVSTVGDPILNST YWSGSLMMTRLAVKPKSNGGGYNQHQLALRSIEKGRYDKVMPYG PSGIKQGDTLYFPAVGFLVRTEFKYNDSNCPITKCQYSKPENCR LSMGIRPNSHYILRSGLLKYNLSDGENPKVVFIEISDQRLSIGS PSKIYDSLGQPVFYQASFSWDTMIKFGDVLTVNPLVVNWRNNTV ISRPGQSQCPRFNTCPEICWEGVYNDAFLIDRINWISAGVFLDS NQTAENPVFTVFKDNEILYRAQLASEDTNAQKTITNCFLLKNKI WCISLVEIYDTGDNVIRPKLFAVKIPEQCT	81
Rotavirus VP4 protein	>sp|P11193|VP4_ROTHW Outer capsid protein VP4 OS=Rotavirus A (strain RVA/Human/United States/Wa/1974/G1P1A[8]) PE=1 SV=3 MASLIYRQLLTNSYSVDLHDEIEQIGSEKTQNVTINPSPFAQTR YAPVNWGHGEINDSTTVEPILDGPYQPTTFTPPNDYWILINSNT NGVVYESTNNSDFWTAVVAIEPHVNPVDRQYTIFGESKQFNVSN DSNKWKFLEMFRSSSQNEFYNRRTLTSDTRFVGILKYGGRVWTF HGETPRATTDSSSTANLNNISITIHSEFYIIPRSQESKCNEYIN NGLPPIQNTRNVVPLPLSSRSIQYKRAQVNEDIIVSKTSLWKEM QYNRDIIIRFKFGNSIVKMGGLGYKWSEISYKAANYQYNYLRDG EQVTAHTTCSVNGVNNFSYNGGSLPTDFGISRYEVIKENSYVYV DYWDDSKAFRNMVYVRSLAANLNSVKCTGGSYNFSIPVGAWPVM NGGAVSLHFAGVTLSTQFTDFVSLNSLRFRFSLTVDEPPFSILR TRTVNLYGLPAANPNNGNEYYEISGRFSLIYLVPTNDDYQTPIM NSVTVRQDLERQLTDLREEFNSLSQEIAMAQLIDLALLPLDMFS MFSGIKSTIDLTKSMATSVMKKFRKSKLATSISEMTNSLSDAAS SASRNVSIRSNLSAISNWTNVSNDVSNVTNSLNDISTQTSTISK KFRLKEMITQTEGMSFDDISAAVLKTKIDMSTQIGKNTLPDIVT EASEKFIPKRSYRILKDDEVMEINTEGKFFAYKINTFDEVPFDV NKFAELVTDSPVISAIIDFKTLKNLNDNYGITRTEALNLIKSNP NMLRNFINQNNPIIRNRIEQLILQCKL	82
Rotavirus VP8 protein	>sp|P11193|1-230 MASLIYRQLLTNSYSVDLHDEIEQIGSEKTQNVTINPSPFAQTR YAPVNWGHGEINDSTTVEPILDGPYQPTTFTPPNDYWILINSNT NGVVYESTNNSDFWTAVVAIEPHVNPVDRQYTIFGESKQFNVSN DSNKWKFLEMFRSSSQNEFYNRRTLTSDTRFVGILKYGGRVWTF HGETPRATTDSSSTANLNNISITIHSEFYIIPRSQESKCNEYIN NGLPPIQNTR	83
Human metapneumovirus (hMPV) F protein	>sp|Q6WB98|FUS_HMPVC Fusion glycoprotein F0 OS=Human metapneumovirus (strain CAN97-83) GN=F PE=1 SV=1 MSWKVVIIFSLLITPQHGLKESYLEESCSTITEGYLSVLRTGWY TNVFTLEVGDVENLTCSDGPSLIKTELDLTKSALRELKTVSADQ LAREEQIENPRQSRFVLGAIALGVATAAAVTAGVAIAKTIRLES EVTAIKNALKTTNEAVSTLGNGVRVLATAVRELKDFVSKNLTRA INKNKCDIDDLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLD LMTDAELARAVSNMPTSAGQIKLMLENRAMVRRKGFGILIGVYG SSVIYMVQLPIFGVIDTPCWIVKAAPSCSGKKGNYACLLREDQG WYCQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNI NISTTNYPCKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNR	84

	VGIIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIKGR PVSSSFDPIKFPEDQFNVALDQVFENIENSQALVDQSNRILSSA EKGNTGFIIVIILIAVLGSSMILVSIFIIIKKTKKPTGAPPELS GVTNNGFIPHS	
Human metapneumovirus (hMPV) G protein	>sp|Q6WB94|VGLG_HMPVC Major surface glycoprotein G OS=Human metapneumovirus (strain CAN97-83) GN=G PE=1 SV=1 MEVKVENIRAIDMLKARVKNRVARSKCFKNASLILIGITTLSIA LNIYLIINYTIQKTSSESEHHTSSPPTESNKEASTISTDNPDIN PNSQHPTQQSTENPTLNFAASVSPSETEPASTPDTTNRLSSVDR STAQPSESRTKTKPTVHTRNNFSTASSTQSPPRATTKAIRRATT FRMSSTGKRPTTTSVQSDSSTTTQNHEETGSANPQASVSTMQN	85
Human parainfluenza virus (PV) F protein	>sp|P12605|FUS_PI1HC Fusion glycoprotein F0 OS=Human parainfluenza 1 virus (strain C39) GN=F PE=2 SV=1 MQKSEILFLIYSSLLLSSSLCQIPVDKLSNVGVIINEGKLLKIA GSYESRYIVLSLVPSIDLEDGCGTTQIIQYKNLLNRLLIPLKDA LDLQESLITITNDTTVPNDNPQSRFFGAVIGTIALGVATAAQIT AGIALAEAREARKDIALIKDSIIKTHNSVELIQRGIGEQIIALK TLQDFVNNEIRPAIGELRCETTALKLGIKLTQHYSELATAFSSN LGTIGEKSLTLQALSSLYSANITEILSTIKKDKSDIYDIIYTEQ VKGTVIDVDLEKYMVTLLVKIPILSEIPGVLIYRASSISYNIEG EEWHVAIPNYIINKASSLGGADVTNCIESRLAYICPRDPTQLIP DNQQKCILGDVSKCPVTKVINNLVPKFAFINGGVVANCIASTCT CGTNRIPVNQDRSRGVTFLTYTNCGLIGINGIELYANKRGRDTT WGNQIIKVGPAVSIRPVDISLNLASATNFLEESKIELMKAKAII SAVGGWHNTESTQIIIIIIVCILIIICGILYYLYRVRRLLVMI NSTHNSPVNTYTLESRMRNPYIGNNSN	86
Human parainfluenza virus HN protein	>sp|P25466|HN_PI2HT Hemagglutinin-neuraminidase OS=Human parainfluenza 2 virus (strain Toshiba) GN=HN PE=2 SV=1 MEDYSNLSLKSIPKRTCRIIFRTATILGICTLIVLCSSILHEII HLDVSSGLMDSDDSQQGIIQPIIESLKSLIALANQILYNVAIKI PLKIDSIETVIFSALKDMHTGSMSNTNCTPGNLLLHDAAYINGI NKFLVLKSYNGTPKYGPLLNIPSFIPSATSPNGCTRIPSFSLIK THWCYTHNVMLGDCLDFTTSNQYLAMGIIQQSAAAFPIFRTMKT IYLSDGINRKSCSVTAIPGGCVLYCYVATRSEKEDYATTDLAEL RLAFYYYNDTFIERVISLPNTTGQWATINPAVGSGIYHLGFILF PVYGGLISGTPSYNKQSSRYFIPKHPNITCAGNSSEQAAAARSS YVIRYHSNRLIQSAVLICPLSDMHTARCNLVMFNNSQVMMGAEG RLYVIDNNLYYYQRSSSWWSASLFYRINTDFSKGIPPIIEAQWV PSYQVPRPGVMPCNATSFCPANCITGVYADVWPLNDPEPTSQNA LNPNYRFAGAFLRNESNRTNPTFYTASASALLNTTGFNNTNHKA AYTSSTCFKNTGTQKIYCLIIIEMGSSLLGEFQIIPFLRELIP	87
Malaria Pfs25 surface antigen	>sp|P13829|OS25_PLAFO 25 kDa ookinete surface antigen OS=Plasmodium falciparum (isolate NF54) PE=1 SV=1 MNKLYSLFLFLFIQLSIKYNNAKVTVDTVCKRGFLIQMSGHLEC KCENDLVLVNEETCEEKVLKCDEKTVNKPCGDFSKCIKIDGNPV SYACKCNLGYDMVNNVCIPNECKNVTCGNGKCILDTSNPVKTGV CSCNIGKVPNVQDQNKCSKDGETKCSLKCLKENETCKAVDGIYK CDCKDGFIIDNESSICTAFSAYNILNLSIMFILFSVCFFIM	88
serogroup B Neisseria meningitidis (MenB) fHbp	>tr|Q6QCC2|Q6QCC2_NEIME Factor H-binding protein OS=Neisseria meningitidis OX=487 GN=gna1870 PE=1 SV=1 MNRTAFCCLSLTTALILTACSSGGGGVAADIGAGLADALTAPLD HKDKGLQSLTLDQSVRKNEKLKLAAQGAEKTYGNGDSLNTGKLK NDKVSRFDFIRQIEVDGQLITLESGEFQVYKQSHSALTAFQTEQ IQDSEHSGKMVAKRQFRIGDIAGEHTSFDKLPEGGRATYRGTAF GSDDAGGKLTYTIDFAAKQGNGKIEHLKSPELNVDLAAADIKPD GKRHAVISGSVLYNQAEKGSYSLGIFGGKAQEVAGSAEVKTVNG IRHIGLAAKQ	98
serogroup B Neisseria meningitidis (MenB) NadA	>tr|X5F9B9|X5F9B9_NEIME Quinolinate synthase A OS=Neisseria meningitidis OX=487 GN=nadA2 PE=3 SV=1 MQTAARRSFDYDMPLIQTPTSACQIRQAWAKVADTPDRETAGRL KDEIKALLKETNAVLVAHYYVDPLIQDLALETGGCVGDSLEMAR FGAEHEAGTLVVAGVRFMGESAKILCPEKTVLMPDLEAECSLDL GCPEEAFSAFCDQHPDRTVVVYANTSAAVKARADWVVTSSVALE IVSYLKSRGEKLIWGPDRHLGDYIRRETGADMLLWQGSCIVHNE FKGQELAALKAEHPDAVVLVHPESPQSVIELGDVVGSTSKLLKA AVSRPEKKFIVATDLGILHEMQKQAPDKQFIAAPTAGNGGSCKS CAFCPWMAMNSLGGIKYALTSGHNEILLDRKLGEAAKLPLQRML DFAAGLKRGDVFNGMGPA	99

serogroup B Neisseria meningitidis (MenB) NHBA	>tr|Q9JPH1|Q9JPH1_NEIME Gna2132 OS=Neisseria meningitidis OX=487 GN=gna2132 PE=4 SV=1 MFKRSVIAMACIFALSACGGGGGGSPDVKSADTLSKPAAPVVSE KETEAKEDAPQAGSQGQGAPSAQGGQDMAAVSEENTGNGGAAAT DKPKNEDEGAQNDMPQNAADTDSLTPNHTPASNMPAGNMENQAP DAGESEQPANQPDMANTADGMQGDDPSAGGENAGNTAAQGTNQA ENNQTAGSQNPASSTNPSATNSGGDFGRTNVGNSVVIDGPSQNI TLTHCKGDSCSGNNFLDEEVQLKSEFEKLSDADKISNYKKDGKN DGKNDKFVGLVADSVQMKGINQYIIFYKPKPTSFARFRRSARSR RSLPAEMPLIPVNQADTLIVDGEAVSLTGHSGNIFAPEGNYRYL TYGAEKLPGGSYALRVQGEPSKGEMLAGTAVYNGEVLHFHTENG RPSPSRGRFAAKVDFGSKSVDGIIDSGDGLHMGTQKFKAAIDGN GFKGTWTENGGGDVSGKFYGPAGEEVAGKYSYRPTDAEKGGFGV FAGKKEQD	100

4. Assembly Domains and Linkers

[0058] In an embodiment, the nanostructure comprises a trimeric assembly. The trimeric assembly comprises a protein-protein interface that induces three copies of the first polypeptides to self-associate to form trimeric building blocks. Each copy of the first polypeptides further comprises a surface-exposed interface that interacts with a complementary surface-exposed interface on a second assembly domain. As described in King et al. (Nature 510, 103-108, 2014), Bale et al. (Science 353, 389-394, 2016), and patent publications WO2014124301 A1 and US20160122392 A1, the complementary protein-protein interface between the trimeric assembly domain and second assembly domain drives the assembly of multiple copies of the trimeric assembly domain and second assembly domain to a target nanostructure. In some embodiments, each copy of the trimeric assembly domains of the nanostructure bears an antigenic proteins, or antigenic fragment thereof, as a genetic fusion; these nanostructures display the proteins at full valency. In other embodiments, the nanostructures of the invention comprise one or more copies of trimeric assembly domains bearing antigens proteins, or antigenic fragments thereof as genetic fusions as well as one or more trimeric assembly domains that do not bear antigenic proteins as genetic fusions; these nanostructures display the F proteins at partial valency. The trimeric assembly domain can be any polypeptide sequence that forms a trimer and interacts with a second assembly domain to drive assembly to a target nanostructure. In some embodiments, the nanostructure comprises first and second polypeptides selected from those disclosed in US 20130274441 A1, US 2015/0356240 A1, US 2016/0122392 A1, WO 2018/187325 A1, each of which is incorporated by reference herein in its entirety.

[0059] In the nanostructures of the present disclosure, the antigenic protein and the core of the nanostructure may be genetically fused such that they are both present in a single polypeptide. Preferably, the linkage between the protein and the core of the nanostructure

allows the protein, or antigenic fragment thereof, to be displayed on the exterior of the nanostructure. As such, the point of connection to the core of the nanostructure should be on the exterior of the core of the nanostructure formed. As will be understood by those of skill in the art, a wide variety of polypeptide sequences can be used to link the proteins, or antigenic fragments thereof and the core of the nanostructure. These polypeptide sequences are referred to as linkers. Any suitable linker can be used; there is no amino acid sequence requirement to serve as an appropriate linker. There is no requirement that the linker impose a rigid relative orientation of the protein or antigenic fragment thereof to the core of the nanostructure beyond enabling the protein or antigenic fragment thereof to be displayed on the exterior of the nanostructure. In some embodiments, the linker includes additional trimerization domains (e.g., the foldon domain of T4 fibritin) that assist in stabilizing the trimeric form of the F protein.

>T4 fibritin foldon domain (optional in the linker region)
GYIPEAPRDGQAYVRKDGEWVLLSTFL (SEQ ID NO: 89)

[0060] In some embodiments, the linker may comprise a Gly-Ser linker (*i.e.* a linker consisting of glycine and serine residues) of any suitable length. In some embodiments, the Gly-Ser linker may be 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, or more amino acids in length. In some embodiments, the Gly-Ser linker may comprise or consist of the amino acid sequence of GSGGSGSGSGGGSGSG, GGSGGGSGS or GSGGSGSG.

5. Assembly of nanostructures

[0061] In some embodiments, one or more purified samples of pluralities of the polypeptides for use in forming a nanostructure are mixed in an approximately equimolar molar ratio in aqueous conditions. The polypeptides interact with one another to drive assembly of the target nanostructure. Successful assembly of the target nanostructure can be confirmed by analyzing the *in vitro* assembly reaction by common biochemical or biophysical methods used to assess the physical size of proteins or protein assemblies, including but not limited to size exclusion chromatography, native (non-denaturing) gel electrophoresis, dynamic light scattering, multi-angle light scattering, analytical ultracentrifugation, negative stain electron microscopy, cryo-electron microscopy, or X-ray crystallography. If necessary, the assembled nanostructure can be purified from other species or molecules present in the *in vitro* assembly reaction using preparative techniques commonly

used to isolate proteins by their physical size, including but not limited to size exclusion chromatography, preparative ultracentrifugation, tangential flow filtration, or preparative gel electrophoresis. The presence of the antigenic protein in the nanostructure can be assessed by techniques commonly used to determine the identity of protein molecules in aqueous solutions, including but not limited to SDS-PAGE, mass spectrometry, protein sequencing, or amino acid analysis. The accessibility of the protein on the exterior of the particle, as well as its conformation or antigenicity, can be assessed by techniques commonly used to detect the presence and conformation of an antigen, including but not limited to binding by monoclonal antibodies, conformation-specific monoclonal antibodies, or anti-sera specific to the antigen.

[0062] In other embodiments, the nanostructures of the invention comprise two or more distinct first polypeptides bearing different antigenic proteins as genetic fusions; these nanostructures co-display multiple different proteins on the same nanostructure. These multi-antigen nanostructures are produced by performing *in vitro* assembly with mixtures of first polypeptides in which each first polypeptide bears one of two or more distinct proteins as a genetic fusion. The fraction of each first polypeptide in the mixture determines the average valency of each antigenic protein in the resulting nanostructures.. The presence and average valency of each protein-bearing first polypeptides in a given sample can be assessed by quantitative analysis using the techniques described above for evaluating the presence of antigenic proteins in full-valency nanostructures.

[0063] In various embodiments, the nanostructures are between about 20 nanometers (nm) to about 40 nm in diameter, with interior lumens between about 15 nm to about 32 nm across and pore sizes in the protein shells between about 1 nm to about 14 nm in their longest dimensions.

[0064] In one embodiment, the nanostructure has icosahedral symmetry. In this embodiment, the nanostructure may comprise 60 copies of a first polypeptide and 60 copies of a second polypeptide. In one such embodiment, the number of identical first polypeptides in each first assembly is different than the number of identical second polypeptides in each second assembly. For example, in one embodiment, the nanostructure comprises twelve first assemblies and twenty second assemblies; in this embodiment, each first assembly may, for example, comprise five copies of the identical first polypeptide, and each second assembly may, for example, comprise three copies of the identical second polypeptide. In another embodiment, the nanostructure comprises twelve first assemblies and thirty second

assemblies; in this embodiment, each first assembly may, for example, comprise five copies of the identical first polypeptide, and each second assembly may, for example, comprise two copies of the identical second polypeptide. In a further embodiment, the nanostructure comprises twenty first assemblies and thirty second assemblies; in this embodiment, each first assembly may, for example, comprise three copies of the identical first polypeptide, and each second assembly may, for example, comprise two copies of the identical second polypeptide. All of these embodiments are capable of forming synthetic nanomaterials with regular icosahedral symmetry.

[0065] In various further embodiments, oligomeric states of the first and second polypeptides are as follows:

I53-34A: trimer + I53-34B: pentamer;

I53-40A: pentamer + I53-40B: trimer;

I53-47A: trimer + I53-47B: pentamer;

I53-50A: trimer + I53-50B: pentamer;

I53-51A: trimer + I53-51B: pentamer;

I32-06A: dimer + I32-06B: trimer;

I32-19A: trimer + I32-19B: dimer;

I32-28A: trimer + I32-28B: dimer;

I52-03A: pentamer + I52-03B: dimer;

I52-32A: dimer + I52-32B: pentamer; and

I52-33A: pentamer + I52-33B: dimer

6. Nucleic Acids

[0066] In another aspect, the present disclosure provides isolated nucleic acids encoding a fusion protein of the present disclosure. The isolated nucleic acid sequence may comprise RNA or DNA. As used herein, "isolated nucleic acids" are those that have been removed from their normal surrounding nucleic acid sequences in the genome or in cDNA sequences. Such isolated nucleic acid sequences may comprise additional sequences useful for promoting expression and/or purification of the encoded protein, including but not limited to polyA sequences, modified Kozak sequences, and sequences encoding epitope tags, export signals, and secretory signals, nuclear localization signals, and plasma membrane localization signals. It will be apparent to those of skill in the art, based on the teachings herein, what nucleic acid sequences will encode the proteins of the disclosure.

[0067] In a further aspect, the present disclosure provides recombinant expression vectors comprising the isolated nucleic acid of any embodiment or combination of embodiments of the disclosure operatively linked a suitable control sequence. "Recombinant expression vector" includes vectors that operatively link a nucleic acid coding region or gene to any control sequences capable of effecting expression of the gene product. "Control sequences" operably linked to the nucleic acid sequences of the disclosure are nucleic acid sequences capable of effecting the expression of the nucleic acid molecules. The control sequences need not be contiguous with the nucleic acid sequences, so long as they function to direct the expression thereof. Thus, for example, intervening untranslated yet transcribed sequences can be present between a promoter sequence and the nucleic acid sequences and the promoter sequence can still be considered "operably linked" to the coding sequence. Other such control sequences include, but are not limited to, polyadenylation signals, termination signals, and ribosome binding sites. Such expression vectors can be of any type known in the art, including but not limited to plasmid and viral-based expression vectors. The control sequence used to drive expression of the disclosed nucleic acid sequences in a mammalian system may be constitutive (driven by any of a variety of promoters, including but not limited to, CMV, SV40, RSV, actin, EF) or inducible (driven by any of a number of inducible promoters including, but not limited to, tetracycline, ecdysone, steroid responsive). The construction of expression vectors for use in transfecting prokaryotic cells is also well known in the art, and thus can be accomplished via standard techniques. (See, for example, Sambrook, Fritsch, and Maniatis, in: Molecular Cloning, A Laboratory Manual, Cold Spring Harbor Laboratory Press, 1989; Gene Transfer and Expression Protocols, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, N.J.), and the Ambion 1998 Catalog (Ambion, Austin, TX). The expression vector must be replicable in the host organisms either as an episome or by integration into host chromosomal DNA. In a preferred embodiment, the expression vector comprises a plasmid. However, the disclosure is intended to include other expression vectors that serve equivalent functions, such as viral vectors.

[0068] In another aspect, the present disclosure provides host cells that have been transfected with the recombinant expression vectors disclosed herein, wherein the host cells can be either prokaryotic or eukaryotic. The cells can be transiently or stably transfected. Such transfection of expression vectors into prokaryotic and eukaryotic cells can be accomplished via any technique known in the art, including but not limited to standard bacterial transformations, calcium phosphate co-precipitation, electroporation, or liposome

mediated-, DEAE dextran mediated-, polycationic mediated-, or viral mediated transfection. (See, for example, Molecular Cloning: A Laboratory Manual (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press; Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed. (R.I. Freshney. 1987. Liss, Inc. New York, NY). A method of producing a polypeptide according to the disclosure is an additional part of the disclosure. The method comprises the steps of (a) culturing a host according to this aspect of the disclosure under conditions conducive to the expression of the polypeptide, and (b) optionally, recovering the expressed polypeptide.

7. Vaccines and Administration

[0069] The disclosure also provides vaccines comprising the nanostructures described herein. Such compositions can be used to raise antibodies in a mammal (e.g. a human). The vaccines compositions of the disclosure typically include a pharmaceutically acceptable carrier, and a thorough discussion of such carriers is available in Remington: The Science and Practice of Pharmacy.

[0070] The pH of the composition is usually between about 4.5 to about 11, such as between about 5 to about 11, between about 5.5 to about 11, between about 6 to about 11, between about 5 to about 10.5, between about 5.5 to about 10.5, between about 6 to about 10.5, between about 5 to about 10, between about 5.5 to about 10, between about 6 to about 10, between about 5 to about 9.5, between about 5.5 to about 9.5, between about 6 to about 9.5, between about 5 to about 9, between about 5.5 to about 9, between about 6 to about 9, between about 5 to about 8.5, between about 5.5 to about 8.5, between about 6 to about 8.5, between about 5 to about 8, between about 5.5 to about 8, between about 6 to about 8, about 4.5, about 5, about 6.5, about 6, about 6.5, about 7, about 7.5, about 8, about 8.5, about 9, about 9.5, about 10, about 10.5, about 11, etc. Stable pH may be maintained by the use of a buffer e.g. a Tris buffer, a citrate buffer, phosphate buffer, or a histidine buffer. Thus a composition will generally include a buffer.

[0071] A composition may be sterile and/or pyrogen free. Compositions may be isotonic with respect to humans.

[0072] A vaccine composition comprises an immunologically effective amount of its antigen(s). An "immunologically effective amount" is an amount which, when administered to a subject, is effective for eliciting an antibody response against the antigen. This amount

can vary depending upon the health and physical condition of the individual to be treated, their age, the capacity of the individual's immune system to synthesize antibodies, the degree of protection desired, the formulation of the vaccine, the treating doctor's assessment of the medical situation, and other relevant factors. It is expected that the amount will fall in a relatively broad range that can be determined through routine trials. The antigen content of compositions of the disclosure will generally be expressed in terms of the mass of protein per dose. A dose of 10-500μg (e.g. 50μg) per antigen can be useful.

[0073] Vaccine compositions may include an immunological adjuvant. Exemplary adjuvants include the following: 1. mineral-containing compositions; 2. oil emulsions; 3. saponin formulations; 4. virosomes and virus-like particles; 5. bacterial or microbial derivatives; 6. bioadhesives and mucoadhesives; 7. liposomes; 8. polyoxyethylene ether and polyoxyethylene ester formulations; 9. polyphosphazene (pcpp); 10. muramyl peptides; 11. imidazoquinolone compounds; 12. thiosemicarbazone compounds; 13. tryptanthrin compounds; 14. human immunomodulators; 15. lipopeptides; 16. benzonaphthyridines; 17. microparticles; 18. immunostimulatory polynucleotide (such as rna or dna; e.g., cpg-containing oligonucleotides).

[0074] For example, the composition may include an aluminum salt adjuvant, an oil in water emulsion (e.g. an oil-in-water emulsion comprising squalene, such as MF59 or AS03), a TLR7 agonist (such as imidazoquinoline or imiquimod), or a combination thereof. Suitable aluminum salts include hydroxides (e.g. oxyhydroxides), phosphates (e.g. hydroxyphosphates, orthophosphates), (e.g. see chapters 8 & 9 of Vaccine Design... (1995) eds. Powell & Newman. ISBN: 030644867X. Plenum), or mixtures thereof. The salts can take any suitable form (e.g. gel, crystalline, amorphous, etc.), with adsorption of antigen to the salt being an example. The concentration of Al^{+++} in a composition for administration to a patient may be less than 5mg/ml e.g. <4 mg/ml, <3 mg/ml, <2 mg/ml, <1 mg/ml, etc. A preferred range is between 0.3 and 1 mg/ml. A maximum of 0.85mg/dose is preferred. Aluminum hydroxide and aluminium phosphate adjuvants are suitable for use with the disclosure.

[0075] Exemplary adjuvants include, but are not limited to, Adju-Phos, Adjumerlm, albumin-heparin microparticles, Algal Glucan, Algammulin, Alum, Antigen Formulation, AS-2 adjuvant, autologous dendritic cells, autologous PBMC, Avridine™, B7-2, BAK, BAY R1005, Bupivacaine, Bupivacaine-HCl, BWZL, Calcitriol, Calcium Phosphate Gel, CCR5

peptides, CFA, Cholera holotoxin (CT) and Cholera toxin B subunit (CTB), Cholera toxin A1-subunit-Protein A D-fragment fusion protein, CpG, CRL1005, Cytokine-containing Liposomes, D-Murapalmitine, DDA, DHEA, Diphtheria toxoid, DL-PGL, DMPC, DMPG, DOC/Alum Complex, Fowlpox, Freund's Complete Adjuvant, Gamma Inulin, Gerbu Adjuvant, GM-CSF, GMDP, hGM-CSF, hIL-12 (N222L), hTNF-alpha, IFA, IFN-gamma in pcDNA3, IL-12 DNA, IL-12 plasmid, IL-12/GMCSF plasmid (Sykes), IL-2 in pcDNA3, IL-2/Ig plasmid, IL-2/Ig protein, IL-4, IL-4 in pcDNA3, Imiquimod, ImmTher™, Immunoliposomes Containing Antibodies to Costimulatory Molecules, Interferon-gamma, Interleukin-1 beta, Interleukin-12, Interleukin-2, Interleukin-7, ISCOM(s)™, Iscoprep 7.0.3™, Keyhole Limpet Hemocyanin, Lipid-based Adjuvant, Liposomes, Loxoribine, LT(R192G), LT-OA or LT Oral Adjuvant, LT-R192G, LTK63, LTK72, MF59, MONTANIDE ISA 51, MONTANIDE ISA 720, MPL.TM., MPL-SE, MTP-PE, MTP-PE Liposomes, Murametide, Murapalmitine, NAGO, nCT native Cholera Toxin, Non-Ionic Surfactant Vesicles, non-toxic mutant E1 12K of Cholera Toxin mCT-E112K, p-Hydroxybenzoique acid methyl ester, pCIL-10, pCIL12, pCMVmCAT1, pCMVN, Peptomer-NP, Pleuran, PLG, PLGA, PGA, and PLA, Pluronic L121, PMMA, PODDS™, Poly rA: Poly rU, Polysorbate 80, Protein Cochleates, QS-21, Quadri A saponin, Quil-A, Rehydragel HPA, Rehydragel LV, RIBI, Ribilike adjuvant system (MPL, TMD, CWS), S-28463, SAF-1, Sclavo peptide, Sendai Proteoliposomes, Sendai-containing Lipid Matrices, Span 85, Specol, Squalane 1, Squalene 2, Stearyl Tyrosine, Tetanus toxoid (TT), Theramide™, Threonyl muramyl dipeptide (TMDP), Ty Particles, and Walter Reed Liposomes. Selection of an adjuvant depends on the subject to be treated. Preferably, a pharmaceutically acceptable adjuvant is used.

[0076] One suitable immunological adjuvant comprises a compound of Formula (I) as defined in WO2011/027222, or a pharmaceutically acceptable salt thereof, adsorbed to an aluminum salt. Many further adjuvants can be used, including any of those disclosed in Powell & Newman (1995).

[0077] Compositions may include an antimicrobial, particularly when packaged in multiple dose format. Antimicrobials such as thiomersal and 2-phenoxyethanol are commonly found in vaccines, but sometimes it may be desirable to use either a mercury-free preservative or no preservative at all.

[0078] Compositions may comprise detergent e.g. a polysorbate, such as polysorbate 80. Detergents are generally present at low levels e.g. <0.01%.

[0079] Compositions may include sodium salts (e.g. sodium chloride) to give tonicity. A concentration of 10±2 mg/ml NaCl is typical e.g. about 9 mg/ml.

[0080] In some embodiments, the buffer in the vaccine composition is a Tris buffer, a histidine buffer, a phosphate buffer, a citrate buffer or an acetate buffer. The composition may also include a lyoprotectant, e.g. sucrose, sorbitol or trehalose. In certain embodiments, the composition includes a preservative e.g. benzalkonium chloride, benzethonium, chlorohexidine, phenol, m-cresol, benzyl alcohol, methylparaben, propylparaben, chlorobutanol, o-cresol, p-cresol, chlorocresol, phenylmercuric nitrate, thimerosal, benzoic acid, and various mixtures thereof. In other embodiments, the composition includes a bulking agent, like glycine. In yet other embodiments, the composition includes a surfactant e.g., polysorbate-20, polysorbate-40, polysorbate- 60, polysorbate-65, polysorbate-80 polysorbate-85, poloxamer-188, sorbitan monolaurate, sorbitan monopalmitate, sorbitan monostearate, sorbitan monooleate, sorbitan trilaurate, sorbitan tristearate, sorbitan trioleaste, or a combination thereof. The composition may also include a tonicity adjusting agent, e.g., a compound that renders the formulation substantially isotonic or isoosmotic with human blood. Exemplary tonicity adjusting agents include sucrose, sorbitol, glycine, methionine, mannitol, dextrose, inositol, sodium chloride, arginine and arginine hydrochloride. In other embodiments, the composition additionally includes a stabilizer, e.g., a molecule which substantially prevents or reduces chemical and/or physical instability of the nanostructure, in lyophilized or liquid form. Exemplary stabilizers include sucrose, sorbitol, glycine, inositol, sodium chloride, methionine, arginine, and arginine hydrochloride.

[0081] In another aspect, the disclosure provides a method of inducing an immune response against an infectious agent, comprising administering to a subject in need thereof an immunologically effective amount of the immunogenic composition described herein, which comprises the nanostructure as described herein.

[0082] In certain embodiments, the immune response comprises the production of neutralizing antibodies against an infectious agent. In certain embodiments, the neutralizing antibodies are complement-independent.

[0083] The immune response can comprise a humoral immune response, a cell-mediated immune response, or both. In some embodiments an immune response is induced against each delivered antigenic protein. A cell-mediated immune response can comprise a Helper T-cell (Th) response, a CD8+ cytotoxic T-cell (CTL) response, or both. In some embodiments the immune response comprises a humoral immune response, and the antibodies are neutralizing antibodies. Neutralizing antibodies block viral infection of cells. Viruses infect epithelial cells and also fibroblast cells. In some embodiments the immune response reduces or prevents infection of both cell types. Neutralizing antibody responses can be complement-dependent or complement-independent. In some embodiments the neutralizing antibody response is complement-independent. In some embodiments the neutralizing antibody response is cross-neutralizing; i.e., an antibody generated against an administered composition neutralizes a virus of a strain other than the strain used in the composition.

[0084] A useful measure of antibody potency in the art is "50% neutralization titer." To determine 50% neutralizing titer, serum from immunized animals is diluted to assess how dilute serum can be yet retain the ability to block entry of 50% of viruses into cells. For example, a titer of 700 means that serum retained the ability to neutralize 50% of virus after being diluted 700-fold. Thus, higher titers indicate more potent neutralizing antibody responses. In some embodiments, this titer is in a range having a lower limit of about 200, about 400, about 600, about 800, about 1000, about 1500, about 2000, about 2500, about 3000, about 3500, about 4000, about 4500, about 5000, about 5500, about 6000, about 6500, or about 7000. The 50% neutralization titer range can have an upper limit of about 400, about 600, about 800, about 1000, about 1500, about 2000, about 2500, about 3000, about 3500, about 4000, about 4500, about 5000, about 5500, about 6000, about 6500, about 7000, about 8000, about 9000, about 10000, about 11000, about 12000, about 13000, about 14000, about 15000, about 16000, about 17000, about 18000, about 19000, about 20000, about 21000, about 22000, about 23000, about 24000, about 25000, about 26000, about 27000, about 28000, about 29000, or about 30000. For example, the 50% neutralization titer can be about 3000 to about 25000. "About" means plus or minus 10% of the recited value.

[0085] Compositions of the disclosure will generally be administered directly to a subject. Direct delivery may be accomplished by parenteral injection (e.g. subcutaneously, intraperitoneally, intravenously, intramuscularly, or to the interstitial space of a tissue), or by any other suitable route. For example, intramuscular administration may be used e.g. to the

thigh or the upper arm. Injection may be via a needle (e.g. a hypodermic needle), but needle-free injection may alternatively be used. A typical intramuscular dosage volume is 0.5 ml.

[0086] Dosage can be by a single dose schedule or a multiple dose schedule. Multiple doses may be used in a primary immunization schedule and/or in a booster immunization schedule. In a multiple dose schedule the various doses may be given by the same or different routes, e.g., a parenteral prime and mucosal boost, a mucosal prime and parenteral boost, etc. Multiple doses will typically be administered at least 1 week apart (e.g., about 2 weeks, about 3 weeks, about 4 weeks, about 6 weeks, about 8 weeks, about 10 weeks, about 12 weeks, about 16 weeks, etc.).

[0087] The subject may be an animal, preferably a vertebrate, more preferably a mammal. Exemplary subject includes, e.g., a human, a cow, a pig, a chicken, a cat or a dog, as the infectious agents covered herein may be problematic across a wide range of species. Where the vaccine is for prophylactic use, the human is preferably a child (e.g., a toddler or infant), a teenager, or an adult; where the vaccine is for therapeutic use, the human is preferably a teenager or an adult. A vaccine intended for children may also be administered to adults, e.g., to assess safety, dosage, immunogenicity, etc.

[0088] Vaccines of the disclosure may be prophylactic (i.e. to prevent disease) or therapeutic (i.e. to reduce or eliminate the symptoms of a disease). The term prophylactic may be considered as reducing the severity of or preventing the onset of a particular condition. For the avoidance of doubt, the term prophylactic vaccine may also refer to vaccines that ameliorate the effects of a future infection, for example by reducing the severity or duration of such an infection.

[0089] Isolated and/or purified nanostructures described herein can be administered alone or as either prime or boost in mixed-modality regimes, such as a RNA prime followed by a protein boost. Benefits of the RNA-prime/protein-boost strategy, as compared to a protein-prime/protein-boost strategy, include, for example, increased antibody titers, a more balanced IgG1:IgG2a subtype profile, induction of TH1-type CD4+ T cell-mediated immune response that was similar to that of viral particles, and reduced production of non-neutralizing antibodies. The RNA prime can increase the immunogenicity of compositions regardless of whether they contain or do not contain an adjuvant.

[0090] In the RNA-prime/protein boost-strategy, the RNA and the protein are directed to the same target antigen. Examples of suitable modes of delivering RNAs include virus-like replicon particles (VRPs), alphavirus RNA, replicons encapsulated in lipid nanoparticles (LNPs) or formulated RNAs, such as replicons formulated with cationic nanoemulsions (CNEs). Suitable cationic oil-in-water nanoemulsions are disclosed in WO2012/006380 e.g. comprising an oil core (e.g. comprising squalene) and a cationic lipid (e.g. DOTAP, DMTAP, DSTAP, DC-cholesterol, etc.).

[0091] In some embodiments, the RNA molecule is encapsulated in, bound to or adsorbed on a cationic lipid, a liposome, a cochleate, a virosome, an immune-stimulating complex, a microparticle, a microsphere, a nanosphere, a unilamellar vesicle, a multilamellar vesicle, an oil-in-water emulsion, a water-in-oil emulsion, an emulsome, a polycationic peptide, a cationic nanoemulsion, or combinations thereof.

[0092] Also provided herein are kits for administration of nucleic acid (e.g., RNA), purified proteins, and purified nanostructures described herein, and instructions for use. The disclosure also provides a delivery device pre-filled with a composition or a vaccine disclosed herein.

[0093] The pharmaceutical compositions described herein can be administered in combination with one or more additional therapeutic agents. The additional therapeutic agents may include, but are not limited to antibiotics or antibacterial agents, antiemetic agents, antifungal agents, anti-inflammatory agents, antiviral agents, immunomodulatory agents, cytokines, antidepressants, hormones, alkylating agents, antimetabolites, antitumour antibiotics, antimitotic agents, topoisomerase inhibitors, cytostatic agents, anti-invasion agents, antiangiogenic agents, inhibitors of growth factor function inhibitors of viral replication, viral enzyme inhibitors, anticancer agents, α-interferons, β-interferon, ribavirin, hormones, and other toll-like receptor modulators, immunoglobulins (Igs), and antibodies modulating Ig function (such as anti-IgE (omalizumab)).

[0094] In certain embodiments, the compositions disclosed herein may be used as a medicament, e.g., for use in inducing or enhancing an immune response in a subject in need thereof, such as a mammal.

[0095] In certain embodiments, the compositions disclosed herein may be used in the manufacture of a medicament for inducing or enhancing an immune response in a subject in need thereof, such as a mammal.

[0096] One way of checking efficacy of therapeutic treatment involves monitoring infection by an infectious agent after administration of the compositions or vaccines disclosed herein. One way of checking efficacy of prophylactic treatment involves monitoring immune responses, systemically (such as monitoring the level of IgG1 and IgG2a production) and/or mucosally (such as monitoring the level of IgA production), against the antigen. Typically, antigen-specific serum antibody responses are determined post-immunization but pre-challenge whereas antigen-specific mucosal antibody responses are determined post-immunization and post-challenge.

8. Terminology

[0097] All publications and patents mentioned herein are hereby incorporated by reference in their entirety as if each individual publication or patent was specifically and individually indicated to be incorporated by reference. In case of conflict, the present application, including any definitions herein, will control. However, mention of any reference, article, publication, patent, patent publication, and patent application cited herein is not, and should not be taken as an acknowledgment, or any form of suggestion, that they constitute valid prior art or form part of the common general knowledge in any country in the world.

[0098] Within this application, unless otherwise stated, the techniques utilized may be found in any of several well-known references such as: *Molecular Cloning: A Laboratory Manual* (Sambrook, et al., 1989, Cold Spring Harbor Laboratory Press), *Gene Expression Technology* (Methods in Enzymology, Vol. 185, edited by D. Goeddel, 1991. Academic Press, San Diego, CA), "Guide to Protein Purification" in *Methods in Enzymology* (M.P. Deutsheer, ed., (1990) Academic Press, Inc.); *PCR Protocols: A Guide to Methods and Applications* (Innis, et al. 1990. Academic Press, San Diego, CA), *Culture of Animal Cells: A Manual of Basic Technique, 2nd Ed* (RI. Freshney. 1987. Liss, Inc. New York, NY), *Gene Transfer and Expression Protocols*, pp. 109-128, ed. E.J. Murray, The Humana Press Inc., Clifton, NJ.), and the Ambion 1998 Catalog (Ambion, Austin, TX).

[0099] In the present description, any concentration range, percentage range, ratio range, or integer range is to be understood to include the value of any integer within the recited range and, when appropriate, fractions thereof (such as one tenth and one hundredth of an integer), unless otherwise indicated. The term "about", when immediately preceding a number or numeral, means that the number or numeral ranges plus or minus 10%. It should be understood that the terms "a" and "an" as used herein refer to "one or more" of the enumerated components unless otherwise indicated. The use of the alternative (*e.g.*, "or") should be understood to mean either one, both, or any combination thereof of the alternatives. The term "and/or" should be understood to mean either one, or both of the alternatives. As used herein, the terms "include" and "comprise" are used synonymously.

[00100] The section headings used herein are for organizational purposes only and are not to be construed as limiting the subject matter described.

[00101] Unless specifically defined otherwise, the following terms and phrases, which are common to the various embodiments disclosed herein, are defined as follows:

[00102] As used herein, the term protein refers to a protein or a glycoprotein.

[00103] As used herein, the term immunogenic refers to the ability of a specific protein, or a specific region thereof, to elicit an immune response to the specific protein, or to proteins comprising an amino acid sequence having a high degree of identity with the specific protein. According to the present disclosure, two proteins having a high degree of identity have amino acid sequences at least 80% identical, at least 85% identical, at least 87% identical, at least 90% identical, at least 92% identical, at least 94% identical, at least 96% identical, at least 98% identical or at least 99% identical.

[00104] As used herein, an immune response to a vaccine, or nanostructure, of the present disclosure is the development in a subject of a humoral and/or a cellular immune response to an antigenic protein present in the vaccine. For purposes of the present disclosure, a "humoral immune response" refers to an immune response mediated by antibody molecules, including secretory (IgA) or IgG molecules, while a "cellular immune response" is one mediated by T-lymphocytes and/or other white blood cells. One important aspect of cellular immunity involves an antigen-specific response by cytolytic T-cells ("CTLs"). CTLs have specificity

for peptide antigens that are presented in association with proteins encoded by the major histocompatibility complex (MHC) and expressed on the surfaces of cells. CTLs help induce and promote the destruction of intracellular microbes, or the lysis of cells infected with such microbes. Another aspect of cellular immunity involves an antigen-specific response by helper T-cells. Helper T-cells act to help stimulate the function, and focus the activity of, nonspecific effector cells against cells displaying peptide antigens in association with MHC molecules on their surface. A cellular immune response also refers to the production of cytokines, chemokines and other such molecules produced by activated T-cells and/or other white blood cells, including those derived from CD4+ and CD8+ T-cells.

[00105] Thus, an immunological response may be one that stimulates CTLs, and/or the production or activation of helper T-cells. The production of chemokines and/or cytokines may also be stimulated. The vaccine may also elicit an antibody-mediated immune response. Hence, an immunological response may include one or more of the following effects: the production of antibodies (e.g., IgA or IgG) by B-cells; and/or the activation of suppressor, cytotoxic, or helper T-cells and/or T-cells directed specifically to a hemagglutinin protein present in the vaccine. These responses may serve to neutralize infectivity, and/or mediate antibody-complement, or antibody dependent cell cytotoxicity (ADCC) to provide protection to an immunized individual. Such responses can be determined using standard immunoassays and neutralization assays, well known in the art.

[00106] As used herein the term "antibody" includes intact molecules as well as functional fragments thereof, such as Fab, F(ab')2, Fv, scFv, dsFv, or single domain molecules such as VH and VL that are capable of specifically binding to an epitope of an antigen. The term "antibody" encompasses B-cell receptors. The term "antibody" further encompasses camelid antibodies.

[00107] As used herein in describing viruses, neutralizing antibodies are antibodies that prevent virus from completing one round of replication. As defined herein, one round of replication refers the life cycle of the virus, starting with attachment of the virus to a host cell and ending with budding of newly formed virus from the host cell. This life cycle includes, but is not limited to, the steps of attaching to a cell, entering a cell, cleavage and rearrangement of viral proteins, fusion of the viral membrane with the endosomal membrane, release of viral ribonucleoproteins into the cytoplasm, formation of new viral particles and budding of viral particles from the host cell membrane.

[00108] As used herein, broadly neutralizing antibodies are antibodies that neutralize more than one type, subtype and/or strain of bacteria, virus, or parasite. For example, broadly neutralizing antibodies elicited against an influenza HA protein from a Type A influenza virus may neutralize a Type B or Type C virus. As a further example, broadly neutralizing antibodies elicited against an influenza HA protein from Group I influenza virus may neutralize a Group 2 virus. As an additional example, broadly neutralizing antibodies elicited against an HA protein from one sub-type or strain of virus, may neutralize another sub-type or strain of virus. For example, broadly neutralizing antibodies elicited against an HA protein from an H1 influenza virus may neutralize viruses from one or more sub-types selected from the group consisting of H2, H3, H4, H5, H6, H7, H8, H8, H10, H11, H12, H13, H14, H15 or H16.

[00109] With regard to antigens, it is understood by those skilled in the art that antigen proteins from different strains may have different lengths due to mutations (insertions, deletions) in the protein. Thus, reference to a corresponding region refers to a region of another proteins that is identical, or nearly so (e.g., at least 95%, identical, at least 98% identical or at least 99% identical), in sequence, structure and/or function to the region being compared. For example, with regard to an epitope of a protein, the corresponding region in a corresponding protein from a different strain of the organism may not have the same residue numbers, but will have a similar or nearly identical sequence and will perform the same function. To better clarify sequences comparisons between strains, numbering systems are used by those in the field, which relate amino acid positions to a reference sequence. Thus, corresponding amino acid residues in antigen proteins from different strains may not have the same residue number with respect to their distance from the N-terminal amino acid of the protein. The use of such numbering systems is understood by those skilled in the art.

[00110] According to the present disclosure, a trimerization domain is a series of amino acids that when joined (also referred to as fused) to a protein or peptide, allow the fusion protein to interact with other fusion proteins containing the trimerization domain, such that a trimeric structure is formed. Any known trimerization domain can be used in the present disclosure. Examples of trimerization domains include, but are not limited to, the HIV-1 gp41 trimerization domain, the SIV gp41 trimerization domain, the Ebola virus gp-2 trimerization domain, the HTLV-1 gp-21 trimerization domain, the T4 fibritin trimerization domain (i.e.,

foldon), the yeast heat shock transcription factor trimerization domain, and the human collagen trimerization domain.

[00111] As used herein, a variant refers to a protein, or nucleic acid molecule, the sequence of which is similar, but not identical to, a reference sequence, wherein the activity of the variant protein (or the protein encoded by the variant nucleic acid molecule) is not significantly altered. These variations in sequence can be naturally occurring variations or they can be engineered through the use of genetic engineering technique known to those skilled in the art. Examples of such techniques are found in Sambrook J, Fritsch E F, Maniatis T et al., in Molecular Cloning—A Laboratory Manual, 2nd Edition, Cold Spring Harbor Laboratory Press, 1989, pp. 9.31-9.57), or in Current Protocols in Molecular Biology, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6, both of which are incorporated herein by reference in their entirety.

[00112] With regard to variants, any type of alteration in the amino acid, or nucleic acid, sequence is permissible so long as the resulting variant protein retains the ability to elicit neutralizing antibodies against an influenza virus. Examples of such variations include, but are not limited to, deletions, insertions, substitutions and combinations thereof. For example, with regard to proteins, it is well understood by those skilled in the art that one or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9 or 10), amino acids can often be removed from the amino and/or carboxy terminal ends of a protein without significantly affecting the activity of that protein. Similarly, one or more (e.g., 2, 3, 4, 5, 6, 7, 8, 9 or 10) amino acids can often be inserted into a protein without significantly affecting the activity of the protein.

[00113] As noted, variant proteins of the present disclosure can contain amino acid substitutions relative to the nanostructure antigen proteins disclosed herein. Any amino acid substitution is permissible so long as the activity of the protein is not significantly affected. In this regard, it is appreciated in the art that amino acids can be classified into groups based on their physical properties. Examples of such groups include, but are not limited to, charged amino acids, uncharged amino acids, polar uncharged amino acids, and hydrophobic amino acids. Preferred variants that contain substitutions are those in which an amino acid is substituted with an amino acid from the same group. Such substitutions are referred to as conservative substitutions.

[00114] As used herein, the amino acid residues are abbreviated as follows: alanine (Ala; A), asparagine (Asn; N), aspartic acid (Asp; D), arginine (Arg; R), cysteine (Cys; C), glutamic acid (Glu; E), glutamine (Gln; Q), glycine (Gly; G), histidine (His; H), isoleucine (Ile; I), leucine (Leu; L), lysine (Lys; K), methionine (Met; M), phenylalanine (Phe; F), praline (Pro; P), serine (Ser; S), threonine (Thr; T), tryptophan (Trp; W), tyrosine (Tyr; Y), and valine (Val; V). As used herein, "about" means+/- 5% of the recited parameter.

[00115] Naturally occurring residues may be divided into classes based on common side chain properties: 1) hydrophobic: Met, Ala, Val, Leu, Ile; 2) neutral hydrophilic: Cys, Ser, Thr; 3) acidic: Asp, Glu; 4) basic: Asn, Gln, His, Lys, Arg; 5) residues that influence chain orientation: Gly, Pro; and 6) aromatic: Trp, Tyr, Phe. For example, non-conservative substitutions may involve the exchange of a member of one of these classes for a member from another class.

[00116] In making amino acid changes, the hydropathic index of amino acids may be considered. Each amino acid has been assigned a hydropathic index on the basis of its hydrophobicity and charge characteristics. The hydropathic indices are: isoleucine (+4.5); valine (+4.2); leucine (+3.8); phenylalanine (+2.8); cysteine/cystine (+2.5); methionine (+1.9); alanine (+1.8); glycine (−0.4); threonine (−0.7); serine (−0.8); tryptophan (−0.9); tyrosine (−1.3); proline (−1.6); histidine (−3.2); glutamate (−3.5); glutamine (−3.5); aspartate (−3.5); asparagine (−3.5); lysine (−3.9); and arginine (−4.5). The importance of the hydropathic amino acid index in conferring interactive biological function on a protein is generally understood in the art (Kyte et al., 1982, J. Mol. Biol. 157:105-31). It is known that certain amino acids may be substituted for other amino acids having a similar hydropathic index or score and still retain a similar biological activity. In making changes based upon the hydropathic index, the substitution of amino acids whose hydropathic indices are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred.

[00117] It is also understood in the art that the substitution of like amino acids can be made effectively on the basis of hydrophilicity, particularly where the biologically functionally equivalent protein or peptide thereby created is intended for use in immunological disclosure, as in the present case. The greatest local average hydrophilicity of a protein, as governed by the hydrophilicity of its adjacent amino acids, correlates with its

immunogenicity and antigenicity, i.e., with a biological property of the protein. The following hydrophilicity values have been assigned to these amino acid residues: arginine (+3.0); lysine (+3.0); aspartate (+3.0±1); glutamate (+3.0±1); serine (+0.3); asparagine (+0.2); glutamine (+0.2); glycine (0); threonine (−0.4); proline (−0.5±1); alanine (−0.5); histidine (−0.5); cysteine (−1.0); methionine (−1.3); valine (−1.5); leucine (−1.8); isoleucine (−1.8); tyrosine (−2.3); phenylalanine (−2.5); and tryptophan (−3.4). In making changes based upon similar hydrophilicity values, the substitution of amino acids whose hydrophilicity values are within ±2 is preferred, those within ±1 are particularly preferred, and those within ±0.5 are even more particularly preferred. One may also identify epitopes from primary amino acid sequences on the basis of hydrophilicity.

[00118] Desired amino acid substitutions (whether conservative or non-conservative) can be determined by those skilled in the art at the time such substitutions are desired. For example, amino acid substitutions can be used to identify important residues of the HA protein, or to increase or decrease the immunogenicity, solubility or stability of the HA proteins described herein. Exemplary amino acid substitutions are shown below in Table 4.

TABLE 4
Amino Acid Substitutions

Original Amino Acid	Exemplary Substitutions
Ala	Val, Leu, Ile
Arg	Lys, Gln, Asn
Asn	Gln
Asp	Glu
Cys	Ser, Ala
Gln	Asn
Glu	Asp
Gly	Pro, Ala
His	Asn, Gln, Lys, Arg
Ile	Leu, Val, Met, Ala
Leu	Ile, Val, Met, Ala
Lys	Arg, Gln, Asn
Met	Leu, Phe, Ile
Phe	Leu, Val, Ile, Ala, Tyr
Pro	Ala
Ser	Thr, Ala, Cys
Thr	Ser
Trp	Tyr, Phe
Tyr	Trp, Phe, Thr, Ser
Val	Ile, Met, Leu, Phe, Ala

[00119] As used herein, the phrase "significantly affect a protein's activity" refers to a decrease in the activity of a protein by at least 10%, at least 20%, at least 30%, at least 40% or at least 50%. With regard to the present disclosure, such an activity may be measured, for example, as the ability of a protein to elicit neutralizing antibodies against a virus. Such activity may be measured by measuring the titer of such antibodies against virus, or by measuring the number of types, subtypes or strains neutralized by the elicited antibodies. Methods of determining antibody titers and methods of performing virus neutralization assays are known to those skilled in the art. In addition to the activities described above, other activities that may be measured include the ability to agglutinate red blood cells and the binding affinity of the protein for a cell. Methods of measuring such activities are known to those skilled in the art.

[00120] As used herein, a fusion protein is a recombinant protein containing amino acid sequence from at least two unrelated proteins that have been joined together, via a peptide bond, to make a single protein. The unrelated amino acid sequences can be joined directly to each other or they can be joined using a linker sequence. As used herein, proteins are unrelated, if their amino acid sequences are not normally found joined together via a peptide bond in their natural environment(s) (e.g., inside a cell). For example, the amino acid sequences of monomeric subunits that make up a polypeptide, and the amino acid sequences of antigen proteins are not normally found joined together via a peptide bond.

[00121] The terms individual, subject, and patient are well-recognized in the art, and are herein used interchangeably to refer to any human or other animal susceptible to infection. Examples include, but are not limited to, humans and other primates, including non-human primates such as chimpanzees and other apes and monkey species; farm animals such as cattle, sheep, pigs, seals, goats and horses; domestic mammals such as dogs and cats; laboratory animals including rodents such as mice, rats and guinea pigs; birds, including domestic, wild and game birds such as chickens, turkeys and other gallinaceous birds, ducks, geese, and the like. The terms individual, subject, and patient by themselves, do not denote a particular age, sex, race, and the like. Thus, individuals of any age, whether male or female, are intended to be covered by the present disclosure and include, but are not limited to the elderly, adults, children, babies, infants, and toddlers. Likewise, the methods of the present disclosure can be applied to any race, including, for example, Caucasian (white), African-

American (black), Native American, Native Hawaiian, Hispanic, Latino, Asian, and European.

[00122] As used herein, a vaccinated subject is a subject that has been administered a vaccine that is intended to provide a protective effect against a bacteria, virus, or parasite.

[00123] As used herein, the terms exposed, exposure, and the like, indicate the subject has come in contact with a person of animal that is known to be infected with a bacteria, virus, or parasite.

[00124] The publications discussed herein are provided solely for their disclosure prior to the filing date of the present application. Nothing herein is to be construed as an admission that the present disclosure is not entitled to antedate such publication by virtue of prior disclosure. Further, the dates of publication provided may be different from the actual publication dates, which may need to be independently confirmed.

[00125] Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this disclosure belongs. Although any methods and materials similar or equivalent to those described herein can also be used in the practice or testing of the present disclosure, the preferred methods and materials are now described. All publications mentioned herein are incorporated herein by reference to disclose and describe the methods and/or materials in connection with which the publications are cited.

[00126] It is appreciated that certain features of the disclosure, which are, for clarity, described in the context of separate embodiments, may also be provided in combination in a single embodiment. Conversely, various features of the disclosure, which are, for brevity, described in the context of a single embodiment, may also be provided separately or in any suitable sub-combination. All combinations of the embodiments are specifically embraced by the present disclosure and are disclosed herein just as if each and every combination was individually and explicitly disclosed. In addition, all sub-combinations are also specifically embraced by the present disclosure and are disclosed herein just as if each and every such sub-combination was individually and explicitly disclosed herein.

[00127] The disclosure is further described in the following Examples, which do not limit the scope of the disclosure described in the claims.

9. Examples

9.1. Example 1: Respiratory Syncytial Virus (RSV)

9.1.1. Sequences

[00128] In embodiments of the present disclosure, RSV F protein is present as a fusion protein with the first polypeptide and a linker is used, the F protein-linker sequence may comprise the following:

>DS-Cav1-foldon (SEQ ID NO: 90)

(MELLILKANAITTILTAVTFCFASG)QNITEEFYQSTCSAVSKGYLSALRTGWYTSVIT
IELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFM
NYTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALL
STNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLL
EITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIM
CIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNA
GSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSS
SVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNK
QEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIR(KSDELL)**GYIPEAP
RDGQAYVRKDGEWVLLSTFL**

[00129] In various further embodiments, the first polypeptides comprise or consist of first polypeptides having a sequence selected from the following (optional residues in parentheses):

>DS-Cav1-foldon-T33-31A (SEQ ID NO: 91)

(MELLILKANVIATILTAVTFCFASS)QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITI
ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFM
NYTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALL
STNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLL
EITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIM
CIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNA
GSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSS
SVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNK
QEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIR(KSDELL)GYIPEAP
RDGQAYVRKDGEWVLLSTFLGGSMEEVVLITVPSALVAVKIAHALVEERLAACVNI

VPGLTSIYREEGSVVSDHELLLLVKTTTDAFPKLKERVKELHPYEVPEIVALPIAEGNR
EYLDWLRENTG

>DS-Cav1-T33-31A (SEQ ID NO: 92)

(MELLILKANVIATILTAVTFCFASS)QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITI
ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFM
NYTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALL
STNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLL
EITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIM
CIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNA
GSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSS
SVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNK
QEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIR(KSDELL)GGSMEE
VVLITVPSALVAVKIAHALVEERLAACVNIVPGLTSIYREEGSVVSDHELLLLVKTTT
DAFPKLKERVKELHPYEVPEIVALPIAEGNREYLDWLRENTG

>DS-Cav1-foldon-T33-15B (SEQ ID NO: 93)

(MELLILKANVIATILTAVTFCFASS)QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITI
ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFM
NYTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALL
STNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLL
EITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIM
CIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNA
GSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSS
SVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNK
QEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIR(KSDELL)GYIPEAP
RDGQAYVRKDGEWVLLSTFLGGSMVRGIRGAITVNSDTPTSIIIATILLLEKMLEANGI
QSYEELAAVIFTVTEDLTSAFPAEAARQIGMHRVPLLSAREVPVPGSLPRVIRVLALW
NTDTPQDRVRHVYLSEAVRLRPDLESAQ

>DS-Cav1-T33-15B (SEQ ID NO: 94)

(MELLILKANVIATILTAVTFCFASS)QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITI
ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFM
NYTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALL
STNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLL

EITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIM
CIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNA
GSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSS
SVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNK
QEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIR(KSDELL)GGSMVR
GIRGAITVNSDTPTSIIIATILLLEKMLEANGIQSYEELAAVIFTVTEDLTSAFPAEAARQ
IGMHRVPLLSAREVPVPGSLPRVIRVLALWNTDTPQDRVRHVYLSEAVRLRPDLESA
Q

>DS-Cav1-foldon-I53-50A (SEQ ID NO: 95)

(MELLILKANAITTILTAVTFCFASG)QNITEEFYQSTCSAVSKGYLSALRTGWYTSVIT
IELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFM
NYTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALL
STNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLL
EITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIM
CIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNA
GSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSS
SVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNK
QEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRGYIPEAPRDGQAY
VRKDGEWVLLSTFLGSGSHHHHHHHHGGSGGSGSEKAAKAEEAARKMEELFKKHK
IVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIKALSVLKEKGAIIGAGTV
TSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMTPTELVKAMKLGHTI
LKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGVNLDNVCEWFKAGVLAVGVGSALV
KGTPDEVREKAKAFVEKIRGCTE

>DS-Cav1-I53-50A (SEQ ID NO: 96)

(MELLILKANVIATILTAVTFCFASS)QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITI
ELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFM
NYTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALL
STNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLL
EITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIM
CIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNA
GSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSS
SVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNK

QEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRGGSGGSGSEKAAK
AEEAARKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIK
ALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGV
MTPTELVKAMKLGHTILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGVNLDNVCE
WFKAGVLAVGVGSALVKGTPDEVREKAKAFVEKIRGCTE

>DS-Cav1-I32-28A (SEQ ID NO: 97)

(MELLILKANAITTILTAVTFCFASG)QNITEEFYQSTCSAVSKGYLSALRTGWYTSVIT
IELSNIKENKCNGTDAKVKLIKQELDKYKNAVTELQLLMQSTPATNNRARRELPRFM
NYTLNNAKKTNVTLSKKRKRRFLGFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALL
STNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLL
EITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIM
CIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNA
GSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSS
SVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNK
QEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIR(KSDELL)GGSGGS
GSDDARIAAIGDVDELNSQIGVLLAEPLPDDVRAALSAIQHDLFDLGGELCIPGHAAIT
EDHLLRLALWLVHYNGQLPPLEEFILPGGARGAALAHVCRTVCRRAERSIKALGASE
PLNIAPAAYVNLLSDLLFVLARVLNRAAGGADVLWDRTRAH

>DS-Cav1-Tr-foldon-T33-31A (SEQ ID NO: 101)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLNNAKKTNVTLSKKRKRRFL
GFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALLSTNKAVVSLSNGVSVLTFKVLDL
KNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNS
ELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMCIIKEEVLAYVVQLPLYGVIDTPC
WKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKVQSNRVFCDT
MNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKTKCTASNK
NRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDPLVFPS
DEFDASISQVNEKINQSLAFIRGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSMEEVVL
ITVPSALVAVKIAHALVEERLAACVNIVPGLTSIYREEGSVVSDHELLLLVKTTTDAFP
KLKERVKELHPYEVPEIVALPIAEGNREYLDWLRENTG

>DS-Cav1-Tr-T33-31A (SEQ ID NO: 102)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL

DKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLNNAKKTNVTLSKKRKRRFL
GFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALLSTNKAVVSLSNGVSVLTFKVLDL
KNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNS
ELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMCIIKEEVLAYVVQLPLYGVIDTPC
WKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKVQSNRVFCDT
MNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKTKCTASNK
NRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDPLVFPS
DEFDASISQVNEKINQSLAFIRGGSMEEVVLITVPSALVAVKIAHALVEERLAACVNIV
PGLTSIYREEGSVVSDHELLLLVKTTTDAFPKLKERVKELHPYEVPEIVALPIAEGNRE
YLDWLRENTG

>DS-Cav1-Tr-foldon-T33-15B (SEQ ID NO: 103)
QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLNNAKKTNVTLSKKRKRRFL
GFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALLSTNKAVVSLSNGVSVLTFKVLDL
KNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNS
ELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMCIIKEEVLAYVVQLPLYGVIDTPC
WKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKVQSNRVFCDT
MNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKTKCTASNK
NRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDPLVFPS
DEFDASISQVNEKINQSLAFIRGYIPEAPRDGQAYVRKDGEWVLLSTFLGGSMVRGIR
GAITVNSDTPTSIIIATILLLEKMLEANGIQSYEELAAVIFTVTEDLTSAFPAEAARQIG
MHRVPLLSAREVPVPGSLPRVIRVLALWNTDTPQDRVRHVYLSEAVRLRPDLESAQ

>DS-Cav1-Tr-T33-15B (SEQ ID NO: 104)
QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLNNAKKTNVTLSKKRKRRFL
GFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALLSTNKAVVSLSNGVSVLTFKVLDL
KNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNS
ELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMCIIKEEVLAYVVQLPLYGVIDTPC
WKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKVQSNRVFCDT
MNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKTKCTASNK
NRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDPLVFPS
DEFDASISQVNEKINQSLAFIRGGSMVRGIRGAITVNSDTPTSIIIATILLLEKMLEANGI

QSYEELAAVIFTVTEDLTSAFPAEAARQIGMHRVPLLSAREVPVPGSLPRVIRVLALW
NTDTPQDRVRHVYLSEAVRLRPDLESAQ

>DS-Cav1-Tr-foldon-I53-50A (SEQ ID NO: 105)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLNNAKKTNVTLSKKRKRRFL
GFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALLSTNKAVVSLSNGVSVLTFKVLDL
KNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNS
ELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMCIIKEEVLAYVVQLPLYGVIDTPC
WKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKVQSNRVFCDT
MNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKTKCTASNK
NRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDPLVFPS
DEFDASISQVNEKINQSLAFIRGYIPEAPRDGQAYVRKDGEWVLLSTFLGSGSHHHHH
HHHGGSGGSGSEKAAKAEEAARKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGG
VHLIEITFTVPDADTVIKALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDE
EISQFCKEKGVFYMPGVMTPTELVKAMKLGHTILKLFPGEVVGPQFVKAMKGPFPN
VKFVPTGGVNLDNVCEWFKAGVLAVGVGSALVKGTPDEVREKAKAFVEKIRGCTE

>DS-Cav1-Tr-I53-50A (SEQ ID NO: 106)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLNNAKKTNVTLSKKRKRRFL
GFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALLSTNKAVVSLSNGVSVLTFKVLDL
KNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNS
ELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMCIIKEEVLAYVVQLPLYGVIDTPC
WKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKVQSNRVFCDT
MNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKTKCTASNK
NRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDPLVFPS
DEFDASISQVNEKINQSLAFIRGGSGGSGSEKAAKAEEAARKMEELFKKHKIVAVLR
ANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIKALSVLKEKGAIIGAGTVTSVEQ
CRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMTPTELVKAMKLGHTILKLFP
GEVVGPQFVKAMKGPFPNVKFVPTGGVNLDNVCEWFKAGVLAVGVGSALVKGTP
DEVREKAKAFVEKIRGCTE

>DS-Cav1-Tr-I32-28A (SEQ ID NO: 107)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL

DKYKNAVTELQLLMQSTPATNNRARRELPRFMNYTLNNAKKTNVTLSKKRKRRFL
GFLLGVGSAIASGVAVCKVLHLEGEVNKIKSALLSTNKAVVSLSNGVSVLTFKVLDL
KNYIDKQLLPILNKQSCSISNIETVIEFQQKNNRLLEITREFSVNAGVTTPVSTYMLTNS
ELLSLINDMPITNDQKKLMSNNVQIVRQQSYSIMCIIKEEVLAYVVQLPLYGVIDTPC
WKLHTSPLCTTNTKEGSNICLTRTDRGWYCDNAGSVSFFPQAETCKVQSNRVFCDT
MNSLTLPSEVNLCNVDIFNPKYDCKIMTSKTDVSSSVITSLGAIVSCYGKTKCTASNK
NRGIIKTFSNGCDYVSNKGVDTVSVGNTLYYVNKQEGKSLYVKGEPIINFYDPLVFPS
DEFDASISQVNEKINQSLAFIRGGSGGSGSDDARIAAIGDVDELNSQIGVLLAEPLPDD
VRAALSAIQHDLFDLGGELCIPGHAAITEDHLLRLALWLVHYNGQLPPLEEFILPGGA
RGAALAHVCRTVCRRAERSIKALGASEPLNIAPAAYVNLLSDLLFVLARVLNRAAGG
ADVLWDRTRAH

9.1.2. Methods

Expression and screening of trimeric building blocks comprising an F protein and a trimeric assembly domain.

[00130] Human codon-optimized sequences for trimeric building blocks including and lacking DS-Cav1 fusions were ordered from Genscript. Building blocks for single-component nanostructures (i.e., I3-01) were cloned into the pcDNA3.1 vector (ThermoFisher Scientific) containing one CMV promoter, while building blocks for two-component nanostructures (e.g., I53-50) were cloned into the pBudCE4.1 vector (ThermoFisher Scientific) containing both CMV and EF-1α promoters. Recombinant proteins were expressed by transient transfection of Expi293F cells (ThermoFisher Scientific) using polyethylenimine (PEI). Cell cultures were harvested five days post-transfection by centrifugation. Secreted proteins were analysed by ELISA, using either direct coating of the cell supernatants or by sandwich ELISA. Briefly, 96-well MaxiSorp plates (Nunc) were coated with cell supernatant for direct ELISA or murine anti-His tag monoclonal antibody (ThermoFisher Scientific) for sandwich ELISA. Secreted proteins were detected using the human Palivizumab, MPE8, RSD5, and D25 monoclonal antibodies. Transfected Expi293F cells were fixed and permeabilized with BD cytofix/cytoperm (BD Biosciences), incubated with human Palivizumab, MPE8, and D25 monoclonal antibodies, and stained with Alexa Fluor 647-conjugated anti-human IgG antibody (Jackson ImmunoResearch). Stained cells were counted with a FACS Fortessa flow cytometer (BD Biosciences). Analysis was performed with FlowJo software. Cell lines were routinely tested for mycoplasma contamination.

Expression and purification of DS-Cav1-I53-50A

[00131] Lentivirus was produced by transient transfection of 293T (ATCC) cells using linear 25- kDa polyethyleneimine (PEI; Polysciences). Briefly, 4x 10^6 cells were plated onto 10 cm tissue culture plates. After 24 h, 3 μg of psPAX2, 1.5 μg of pMD2G (Addgene plasmid #12260 and #12259, respectively) and 6 μg of lentiviral vector plasmid were mixed in 500 pi diluent (5 mM HEPES, 150 mM NaCl, pH = 7.05) and 42 μl of PEI (1 mg/ml) and incubated for 15 min. The DNA/PEI complex was then added to the plate drop-wise. Lentivirus was harvested 48 h post-transfection and concentrated 100-fold by low-speed centrifugation at 8000g for 18 h. Transduction of the target cell line was carried out in 125 mL shake flasks containing 10 x 10^6 cells in 10 mL of growth media. 100 uL of 100x lentivirus was added to the flask and the cells were incubated with shaking (225 rpm) at 37 °C, in 8% CO_2 for 4-6 h. 20 mL of growth media was added to the shake flask after 4-6 h.

[00132] Transduced cells were expanded every other day to a density of 1 x 10^6 cells/ml until a final culture size of 4 L was reached. The media was harvested after 17 days of total incubation after measuring final cell concentration (~5 x 10^6 cells/mL) and viability (~90% viable). Culture supernatant was harvested by low-speed centrifugation to remove cells from the supernatant. NaCl and NaN_3 were added to final concentrations of 250 mM and 0.02%, respectively. The supernatant was loaded over one 5 mL HisTrap FF Crude column (GE Healthsciences) at 5 ml/min by an AKTA Pure (GE Healthsciences). The nickel elution was applied to a HiLoad 16/600 Superdex 200 pg column (GE Healthsciences) to further purify the target protein by size-exclusion chromatography. The size-exclusion purified target protein was snap frozen in liquid nitrogen and stored at -80 °C.

In vitro assembly of DS-Cav1-bearing nanostructures

[00133] 100% valency particles (20 DS-Cav1 trimers per icosahedral nanostructure) were prepared by mixing DS-Cav1-foldon-I53-50A trimers and I53-50B.4PT1 pentamers at 50 μM each and incubating with rocking overnight at 4 °C. In some cases, assembled nanostructures were purified from excess components remaining in the *in vitro* assembly reaction using a GE Sephacryl S-500 HR 16/60 column in a buffer comprising 25 mM Tris pH 8, 250 mM NaCl, 5% glycerol. Sample load and SEC fractions were analyzed by SDS-PAGE in the presence and absence of reducing agent. Peak fractions were pooled, concentrated using a GE

Vivaspin 20 30kDa MWCO centrifugal filter, and quantified using an Agilent 8454 spectrophotometer.

[00134] 66% valency particles (~14 DS-Cav1 trimers per icosahedral nanostructure) were prepared by mixing DS-Cav1-foldon-I53-50A trimers, I53-50A trimers, and I53-50B.4PosT1 pentamers at 50, 25, and 75 μM, respectively. 33% valency particles (~7 DS-Cav1 trimers per icosahedral nanostructure) were prepared by mixing DS-Cav1 -foldon-I53-50A trimers, I53-50A trimers, and I53-50B.4PosT1 pentamers at 25, 50, and 75 μM, respectively. The *in vitro* assembly reactions were allowed to incubate with rocking overnight at 4 °C. In some cases, assembled nanostructures were purified from excess components remaining in the *in vitro* assembly reaction using a GE Sephacryl S-500 HR 16/60 column in a buffer comprising 25 mM Tris pH 8, 250 mM NaCl, 5% glycerol. Sample load and SEC fractions were analyzed by SDS-PAGE in the presence and absence of reducing agent. Peak fractions were pooled, concentrated using a GE Vivaspin 20 30kDa MWCO centrifugal filter, and quantified using an Agilent 8454 spectrophotometer after centrifuging at ~21,000 g for 10 minutes at 4 °C. Samples were then transferred to cryogenic tubes in 1 mL aliquots at 1.1 mg/mL for the 33% valency particles and 0.6 mg/mL for the 66% valency particles, flash frozen in liquid nitrogen, and stored at -80 °C.

Electron microscopy of DS-Cav1-bearing nanostructures

[00135] Samples were prepared for negative stain EM by diluting to 0.01 mg/mL using 25 mM Tris pH 8, 250 mM NaCl, 5% glycerol and 3.5 μL was incubated on a glow-discharged, copper, carbon-coated grid for 20 seconds before blotting away the liquid with a piece of Whatman No. 1 filter paper. Within seconds of blotting away the sample, a 3.5 μL droplet of stain (2% w/v uranyl formate) was deposited and blotted away immediately, and then a second cycle of staining/blotting was performed.

Circular dichroism (CD) spectropolarimetry

[00136] CD spectra from F proteins (0.5 mg ml^{-1}) were recorded on a Chirascan spectropolarimeter (Applied Photophysics) over the wavelength range of 195 to 260 nm at a bandwidth of 1 nm, step size of 0.5 nm, and 1 s per step. The spectra in the far-ultraviolet region required an average of three scans and were subtracted from blank spectra performed with buffer. Thermal denaturation was monitored by performing scans at intervals of 1 °C, after equilibration for 1 min at each temperature. Data were fitted to a simple first order

curve. The values of ΔA222 are represented on the y axis as the percentage of the values recorded at 20 °C.

Enzyme-linked immunosorbent assay (ELISA)

[00137] To test specific binding of antibody or sera, 96-well MaxiSorp plates (Nunc) were coated with serial dilutions of tissue culture supernatants from cells expressing trimeric building blocks comprising F proteins and a trimeric assembly domain or 2 μg ml^{-1} of the following purified proteins: Ds-Cav1 with foldon, Ds-Cav1 fused to a trimeric first polypeptide or DS-Cav1-displaying nanostructures. Plates were blocked with 1% bovine serum albumin (BSA) and incubated with titrated antibodies (D25, MPE8, Palivizumab, RSD5) or murine sera followed by AP-conjugated goat anti-human IgG (Southern Biotech, 2040-04) or goat anti-mouse IgG (Southern Biotech, 1030-04). Plates were then washed with PBS buffer (Gibco, Invitrogen), 0.05% Tween-20 and substrate (p-NPP, Sigma) was added and plates were read at 405 nm.

Surface plasmon resonance (SPR)

[00138] The experiments were carried out at 25 °C on a ProteON XPR-36 instrument (Bio-Rad Laboratories) in a PBS buffer (Gibco, Invitrogen), 0.05% Tween-20. The D25 mAb was immobilized on a GLM sensor chip surface through amine coupling at 1000 response units (RU) and a blank surface with no protein was created under identical coupling conditions for use as a reference. Monoclonal antibodies (D25, MPE8, Palivizumab and 131-2a) were injected at a flow rate of 100 μl/min, at concentrations of 50 nM in different sensor channels. The data were processed using Proteon software and double referenced by subtraction of the blank surface and buffer only injection before local fitting of the data.

Vaccination and Serological Analysis

[00139] Female BALB/c mice 6-9 wk of age were obtained from Harlan Laboratories Inc. All procedures were performed in accordance with guidelines of the Swiss Federal Veterinary Office and after obtaining local ethical approval. Mice were immunized i.p. with 100 μL of immunogen formulation on day 0, 14, and 28. Priming infection at day 0 was performed with the Murine TLR9 ligand agonist (ODN 1668, InvivoGen). Mice were bled on day 10, 20 and 40, and antigen-and site-specific IgG titers were measured in the serum by ELISA. Neutralizing titers were also determined on HEp-2 cell as described below.

Virus neutralization assay and microscopy analysis

[00140] Confluent layers of HEp-2 cells in 96-well flat-bottom plates were infected with a fixed amount of Human Respiratory Syncytial Virus with Green Fluorescent Protein (RSV strain A2, Vira Tree#R121) at MOI of 1. 48 hours post-infection the cells were stained with Hoechst (Sigma#H6024) and images were acquired on BD Pathway bioimaging system. Percentage of the infected cells was automatically calculated by BD AttoVision software. The number of infected cells was plotted as dose response curves by plotting the relative infected cells against the antibodies dilutions.

Stability of DS-Cav1-bearing nanostructures

[00141] Physical stability of the prefusion conformation of designed DS-Cav1-foldon-I53-50 was assessed by incubating protein at various concentrations in a PCR cycler with heated lid at 80°C for 1 h. Residual prefusion conformation was evaluated by direct coating of the protein and ELISA with the prefusion-specific antibody D25.

Statistical analysis

[00142] No statistical methods were used to predetermine sample size. Data were analyzed with Prism 6 (GraphPad Software) using the two-tailed non-parametric Mann-Whitney U test for two groups' comparison, or Kruskall-Wallis test (and Dunn's posttest) when three or more groups were compared.

9.1.3. Results

Trimeric building blocks comprising an F protein and a trimeric assembly domain

[00143] Several trimeric building blocks, each comprising an F protein genetically fused to a trimeric assembly domain, were found to be secreted from HEK293F cells with their F proteins in a well-folded, prefusion conformation as judged by prefusion-specific monoclonal antibody binding in ELISA assays. FIG. 2 shows an example of ELISA data analyzing the supernatant of HEK293F cells expressing DS-Cav1-foldon, DS-Cav1-foldon-T33-31A, and DS-Cav1-T33-31A. Several other trimeric building blocks yielded detectable secretion of well-folded, prefusion F proteins.

Expression and purification of DS-Cav1-foldon-I53-50A

[00144] A lentiviral vector encoding DS-Cav1-foldon-I53-50A was used to transduce HEK293F cells for large-scale expression. The secreted protein was purified from tissue culture supernatants by immobilized metal affinity chromatography and size exclusion chromatography. Size exclusion chromatograms (FIG. 3) indicated that the purified protein formed a single, monodisperse species.

Expression and purification of I53-50B.4PT1

[00145] I53-50B.4PT1, a pentameric protein comprising a second assembly domain that interacts with the trimeric assembly domain in I53-50A or DS-Cav1-foldon-I53-50A to drive assembly of icosahedral I53-50-based nanostructures, was expressed and purified as described in Bale et al. and patent publication US20160122392 A1.

In vitro assembly and characterization of DS-Cav1-bearing I53-50 nanostructures

[00146] I53-50 is a 120-subunit two-component nanostructure with icosahedral symmetry comprising 20 trimeric (I53-50A) and 12 pentameric (I53-50B) building blocks, as recently described by Bale et al. The N terminus of I53-50A is exposed on the exterior of the I53-50 nanostructure, which enables the display of antigens on the nanostructure exterior through genetic fusion to the I53-530A N terminus. Purified DS-Cav1-foldon-I53-50A and I53-50B.4PT1 were assembled *in vitro* to form 120-subunit icosahedral nanostructures displaying various amounts of DS-Cav1 on the nanostructure exteriors by mixing the two purified proteins in various molar ratios. In separate preparations, nanostructures displaying DS-Cav1 at valencies of 100% (20 trimers), 66% (~14 trimers), and 33% (~7 trimers) were prepared as described above. The species present in the *in vitro* assembly reactions after overnight incubation were assessed by several techniques, including size exclusion chromatography-multi-angle light scattering (SEC-MALS), dynamic light scattering, and UV/vis spectroscopy. Assembled, 120-subunit nanostructures were purified from the *in vitro* assembly reactions using size exclusion chromatography (an example chromatogram obtained using the 100% valency nanostructures is presented in FIG. 4). The purified nanostructures were characterized by negative stain electron microscopy, which revealed fields of monodiperse particles in which DS-Cav1 was clearly visible as spikes projecting outward from the core icosahedral I53-50 assembly (an example micrograph obtained using the 100% valency particles is presented in FIG. 5). ELISA assays using monomclonal antibodies specific to the prefusion conformation confirmed that the DS-Cav1 thus displayed

on the nanostructure exteriors was well-folded and antigenically intact (FIG. 6). Surface plasmon resonance experiments evaluating the kinetics of monoclonal antibody binding revealed that antibody dissociation from the 100% valency DS-Cav1-foldon-I53-50 nanostructures was slower than from DS-Cav1-foldon trimers, likely due to avidity effects deriving from the multivalent presentation of DS-Cav1 on the nanostructure exterior (FIG. 6). Together, these experiments confirmed that the DS-Cav1-foldon-I53-50 nanostructures formed monodisperse, icosahedral nanostructures that display well-folded, antigenically intact DS-Cav1 trimers on their exteriors. These findings motivated experiments to evaluate the utility of the DS-Cav1-foldon-I53-50 nanostructures as immunogens for inducing humoral immune responses against DS-Cav1 in animals.

Immunogenicity of DS-Cav1-foldon-I53-50 nanostructures

[00147] The DS-Cav1-foldon-I53-50 nanostructures displaying DS-Cav1 at 33%, 66%, and 100% valency were injected into mice using a prime-boost strategy as described above. Additional groups of mice were injected with trimeric DS-Cav1-foldon as a benchmark for the humoral immune response induced against DS-Cav1 by the nanostructures or I53-50 nanostructures lacking displayed DS-Cav1 as negative controls for a DS-Cav1 specific response. ELISA assays of serum extracted from the mice at defined timepoints after the injections were used to measure DS-Cav1 specific antibody titers present in the sera of the injected animals (FIG. 7). As expected, sera from animals injected with the I53-50 nanostructures lacking displayed DS-Cav1 did not contain antibodies specific to DS-Cav1. Trimeric DS-Cav1-foldon induced DS-Cav1-specific antibodies, in accordance with previous results (McClellan et al.). The 33%, 66%, and 100% valency DS-Cav1 nanostructures all induced higher DS-Cav1-specific antibody titers than trimeric DS-Cav1-foldon, with the antibody titers increasing with increasing DS-Cav1 valency. DS-Cav1-specific titers were roughy 2.5-fold higher on average in mice injected with 100% valency DS-Cav1-foldon-I53-50 nanostructures compared to DS-Cav1. These results demonstrate that immunogens in which paramyxovirus F proteins are multivalently displayed on self-assembling protein nanostructures can induce higher humoral immune responses when injected into animals.

[00148] The sera from the mice injected with the series of immunogens described above was also evaluated for the presence of neutralizing antibody titers using the standard neutralization assay in HEp-2 cells (FIG. 8). The trend in serum neutralizing antibody titers correlated highly with the trend observed in DS-Cav1-specific binding antibody titers. Sera

from animals injected with the I53-50 nanostructures lacking displayed DS-Cav1 did not neutralize virus, consistent with the lack of DS-Cav1-specific antibodies in these sera. The sera from animals injected with trimeric DS-Cav-l-foldon neutralized virus with an average titer ($1/ID_{50}$) of 3,030. The 33%, 66%, and 100% valency DS-Cav1-I53-50 nanostructures induced higher neutralizing antibody titers than trimeric DS-Cav1-foldon, with average titers of 9,400, 20,000, and 30,500, respectively. These results demonstrate that the higher response induced by immunogens in which paramyxovirus F proteins are multivalently displayed on self-assembling protein nanostructures result in more effective virus neutralization.

Physical stabilization of DS-Cav1 by fusion to I53-50A

[00149] Given the key antigenic properties of prefusion F, we used two orthogonal approaches to measure the physical stability of DS-Cav1 when fused to I53-50A and/or when further assembled into the icosahedral nanostructure. The first assay measured the retention of binding by a prefusion-specific mAb (D25) after thermal stress, an approach that has been used previously to characterize prefusion F stability (McLellan et al. 2013; Joyce et al. 2016; Krarup et al. 2015). Samples of trimeric DS-Cav1, trimeric DS-Cav1–I53-50A, and DS-Cav1–I53-50 nanostructures containing equivalent concentrations (50 nM) of DS-Cav1 were split into four aliquots and incubated at 20, 50, 70 or 80 °C for 1 hour. After cooling to room temperature, D25 binding was assayed by surface plasmon resonance (SPR). We found that all samples bound D25 equivalently at 20 and 50 °C, but lost most of their reactivity to D25 after 1 hour at 80 °C as previously reported for DS-Cav1 (McLellan et al. 2013; Joyce et al. 2016) (FIG. 10). Interestingly, while D25 was also unable to bind trimeric DS-Cav1 incubated at 70 °C for 1 hour, trimeric DS-Cav1–I53-50A and the DS-Cav1–I53-50 nanostructures retained 50 and 80% of their respective binding signals (FIG. 10). While the multivalent nature of the DS-Cav1–I53-50 nanostructures complicates direct quantitative comparisons to trimeric DS-Cav1, these results indicate that genetic fusion to the I53-50A trimer further stabilizes the prefusion conformation of DS-Cav1, and suggest that this increased stability is maintained in the context of the assembled nanostructure immunogen.

[00150] We used chemical denaturation in guanidine hydrochloride (GdnHCl), monitored by intrinsic tryptophan fluorescence, as a second, antibody-independent technique to evaluate physical stability. Analyzing fluorescence emission from DS-Cav1 incubated in 0–6.5 M GdnHCl revealed that the protein undergoes two subtly distinct transitions, one between 0.25 and 2.25 M GdnHCl and another between 2.25 and 5.75 M (FIGs 11A-11J). In contrast, only

a single transition is apparent for trimeric DS-Cav1–I53-50A, occurring between 2.25 and 6.25 M GdnHCl (FIGs 11A-11J). It is unclear at present whether the transition at lower [GdnHCl] observed for DS-Cav1 is absent from trimeric DS-Cav1–I53-50A or simply shifted to higher [GdnHCl]. However, it is clear that the native conformation of DS-Cav1 is stabilized by genetic fusion to trimeric I53-50A, mirroring the results obtained by measuring D25 binding after thermal stress. Comparing the data for the DS-Cav1–I53-50 nanostructure and the I53-50 nanostructure alone (lacking fused DS-Cav1) indicated that the stabilization is maintained upon assembly to the icosahedral nanostructure (FIGs 11A-11J). The source of this effect is likely the extreme stability of the I53-50A trimer. I53-50A is derived from the KDPG aldolase of the hyperthermophilic bacterium *T. maritima* and only began to exhibit changes in fluorescence at very high (≥5.75 M) GdnHCl concentrations (FIGs 11A-11J).

[00151] We made addition constructs to assess the number of GS repeats and the need for a stabilization domain such as the Foldon moiety.

[00152] Sequence Information

IPD Name	MS (Da)	Construct Information
RSV_F-10	74005.38	DS-Cav1-8GS-HelExt-50A (SEQ ID NO: 108)
RSV_F-11	74293.64	DS-Cav1-12GS-HelExt-50A (SEQ ID NO: 109)
RSV_F-12	74551.87	DS-Cav1-16GS-HelExt-50A (SEQ ID NO: 110)
RSV_F-13	77212.97	DS-Cav1-foldon-10GS-HelExt-50A (SEQ ID NO: 111)
RSV_F-14	77558.28	DS-Cav1-foldon-15GS-HelExt-50A (SEQ ID NO: 112)
RSV_F-15	77933.62	DS-Cav1-foldon-20GS-HelExt-50A (SEQ ID NO: 113)

> RSV_F-10 (SEQ ID NO: 108)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRFLGFLLGVGSAIASGVAVCKVLHLEGEVNK
IKSALLSTNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQK
NNRLLEITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQ
SYSIMCIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWY
CDNAGSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSK
TDVSSSVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLY
YVNKQEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRGSGGSGSGE
KAAKAEEAARKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDA
DTVIKALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFY

MPGVMTPTELVKAMKLGHTILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGVNLD
NVCEWFKAGVLAVGVGSALVKGTPDEVREKAKAFVEKIRGCTE

> **RSV_F-11** (SEQ ID NO: 109)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRFLGFLLGVGSAIASGVAVCKVLHLEGEVNK
IKSALLSTNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQK
NNRLLEITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQ
SYSIMCIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWY
CDNAGSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSK
TDVSSSVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLY
YVNKQEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRGSGGSGSGS
GGSEKAAKAEEAARKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFT
VPDADTVIKALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEK
GVFYMPGVMTPTELVKAMKLGHTILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGG
VNLDNVCEWFKAGVLAVGVGSALVKGTPDEVREKAKAFVEKIRGCTE

> **RSV_F-12** (SEQ ID NO: 110)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRFLGFLLGVGSAIASGVAVCKVLHLEGEVNK
IKSALLSTNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQK
NNRLLEITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQ
SYSIMCIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWY
CDNAGSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSK
TDVSSSVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLY
YVNKQEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRGSGGSGSGS
GGSGSGGEKAAKAEEAARKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLI
EITFTVPDADTVIKALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQF
CKEKGVFYMPGVMTPTELVKAMKLGHTILKLFPGEVVGPQFVKAMKGPFPNVKFVP
TGGVNLDNVCEWFKAGVLAVGVGSALVKGTPDEVREKAKAFVEKIRGCTE

> **RSV_F-13** (SEQ ID NO: 111)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRFLGFLLGVGSAIASGVAVCKVLHLEGEVNK
IKSALLSTNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQK

NNRLLEITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQ
SYSIMCIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWY
CDNAGSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSK
TDVSSSVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLY
YVNKQEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRGSGGSGSGS
GEKAAKAEEAARKMEELFKKHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVP
DADTVIKALSVLKEKGAIIGAGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKG
VFYMPGVMTPTELVKAMKLGHTILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGV
NLDNVCEWFKAGVLAVGVGSALVKGTPDEVREKAKAFVEKIRGCTE

> **RSV_F-14** (SEQ ID NO: 112)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRFLGFLLGVGSAIASGVAVCKVLHLEGEVNK
IKSALLSTNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQK
NNRLLEITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQ
SYSIMCIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWY
CDNAGSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSK
TDVSSSVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLY
YVNKQEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRGYIPEAPRD
GQAYVRKDGEWVLLSTFLGSGGSGSGSGGSGSGEKAAKAEEAARKMEELFKKHKIV
AVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIKALSVLKEKGAIIGAGTVT
SVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMTPTELVKAMKLGHTIL
KLFPGEVVGPQFVKAMKGPFPNVKFVPTGGVNLDNVCEWFKAGVLAVGVGSALVK
GTPDEVREKAKAFVEKIRGCTE

> **RSV_F-15** (SEQ ID NO: 113)

QNITEEFYQSTCSAVSKGYLSALRTGWYTSVITIELSNIKENKCNGTDAKVKLIKQEL
DKYKNAVTELQLLMQSTPATNNRARRFLGFLLGVGSAIASGVAVCKVLHLEGEVNK
IKSALLSTNKAVVSLSNGVSVLTFKVLDLKNYIDKQLLPILNKQSCSISNIETVIEFQQK
NNRLLEITREFSVNAGVTTPVSTYMLTNSELLSLINDMPITNDQKKLMSNNVQIVRQQ
SYSIMCIIKEEVLAYVVQLPLYGVIDTPCWKLHTSPLCTTNTKEGSNICLTRTDRGWY
CDNAGSVSFFPQAETCKVQSNRVFCDTMNSLTLPSEVNLCNVDIFNPKYDCKIMTSK
TDVSSSVITSLGAIVSCYGKTKCTASNKNRGIIKTFSNGCDYVSNKGVDTVSVGNTLY
YVNKQEGKSLYVKGEPIINFYDPLVFPSDEFDASISQVNEKINQSLAFIRGYIPEAPRD

GQAYVRKDGEWVLLSTFLGSGGSGSGSGGSGSGGSSGSEKAAKAEEAARKMEELFK
KHKIVAVLRANSVEEAIEKAVAVFAGGVHLIEITFTVPDADTVIKALSVLKEKGAIIG
AGTVTSVEQCRKAVESGAEFIVSPHLDEEISQFCKEKGVFYMPGVMTPTELVKAMKL
GHTILKLFPGEVVGPQFVKAMKGPFPNVKFVPTGGVNLDNVCEWFKAGVLAVGVG
SALVKGTPDEVREKAKAFVEKIRGCTE

[00153] Studies were based on expression yield in a small-scale transient transfection. Plasmids capable of expressing the relevant constructs were transformed into NEB 5α *E. coli* cells and selected on LB + carbenicillin agar plates. 1 mL cultures were prepared by inoculating TB media with a bacterial colony and again selecting with 50 ug/mL carbenicillin. A Qiagen Mini Prep kit was used to purify plasmid from the *E. coli* cultures in accordance with their protocol. Expi293F™ Cells (ThermoFisher) were cultured in Expi293™ Expression Medium (ThermoFisher) supplemented with penicillin (100 u/mL) and streptomycin (100 µg/mL) at 8% CO_2, 37° C, and 125 rpm shaking.

[00154] On the day prior to transfection, cells were seeded at a concentration of 2E6 cells/mL. On the day of transfection, cells were counted by a Countess II (ThermoFisher) with trypan blue to determine cell viability. Cell concentration was adjusted to 2.5E6 cells/mL, and cells where plated into untreated 12-well plates (Corning) in 1 mL volumes. 1 µg of DNA plasmid were transfected per each well using Expifectamine™ (ThermoFisher), following the manufacturer's directions. Enhancers, components of ThermoFisher's Expifectamine™ Transfection Kit, were added 18 hours after transfection. The 1 mL cultures were harvested 5 days post-transfection, and the cells were pelleted from the supernatant by centrifugation at 1,500xg for 5 minutes at 4° C. Supernatants were filtered through a 0.45 µM filter with a PVDF membrane.

[00155] Filtered supernatants containing DS-Cav1–I53-50A constructs were denatured and boiled for 10 minutes at 95° C for 10 minutes in 2x Laemmli buffer with 2-mercaptoethanol. SDS-PAGE separated the sample fractions, which were then transferred to a nitrocellulose membrane and probed withpalivizumab, followed with a secondary antibody, anti-human conjugated to HRP. Blot was imaged using Clarity Western ECL Blotting Substrate (Bio-Rad).

[00156] Filtered supernatants containing DS-Cav1–I53-50A constructs were bound to Nunc MaxiSorp 96-well plates in a two-fold dilution series. The pre-fusion conformation-

specific antibody D25 was used to detect DS-Cav1–I53-50A, followed by a secondary anti-human antibody conjugated to HRP. Protein yield was determined colorimetrically via the substrate TMB and absorbances were collected at 450 nm.

[00157] The expression yields and binding of the prefusion-specific mAb D25 (data not shown) indicate that all constructs express well and are in the prefusion conformation. As is known to those of skill in the art, a heterologous trimerization domain (*e.g.*, the foldon) is typically required for proper expression and folding of prefusion F constructs. Our results indicate that the I53-50A nanostructure component can support the expression and proper folding of DS-Cav1 without the use of a trimerization domain like the foldon. Binding of D25 to these constructs suggests that they are antigenically intact and would be expected to induce potent immune responses, including neutralizing antibodies, similarly to nanostructures comprising the DS-Cav1-foldon–I53-50 fusion polypeptide.

9.2. Example 2: Cytomegalovirus (CMV)

[00158] Protein-based vaccines for CMV are described, for example, in U.S. Patent Pub. Nos. US 2016/0159864 A1 and US 2017/0369532 A1; International Patent Pub No. WO 2016/092460 A3; and Kirchmeier al. Enveloped virus-like particle expression of human cytomegalovirus glycoprotein B antigen induces antibodies with potent and broad neutralizing activity. Clin Vaccine Immunol. 2014; 21(2):174–80. The homotrimer complex of gB, the trimeric gH/gL/gO complex, or the pentameric gH/gL/pUL128/pUL130/pUL131A complex are considered the three major targets for CMV vaccination.

[00159] The first of these targets, gB, forms a trimeric structure which comprises several hydrophobic surfaces. The C terminus of the extracellular domain of gB is proximal to the transmembrane region and lies near the 3-fold axis of the molecule. *See* Chandramouli et al. Structure of HCMV glycoprotein B in the postfusion conformation bound to a neutralizing human antibody. Nat Commun. 2015 Sep 14;6:8176. By substitution of the transmembrane region of gB for a linker, the gB protein of CMV is N-terminally linked to a nanostructure having a free N terminus at or near the 3-fold axis of the nanostructure. The resulting nanostructure has displays 20 copies of the gB trimer on its surface and effectively elicits a immune response to CMV gB. Mutations to the gB protein as described in International Patent Pub No. WO 2016/092460 A3, improve the solubility and immunogenicity of the nanostructure-based vaccine.

[00160] The second of these targets, the trimeric gH/gL/gO complex, and the third of these targets, the pentameric gH/gL/pUL128/pUL130/pUL131A, form by mutually exclusive interactions of the envelope glycoproteins gH/gL with either gO or pUL128/pUL130/pUL131A. *See* Ciferri et al. Structural and biochemical studies of HCMV gH/gL/gO and Pentamer reveal mutually exclusive cell entry complexes. Proc. Natl. Acad. Sci. U.S.A. 112, 1767–1772 (2015). The gH component is targeted by antibodies neutralizing infection of both fibroblasts and endothelial/epithelial cells. The UL region contains the binding sites for potently neutralizing antibodies of epithelial and endothelial cells infection.

[00161] The gH component is expressed as a gene fusion to a nanostructure polypeptide and either gL/gO or gL/pUL128/pUL130/pUL131A are co-expressed. The expressed proteins self-assemble into either gH/gL/gO or gH/gL/pUL128/pUL130/pUL131A nanostructure-based vaccines, respectively. Expression and correct folding of the nanostructure is assessed by binding of the MSL-109 antibody of an Fab fragment thereof to the nanostructure. Correct folding and antigenicity of the pentameric complex is assessed using antibodies and Fab fragments described in Chandramouli et al. Structural basis for potent antibody-mediated neutralization of human cytomegalovirus Sci. Immunol. 2, eaan1457 (2017).

9.3. Example 3: Epstein-Barr Virus (EBV)

[00162] Epstein-Barr virus (EBV) represents a major global health problem. Though it is associated with infectious mononucleosis and ~200,000 cancers annually worldwide, a vaccine is not available. The major target of immunity is EBV glycoprotein 350/220 (gp350) that mediates attachment to B cells through complement receptor 2 (CR2/CD21). *See* Kanekiyo et al. Rational Design of an Epstein-Barr Virus Vaccine Targeting the Receptor-Binding Site. Cell 162(5):1090-1100 (2015). The gp350 ectodomain or the D_{123} fragment of gp350 is expressed as a gene fusion to a nanostructure polypeptides as either an N-terminal or C-terminal fusion. The resulting gene fusions are expressed, assembled, and formulated into nanostructure-based vaccines. Antigenicity is determined using the monoclonal antibodies 72A1 and 2L10.

What is claimed:

1. A nanostructure, comprising a first plurality of polypeptides, wherein:

the first plurality of polypeptides are arranged according to at least one symmetry operator;

the nanostructure comprises a first plurality of antigens;

each of the first plurality of the antigens has a proximal end and a distal end; and

the proximal ends of the antigens are each attached to a member of the first plurality of polypeptides.

2. The nanostructure of claim 1, further comprising a second plurality of polypeptides, wherein the second plurality of polypeptides is attached to the first plurality of polypeptides.

3. The nanostructure of claim 1, further comprising a second plurality of antigens.

4. The nanostructure of claim 1, further comprising a second plurality of antigens, wherein:

each of the second plurality of second antigens has a proximal end and a distal end, and

the proximal ends of the second antigens are each attached to a member of the second plurality of polypeptides

5. The nanostructure of claim 1, wherein the proximal ends of the antigens are the N termini of the antigens.

6. The nanostructure of claim 1, wherein the proximal ends of the antigens are the C termini of the antigens.

7. The nanostructure of claim 1, wherein the plurality of antigens is a plurality of antigenic proteins or antigenic fragments thereof.

8. The nanostructure of claim 7, wherein the antigenic protein is selected from a polypeptide of SEQ ID NOs: 52-56, 59-85,88 and 90-113 or a variant thereof.

9. The nanostructure of claim 7, wherein the antigenic protein is at least 75, 80, 85, 90, 95, or 99% identical to a polypeptide selected from SEQ ID NOs: 52-56, 59-85, 88 and 90-113.

10. The nanostructure of claim 7, wherein the antigenic protein is selected from the group consisting of:

a) HIV Env,
b) RSV F,
c) EBV gp350,
d) CMV gB,
e) CMV UL128,
f) CMV UL130,
g) CMV UL131A,
h) CMV gH,
i) CMV gL,
j) Lyme OspA,
k) Pertussis toxin,
l) Dengue E,
m) SARS S,
n) MERS S,
o) Zaire ebolavirus GP,
p) Sudan ebolavirus GP,
q) Marburg virus GP,
r) Hanta virus Gn,
s) Hanta virus Gc,
t) HepB surface antigen,
u) Measles H,
v) Zika envelope domain III,
w) Malaria CSP,
x) Malaria Pfs25,
y) Nipah virus F,
z) Nipah virus G,
aa) Rotavirus VP4,

bb) Rotavirus VP8*,

cc) hMPV F,

dd) hMPV G,

ee) PV F,

ff) PV HN,

gg) MenB fHbp,

hh) MenB NadA, and

ii) MenB NHBA.

11. The nanostructure of claim 1, wherein the first plurality of antigens comprises a target epitope, and the nanostructure is configured to display the target epitope.

12. The nanostructure of claim 11, wherein the target epitope is accessible to an antibody.

13. The nanostructure of claim 11, wherein the nanostructure is configured to elicit an immune response to the first plurality of antigenic proteins, said immune response being preferentially directed to the target epitope.

14. The nanostructure of claim 11, wherein the target epitope is conserved.

15. The nanostructure of claim 11, wherein the target epitope is an epitope for neutralizing antibodies.

16. The nanostructure of claim 11, wherein the target epitope is an epitope for cross-reactive antibodies.

17. The nanostructure of claim 11, wherein the target epitope is an epitope for a broadly-neutralizing antibody.

18. The nanostructure of claim 1, wherein the plurality of antigens comprises at least one mutation selected from the group consisting of an interface-stabilizing mutation, complementary cysteine mutations configured to result in a disulfide bond, deletion of a loop, addition of an N-linked glycosylation site, removal of an N-linked glycosylation site, an epitope-destroying mutation, and an epitope-creating mutation.

19. The nanostructure of claim 1, wherein the plurality of antigens comprises an antigenic oligosaccharide.

20. A vaccine comprising a nanostructure of any of claim 1-17, wherein the vaccine is capable of eliciting a neutralizing antibody response to an infectious agent.

21. The vaccine of claim 20, wherein the neutralizing antibody response is protective against infection by an infectious agent.

22. The vaccine of claim 20, wherein the neutralizing antibody response is broadly-neutralizing against diverse strains of an infectious agent.

23. The vaccine of claim 21 or 22, wherein the infectious agent is selected from the group consisting of lyme disease, pertussis, herpesvirus, paramyxovirus, pneumovirus, filovirus, flavivirus, reovirus, retrovirus, meningococcus, and malaria.

24. The vaccine of claim 21 or 22, wherein the infectious agent is a virus selected from the group consisting of

a) HIV,
b) RSV,
c) EBV,
d) CMV,
e) Dengue,
f) Severe Acute Respiratory Syndrome (SARS) virus,
g) Middle East Respiratory Syndrome (MERS) virus,
h) Ebola virus,
i) Marburg virus,
j) Hanta virus,
k) Hepatitis B,
l) HPV,
m) Measles,
n) Nipah virus,
o) Rotavirus,

p) Metapneumo virus, and

q) Zika.

25. The vaccine of claim 20, wherein the infectious agent is lyme disease or pertussis.

26. The vaccine of claim 20, wherein the infectious agent is malaria.

27. A method of generating immunity to an infectious agent in a subject, comprising administering a vaccine of any of claims 20-26.

28. The method of claim 27, further comprising administering an adjuvant.

29. The method of claim 27, further comprising administering the vaccine repeatedly.

30. The method of claim 27, further comprising administering a second vaccine and wherein the second vaccine is selected from the group consisting of a nanoparticle-based vaccine, a protein-based vaccine, a live vaccine, a live attenuated vaccine, a whole germ vaccine, a DNA vaccine, or a RNA vaccine.

31. The method of claim 30, wherein the first vaccine is a prime and the second vaccine is a boost.

32. The method of claim 30, wherein the second vaccine is a prime and the first vaccine is a boost.

33. The method of any of claims 27-32, wherein the method induces directed affinity maturation.

34. The method of any of claims 27-33, wherein the method results in a broadly-neutralizing immune response.

35. A pharmaceutical composition comprising a vaccine of any of claims 20-26.

36. A method of making the nanostructure of claim 1 by *in vitro* assembly, comprising:

expressing the first plurality of polypeptides in a first recombinant expression system,

expressing the first plurality of antigens in a second recombinant expression system,

purifying the first plurality of polypeptides,

purifying the first plurality of antigens, and

mixing the first plurality of polypeptides and the first plurality of antigens;

thereby generating the nanostructure.

37. A method of making the nanostructure of claim 2 by *in vitro* assembly, comprising:

expressing the first plurality of polypeptides in a first recombinant expression system,

expressing the first plurality of antigens in a second recombinant expression system,

expressing the second plurality of polypeptides in a third recombinant expression system,

purifying the first plurality of polypeptides,

purifying the first plurality of antigens,

purifying the second plurality of polypeptides, and

mixing the first plurality of polypeptides, the first plurality of antigens, and the second plurality of polypeptides;

thereby generating the nanostructure.

38. The method of claim 37, wherein:

the first recombinant expression system and the second recombinant expression system are the same, and

the first plurality of polypeptides and the first plurality of antigens are purified together.

39. A method of making the nanostructure of claim 1 by co-expression, comprising:

expressing the first plurality of polypeptides and the first plurality of antigens in a single recombinant expression system,

thereby generating the nanostructure, and

purifying the nanostructure.

40. A method of making the nanostructure of claim 2 by co-expression, comprising:

expressing the first plurality of polypeptides, the first plurality of antigens, and the second plurality of polypeptides in a single recombinant expression system,

thereby generating the nanostructure, and

purifying the nanostructure.

41. The method of claim 38-40, wherein the first plurality of polypeptides and the first plurality of antigens are encoded by a single open reading frame.

42. The method of making of claim 41, wherein the single open reading frame encodes a fusion protein of the polypeptide and the antigen.

43. The method of making of claim 42, wherein the single open reading frame encodes a self-cleaving peptide.

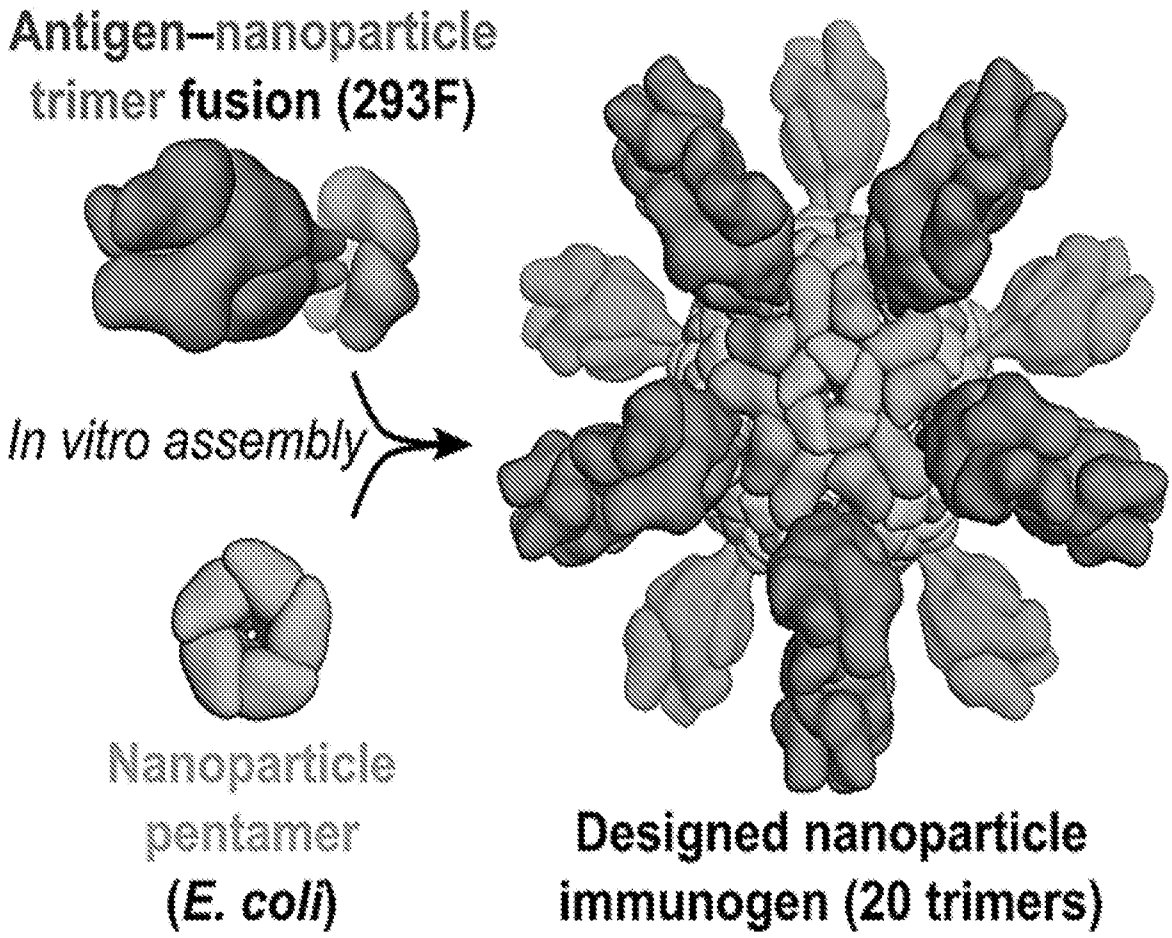

Antigen–nanoparticle
trimer fusion (293F)
In vitro assembly
Nanoparticle
pentamer
(E. coli)
Designed nanoparticle
immunogen (20 trimers)

FIG. 1A

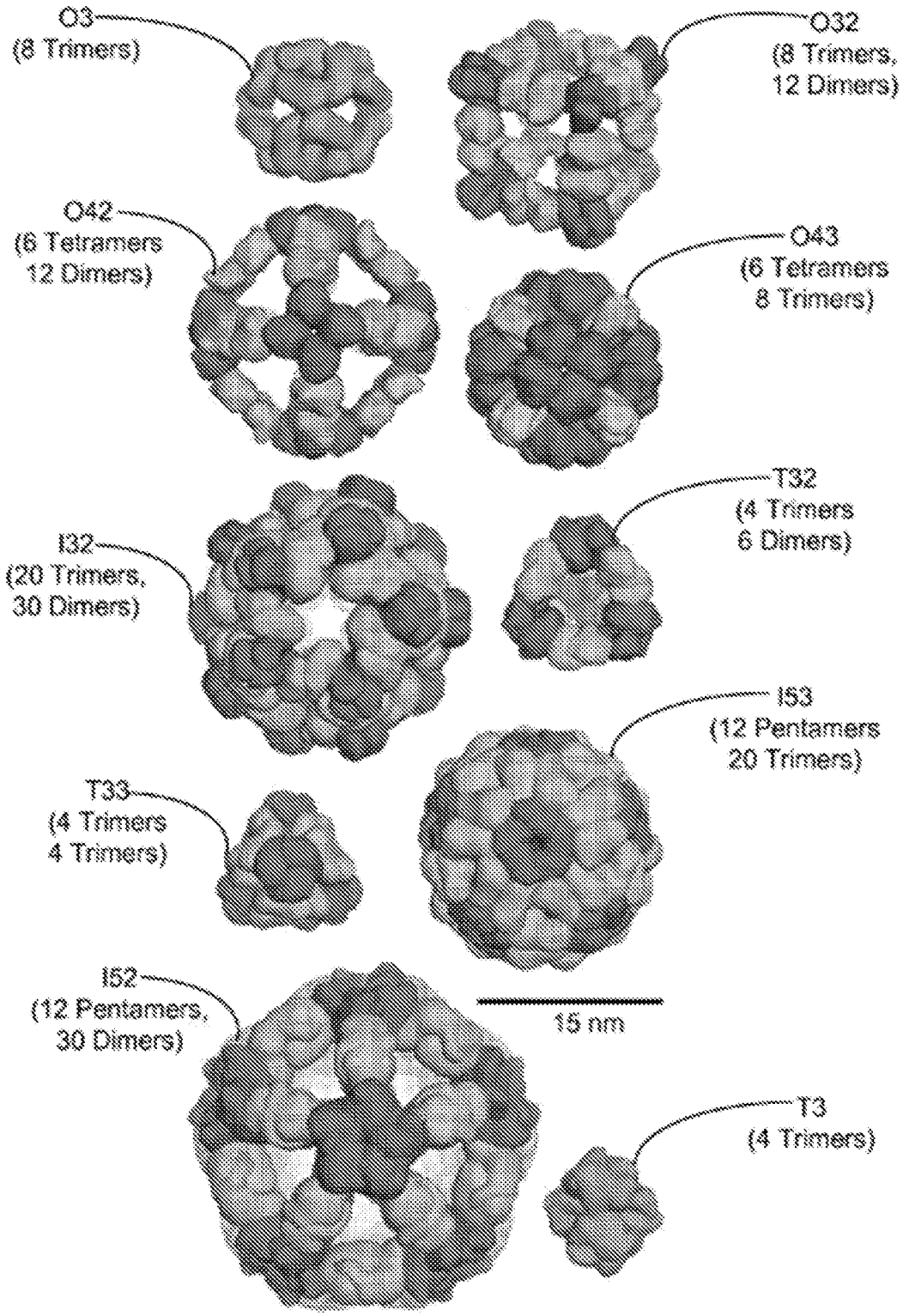
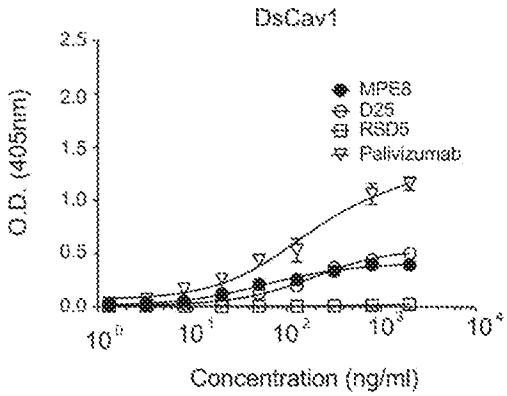

O3
(8 Trimers)
O32
(8 Trimers,
12 Dimers)
O42
(6 Tetramers
12 Dimers)
O43
(6 Tetramers
8 Trimers)
T32
(4 Trimers
6 Dimers)
I32
(20 Trimers,
30 Dimers)
I53
(12 Pentamers
20 Trimers)
T33
(4 Trimers
4 Trimers)
I52
(12 Pentamers,
30 Dimers)
15 nm
T3
(4 Trimers)

FIG. 1B

FIG. 2A



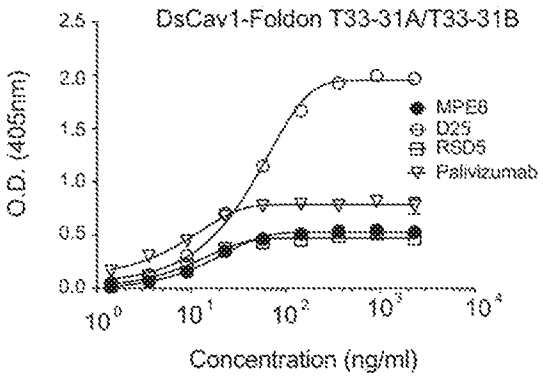


FIG. 2B

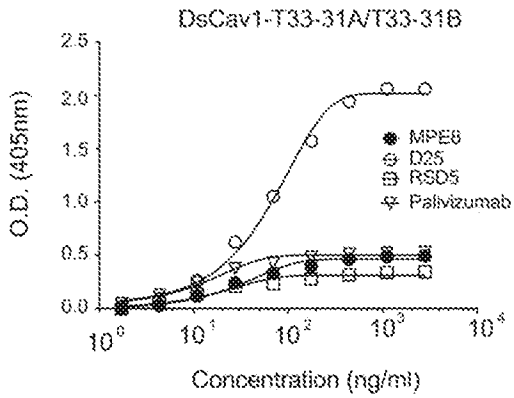


FIG. 2C

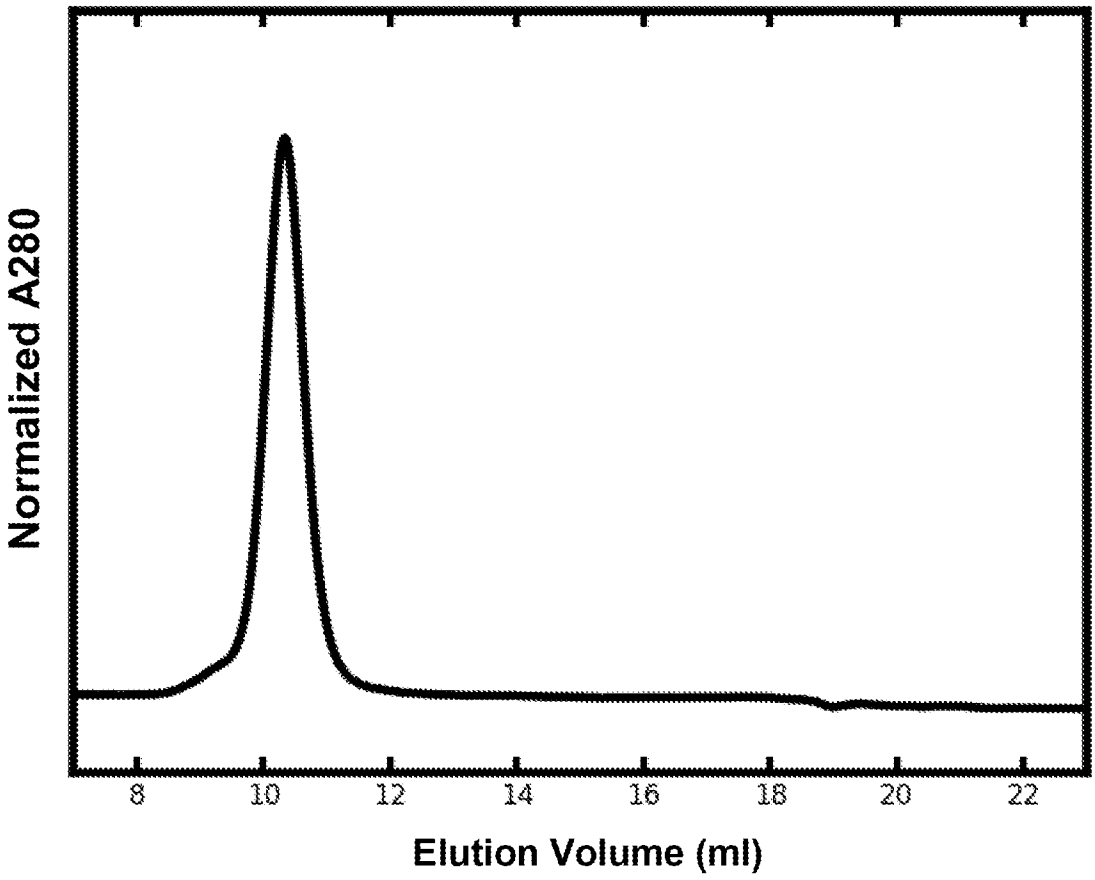


FIG. 3

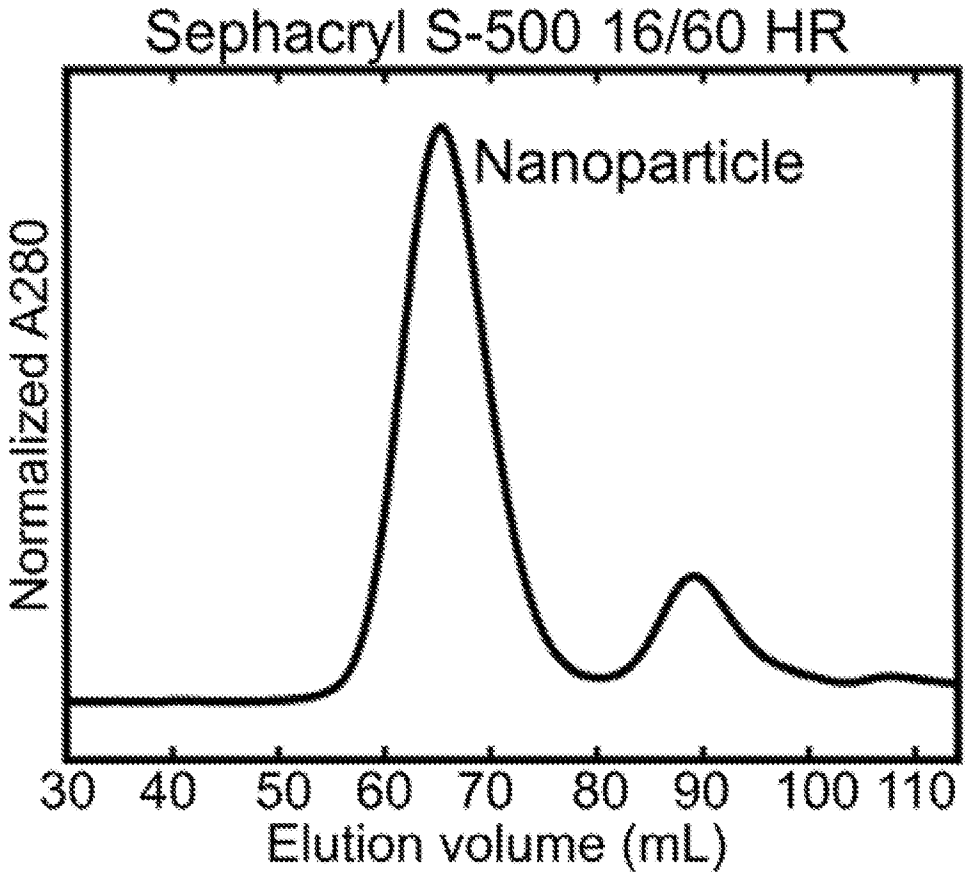

Sephacryl S-500 16/60 HR
Nanoparticle
Normalized A280
30 40 50 60 70 80 90 100 110
Elution volume (mL)

FIG. 4

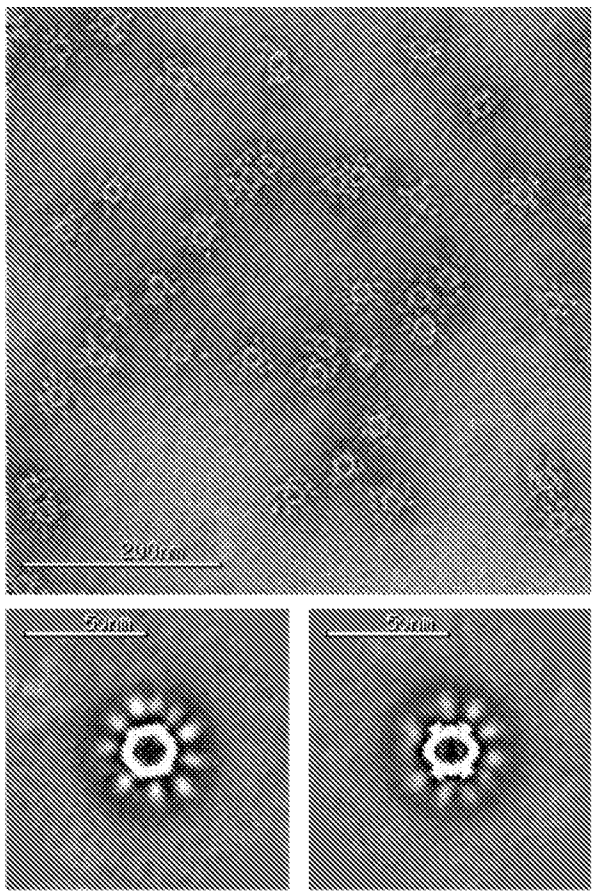


FIG. 5

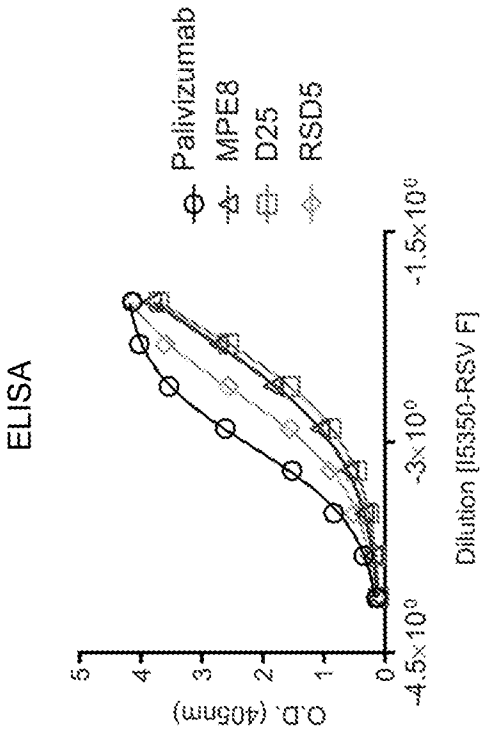


FIG. 6A

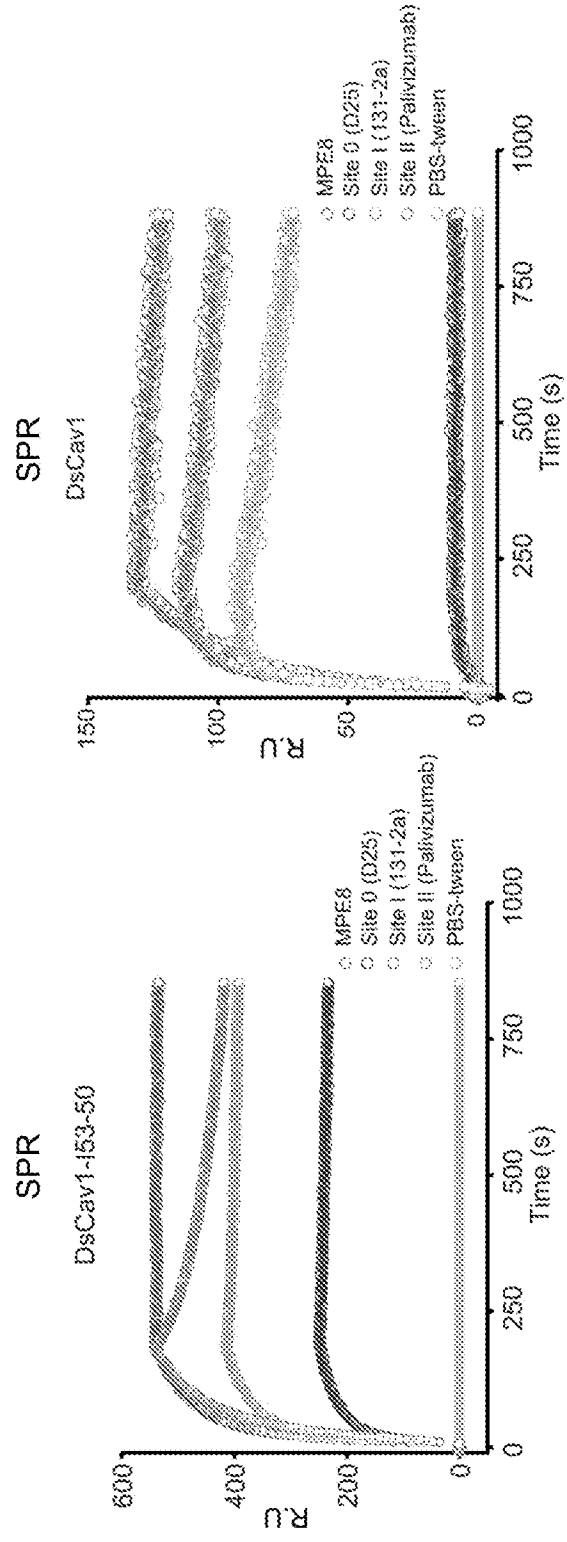


FIG. 6B

FIG. 6C

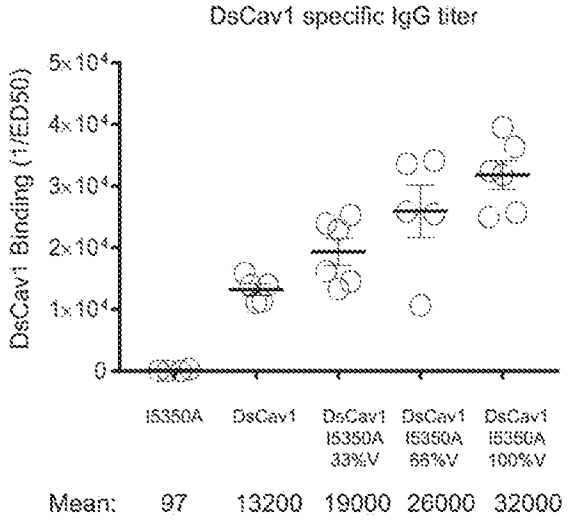

DsCav1 specific IgG titer
DsCav1 Binding (1/ED50)
5x10⁴
4x10⁴
3x10⁴
2x10⁴
1x10⁴
0
I5350A
DsCav1
DsCav1 I5350A 33%V
DsCav1 I5350A 66%V
DsCav1 I5350A 100%V
Mean: 97 13200 19000 26000 32000

FIG. 7

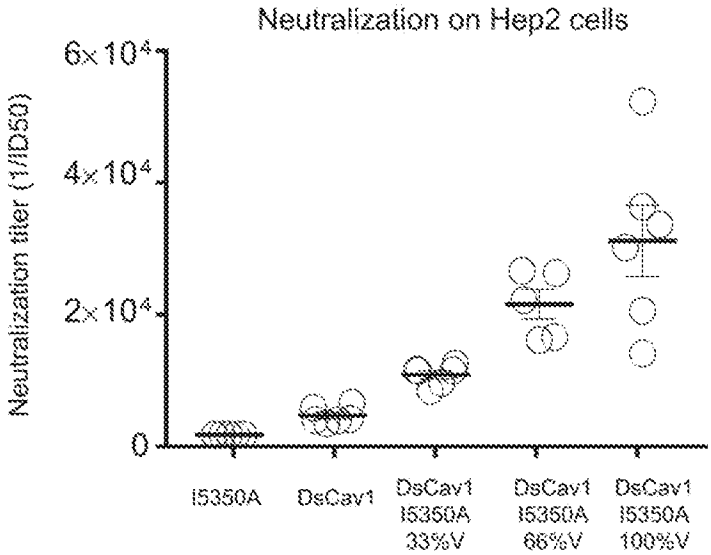

Neutralization on Hep2 cells
Neutralization titer (1/ID50)
6x10⁴
4x10⁴
2x10⁴
0
I5350A
DsCav1
DsCav1 I5350A 33%V
DsCav1 I5350A 66%V
DsCav1 I5350A 100%V

FIG. 8

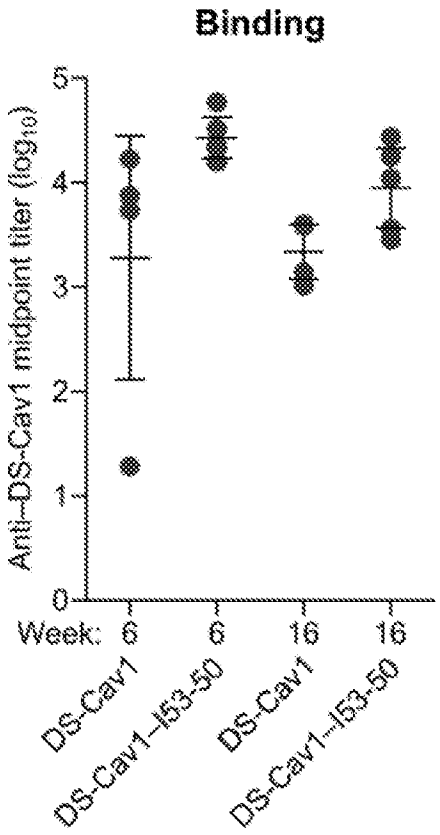

Binding
Anti–DS-Cav1 midpoint titer (log_{10})
0
1
2
3
4
5
Week: 6 6 16 16
DS-Cav1
DS-Cav1–I53-50
DS-Cav1
DS-Cav1–I53-50

FIG. 9A

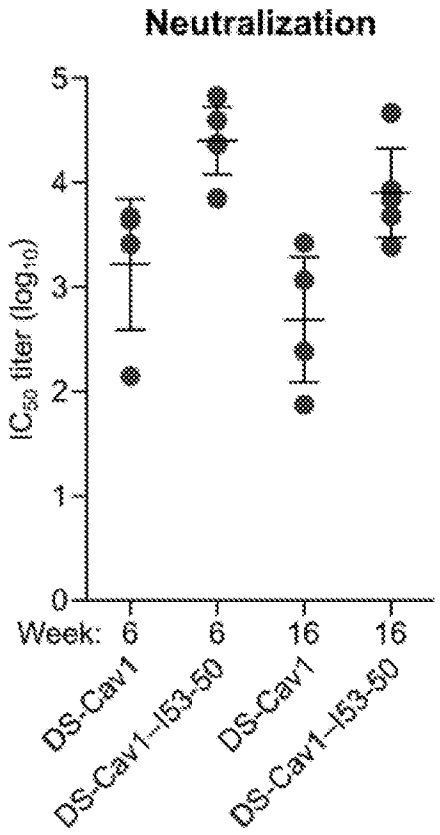

Neutralization
IC_{50} titer (log_{10})
0
1
2
3
4
5
Week: 6 6 16 16
DS-Cav1
DS-Cav1–I53-50
DS-Cav1
DS-Cav1–I53-50

FIG. 9B

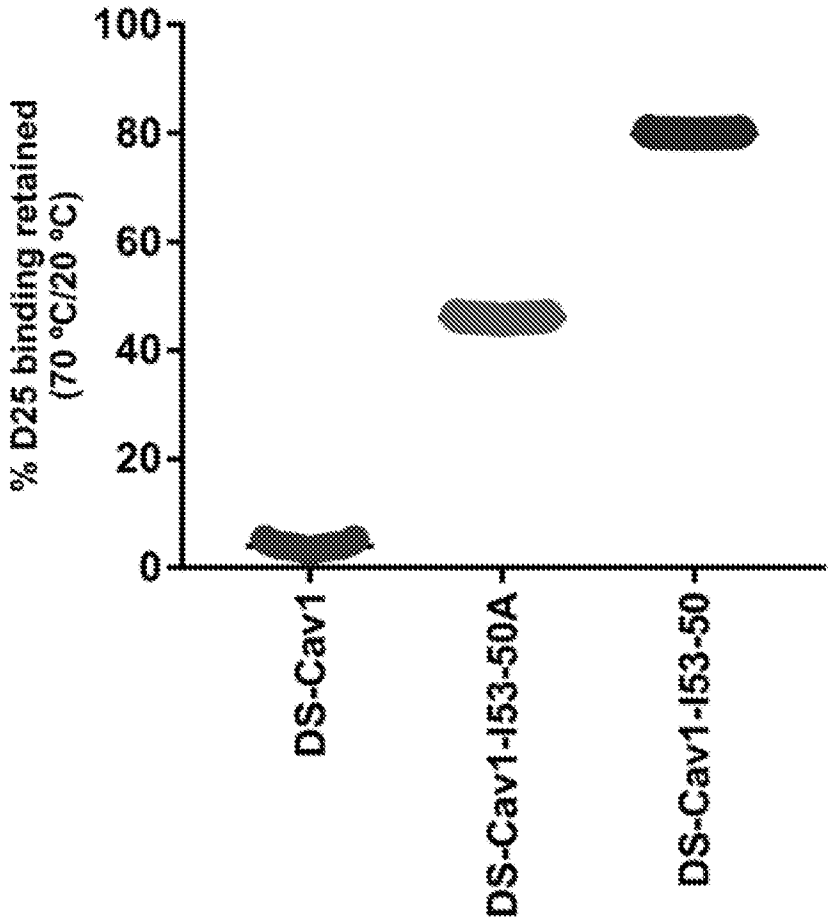

% D25 binding retained
(70 °C/20 °C)
100
80
60
40
20
0
DS-Cav1
DS-Cav1-I53-50A
DS-Cav1-I53-50

FIG. 10

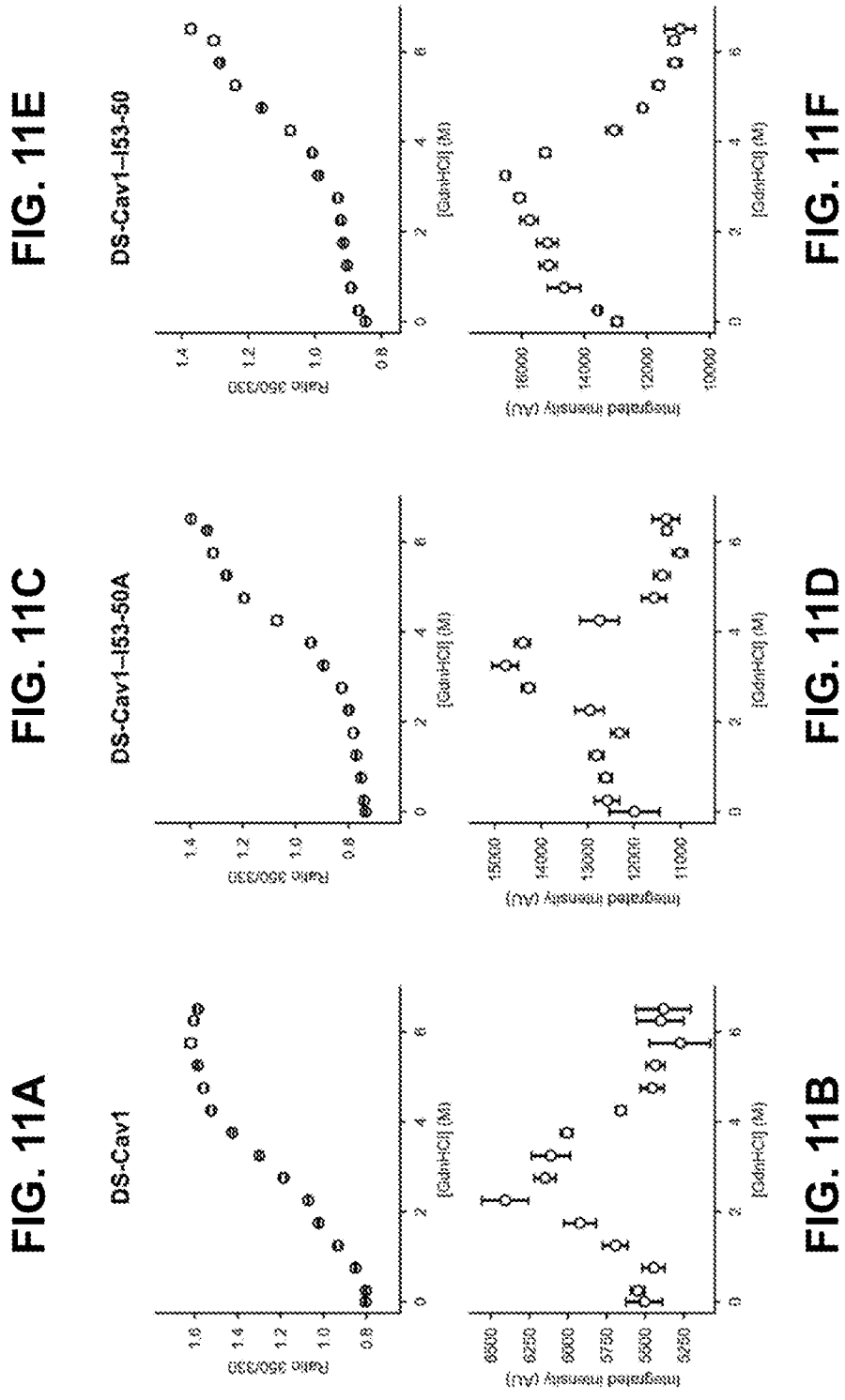


FIG. 11A FIG. 11B FIG. 11C FIG. 11D FIG. 11E FIG. 11F

FIG. 11I

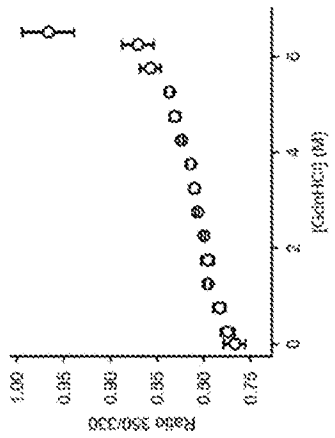


FIG. 11J

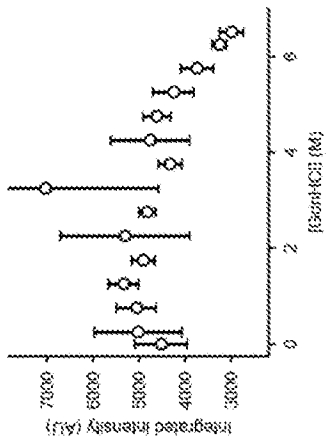


FIG. 11G

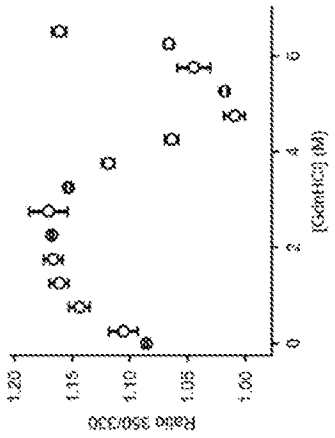
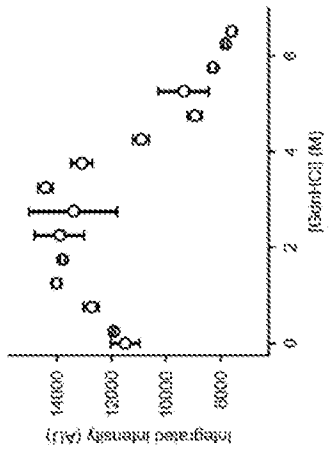


FIG. 11H



SEQUENCE LISTING

<110> University of Washington
King, Neil
Baker, David
Stewart, Lance

<120> SELF-ASSSEMBLING NANOSTRUCTURE VACCINES

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

Val Leu Glu Leu Met Gly Val Gly Ala Leu Glu Ile Thr Leu Arg Thr
35 40 45

Glu Lys Gly Leu Glu Ala Leu Lys Ala Leu Arg Lys Ser Gly Leu Leu
50 55 60

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

Glu Ala Gly Ala Ala Phe Leu Val Ser Pro Gly Leu Leu Glu Glu Val
85 90 95

Ala Ala Leu Ala Gln Ala Arg Gly Val Pro Tyr Leu Pro Gly Val Leu
100 105 110

Thr Pro Thr Glu Val Glu Arg Ala Leu Ala Leu Gly Leu Ser Ala Leu
115 120 125

Lys Phe Phe Pro Ala Glu Pro Phe Gln Gly Val Arg Val Leu Arg Ala
130 135 140

Tyr Ala Glu Val Phe Pro Glu Val Arg Phe Leu Pro Thr Gly Gly Ile
145 150 155 160

Lys Glu Glu His Leu Pro His Tyr Ala Ala Leu Pro Asn Leu Leu Ala
165 170 175

Val Gly Gly Ser Trp Leu Leu Gln Gly Asp Leu Ala Ala Val Met Lys
180 185 190

Lys Val Lys Ala Ala Lys Ala Leu Leu Ser Pro Gln Ala Pro Gly
195 200 205

<210> 2
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 2

Met Thr Lys Lys Val Gly Ile Val Asp Thr Thr Phe Ala Arg Val Asp
1 5 10 15

Met Ala Glu Ala Ala Ile Arg Thr Leu Lys Ala Leu Ser Pro Asn Ile
20 25 30

Lys Ile Ile Arg Lys Thr Val Pro Gly Ile Lys Asp Leu Pro Val Ala
35 40 45

Cys Lys Lys Leu Leu Glu Glu Glu Gly Cys Asp Ile Val Met Ala Leu
50 55 60

Gly Met Pro Gly Lys Ala Glu Lys Asp Lys Val Cys Ala His Glu Ala
65 70 75 80

Ser Leu Gly Leu Met Leu Ala Gln Leu Met Thr Asn Lys His Ile Ile
85 90 95

Glu Val Phe Val His Glu Asp Glu Ala Lys Asp Asp Asp Glu Leu Asp
100 105 110

Ile Leu Ala Leu Val Arg Ala Ile Glu His Ala Ala Asn Val Tyr Tyr
115 120 125

Leu Leu Phe Lys Pro Glu Tyr Leu Thr Arg Met Ala Gly Lys Gly Leu
130 135 140

Arg Gln Gly Arg Glu Asp Ala Gly Pro Ala Arg Glu
145 150 155

<210> 3
<211> 156

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 3

Met Thr Lys Lys Val Gly Ile Val Asp Thr Thr Phe Ala Arg Val Asp
1 5 10 15

Met Ala Ser Ala Ala Ile Leu Thr Leu Lys Met Glu Ser Pro Asn Ile
20 25 30

Lys Ile Ile Arg Lys Thr Val Pro Gly Ile Lys Asp Leu Pro Val Ala
35 40 45

Cys Lys Lys Leu Leu Glu Glu Glu Gly Cys Asp Ile Val Met Ala Leu
50 55 60

Gly Met Pro Gly Lys Ala Glu Lys Asp Lys Val Cys Ala His Glu Ala
65 70 75 80

Ser Leu Gly Leu Met Leu Ala Gln Leu Met Thr Asn Lys His Ile Ile
85 90 95

Glu Val Phe Val His Glu Asp Glu Ala Lys Asp Asp Ala Glu Leu Lys
100 105 110

Ile Leu Ala Ala Arg Arg Ala Ile Glu His Ala Leu Asn Val Tyr Tyr
115 120 125

Leu Leu Phe Lys Pro Glu Tyr Leu Thr Arg Met Ala Gly Lys Gly Leu
130 135 140

Arg Gln Gly Phe Glu Asp Ala Gly Pro Ala Arg Glu

145 150 155

<210> 4
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 4

Met Ser Thr Ile Asn Asn Gln Leu Lys Ala Leu Lys Val Ile Pro Val
1 5 10 15

Ile Ala Ile Asp Asn Ala Glu Asp Ile Ile Pro Leu Gly Lys Val Leu
20 25 30

Ala Glu Asn Gly Leu Pro Ala Ala Glu Ile Thr Phe Arg Ser Ser Ala
35 40 45

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

Ile Gly Ala Gly Thr Ile Leu Asn Gly Val Gln Ala Leu Ala Ala Lys
65 70 75 80

Glu Ala Gly Ala Thr Phe Val Val Ser Pro Gly Phe Asn Pro Asn Thr
85 90 95

Val Arg Ala Cys Gln Ile Ile Gly Ile Asp Ile Val Pro Gly Val Asn
100 105 110

Asn Pro Ser Thr Val Glu Ala Ala Leu Glu Met Gly Leu Thr Thr Leu
115 120 125

Lys Phe Phe Pro Ala Glu Ala Ser Gly Gly Ile Ser Met Val Lys Ser
130 135 140

Leu Val Gly Pro Tyr Gly Asp Ile Arg Leu Met Pro Thr Gly Gly Ile
145 150 155 160

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

Cys Gly Gly Thr Trp Met Val Asp Lys Lys Leu Val Thr Asn Gly Glu
180 185 190

Trp Asp Glu Ile Ala Arg Leu Thr Arg Glu Ile Val Glu Gln Val Asn
195 200 205

Pro

<210> 5
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 5

Met Pro Ile Phe Thr Leu Asn Thr Asn Ile Lys Ala Thr Asp Val Pro
1 5 10 15

Ser Asp Phe Leu Ser Leu Thr Ser Arg Leu Val Gly Leu Ile Leu Ser
20 25 30

Lys Pro Gly Ser Tyr Val Ala Val His Ile Asn Thr Asp Gln Gln Leu
35 40 45

Ser Phe Gly Gly Ser Thr Asn Pro Ala Ala Phe Gly Thr Leu Met Ser
50 55 60

Ile Gly Gly Ile Glu Pro Ser Lys Asn Arg Asp His Ser Ala Val Leu
65 70 75 80

Phe Asp His Leu Asn Ala Met Leu Gly Ile Pro Lys Asn Arg Met Tyr
85 90 95

Ile His Phe Val Asn Leu Asn Gly Asp Asp Val Gly Trp Asn Gly Thr
100 105 110

Thr Phe

<210> 6
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 6

Met Asn Gln His Ser His Lys Asp Tyr Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Ala Cys Val Glu Ala
20 25 30

Phe Glu Ile Ala Met Ala Ala Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Ser Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Arg Tyr Arg Asp Ser Ala Glu His His Arg
115 120 125

Phe Phe Ala Ala His Phe Ala Val Lys Gly Val Glu Ala Ala Arg Ala
130 135 140

Cys Ile Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 7
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 7

Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1 5 10 15

Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
20 25 30

Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala

35 40 45

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

Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65 70 75 80

Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
85 90 95

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
100 105 110

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu
115 120 125

Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met
130 135 140

Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn
145 150 155 160

Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly
165 170 175

Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys
180 185 190

Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
195 200 205

<210> 8
<211> 157

<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 8

Met Asn Gln His Ser His Lys Asp Tyr Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
20 25 30

Phe Glu Ala Ala Met Ala Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Ser Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Arg Tyr Arg Asp Ser Asp Ala His Thr Leu
115 120 125

Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
130 135 140

Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala

145 150 155

<210> 9
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 9

Met Phe Thr Lys Ser Gly Asp Asp Gly Asn Thr Asn Val Ile Asn Lys
1 5 10 15

Arg Val Gly Lys Asp Ser Pro Leu Val Asn Phe Leu Gly Asp Leu Asp
20 25 30

Glu Leu Asn Ser Phe Ile Gly Phe Ala Ile Ser Lys Ile Pro Trp Glu
35 40 45

Asp Met Lys Lys Asp Leu Glu Arg Val Gln Val Glu Leu Phe Glu Ile
50 55 60

Gly Glu Asp Leu Ser Thr Gln Ser Ser Lys Lys Lys Ile Asp Glu Ser
65 70 75 80

Tyr Val Leu Trp Leu Leu Ala Ala Thr Ala Ile Tyr Arg Ile Glu Ser
85 90 95

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

Val Leu His Val Thr Arg Ser Val Ala Arg Arg Val Glu Arg Asn Ala
115 120 125

Val Lys Tyr Thr Lys Glu Leu Pro Glu Ile Asn Arg Met Ile Ile Val
130 135 140

Tyr Leu Asn Arg Leu Ser Ser Leu Leu Phe Ala Met Ala Leu Val Ala
145 150 155 160

Asn Lys Arg Arg Asn Gln Ser Glu Lys Ile Tyr Glu Ile Gly Lys Ser
165 170 175

Trp

<210> 10
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 10

Met Asn Gln His Ser His Lys Asp Tyr Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Gln Cys Val Arg Ala
20 25 30

Phe Glu Glu Ala Met Ala Asp Ala Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Ser Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Arg Tyr Arg Ser Ser Arg Glu His His Glu
115 120 125

Phe Phe Arg Glu His Phe Met Val Lys Gly Val Glu Ala Ala Ala Ala
130 135 140

Cys Ile Thr Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 11
<211> 201
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 11

Met Gly His Thr Lys Gly Pro Thr Pro Gln Gln His Asp Gly Ser Ala
1 5 10 15

Leu Arg Ile Gly Ile Val His Ala Arg Trp Asn Lys Thr Ile Ile Met
20 25 30

Pro Leu Leu Ile Gly Thr Ile Ala Lys Leu Leu Glu Cys Gly Val Lys
35 40 45

Ala Ser Asn Ile Val Val Gln Ser Val Pro Gly Ser Trp Glu Leu Pro
50 55 60

Ile Ala Val Gln Arg Leu Tyr Ser Ala Ser Gln Leu Gln Thr Pro Ser
65 70 75 80

Ser Gly Pro Ser Leu Ser Ala Gly Asp Leu Leu Gly Ser Ser Thr Thr
85 90 95

Asp Leu Thr Ala Leu Pro Thr Thr Thr Ala Ser Ser Thr Gly Pro Phe
100 105 110

Asp Ala Leu Ile Ala Ile Gly Val Leu Ile Lys Gly Glu Thr Met His
115 120 125

Phe Glu Tyr Ile Ala Asp Ser Val Ser His Gly Leu Met Arg Val Gln
130 135 140

Leu Asp Thr Gly Val Pro Val Ile Phe Gly Val Leu Thr Val Leu Thr
145 150 155 160

Asp Asp Gln Ala Lys Ala Arg Ala Gly Val Ile Glu Gly Ser His Asn
165 170 175

His Gly Glu Asp Trp Gly Leu Ala Ala Val Glu Met Gly Val Arg Arg
180 185 190

Arg Asp Trp Ala Ala Gly Lys Thr Glu
195 200

<210> 12
<211> 237
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 12

Met Tyr Glu Val Asp His Ala Asp Val Tyr Asp Leu Phe Tyr Leu Gly
1 5 10 15

Arg Gly Lys Asp Tyr Ala Ala Glu Ala Ser Asp Ile Ala Asp Leu Val
20 25 30

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

Thr Gly Thr His Leu Glu His Phe Thr Lys Glu Phe Gly Asp Thr Ala
50 55 60

Gly Leu Glu Leu Ser Glu Asp Met Leu Thr His Ala Arg Lys Arg Leu
65 70 75 80

Pro Asp Ala Thr Leu His Gln Gly Asp Met Arg Asp Phe Gln Leu Gly
85 90 95

Arg Lys Phe Ser Ala Val Val Ser Met Phe Ser Ser Val Gly Tyr Leu
100 105 110

Lys Thr Val Ala Glu Leu Gly Ala Ala Val Ala Ser Phe Ala Glu His
115 120 125

Leu Glu Pro Gly Gly Val Val Val Val Glu Pro Trp Trp Phe Pro Glu
130 135 140

Thr Phe Ala Asp Gly Trp Val Ser Ala Asp Val Val Arg Arg Asp Gly
145 150 155 160

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

Arg Met Glu Val His Phe Thr Val Ala Asp Pro Gly Lys Gly Val Arg
180 185 190

His Phe Ser Asp Val His Leu Ile Thr Leu Phe His Gln Arg Glu Tyr
195 200 205

Glu Ala Ala Phe Met Ala Ala Gly Leu Arg Val Glu Tyr Leu Glu Gly
210 215 220

Gly Pro Ser Gly Arg Gly Leu Phe Val Gly Val Pro Ala
225 230 235

<210> 13
<211> 138
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 13

Met Gly Met Lys Glu Lys Phe Val Leu Ile Ile Thr His Gly Asp Phe
1 5 10 15

Gly Lys Gly Leu Leu Ser Gly Ala Glu Val Ile Ile Gly Lys Gln Glu
20 25 30

Asn Val His Thr Val Gly Leu Asn Leu Gly Asp Asn Ile Glu Lys Val
35 40 45

Ala Lys Glu Val Met Arg Ile Ile Ile Ala Lys Leu Ala Glu Asp Lys
50 55 60

Glu Ile Ile Ile Val Val Asp Leu Phe Gly Gly Ser Pro Phe Asn Ile

65 70 75 80

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

Asn Met Pro Met Leu Val Glu Leu Leu Thr Ser Ile Asn Val Tyr Asp
100 105 110

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

Lys Val Ile Glu Lys Ser Ser Leu Lys Met
130 135

<210> 14
<211> 154
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 14

Met Lys Tyr Asp Gly Ser Lys Leu Arg Ile Gly Ile Leu His Ala Arg
1 5 10 15

Trp Asn Leu Glu Ile Ile Ala Ala Leu Val Ala Gly Ala Ile Lys Arg
20 25 30

Leu Gln Glu Phe Gly Val Lys Ala Glu Asn Ile Ile Ile Glu Thr Val
35 40 45

Pro Gly Ser Phe Glu Leu Pro Tyr Gly Ser Lys Leu Phe Val Glu Lys
50 55 60

Gln Lys Arg Leu Gly Lys Pro Leu Asp Ala Ile Ile Pro Ile Gly Val
65 70 75 80

Leu Ile Lys Gly Ser Thr Met His Phe Glu Tyr Ile Cys Asp Ser Thr
85 90 95

Thr His Gln Leu Met Lys Leu Asn Phe Glu Leu Gly Ile Pro Val Ile
100 105 110

Phe Gly Val Leu Thr Cys Leu Thr Asp Glu Gln Ala Glu Ala Arg Ala
115 120 125

Gly Leu Ile Glu Gly Lys Met His Asn His Gly Glu Asp Trp Gly Ala
130 135 140

Ala Ala Val Glu Met Ala Thr Lys Phe Asn
145 150

<210> 15
<211> 164
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 15

Met Ala Val Lys Gly Leu Gly Glu Val Asp Gln Lys Tyr Asp Gly Ser
1 5 10 15

Lys Leu Arg Ile Gly Ile Leu His Ala Arg Trp Asn Arg Lys Ile Ile
20 25 30

Leu Ala Leu Val Ala Gly Ala Val Leu Arg Leu Leu Glu Phe Gly Val
35 40 45

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

Pro Tyr Gly Ser Lys Leu Phe Val Glu Lys Gln Lys Arg Leu Gly Lys
65 70 75 80

Pro Leu Asp Ala Ile Ile Pro Ile Gly Val Leu Ile Lys Gly Ser Thr
85 90 95

Met His Phe Glu Tyr Ile Cys Asp Ser Thr Thr His Gln Leu Met Lys
100 105 110

Leu Asn Phe Glu Leu Gly Ile Pro Val Ile Phe Gly Val Leu Thr Cys
115 120 125

Leu Thr Asp Glu Gln Ala Glu Ala Arg Ala Gly Leu Ile Glu Gly Lys
130 135 140

Met His Asn His Gly Glu Asp Trp Gly Ala Ala Ala Val Glu Met Ala
145 150 155 160

Thr Lys Phe Asn

<210> 16
<211> 175
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 16

Met Gly Ala Asn Trp Tyr Leu Asp Asn Glu Ser Ser Arg Leu Ser Phe
1 5 10 15

Thr Ser Thr Lys Asn Ala Asp Ile Ala Glu Val His Arg Phe Leu Val
20 25 30

Leu His Gly Lys Val Asp Pro Lys Gly Leu Ala Glu Val Glu Val Glu
35 40 45

Thr Glu Ser Ile Ser Thr Gly Ile Pro Leu Arg Asp Met Leu Leu Arg
50 55 60

Val Leu Val Phe Gln Val Ser Lys Phe Pro Val Ala Gln Ile Asn Ala
65 70 75 80

Gln Leu Asp Met Arg Pro Ile Asn Asn Leu Ala Pro Gly Ala Gln Leu
85 90 95

Glu Leu Arg Leu Pro Leu Thr Val Ser Leu Arg Gly Lys Ser His Ser
100 105 110

Tyr Asn Ala Glu Leu Leu Ala Thr Arg Leu Asp Glu Arg Arg Phe Gln
115 120 125

Val Val Thr Leu Glu Pro Leu Val Ile His Ala Gln Asp Phe Asp Met
130 135 140

Val Arg Ala Phe Asn Ala Leu Arg Leu Val Ala Gly Leu Ser Ala Val
145 150 155 160

Ser Leu Ser Val Pro Val Gly Ala Val Leu Ile Phe Thr Ala Arg
165 170 175

<210> 17
<211> 208
<212> PRT

<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 17

Met Thr Asp Tyr Ile Arg Asp Gly Ser Ala Ile Lys Ala Leu Ser Phe
1 5 10 15

Ala Ile Ile Leu Ala Glu Ala Asp Leu Arg His Ile Pro Gln Asp Leu
20 25 30

Gln Arg Leu Ala Val Arg Val Ile His Ala Cys Gly Met Val Asp Val
35 40 45

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

Ala Leu Leu Ala Gly Ala Pro Ile Leu Cys Asp Ala Arg Met Val Ala
65 70 75 80

Glu Gly Ile Thr Arg Ser Arg Leu Pro Ala Asp Asn Arg Val Ile Tyr
85 90 95

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

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

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

Glu Leu Leu Asp Ala Gly Ala Pro Lys Pro Ala Leu Ile Ile Gly Met
145 150 155 160

Pro Val Gly Phe Val Gly Ala Ala Glu Ser Lys Asp Glu Leu Ala Ala
165 170 175

Asn Ser Arg Gly Val Pro Tyr Val Ile Val Arg Gly Arg Arg Gly Gly
180 185 190

Ser Ala Met Thr Ala Ala Ala Val Asn Ala Leu Ala Ser Glu Arg Glu
195 200 205

<210> 18
<211> 128
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 18

Met Ile Thr Val Phe Gly Leu Lys Ser Lys Leu Ala Pro Arg Arg Glu
1 5 10 15

Lys Leu Ala Glu Val Ile Tyr Ser Ser Leu His Leu Gly Leu Asp Ile
20 25 30

Pro Lys Gly Lys His Ala Ile Arg Phe Leu Cys Leu Glu Lys Glu Asp
35 40 45

Phe Tyr Tyr Pro Phe Asp Arg Ser Asp Asp Tyr Thr Val Ile Glu Ile
50 55 60

Asn Leu Met Ala Gly Arg Ser Glu Glu Thr Lys Met Leu Leu Ile Phe
65 70 75 80

Leu Leu Phe Ile Ala Leu Glu Arg Lys Leu Gly Ile Arg Ala His Asp

85 90 95

Val Glu Ile Thr Ile Lys Glu Gln Pro Ala His Cys Trp Gly Phe Arg
100 105 110

Gly Arg Thr Gly Asp Ser Ala Arg Asp Leu Asp Tyr Asp Ile Tyr Val
115 120 125

<210> 19
<211> 235
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 19

Met Gly Ser Asp Leu Gln Lys Leu Gln Arg Phe Ser Thr Cys Asp Ile
1 5 10 15

Ser Asp Gly Leu Leu Asn Val Tyr Asn Ile Pro Thr Gly Gly Tyr Phe
20 25 30

Pro Asn Leu Thr Ala Ile Ser Pro Pro Gln Asn Ser Ser Ile Val Gly
35 40 45

Thr Ala Tyr Thr Val Leu Phe Ala Pro Ile Asp Asp Pro Arg Pro Ala
50 55 60

Val Asn Tyr Ile Asp Ser Val Pro Pro Asn Ser Ile Leu Val Leu Ala
65 70 75 80

Leu Glu Pro His Leu Gln Ser Gln Phe His Pro Phe Ile Lys Ile Thr
85 90 95

Gln Ala Met Tyr Gly Gly Leu Met Ser Thr Arg Ala Gln Tyr Leu Lys
100 105 110

Ser Asn Gly Thr Val Val Phe Gly Arg Ile Arg Asp Val Asp Glu His
115 120 125

Arg Thr Leu Asn His Pro Val Phe Ala Tyr Gly Val Gly Ser Cys Ala
130 135 140

Pro Lys Ala Val Val Lys Ala Val Gly Thr Asn Val Gln Leu Lys Ile
145 150 155 160

Leu Thr Ser Asp Gly Val Thr Gln Thr Ile Cys Pro Gly Asp Tyr Ile
165 170 175

Ala Gly Asp Asn Asn Gly Ile Val Arg Ile Pro Val Gln Glu Thr Asp
180 185 190

Ile Ser Lys Leu Val Thr Tyr Ile Glu Lys Ser Ile Glu Val Asp Arg
195 200 205

Leu Val Ser Glu Ala Ile Lys Asn Gly Leu Pro Ala Lys Ala Ala Gln
210 215 220

Thr Ala Arg Arg Met Val Leu Lys Asp Tyr Ile
225 230 235

<210> 20
<211> 162
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 20

Met Ser Gly Met Arg Val Tyr Leu Gly Ala Asp His Ala Gly Tyr Glu
1 5 10 15

Leu Lys Gln Ala Ile Ile Ala Phe Leu Lys Met Thr Gly His Glu Pro
20 25 30

Ile Asp Cys Gly Ala Leu Arg Tyr Asp Ala Asp Asp Asp Tyr Pro Ala
35 40 45

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

Gly Ile Val Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn
65 70 75 80

Lys Val Pro Gly Ala Arg Cys Ala Leu Ala Trp Ser Val Gln Thr Ala
85 90 95

Ala Leu Ala Arg Glu His Asn Asn Ala Gln Leu Ile Gly Ile Gly Gly
100 105 110

Arg Met His Thr Leu Glu Glu Ala Leu Arg Ile Val Lys Ala Phe Val
115 120 125

Thr Thr Pro Trp Ser Lys Ala Gln Arg His Gln Arg Arg Ile Asp Ile
130 135 140

Leu Ala Glu Tyr Glu Arg Thr His Glu Ala Pro Pro Val Pro Gly Ala
145 150 155 160

Pro Ala

<210> 21
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 21

Met Gly Asp Asp Ala Arg Ile Ala Ala Ile Gly Asp Val Asp Glu Leu
1 5 10 15

Asn Ser Gln Ile Gly Val Leu Leu Ala Glu Pro Leu Pro Asp Asp Val
20 25 30

Arg Ala Ala Leu Ser Ala Ile Gln His Asp Leu Phe Asp Leu Gly Gly
35 40 45

Glu Leu Cys Ile Pro Gly His Ala Ala Ile Thr Glu Asp His Leu Leu
50 55 60

Arg Leu Ala Leu Trp Leu Val His Tyr Asn Gly Gln Leu Pro Pro Leu
65 70 75 80

Glu Glu Phe Ile Leu Pro Gly Gly Ala Arg Gly Ala Ala Leu Ala His
85 90 95

Val Cys Arg Thr Val Cys Arg Arg Ala Glu Arg Ser Ile Lys Ala Leu
100 105 110

Gly Ala Ser Glu Pro Leu Asn Ile Ala Pro Ala Ala Tyr Val Asn Leu
115 120 125

Leu Ser Asp Leu Leu Phe Val Leu Ala Arg Val Leu Asn Arg Ala Ala
130 135 140

Gly Gly Ala Asp Val Leu Trp Asp Arg Thr Arg Ala His
145 150 155

<210> 22
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 22

Met Ile Leu Ser Ala Glu Gln Ser Phe Thr Leu Arg His Pro His Gly
1 5 10 15

Gln Ala Ala Ala Leu Ala Phe Val Arg Glu Pro Ala Ala Ala Leu Ala
20 25 30

Gly Val Gln Arg Leu Arg Gly Leu Asp Ser Asp Gly Glu Gln Val Trp
35 40 45

Gly Glu Leu Leu Val Arg Val Pro Leu Leu Gly Glu Val Asp Leu Pro
50 55 60

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

Leu Thr Leu Thr Gly Glu Arg Ala Trp Val Ala Val Ser Gly Gln Ala
85 90 95

Thr Ala Ala Glu Gly Gly Glu Met Ala Phe Ala Phe Gln Phe Gln Ala
100 105 110

His Leu Ala Thr Pro Glu Ala Glu Gly Glu Gly Gly Ala Ala Phe Glu
115 120 125

Val Met Val Gln Ala Ala Ala Gly Val Thr Leu Leu Leu Val Ala Met
130 135 140

Ala Leu Pro Gln Gly Leu Ala Ala Gly Leu Pro Pro Ala
145 150 155

<210> 23
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 23

Met Thr Lys Lys Val Gly Ile Val Asp Thr Thr Phe Ala Arg Val Asp
1 5 10 15

Met Ala Ser Ala Ala Ile Leu Thr Leu Lys Met Glu Ser Pro Asn Ile
20 25 30

Lys Ile Ile Arg Lys Thr Val Pro Gly Ile Lys Asp Leu Pro Val Ala
35 40 45

Cys Lys Lys Leu Leu Glu Glu Glu Gly Cys Asp Ile Val Met Ala Leu
50 55 60

Gly Met Pro Gly Lys Lys Glu Lys Asp Lys Val Cys Ala His Glu Ala
65 70 75 80

Ser Leu Gly Leu Met Leu Ala Gln Leu Met Thr Asn Lys His Ile Ile
85 90 95

Glu Val Phe Val His Glu Asp Glu Ala Lys Asp Asp Ala Glu Leu Lys

100 105 110

Ile Leu Ala Ala Arg Arg Ala Ile Glu His Ala Leu Asn Val Tyr Tyr
115 120 125

Leu Leu Phe Lys Pro Glu Tyr Leu Thr Arg Met Ala Gly Lys Gly Leu
130 135 140

Arg Gln Gly Phe Glu Asp Ala Gly Pro Ala Arg Glu
145 150 155

<210> 24
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 24

Met Asp Asp Ile Asn Asn Gln Leu Lys Arg Leu Lys Val Ile Pro Val
1 5 10 15

Ile Ala Ile Asp Asn Ala Glu Asp Ile Ile Pro Leu Gly Lys Val Leu
20 25 30

Ala Glu Asn Gly Leu Pro Ala Ala Glu Ile Thr Phe Arg Ser Ser Ala
35 40 45

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

Ile Gly Ala Gly Thr Ile Leu Asn Gly Val Gln Ala Leu Ala Ala Lys
65 70 75 80

Glu Ala Gly Ala Asp Phe Val Val Ser Pro Gly Phe Asn Pro Asn Thr
85 90 95

Val Arg Ala Cys Gln Ile Ile Gly Ile Asp Ile Val Pro Gly Val Asn
100 105 110

Asn Pro Ser Thr Val Glu Gln Ala Leu Glu Met Gly Leu Thr Thr Leu
115 120 125

Lys Phe Phe Pro Ala Glu Ala Ser Gly Gly Ile Ser Met Val Lys Ser
130 135 140

Leu Val Gly Pro Tyr Gly Asp Ile Arg Leu Met Pro Thr Gly Gly Ile
145 150 155 160

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

Cys Gly Gly Thr Trp Met Val Asp Lys Lys Leu Val Arg Asn Gly Glu
180 185 190

Trp Asp Glu Ile Ala Arg Leu Thr Arg Glu Ile Val Glu Gln Val Asn
195 200 205

Pro

<210> 25
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
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<400> 25

Met Pro Ile Phe Thr Leu Asn Thr Asn Ile Lys Ala Asp Asp Val Pro
1 5 10 15

Ser Asp Phe Leu Ser Leu Thr Ser Arg Leu Val Gly Leu Ile Leu Ser
20 25 30

Lys Pro Gly Ser Tyr Val Ala Val His Ile Asn Thr Asp Gln Gln Leu
35 40 45

Ser Phe Gly Gly Ser Thr Asn Pro Ala Ala Phe Gly Thr Leu Met Ser
50 55 60

Ile Gly Gly Ile Glu Pro Asp Lys Asn Arg Asp His Ser Ala Val Leu
65 70 75 80

Phe Asp His Leu Asn Ala Met Leu Gly Ile Pro Lys Asn Arg Met Tyr
85 90 95

Ile His Phe Val Asn Leu Asn Gly Asp Asp Val Gly Trp Asn Gly Thr
100 105 110

Thr Phe

<210> 26
<211> 114
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 26

Met Pro Ile Phe Thr Leu Asn Thr Asn Ile Lys Ala Asp Asp Val Pro
1 5 10 15

Ser Asp Phe Leu Ser Leu Thr Ser Arg Leu Val Gly Leu Ile Leu Ser
            20   25   30

Glu Pro Gly Ser Tyr Val Ala Val His Ile Asn Thr Asp Gln Gln Leu
        35   40   45

Ser Phe Gly Gly Ser Thr Asn Pro Ala Ala Phe Gly Thr Leu Met Ser
    50   55   60

Ile Gly Gly Ile Glu Pro Asp Lys Asn Glu Asp His Ser Ala Val Leu
65   70   75   80

Phe Asp His Leu Asn Ala Met Leu Gly Ile Pro Lys Asn Arg Met Tyr
                85   90   95

Ile His Phe Val Asp Leu Asp Gly Asp Asp Val Gly Trp Asn Gly Thr
            100   105   110

Thr Phe

<210> 27
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 27

Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1   5   10   15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Ala Cys Val Glu Ala

20 25 30

Phe Glu Ile Ala Met Ala Ala Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Asp Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Arg Tyr Arg Asp Ser Asp Glu His His Arg
115 120 125

Phe Phe Ala Ala His Phe Ala Val Lys Gly Val Glu Ala Ala Arg Ala
130 135 140

Cys Ile Glu Ile Leu Asn Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 28
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 28

Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Ala Cys Val Glu Ala
20 25 30

Phe Glu Ile Ala Met Ala Ala Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asp Gly Gly Ile Tyr Asp His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Asp Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Glu Tyr Glu Asp Ser Asp Glu Asp His Glu
115 120 125

Phe Phe Ala Ala His Phe Ala Val Lys Gly Val Glu Ala Ala Arg Ala
130 135 140

Cys Ile Glu Ile Leu Asn Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 29
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
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<400> 29

Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1 5 10 15

Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
20 25 30

Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
35 40 45

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

Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65 70 75 80

Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
85 90 95

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
100 105 110

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Asp Ile Leu
115 120 125

Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met
130 135 140

Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn
145 150 155 160

Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly
165 170 175

Val Gly Asp Ala Leu Val Lys Gly Asp Pro Asp Glu Val Arg Glu Lys
180 185 190

Ala Lys Lys Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
195 200 205

<210> 30
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 30

Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1 5 10 15

Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
20 25 30

Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
35 40 45

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

Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65 70 75 80

Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
85 90 95

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
100 105 110

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Asp Ile Leu
115 120 125

Lys Leu Phe Pro Gly Glu Val Val Gly Pro Glu Phe Val Glu Ala Met
130 135 140

Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asp
145 150 155 160

Leu Asp Asp Val Cys Glu Trp Phe Asp Ala Gly Val Leu Ala Val Gly
165 170 175

Val Gly Asp Ala Leu Val Glu Gly Asp Pro Asp Glu Val Arg Glu Asp
180 185 190

Ala Lys Glu Phe Val Glu Glu Ile Arg Gly Cys Thr Glu
195 200 205

<210> 31
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 31

Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1 5 10 15

Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
20 25 30

Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
35 40 45

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

Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65 70 75 80

Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
85 90 95

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
100 105 110

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Asp Ile Leu
115 120 125

Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met
130 135 140

Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn
145 150 155 160

Leu Asp Asn Val Cys Lys Trp Phe Lys Ala Gly Val Leu Ala Val Gly
165 170 175

Val Gly Lys Ala Leu Val Lys Gly Lys Pro Asp Glu Val Arg Glu Lys
180 185 190

Ala Lys Lys Phe Val Lys Lys Ile Arg Gly Cys Thr Glu
195 200 205

<210> 32
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 32

Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
20 25 30

Phe Glu Ala Ala Met Arg Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Asp Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Arg Tyr Arg Asp Ser Asp Ala His Thr Leu
115 120 125

Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
130 135 140

Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 33
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 33

Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
20 25 30

Phe Glu Ala Ala Met Arg Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asp Gly Gly Ile Tyr Asp His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asp Gly Met Met Asn Val Gln Leu Asp Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Glu Tyr Glu Asp Ser Asp Ala Asp Thr Leu

115 120 125

Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
130 135 140

Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 34
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 34

Met Asn Gln His Ser His Lys Asp His Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
20 25 30

Phe Glu Ala Ala Met Arg Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Asn Gly Gly Ile Tyr Arg His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Asn Gly Met Met Asn Val Gln Leu Asn Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Asn Tyr Asp Lys Ser Lys Ala His Thr Leu
115 120 125

Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
130 135 140

Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 35
<211> 156
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (70)..(70)
<223> Xaa is Ala or Lys

<400> 35

Met Thr Lys Lys Val Gly Ile Val Asp Thr Thr Phe Ala Arg Val Asp
1 5 10 15

Met Ala Ser Ala Ala Ile Leu Thr Leu Lys Met Glu Ser Pro Asn Ile
20 25 30

Lys Ile Ile Arg Lys Thr Val Pro Gly Ile Lys Asp Leu Pro Val Ala
35 40 45

Cys Lys Lys Leu Leu Glu Glu Glu Gly Cys Asp Ile Val Met Ala Leu

50 55 60

Gly Met Pro Gly Lys Xaa Glu Lys Asp Lys Val Cys Ala His Glu Ala
65 70 75 80

Ser Leu Gly Leu Met Leu Ala Gln Leu Met Thr Asn Lys His Ile Ile
85 90 95

Glu Val Phe Val His Glu Asp Glu Ala Lys Asp Asp Ala Glu Leu Lys
100 105 110

Ile Leu Ala Ala Arg Arg Ala Ile Glu His Ala Leu Asn Val Tyr Tyr
115 120 125

Leu Leu Phe Lys Pro Glu Tyr Leu Thr Arg Met Ala Gly Lys Gly Leu
130 135 140

Arg Gln Gly Phe Glu Asp Ala Gly Pro Ala Arg Glu
145 150 155

<210> 36
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (2)..(2)
<223> Xaa is Ser or Asp

<220>
<221> misc_feature
<222> (3)..(3)
<223> Xaa is Thr or Asp

<220>
<221> misc_feature
<222> (10)..(10)
<223> Xaa is Ala or Arg

<220>
<221> misc_feature
<222> (85)..(85)
<223> Xaa is Thr or Asp

<220>
<221> misc_feature
<222> (119)..(119)
<223> Xaa is Ala or Gln

<220>
<221> misc_feature
<222> (163)..(163)
<223> Xaa is Ser or Asp

<220>
<221> misc_feature
<222> (189)..(189)
<223> Xaa is Thr or Arg

<400> 36

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Met Xaa Xaa Ile Asn Asn Gln Leu Lys Xaa Leu Lys Val Ile Pro Val
1               5                  10                  15


Ile Ala Ile Asp Asn Ala Glu Asp Ile Ile Pro Leu Gly Lys Val Leu
            20                  25                  30


Ala Glu Asn Gly Leu Pro Ala Ala Glu Ile Thr Phe Arg Ser Ser Ala
        35                  40                  45


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


Ile Gly Ala Gly Thr Ile Leu Asn Gly Val Gln Ala Leu Ala Ala Lys
```

65 70 75 80

Glu Ala Gly Ala Xaa Phe Val Val Ser Pro Gly Phe Asn Pro Asn Thr
85 90 95

Val Arg Ala Cys Gln Ile Ile Gly Ile Asp Ile Val Pro Gly Val Asn
100 105 110

Asn Pro Ser Thr Val Glu Xaa Ala Leu Glu Met Gly Leu Thr Thr Leu
115 120 125

Lys Phe Phe Pro Ala Glu Ala Ser Gly Gly Ile Ser Met Val Lys Ser
130 135 140

Leu Val Gly Pro Tyr Gly Asp Ile Arg Leu Met Pro Thr Gly Gly Ile
145 150 155 160

Thr Pro Xaa Asn Ile Asp Asn Tyr Leu Ala Ile Pro Gln Val Leu Ala
165 170 175

Cys Gly Gly Thr Trp Met Val Asp Lys Lys Leu Val Xaa Asn Gly Glu
180 185 190

Trp Asp Glu Ile Ala Arg Leu Thr Arg Glu Ile Val Glu Gln Val Asn
195 200 205

Pro

<210> 37
<211> 114
<212> PRT
<213> Artificial Sequence

<220>

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<220>
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<223> Xaa is Thr or Asp

<220>
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<222> (33)..(33)
<223> Xaa is Lys or Glu

<220>
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<222> (71)..(71)
<223> Xaa is Ser or Asp

<220>
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<222> (74)..(74)
<223> Xaa is Arg or Glu

<220>
<221> misc_feature
<222> (101)..(101)
<223> Xaa is Asn or Asp

<220>
<221> misc_feature
<222> (103)..(103)
<223> Xaa is Asn or Asp

<400> 37

Met Pro Ile Phe Thr Leu Asn Thr Asn Ile Lys Ala Xaa Asp Val Pro
1 5 10 15

Ser Asp Phe Leu Ser Leu Thr Ser Arg Leu Val Gly Leu Ile Leu Ser
20 25 30

Xaa Pro Gly Ser Tyr Val Ala Val His Ile Asn Thr Asp Gln Gln Leu
35 40 45

Ser Phe Gly Gly Ser Thr Asn Pro Ala Ala Phe Gly Thr Leu Met Ser
50 55 60

Ile Gly Gly Ile Glu Pro Xaa Lys Asn Xaa Asp His Ser Ala Val Leu
65 70 75 80

Phe Asp His Leu Asn Ala Met Leu Gly Ile Pro Lys Asn Arg Met Tyr
85 90 95

Ile His Phe Val Xaa Leu Xaa Gly Asp Asp Val Gly Trp Asn Gly Thr
100 105 110

Thr Phe

<210> 38
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<222> (9)..(9)
<223> Xaa is Tyr or His

<220>
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<222> (82)..(82)
<223> Xaa is Asn or Asp

<220>
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<222> (87)..(87)
<223> Xaa is Arg or Asp

<220>
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<222> (105)..(105)
<223> Xaa is Ser or Asp

<220>
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<222> (119)..(119)
<223> Xaa is Arg or Glu

<220>
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<222> (121)..(121)
<223> Xaa is Arg or Glu

<220>
<221> misc_feature
<222> (124)..(124)
<223> Xaa is Ala or Asp

<220>
<221> misc_feature
<222> (126)..(126)
<223> Xaa is His or Asp

<220>
<221> misc_feature
<222> (128)..(128)
<223> Xaa is Arg or Glu

<220>
<221> misc_feature
<222> (150)..(150)
<223> Xaa is Ala or Asn

<400> 38

Met Asn Gln His Ser His Lys Asp Xaa Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Asp Ile Val Asp Ala Cys Val Glu Ala
20 25 30

Phe Glu Ile Ala Met Ala Ala Ile Gly Gly Asp Arg Phe Ala Val Asp
        35   40   45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
    50   55   60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65   70   75   80

Val Xaa Gly Gly Ile Tyr Xaa His Glu Phe Val Ala Ser Ala Val Ile
                85   90   95

Asp Gly Met Met Asn Val Gln Leu Xaa Thr Gly Val Pro Val Leu Ser
            100   105   110

Ala Val Leu Thr Pro His Xaa Tyr Xaa Asp Ser Xaa Glu Xaa His Xaa
        115   120   125

Phe Phe Ala Ala His Phe Ala Val Lys Gly Val Glu Ala Ala Arg Ala
    130   135   140

Cys Ile Glu Ile Leu Xaa Ala Arg Glu Lys Ile Ala Ala
145   150   155

<210> 39
<211> 205
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> Xaa is Thr or Asp

<220>
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<222> (139)..(139)
<223> Xaa is Gln or Glu

<220>
<221> misc_feature
<222> (142)..(142)
<223> Xaa is Lys or Glu

<220>
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<222> (160)..(160)
<223> Xaa is Asn or Asp

<220>
<221> misc_feature
<222> (163)..(163)
<223> Xaa is Asn or Asp

<220>
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<222> (166)..(166)
<223> Xaa is Glu or Lys

<220>
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<222> (169)..(169)
<223> Xaa is Lys or Asp

<220>
<221> misc_feature
<222> (179)..(179)
<223> Xaa is Ser, Lys or Asp

<220>
<221> misc_feature
<222> (183)..(183)
<223> Xaa is Lys or Glu

<220>
<221> misc_feature
<222> (185)..(185)

<223> Xaa is Thr, Asp or Lys

<220>
<221> misc_feature
<222> (192)..(192)
<223> Xaa is Lys or Asp

<220>
<221> misc_feature
<222> (195)..(195)
<223> Xaa is Ala, Glu or Lys

<220>
<221> misc_feature
<222> (198)..(198)
<223> Xaa is Glu or Lys

<220>
<221> misc_feature
<222> (199)..(199)
<223> Xaa is Lys or Glu

<400> 39

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Met Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
1               5                  10                  15


Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
            20                  25                  30


Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
        35                  40                  45


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


Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
65                  70                  75                  80


Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
```

85 90 95

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met
100 105 110

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Xaa Ile Leu
115 120 125

Lys Leu Phe Pro Gly Glu Val Val Gly Pro Xaa Phe Val Xaa Ala Met
130 135 140

Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Xaa
145 150 155 160

Leu Asp Xaa Val Cys Xaa Trp Phe Xaa Ala Gly Val Leu Ala Val Gly
165 170 175

Val Gly Xaa Ala Leu Val Xaa Gly Xaa Pro Asp Glu Val Arg Glu Xaa
180 185 190

Ala Lys Xaa Phe Val Xaa Xaa Ile Arg Gly Cys Thr Glu
195 200 205

<210> 40
<211> 157
<212> PRT
<213> Artificial Sequence

<220>
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<220>
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<223> Xaa is Tyr or His

<220>
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<222> (38)..(38)
<223> Xaa is Ala or Arg

<220>
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<222> (82)..(82)
<223> Xaa is Asn or Asp

<220>
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<222> (87)..(87)
<223> Xaa is Arg or Asp

<220>
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<222> (97)..(97)
<223> Xaa is Asp or Asn

<220>
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<222> (105)..(105)
<223> Xaa is Ser, Asp or Asn

<220>
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<222> (119)..(119)
<223> Xaa is Arg, Glu or Asn

<220>
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<222> (121)..(121)
<223> Xaa is Arg, Asp or Glu

<220>
<221> misc_feature
<222> (122)..(122)
<223> Xaa is Asp or Lys

<220>
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<222> (124)..(124)
<223> Xaa is Asp or Lys

<220>
<221> misc_feature
<222> (126)..(126)
<223> Xaa is His or Asp

<400> 40

Met Asn Gln His Ser His Lys Asp Xaa Glu Thr Val Arg Ile Ala Val
1 5 10 15

Val Arg Ala Arg Trp His Ala Glu Ile Val Asp Ala Cys Val Ser Ala
20 25 30

Phe Glu Ala Ala Met Xaa Asp Ile Gly Gly Asp Arg Phe Ala Val Asp
35 40 45

Val Phe Asp Val Pro Gly Ala Tyr Glu Ile Pro Leu His Ala Arg Thr
50 55 60

Leu Ala Glu Thr Gly Arg Tyr Gly Ala Val Leu Gly Thr Ala Phe Val
65 70 75 80

Val Xaa Gly Gly Ile Tyr Xaa His Glu Phe Val Ala Ser Ala Val Ile
85 90 95

Xaa Gly Met Met Asn Val Gln Leu Xaa Thr Gly Val Pro Val Leu Ser
100 105 110

Ala Val Leu Thr Pro His Xaa Tyr Xaa Xaa Ser Xaa Ala Xaa Thr Leu
115 120 125

Leu Phe Leu Ala Leu Phe Ala Val Lys Gly Met Glu Ala Ala Arg Ala
130 135 140

Cys Val Glu Ile Leu Ala Ala Arg Glu Lys Ile Ala Ala
145 150 155

<210> 41
<211> 159
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 41

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Met Gly Glu Val Pro Ile Gly Asp Pro Lys Glu Leu Asn Gly Met Glu
1               5                  10                  15


Ile Ala Ala Val Tyr Leu Gln Pro Ile Glu Met Glu Pro Arg Gly Ile
            20                  25                  30


Asp Leu Ala Ala Ser Leu Ala Asp Ile His Leu Glu Ala Asp Ile His
        35                  40                  45


Ala Leu Lys Asn Asn Pro Asn Gly Phe Pro Glu Gly Phe Trp Met Pro
    50                  55                  60


Tyr Leu Thr Ile Ala Tyr Ala Leu Ala Asn Ala Asp Thr Gly Ala Ile
65                  70                  75                  80


Lys Thr Gly Thr Leu Met Pro Met Val Ala Asp Asp Gly Pro His Tyr
                85                  90                  95


Gly Ala Asn Ile Ala Met Glu Lys Asp Lys Lys Gly Gly Phe Gly Val
            100                 105                 110


Gly Thr Tyr Ala Leu Thr Phe Leu Ile Ser Asn Pro Glu Lys Gln Gly
        115                 120                 125


Phe Gly Arg His Val Asp Glu Glu Thr Gly Val Gly Lys Trp Phe Glu
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130 135 140

Pro Phe Val Val Thr Tyr Phe Phe Lys Tyr Thr Gly Thr Pro Lys
145 150 155

<210> 42
<211> 184
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 42

Met Ser Gln Ala Ile Gly Ile Leu Glu Leu Thr Ser Ile Ala Lys Gly
1 5 10 15

Met Glu Leu Gly Asp Ala Met Leu Lys Ser Ala Asn Val Asp Leu Leu
20 25 30

Val Ser Lys Thr Ile Ser Pro Gly Lys Phe Leu Leu Met Leu Gly Gly
35 40 45

Asp Ile Gly Ala Ile Gln Gln Ala Ile Glu Thr Gly Thr Ser Gln Ala
50 55 60

Gly Glu Met Leu Val Asp Ser Leu Val Leu Ala Asn Ile His Pro Ser
65 70 75 80

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

Val Gly Ile Val Glu Thr Trp Ser Val Ala Ala Cys Ile Ser Ala Ala
100 105 110

Asp Leu Ala Val Lys Gly Ser Asn Val Thr Leu Val Arg Val His Met
115 120 125

Ala Phe Gly Ile Gly Gly Lys Cys Tyr Met Val Val Ala Gly Asp Val
130 135 140

Leu Asp Val Ala Ala Ala Val Ala Thr Ala Ser Leu Ala Ala Gly Ala
145 150 155 160

Lys Gly Leu Leu Val Tyr Ala Ser Ile Ile Pro Arg Pro His Glu Ala
165 170 175

Met Trp Arg Gln Met Val Glu Gly
180

<210> 43
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 43

Met Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala Leu Val Ala Val
1 5 10 15

Lys Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala Ala Cys Val Asn
20 25 30

Ile Val Pro Gly Leu Thr Ser Ile Tyr Arg Trp Gln Gly Ser Val Val
35 40 45

Ser Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr Thr His Ala Phe
50 55 60

Pro Lys Leu Lys Glu Arg Val Lys Ala Leu His Pro Tyr Thr Val Pro
65 70 75 80

Glu Ile Val Ala Leu Pro Ile Ala Glu Gly Asn Arg Glu Tyr Leu Asp
85 90 95

Trp Leu Arg Glu Asn Thr Gly
100

<210> 44
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 44

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

Ala Ala Ile Leu Ala Ala Thr Ile Glu Leu Leu Leu Lys Met Leu Glu
20 25 30

Ala Asn Gly Ile Gln Ser Tyr Glu Glu Leu Ala Ala Val Ile Phe Thr
35 40 45

Val Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala Glu Ala Ala Arg Leu
50 55 60

Ile Gly Met His Arg Val Pro Leu Leu Ser Ala Arg Glu Val Pro Val
65 70 75 80

Pro Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala Leu Trp Asn Thr
85 90 95

Asp Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu Asn Glu Ala Val
100 105 110

Arg Leu Arg Pro Asp Leu Glu Ser Ala Gln
115 120

<210> 45
<211> 177
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 45

Met Ser Lys Ala Lys Ile Gly Ile Val Thr Val Ser Asp Arg Ala Ser
1 5 10 15

Ala Gly Ile Thr Ala Asp Ile Ser Gly Lys Ala Ile Ile Leu Ala Leu
20 25 30

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

Asp Glu Gln Asp Val Ile Glu Thr Thr Leu Ile Lys Met Ala Asp Glu
50 55 60

Gln Asp Cys Cys Leu Ile Val Thr Thr Gly Gly Thr Gly Pro Ala Lys
65 70 75 80

Arg Asp Val Thr Pro Glu Ala Thr Glu Ala Val Cys Asp Arg Met Met
85 90 95

Pro Gly Phe Gly Glu Leu Met Arg Ala Glu Ser Leu Lys Glu Val Pro

100 105 110

Thr Ala Ile Leu Ser Arg Gln Thr Ala Gly Leu Arg Gly Asp Ser Leu
115 120 125

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

Ala Val Phe Pro Ala Ile Pro Tyr Cys Ile Asp Leu Met Glu Gly Pro
145 150 155 160

Tyr Leu Glu Cys Asn Glu Ala Met Ile Lys Pro Phe Arg Pro Lys Ala
165 170 175

Lys

<210> 46
<211> 122
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 46

Met Val Arg Gly Ile Arg Gly Ala Ile Thr Val Asn Ser Asp Thr Pro
1 5 10 15

Thr Ser Ile Ile Ile Ala Thr Ile Leu Leu Leu Glu Lys Met Leu Glu
20 25 30

Ala Asn Gly Ile Gln Ser Tyr Glu Glu Leu Ala Ala Val Ile Phe Thr
35 40 45

Val Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala Glu Ala Ala Arg Gln
50 55 60

Ile Gly Met His Arg Val Pro Leu Leu Ser Ala Arg Glu Val Pro Val
65 70 75 80

Pro Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala Leu Trp Asn Thr
85 90 95

Asp Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu Ser Glu Ala Val
100 105 110

Arg Leu Arg Pro Asp Leu Glu Ser Ala Gln
115 120

<210> 47
<211> 172
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 47

Met Arg Ile Thr Thr Lys Val Gly Asp Lys Gly Ser Thr Arg Leu Phe
1 5 10 15

Gly Gly Glu Glu Val Trp Lys Asp Ser Pro Ile Ile Glu Ala Asn Gly
20 25 30

Thr Leu Asp Glu Leu Thr Ser Phe Ile Gly Glu Ala Lys His Tyr Val
35 40 45

Asp Glu Glu Met Lys Gly Ile Leu Glu Glu Ile Gln Asn Asp Ile Tyr
50 55 60

Lys Ile Met Gly Glu Ile Gly Ser Lys Gly Lys Ile Glu Gly Ile Ser
65 70 75 80

Glu Glu Arg Ile Ala Trp Leu Leu Lys Leu Ile Leu Arg Tyr Met Glu
85 90 95

Met Val Asn Leu Lys Ser Phe Val Leu Pro Gly Gly Thr Leu Glu Ser
100 105 110

Ala Lys Leu Asp Val Cys Arg Thr Ile Ala Arg Arg Ala Leu Arg Lys
115 120 125

Val Leu Thr Val Thr Arg Glu Phe Gly Ile Gly Ala Glu Ala Ala Ala
130 135 140

Tyr Leu Leu Ala Leu Ser Asp Leu Leu Phe Leu Leu Ala Arg Val Ile
145 150 155 160

Glu Ile Glu Lys Asn Lys Leu Lys Glu Val Arg Ser
165 170

<210> 48
<211> 123
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 48

Met Pro His Leu Val Ile Glu Ala Thr Ala Asn Leu Arg Leu Glu Thr
1 5 10 15

Ser Pro Gly Glu Leu Leu Glu Gln Ala Asn Lys Ala Leu Phe Ala Ser
20 25 30

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

Ala Tyr Arg Gln Gly Thr Ala Ala Val Glu Arg Ala Tyr Leu His Ala
50 55 60

Cys Leu Ser Ile Leu Asp Gly Arg Asp Ile Ala Thr Arg Thr Leu Leu
65 70 75 80

Gly Ala Ser Leu Cys Ala Val Leu Ala Glu Ala Val Ala Gly Gly Gly
85 90 95

Glu Glu Gly Val Gln Val Ser Val Glu Val Arg Glu Met Glu Arg Leu
100 105 110

Ser Tyr Ala Lys Arg Val Val Ala Arg Gln Arg
115 120

<210> 49
<211> 158
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 49

Met Glu Ser Val Asn Thr Ser Phe Leu Ser Pro Ser Leu Val Thr Ile
1 5 10 15

Arg Asp Phe Asp Asn Gly Gln Phe Ala Val Leu Arg Ile Gly Arg Thr
20 25 30

Gly Phe Pro Ala Asp Lys Gly Asp Ile Asp Leu Cys Leu Asp Lys Met

35 40 45

Ile Gly Val Arg Ala Ala Gln Ile Phe Leu Gly Asp Asp Thr Glu Asp
50 55 60

Gly Phe Lys Gly Pro His Ile Arg Ile Arg Cys Val Asp Ile Asp Asp
65 70 75 80

Lys His Thr Tyr Asn Ala Met Val Tyr Val Asp Leu Ile Val Gly Thr
85 90 95

Gly Ala Ser Glu Val Glu Arg Glu Thr Ala Glu Glu Glu Ala Lys Leu
100 105 110

Ala Leu Arg Val Ala Leu Gln Val Asp Ile Ala Asp Glu His Ser Cys
115 120 125

Val Thr Gln Phe Glu Met Lys Leu Arg Glu Glu Leu Leu Ser Ser Asp
130 135 140

Ser Phe His Pro Asp Lys Asp Glu Tyr Tyr Lys Asp Phe Leu
145 150 155

<210> 50
<211> 113
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 50

Met Pro Val Ile Gln Thr Phe Val Ser Thr Pro Leu Asp His His Lys
1 5 10 15

Arg Leu Leu Leu Ala Ile Ile Tyr Arg Ile Val Thr Arg Val Val Leu
            20   25   30

Gly Lys Pro Glu Asp Leu Val Met Met Thr Phe His Asp Ser Thr Pro
        35   40   45

Met His Phe Phe Gly Ser Thr Asp Pro Val Ala Cys Val Arg Val Glu
    50   55   60

Ala Leu Gly Gly Tyr Gly Pro Ser Glu Pro Glu Lys Val Thr Ser Ile
65   70   75   80

Val Thr Ala Ala Ile Thr Ala Val Cys Gly Ile Val Ala Asp Arg Ile
                85   90   95

Phe Val Leu Tyr Phe Ser Pro Leu His Cys Gly Trp Asn Gly Thr Asn
            100   105   110

Phe

<210> 51
<211> 103
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed nanostructure polypeptide

<400> 51

Met Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala Leu Val Ala Val
1   5   10   15

Lys Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala Ala Cys Val Asn
            20   25   30

Ile Val Pro Gly Leu Thr Ser Ile Tyr Arg Glu Glu Gly Ser Val Val
        35   40   45

Ser Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr Thr Asp Ala Phe
    50   55   60

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

Glu Ile Val Ala Leu Pro Ile Ala Glu Gly Asn Arg Glu Tyr Leu Asp
                85   90   95

Trp Leu Arg Glu Asn Thr Gly
            100

<210> 52
<211> 869
<212> PRT
<213> Human immunodeficiency virus 1

<400> 52

Met Arg Val Lys Gly Ile Lys Lys Asn Tyr Gln His Trp Trp Arg Gly
1   5   10   15

Gly Ile Met Leu Leu Gly Met Leu Met Ile Cys Ser Ser Ala Glu Lys
            20   25   30

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
        35   40   45

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Gln Asn Pro Glu Met
    50   55   60

His Asn Ile Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro

65 70 75 80

Gln Glu Val Ile Leu Lys Asn Leu Thr Glu Glu Phe Asn Met Trp Lys
85 90 95

Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
100 105 110

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
115 120 125

Asn Cys Thr Asn Ala Glu Ser Leu Asn Cys Thr Ala Thr Asn Gly Thr
130 135 140

Asn Asn Cys Ser Ala Ser Thr Lys Pro Met Glu Glu Met Lys Asn Cys
145 150 155 160

Ser Phe Asn Ile Thr Thr Ser Val Gln Asp Lys Lys Gln Gln Glu Tyr
165 170 175

Ala Leu Phe Tyr Lys Leu Asp Ile Ile Pro Ile Asp Asn Asn Glu Asn
180 185 190

Asp Leu Asn Asn Thr Asn Tyr Thr Ser Tyr Arg Leu Ile Ser Cys Asn
195 200 205

Thr Ser Val Ile Thr Gln Ala Cys Pro Lys Ile Thr Phe Glu Pro Ile
210 215 220

Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Lys
225 230 235 240

Asp Lys Arg Phe Asn Gly Thr Gly Pro Cys Lys Asn Val Ser Thr Val
245 250 255

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

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

Thr Asp Asn Ala Lys Asn Ile Ile Val Gln Leu Lys Asp Pro Val Asn
290 295 300

Ile Thr Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile
305 310 315 320

Gly Pro Gly Arg Ala Phe Tyr Ala Thr Gly Gln Val Ile Gly Asp Ile
325 330 335

Arg Lys Ala His Cys Asp Leu Asn Gly Thr Glu Trp Asp Asn Ala Leu
340 345 350

Lys Gln Ile Val Glu Glu Leu Arg Lys Gln Tyr Gly Asn Asn Ile Thr
355 360 365

Ile Phe Asn Ser Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser
370 375 380

Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe
385 390 395 400

Asn Ser Thr Trp Leu Phe Asn Ser Thr Trp Asn Ser Thr Glu Arg Leu
405 410 415

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

Ile Lys Gln Val Ile Asn Met Trp Gln Thr Val Gly Lys Ala Met Tyr
435 440 445

Ala Pro Pro Ile Arg Gly Leu Ile Arg Cys Ser Ser Asn Ile Thr Gly
450 455 460

Leu Ile Leu Thr Arg Asp Gly Ser Gly Asn Thr Thr Gly Asn Glu Thr
465 470 475 480

Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu
485 490 495

Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr
500 505 510

Arg Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg Ala Ala Gly Leu
515 520 525

Gly Ala Leu Phe Leu Gly Phe Leu Gly Met Ala Gly Ser Thr Met Gly
530 535 540

Ala Ala Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu Ser Gly
545 550 555 560

Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala Gln Gln
565 570 575

His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln Ala Arg
580 585 590

Val Leu Ala Val Glu Arg Tyr Leu Arg Asp Gln Gln Leu Leu Gly Ile
595 600 605

Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Thr Val Pro Trp Asn
610 615 620

Ala Ser Trp Ser Asn Lys Ser Leu Asp Asn Ile Trp Glu Asn Met Thr
625 630 635 640

Trp Met Gln Trp Glu Lys Glu Ile Asp Asn Tyr Thr Asp Val Ile Tyr
645 650 655

Lys Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu Gln Glu
660 665 670

Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile
675 680 685

Thr Arg Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val Gly Gly
690 695 700

Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Ile Val Asn Arg
705 710 715 720

Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu Phe Pro Ala
725 730 735

Pro Arg Gly Pro Asp Arg Pro Glu Gly Thr Glu Glu Gly Gly Gly Glu
740 745 750

Arg Gly Arg Asp Ser Ser Asp Arg Ser Ala His Gly Phe Leu Ala Leu
755 760 765

Ile Trp Gly Asp Leu Trp Ser Leu Cys Leu Phe Ser Tyr Arg Arg Leu
770 775 780

Arg Asp Leu Leu Leu Ile Ala Ala Arg Ile Val Glu Leu Leu Gly Arg

785 790 795 800

Arg Gly Trp Glu Val Leu Lys Tyr Trp Trp Ser Leu Leu Gln Tyr Trp
805 810 815

Ser Gln Glu Leu Lys Lys Ser Ala Val Ser Leu Leu Asn Ala Thr Ala
820 825 830

Ile Ala Val Ala Glu Gly Thr Asp Arg Ile Ile Glu Ile Val Gln Arg
835 840 845

Ala Gly Arg Ala Ile Ile His Ile Pro Arg Arg Ile Arg Gln Gly Ala
850 855 860

Glu Arg Ala Leu Leu
865

<210> 53
<211> 492
<212> PRT
<213> Human immunodeficiency virus 1

<400> 53

Leu Trp Val Thr Val Tyr Tyr Gly Val Pro Val Trp Lys Glu Ala Thr
1 5 10 15

Thr Thr Leu Phe Cys Ala Ser Asp Ala Lys Ala Gln Asn Pro Glu Met
20 25 30

His Asn Ile Trp Ala Thr His Ala Cys Val Pro Thr Asp Pro Asn Pro
35 40 45

Gln Glu Val Ile Leu Lys Asn Leu Thr Glu Glu Phe Asn Met Trp Lys
50 55 60

```
Asn Asn Met Val Glu Gln Met His Glu Asp Ile Ile Ser Leu Trp Asp
65                  70                  75                  80

Gln Ser Leu Lys Pro Cys Val Lys Leu Thr Pro Leu Cys Val Thr Leu
                85                  90                  95

Asn Cys Thr Asn Ala Glu Ser Leu Asn Cys Thr Ala Thr Asn Gly Thr
            100                 105                 110

Asn Asn Cys Ser Ala Ser Thr Lys Pro Met Glu Glu Met Lys Asn Cys
        115                 120                 125

Ser Phe Asn Ile Thr Thr Ser Val Gln Asp Lys Lys Gln Gln Glu Tyr
    130                 135                 140

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

Asp Leu Asn Asn Thr Asn Tyr Thr Ser Tyr Arg Leu Ile Ser Cys Asn
                165                 170                 175

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

Pro Ile His Tyr Cys Ala Pro Ala Gly Phe Ala Ile Leu Lys Cys Lys
        195                 200                 205

Asp Lys Arg Phe Asn Gly Thr Gly Pro Cys Lys Asn Val Ser Thr Val
    210                 215                 220

Gln Cys Thr His Gly Ile Arg Pro Val Val Ser Thr Gln Leu Leu Leu
225                 230                 235                 240
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Asn Gly Ser Leu Ala Glu Glu Gly Val Val Leu Arg Ser Glu Asn Phe
245 250 255

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

Ile Thr Cys Thr Arg Pro Asn Asn Asn Thr Arg Lys Ser Ile Thr Ile
275 280 285

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

Arg Lys Ala His Cys Asp Leu Asn Gly Thr Glu Trp Asp Asn Ala Leu
305 310 315 320

Lys Gln Ile Val Glu Glu Leu Arg Lys Gln Tyr Gly Asn Asn Ile Thr
325 330 335

Ile Phe Asn Ser Ser Ser Gly Gly Asp Pro Glu Ile Val Met His Ser
340 345 350

Phe Asn Cys Gly Gly Glu Phe Phe Tyr Cys Asn Thr Ala Gln Leu Phe
355 360 365

Asn Ser Thr Trp Leu Phe Asn Ser Thr Trp Asn Ser Thr Glu Arg Leu
370 375 380

Gly Asn Asp Thr Glu Arg Thr Asn Asp Thr Ile Thr Leu Pro Cys Lys
385 390 395 400

Ile Lys Gln Val Ile Asn Met Trp Gln Thr Val Gly Lys Ala Met Tyr
405 410 415

Ala Pro Pro Ile Arg Gly Leu Ile Arg Cys Ser Ser Asn Ile Thr Gly

420 425 430

Leu Ile Leu Thr Arg Asp Gly Ser Gly Asn Thr Thr Gly Asn Glu Thr
435 440 445

Phe Arg Pro Gly Gly Gly Asn Met Lys Asp Asn Trp Arg Ser Glu Leu
450 455 460

Tyr Lys Tyr Lys Val Val Lys Ile Glu Pro Leu Gly Val Ala Pro Thr
465 470 475 480

Arg Ala Lys Arg Arg Val Val Gln Arg Glu Lys Arg
485 490

<210> 54
<211> 191
<212> PRT
<213> Human immunodeficiency virus 1

<400> 54

Met Gly Ala Ala Ser Leu Thr Leu Thr Val Gln Ala Arg Gln Leu Leu
1 5 10 15

Ser Gly Ile Val Gln Gln Gln Asn Asn Leu Leu Arg Ala Ile Glu Ala
20 25 30

Gln Gln His Leu Leu Gln Leu Thr Val Trp Gly Ile Lys Gln Leu Gln
35 40 45

Ala Arg Val Leu Ala Val Glu Arg Tyr Leu Arg Asp Gln Gln Leu Leu
50 55 60

Gly Ile Trp Gly Cys Ser Gly Lys Leu Ile Cys Thr Thr Thr Val Pro
65 70 75 80

Trp Asn Ala Ser Trp Ser Asn Lys Ser Leu Asp Asn Ile Trp Glu Asn
85 90 95

Met Thr Trp Met Gln Trp Glu Lys Glu Ile Asp Asn Tyr Thr Asp Val
100 105 110

Ile Tyr Lys Leu Leu Glu Glu Ser Gln Asn Gln Gln Glu Lys Asn Glu
115 120 125

Gln Glu Leu Leu Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe
130 135 140

Asp Ile Thr Arg Trp Leu Trp Tyr Ile Lys Ile Phe Ile Met Ile Val
145 150 155 160

Gly Gly Leu Val Gly Leu Arg Ile Val Phe Ala Val Leu Ser Ile Val
165 170 175

Asn Arg Val Arg Gln Gly Tyr Ser Pro Leu Ser Phe Gln Thr Leu
180 185 190

<210> 55
<211> 22
<212> PRT
<213> Human immunodeficiency virus 1

<400> 55

Glu Leu Asp Lys Trp Ala Ser Leu Trp Asn Trp Phe Asp Ile Thr Arg
1 5 10 15

Trp Leu Trp Tyr Ile Lys
20

<210> 56

<211> 574
<212> PRT
<213> Respiratory syncytial virus type A

<400> 56

Met Glu Leu Pro Ile Leu Lys Thr Asn Ala Ile Thr Thr Ile Leu Ala
1 5 10 15

Ala Val Thr Leu Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95

Met Gln Ser Thr Pro Ala Ala Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Thr Lys Asn Asn Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Ile Ala Val Ser Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Ser Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Val Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Ser Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Ile
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

Leu His Asn Val Asn Val Gly Lys Ser Thr Thr Asn Ile Met Ile Thr

515 520 525

Thr Ile Ile Ile Val Ile Ile Val Ile Leu Leu Leu Leu Ile Ala Val
530 535 540

Gly Leu Phe Leu Tyr Cys Lys Ala Arg Ser Thr Pro Val Thr Leu Ser
545 550 555 560

Lys Asp Gln Leu Ser Gly Ile Asn Asn Ile Ala Phe Ser Asn
565 570

<210> 57
<211> 566
<212> PRT
<213> Influenza A virus

<400> 57

Met Lys Ala Ile Leu Val Val Leu Leu Tyr Thr Phe Ala Thr Ala Asn
1 5 10 15

Ala Asp Thr Leu Cys Ile Gly Tyr His Ala Asn Asn Ser Thr Asp Thr
20 25 30

Val Asp Thr Val Leu Glu Lys Asn Val Thr Val Thr His Ser Val Asn
35 40 45

Leu Leu Glu Asp Lys His Asn Gly Lys Leu Cys Lys Leu Arg Gly Val
50 55 60

Ala Pro Leu His Leu Gly Lys Cys Asn Ile Ala Gly Trp Ile Leu Gly
65 70 75 80

Asn Pro Glu Cys Glu Ser Leu Ser Thr Ala Ser Ser Trp Ser Tyr Ile
85 90 95

Val Glu Thr Pro Ser Ser Asp Asn Gly Thr Cys Tyr Pro Gly Asp Phe
100 105 110

Ile Asp Tyr Glu Glu Leu Arg Glu Gln Leu Ser Ser Val Ser Ser Phe
115 120 125

Glu Arg Phe Glu Ile Phe Pro Lys Thr Ser Ser Trp Pro Asn His Asp
130 135 140

Ser Asn Lys Gly Val Thr Ala Ala Cys Pro His Ala Gly Ala Lys Ser
145 150 155 160

Phe Tyr Lys Asn Leu Ile Trp Leu Val Lys Lys Gly Asn Ser Tyr Pro
165 170 175

Lys Leu Ser Lys Ser Tyr Ile Asn Asp Lys Gly Lys Glu Val Leu Val
180 185 190

Leu Trp Gly Ile His His Pro Ser Thr Ser Ala Asp Gln Gln Ser Leu
195 200 205

Tyr Gln Asn Ala Asp Ala Tyr Val Phe Val Gly Ser Ser Arg Tyr Ser
210 215 220

Lys Lys Phe Lys Pro Glu Ile Ala Ile Arg Pro Lys Val Arg Asp Gln
225 230 235 240

Glu Gly Arg Met Asn Tyr Tyr Trp Thr Leu Val Glu Pro Gly Asp Lys
245 250 255

Ile Thr Phe Glu Ala Thr Gly Asn Leu Val Val Pro Arg Tyr Ala Phe
260 265 270

Ala Met Glu Arg Asn Ala Gly Ser Gly Ile Ile Ile Ser Asp Thr Pro
275 280 285

Val His Asp Cys Asn Thr Thr Cys Gln Thr Pro Lys Gly Ala Ile Asn
290 295 300

Thr Ser Leu Pro Phe Gln Asn Ile His Pro Ile Thr Ile Gly Lys Cys
305 310 315 320

Pro Lys Tyr Val Lys Ser Thr Lys Leu Arg Leu Ala Thr Gly Leu Arg
325 330 335

Asn Ile Pro Ser Ile Gln Ser Arg Gly Leu Phe Gly Ala Ile Ala Gly
340 345 350

Phe Ile Glu Gly Gly Trp Thr Gly Met Val Asp Gly Trp Tyr Gly Tyr
355 360 365

His His Gln Asn Glu Gln Gly Ser Gly Tyr Ala Ala Asp Leu Lys Ser
370 375 380

Thr Gln Asn Ala Ile Asp Glu Ile Thr Asn Lys Val Asn Ser Val Ile
385 390 395 400

Glu Lys Met Asn Thr Gln Phe Thr Ala Val Gly Lys Glu Phe Asn His
405 410 415

Leu Glu Lys Arg Ile Glu Asn Leu Asn Lys Lys Val Asp Asp Gly Phe
420 425 430

Leu Asp Ile Trp Thr Tyr Asn Ala Glu Leu Leu Val Leu Leu Glu Asn
435 440 445

Glu Arg Thr Leu Asp Tyr His Asp Ser Asn Val Lys Asn Leu Tyr Glu

450 455 460

Lys Val Arg Ser Gln Leu Lys Asn Asn Ala Lys Glu Ile Gly Asn Gly
465 470 475 480

Cys Phe Glu Phe Tyr His Lys Cys Asp Asn Thr Cys Met Glu Ser Val
485 490 495

Lys Asn Gly Thr Tyr Asp Tyr Pro Lys Tyr Ser Glu Glu Ala Lys Leu
500 505 510

Asn Arg Glu Glu Ile Asp Gly Val Lys Leu Glu Ser Thr Arg Ile Tyr
515 520 525

Gln Ile Leu Ala Ile Tyr Ser Thr Val Ala Ser Ser Leu Val Leu Val
530 535 540

Val Ser Leu Gly Ala Ile Ser Phe Trp Met Cys Ser Asn Gly Ser Leu
545 550 555 560

Gln Cys Arg Ile Cys Ile
565

<210> 58
<211> 584
<212> PRT
<213> Influenza B virus

<400> 58

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

Arg Ile Cys Thr Gly Ile Thr Ser Ser Asn Ser Pro His Val Val Lys
20 25 30

Thr Ala Thr Gln Gly Glu Val Asn Val Thr Gly Val Ile Pro Leu Thr
35 40 45

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

Arg Gly Lys Leu Cys Pro Asp Cys Leu Asn Cys Thr Asp Leu Asp Val
65 70 75 80

Ala Leu Gly Arg Pro Met Cys Val Gly Thr Thr Pro Ser Ala Lys Ala
85 90 95

Ser Ile Leu His Glu Val Arg Pro Val Thr Ser Gly Cys Phe Pro Ile
100 105 110

Met His Asp Arg Thr Lys Ile Arg Gln Leu Ala Asn Leu Leu Arg Gly
115 120 125

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

Ala Pro Gly Gly Pro Tyr Arg Leu Gly Thr Ser Gly Ser Cys Pro Asn
145 150 155 160

Ala Thr Ser Lys Ser Gly Phe Phe Ala Thr Met Ala Trp Ala Val Pro
165 170 175

Lys Asp Asn Asn Lys Asn Ala Thr Asn Pro Leu Thr Val Glu Val Pro
180 185 190

Tyr Ile Cys Ala Glu Gly Glu Asp Gln Ile Thr Val Trp Gly Phe His
195 200 205

Ser Asp Asn Lys Thr Gln Met Lys Asn Leu Tyr Gly Asp Ser Asn Pro
210 215 220

Gln Lys Phe Thr Ser Ser Ala Asn Gly Val Thr Thr His Tyr Val Ser
225 230 235 240

Gln Ile Gly Gly Phe Pro Asp Gln Thr Glu Asp Gly Gly Leu Pro Gln
245 250 255

Ser Gly Arg Ile Val Val Asp Tyr Met Met Gln Lys Pro Gly Lys Thr
260 265 270

Gly Thr Ile Val Tyr Gln Arg Gly Val Leu Leu Pro Gln Lys Val Trp
275 280 285

Cys Ala Ser Gly Arg Ser Lys Val Ile Lys Gly Ser Leu Pro Leu Ile
290 295 300

Gly Glu Ala Asp Cys Leu His Glu Lys Tyr Gly Gly Leu Asn Lys Ser
305 310 315 320

Lys Pro Tyr Tyr Thr Gly Glu His Ala Lys Ala Ile Gly Asn Cys Pro
325 330 335

Ile Trp Val Lys Thr Pro Leu Lys Leu Ala Asn Gly Thr Lys Tyr Arg
340 345 350

Pro Pro Ala Lys Leu Leu Lys Glu Arg Gly Phe Phe Gly Ala Ile Ala
355 360 365

Gly Phe Leu Glu Gly Gly Trp Glu Gly Met Ile Ala Gly Trp His Gly
370 375 380

Tyr Thr Ser His Gly Ala His Gly Val Ala Val Ala Ala Asp Leu Lys

385 390 395 400

Ser Thr Gln Glu Ala Ile Asn Lys Ile Thr Lys Asn Leu Asn Ser Leu
405 410 415

Ser Glu Leu Glu Val Lys Asn Leu Gln Arg Leu Ser Gly Ala Met Asp
420 425 430

Glu Leu His Asn Glu Ile Leu Glu Leu Asp Glu Lys Val Asp Asp Leu
435 440 445

Arg Ala Asp Thr Ile Ser Ser Gln Ile Glu Leu Ala Val Leu Leu Ser
450 455 460

Asn Glu Gly Ile Ile Asn Ser Glu Asp Glu His Leu Leu Ala Leu Glu
465 470 475 480

Arg Lys Leu Lys Lys Met Leu Gly Pro Ser Ala Val Asp Ile Gly Asn
485 490 495

Gly Cys Phe Glu Thr Lys His Lys Cys Asn Gln Thr Cys Leu Asp Arg
500 505 510

Ile Ala Ala Gly Thr Phe Asn Ala Gly Glu Phe Ser Leu Pro Thr Phe
515 520 525

Asp Ser Leu Asn Ile Thr Ala Ala Ser Leu Asn Asp Asp Gly Leu Asp
530 535 540

Asn His Thr Ile Leu Leu Tyr Tyr Ser Thr Ala Ala Ser Ser Leu Ala
545 550 555 560

Val Thr Leu Met Leu Ala Ile Phe Ile Val Tyr Met Val Ser Arg Asp
565 570 575

Asn Val Ser Cys Ser Ile Cys Leu
580

<210> 59
<211> 907
<212> PRT
<213> Epstein-Barr virus

<400> 59

Met Glu Ala Ala Leu Leu Val Cys Gln Tyr Thr Ile Gln Ser Leu Ile
1 5 10 15

His Leu Thr Gly Glu Asp Pro Gly Phe Phe Asn Val Glu Ile Pro Glu
20 25 30

Phe Pro Phe Tyr Pro Thr Cys Asn Val Cys Thr Ala Asp Val Asn Val
35 40 45

Thr Ile Asn Phe Asp Val Gly Gly Lys Lys His Gln Leu Asp Leu Asp
50 55 60

Phe Gly Gln Leu Thr Pro His Thr Lys Ala Val Tyr Gln Pro Arg Gly
65 70 75 80

Ala Phe Gly Gly Ser Glu Asn Ala Thr Asn Leu Phe Leu Leu Glu Leu
85 90 95

Leu Gly Ala Gly Glu Leu Ala Leu Thr Met Arg Ser Lys Lys Leu Pro
100 105 110

Ile Asn Val Thr Thr Gly Glu Glu Gln Gln Val Ser Leu Glu Ser Val
115 120 125

Asp Val Tyr Phe Gln Asp Val Phe Gly Thr Met Trp Cys His His Ala
130 135 140

Glu Met Gln Asn Pro Val Tyr Leu Ile Pro Glu Thr Val Pro Tyr Ile
145 150 155 160

Lys Trp Asp Asn Cys Asn Ser Thr Asn Ile Thr Ala Val Val Arg Ala
165 170 175

Gln Gly Leu Asp Val Thr Leu Pro Leu Ser Leu Pro Thr Ser Ala Gln
180 185 190

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

Ile Glu Cys Ile Met Glu Asp Gly Glu Ile Ser Gln Val Leu Pro Gly
210 215 220

Asp Asn Lys Phe Asn Ile Thr Cys Ser Gly Tyr Glu Ser His Val Pro
225 230 235 240

Ser Gly Gly Ile Leu Thr Ser Thr Ser Pro Val Ala Thr Pro Ile Pro
245 250 255

Gly Thr Gly Tyr Ala Tyr Ser Leu Arg Leu Thr Pro Arg Pro Val Ser
260 265 270

Arg Phe Leu Gly Asn Asn Ser Ile Leu Tyr Val Phe Tyr Ser Gly Asn
275 280 285

Gly Pro Lys Ala Ser Gly Gly Asp Tyr Cys Ile Gln Ser Asn Ile Val
290 295 300

Phe Ser Asp Glu Ile Pro Ala Ser Gln Asp Met Pro Thr Asn Thr Thr

305 310 315 320

Asp Ile Thr Tyr Val Gly Asp Asn Ala Thr Tyr Ser Val Pro Met Val
325 330 335

Thr Ser Glu Asp Ala Asn Ser Pro Asn Val Thr Val Thr Ala Phe Trp
340 345 350

Ala Trp Pro Asn Asn Thr Glu Thr Asp Phe Lys Cys Lys Trp Thr Leu
355 360 365

Thr Ser Gly Thr Pro Ser Gly Cys Glu Asn Ile Ser Gly Ala Phe Ala
370 375 380

Ser Asn Arg Thr Phe Asp Ile Thr Val Ser Gly Leu Gly Thr Ala Pro
385 390 395 400

Lys Thr Leu Ile Ile Thr Arg Thr Ala Thr Asn Ala Thr Thr Thr Thr
405 410 415

His Lys Val Ile Phe Ser Lys Ala Pro Glu Ser Thr Thr Thr Ser Pro
420 425 430

Thr Leu Asn Thr Thr Gly Phe Ala Asp Pro Asn Thr Thr Thr Gly Leu
435 440 445

Pro Ser Ser Thr His Val Pro Thr Asn Leu Thr Ala Pro Ala Ser Thr
450 455 460

Gly Pro Thr Val Ser Thr Ala Asp Val Thr Ser Pro Thr Pro Ala Gly
465 470 475 480

Thr Thr Ser Gly Ala Ser Pro Val Thr Pro Ser Pro Ser Pro Trp Asp
485 490 495

Asn Gly Thr Glu Ser Lys Ala Pro Asp Met Thr Ser Ser Thr Ser Pro
500 505 510

Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr
515 520 525

Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Pro Ala Val Thr Thr Pro
530 535 540

Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser
545 550 555 560

Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Ser Pro Thr Leu Gly Lys
565 570 575

Thr Ser Pro Thr Ser Ala Val Thr Thr Pro Thr Pro Asn Ala Thr Ser
580 585 590

Pro Thr Leu Gly Lys Thr Ser Pro Thr Ser Ala Val Thr Thr Pro Thr
595 600 605

Pro Asn Ala Thr Gly Pro Thr Val Gly Glu Thr Ser Pro Gln Ala Asn
610 615 620

Ala Thr Asn His Thr Leu Gly Gly Thr Ser Pro Thr Pro Val Val Thr
625 630 635 640

Ser Gln Pro Lys Asn Ala Thr Ser Ala Val Thr Thr Gly Gln His Asn
645 650 655

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

Pro Glu Thr Leu Ser Pro Ser Thr Ser Asp Asn Ser Thr Ser His Met
675 680 685

Pro Leu Leu Thr Ser Ala His Pro Thr Gly Gly Glu Asn Ile Thr Gln
690 695 700

Val Thr Pro Ala Ser Ile Ser Thr His His Val Ser Thr Ser Ser Pro
705 710 715 720

Ala Pro Arg Pro Gly Thr Thr Ser Gln Ala Ser Gly Pro Gly Asn Ser
725 730 735

Ser Thr Ser Thr Lys Pro Gly Glu Val Asn Val Thr Lys Gly Thr Pro
740 745 750

Pro Gln Asn Ala Thr Ser Pro Gln Ala Pro Ser Gly Gln Lys Thr Ala
755 760 765

Val Pro Thr Val Thr Ser Thr Gly Gly Lys Ala Asn Ser Thr Thr Gly
770 775 780

Gly Lys His Thr Thr Gly His Gly Ala Arg Thr Ser Thr Glu Pro Thr
785 790 795 800

Thr Asp Tyr Gly Gly Asp Ser Thr Thr Pro Arg Pro Arg Tyr Asn Ala
805 810 815

Thr Thr Tyr Leu Pro Pro Ser Thr Ser Ser Lys Leu Arg Pro Arg Trp
820 825 830

Thr Phe Thr Ser Pro Pro Val Thr Thr Ala Gln Ala Thr Val Pro Val
835 840 845

Pro Pro Thr Ser Gln Pro Arg Phe Ser Asn Leu Ser Met Leu Val Leu
850 855 860

Gln Trp Ala Ser Leu Ala Val Leu Thr Leu Leu Leu Leu Leu Val Met
865 870 875 880

Ala Asp Cys Ala Phe Arg Arg Asn Leu Ser Thr Ser His Thr Tyr Thr
885 890 895

Thr Pro Pro Tyr Asp Asp Ala Glu Thr Tyr Val
900 905

<210> 60
<211> 906
<212> PRT
<213> Human cytomegalovirus

<400> 60

Met Glu Ser Arg Ile Trp Cys Leu Val Val Cys Val Asn Leu Cys Ile
1 5 10 15

Val Cys Leu Gly Ala Ala Val Ser Ser Ser Ser Thr Ser His Ala Thr
20 25 30

Ser Ser Thr His Asn Gly Ser His Thr Ser Arg Thr Thr Ser Ala Gln
35 40 45

Thr Arg Ser Val Tyr Ser Gln His Val Thr Ser Ser Glu Ala Val Ser
50 55 60

His Arg Ala Asn Glu Thr Ile Tyr Asn Thr Thr Leu Lys Tyr Gly Asp
65 70 75 80

Val Val Gly Val Asn Thr Thr Lys Tyr Pro Tyr Arg Val Cys Ser Met
85 90 95

Ala Gln Gly Thr Asp Leu Ile Arg Phe Glu Arg Asn Ile Ile Cys Thr
100 105 110

Ser Met Lys Pro Ile Asn Glu Asp Leu Asp Glu Gly Ile Met Val Val
115 120 125

Tyr Lys Arg Asn Ile Val Ala His Thr Phe Lys Val Arg Val Tyr Gln
130 135 140

Lys Val Leu Thr Phe Arg Arg Ser Tyr Ala Tyr Ile Tyr Thr Thr Tyr
145 150 155 160

Leu Leu Gly Ser Asn Thr Glu Tyr Val Ala Pro Pro Met Trp Glu Ile
165 170 175

His His Ile Asn Lys Phe Ala Gln Cys Tyr Ser Ser Tyr Ser Arg Val
180 185 190

Ile Gly Gly Thr Val Phe Val Ala Tyr His Arg Asp Ser Tyr Glu Asn
195 200 205

Lys Thr Met Gln Leu Ile Pro Asp Asp Tyr Ser Asn Thr His Ser Thr
210 215 220

Arg Tyr Val Thr Val Lys Asp Gln Trp His Ser Arg Gly Ser Thr Trp
225 230 235 240

Leu Tyr Arg Glu Thr Cys Asn Leu Asn Cys Met Leu Thr Ile Thr Thr
245 250 255

Ala Arg Ser Lys Tyr Pro Tyr His Phe Phe Ala Thr Ser Thr Gly Asp
260 265 270

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

Tyr Phe Gly Glu Asn Ala Asp Lys Phe Phe Ile Phe Pro Asn Tyr Thr
290 295 300

Ile Val Ser Asp Phe Gly Arg Pro Asn Ala Ala Pro Glu Thr His Arg
305 310 315 320

Leu Val Ala Phe Leu Glu Arg Ala Asp Ser Val Ile Ser Trp Asp Ile
325 330 335

Gln Asp Glu Lys Asn Val Thr Cys Gln Leu Thr Phe Trp Glu Ala Ser
340 345 350

Glu Arg Thr Ile Arg Ser Glu Ala Glu Asp Ser Tyr His Phe Ser Ser
355 360 365

Ala Lys Met Thr Ala Thr Phe Leu Ser Lys Lys Gln Glu Val Asn Met
370 375 380

Ser Asp Ser Ala Leu Asp Cys Val Arg Asp Glu Ala Ile Asn Lys Leu
385 390 395 400

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

Asn Val Ser Val Phe Glu Thr Ser Gly Gly Leu Val Val Phe Trp Gln
420 425 430

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

Ser Ser Leu Asn Ile Thr His Arg Thr Arg Arg Ser Thr Ser Asp Asn
450 455 460

Asn Thr Thr His Leu Ser Ser Met Glu Ser Val His Asn Leu Val Tyr
465 470 475 480

Ala Gln Leu Gln Phe Thr Tyr Asp Thr Leu Arg Gly Tyr Ile Asn Arg
485 490 495

Ala Leu Ala Gln Ile Ala Glu Ala Trp Cys Val Asp Gln Arg Arg Thr
500 505 510

Leu Glu Val Phe Lys Glu Leu Ser Lys Ile Asn Pro Ser Ala Ile Leu
515 520 525

Ser Ala Ile Tyr Asn Lys Pro Ile Ala Ala Arg Phe Met Gly Asp Val
530 535 540

Leu Gly Leu Ala Ser Cys Val Thr Ile Asn Gln Thr Ser Val Lys Val
545 550 555 560

Leu Arg Asp Met Asn Val Lys Glu Ser Pro Gly Arg Cys Tyr Ser Arg
565 570 575

Pro Val Val Ile Phe Asn Phe Ala Asn Ser Ser Tyr Val Gln Tyr Gly
580 585 590

Gln Leu Gly Glu Asp Asn Glu Ile Leu Leu Gly Asn His Arg Thr Glu
595 600 605

Glu Cys Gln Leu Pro Ser Leu Lys Ile Phe Ile Ala Gly Asn Ser Ala
610 615 620

Tyr Glu Tyr Val Asp Tyr Leu Phe Lys Arg Met Ile Asp Leu Ser Ser

625 630 635 640

Ile Ser Thr Val Asp Ser Met Ile Ala Leu Asp Ile Asp Pro Leu Glu
645 650 655

Asn Thr Asp Phe Arg Val Leu Glu Leu Tyr Ser Gln Lys Glu Leu Arg
660 665 670

Ser Ser Asn Val Phe Asp Leu Glu Glu Ile Met Arg Glu Phe Asn Ser
675 680 685

Tyr Lys Gln Arg Val Lys Tyr Val Glu Asp Lys Val Val Asp Pro Leu
690 695 700

Pro Pro Tyr Leu Lys Gly Leu Asp Asp Leu Met Ser Gly Leu Gly Ala
705 710 715 720

Ala Gly Lys Ala Val Gly Val Ala Ile Gly Ala Val Gly Gly Ala Val
725 730 735

Ala Ser Val Val Glu Gly Val Ala Thr Phe Leu Lys Asn Pro Phe Gly
740 745 750

Ala Phe Thr Ile Ile Leu Val Ala Ile Ala Val Val Ile Ile Thr Tyr
755 760 765

Leu Ile Tyr Thr Arg Gln Arg Arg Leu Cys Thr Gln Pro Leu Gln Asn
770 775 780

Leu Phe Pro Tyr Leu Val Ser Ala Asp Gly Thr Thr Val Thr Ser Gly
785 790 795 800

Ser Thr Lys Asp Thr Ser Leu Gln Ala Pro Pro Ser Tyr Glu Glu Ser
805 810 815

Val Tyr Asn Ser Gly Arg Lys Gly Pro Gly Pro Pro Ser Ser Asp Ala
820 825 830

Ser Thr Ala Ala Pro Pro Tyr Thr Asn Glu Gln Ala Tyr Gln Met Leu
835 840 845

Leu Ala Leu Ala Arg Leu Asp Ala Glu Gln Arg Ala Gln Gln Asn Gly
850 855 860

Thr Asp Ser Leu Asp Gly Gln Thr Gly Thr Gln Asp Lys Gly Gln Lys
865 870 875 880

Pro Asn Leu Leu Asp Arg Leu Arg His Arg Lys Asn Gly Tyr Arg His
885 890 895

Leu Lys Asp Ser Asp Glu Glu Glu Asn Val
900 905

<210> 61
<211> 171
<212> PRT
<213> Human cytomegalovirus

<400> 61

Met Ser Pro Lys Asp Leu Thr Pro Phe Leu Thr Thr Leu Trp Leu Leu
1 5 10 15

Leu Gly His Ser Arg Val Pro Arg Val Arg Ala Glu Glu Cys Cys Glu
20 25 30

Phe Ile Asn Val Asn His Pro Pro Glu Arg Cys Tyr Asp Phe Lys Met
35 40 45

Cys Asn Arg Phe Thr Val Ala Leu Arg Cys Pro Asp Gly Glu Val Cys
50 55 60

Tyr Ser Pro Glu Lys Thr Ala Glu Ile Arg Gly Ile Val Thr Thr Met
65 70 75 80

Thr His Ser Leu Thr Arg Gln Val Val His Asn Lys Leu Thr Ser Cys
85 90 95

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

Lys Val Asn Asp Lys Ala Gln Tyr Leu Leu Gly Ala Ala Gly Ser Val
115 120 125

Pro Tyr Arg Trp Ile Asn Leu Glu Tyr Asp Lys Ile Thr Arg Ile Val
130 135 140

Gly Leu Asp Gln Tyr Leu Glu Ser Val Lys Lys His Lys Arg Leu Asp
145 150 155 160

Val Cys Arg Ala Lys Met Gly Tyr Met Leu Gln
165 170

<210> 62
<211> 214
<212> PRT
<213> Human cytomegalovirus

<400> 62

Met Leu Arg Leu Leu Leu Arg His His Phe His Cys Leu Leu Leu Cys
1 5 10 15

Ala Val Trp Ala Thr Pro Cys Leu Ala Ser Pro Trp Ser Thr Leu Thr
20 25 30

Ala Asn Gln Asn Pro Ser Pro Pro Trp Ser Lys Leu Thr Tyr Ser Lys
35 40 45

Pro His Asp Ala Ala Thr Phe Tyr Cys Pro Phe Leu Tyr Pro Ser Pro
50 55 60

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

Pro Glu Cys Arg Asn Glu Thr Leu Tyr Leu Leu Tyr Asn Arg Glu Gly
85 90 95

Gln Thr Leu Val Glu Arg Ser Ser Thr Trp Val Lys Lys Val Ile Trp
100 105 110

Tyr Leu Ser Gly Arg Asn Gln Thr Ile Leu Gln Arg Met Pro Arg Thr
115 120 125

Ala Ser Lys Pro Ser Asp Gly Asn Val Gln Ile Ser Val Glu Asp Ala
130 135 140

Lys Ile Phe Gly Ala His Met Val Pro Lys Gln Thr Lys Leu Leu Arg
145 150 155 160

Phe Val Val Asn Asp Gly Thr Arg Tyr Gln Met Cys Val Met Lys Leu
165 170 175

Glu Ser Trp Ala His Val Phe Arg Asp Tyr Ser Val Ser Phe Gln Val
180 185 190

Arg Leu Thr Phe Thr Glu Ala Asn Asn Gln Thr Tyr Thr Phe Cys Thr
195 200 205

His Pro Asn Leu Ile Val
    210

<210> 63
<211> 129
<212> PRT
<213> Human cytomegalovirus

<400> 63

Met Arg Leu Cys Arg Val Trp Leu Ser Val Cys Leu Cys Ala Val Val
1   5   10   15

Leu Gly Gln Cys Gln Arg Glu Thr Ala Glu Lys Asn Asp Tyr Tyr Arg
            20   25   30

Val Pro His Tyr Trp Asp Ala Cys Ser Arg Ala Leu Pro Asp Gln Thr
        35   40   45

Arg Tyr Lys Tyr Val Glu Gln Leu Val Asp Leu Thr Leu Asn Tyr His
    50   55   60

Tyr Asp Ala Ser His Gly Leu Asp Asn Phe Asp Val Leu Lys Arg Ile
65   70   75   80

Asn Val Thr Glu Val Ser Leu Leu Ile Ser Asp Phe Arg Arg Gln Asn
                85   90   95

Arg Arg Gly Gly Thr Asn Lys Arg Thr Thr Phe Asn Ala Ala Gly Ser
            100   105   110

Leu Ala Pro His Ala Arg Ser Leu Glu Phe Ser Val Arg Leu Phe Ala
        115   120   125

Asn

<210> 64
<211> 743
<212> PRT
<213> Human cytomegalovirus

<400> 64

Met Arg Pro Gly Leu Pro Pro Tyr Leu Thr Val Phe Thr Val Tyr Leu
1 5 10 15

Leu Ser His Leu Pro Ser Gln Arg Tyr Gly Ala Asp Ala Ala Ser Glu
20 25 30

Ala Leu Asp Pro His Ala Phe His Leu Leu Leu Asn Thr Tyr Gly Arg
35 40 45

Pro Ile Arg Phe Leu Arg Glu Asn Thr Thr Gln Cys Thr Tyr Asn Ser
50 55 60

Ser Leu Arg Asn Ser Thr Val Val Arg Glu Asn Ala Ile Ser Phe Asn
65 70 75 80

Phe Phe Gln Ser Tyr Asn Gln Tyr Tyr Val Phe His Met Pro Arg Cys
85 90 95

Leu Phe Ala Gly Pro Leu Ala Glu Gln Phe Leu Asn Gln Val Asp Leu
100 105 110

Thr Glu Thr Leu Glu Arg Tyr Gln Gln Arg Leu Asn Thr Tyr Ala Leu
115 120 125

Val Ser Lys Asp Leu Ala Ser Tyr Arg Ser Phe Ser Gln Gln Leu Lys
130 135 140

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Ala Gln Asp Ser Leu Gly Gln Gln Pro Thr Thr Val Pro Pro Pro Ile
145                 150                 155                 160

Asp Leu Ser Ile Pro His Val Trp Met Pro Pro Gln Thr Thr Pro His
                165                 170                 175

Asp Trp Lys Gly Ser His Thr Thr Ser Gly Leu His Arg Pro His Phe
            180                 185                 190

Asn Gln Thr Cys Ile Leu Phe Asp Gly His Asp Leu Leu Phe Ser Thr
        195                 200                 205

Val Thr Pro Cys Leu His Gln Gly Phe Tyr Leu Met Asp Glu Leu Arg
    210                 215                 220

Tyr Val Lys Ile Thr Leu Thr Glu Asp Phe Phe Val Val Thr Val Ser
225                 230                 235                 240

Ile Asp Asp Asp Thr Pro Met Leu Leu Ile Phe Gly His Leu Pro Arg
                245                 250                 255

Val Leu Phe Lys Ala Pro Tyr Gln Arg Asp Asn Phe Ile Leu Arg Gln
            260                 265                 270

Thr Glu Lys His Glu Leu Leu Val Leu Val Lys Lys Ala Gln Leu Asn
        275                 280                 285

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

Phe Asn Tyr Leu Asp Leu Ser Ala Leu Leu Arg Asn Ser Phe His Arg
305                 310                 315                 320
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Tyr Ala Val Asp Val Leu Lys Ser Gly Arg Cys Gln Met Leu Asp Arg
325 330 335

Arg Thr Val Glu Met Ala Phe Ala Tyr Ala Leu Ala Leu Phe Ala Ala
340 345 350

Ala Arg Gln Glu Glu Ala Gly Thr Glu Ile Ser Ile Pro Arg Ala Leu
355 360 365

Asp Arg Gln Ala Ala Leu Leu Gln Ile Gln Glu Phe Met Ile Thr Cys
370 375 380

Leu Ser Gln Thr Pro Pro Arg Thr Thr Leu Leu Leu Tyr Pro Thr Ala
385 390 395 400

Val Asp Leu Ala Lys Arg Ala Leu Trp Thr Pro Asp Gln Ile Thr Asp
405 410 415

Ile Thr Ser Leu Val Arg Leu Val Tyr Ile Leu Ser Lys Gln Asn Gln
420 425 430

Gln His Leu Ile Pro Gln Trp Ala Leu Arg Gln Ile Ala Asp Phe Ala
435 440 445

Leu Gln Leu His Lys Thr His Leu Ala Ser Phe Leu Ser Ala Phe Ala
450 455 460

Arg Gln Glu Leu Tyr Leu Met Gly Ser Leu Val His Ser Met Leu Val
465 470 475 480

His Thr Thr Glu Arg Arg Glu Ile Phe Ile Val Glu Thr Gly Leu Cys
485 490 495

Ser Leu Ala Glu Leu Ser His Phe Thr Gln Leu Leu Ala His Pro His

500 505 510

His Glu Tyr Leu Ser Asp Leu Tyr Thr Pro Cys Ser Ser Ser Gly Arg
515 520 525

Arg Asp His Ser Leu Glu Arg Leu Thr Arg Leu Phe Pro Asp Ala Thr
530 535 540

Val Pro Ala Thr Val Pro Ala Ala Leu Ser Ile Leu Ser Thr Met Gln
545 550 555 560

Pro Ser Thr Leu Glu Thr Phe Pro Asp Leu Phe Cys Leu Pro Leu Gly
565 570 575

Glu Ser Phe Ser Ala Leu Thr Val Ser Glu His Val Ser Tyr Val Val
580 585 590

Thr Asn Gln Tyr Leu Ile Lys Gly Ile Ser Tyr Pro Val Ser Thr Thr
595 600 605

Val Val Gly Gln Ser Leu Ile Ile Thr Gln Thr Asp Ser Gln Thr Lys
610 615 620

Cys Glu Leu Thr Arg Asn Met His Thr Thr His Ser Ile Thr Ala Ala
625 630 635 640

Leu Asn Ile Ser Leu Glu Asn Cys Ala Phe Cys Gln Ser Ala Leu Leu
645 650 655

Glu Tyr Asp Asp Thr Gln Gly Val Ile Asn Ile Met Tyr Met His Asp
660 665 670

Ser Asp Asp Val Leu Phe Ala Leu Asp Pro Tyr Asn Glu Val Val Val
675 680 685

Ser Ser Pro Arg Thr His Tyr Leu Met Leu Leu Lys Asn Gly Thr Val
690 695 700

Leu Glu Val Thr Asp Val Val Val Asp Ala Thr Asp Ser Arg Leu Leu
705 710 715 720

Met Met Ser Val Tyr Ala Leu Ser Ala Ile Ile Gly Ile Tyr Leu Leu
725 730 735

Tyr Arg Met Leu Lys Thr Cys
740

<210> 65
<211> 278
<212> PRT
<213> Human cytomegalovirus

<400> 65

Met Cys Arg Arg Pro Asp Cys Gly Phe Ser Phe Ser Pro Gly Pro Val
1 5 10 15

Val Leu Leu Trp Cys Cys Leu Leu Leu Pro Ile Val Ser Ser Val Ala
20 25 30

Val Ser Val Ala Pro Thr Ala Ala Glu Lys Val Pro Ala Glu Cys Pro
35 40 45

Glu Leu Thr Arg Arg Cys Leu Leu Gly Glu Val Phe Gln Gly Asp Lys
50 55 60

Tyr Glu Ser Trp Leu Arg Pro Leu Val Asn Val Thr Arg Arg Asp Gly
65 70 75 80

Pro Leu Ser Gln Leu Ile Arg Tyr Arg Pro Val Thr Pro Glu Ala Ala
85 90 95

Asn Ser Val Leu Leu Asp Asp Ala Phe Leu Asp Thr Leu Ala Leu Leu
100 105 110

Tyr Asn Asn Pro Asp Gln Leu Arg Ala Leu Leu Thr Leu Leu Ser Ser
115 120 125

Asp Thr Ala Pro Arg Trp Met Thr Val Met Arg Gly Tyr Ser Glu Cys
130 135 140

Gly Asp Gly Ser Pro Ala Val Tyr Thr Cys Val Asp Asp Leu Cys Arg
145 150 155 160

Gly Tyr Asp Leu Thr Arg Leu Ser Tyr Gly Arg Ser Ile Phe Thr Glu
165 170 175

His Val Leu Gly Phe Glu Leu Val Pro Pro Ser Leu Phe Asn Val Val
180 185 190

Val Ala Ile Arg Asn Glu Ala Thr Arg Thr Asn Arg Ala Val Arg Leu
195 200 205

Pro Val Ser Thr Ala Ala Ala Pro Glu Gly Ile Thr Leu Phe Tyr Gly
210 215 220

Leu Tyr Asn Ala Val Lys Glu Phe Cys Leu Arg His Gln Leu Asp Pro
225 230 235 240

Pro Leu Leu Arg His Leu Asp Lys Tyr Tyr Ala Gly Leu Pro Pro Glu
245 250 255

Leu Lys Gln Thr Arg Val Asn Leu Pro Ala His Ser Arg Tyr Gly Pro

260 265 270

Gln Ala Val Asp Ala Arg
275

<210> 66
<211> 272
<212> PRT
<213> Borreliella burgdorferi

<400> 66

Met Lys Lys Tyr Leu Leu Gly Ile Gly Leu Ile Leu Ala Leu Ile Ala
1 5 10 15

Cys Lys Gln Asn Val Ser Ser Leu Asp Glu Lys Asn Ser Val Ser Val
20 25 30

Asp Val Pro Gly Gly Met Lys Val Leu Val Ser Lys Glu Lys Asn Lys
35 40 45

Asp Gly Lys Tyr Asp Leu Met Ala Thr Val Asp Asn Val Asp Leu Lys
50 55 60

Gly Thr Ser Asp Lys Asn Asn Gly Ser Gly Ile Leu Glu Gly Val Lys
65 70 75 80

Ala Asp Lys Ser Lys Val Lys Leu Thr Val Ala Asp Asp Leu Ser Lys
85 90 95

Thr Thr Leu Glu Val Leu Lys Glu Asp Gly Thr Val Val Ser Arg Lys
100 105 110

Val Thr Ser Lys Asp Lys Ser Thr Thr Glu Ala Lys Phe Asn Glu Lys
115 120 125

Gly Glu Leu Ser Glu Lys Thr Met Thr Arg Ala Asn Gly Thr Thr Leu
130 135 140

Glu Tyr Ser Gln Met Thr Asn Glu Asp Asn Ala Ala Lys Ala Val Glu
145 150 155 160

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

Thr Ala Val Glu Ile Lys Glu Gly Thr Val Thr Leu Lys Arg Glu Ile
180 185 190

Asp Lys Asn Gly Lys Val Thr Val Ser Leu Asn Asp Thr Ala Ser Gly
195 200 205

Ser Lys Lys Thr Ala Ser Trp Gln Glu Ser Thr Ser Thr Leu Thr Ile
210 215 220

Ser Ala Asn Ser Lys Lys Thr Lys Asp Leu Val Phe Leu Thr Asn Gly
225 230 235 240

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

Ser Ala Ala Glu Ile Lys Lys Leu Asp Glu Leu Lys Asn Ala Leu Arg
260 265 270

<210> 67
<211> 269
<212> PRT
<213> Bordetella pertussis

<400> 67

Met Arg Cys Thr Arg Ala Ile Arg Gln Thr Ala Arg Thr Gly Trp Leu

1 5 10 15

Thr Trp Leu Ala Ile Leu Ala Val Thr Ala Pro Val Thr Ser Pro Ala
20 25 30

Trp Ala Asp Asp Pro Pro Ala Thr Val Tyr Arg Tyr Asp Ser Arg Pro
35 40 45

Pro Glu Asp Val Phe Gln Asn Gly Phe Thr Ala Trp Gly Asn Asn Asp
50 55 60

Asn Val Leu Asp His Leu Thr Gly Arg Ser Cys Gln Val Gly Ser Ser
65 70 75 80

Asn Ser Ala Phe Val Ser Thr Ser Ser Ser Arg Arg Tyr Thr Glu Val
85 90 95

Tyr Leu Glu His Arg Met Gln Glu Ala Val Glu Ala Glu Arg Ala Gly
100 105 110

Arg Gly Thr Gly His Phe Ile Gly Tyr Ile Tyr Glu Val Arg Ala Asp
115 120 125

Asn Asn Phe Tyr Gly Ala Ala Ser Ser Tyr Phe Glu Tyr Val Asp Thr
130 135 140

Tyr Gly Asp Asn Ala Gly Arg Ile Leu Ala Gly Ala Leu Ala Thr Tyr
145 150 155 160

Gln Ser Glu Tyr Leu Ala His Arg Arg Ile Pro Pro Glu Asn Ile Arg
165 170 175

Arg Val Thr Arg Val Tyr His Asn Gly Ile Thr Gly Glu Thr Thr Thr
180 185 190

Thr Glu Tyr Ser Asn Ala Arg Tyr Val Ser Gln Gln Thr Arg Ala Asn
195 200 205

Pro Asn Pro Tyr Thr Ser Arg Arg Ser Val Ala Ser Ile Val Gly Thr
210 215 220

Leu Val Arg Met Ala Pro Val Ile Gly Ala Cys Met Ala Arg Gln Ala
225 230 235 240

Glu Ser Ser Glu Ala Met Ala Ala Trp Ser Glu Arg Ala Gly Glu Ala
245 250 255

Met Val Leu Val Tyr Tyr Glu Ser Ile Ala Tyr Ser Phe
260 265

<210> 68
<211> 495
<212> PRT
<213> Dengue virus

<400> 68

Met Arg Cys Val Gly Ile Gly Asn Arg Asp Phe Val Glu Gly Leu Ser
1 5 10 15

Gly Ala Thr Trp Val Asp Val Val Leu Glu His Gly Ser Cys Val Thr
20 25 30

Thr Met Ala Lys Asp Lys Pro Thr Leu Asp Ile Glu Leu Leu Lys Thr
35 40 45

Glu Val Thr Asn Pro Ala Val Leu Arg Lys Leu Cys Ile Glu Ala Lys
50 55 60

Ile Ser Asn Thr Thr Thr Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Thr Leu Val Glu Glu Gln Asp Thr Asn Phe Val Cys Arg Arg Thr Phe
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Ile Thr Cys Ala Lys Phe Lys Cys Val Thr Lys Leu Glu Gly Lys
115 120 125

Ile Val Gln Tyr Glu Asn Leu Lys Tyr Ser Val Ile Val Thr Val His
130 135 140

Thr Gly Asp Gln His Gln Val Gly Asn Glu Thr Thr Glu His Gly Thr
145 150 155 160

Thr Ala Thr Ile Thr Pro Gln Ala Pro Thr Ser Glu Ile Gln Leu Thr
165 170 175

Asp Tyr Gly Ala Leu Thr Leu Asp Cys Ser Pro Arg Thr Gly Leu Asp
180 185 190

Phe Asn Glu Met Val Leu Leu Thr Met Glu Lys Lys Ser Trp Leu Val
195 200 205

His Lys Gln Trp Phe Leu Asp Leu Pro Leu Pro Trp Thr Ser Gly Ala
210 215 220

Ser Thr Ser Gln Glu Thr Trp Asn Arg Gln Asp Leu Leu Val Thr Phe
225 230 235 240

Lys Thr Ala His Ala Lys Lys Gln Glu Val Val Val Leu Gly Ser Gln

245 250 255

Glu Gly Ala Met His Thr Ala Leu Thr Gly Ala Thr Glu Ile Gln Thr
260 265 270

Ser Gly Thr Thr Thr Ile Phe Ala Gly His Leu Lys Cys Arg Leu Lys
275 280 285

Met Asp Lys Leu Thr Leu Lys Gly Met Ser Tyr Val Met Cys Thr Gly
290 295 300

Ser Phe Lys Leu Glu Lys Glu Val Ala Glu Thr Gln His Gly Thr Val
305 310 315 320

Leu Val Gln Val Lys Tyr Glu Gly Thr Asp Ala Pro Cys Lys Ile Pro
325 330 335

Phe Ser Ser Gln Asp Glu Lys Gly Val Thr Gln Asn Gly Arg Leu Ile
340 345 350

Thr Ala Asn Pro Ile Val Thr Asp Lys Glu Lys Pro Val Asn Ile Glu
355 360 365

Ala Glu Pro Pro Phe Gly Glu Ser Tyr Ile Val Val Gly Ala Gly Glu
370 375 380

Lys Ala Leu Lys Leu Ser Trp Phe Lys Lys Gly Ser Ser Ile Gly Lys
385 390 395 400

Met Phe Glu Ala Thr Ala Arg Gly Ala Arg Arg Met Ala Ile Leu Gly
405 410 415

Asp Thr Ala Trp Asp Phe Gly Ser Ile Gly Gly Val Phe Thr Ser Val
420 425 430

Gly Lys Leu Ile His Gln Ile Phe Gly Thr Ala Tyr Gly Val Leu Phe
435 440 445

Ser Gly Val Ser Trp Thr Met Lys Ile Gly Ile Gly Ile Leu Leu Thr
450 455 460

Trp Leu Gly Leu Asn Ser Arg Ser Thr Ser Leu Ser Met Thr Cys Ile
465 470 475 480

Ala Val Gly Met Val Thr Leu Tyr Leu Gly Val Met Val Gln Ala
485 490 495

<210> 69
<211> 1255
<212> PRT
<213> Human SARS coronavirus

<400> 69

Met Phe Ile Phe Leu Leu Phe Leu Thr Leu Thr Ser Gly Ser Asp Leu
1 5 10 15

Asp Arg Cys Thr Thr Phe Asp Asp Val Gln Ala Pro Asn Tyr Thr Gln
20 25 30

His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg
35 40 45

Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
50 55 60

Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65 70 75 80

Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
85 90 95

Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
100 105 110

Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
115 120 125

Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
130 135 140

Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
145 150 155 160

Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
165 170 175

Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
180 185 190

Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
195 200 205

Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
210 215 220

Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225 230 235 240

Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
245 250 255

Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile

260 265 270

Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
275 280 285

Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
290 295 300

Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305 310 315 320

Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
325 330 335

Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
340 345 350

Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
355 360 365

Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
370 375 380

Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385 390 395 400

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

Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
420 425 430

Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
435 440 445

Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
450 455 460

Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465 470 475 480

Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
485 490 495

Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
500 505 510

Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
515 520 525

Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
530 535 540

Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
545 550 555 560

Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
565 570 575

Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
580 585 590

Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
595 600 605

Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
610 615 620

Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625 630 635 640

His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
645 650 655

Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
660 665 670

Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
675 680 685

Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
690 695 700

Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705 710 715 720

Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
725 730 735

Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
740 745 750

Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
755 760 765

Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
770 775 780

Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785 790 795 800

Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
805 810 815

Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
820 825 830

Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
835 840 845

Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
850 855 860

Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865 870 875 880

Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
885 890 895

Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
900 905 910

Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
915 920 925

Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
930 935 940

Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945 950 955 960

Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
965 970 975

Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln

980 985 990

Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
995 1000 1005

Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
1010 1015 1020

Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala
1025 1030 1035

Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
1040 1045 1050

Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
1055 1060 1065

Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
1070 1075 1080

Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr
1085 1090 1095

Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
1100 1105 1110

Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
1115 1120 1125

Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
1130 1135 1140

Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
1145 1150 1155

Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys
1160 1165 1170

Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
1175 1180 1185

Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Val Trp Leu Gly Phe Ile
1190 1195 1200

Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Leu Leu Cys Cys
1205 1210 1215

Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys Gly
1220 1225 1230

Ser Cys Cys Lys Phe Asp Glu Asp Asp Ser Glu Pro Val Leu Lys
1235 1240 1245

Gly Val Lys Leu His Tyr Thr
1250 1255

<210> 70
<211> 1353
<212> PRT
<213> Middle East respiratory syndrome-related coronavirus

<400> 70

Met Ile His Ser Val Phe Leu Leu Met Phe Leu Leu Thr Pro Thr Glu
1 5 10 15

Ser Tyr Val Asp Val Gly Pro Asp Ser Ile Lys Ser Ala Cys Ile Glu
20 25 30

Val Asp Ile Gln Gln Thr Phe Phe Asp Lys Thr Trp Pro Arg Pro Ile
35 40 45

Asp Val Ser Lys Ala Asp Gly Ile Ile Tyr Pro Gln Gly Arg Thr Tyr
50 55 60

Ser Asn Ile Thr Ile Thr Tyr Gln Gly Leu Phe Pro Tyr Gln Gly Asp
65 70 75 80

His Gly Asp Met Tyr Val Tyr Ser Ala Gly His Ala Thr Gly Thr Thr
85 90 95

Pro Gln Lys Leu Phe Val Ala Asn Tyr Ser Gln Asp Val Lys Gln Phe
100 105 110

Ala Asn Gly Phe Val Val Arg Ile Gly Ala Ala Ala Asn Ser Thr Gly
115 120 125

Thr Val Ile Ile Ser Pro Ser Thr Ser Ala Thr Ile Arg Lys Ile Tyr
130 135 140

Pro Ala Phe Met Leu Gly Ser Ser Val Gly Asn Phe Ser Asp Gly Lys
145 150 155 160

Met Gly Arg Phe Phe Asn His Thr Leu Val Leu Leu Pro Asp Gly Cys
165 170 175

Gly Thr Leu Leu Arg Ala Phe Tyr Cys Ile Leu Glu Pro Arg Ser Gly
180 185 190

Asn His Cys Pro Ala Gly Asn Ser Tyr Thr Ser Phe Ala Thr Tyr His
195 200 205

Thr Pro Ala Thr Asp Cys Ser Asp Gly Asn Tyr Asn Arg Asn Ala Ser

210 215 220

Leu Asn Ser Phe Lys Glu Tyr Phe Asn Leu Arg Asn Cys Thr Phe Met
225 230 235 240

Tyr Thr Tyr Asn Ile Thr Glu Asp Glu Ile Leu Glu Trp Phe Gly Ile
245 250 255

Thr Gln Thr Ala Gln Gly Val His Leu Phe Ser Ser Arg Tyr Val Asp
260 265 270

Leu Tyr Gly Gly Asn Met Phe Gln Phe Ala Thr Leu Pro Val Tyr Asp
275 280 285

Thr Ile Lys Tyr Tyr Ser Ile Ile Pro His Ser Ile Arg Ser Ile Gln
290 295 300

Ser Asp Arg Lys Ala Trp Ala Ala Phe Tyr Val Tyr Lys Leu Gln Pro
305 310 315 320

Leu Thr Phe Leu Leu Asp Phe Ser Val Asp Gly Tyr Ile Arg Arg Ala
325 330 335

Ile Asp Cys Gly Phe Asn Asp Leu Ser Gln Leu His Cys Ser Tyr Glu
340 345 350

Ser Phe Asp Val Glu Ser Gly Val Tyr Ser Val Ser Ser Phe Glu Ala
355 360 365

Lys Pro Ser Gly Ser Val Val Glu Gln Ala Glu Gly Val Glu Cys Asp
370 375 380

Phe Ser Pro Leu Leu Ser Gly Thr Pro Pro Gln Val Tyr Asn Phe Lys
385 390 395 400

Arg Leu Val Phe Thr Asn Cys Asn Tyr Asn Leu Thr Lys Leu Leu Ser
405 410 415

Leu Phe Ser Val Asn Asp Phe Thr Cys Ser Gln Ile Ser Pro Ala Ala
420 425 430

Ile Ala Ser Asn Cys Tyr Ser Ser Leu Ile Leu Asp Tyr Phe Ser Tyr
435 440 445

Pro Leu Ser Met Lys Ser Asp Leu Ser Val Ser Ser Ala Gly Pro Ile
450 455 460

Ser Gln Phe Asn Tyr Lys Gln Ser Phe Ser Asn Pro Thr Cys Leu Ile
465 470 475 480

Leu Ala Thr Val Pro His Asn Leu Thr Thr Ile Thr Lys Pro Leu Lys
485 490 495

Tyr Ser Tyr Ile Asn Lys Cys Ser Arg Leu Leu Ser Asp Asp Arg Thr
500 505 510

Glu Val Pro Gln Leu Val Asn Ala Asn Gln Tyr Ser Pro Cys Val Ser
515 520 525

Ile Val Pro Ser Thr Val Trp Glu Asp Gly Asp Tyr Tyr Arg Lys Gln
530 535 540

Leu Ser Pro Leu Glu Gly Gly Gly Trp Leu Val Ala Ser Gly Ser Thr
545 550 555 560

Val Ala Met Thr Glu Gln Leu Gln Met Gly Phe Gly Ile Thr Val Gln
565 570 575

Tyr Gly Thr Asp Thr Asn Ser Val Cys Pro Lys Leu Glu Phe Ala Asn
580 585 590

Asp Thr Lys Ile Ala Ser Gln Leu Gly Asn Cys Val Glu Tyr Ser Leu
595 600 605

Tyr Gly Val Ser Gly Arg Gly Val Phe Gln Asn Cys Thr Ala Val Gly
610 615 620

Val Arg Gln Gln Arg Phe Val Tyr Asp Ala Tyr Gln Asn Leu Val Gly
625 630 635 640

Tyr Tyr Ser Asp Asp Gly Asn Tyr Tyr Cys Leu Arg Ala Cys Val Ser
645 650 655

Val Pro Val Ser Val Ile Tyr Asp Lys Glu Thr Lys Thr His Ala Thr
660 665 670

Leu Phe Gly Ser Val Ala Cys Glu His Ile Ser Ser Thr Met Ser Gln
675 680 685

Tyr Ser Arg Ser Thr Arg Ser Met Leu Lys Arg Arg Asp Ser Thr Tyr
690 695 700

Gly Pro Leu Gln Thr Pro Val Gly Cys Val Leu Gly Leu Val Asn Ser
705 710 715 720

Ser Leu Phe Val Glu Asp Cys Lys Leu Pro Leu Gly Gln Ser Leu Cys
725 730 735

Ala Leu Pro Asp Thr Pro Ser Thr Leu Thr Pro Arg Ser Val Arg Ser
740 745 750

Val Pro Gly Glu Met Arg Leu Ala Ser Ile Ala Phe Asn His Pro Ile
        755   760   765

Gln Val Asp Gln Leu Asn Ser Ser Tyr Phe Lys Leu Ser Ile Pro Thr
    770   775   780

Asn Phe Ser Phe Gly Val Thr Gln Glu Tyr Ile Gln Thr Thr Ile Gln
785   790   795   800

Lys Val Thr Val Asp Cys Lys Gln Tyr Val Cys Asn Gly Phe Gln Lys
                805   810   815

Cys Glu Gln Leu Leu Arg Glu Tyr Gly Gln Phe Cys Ser Lys Ile Asn
            820   825   830

Gln Ala Leu His Gly Ala Asn Leu Arg Gln Asp Asp Ser Val Arg Asn
        835   840   845

Leu Phe Ala Ser Val Lys Ser Ser Gln Ser Ser Pro Ile Ile Pro Gly
    850   855   860

Phe Gly Gly Asp Phe Asn Leu Thr Leu Leu Glu Pro Val Ser Ile Ser
865   870   875   880

Thr Gly Ser Arg Ser Ala Arg Ser Ala Ile Glu Asp Leu Leu Phe Asp
                885   890   895

Lys Val Thr Ile Ala Asp Pro Gly Tyr Met Gln Gly Tyr Asp Asp Cys
            900   905   910

Met Gln Gln Gly Pro Ala Ser Ala Arg Asp Leu Ile Cys Ala Gln Tyr
        915   920   925

Val Ala Gly Tyr Lys Val Leu Pro Pro Leu Met Asp Val Asn Met Glu

930 935 940

Ala Ala Tyr Thr Ser Ser Leu Leu Gly Ser Ile Ala Gly Val Gly Trp
945 950 955 960

Thr Ala Gly Leu Ser Ser Phe Ala Ala Ile Pro Phe Ala Gln Ser Ile
965 970 975

Phe Tyr Arg Leu Asn Gly Val Gly Ile Thr Gln Gln Val Leu Ser Glu
980 985 990

Asn Gln Lys Leu Ile Ala Asn Lys Phe Asn Gln Ala Leu Gly Ala Met
995 1000 1005

Gln Thr Gly Phe Thr Thr Thr Asn Glu Ala Phe His Lys Val Gln
1010 1015 1020

Asp Ala Val Asn Asn Asn Ala Gln Ala Leu Ser Lys Leu Ala Ser
1025 1030 1035

Glu Leu Ser Asn Thr Phe Gly Ala Ile Ser Ala Ser Ile Gly Asp
1040 1045 1050

Ile Ile Gln Arg Leu Asp Val Leu Glu Gln Asp Ala Gln Ile Asp
1055 1060 1065

Arg Leu Ile Asn Gly Arg Leu Thr Thr Leu Asn Ala Phe Val Ala
1070 1075 1080

Gln Gln Leu Val Arg Ser Glu Ser Ala Ala Leu Ser Ala Gln Leu
1085 1090 1095

Ala Lys Asp Lys Val Asn Glu Cys Val Lys Ala Gln Ser Lys Arg
1100 1105 1110

Ser Gly Phe Cys Gly Gln Gly Thr His Ile Val Ser Phe Val Val
1115 1120 1125

Asn Ala Pro Asn Gly Leu Tyr Phe Met His Val Gly Tyr Tyr Pro
1130 1135 1140

Ser Asn His Ile Glu Val Val Ser Ala Tyr Gly Leu Cys Asp Ala
1145 1150 1155

Ala Asn Pro Thr Asn Cys Ile Ala Pro Val Asn Gly Tyr Phe Ile
1160 1165 1170

Lys Thr Asn Asn Thr Arg Ile Val Asp Glu Trp Ser Tyr Thr Gly
1175 1180 1185

Ser Ser Phe Tyr Ala Pro Glu Pro Ile Thr Ser Leu Asn Thr Lys
1190 1195 1200

Tyr Val Ala Pro Gln Val Thr Tyr Gln Asn Ile Ser Thr Asn Leu
1205 1210 1215

Pro Pro Pro Leu Leu Gly Asn Ser Thr Gly Ile Asp Phe Gln Asp
1220 1225 1230

Glu Leu Asp Glu Phe Phe Lys Asn Val Ser Thr Ser Ile Pro Asn
1235 1240 1245

Phe Gly Ser Leu Thr Gln Ile Asn Thr Thr Leu Leu Asp Leu Thr
1250 1255 1260

Tyr Glu Met Leu Ser Leu Gln Gln Val Val Lys Ala Leu Asn Glu
1265 1270 1275

Ser Tyr Ile Asp Leu Lys Glu Leu Gly Asn Tyr Thr Tyr Tyr Asn
1280 1285 1290

Lys Trp Pro Trp Tyr Ile Trp Leu Gly Phe Ile Ala Gly Leu Val
1295 1300 1305

Ala Leu Ala Leu Cys Val Phe Phe Ile Leu Cys Cys Thr Gly Cys
1310 1315 1320

Gly Thr Asn Cys Met Gly Lys Leu Lys Cys Asn Arg Cys Cys Asp
1325 1330 1335

Arg Tyr Glu Glu Tyr Asp Leu Glu Pro His Lys Val His Val His
1340 1345 1350

<210> 71
<211> 676
<212> PRT
<213> Zaire ebolavirus

<400> 71

Met Gly Val Thr Gly Ile Leu Gln Leu Pro Arg Asp Arg Phe Lys Arg
1 5 10 15

Thr Ser Phe Phe Leu Trp Val Ile Ile Leu Phe Gln Arg Thr Phe Ser
20 25 30

Ile Pro Leu Gly Val Ile His Asn Ser Thr Leu Gln Val Ser Asp Val
35 40 45

Asp Lys Leu Val Cys Arg Asp Lys Leu Ser Ser Thr Asn Gln Leu Arg
50 55 60

Ser Val Gly Leu Asn Leu Glu Gly Asn Gly Val Ala Thr Asp Val Pro

65 70 75 80

Ser Ala Thr Lys Arg Trp Gly Phe Arg Ser Gly Val Pro Pro Lys Val
85 90 95

Val Asn Tyr Glu Ala Gly Glu Trp Ala Glu Asn Cys Tyr Asn Leu Glu
100 105 110

Ile Lys Lys Pro Asp Gly Ser Glu Cys Leu Pro Ala Ala Pro Asp Gly
115 120 125

Ile Arg Gly Phe Pro Arg Cys Arg Tyr Val His Lys Val Ser Gly Thr
130 135 140

Gly Pro Cys Ala Gly Asp Phe Ala Phe His Lys Glu Gly Ala Phe Phe
145 150 155 160

Leu Tyr Asp Arg Leu Ala Ser Thr Val Ile Tyr Arg Gly Thr Thr Phe
165 170 175

Ala Glu Gly Val Val Ala Phe Leu Ile Leu Pro Gln Ala Lys Lys Asp
180 185 190

Phe Phe Ser Ser His Pro Leu Arg Glu Pro Val Asn Ala Thr Glu Asp
195 200 205

Pro Ser Ser Gly Tyr Tyr Ser Thr Thr Ile Arg Tyr Gln Ala Thr Gly
210 215 220

Phe Gly Thr Asn Glu Thr Glu Tyr Leu Phe Glu Val Asp Asn Leu Thr
225 230 235 240

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

Asn Glu Thr Ile Tyr Thr Ser Gly Lys Arg Ser Asn Thr Thr Gly Lys
260 265 270

Leu Ile Trp Lys Val Asn Pro Glu Ile Asp Thr Thr Ile Gly Glu Trp
275 280 285

Ala Phe Trp Glu Thr Lys Lys Asn Leu Thr Arg Lys Ile Arg Ser Glu
290 295 300

Glu Leu Ser Phe Thr Val Val Ser Asn Gly Ala Lys Asn Ile Ser Gly
305 310 315 320

Gln Ser Pro Ala Arg Thr Ser Ser Asp Pro Gly Thr Asn Thr Thr Thr
325 330 335

Glu Asp His Lys Ile Met Ala Ser Glu Asn Ser Ser Ala Met Val Gln
340 345 350

Val His Ser Gln Gly Arg Glu Ala Ala Val Ser His Leu Thr Thr Leu
355 360 365

Ala Thr Ile Ser Thr Ser Pro Gln Ser Leu Thr Thr Lys Pro Gly Pro
370 375 380

Asp Asn Ser Thr His Asn Thr Pro Val Tyr Lys Leu Asp Ile Ser Glu
385 390 395 400

Ala Thr Gln Val Glu Gln His His Arg Arg Thr Asp Asn Asp Ser Thr
405 410 415

Ala Ser Asp Thr Pro Ser Ala Thr Thr Ala Ala Gly Pro Pro Lys Ala
420 425 430

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

Thr Thr Ser Pro Gln Asn His Ser Glu Thr Ala Gly Asn Asn Asn Thr
450 455 460

His His Gln Asp Thr Gly Glu Glu Ser Ala Ser Ser Gly Lys Leu Gly
465 470 475 480

Leu Ile Thr Asn Thr Ile Ala Gly Val Ala Gly Leu Ile Thr Gly Gly
485 490 495

Arg Arg Thr Arg Arg Glu Ala Ile Val Asn Ala Gln Pro Lys Cys Asn
500 505 510

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

Leu Ala Trp Ile Pro Tyr Phe Gly Pro Ala Ala Glu Gly Ile Tyr Ile
530 535 540

Glu Gly Leu Met His Asn Gln Asp Gly Leu Ile Cys Gly Leu Arg Gln
545 550 555 560

Leu Ala Asn Glu Thr Thr Gln Ala Leu Gln Leu Phe Leu Arg Ala Thr
565 570 575

Thr Glu Leu Arg Thr Phe Ser Ile Leu Asn Arg Lys Ala Ile Asp Phe
580 585 590

Leu Leu Gln Arg Trp Gly Gly Thr Cys His Ile Leu Gly Pro Asp Cys
595 600 605

Cys Ile Glu Pro His Asp Trp Thr Lys Asn Ile Thr Asp Lys Ile Asp
610 615 620

Gln Ile Ile His Asp Phe Val Asp Lys Thr Leu Pro Asp Gln Gly Asp
625 630 635 640

Asn Asp Asn Trp Trp Thr Gly Trp Arg Gln Trp Ile Pro Ala Gly Ile
645 650 655

Gly Val Thr Gly Val Ile Ile Ala Val Ile Ala Leu Phe Cys Ile Cys
660 665 670

Lys Phe Val Phe
675

<210> 72
<211> 681
<212> PRT
<213> Lake Victoria marburgvirus

<400> 72

Met Lys Thr Thr Cys Phe Leu Ile Ser Leu Ile Leu Ile Gln Gly Thr
1 5 10 15

Lys Asn Leu Pro Ile Leu Glu Ile Ala Ser Asn Asn Gln Pro Gln Asn
20 25 30

Val Asp Ser Val Cys Ser Gly Thr Leu Gln Lys Thr Glu Asp Val His
35 40 45

Leu Met Gly Phe Thr Leu Ser Gly Gln Lys Val Ala Asp Ser Pro Leu
50 55 60

Glu Ala Ser Lys Arg Trp Ala Phe Arg Thr Gly Val Pro Pro Lys Asn
65 70 75 80

Val Glu Tyr Thr Glu Gly Glu Glu Ala Lys Thr Cys Tyr Asn Ile Ser
85 90 95

Val Thr Asp Pro Ser Gly Lys Ser Leu Leu Leu Asp Pro Pro Thr Asn
100 105 110

Ile Arg Asp Tyr Pro Lys Cys Lys Thr Ile His His Ile Gln Gly Gln
115 120 125

Asn Pro His Ala Gln Gly Ile Ala Leu His Leu Trp Gly Ala Phe Phe
130 135 140

Leu Tyr Asp Arg Ile Ala Ser Thr Thr Met Tyr Arg Gly Lys Val Phe
145 150 155 160

Thr Glu Gly Asn Ile Ala Ala Met Ile Val Asn Lys Thr Val His Lys
165 170 175

Met Ile Phe Ser Arg Gln Gly Gln Gly Tyr Arg His Met Asn Leu Thr
180 185 190

Ser Thr Asn Lys Tyr Trp Thr Ser Ser Asn Gly Thr Gln Thr Asn Asp
195 200 205

Thr Gly Cys Phe Gly Ala Leu Gln Glu Tyr Asn Ser Thr Lys Asn Gln
210 215 220

Thr Cys Ala Pro Ser Lys Ile Pro Pro Pro Leu Pro Thr Ala Arg Pro
225 230 235 240

Glu Ile Lys Leu Thr Ser Thr Pro Thr Asp Ala Thr Lys Leu Asn Thr
245 250 255

Thr Asp Pro Ser Ser Asp Asp Glu Asp Leu Ala Thr Ser Gly Ser Gly
260 265 270

Ser Gly Glu Arg Glu Pro His Thr Thr Ser Asp Ala Val Thr Lys Gln
275 280 285

Gly Leu Ser Ser Thr Met Pro Pro Thr Pro Ser Pro Gln Pro Ser Thr
290 295 300

Pro Gln Gln Gly Gly Asn Asn Thr Asn His Ser Gln Asp Ala Val Thr
305 310 315 320

Glu Leu Asp Lys Asn Asn Thr Thr Ala Gln Pro Ser Met Pro Pro His
325 330 335

Asn Thr Thr Thr Ile Ser Thr Asn Asn Thr Ser Lys His Asn Phe Ser
340 345 350

Thr Leu Ser Ala Pro Leu Gln Asn Thr Thr Asn Asp Asn Thr Gln Ser
355 360 365

Thr Ile Thr Glu Asn Glu Gln Thr Ser Ala Pro Ser Ile Thr Thr Leu
370 375 380

Pro Pro Thr Gly Asn Pro Thr Thr Ala Lys Ser Thr Ser Ser Lys Lys
385 390 395 400

Gly Pro Ala Thr Thr Ala Pro Asn Thr Thr Asn Glu His Phe Thr Ser
405 410 415

Pro Pro Pro Thr Pro Ser Ser Thr Ala Gln His Leu Val Tyr Phe Arg
420 425 430

Arg Lys Arg Ser Ile Leu Trp Arg Glu Gly Asp Met Phe Pro Phe Leu
435 440 445

Asp Gly Leu Ile Asn Ala Pro Ile Asp Phe Asp Pro Val Pro Asn Thr
450 455 460

Lys Thr Ile Phe Asp Glu Ser Ser Ser Ser Gly Ala Ser Ala Glu Glu
465 470 475 480

Asp Gln His Ala Ser Pro Asn Ile Ser Leu Thr Leu Ser Tyr Phe Pro
485 490 495

Asn Ile Asn Glu Asn Thr Ala Tyr Ser Gly Glu Asn Glu Asn Asp Cys
500 505 510

Asp Ala Glu Leu Arg Ile Trp Ser Val Gln Glu Asp Asp Leu Ala Ala
515 520 525

Gly Leu Ser Trp Ile Pro Phe Phe Gly Pro Gly Ile Glu Gly Leu Tyr
530 535 540

Thr Ala Val Leu Ile Lys Asn Gln Asn Asn Leu Val Cys Arg Leu Arg
545 550 555 560

Arg Leu Ala Asn Gln Thr Ala Lys Ser Leu Glu Leu Leu Leu Arg Val
565 570 575

Thr Thr Glu Glu Arg Thr Phe Ser Leu Ile Asn Arg His Ala Ile Asp
580 585 590

Phe Leu Leu Thr Arg Trp Gly Gly Thr Cys Lys Val Leu Gly Pro Asp
595 600 605

Cys Cys Ile Gly Ile Glu Asp Leu Ser Lys Asn Ile Ser Glu Gln Ile

610 615 620

Asp Gln Ile Lys Lys Asp Glu Gln Lys Glu Gly Thr Gly Trp Gly Leu
625 630 635 640

Gly Gly Lys Trp Trp Thr Ser Asp Trp Gly Val Leu Thr Asn Leu Gly
645 650 655

Ile Leu Leu Leu Leu Ser Ile Ala Val Leu Ile Ala Leu Ser Cys Ile
660 665 670

Cys Arg Ile Phe Thr Lys Tyr Ile Gly
675 680

<210> 73
<211> 630
<212> PRT
<213> Hanta virus

<400> 73

Leu Arg Asn Val Tyr Asp Met Lys Ile Glu Cys Pro His Thr Val Ser
1 5 10 15

Phe Gly Glu Asn Ser Val Ile Gly Tyr Val Glu Leu Pro Pro Val Pro
20 25 30

Leu Ala Asp Thr Ala Gln Met Val Pro Glu Ser Ser Cys Asn Met Asp
35 40 45

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

Arg Gly Lys Ala Asp Gln Ser Gln Ser Ser Gln Asn Ser Phe Glu Thr
65 70 75 80

Val Ser Thr Glu Val Asp Leu Lys Gly Thr Cys Val Leu Lys His Lys
85 90 95

Met Val Glu Glu Ser Tyr Arg Ser Arg Lys Ser Val Thr Cys Tyr Asp
100 105 110

Leu Ser Cys Asn Ser Thr Tyr Cys Lys Pro Thr Leu Tyr Met Ile Val
115 120 125

Pro Ile His Ala Cys Asn Met Met Lys Ser Cys Leu Ile Ala Leu Gly
130 135 140

Pro Tyr Arg Val Gln Val Val Tyr Glu Arg Ser Tyr Cys Met Thr Gly
145 150 155 160

Val Leu Ile Glu Gly Lys Cys Phe Val Pro Asp Gln Ser Val Val Ser
165 170 175

Ile Ile Lys His Gly Ile Phe Asp Ile Ala Ser Val His Ile Val Cys
180 185 190

Phe Phe Val Ala Val Lys Gly Asn Thr Tyr Lys Ile Phe Glu Gln Val
195 200 205

Lys Lys Ser Phe Glu Ser Thr Cys Asn Asp Thr Glu Asn Lys Val Gln
210 215 220

Gly Tyr Tyr Ile Cys Ile Val Gly Gly Asn Ser Ala Pro Ile Tyr Val
225 230 235 240

Pro Thr Leu Asp Asp Phe Arg Ser Met Glu Ala Phe Thr Gly Ile Phe
245 250 255

Arg Ser Pro His Gly Glu Asp His Asp Leu Ala Gly Glu Glu Ile Ala
260 265 270

Ser Tyr Ser Ile Val Gly Pro Ala Asn Ala Lys Val Pro His Ser Ala
275 280 285

Ser Ser Asp Thr Leu Ser Leu Ile Ala Tyr Ser Gly Ile Pro Ser Tyr
290 295 300

Ser Ser Leu Ser Ile Leu Thr Ser Ser Thr Glu Ala Lys His Val Phe
305 310 315 320

Ser Pro Gly Leu Phe Pro Lys Leu Asn His Thr Asn Cys Asp Lys Ser
325 330 335

Ala Ile Pro Leu Ile Trp Thr Gly Met Ile Asp Leu Pro Gly Tyr Tyr
340 345 350

Glu Ala Val His Pro Cys Thr Val Phe Cys Val Leu Ser Gly Pro Gly
355 360 365

Ala Ser Cys Glu Ala Phe Ser Glu Gly Gly Ile Phe Asn Ile Thr Ser
370 375 380

Pro Met Cys Leu Val Ser Lys Gln Asn Arg Phe Arg Leu Thr Glu Gln
385 390 395 400

Gln Val Asn Phe Val Cys Gln Arg Val Asp Met Asp Ile Val Val Tyr
405 410 415

Cys Asn Gly Gln Arg Lys Val Ile Leu Thr Lys Thr Leu Val Ile Gly
420 425 430

Gln Cys Ile Tyr Thr Ile Thr Ser Leu Phe Ser Leu Leu Pro Gly Val

435 440 445

Ala His Ser Ile Ala Val Glu Leu Cys Val Pro Gly Phe His Gly Trp
450 455 460

Ala Thr Ala Ala Leu Leu Val Thr Phe Cys Phe Gly Trp Val Leu Ile
465 470 475 480

Pro Ala Ile Thr Phe Ile Ile Leu Thr Val Leu Lys Phe Ile Ala Asn
485 490 495

Ile Phe His Thr Ser Asn Gln Glu Asn Arg Leu Lys Ser Val Leu Arg
500 505 510

Lys Ile Lys Glu Glu Phe Glu Lys Thr Lys Gly Ser Met Val Cys Asp
515 520 525

Val Cys Lys Tyr Glu Cys Glu Thr Tyr Lys Glu Leu Lys Ala His Gly
530 535 540

Val Ser Cys Pro Gln Ser Gln Cys Pro Tyr Cys Phe Thr His Cys Glu
545 550 555 560

Pro Thr Glu Ala Ala Phe Gln Ala His Tyr Lys Val Cys Gln Val Thr
565 570 575

His Arg Phe Arg Asp Asp Leu Lys Lys Thr Val Thr Pro Gln Asn Phe
580 585 590

Thr Pro Gly Cys Tyr Arg Thr Leu Asn Leu Phe Arg Tyr Lys Ser Arg
595 600 605

Cys Tyr Ile Phe Thr Met Trp Ile Phe Leu Leu Val Leu Glu Ser Ile
610 615 620

Leu Trp Ala Ala Ser Ala
625 630

<210> 74
<211> 487
<212> PRT
<213> Hanta virus

<400> 74

Ser Glu Thr Pro Leu Thr Pro Val Trp Asn Asp Asn Ala His Gly Val
1 5 10 15

Gly Ser Val Pro Met His Thr Asp Leu Glu Leu Asp Phe Ser Leu Thr
20 25 30

Ser Ser Ser Lys Tyr Thr Tyr Arg Arg Lys Leu Thr Asn Pro Leu Glu
35 40 45

Glu Ala Gln Ser Ile Asp Leu His Ile Glu Ile Glu Glu Gln Thr Ile
50 55 60

Gly Val Asp Val His Ala Leu Gly His Trp Phe Asp Gly Arg Leu Asn
65 70 75 80

Leu Lys Thr Ser Phe His Cys Tyr Gly Ala Cys Thr Lys Tyr Glu Tyr
85 90 95

Pro Trp His Thr Ala Lys Cys His Tyr Glu Arg Asp Tyr Gln Tyr Glu
100 105 110

Thr Ser Trp Gly Cys Asn Pro Ser Asp Cys Pro Gly Val Gly Thr Gly
115 120 125

Cys Thr Ala Cys Gly Leu Tyr Leu Asp Gln Leu Lys Pro Val Gly Ser
130 135 140

Ala Tyr Lys Ile Ile Thr Ile Arg Tyr Ser Arg Arg Val Cys Val Gln
145 150 155 160

Phe Gly Glu Glu Asn Leu Cys Lys Ile Ile Asp Met Asn Asp Cys Phe
165 170 175

Val Ser Arg His Val Lys Val Cys Ile Ile Gly Thr Val Ser Lys Phe
180 185 190

Ser Gln Gly Asp Thr Leu Leu Phe Phe Gly Pro Leu Glu Gly Gly Gly
195 200 205

Leu Ile Phe Lys His Trp Cys Thr Ser Thr Cys Gln Phe Gly Asp Pro
210 215 220

Gly Asp Ile Met Ser Pro Arg Asp Lys Gly Phe Leu Cys Pro Glu Phe
225 230 235 240

Pro Gly Ser Phe Arg Lys Lys Cys Asn Phe Ala Thr Thr Pro Ile Cys
245 250 255

Glu Tyr Asp Gly Asn Met Val Ser Gly Tyr Lys Lys Val Met Ala Thr
260 265 270

Ile Asp Ser Phe Gln Ser Phe Asn Thr Ser Thr Met His Phe Thr Asp
275 280 285

Glu Arg Ile Glu Trp Lys Asp Pro Asp Gly Met Leu Arg Asp His Ile
290 295 300

Asn Ile Leu Val Thr Lys Asp Ile Asp Phe Asp Asn Leu Gly Glu Asn

305 310 315 320

Pro Cys Lys Ile Gly Leu Gln Thr Ser Ser Ile Glu Gly Ala Trp Gly
325 330 335

Ser Gly Val Gly Phe Thr Leu Thr Cys Leu Val Ser Leu Thr Glu Cys
340 345 350

Pro Thr Phe Leu Thr Ser Ile Lys Ala Cys Asp Lys Ala Ile Cys Tyr
355 360 365

Gly Ala Glu Ser Val Thr Leu Thr Arg Gly Gln Asn Thr Val Lys Val
370 375 380

Ser Gly Lys Gly Gly His Ser Gly Ser Thr Phe Arg Cys Cys His Gly
385 390 395 400

Glu Asp Cys Ser Gln Ile Gly Leu His Ala Ala Ala Pro His Leu Asp
405 410 415

Lys Val Asn Gly Ile Ser Glu Ile Glu Asn Ser Lys Val Tyr Asp Asp
420 425 430

Gly Ala Pro Gln Cys Gly Ile Lys Cys Trp Phe Val Lys Ser Gly Glu
435 440 445

Trp Ile Ser Gly Ile Phe Ser Gly Asn Trp Ile Val Leu Ile Val Leu
450 455 460

Cys Val Phe Leu Leu Phe Ser Leu Val Leu Leu Ser Ile Leu Cys Pro
465 470 475 480

Val Arg Lys His Lys Lys Ser
485

<210> 75
<211> 226
<212> PRT
<213> Hepatitis B

<400> 75

Met Glu Asn Ile Thr Ser Gly Phe Leu Gly Pro Leu Leu Val Leu Gln
1 5 10 15

Ala Gly Phe Phe Leu Leu Thr Lys Ile Leu Thr Ile Pro Gln Ser Leu
20 25 30

Asn Ser Trp Trp Thr Ser Leu Ser Phe Leu Gly Gly Asn Thr Val Cys
35 40 45

Leu Gly Gln Asn Ser Gln Ser Pro Thr Ser Asn His Ser Pro Thr Ser
50 55 60

Cys Pro Pro Thr Cys Pro Gly Tyr Arg Trp Met Cys Leu Arg Arg Phe
65 70 75 80

Ile Ile Phe Leu Phe Ile Leu Leu Leu Cys Leu Ile Phe Leu Leu Val
85 90 95

Leu Leu Asp Tyr Gln Gly Met Leu Pro Val Cys Pro Leu Ile Pro Gly
100 105 110

Ser Ser Thr Thr Ser Thr Gly Pro Cys Arg Thr Cys Lys Thr Pro Ala
115 120 125

Gln Gly Thr Ser Met Tyr Pro Ser Cys Cys Cys Thr Lys Pro Ser Asp
130 135 140

Gly Asn Cys Thr Cys Ile Pro Ile Pro Ser Ser Trp Ala Phe Gly Lys
145 150 155 160

Phe Leu Trp Glu Trp Ala Ser Ala Arg Phe Ser Trp Leu Ser Leu Ile
165 170 175

Val Pro Phe Val Gln Trp Phe Val Gly Leu Ser Pro Thr Val Trp Leu
180 185 190

Ser Val Ile Trp Met Met Trp Tyr Trp Gly Pro Ser Leu Tyr Ser Ile
195 200 205

Leu Ser Pro Phe Leu Pro Leu Leu Pro Ile Phe Phe Cys Leu Trp Val
210 215 220

Tyr Ile
225

<210> 76
<211> 617
<212> PRT
<213> Measles virus

<400> 76

Met Ser Pro Gln Arg Asp Arg Ile Asn Ala Phe Tyr Lys Asp Asn Pro
1 5 10 15

His Pro Lys Gly Ser Arg Ile Val Ile Asn Arg Glu His Leu Met Ile
20 25 30

Asp Arg Pro Tyr Val Leu Leu Ala Val Leu Phe Val Met Phe Leu Ser
35 40 45

Leu Ile Gly Leu Leu Ala Ile Ala Gly Ile Arg Leu His Arg Ala Ala
50 55 60

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Ile Tyr Thr Ala Glu Ile His Lys Ser Leu Ser Thr Asn Leu Asp Val
65                  70                  75                  80

Thr Asn Ser Ile Glu His Gln Val Lys Asp Val Leu Thr Pro Leu Phe
                85                  90                  95

Lys Ile Ile Gly Asp Glu Val Gly Leu Arg Thr Pro Gln Arg Phe Thr
            100                 105                 110

Asp Leu Val Lys Phe Ile Ser Asp Lys Ile Lys Phe Leu Asn Pro Asp
        115                 120                 125

Arg Glu Tyr Asp Phe Arg Asp Leu Thr Trp Cys Ile Asn Pro Pro Glu
    130                 135                 140

Arg Ile Lys Leu Asp Tyr Asp Gln Tyr Cys Ala Asp Val Ala Ala Glu
145                 150                 155                 160

Glu Leu Met Asn Ala Leu Val Asn Ser Thr Leu Leu Glu Thr Arg Thr
                165                 170                 175

Thr Asn Gln Phe Leu Ala Val Ser Lys Gly Asn Cys Ser Gly Pro Thr
            180                 185                 190

Thr Ile Arg Gly Gln Phe Ser Asn Met Ser Leu Ser Leu Leu Asp Leu
        195                 200                 205

Tyr Leu Gly Arg Gly Tyr Asn Val Ser Ser Ile Val Thr Met Thr Ser
    210                 215                 220

Gln Gly Met Tyr Gly Gly Thr Tyr Leu Val Glu Lys Pro Asn Leu Ser
225                 230                 235                 240
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Ser Lys Arg Ser Glu Leu Ser Gln Leu Ser Met Tyr Arg Val Phe Glu
245 250 255

Val Gly Val Ile Arg Asn Pro Gly Leu Gly Ala Pro Val Phe His Met
260 265 270

Thr Asn Tyr Leu Glu Gln Pro Val Ser Asn Asp Leu Ser Asn Cys Met
275 280 285

Val Ala Leu Gly Glu Leu Lys Leu Ala Ala Leu Cys His Gly Glu Asp
290 295 300

Ser Ile Thr Ile Pro Tyr Gln Gly Ser Gly Lys Gly Val Ser Phe Gln
305 310 315 320

Leu Val Lys Leu Gly Val Trp Lys Ser Pro Thr Asp Met Gln Ser Trp
325 330 335

Val Pro Leu Ser Thr Asp Asp Pro Val Ile Asp Arg Leu Tyr Leu Ser
340 345 350

Ser His Arg Gly Val Ile Ala Asp Asn Gln Ala Lys Trp Ala Val Pro
355 360 365

Thr Thr Arg Thr Asp Asp Lys Leu Arg Met Glu Thr Cys Phe Gln Gln
370 375 380

Ala Cys Lys Gly Lys Ile Gln Ala Leu Cys Glu Asn Pro Glu Trp Ala
385 390 395 400

Pro Leu Lys Asp Asn Arg Ile Pro Ser Tyr Gly Val Leu Ser Val Asp
405 410 415

Leu Ser Leu Thr Val Glu Leu Lys Ile Lys Ile Ala Ser Gly Phe Gly
420 425 430

Pro Leu Ile Thr His Gly Ser Gly Met Asp Leu Tyr Lys Ser Asn His
435 440 445

Asn Asn Val Tyr Trp Leu Thr Ile Pro Pro Met Lys Asn Leu Ala Leu
450 455 460

Gly Val Ile Asn Thr Leu Glu Trp Ile Pro Arg Phe Lys Val Ser Pro
465 470 475 480

Tyr Leu Phe Asn Val Pro Ile Lys Glu Ala Gly Glu Asp Cys His Ala
485 490 495

Pro Thr Tyr Leu Pro Ala Glu Val Asp Gly Asp Val Lys Leu Ser Ser
500 505 510

Asn Leu Val Ile Leu Pro Gly Gln Asp Leu Gln Tyr Val Leu Ala Thr
515 520 525

Tyr Asp Thr Ser Arg Val Glu His Ala Val Val Tyr Tyr Val Tyr Ser
530 535 540

Pro Ser Arg Ser Phe Ser Tyr Phe Tyr Pro Phe Arg Leu Pro Ile Lys
545 550 555 560

Gly Val Pro Ile Glu Leu Gln Val Glu Cys Phe Thr Trp Asp Gln Lys
565 570 575

Leu Trp Cys Arg His Phe Cys Val Leu Ala Asp Ser Glu Ser Gly Gly
580 585 590

His Ile Thr His Ser Gly Met Glu Gly Met Gly Val Ser Cys Thr Val

595 600 605

Thr Arg Glu Asp Gly Thr Asn Arg Arg
610 615

<210> 77
<211> 550
<212> PRT
<213> Measles virus

<400> 77

Met Gly Leu Lys Val Asn Val Ser Ala Ile Phe Met Ala Val Leu Leu
1 5 10 15

Thr Leu Gln Thr Pro Thr Gly Gln Ile His Trp Gly Asn Leu Ser Lys
20 25 30

Ile Gly Val Val Gly Ile Gly Ser Ala Ser Tyr Lys Val Met Thr Arg
35 40 45

Ser Ser His Gln Ser Leu Val Ile Lys Leu Met Pro Asn Ile Thr Leu
50 55 60

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

Arg Thr Val Leu Glu Pro Ile Arg Asp Ala Leu Asn Ala Met Thr Gln
85 90 95

Asn Ile Arg Pro Val Gln Ser Val Ala Ser Ser Arg Arg His Lys Arg
100 105 110

Phe Ala Gly Val Val Leu Ala Gly Ala Ala Leu Gly Val Ala Thr Ala
115 120 125

Ala Gln Ile Thr Ala Gly Ile Ala Leu His Gln Ser Met Leu Asn Ser
130 135 140

Gln Ala Ile Asp Asn Leu Arg Ala Ser Leu Glu Thr Thr Asn Gln Ala
145 150 155 160

Ile Glu Ala Ile Arg Gln Ala Gly Gln Glu Met Ile Leu Ala Val Gln
165 170 175

Gly Val Gln Asp Tyr Ile Asn Asn Glu Leu Ile Pro Ser Met Asn Gln
180 185 190

Leu Ser Cys Asp Leu Ile Gly Gln Lys Leu Gly Leu Lys Leu Leu Arg
195 200 205

Tyr Tyr Thr Glu Ile Leu Ser Leu Phe Gly Pro Ser Leu Arg Asp Pro
210 215 220

Ile Ser Ala Glu Ile Ser Ile Gln Ala Leu Ser Tyr Ala Leu Gly Gly
225 230 235 240

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

Leu Gly Ile Leu Glu Ser Arg Gly Ile Lys Ala Arg Ile Thr His Val
260 265 270

Asp Thr Glu Ser Tyr Phe Ile Val Leu Ser Ile Ala Tyr Pro Thr Leu
275 280 285

Ser Glu Ile Lys Gly Val Ile Val His Arg Leu Glu Gly Val Ser Tyr
290 295 300

Asn Ile Gly Ser Gln Glu Trp Tyr Thr Thr Val Pro Lys Tyr Val Ala
305 310 315 320

Thr Gln Gly Tyr Leu Ile Ser Asn Phe Asp Glu Ser Ser Cys Thr Phe
325 330 335

Met Pro Glu Gly Thr Val Cys Ser Gln Asn Ala Leu Tyr Pro Met Ser
340 345 350

Pro Leu Leu Gln Glu Cys Leu Arg Gly Ser Thr Lys Ser Cys Ala Arg
355 360 365

Thr Leu Val Ser Gly Ser Phe Gly Asn Arg Phe Ile Leu Ser Gln Gly
370 375 380

Asn Leu Ile Ala Asn Cys Ala Ser Ile Leu Cys Lys Cys Tyr Thr Thr
385 390 395 400

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

Ala Asp His Cys Pro Val Val Glu Val Asn Gly Val Thr Ile Gln Val
420 425 430

Gly Ser Arg Arg Tyr Pro Asp Ala Val Tyr Leu His Arg Ile Asp Leu
435 440 445

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

Asn Ala Ile Ala Lys Leu Glu Asp Ala Lys Glu Leu Leu Glu Ser Ser
465 470 475 480

Asp Gln Ile Leu Arg Ser Met Lys Gly Leu Ser Ser Thr Ser Ile Val

485 490 495

Tyr Ile Leu Ile Ala Val Cys Leu Gly Gly Leu Ile Gly Ile Pro Ala
500 505 510

Leu Ile Cys Cys Cys Arg Gly Arg Cys Asn Lys Lys Gly Glu Gln Val
515 520 525

Gly Met Ser Arg Pro Gly Leu Lys Pro Asp Leu Thr Gly Thr Ser Lys
530 535 540

Ser Tyr Val Arg Ser Leu
545 550

<210> 78
<211> 500
<212> PRT
<213> Zika virus

<400> 78

Ile Arg Cys Ile Gly Val Ser Asn Arg Asp Phe Val Glu Gly Met Ser
1 5 10 15

Gly Gly Thr Trp Val Asp Val Val Leu Glu His Gly Gly Cys Val Thr
20 25 30

Val Met Ala Gln Asp Lys Pro Thr Val Asp Ile Glu Leu Val Thr Thr
35 40 45

Thr Val Ser Asn Met Ala Glu Val Arg Ser Tyr Cys Tyr Glu Ala Ser
50 55 60

Ile Ser Asp Met Ala Ser Asp Ser Arg Cys Pro Thr Gln Gly Glu Ala
65 70 75 80

Tyr Leu Asp Lys Gln Ser Asp Thr Gln Tyr Val Cys Lys Arg Thr Leu
85 90 95

Val Asp Arg Gly Trp Gly Asn Gly Cys Gly Leu Phe Gly Lys Gly Ser
100 105 110

Leu Val Thr Cys Ala Lys Phe Thr Cys Ser Lys Lys Met Thr Gly Lys
115 120 125

Ser Ile Gln Pro Glu Asn Leu Glu Tyr Arg Ile Met Leu Ser Val His
130 135 140

Gly Ser Gln His Ser Gly Met Ile Gly Tyr Glu Thr Asp Glu Asp Arg
145 150 155 160

Ala Lys Val Glu Val Thr Pro Asn Ser Pro Arg Ala Glu Ala Thr Leu
165 170 175

Gly Gly Phe Gly Ser Leu Gly Leu Asp Cys Glu Pro Arg Thr Gly Leu
180 185 190

Asp Phe Ser Asp Leu Tyr Tyr Leu Thr Met Asn Asn Lys His Trp Leu
195 200 205

Val His Lys Glu Trp Phe His Asp Ile Pro Leu Pro Trp His Ala Gly
210 215 220

Ala Asp Thr Gly Thr Pro His Trp Asn Asn Lys Glu Ala Leu Val Glu
225 230 235 240

Phe Lys Asp Ala His Ala Lys Arg Gln Thr Val Val Val Leu Gly Ser
245 250 255

Gln Glu Gly Ala Val His Thr Ala Leu Ala Gly Ala Leu Glu Ala Glu
260 265 270

Met Asp Gly Ala Lys Gly Arg Leu Phe Ser Gly His Leu Lys Cys Arg
275 280 285

Leu Lys Met Asp Lys Leu Arg Leu Lys Gly Val Ser Tyr Ser Leu Cys
290 295 300

Thr Ala Ala Phe Thr Phe Thr Lys Val Pro Ala Glu Thr Leu His Gly
305 310 315 320

Thr Val Thr Val Glu Val Gln Tyr Ala Gly Thr Asp Gly Pro Cys Lys
325 330 335

Ile Pro Val Gln Met Ala Val Asp Met Gln Thr Leu Thr Pro Val Gly
340 345 350

Arg Leu Ile Thr Ala Asn Pro Val Ile Thr Glu Ser Thr Glu Asn Ser
355 360 365

Lys Met Met Leu Glu Leu Asp Pro Pro Phe Gly Asp Ser Tyr Ile Val
370 375 380

Ile Gly Val Gly Asp Lys Lys Ile Thr His His Trp His Arg Ser Gly
385 390 395 400

Ser Thr Ile Gly Lys Ala Phe Glu Ala Thr Val Arg Gly Ala Lys Arg
405 410 415

Met Ala Val Leu Gly Asp Thr Ala Trp Asp Phe Gly Ser Val Gly Gly
420 425 430

Val Phe Asn Ser Leu Gly Lys Gly Ile His Gln Ile Phe Gly Ala Ala

435 440 445

Phe Lys Ser Leu Phe Gly Gly Met Ser Trp Phe Ser Gln Ile Leu Ile
450 455 460

Gly Thr Leu Leu Val Trp Leu Gly Leu Asn Thr Lys Asn Gly Ser Ile
465 470 475 480

Ser Leu Thr Cys Leu Ala Leu Gly Gly Val Met Ile Phe Leu Ser Thr
485 490 495

Ala Val Ser Ala
500

<210> 79
<211> 378
<212> PRT
<213> Plasmodium vivax

<400> 79

Met Lys Asn Phe Ile Leu Leu Ala Val Ser Ser Ile Leu Leu Val Asp
1 5 10 15

Leu Phe Pro Thr His Cys Gly His Asn Val Asp Leu Ser Lys Ala Ile
20 25 30

Asn Leu Asn Gly Val Asn Phe Asn Asn Val Asp Ala Ser Ser Leu Gly
35 40 45

Ala Ala His Val Gly Gln Ser Ala Ser Arg Gly Arg Gly Leu Gly Glu
50 55 60

Asn Pro Asp Asp Glu Glu Gly Asp Ala Lys Lys Lys Lys Asp Gly Lys
65 70 75 80

Lys Ala Glu Pro Lys Asn Pro Arg Glu Asn Lys Leu Lys Gln Pro Gly
85 90 95

Asp Arg Ala Asp Gly Gln Pro Ala Gly Asp Arg Ala Asp Gly Gln Pro
100 105 110

Ala Gly Asp Arg Ala Asp Gly Gln Pro Ala Gly Asp Arg Ala Ala Gly
115 120 125

Gln Pro Ala Gly Asp Arg Ala Asp Gly Gln Pro Ala Gly Asp Arg Ala
130 135 140

Asp Gly Gln Pro Ala Gly Asp Arg Ala Asp Gly Gln Pro Ala Gly Asp
145 150 155 160

Arg Ala Asp Gly Gln Pro Ala Gly Asp Arg Ala Ala Gly Gln Pro Ala
165 170 175

Gly Asp Arg Ala Ala Gly Gln Pro Ala Gly Asp Arg Ala Asp Gly Gln
180 185 190

Pro Ala Gly Asp Arg Ala Ala Gly Gln Pro Ala Gly Asp Arg Ala Asp
195 200 205

Gly Gln Pro Ala Gly Asp Arg Ala Ala Gly Gln Pro Ala Gly Asp Arg
210 215 220

Ala Asp Gly Gln Pro Ala Gly Asp Arg Ala Ala Gly Gln Pro Ala Gly
225 230 235 240

Asp Arg Ala Ala Gly Gln Pro Ala Gly Asp Arg Ala Ala Gly Gln Pro
245 250 255

Ala Gly Asp Arg Ala Ala Gly Gln Pro Ala Gly Asn Gly Ala Gly Gly
260 265 270

Gln Ala Ala Gly Gly Asn Ala Gly Gly Gly Gln Gly Gln Asn Asn Glu
275 280 285

Gly Ala Asn Ala Pro Asn Glu Lys Ser Val Lys Glu Tyr Leu Asp Lys
290 295 300

Val Arg Ala Thr Val Gly Thr Glu Trp Thr Pro Cys Ser Val Thr Cys
305 310 315 320

Gly Val Gly Val Arg Val Arg Arg Arg Val Asn Ala Ala Asn Lys Lys
325 330 335

Pro Glu Asp Leu Thr Leu Asn Asp Leu Glu Thr Asp Val Cys Thr Met
340 345 350

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

Val Ile Leu Leu Val Leu Ala Leu Phe Asn
370 375

<210> 80
<211> 546
<212> PRT
<213> Nipah virus

<400> 80

Met Val Val Ile Leu Asp Lys Arg Cys Tyr Cys Asn Leu Leu Ile Leu
1 5 10 15

Ile Leu Met Ile Ser Glu Cys Ser Val Gly Ile Leu His Tyr Glu Lys
20 25 30

Leu Ser Lys Ile Gly Leu Val Lys Gly Val Thr Arg Lys Tyr Lys Ile
35 40 45

Lys Ser Asn Pro Leu Thr Lys Asp Ile Val Ile Lys Met Ile Pro Asn
50 55 60

Val Ser Asn Met Ser Gln Cys Thr Gly Ser Val Met Glu Asn Tyr Lys
65 70 75 80

Thr Arg Leu Asn Gly Ile Leu Thr Pro Ile Lys Gly Ala Leu Glu Ile
85 90 95

Tyr Lys Asn Asn Thr His Asp Leu Val Gly Asp Val Arg Leu Ala Gly
100 105 110

Val Ile Met Ala Gly Val Ala Ile Gly Ile Ala Thr Ala Ala Gln Ile
115 120 125

Thr Ala Gly Val Ala Leu Tyr Glu Ala Met Lys Asn Ala Asp Asn Ile
130 135 140

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

Leu Gln Glu Thr Ala Glu Lys Thr Val Tyr Val Leu Thr Ala Leu Gln
165 170 175

Asp Tyr Ile Asn Thr Asn Leu Val Pro Thr Ile Asp Lys Ile Ser Cys
180 185 190

Lys Gln Thr Glu Leu Ser Leu Asp Leu Ala Leu Ser Lys Tyr Leu Ser
195 200 205

Asp Leu Leu Phe Val Phe Gly Pro Asn Leu Gln Asp Pro Val Ser Asn
210 215 220

Ser Met Thr Ile Gln Ala Ile Ser Gln Ala Phe Gly Gly Asn Tyr Glu
225 230 235 240

Thr Leu Leu Arg Thr Leu Gly Tyr Ala Thr Glu Asp Phe Asp Asp Leu
245 250 255

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

Ser Tyr Tyr Ile Ile Val Arg Val Tyr Phe Pro Ile Leu Thr Glu Ile
275 280 285

Gln Gln Ala Tyr Ile Gln Glu Leu Leu Pro Val Ser Phe Asn Asn Asp
290 295 300

Asn Ser Glu Trp Ile Ser Ile Val Pro Asn Phe Ile Leu Val Arg Asn
305 310 315 320

Thr Leu Ile Ser Asn Ile Glu Ile Gly Phe Cys Leu Ile Thr Lys Arg
325 330 335

Ser Val Ile Cys Asn Gln Asp Tyr Ala Thr Pro Met Thr Asn Asn Met
340 345 350

Arg Glu Cys Leu Thr Gly Ser Thr Glu Lys Cys Pro Arg Glu Leu Val
355 360 365

Val Ser Ser His Val Pro Arg Phe Ala Leu Ser Asn Gly Val Leu Phe
370 375 380

Ala Asn Cys Ile Ser Val Thr Cys Gln Cys Gln Thr Thr Gly Arg Ala
385 390 395 400

Ile Ser Gln Ser Gly Glu Gln Thr Leu Leu Met Ile Asp Asn Thr Thr
405 410 415

Cys Pro Thr Ala Val Leu Gly Asn Val Ile Ile Ser Leu Gly Lys Tyr
420 425 430

Leu Gly Ser Val Asn Tyr Asn Ser Glu Gly Ile Ala Ile Gly Pro Pro
435 440 445

Val Phe Thr Asp Lys Val Asp Ile Ser Ser Gln Ile Ser Ser Met Asn
450 455 460

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

Leu Asp Thr Val Asn Pro Ser Leu Ile Ser Met Leu Ser Met Ile Ile
485 490 495

Leu Tyr Val Leu Ser Ile Ala Ser Leu Cys Ile Gly Leu Ile Thr Phe
500 505 510

Ile Ser Phe Ile Ile Val Glu Lys Lys Arg Asn Thr Tyr Ser Arg Leu
515 520 525

Glu Asp Arg Arg Val Arg Pro Thr Ser Ser Gly Asp Leu Tyr Tyr Ile
530 535 540

Gly Thr
545

<210> 81

<211> 602
<212> PRT
<213> Nipah virus

<400> 81

Met Pro Ala Glu Asn Lys Lys Val Arg Phe Glu Asn Thr Thr Ser Asp
1 5 10 15

Lys Gly Lys Ile Pro Ser Lys Val Ile Lys Ser Tyr Tyr Gly Thr Met
20 25 30

Asp Ile Lys Lys Ile Asn Glu Gly Leu Leu Asp Ser Lys Ile Leu Ser
35 40 45

Ala Phe Asn Thr Val Ile Ala Leu Leu Gly Ser Ile Val Ile Ile Val
50 55 60

Met Asn Ile Met Ile Ile Gln Asn Tyr Thr Arg Ser Thr Asp Asn Gln
65 70 75 80

Ala Val Ile Lys Asp Ala Leu Gln Gly Ile Gln Gln Gln Ile Lys Gly
85 90 95

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

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

Ser Lys Ile Ser Gln Ser Thr Ala Ser Ile Asn Glu Asn Val Asn Glu
130 135 140

Lys Cys Lys Phe Thr Leu Pro Pro Leu Lys Ile His Glu Cys Asn Ile
145 150 155 160

Ser Cys Pro Asn Pro Leu Pro Phe Arg Glu Tyr Arg Pro Gln Thr Glu
165 170 175

Gly Val Ser Asn Leu Val Gly Leu Pro Asn Asn Ile Cys Leu Gln Lys
180 185 190

Thr Ser Asn Gln Ile Leu Lys Pro Lys Leu Ile Ser Tyr Thr Leu Pro
195 200 205

Val Val Gly Gln Ser Gly Thr Cys Ile Thr Asp Pro Leu Leu Ala Met
210 215 220

Asp Glu Gly Tyr Phe Ala Tyr Ser His Leu Glu Arg Ile Gly Ser Cys
225 230 235 240

Ser Arg Gly Val Ser Lys Gln Arg Ile Ile Gly Val Gly Glu Val Leu
245 250 255

Asp Arg Gly Asp Glu Val Pro Ser Leu Phe Met Thr Asn Val Trp Thr
260 265 270

Pro Pro Asn Pro Asn Thr Val Tyr His Cys Ser Ala Val Tyr Asn Asn
275 280 285

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

Leu Asn Ser Thr Tyr Trp Ser Gly Ser Leu Met Met Thr Arg Leu Ala
305 310 315 320

Val Lys Pro Lys Ser Asn Gly Gly Gly Tyr Asn Gln His Gln Leu Ala
325 330 335

Leu Arg Ser Ile Glu Lys Gly Arg Tyr Asp Lys Val Met Pro Tyr Gly
340 345 350

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

Phe Leu Val Arg Thr Glu Phe Lys Tyr Asn Asp Ser Asn Cys Pro Ile
370 375 380

Thr Lys Cys Gln Tyr Ser Lys Pro Glu Asn Cys Arg Leu Ser Met Gly
385 390 395 400

Ile Arg Pro Asn Ser His Tyr Ile Leu Arg Ser Gly Leu Leu Lys Tyr
405 410 415

Asn Leu Ser Asp Gly Glu Asn Pro Lys Val Val Phe Ile Glu Ile Ser
420 425 430

Asp Gln Arg Leu Ser Ile Gly Ser Pro Ser Lys Ile Tyr Asp Ser Leu
435 440 445

Gly Gln Pro Val Phe Tyr Gln Ala Ser Phe Ser Trp Asp Thr Met Ile
450 455 460

Lys Phe Gly Asp Val Leu Thr Val Asn Pro Leu Val Val Asn Trp Arg
465 470 475 480

Asn Asn Thr Val Ile Ser Arg Pro Gly Gln Ser Gln Cys Pro Arg Phe
485 490 495

Asn Thr Cys Pro Glu Ile Cys Trp Glu Gly Val Tyr Asn Asp Ala Phe
500 505 510

Leu Ile Asp Arg Ile Asn Trp Ile Ser Ala Gly Val Phe Leu Asp Ser

515 520 525

Asn Gln Thr Ala Glu Asn Pro Val Phe Thr Val Phe Lys Asp Asn Glu
530 535 540

Ile Leu Tyr Arg Ala Gln Leu Ala Ser Glu Asp Thr Asn Ala Gln Lys
545 550 555 560

Thr Ile Thr Asn Cys Phe Leu Leu Lys Asn Lys Ile Trp Cys Ile Ser
565 570 575

Leu Val Glu Ile Tyr Asp Thr Gly Asp Asn Val Ile Arg Pro Lys Leu
580 585 590

Phe Ala Val Lys Ile Pro Glu Gln Cys Thr
595 600

<210> 82
<211> 775
<212> PRT
<213> Rotavirus A

<400> 82

Met Ala Ser Leu Ile Tyr Arg Gln Leu Leu Thr Asn Ser Tyr Ser Val
1 5 10 15

Asp Leu His Asp Glu Ile Glu Gln Ile Gly Ser Glu Lys Thr Gln Asn
20 25 30

Val Thr Ile Asn Pro Ser Pro Phe Ala Gln Thr Arg Tyr Ala Pro Val
35 40 45

Asn Trp Gly His Gly Glu Ile Asn Asp Ser Thr Thr Val Glu Pro Ile
50 55 60

Leu Asp Gly Pro Tyr Gln Pro Thr Thr Phe Thr Pro Pro Asn Asp Tyr
65 70 75 80

Trp Ile Leu Ile Asn Ser Asn Thr Asn Gly Val Val Tyr Glu Ser Thr
85 90 95

Asn Asn Ser Asp Phe Trp Thr Ala Val Val Ala Ile Glu Pro His Val
100 105 110

Asn Pro Val Asp Arg Gln Tyr Thr Ile Phe Gly Glu Ser Lys Gln Phe
115 120 125

Asn Val Ser Asn Asp Ser Asn Lys Trp Lys Phe Leu Glu Met Phe Arg
130 135 140

Ser Ser Ser Gln Asn Glu Phe Tyr Asn Arg Arg Thr Leu Thr Ser Asp
145 150 155 160

Thr Arg Phe Val Gly Ile Leu Lys Tyr Gly Gly Arg Val Trp Thr Phe
165 170 175

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

Leu Asn Asn Ile Ser Ile Thr Ile His Ser Glu Phe Tyr Ile Ile Pro
195 200 205

Arg Ser Gln Glu Ser Lys Cys Asn Glu Tyr Ile Asn Asn Gly Leu Pro
210 215 220

Pro Ile Gln Asn Thr Arg Asn Val Val Pro Leu Pro Leu Ser Ser Arg
225 230 235 240

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

Lys Thr Ser Leu Trp Lys Glu Met Gln Tyr Asn Arg Asp Ile Ile Ile
260 265 270

Arg Phe Lys Phe Gly Asn Ser Ile Val Lys Met Gly Gly Leu Gly Tyr
275 280 285

Lys Trp Ser Glu Ile Ser Tyr Lys Ala Ala Asn Tyr Gln Tyr Asn Tyr
290 295 300

Leu Arg Asp Gly Glu Gln Val Thr Ala His Thr Thr Cys Ser Val Asn
305 310 315 320

Gly Val Asn Asn Phe Ser Tyr Asn Gly Gly Ser Leu Pro Thr Asp Phe
325 330 335

Gly Ile Ser Arg Tyr Glu Val Ile Lys Glu Asn Ser Tyr Val Tyr Val
340 345 350

Asp Tyr Trp Asp Asp Ser Lys Ala Phe Arg Asn Met Val Tyr Val Arg
355 360 365

Ser Leu Ala Ala Asn Leu Asn Ser Val Lys Cys Thr Gly Gly Ser Tyr
370 375 380

Asn Phe Ser Ile Pro Val Gly Ala Trp Pro Val Met Asn Gly Gly Ala
385 390 395 400

Val Ser Leu His Phe Ala Gly Val Thr Leu Ser Thr Gln Phe Thr Asp
405 410 415

Phe Val Ser Leu Asn Ser Leu Arg Phe Arg Phe Ser Leu Thr Val Asp

420 425 430

Glu Pro Pro Phe Ser Ile Leu Arg Thr Arg Thr Val Asn Leu Tyr Gly
435 440 445

Leu Pro Ala Ala Asn Pro Asn Asn Gly Asn Glu Tyr Tyr Glu Ile Ser
450 455 460

Gly Arg Phe Ser Leu Ile Tyr Leu Val Pro Thr Asn Asp Asp Tyr Gln
465 470 475 480

Thr Pro Ile Met Asn Ser Val Thr Val Arg Gln Asp Leu Glu Arg Gln
485 490 495

Leu Thr Asp Leu Arg Glu Glu Phe Asn Ser Leu Ser Gln Glu Ile Ala
500 505 510

Met Ala Gln Leu Ile Asp Leu Ala Leu Leu Pro Leu Asp Met Phe Ser
515 520 525

Met Phe Ser Gly Ile Lys Ser Thr Ile Asp Leu Thr Lys Ser Met Ala
530 535 540

Thr Ser Val Met Lys Lys Phe Arg Lys Ser Lys Leu Ala Thr Ser Ile
545 550 555 560

Ser Glu Met Thr Asn Ser Leu Ser Asp Ala Ala Ser Ser Ala Ser Arg
565 570 575

Asn Val Ser Ile Arg Ser Asn Leu Ser Ala Ile Ser Asn Trp Thr Asn
580 585 590

Val Ser Asn Asp Val Ser Asn Val Thr Asn Ser Leu Asn Asp Ile Ser
595 600 605

Thr Gln Thr Ser Thr Ile Ser Lys Lys Phe Arg Leu Lys Glu Met Ile
610 615 620

Thr Gln Thr Glu Gly Met Ser Phe Asp Asp Ile Ser Ala Ala Val Leu
625 630 635 640

Lys Thr Lys Ile Asp Met Ser Thr Gln Ile Gly Lys Asn Thr Leu Pro
645 650 655

Asp Ile Val Thr Glu Ala Ser Glu Lys Phe Ile Pro Lys Arg Ser Tyr
660 665 670

Arg Ile Leu Lys Asp Asp Glu Val Met Glu Ile Asn Thr Glu Gly Lys
675 680 685

Phe Phe Ala Tyr Lys Ile Asn Thr Phe Asp Glu Val Pro Phe Asp Val
690 695 700

Asn Lys Phe Ala Glu Leu Val Thr Asp Ser Pro Val Ile Ser Ala Ile
705 710 715 720

Ile Asp Phe Lys Thr Leu Lys Asn Leu Asn Asp Asn Tyr Gly Ile Thr
725 730 735

Arg Thr Glu Ala Leu Asn Leu Ile Lys Ser Asn Pro Asn Met Leu Arg
740 745 750

Asn Phe Ile Asn Gln Asn Asn Pro Ile Ile Arg Asn Arg Ile Glu Gln
755 760 765

Leu Ile Leu Gln Cys Lys Leu
770 775

<210> 83
<211> 230
<212> PRT
<213> Rotavirus A

<400> 83

Met Ala Ser Leu Ile Tyr Arg Gln Leu Leu Thr Asn Ser Tyr Ser Val
1 5 10 15

Asp Leu His Asp Glu Ile Glu Gln Ile Gly Ser Glu Lys Thr Gln Asn
20 25 30

Val Thr Ile Asn Pro Ser Pro Phe Ala Gln Thr Arg Tyr Ala Pro Val
35 40 45

Asn Trp Gly His Gly Glu Ile Asn Asp Ser Thr Thr Val Glu Pro Ile
50 55 60

Leu Asp Gly Pro Tyr Gln Pro Thr Thr Phe Thr Pro Pro Asn Asp Tyr
65 70 75 80

Trp Ile Leu Ile Asn Ser Asn Thr Asn Gly Val Val Tyr Glu Ser Thr
85 90 95

Asn Asn Ser Asp Phe Trp Thr Ala Val Val Ala Ile Glu Pro His Val
100 105 110

Asn Pro Val Asp Arg Gln Tyr Thr Ile Phe Gly Glu Ser Lys Gln Phe
115 120 125

Asn Val Ser Asn Asp Ser Asn Lys Trp Lys Phe Leu Glu Met Phe Arg
130 135 140

Ser Ser Ser Gln Asn Glu Phe Tyr Asn Arg Arg Thr Leu Thr Ser Asp

145 150 155 160

Thr Arg Phe Val Gly Ile Leu Lys Tyr Gly Gly Arg Val Trp Thr Phe
165 170 175

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

Leu Asn Asn Ile Ser Ile Thr Ile His Ser Glu Phe Tyr Ile Ile Pro
195 200 205

Arg Ser Gln Glu Ser Lys Cys Asn Glu Tyr Ile Asn Asn Gly Leu Pro
210 215 220

Pro Ile Gln Asn Thr Arg
225 230

<210> 84
<211> 539
<212> PRT
<213> Human metapneumovirus

<400> 84

Met Ser Trp Lys Val Val Ile Ile Phe Ser Leu Leu Ile Thr Pro Gln
1 5 10 15

His Gly Leu Lys Glu Ser Tyr Leu Glu Glu Ser Cys Ser Thr Ile Thr
20 25 30

Glu Gly Tyr Leu Ser Val Leu Arg Thr Gly Trp Tyr Thr Asn Val Phe
35 40 45

Thr Leu Glu Val Gly Asp Val Glu Asn Leu Thr Cys Ser Asp Gly Pro
50 55 60

Ser Leu Ile Lys Thr Glu Leu Asp Leu Thr Lys Ser Ala Leu Arg Glu
65 70 75 80

Leu Lys Thr Val Ser Ala Asp Gln Leu Ala Arg Glu Glu Gln Ile Glu
85 90 95

Asn Pro Arg Gln Ser Arg Phe Val Leu Gly Ala Ile Ala Leu Gly Val
100 105 110

Ala Thr Ala Ala Ala Val Thr Ala Gly Val Ala Ile Ala Lys Thr Ile
115 120 125

Arg Leu Glu Ser Glu Val Thr Ala Ile Lys Asn Ala Leu Lys Thr Thr
130 135 140

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

Ala Val Arg Glu Leu Lys Asp Phe Val Ser Lys Asn Leu Thr Arg Ala
165 170 175

Ile Asn Lys Asn Lys Cys Asp Ile Asp Asp Leu Lys Met Ala Val Ser
180 185 190

Phe Ser Gln Phe Asn Arg Arg Phe Leu Asn Val Val Arg Gln Phe Ser
195 200 205

Asp Asn Ala Gly Ile Thr Pro Ala Ile Ser Leu Asp Leu Met Thr Asp
210 215 220

Ala Glu Leu Ala Arg Ala Val Ser Asn Met Pro Thr Ser Ala Gly Gln
225 230 235 240

Ile Lys Leu Met Leu Glu Asn Arg Ala Met Val Arg Arg Lys Gly Phe
245 250 255

Gly Ile Leu Ile Gly Val Tyr Gly Ser Ser Val Ile Tyr Met Val Gln
260 265 270

Leu Pro Ile Phe Gly Val Ile Asp Thr Pro Cys Trp Ile Val Lys Ala
275 280 285

Ala Pro Ser Cys Ser Gly Lys Lys Gly Asn Tyr Ala Cys Leu Leu Arg
290 295 300

Glu Asp Gln Gly Trp Tyr Cys Gln Asn Ala Gly Ser Thr Val Tyr Tyr
305 310 315 320

Pro Asn Glu Lys Asp Cys Glu Thr Arg Gly Asp His Val Phe Cys Asp
325 330 335

Thr Ala Ala Gly Ile Asn Val Ala Glu Gln Ser Lys Glu Cys Asn Ile
340 345 350

Asn Ile Ser Thr Thr Asn Tyr Pro Cys Lys Val Ser Thr Gly Arg His
355 360 365

Pro Ile Ser Met Val Ala Leu Ser Pro Leu Gly Ala Leu Val Ala Cys
370 375 380

Tyr Lys Gly Val Ser Cys Ser Ile Gly Ser Asn Arg Val Gly Ile Ile
385 390 395 400

Lys Gln Leu Asn Lys Gly Cys Ser Tyr Ile Thr Asn Gln Asp Ala Asp
405 410 415

Thr Val Thr Ile Asp Asn Thr Val Tyr Gln Leu Ser Lys Val Glu Gly

420 425 430

Glu Gln His Val Ile Lys Gly Arg Pro Val Ser Ser Ser Phe Asp Pro
435 440 445

Ile Lys Phe Pro Glu Asp Gln Phe Asn Val Ala Leu Asp Gln Val Phe
450 455 460

Glu Asn Ile Glu Asn Ser Gln Ala Leu Val Asp Gln Ser Asn Arg Ile
465 470 475 480

Leu Ser Ser Ala Glu Lys Gly Asn Thr Gly Phe Ile Ile Val Ile Ile
485 490 495

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

Ile Ile Lys Lys Thr Lys Lys Pro Thr Gly Ala Pro Pro Glu Leu Ser
515 520 525

Gly Val Thr Asn Asn Gly Phe Ile Pro His Ser
530 535

<210> 85
<211> 219
<212> PRT
<213> Human metapneumovirus

<400> 85

Met Glu Val Lys Val Glu Asn Ile Arg Ala Ile Asp Met Leu Lys Ala
1 5 10 15

Arg Val Lys Asn Arg Val Ala Arg Ser Lys Cys Phe Lys Asn Ala Ser
20 25 30

Leu Ile Leu Ile Gly Ile Thr Thr Leu Ser Ile Ala Leu Asn Ile Tyr
35 40 45

Leu Ile Ile Asn Tyr Thr Ile Gln Lys Thr Ser Ser Glu Ser Glu His
50 55 60

His Thr Ser Ser Pro Pro Thr Glu Ser Asn Lys Glu Ala Ser Thr Ile
65 70 75 80

Ser Thr Asp Asn Pro Asp Ile Asn Pro Asn Ser Gln His Pro Thr Gln
85 90 95

Gln Ser Thr Glu Asn Pro Thr Leu Asn Pro Ala Ala Ser Val Ser Pro
100 105 110

Ser Glu Thr Glu Pro Ala Ser Thr Pro Asp Thr Thr Asn Arg Leu Ser
115 120 125

Ser Val Asp Arg Ser Thr Ala Gln Pro Ser Glu Ser Arg Thr Lys Thr
130 135 140

Lys Pro Thr Val His Thr Arg Asn Asn Pro Ser Thr Ala Ser Ser Thr
145 150 155 160

Gln Ser Pro Pro Arg Ala Thr Thr Lys Ala Ile Arg Arg Ala Thr Thr
165 170 175

Phe Arg Met Ser Ser Thr Gly Lys Arg Pro Thr Thr Thr Ser Val Gln
180 185 190

Ser Asp Ser Ser Thr Thr Thr Gln Asn His Glu Glu Thr Gly Ser Ala
195 200 205

Asn Pro Gln Ala Ser Val Ser Thr Met Gln Asn
210 215

<210> 86
<211> 555
<212> PRT
<213> Human parainfluenza virus

<400> 86

Met Gln Lys Ser Glu Ile Leu Phe Leu Ile Tyr Ser Ser Leu Leu Leu
1 5 10 15

Ser Ser Ser Leu Cys Gln Ile Pro Val Asp Lys Leu Ser Asn Val Gly
20 25 30

Val Ile Ile Asn Glu Gly Lys Leu Leu Lys Ile Ala Gly Ser Tyr Glu
35 40 45

Ser Arg Tyr Ile Val Leu Ser Leu Val Pro Ser Ile Asp Leu Glu Asp
50 55 60

Gly Cys Gly Thr Thr Gln Ile Ile Gln Tyr Lys Asn Leu Leu Asn Arg
65 70 75 80

Leu Leu Ile Pro Leu Lys Asp Ala Leu Asp Leu Gln Glu Ser Leu Ile
85 90 95

Thr Ile Thr Asn Asp Thr Thr Val Thr Asn Asp Asn Pro Gln Ser Arg
100 105 110

Phe Phe Gly Ala Val Ile Gly Thr Ile Ala Leu Gly Val Ala Thr Ala
115 120 125

Ala Gln Ile Thr Ala Gly Ile Ala Leu Ala Glu Ala Arg Glu Ala Arg
130 135 140

Lys Asp Ile Ala Leu Ile Lys Asp Ser Ile Ile Lys Thr His Asn Ser
145 150 155 160

Val Glu Leu Ile Gln Arg Gly Ile Gly Glu Gln Ile Ile Ala Leu Lys
165 170 175

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

Leu Arg Cys Glu Thr Thr Ala Leu Lys Leu Gly Ile Lys Leu Thr Gln
195 200 205

His Tyr Ser Glu Leu Ala Thr Ala Phe Ser Ser Asn Leu Gly Thr Ile
210 215 220

Gly Glu Lys Ser Leu Thr Leu Gln Ala Leu Ser Ser Leu Tyr Ser Ala
225 230 235 240

Asn Ile Thr Glu Ile Leu Ser Thr Ile Lys Lys Asp Lys Ser Asp Ile
245 250 255

Tyr Asp Ile Ile Tyr Thr Glu Gln Val Lys Gly Thr Val Ile Asp Val
260 265 270

Asp Leu Glu Lys Tyr Met Val Thr Leu Leu Val Lys Ile Pro Ile Leu
275 280 285

Ser Glu Ile Pro Gly Val Leu Ile Tyr Arg Ala Ser Ser Ile Ser Tyr
290 295 300

Asn Ile Glu Gly Glu Glu Trp His Val Ala Ile Pro Asn Tyr Ile Ile
305 310 315 320

Asn Lys Ala Ser Ser Leu Gly Gly Ala Asp Val Thr Asn Cys Ile Glu
325 330 335

Ser Arg Leu Ala Tyr Ile Cys Pro Arg Asp Pro Thr Gln Leu Ile Pro
340 345 350

Asp Asn Gln Gln Lys Cys Ile Leu Gly Asp Val Ser Lys Cys Pro Val
355 360 365

Thr Lys Val Ile Asn Asn Leu Val Pro Lys Phe Ala Phe Ile Asn Gly
370 375 380

Gly Val Val Ala Asn Cys Ile Ala Ser Thr Cys Thr Cys Gly Thr Asn
385 390 395 400

Arg Ile Pro Val Asn Gln Asp Arg Ser Arg Gly Val Thr Phe Leu Thr
405 410 415

Tyr Thr Asn Cys Gly Leu Ile Gly Ile Asn Gly Ile Glu Leu Tyr Ala
420 425 430

Asn Lys Arg Gly Arg Asp Thr Thr Trp Gly Asn Gln Ile Ile Lys Val
435 440 445

Gly Pro Ala Val Ser Ile Arg Pro Val Asp Ile Ser Leu Asn Leu Ala
450 455 460

Ser Ala Thr Asn Phe Leu Glu Glu Ser Lys Ile Glu Leu Met Lys Ala
465 470 475 480

Lys Ala Ile Ile Ser Ala Val Gly Gly Trp His Asn Thr Glu Ser Thr
485 490 495

Gln Ile Ile Ile Ile Ile Ile Val Cys Ile Leu Ile Ile Ile Ile Cys
500 505 510

Gly Ile Leu Tyr Tyr Leu Tyr Arg Val Arg Arg Leu Leu Val Met Ile
515 520 525

Asn Ser Thr His Asn Ser Pro Val Asn Thr Tyr Thr Leu Glu Ser Arg
530 535 540

Met Arg Asn Pro Tyr Ile Gly Asn Asn Ser Asn
545 550 555

<210> 87
<211> 571
<212> PRT
<213> Human parainfluenza virus

<400> 87

Met Glu Asp Tyr Ser Asn Leu Ser Leu Lys Ser Ile Pro Lys Arg Thr
1 5 10 15

Cys Arg Ile Ile Phe Arg Thr Ala Thr Ile Leu Gly Ile Cys Thr Leu
20 25 30

Ile Val Leu Cys Ser Ser Ile Leu His Glu Ile Ile His Leu Asp Val
35 40 45

Ser Ser Gly Leu Met Asp Ser Asp Asp Ser Gln Gln Gly Ile Ile Gln
50 55 60

Pro Ile Ile Glu Ser Leu Lys Ser Leu Ile Ala Leu Ala Asn Gln Ile
65 70 75 80

Leu Tyr Asn Val Ala Ile Ile Ile Pro Leu Lys Ile Asp Ser Ile Glu
85 90 95

Thr Val Ile Phe Ser Ala Leu Lys Asp Met His Thr Gly Ser Met Ser
100 105 110

Asn Thr Asn Cys Thr Pro Gly Asn Leu Leu Leu His Asp Ala Ala Tyr
115 120 125

Ile Asn Gly Ile Asn Lys Phe Leu Val Leu Lys Ser Tyr Asn Gly Thr
130 135 140

Pro Lys Tyr Gly Pro Leu Leu Asn Ile Pro Ser Phe Ile Pro Ser Ala
145 150 155 160

Thr Ser Pro Asn Gly Cys Thr Arg Ile Pro Ser Phe Ser Leu Ile Lys
165 170 175

Thr His Trp Cys Tyr Thr His Asn Val Met Leu Gly Asp Cys Leu Asp
180 185 190

Phe Thr Thr Ser Asn Gln Tyr Leu Ala Met Gly Ile Ile Gln Gln Ser
195 200 205

Ala Ala Ala Phe Pro Ile Phe Arg Thr Met Lys Thr Ile Tyr Leu Ser
210 215 220

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

Cys Val Leu Tyr Cys Tyr Val Ala Thr Arg Ser Glu Lys Glu Asp Tyr
245 250 255

Ala Thr Thr Asp Leu Ala Glu Leu Arg Leu Ala Phe Tyr Tyr Tyr Asn
260 265 270

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

Trp Ala Thr Ile Asn Pro Ala Val Gly Ser Gly Ile Tyr His Leu Gly
290 295 300

Phe Ile Leu Phe Pro Val Tyr Gly Gly Leu Ile Ser Gly Thr Pro Ser
305 310 315 320

Tyr Asn Lys Gln Ser Ser Arg Tyr Phe Ile Pro Lys His Pro Asn Ile
325 330 335

Thr Cys Ala Gly Asn Ser Ser Glu Gln Ala Ala Ala Ala Arg Ser Ser
340 345 350

Tyr Val Ile Arg Tyr His Ser Asn Arg Leu Ile Gln Ser Ala Val Leu
355 360 365

Ile Cys Pro Leu Ser Asp Met His Thr Ala Arg Cys Asn Leu Val Met
370 375 380

Phe Asn Asn Ser Gln Val Met Met Gly Ala Glu Gly Arg Leu Tyr Val
385 390 395 400

Ile Asp Asn Asn Leu Tyr Tyr Tyr Gln Arg Ser Ser Ser Trp Trp Ser
405 410 415

Ala Ser Leu Phe Tyr Arg Ile Asn Thr Asp Phe Ser Lys Gly Ile Pro
420 425 430

Pro Ile Ile Glu Ala Gln Trp Val Pro Ser Tyr Gln Val Pro Arg Pro
435 440 445

Gly Val Met Pro Cys Asn Ala Thr Ser Phe Cys Pro Ala Asn Cys Ile
450 455 460

Thr Gly Val Tyr Ala Asp Val Trp Pro Leu Asn Asp Pro Glu Pro Thr
465 470 475 480

Ser Gln Asn Ala Leu Asn Pro Asn Tyr Arg Phe Ala Gly Ala Phe Leu
485 490 495

Arg Asn Glu Ser Asn Arg Thr Asn Pro Thr Phe Tyr Thr Ala Ser Ala
500 505 510

Ser Ala Leu Leu Asn Thr Thr Gly Phe Asn Asn Thr Asn His Lys Ala
515 520 525

Ala Tyr Thr Ser Ser Thr Cys Phe Lys Asn Thr Gly Thr Gln Lys Ile
530 535 540

Tyr Cys Leu Ile Ile Ile Glu Met Gly Ser Ser Leu Leu Gly Glu Phe
545 550 555 560

Gln Ile Ile Pro Phe Leu Arg Glu Leu Ile Pro
565 570

<210> 88
<211> 217
<212> PRT
<213> Plasmodium falciparum

<400> 88

Met Asn Lys Leu Tyr Ser Leu Phe Leu Phe Leu Phe Ile Gln Leu Ser
1 5 10 15

Ile Lys Tyr Asn Asn Ala Lys Val Thr Val Asp Thr Val Cys Lys Arg
20 25 30

Gly Phe Leu Ile Gln Met Ser Gly His Leu Glu Cys Lys Cys Glu Asn
35 40 45

Asp Leu Val Leu Val Asn Glu Glu Thr Cys Glu Glu Lys Val Leu Lys
50 55 60

Cys Asp Glu Lys Thr Val Asn Lys Pro Cys Gly Asp Phe Ser Lys Cys
65 70 75 80

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

Gly Tyr Asp Met Val Asn Asn Val Cys Ile Pro Asn Glu Cys Lys Asn
100 105 110

Val Thr Cys Gly Asn Gly Lys Cys Ile Leu Asp Thr Ser Asn Pro Val
115 120 125

Lys Thr Gly Val Cys Ser Cys Asn Ile Gly Lys Val Pro Asn Val Gln
130 135 140

Asp Gln Asn Lys Cys Ser Lys Asp Gly Glu Thr Lys Cys Ser Leu Lys
145 150 155 160

Cys Leu Lys Glu Asn Glu Thr Cys Lys Ala Val Asp Gly Ile Tyr Lys
165 170 175

Cys Asp Cys Lys Asp Gly Phe Ile Ile Asp Asn Glu Ser Ser Ile Cys
180 185 190

Thr Ala Phe Ser Ala Tyr Asn Ile Leu Asn Leu Ser Ile Met Phe Ile
195 200 205

Leu Phe Ser Val Cys Phe Phe Ile Met
210 215

<210> 89
<211> 27
<212> PRT
<213> Artificial Sequence

<220>
<223> T4 fibritin foldon domain

<400> 89

Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys
1 5 10 15

Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
20 25

<210> 90
<211> 540
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 90

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn

225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

Leu Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
515 520 525

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu
530 535 540

<210> 91
<211> 646
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 91

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr

1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

Leu Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
515 520 525

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Met
530 535 540

Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala Leu Val Ala Val Lys
545 550 555 560

Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala Ala Cys Val Asn Ile
565 570 575

Val Pro Gly Leu Thr Ser Ile Tyr Arg Glu Glu Gly Ser Val Val Ser
580 585 590

Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr Thr Asp Ala Phe Pro
595 600 605

Lys Leu Lys Glu Arg Val Lys Glu Leu His Pro Tyr Glu Val Pro Glu
610 615 620

Ile Val Ala Leu Pro Ile Ala Glu Gly Asn Arg Glu Tyr Leu Asp Trp
625 630 635 640

Leu Arg Glu Asn Thr Gly
645

<210> 92
<211> 619
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 92

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr

385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

Leu Gly Gly Ser Met Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala
515 520 525

Leu Val Ala Val Lys Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala
530 535 540

Ala Cys Val Asn Ile Val Pro Gly Leu Thr Ser Ile Tyr Arg Glu Glu
545 550 555 560

Gly Ser Val Val Ser Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr
565 570 575

Thr Asp Ala Phe Pro Lys Leu Lys Glu Arg Val Lys Glu Leu His Pro
580 585 590

Tyr Glu Val Pro Glu Ile Val Ala Leu Pro Ile Ala Glu Gly Asn Arg
595 600 605

Glu Tyr Leu Asp Trp Leu Arg Glu Asn Thr Gly
610 615

<210> 93
<211> 665
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 93

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu

85 90 95

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

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Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510

Leu Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg
        515                 520                 525

Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser Met
    530                 535                 540

Val Arg Gly Ile Arg Gly Ala Ile Thr Val Asn Ser Asp Thr Pro Thr
545                 550                 555                 560

Ser Ile Ile Ile Ala Thr Ile Leu Leu Leu Glu Lys Met Leu Glu Ala
                565                 570                 575

Asn Gly Ile Gln Ser Tyr Glu Glu Leu Ala Ala Val Ile Phe Thr Val
            580                 585                 590

Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala Glu Ala Ala Arg Gln Ile
        595                 600                 605

Gly Met His Arg Val Pro Leu Leu Ser Ala Arg Glu Val Pro Val Pro
    610                 615                 620
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Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala Leu Trp Asn Thr Asp
625 630 635 640

Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu Ser Glu Ala Val Arg
645 650 655

Leu Arg Pro Asp Leu Glu Ser Ala Gln
660 665

<210> 94
<211> 638
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 94

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly

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    450                 455                 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465                 470                 475                 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
                485                 490                 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
            500                 505                 510

Leu Gly Gly Ser Met Val Arg Gly Ile Arg Gly Ala Ile Thr Val Asn
        515                 520                 525

Ser Asp Thr Pro Thr Ser Ile Ile Ile Ala Thr Ile Leu Leu Leu Glu
    530                 535                 540

Lys Met Leu Glu Ala Asn Gly Ile Gln Ser Tyr Glu Glu Leu Ala Ala
545                 550                 555                 560

Val Ile Phe Thr Val Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala Glu
                565                 570                 575

Ala Ala Arg Gln Ile Gly Met His Arg Val Pro Leu Leu Ser Ala Arg
            580                 585                 590

Glu Val Pro Val Pro Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala
        595                 600                 605

Leu Trp Asn Thr Asp Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu
    610                 615                 620

Ser Glu Ala Val Arg Leu Arg Pro Asp Leu Glu Ser Ala Gln
625                 630                 635
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<210> 95
<211> 769
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 95

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val

130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Gly Tyr Ile Pro Glu
500 505 510

Ala Pro Arg Asp Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val
515 520 525

Leu Leu Ser Thr Phe Leu Gly Ser Gly Ser His His His His His His
530 535 540

His His Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala
545 550 555 560

Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile
565 570 575

Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala
580 585 590

Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr
595 600 605

Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu
610 615 620

Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys
625 630 635 640

Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu
645 650 655

Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met
660 665 670

Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly
675 680 685

His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe
690 695 700

Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr
705 710 715 720

Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val
725 730 735

Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu
740 745 750

Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr
755 760 765

Glu

<210> 96
<211> 730
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 96

Met Glu Leu Leu Ile Leu Lys Ala Asn Val Ile Ala Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Ser Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr

385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Gly Gly Ser Gly Gly
500 505 510

Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met
515 520 525

Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn
530 535 540

Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly
545 550 555 560

Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val
565 570 575

Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala
580 585 590

Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly
595 600 605

Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe
610 615 620

Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr
625 630 635 640

Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe
645 650 655

Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro
660 665 670

Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn
675 680 685

Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser
690 695 700

Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala
705 710 715 720

Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
725 730

<210> 97
<211> 676
<212> PRT

<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 97

Met Glu Leu Leu Ile Leu Lys Ala Asn Ala Ile Thr Thr Ile Leu Thr
1 5 10 15

Ala Val Thr Phe Cys Phe Ala Ser Gly Gln Asn Ile Thr Glu Glu Phe
20 25 30

Tyr Gln Ser Thr Cys Ser Ala Val Ser Lys Gly Tyr Leu Ser Ala Leu
35 40 45

Arg Thr Gly Trp Tyr Thr Ser Val Ile Thr Ile Glu Leu Ser Asn Ile
50 55 60

Lys Glu Asn Lys Cys Asn Gly Thr Asp Ala Lys Val Lys Leu Ile Lys
65 70 75 80

Gln Glu Leu Asp Lys Tyr Lys Asn Ala Val Thr Glu Leu Gln Leu Leu
85 90 95

Met Gln Ser Thr Pro Ala Thr Asn Asn Arg Ala Arg Arg Glu Leu Pro
100 105 110

Arg Phe Met Asn Tyr Thr Leu Asn Asn Ala Lys Lys Thr Asn Val Thr
115 120 125

Leu Ser Lys Lys Arg Lys Arg Arg Phe Leu Gly Phe Leu Leu Gly Val
130 135 140

Gly Ser Ala Ile Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu
145 150 155 160

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

Ala Val Val Ser Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val
180 185 190

Leu Asp Leu Lys Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn
195 200 205

Lys Gln Ser Cys Ser Ile Ser Asn Ile Glu Thr Val Ile Glu Phe Gln
210 215 220

Gln Lys Asn Asn Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn
225 230 235 240

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

Leu Leu Ser Leu Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys
260 265 270

Leu Met Ser Asn Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile
275 280 285

Met Cys Ile Ile Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro
290 295 300

Leu Tyr Gly Val Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro
305 310 315 320

Leu Cys Thr Thr Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg
325 330 335

Thr Asp Arg Gly Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe
340 345 350

Pro Gln Ala Glu Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp
355 360 365

Thr Met Asn Ser Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val
370 375 380

Asp Ile Phe Asn Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr
385 390 395 400

Asp Val Ser Ser Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys
405 410 415

Tyr Gly Lys Thr Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile
420 425 430

Lys Thr Phe Ser Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp
435 440 445

Thr Val Ser Val Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly
450 455 460

Lys Ser Leu Tyr Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro
465 470 475 480

Leu Val Phe Pro Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn
485 490 495

Glu Lys Ile Asn Gln Ser Leu Ala Phe Ile Arg Lys Ser Asp Glu Leu
500 505 510

Leu Gly Gly Ser Gly Gly Ser Gly Ser Asp Asp Ala Arg Ile Ala Ala
515 520 525

Ile Gly Asp Val Asp Glu Leu Asn Ser Gln Ile Gly Val Leu Leu Ala
530 535 540

Glu Pro Leu Pro Asp Asp Val Arg Ala Ala Leu Ser Ala Ile Gln His
545 550 555 560

Asp Leu Phe Asp Leu Gly Gly Glu Leu Cys Ile Pro Gly His Ala Ala
565 570 575

Ile Thr Glu Asp His Leu Leu Arg Leu Ala Leu Trp Leu Val His Tyr
580 585 590

Asn Gly Gln Leu Pro Pro Leu Glu Glu Phe Ile Leu Pro Gly Gly Ala
595 600 605

Arg Gly Ala Ala Leu Ala His Val Cys Arg Thr Val Cys Arg Arg Ala
610 615 620

Glu Arg Ser Ile Lys Ala Leu Gly Ala Ser Glu Pro Leu Asn Ile Ala
625 630 635 640

Pro Ala Ala Tyr Val Asn Leu Leu Ser Asp Leu Leu Phe Val Leu Ala
645 650 655

Arg Val Leu Asn Arg Ala Ala Gly Gly Ala Asp Val Leu Trp Asp Arg
660 665 670

Thr Arg Ala His
675

<210> 98
<211> 274

<212> PRT
<213> Neisseria meningitidis

<400> 98

Met Asn Arg Thr Ala Phe Cys Cys Leu Ser Leu Thr Thr Ala Leu Ile
1 5 10 15

Leu Thr Ala Cys Ser Ser Gly Gly Gly Gly Val Ala Ala Asp Ile Gly
20 25 30

Ala Gly Leu Ala Asp Ala Leu Thr Ala Pro Leu Asp His Lys Asp Lys
35 40 45

Gly Leu Gln Ser Leu Thr Leu Asp Gln Ser Val Arg Lys Asn Glu Lys
50 55 60

Leu Lys Leu Ala Ala Gln Gly Ala Glu Lys Thr Tyr Gly Asn Gly Asp
65 70 75 80

Ser Leu Asn Thr Gly Lys Leu Lys Asn Asp Lys Val Ser Arg Phe Asp
85 90 95

Phe Ile Arg Gln Ile Glu Val Asp Gly Gln Leu Ile Thr Leu Glu Ser
100 105 110

Gly Glu Phe Gln Val Tyr Lys Gln Ser His Ser Ala Leu Thr Ala Phe
115 120 125

Gln Thr Glu Gln Ile Gln Asp Ser Glu His Ser Gly Lys Met Val Ala
130 135 140

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

Asp Lys Leu Pro Glu Gly Gly Arg Ala Thr Tyr Arg Gly Thr Ala Phe
165 170 175

Gly Ser Asp Asp Ala Gly Gly Lys Leu Thr Tyr Thr Ile Asp Phe Ala
180 185 190

Ala Lys Gln Gly Asn Gly Lys Ile Glu His Leu Lys Ser Pro Glu Leu
195 200 205

Asn Val Asp Leu Ala Ala Ala Asp Ile Lys Pro Asp Gly Lys Arg His
210 215 220

Ala Val Ile Ser Gly Ser Val Leu Tyr Asn Gln Ala Glu Lys Gly Ser
225 230 235 240

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

Ala Glu Val Lys Thr Val Asn Gly Ile Arg His Ile Gly Leu Ala Ala
260 265 270

Lys Gln

<210> 99
<211> 370
<212> PRT
<213> Neisseria meningitidis

<400> 99

Met Gln Thr Ala Ala Arg Arg Ser Phe Asp Tyr Asp Met Pro Leu Ile
1 5 10 15

Gln Thr Pro Thr Ser Ala Cys Gln Ile Arg Gln Ala Trp Ala Lys Val
20 25 30

Ala Asp Thr Pro Asp Arg Glu Thr Ala Gly Arg Leu Lys Asp Glu Ile
35 40 45

Lys Ala Leu Leu Lys Glu Thr Asn Ala Val Leu Val Ala His Tyr Tyr
50 55 60

Val Asp Pro Leu Ile Gln Asp Leu Ala Leu Glu Thr Gly Gly Cys Val
65 70 75 80

Gly Asp Ser Leu Glu Met Ala Arg Phe Gly Ala Glu His Glu Ala Gly
85 90 95

Thr Leu Val Val Ala Gly Val Arg Phe Met Gly Glu Ser Ala Lys Ile
100 105 110

Leu Cys Pro Glu Lys Thr Val Leu Met Pro Asp Leu Glu Ala Glu Cys
115 120 125

Ser Leu Asp Leu Gly Cys Pro Glu Glu Ala Phe Ser Ala Phe Cys Asp
130 135 140

Gln His Pro Asp Arg Thr Val Val Val Tyr Ala Asn Thr Ser Ala Ala
145 150 155 160

Val Lys Ala Arg Ala Asp Trp Val Val Thr Ser Ser Val Ala Leu Glu
165 170 175

Ile Val Ser Tyr Leu Lys Ser Arg Gly Glu Lys Leu Ile Trp Gly Pro
180 185 190

Asp Arg His Leu Gly Asp Tyr Ile Arg Arg Glu Thr Gly Ala Asp Met
195 200 205

Leu Leu Trp Gln Gly Ser Cys Ile Val His Asn Glu Phe Lys Gly Gln
210 215 220

Glu Leu Ala Ala Leu Lys Ala Glu His Pro Asp Ala Val Val Leu Val
225 230 235 240

His Pro Glu Ser Pro Gln Ser Val Ile Glu Leu Gly Asp Val Val Gly
245 250 255

Ser Thr Ser Lys Leu Leu Lys Ala Ala Val Ser Arg Pro Glu Lys Lys
260 265 270

Phe Ile Val Ala Thr Asp Leu Gly Ile Leu His Glu Met Gln Lys Gln
275 280 285

Ala Pro Asp Lys Gln Phe Ile Ala Ala Pro Thr Ala Gly Asn Gly Gly
290 295 300

Ser Cys Lys Ser Cys Ala Phe Cys Pro Trp Met Ala Met Asn Ser Leu
305 310 315 320

Gly Gly Ile Lys Tyr Ala Leu Thr Ser Gly His Asn Glu Ile Leu Leu
325 330 335

Asp Arg Lys Leu Gly Glu Ala Ala Lys Leu Pro Leu Gln Arg Met Leu
340 345 350

Asp Phe Ala Ala Gly Leu Lys Arg Gly Asp Val Phe Asn Gly Met Gly
355 360 365

Pro Ala
370

<210> 100
<211> 492
<212> PRT
<213> Neisseria meningitidis

<400> 100

Met Phe Lys Arg Ser Val Ile Ala Met Ala Cys Ile Phe Ala Leu Ser
1 5 10 15

Ala Cys Gly Gly Gly Gly Gly Gly Ser Pro Asp Val Lys Ser Ala Asp
20 25 30

Thr Leu Ser Lys Pro Ala Ala Pro Val Val Ser Glu Lys Glu Thr Glu
35 40 45

Ala Lys Glu Asp Ala Pro Gln Ala Gly Ser Gln Gly Gln Gly Ala Pro
50 55 60

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

Gly Asn Gly Gly Ala Ala Ala Thr Asp Lys Pro Lys Asn Glu Asp Glu
85 90 95

Gly Ala Gln Asn Asp Met Pro Gln Asn Ala Ala Asp Thr Asp Ser Leu
100 105 110

Thr Pro Asn His Thr Pro Ala Ser Asn Met Pro Ala Gly Asn Met Glu
115 120 125

Asn Gln Ala Pro Asp Ala Gly Glu Ser Glu Gln Pro Ala Asn Gln Pro
130 135 140

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

Gly Gly Glu Asn Ala Gly Asn Thr Ala Ala Gln Gly Thr Asn Gln Ala
165 170 175

Glu Asn Asn Gln Thr Ala Gly Ser Gln Asn Pro Ala Ser Ser Thr Asn
180 185 190

Pro Ser Ala Thr Asn Ser Gly Gly Asp Phe Gly Arg Thr Asn Val Gly
195 200 205

Asn Ser Val Val Ile Asp Gly Pro Ser Gln Asn Ile Thr Leu Thr His
210 215 220

Cys Lys Gly Asp Ser Cys Ser Gly Asn Asn Phe Leu Asp Glu Glu Val
225 230 235 240

Gln Leu Lys Ser Glu Phe Glu Lys Leu Ser Asp Ala Asp Lys Ile Ser
245 250 255

Asn Tyr Lys Lys Asp Gly Lys Asn Asp Gly Lys Asn Asp Lys Phe Val
260 265 270

Gly Leu Val Ala Asp Ser Val Gln Met Lys Gly Ile Asn Gln Tyr Ile
275 280 285

Ile Phe Tyr Lys Pro Lys Pro Thr Ser Phe Ala Arg Phe Arg Arg Ser
290 295 300

Ala Arg Ser Arg Arg Ser Leu Pro Ala Glu Met Pro Leu Ile Pro Val
305 310 315 320

Asn Gln Ala Asp Thr Leu Ile Val Asp Gly Glu Ala Val Ser Leu Thr
325 330 335

Gly His Ser Gly Asn Ile Phe Ala Pro Glu Gly Asn Tyr Arg Tyr Leu
340 345 350

Thr Tyr Gly Ala Glu Lys Leu Pro Gly Gly Ser Tyr Ala Leu Arg Val
355 360 365

Gln Gly Glu Pro Ser Lys Gly Glu Met Leu Ala Gly Thr Ala Val Tyr
370 375 380

Asn Gly Glu Val Leu His Phe His Thr Glu Asn Gly Arg Pro Ser Pro
385 390 395 400

Ser Arg Gly Arg Phe Ala Ala Lys Val Asp Phe Gly Ser Lys Ser Val
405 410 415

Asp Gly Ile Ile Asp Ser Gly Asp Gly Leu His Met Gly Thr Gln Lys
420 425 430

Phe Lys Ala Ala Ile Asp Gly Asn Gly Phe Lys Gly Thr Trp Thr Glu
435 440 445

Asn Gly Gly Gly Asp Val Ser Gly Lys Phe Tyr Gly Pro Ala Gly Glu
450 455 460

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

Gly Phe Gly Val Phe Ala Gly Lys Lys Glu Gln Asp
485 490

<210> 101
<211> 615
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 101

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
85 90 95

Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
100 105 110

Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
115 120 125

Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
130 135 140

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

Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
165 170 175

Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
180 185 190

Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
195 200 205

Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
210 215 220

Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
225 230 235 240

Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val
245 250 255

Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu Val Leu
260 265 270

Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
275 280 285

Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
290 295 300

Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
305 310 315 320

Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
325 330 335

Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser
340 345 350

Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys
355 360 365

Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
370 375 380

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
385 390 395 400

Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
405 410 415

Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
420 425 430

Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
435 440 445

Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
450 455 460

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
465 470 475 480

Ile Arg Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val
485 490 495

Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser
500 505 510

Met Glu Glu Val Val Leu Ile Thr Val Pro Ser Ala Leu Val Ala Val

515 520 525

Lys Ile Ala His Ala Leu Val Glu Glu Arg Leu Ala Ala Cys Val Asn
530 535 540

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

Ser Asp His Glu Leu Leu Leu Leu Val Lys Thr Thr Thr Asp Ala Phe
565 570 575

Pro Lys Leu Lys Glu Arg Val Lys Glu Leu His Pro Tyr Glu Val Pro
580 585 590

Glu Ile Val Ala Leu Pro Ile Ala Glu Gly Asn Arg Glu Tyr Leu Asp
595 600 605

Trp Leu Arg Glu Asn Thr Gly
610 615

<210> 102
<211> 588
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 102

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
85 90 95

Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
100 105 110

Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
115 120 125

Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
130 135 140

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

Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
165 170 175

Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
180 185 190

Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
195 200 205

Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr

210 215 220

Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
225 230 235 240

Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val
245 250 255

Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu Val Leu
260 265 270

Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
275 280 285

Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
290 295 300

Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
305 310 315 320

Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
325 330 335

Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser
340 345 350

Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys
355 360 365

Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
370 375 380

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
385 390 395 400

Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
405 410 415

Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
420 425 430

Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
435 440 445

Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
450 455 460

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
465 470 475 480

Ile Arg Gly Gly Ser Met Glu Glu Val Val Leu Ile Thr Val Pro Ser
485 490 495

Ala Leu Val Ala Val Lys Ile Ala His Ala Leu Val Glu Glu Arg Leu
500 505 510

Ala Ala Cys Val Asn Ile Val Pro Gly Leu Thr Ser Ile Tyr Arg Glu
515 520 525

Glu Gly Ser Val Val Ser Asp His Glu Leu Leu Leu Leu Val Lys Thr
530 535 540

Thr Thr Asp Ala Phe Pro Lys Leu Lys Glu Arg Val Lys Glu Leu His
545 550 555 560

Pro Tyr Glu Val Pro Glu Ile Val Ala Leu Pro Ile Ala Glu Gly Asn
565 570 575

Arg Glu Tyr Leu Asp Trp Leu Arg Glu Asn Thr Gly
580 585

<210> 103
<211> 634
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 103

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
85 90 95

Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
100 105 110

Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
115 120 125

Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
130 135 140

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

Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
165 170 175

Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
180 185 190

Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
195 200 205

Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
210 215 220

Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
225 230 235 240

Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val
245 250 255

Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu Val Leu
260 265 270

Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
275 280 285

Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
290 295 300

Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
305 310 315 320

Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
325 330 335

Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser
340 345 350

Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys
355 360 365

Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
370 375 380

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
385 390 395 400

Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
405 410 415

Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
420 425 430

Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
435 440 445

Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
450 455 460

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
465 470 475 480

Ile Arg Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val
485 490 495

Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Gly Ser
500 505 510

Met Val Arg Gly Ile Arg Gly Ala Ile Thr Val Asn Ser Asp Thr Pro
515 520 525

Thr Ser Ile Ile Ile Ala Thr Ile Leu Leu Leu Glu Lys Met Leu Glu
530 535 540

Ala Asn Gly Ile Gln Ser Tyr Glu Glu Leu Ala Ala Val Ile Phe Thr
545 550 555 560

Val Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala Glu Ala Ala Arg Gln
565 570 575

Ile Gly Met His Arg Val Pro Leu Leu Ser Ala Arg Glu Val Pro Val
580 585 590

Pro Gly Ser Leu Pro Arg Val Ile Arg Val Leu Ala Leu Trp Asn Thr
595 600 605

Asp Thr Pro Gln Asp Arg Val Arg His Val Tyr Leu Ser Glu Ala Val
610 615 620

Arg Leu Arg Pro Asp Leu Glu Ser Ala Gln
625 630

<210> 104
<211> 607
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 104

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
85 90 95

Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
100 105 110

Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
115 120 125

Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
130 135 140

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

Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
165 170 175

Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
180 185 190

Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
195 200 205

Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
210 215 220

Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
225 230 235 240

Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val
245 250 255

Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu Val Leu
260 265 270

Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
275 280 285

Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
290 295 300

Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
305 310 315 320

Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
325 330 335

Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser

340 345 350

Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys
355 360 365

Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
370 375 380

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
385 390 395 400

Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
405 410 415

Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
420 425 430

Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
435 440 445

Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
450 455 460

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
465 470 475 480

Ile Arg Gly Gly Ser Met Val Arg Gly Ile Arg Gly Ala Ile Thr Val
485 490 495

Asn Ser Asp Thr Pro Thr Ser Ile Ile Ile Ala Thr Ile Leu Leu Leu
500 505 510

Glu Lys Met Leu Glu Ala Asn Gly Ile Gln Ser Tyr Glu Glu Leu Ala
515 520 525

Ala Val Ile Phe Thr Val Thr Glu Asp Leu Thr Ser Ala Phe Pro Ala
530 535 540

Glu Ala Ala Arg Gln Ile Gly Met His Arg Val Pro Leu Leu Ser Ala
545 550 555 560

Arg Glu Val Pro Val Pro Gly Ser Leu Pro Arg Val Ile Arg Val Leu
565 570 575

Ala Leu Trp Asn Thr Asp Thr Pro Gln Asp Arg Val Arg His Val Tyr
580 585 590

Leu Ser Glu Ala Val Arg Leu Arg Pro Asp Leu Glu Ser Ala Gln
595 600 605

<210> 105
<211> 744
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 105

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala

50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
85 90 95

Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
100 105 110

Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
115 120 125

Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
130 135 140

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

Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
165 170 175

Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
180 185 190

Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
195 200 205

Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
210 215 220

Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
225 230 235 240

Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val
245 250 255

Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu Val Leu
260 265 270

Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
275 280 285

Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
290 295 300

Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
305 310 315 320

Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
325 330 335

Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser
340 345 350

Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys
355 360 365

Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
370 375 380

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
385 390 395 400

Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
405 410 415

Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
420 425 430

Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
435 440 445

Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
450 455 460

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
465 470 475 480

Ile Arg Gly Tyr Ile Pro Glu Ala Pro Arg Asp Gly Gln Ala Tyr Val
485 490 495

Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr Phe Leu Gly Ser Gly
500 505 510

Ser His His His His His His His His Gly Gly Ser Gly Gly Ser Gly
515 520 525

Ser Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu
530 535 540

Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val
545 550 555 560

Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His
565 570 575

Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys
580 585 590

Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr
595 600 605

Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu
610 615 620

Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys
625 630 635 640

Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu
645 650 655

Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly
660 665 670

Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro
675 680 685

Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys
690 695 700

Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu
705 710 715 720

Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val
725 730 735

Glu Lys Ile Arg Gly Cys Thr Glu
740

<210> 106
<211> 705
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 106

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
85 90 95

Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
100 105 110

Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
115 120 125

Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
130 135 140

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

Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
165 170 175

Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
180 185 190

Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
195 200 205

Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
210 215 220

Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
225 230 235 240

Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val
245 250 255

Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu Val Leu
260 265 270

Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
275 280 285

Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
290 295 300

Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
305 310 315 320

Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
325 330 335

Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser

340 345 350

Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys
355 360 365

Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
370 375 380

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
385 390 395 400

Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
405 410 415

Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
420 425 430

Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
435 440 445

Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
450 455 460

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
465 470 475 480

Ile Arg Gly Gly Ser Gly Gly Ser Gly Ser Glu Lys Ala Ala Lys Ala
485 490 495

Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile
500 505 510

Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala
515 520 525

Val Ala Val Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr
530 535 540

Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu
545 550 555 560

Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys
565 570 575

Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu
580 585 590

Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met
595 600 605

Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly
610 615 620

His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe
625 630 635 640

Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr
645 650 655

Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val
660 665 670

Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu
675 680 685

Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr
690 695 700

Glu
705

<210> 107
<211> 645
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetically constructed Respiratory Synticial Virus antigen

<400> 107

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Glu Leu Pro Arg Phe Met Asn Tyr Thr Leu Asn Asn
85 90 95

Ala Lys Lys Thr Asn Val Thr Leu Ser Lys Lys Arg Lys Arg Arg Phe
100 105 110

Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile Ala Ser Gly Val Ala
115 120 125

Val Cys Lys Val Leu His Leu Glu Gly Glu Val Asn Lys Ile Lys Ser
130 135 140

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

Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys Asn Tyr Ile Asp Lys
165 170 175

Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys Ser Ile Ser Asn Ile
180 185 190

Glu Thr Val Ile Glu Phe Gln Gln Lys Asn Asn Arg Leu Leu Glu Ile
195 200 205

Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr Thr Pro Val Ser Thr
210 215 220

Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu Ile Asn Asp Met Pro
225 230 235 240

Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn Asn Val Gln Ile Val
245 250 255

Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile Lys Glu Glu Val Leu
260 265 270

Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val Ile Asp Thr Pro Cys
275 280 285

Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr Asn Thr Lys Glu Gly
290 295 300

Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly Trp Tyr Cys Asp Asn
305 310 315 320

Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu Thr Cys Lys Val Gln
325 330 335

Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser Leu Thr Leu Pro Ser
340 345 350

Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn Pro Lys Tyr Asp Cys
355 360 365

Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser Ser Val Ile Thr Ser
370 375 380

Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr Lys Cys Thr Ala Ser
385 390 395 400

Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser Asn Gly Cys Asp Tyr
405 410 415

Val Ser Asn Lys Gly Val Asp Thr Val Ser Val Gly Asn Thr Leu Tyr
420 425 430

Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr Val Lys Gly Glu Pro
435 440 445

Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro Ser Asp Glu Phe Asp
450 455 460

Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn Gln Ser Leu Ala Phe
465 470 475 480

Ile Arg Gly Gly Ser Gly Gly Ser Gly Ser Asp Asp Ala Arg Ile Ala
485 490 495

Ala Ile Gly Asp Val Asp Glu Leu Asn Ser Gln Ile Gly Val Leu Leu
500 505 510

Ala Glu Pro Leu Pro Asp Asp Val Arg Ala Ala Leu Ser Ala Ile Gln
515 520 525

His Asp Leu Phe Asp Leu Gly Gly Glu Leu Cys Ile Pro Gly His Ala
530 535 540

Ala Ile Thr Glu Asp His Leu Leu Arg Leu Ala Leu Trp Leu Val His
545 550 555 560

Tyr Asn Gly Gln Leu Pro Pro Leu Glu Glu Phe Ile Leu Pro Gly Gly
565 570 575

Ala Arg Gly Ala Ala Leu Ala His Val Cys Arg Thr Val Cys Arg Arg
580 585 590

Ala Glu Arg Ser Ile Lys Ala Leu Gly Ala Ser Glu Pro Leu Asn Ile
595 600 605

Ala Pro Ala Ala Tyr Val Asn Leu Leu Ser Asp Leu Leu Phe Val Leu
610 615 620

Ala Arg Val Leu Asn Arg Ala Ala Gly Gly Ala Asp Val Leu Trp Asp
625 630 635 640

Arg Thr Arg Ala His
645

<210> 108

<211> 678
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV F-10 DS-Cav1-8GS-HelExt-50A

<400> 108

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Phe Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile
85 90 95

Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val
100 105 110

Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
115 120 125

Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys
130 135 140

Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys
145 150 155 160

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

Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr
180 185 190

Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu
195 200 205

Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn
210 215 220

Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile
225 230 235 240

Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val
245 250 255

Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr
260 265 270

Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly
275 280 285

Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu
290 295 300

Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser
305 310 315 320

Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn

325 330 335

Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser
340 345 350

Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr
355 360 365

Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser
370 375 380

Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val
385 390 395 400

Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr
405 410 415

Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro
420 425 430

Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn
435 440 445

Gln Ser Leu Ala Phe Ile Arg Gly Ser Gly Gly Ser Gly Ser Gly Glu
450 455 460

Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu Leu Phe
465 470 475 480

Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val Glu Glu
485 490 495

Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His Leu Ile
500 505 510

Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys Ala Leu
515 520 525

Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr Val Thr
530 535 540

Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu Phe Ile
545 550 555 560

Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys Glu Lys
565 570 575

Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu Val Lys
580 585 590

Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly Glu Val
595 600 605

Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro Asn Val
610 615 620

Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys Glu Trp
625 630 635 640

Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu Val Lys
645 650 655

Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val Glu Lys
660 665 670

Ile Arg Gly Cys Thr Glu
675

<210> 109
<211> 682
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV F-11 DS-Cav1-12GS-HelExt-50A

<400> 109

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Phe Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile
85 90 95

Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val
100 105 110

Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
115 120 125

Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys
130 135 140

Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys
145 150 155 160

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

Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr
180 185 190

Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu
195 200 205

Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn
210 215 220

Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile
225 230 235 240

Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val
245 250 255

Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr
260 265 270

Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly
275 280 285

Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu
290 295 300

Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser
305 310 315 320

Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn
325 330 335

Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser
340 345 350

Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr
355 360 365

Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser
370 375 380

Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val
385 390 395 400

Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr
405 410 415

Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro
420 425 430

Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn
435 440 445

Gln Ser Leu Ala Phe Ile Arg Gly Ser Gly Gly Ser Gly Ser Gly Ser
450 455 460

Gly Gly Ser Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met
465 470 475 480

Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn
485 490 495

Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly
500 505 510

Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val
515 520 525

Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala
530 535 540

Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly
545 550 555 560

Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe
565 570 575

Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr
580 585 590

Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe
595 600 605

Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro
610 615 620

Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn
625 630 635 640

Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser
645 650 655

Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala
660 665 670

Phe Val Glu Lys Ile Arg Gly Cys Thr Glu

675 680

<210> 110
<211> 686
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV F-12 DS-Cav1-16GS-HelExt-50A

<400> 110

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Phe Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile
85 90 95

Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val
100 105 110

Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
115 120 125

Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys
130 135 140

Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys
145 150 155 160

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

Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr
180 185 190

Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu
195 200 205

Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn
210 215 220

Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile
225 230 235 240

Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val
245 250 255

Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr
260 265 270

Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly
275 280 285

Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu
290 295 300

Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser

305 310 315 320

Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn
325 330 335

Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser
340 345 350

Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr
355 360 365

Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser
370 375 380

Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val
385 390 395 400

Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr
405 410 415

Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro
420 425 430

Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn
435 440 445

Gln Ser Leu Ala Phe Ile Arg Gly Ser Gly Gly Ser Gly Ser Gly Ser
450 455 460

Gly Gly Ser Gly Ser Gly Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala
465 470 475 480

Ala Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val
485 490 495

Leu Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val
500 505 510

Phe Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp
515 520 525

Ala Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala
530 535 540

Ile Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala
545 550 555 560

Val Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu
565 570 575

Ile Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val
580 585 590

Met Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile
595 600 605

Leu Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala
610 615 620

Met Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val
625 630 635 640

Asn Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val
645 650 655

Gly Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu
660 665 670

Lys Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
675 680 685

<210> 111
<211> 680
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV F-13 DS-Cav1-foldon-10GS-HelExt-50A

<400> 111

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Phe Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile
85 90 95

Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val
100 105 110

Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
115 120 125

Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys
130 135 140

Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys
145 150 155 160

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

Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr
180 185 190

Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu
195 200 205

Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn
210 215 220

Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile
225 230 235 240

Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val
245 250 255

Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr
260 265 270

Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly
275 280 285

Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu
290 295 300

Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser
305 310 315 320

Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn
325 330 335

Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser
340 345 350

Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr
355 360 365

Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser
370 375 380

Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val
385 390 395 400

Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr
405 410 415

Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro
420 425 430

Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn
435 440 445

Gln Ser Leu Ala Phe Ile Arg Gly Ser Gly Gly Ser Gly Ser Gly Ser
450 455 460

Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu
465 470 475 480

Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val
485 490 495

Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His
500 505 510

Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys
515 520 525

Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr
530 535 540

Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu
545 550 555 560

Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys
565 570 575

Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu
580 585 590

Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly
595 600 605

Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro
610 615 620

Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys
625 630 635 640

Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu
645 650 655

Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val

660 665 670

Glu Lys Ile Arg Gly Cys Thr Glu
675 680

<210> 112
<211> 712
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV_F-14 DS-Cav1-foldon-15GS-HelExt-50A

<400> 112

Gln Asn Ile Thr Glu Glu Phe Tyr Gln Ser Thr Cys Ser Ala Val Ser
1 5 10 15

Lys Gly Tyr Leu Ser Ala Leu Arg Thr Gly Trp Tyr Thr Ser Val Ile
20 25 30

Thr Ile Glu Leu Ser Asn Ile Lys Glu Asn Lys Cys Asn Gly Thr Asp
35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Phe Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile
85 90 95

Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val
100 105 110

Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
115 120 125

Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys
130 135 140

Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys
145 150 155 160

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

Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr
180 185 190

Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu
195 200 205

Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn
210 215 220

Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile
225 230 235 240

Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val
245 250 255

Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr
260 265 270

Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly
275 280 285

Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu

290 295 300

Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser
305 310 315 320

Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn
325 330 335

Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser
340 345 350

Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr
355 360 365

Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser
370 375 380

Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val
385 390 395 400

Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr
405 410 415

Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro
420 425 430

Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn
435 440 445

Gln Ser Leu Ala Phe Ile Arg Gly Tyr Ile Pro Glu Ala Pro Arg Asp
450 455 460

Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr
465 470 475 480

Phe Leu Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser
485 490 495

Gly Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala Arg Lys Met Glu Glu
500 505 510

Leu Phe Lys Lys His Lys Ile Val Ala Val Leu Arg Ala Asn Ser Val
515 520 525

Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe Ala Gly Gly Val His
530 535 540

Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala Asp Thr Val Ile Lys
545 550 555 560

Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile Ile Gly Ala Gly Thr
565 570 575

Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val Glu Ser Gly Ala Glu
580 585 590

Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile Ser Gln Phe Cys Lys
595 600 605

Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met Thr Pro Thr Glu Leu
610 615 620

Val Lys Ala Met Lys Leu Gly His Thr Ile Leu Lys Leu Phe Pro Gly
625 630 635 640

Glu Val Val Gly Pro Gln Phe Val Lys Ala Met Lys Gly Pro Phe Pro
645 650 655

Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn Leu Asp Asn Val Cys
660 665 670

Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly Val Gly Ser Ala Leu
675 680 685

Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys Ala Lys Ala Phe Val
690 695 700

Glu Lys Ile Arg Gly Cys Thr Glu
705 710

<210> 113
<211> 717
<212> PRT
<213> Artificial Sequence

<220>
<223> RSV F-15 DS-Cav1-foldon-20GS-HelExt-50A

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35 40 45

Ala Lys Val Lys Leu Ile Lys Gln Glu Leu Asp Lys Tyr Lys Asn Ala
50 55 60

Val Thr Glu Leu Gln Leu Leu Met Gln Ser Thr Pro Ala Thr Asn Asn
65 70 75 80

Arg Ala Arg Arg Phe Leu Gly Phe Leu Leu Gly Val Gly Ser Ala Ile
85 90 95

Ala Ser Gly Val Ala Val Cys Lys Val Leu His Leu Glu Gly Glu Val
100 105 110

Asn Lys Ile Lys Ser Ala Leu Leu Ser Thr Asn Lys Ala Val Val Ser
115 120 125

Leu Ser Asn Gly Val Ser Val Leu Thr Phe Lys Val Leu Asp Leu Lys
130 135 140

Asn Tyr Ile Asp Lys Gln Leu Leu Pro Ile Leu Asn Lys Gln Ser Cys
145 150 155 160

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

Arg Leu Leu Glu Ile Thr Arg Glu Phe Ser Val Asn Ala Gly Val Thr
180 185 190

Thr Pro Val Ser Thr Tyr Met Leu Thr Asn Ser Glu Leu Leu Ser Leu
195 200 205

Ile Asn Asp Met Pro Ile Thr Asn Asp Gln Lys Lys Leu Met Ser Asn
210 215 220

Asn Val Gln Ile Val Arg Gln Gln Ser Tyr Ser Ile Met Cys Ile Ile
225 230 235 240

Lys Glu Glu Val Leu Ala Tyr Val Val Gln Leu Pro Leu Tyr Gly Val
245 250 255

Ile Asp Thr Pro Cys Trp Lys Leu His Thr Ser Pro Leu Cys Thr Thr
260 265 270

Asn Thr Lys Glu Gly Ser Asn Ile Cys Leu Thr Arg Thr Asp Arg Gly
275 280 285

Trp Tyr Cys Asp Asn Ala Gly Ser Val Ser Phe Phe Pro Gln Ala Glu
290 295 300

Thr Cys Lys Val Gln Ser Asn Arg Val Phe Cys Asp Thr Met Asn Ser
305 310 315 320

Leu Thr Leu Pro Ser Glu Val Asn Leu Cys Asn Val Asp Ile Phe Asn
325 330 335

Pro Lys Tyr Asp Cys Lys Ile Met Thr Ser Lys Thr Asp Val Ser Ser
340 345 350

Ser Val Ile Thr Ser Leu Gly Ala Ile Val Ser Cys Tyr Gly Lys Thr
355 360 365

Lys Cys Thr Ala Ser Asn Lys Asn Arg Gly Ile Ile Lys Thr Phe Ser
370 375 380

Asn Gly Cys Asp Tyr Val Ser Asn Lys Gly Val Asp Thr Val Ser Val
385 390 395 400

Gly Asn Thr Leu Tyr Tyr Val Asn Lys Gln Glu Gly Lys Ser Leu Tyr
405 410 415

Val Lys Gly Glu Pro Ile Ile Asn Phe Tyr Asp Pro Leu Val Phe Pro
420 425 430

Ser Asp Glu Phe Asp Ala Ser Ile Ser Gln Val Asn Glu Lys Ile Asn
435 440 445

Gln Ser Leu Ala Phe Ile Arg Gly Tyr Ile Pro Glu Ala Pro Arg Asp
450 455 460

Gly Gln Ala Tyr Val Arg Lys Asp Gly Glu Trp Val Leu Leu Ser Thr
465 470 475 480

Phe Leu Gly Ser Gly Gly Ser Gly Ser Gly Ser Gly Gly Ser Gly Ser
485 490 495

Gly Gly Ser Ser Gly Ser Glu Lys Ala Ala Lys Ala Glu Glu Ala Ala
500 505 510

Arg Lys Met Glu Glu Leu Phe Lys Lys His Lys Ile Val Ala Val Leu
515 520 525

Arg Ala Asn Ser Val Glu Glu Ala Ile Glu Lys Ala Val Ala Val Phe
530 535 540

Ala Gly Gly Val His Leu Ile Glu Ile Thr Phe Thr Val Pro Asp Ala
545 550 555 560

Asp Thr Val Ile Lys Ala Leu Ser Val Leu Lys Glu Lys Gly Ala Ile
565 570 575

Ile Gly Ala Gly Thr Val Thr Ser Val Glu Gln Cys Arg Lys Ala Val
580 585 590

Glu Ser Gly Ala Glu Phe Ile Val Ser Pro His Leu Asp Glu Glu Ile
595 600 605

Ser Gln Phe Cys Lys Glu Lys Gly Val Phe Tyr Met Pro Gly Val Met

610 615 620

Thr Pro Thr Glu Leu Val Lys Ala Met Lys Leu Gly His Thr Ile Leu
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Lys Leu Phe Pro Gly Glu Val Val Gly Pro Gln Phe Val Lys Ala Met
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Lys Gly Pro Phe Pro Asn Val Lys Phe Val Pro Thr Gly Gly Val Asn
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Leu Asp Asn Val Cys Glu Trp Phe Lys Ala Gly Val Leu Ala Val Gly
675 680 685

Val Gly Ser Ala Leu Val Lys Gly Thr Pro Asp Glu Val Arg Glu Lys
690 695 700

Ala Lys Ala Phe Val Glu Lys Ile Arg Gly Cys Thr Glu
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